

UNIVERSITY OF NAIROBI

DNA barcoding, mineral and phytochemical analysis of Cape gooseberry (*Physalis* spp.) accessions in Kenya

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A thesis submitted in fulfillment of the requirements for the award of Doctor of Philosophy Degree (Biochemistry) of the University of Nairobi

DECLARATION

I, the undersigned declare that this is my original work and that it has not been presented to any institution of learning for academic credit. All the sources used herein are duly acknowledged.

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DEDICATION

I dedicate this work firstly to God, for the faithfulness and grace he has provided me with throughout my studies until this level. Secondly, I dedicate this work to my parents, husband and siblings that have been supportive in so many ways and have always encouraged me to focus on the final goal despite all the challenges. I thank everyone, friends and family for their never-ending prayers and encouragement.

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LIST OF ABBREVIATIONS AND ACRONYMS

12S:	12 Svedberg
16S:	16 Svedberg
AAS:	Atomic absorption spectrophotometer
ABGD:	Automatic barcode gap discovery
AFLP:	Amplified fragment length polymorphism
ANOVA:	Analysis of Variance
AtpF:	Adenosine triphosphate (ATP) synthase F
AtpH:	Adenosine triphosphate (ATP) synthase H
BMC:	BioMed Central
BLAST:	Basic local alignment search tool
BLASTn:	Basic local alignment search tool nucleotide
CAPS:	Cleaved amplified polymorphic sequences
CBOL:	Consortium for the Barcode of Life
CO1:	Cytochrome oxidase 1
CoEHM:	Center of Excellence in HIV Medicine
COS:	Conserved ortholog set
cpDNA:	Chloroplast DNA
CTAB:	Cetyltrimethylammonium bromide
CV:	Coefficient of Variance
Cytb:	Cytochrome b
DAF-DNA:	Amplified fingerprinting deoxyribonucleic acid
DnaSP:	Deoxyribonucleic acid sequence polymorphism
DPPH:	2, 2-diphenyl-2-picrylhydrazyl
DW:	Dry weight
Dxy:	Average nucleotide substitution per site between populations
GAE:	Gallic acid equivalent
GTR:	Generalized Time Reversal
HDS:	Honestly significant difference
HIV:	Human immunodeficiency virus
HRS:	Hydrogen peroxide radical scavenging

InDels:	Insertions and deletions
IRG:	Immunity regulated genes
ISSR:	Inter-simple sequence repeats
ITS:	Internal transcribed spacer
ITS1:	Internal transcribed spacer 1
ITS2:	Internal transcribed spacer 2
K2P:	Kimura 2 parameter
K80:	Kimura 80
mat-K:	Maturase K
MCMC:	Markov chain Monte Carlo
MEGA:	Molecular evolutionary genetic analysis
MUSCLE:	MUltiple Sequence Comparison by Log-Expectation
MSA:	Multiple sequence alignment
NA:	Nutrient agar
NCBI:	National Center for Biotechnology Information
OD:	Optical density
PCR:	Polymerase chain reaction
Pi:	Nucleotide diversity
RAPD:	Random amplified polymorphic DNA
rbcL:	Ribulose-1,5-bisphosphate carboxylase large
RFLP:	Restriction fragment length polymorphism
RAM:	Random amplified microsatellites
RNase:	Ribonuclease
rRNA:	Ribosomal Ribonucleic acid
SCARs:	Sequence characterized amplified regions
SD:	Standard deviation
SNPs:	Single nucleotide polymorphisms
SSR:	Simple sequence repeats
TFC:	Total flavonoid content
TPC:	Total phenolic acid content
TTC:	Total tannic acid content

- USA: United States of America
- UV: Ultra-violet
- ycf 1: Yeast cadmium factor protein 1

ABSTRACT

Physalis genus belongs to the *Solanaceae* family and is mostly a wild self-propagating orphan fruit plant. Physalis fruit contains nutritional and phytochemical compounds of importance to public health and is a potential ingredient for fortification of foods and beverages. In Kenya, commercial cultivation of *Physalis* has significantly increased for the last decade and the farmers are concerned about the reliability and identity of the planting material. Challenges facing the production of planting material include difficulty in precise identification of the *Physalis* species due to lack of discriminatory morphological features. DNA barcoding is an effective tool in identification and discrimination of plant species. Therefore, the objectives of this study were to identify and discriminate the different *Physalis* species in the wild and cultivated in Kenya using DNA barcoding as well as determine the nutritional and biochemical profile of selected Physalis accessions. To identify the Physalis species from selected Counties in Kenya, ribulose-1,5bisphosphate carboxylase large (rbcL) gene and internal transcribed spacer 2 (ITS2) DNA barcodes were used. Genomic DNA was extracted from leaves and polymerase chain reaction (PCR) amplification was carried out using ITS2 and rbcL barcodes followed by Sanger sequencing of the amplicons. Sequences were curated and aligned along their reference sequences based on MUltiple Sequence Comparison by Log-Expectation (MUSCLE). The generated multiple sequence alignments were used to prepare phylogenetic trees for Physalis species discrimination based on *rbcL* and ITS2 genes by Bayesian inference based on MrBayes software. Genetic diversity, distance and polymorphism were also assessed for the Physalis species through the use of DNA sequence polymorphism (DnaSP) software. Additionally, assessment of Physalis species mineral content for nine representative accessions was performed on an atomic absorption spectrophotometer and phytochemical content determined by UV-Visible spectrophotometry. Further, the radical scavenging activity of *Physalis* accessions was determined for 2,2-diphenyl-2-picrylhydrazyl (DPPH) and hydrogen peroxide radicals. Success rate of PCR amplification and sequencing of rbcL and ITS2 genes ranged from 82% to 88% and 65% to 67%, respectively. The phylogenetic tree generated for the *rbcL* sequences was unable to distinguish between *Physalis* species. However, the phylogenetic tree generated for the ITS2 sequences successfully identified three species of Physalis: Physalis peruviana, Physalis purpurea and Physalis cordata. There was low nucleotide diversity and genetic distance of 0.01333 and 0.04, respectively, for the *rbcL* genes while high genetic diversity and distance was noted for the ITS2 sequences. The highest genetic diversity and distance between Physalis species was noted between *P. peruviana* and *P. cordata* at 0.36923 and 0.703, respectively based on ITS2 sequences. The highest genetic nucleotide diversity and distance within species was noted for the P. peruviana at 0.26324 and 0.46, respectively, for the ITS2 gene sequences. Tajima D values obtained indicated low frequency mutations among the Physalis sequences based on rbcL and ITS2 barcodes. The mineral content of the Physalis accessions was significantly different (p < 0.05) for calcium, copper, zinc, nickel and lithium between accessions. For the phytochemicals of Physalis fruit accessions, tannic acid content was significantly different (p < 0.05), while the phenolic acid and flavonoid contents were not significantly different (p > 0.05). *Physalis* accessions DPPH radical scavenging activity was significantly different (p < 0.05) while no significant difference (p > 0.05) was noted for hydrogen peroxide scavenging capacity. Therefore, this study identified Kenyan Physalis accessions based on ITS2 barcode region as P. purpurea, P. peruviana and P. cordata. The findings also demonstrated that Physalis accessions in Kenya are rich in mineral and phytochemical contents as well as high antioxidant properties.

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background to the study

Physalis genus is a wild plant that belongs to the nightshade (*Solanaceae*) family (Zhang and Tong, 2016). It is native to South American Andes either Peru or Chile, hence referred to as the Peruvian gooseberry. *Physalis* is now cultivated in various regions of the world and the fruits are exported from several countries including Colombia, Australia, New Zealand, Great Britain, Zimbabwe, Kenya, Egypt, South Africa, Madagascar and South East Asia (Zhang *et al.*, 2013; Ramadan and Moersel, 2003). Colombia is the leading producer, consumer and exporter of *Physalis* fruits (Zhang *et al.*, 2013). In Kenya, the fruits are vastly seen as wild and self-propagating plants, commonly in farms during and after harvesting of maize. *Physalis* has golden yellow edible fruits and inside it has a juicy pulp with many small yellowish seeds. The fruits are protected by papery husks against insects, birds, and adverse conditions. There is growing commercial interest in this orphan fruit crop in Kenya because of its nutritional and pharmacological properties and health benefits.

Nutritional and phytochemical profile of *Physalis* has been studied to a moderate level in the Andes (Ramadhan and Morsel, 2007). The Physalis fruit contains fat and water-soluble vitamins (Bcomplex, C, A, E and K), minerals (mainly phosphorus, magnesium, potassium, zinc and calcium), sugars (e.g., sucrose, glucose and fructose), fatty acids (palmitate, oleic and gamma linoleic acid), phytosterols (sitosterol and stigmasterol) as well as fiber (pectin) (Puente et al., 2011; Ramadhan and Morsel, 2003). The fruit pomace (skin and seed) contains 19.3% oil, 3.1% ash, 17.8% protein, 24.5% carbohydrates and 28.7% crude fiber (Ramadhan and Morsel, 2007). Phytochemicals found in Physalis include withanolides, physalins, carotenoids, phenolics and flavonoids (Puente et al., 2011). The most studied phytochemicals are the poly phenolic compounds and they have been shown to have anti-oxidant properties and medicinal properties (Somani *et al.*, 2015). The key polyphenolics include flavonoids, stilebenes, phenolic acids, coumarins and tannins (Bayir et al., 2019). The high content of vitamins, minerals and antioxidant phytochemicals in Physalis explains its medicinal properties such as anti-cancer, antibacterial and anti-inflammatory activity (Hong et al., 2015). P. alkengi has been used in China to treat sore throats, tumors, urinary problems, hepatitis, eczema, leishmaniasis and cough (Chinese Pharmacopoeia Editorial Committee, 2015). However, there is lack of information on cultivar-specific mineral and phytochemical profiling of *Physalis* species growing in Kenya. The characterization of *Physalis* phytochemical content has been done in Uganda and they were able to identify several types of phytochemicals present in the plant such as phenolic

compounds and flavonoids (Kasali *et al.*, 2021). Characterization of *Physalis* species and major cultivars in terms of their nutritional and chemical composition, functional and physicochemical properties could provide important knowledge for future utilization. The information could accelerate the processing of value-added products from gooseberry fruits.

Due to their ethnobotanical, medical and economic applications and a wide array of species there is a need to authenticate and identify various Physalis species for future species-specific use. Physalis species identification ensures their appropriate utilization, germplasm conservation and formation of future breeding programs (Feng et al., 2018). Identification of Physalis species using traditional identification systems such as morphological appearance has resulted in misidentification due to high similarities in phenotypic characteristics (Feng et al., 2016). Physalis minima and Physalis pubescens are morphologically similar and present a clear challenge in their distinction using their phenotypic characteristics only (Feng et al., 2016). Morphological identification is also affected by environmental and physiological factors which can affect phenotypic characteristics (Vargas-Ponce et al., 2011; Menzel, 1951). Misidentification of Physalis can cause the loss of genetic information due to lack of genetic conservation (Feng et al., 2018). Since morphological identification of Physalis species has proven to be inefficient there is a need to use other robust means of genus and species identification (Yu et al., 2021). In the Solanaceae family, identification of the Physalis genus is also important because plants in this genus are sometimes confused with other plants such Nicandra physalodes (Feng et al., 2016). Molecular identification of plant species has proven to be more efficient than the use of morphology. This has been done successfully using species specific SCAR markers and DNA barcoding (Feng et al., 2018; Feng et al., 2016; Simbaqueba et al., 2011).

DNA barcoding entails a rapid and reliable method of genus and species identification using short universal standardized DNA sequences (Saddhe and Kumar, 2018). DNA barcording has widely been utilized and accepted in the identification of plants and animals (Kress, 2005). Therefore, DNA barcoding has proved to be an effective tool in taxon identification and also in the identification of medicinal plants (Yu *et al.*, 2021; Dormontt *et al.*, 2018). There are several known DNA barcodes utilized in the identification of plants such as chloroplast genes and the nuclear ribosomal DNA (rDNA) genes. The chloroplast DNA barcode genes including ribulose bisphosphate carboxylase large (*rbcL*) and maturase (*matK*) have been reported to be ideal for plant barcoding studies (Kang *et al.*, 2017). Intergenic sequence *psbA-trnH* gene and the nuclear rRNA barcodes including 5.8S, 26S, 18S rRNA and internal transcriber spacer (ITS) 1 and 2 are used as supplements in plant barcoding (Kang *et al.*, 2017). Proper selection of plant DNA barcodes is crucial for the successful

identification of plant genus and species. Among the chloroplast DNA barcodes, the *rbcL* region, which was the first plant gene to be sequenced, has proved to be highly effective and successful in species identification for some plant genera (Ismail *et al.*, 2020). It has a higher amplification rate during polymerase chain reaction (PCR), better universality, and produces high quality sequences with high success rate during sequencing (Newmaster *et al.*, 2006). It is considered the best characterized DNA barcode gene (Duan *et al.*, 2019). The nuclear DNA barcodes ITS2 genes are considered the best candidate to use in DNA barcoding due to their high species discrimination, ability to identify diversity at the interspecies and intra-species level, high rate of success in amplification and sequencing in plants (Kang *et al.*, 2017). It is however important to note that the debate on the best DNA barcode in plant species and taxon identification is still ongoing as certain barcodes work better in the identification of specific plants (Ralte and Singh, 2021; Tran *et al.*, 2021).

DNA barcoding has not been previously used in the identification of *Physalis* species in Kenya. Molecular markers such as simple sequence repeat (SSR) have been used in the genetic characterization of *Physalis* in Kenya (Muraguri *et al.*, 2021; Simbaqueba *et al.*, 2011), with the assumptions that the identity of the species was *P. peruviana*. Therefore, there is need to identify and discriminate the *Physalis* species in Kenya for species-specific uses, genetic conservation of vulnerable species and for use in breeding programs. The efficiency of *rbcL* and ITS2 DNA barcode genes in the identification of *Physalis* species in Kenya was evaluated in the current study.

1.2 Problem statement

Physalis is a wild fruit producing plant that grows without human intervention in Kenyan fields after harvesting of maize or even in forests and on the sides of the roads. It has wide application in ethnomedicine where it is used in the deterrence and treatment of many diseases due to a rich phytochemical profile (Hong *et al.*, 2015). *Physalis* plants also have a rich nutritional profile and can be a source of both macro- and micro-nutrients (Musinguzi *et al.*, 2007). Most *Physalis* species are morphologically similar and difficult to distinguish. *P. minima* and *P. pubescens* are highly similar in appearance, though they have different applications in ethnomedicine. Improper identification of these species can lead to improper utilization of the plants (Feng *et al.*, 2016). There is a lack of a database of *Physalis* species and accessions growing in Kenya as well as studies on their genetic diversity. The lack of genetic diversity studies of the plant in Kenya is also a risk to genetic loss of this important fruit. This can lead to the extinction of important species and accessions due to climate change and urbanization as the plant mostly grows without human intervention in bushes and forests.

There is a need to identify and genetically characterize *Physalis* species to initiate proper utilization and conservation as well as its genetic improvement through breeding programs.

1.3 Justification

Physalis fruits have high nutritional value, and pharmacological properties due to their rich phytochemical profile and many health benefits. This plant is rich in vitamins, minerals and soluble sugars (Puente et al., 2011; Ramadhan and Morsel, 2007). The medicinal usages indicate that it might be rich in a plethora of phytochemicals (Puente et al., 2011). However, it is underutilized in Kenya due to a lack of information on the nutritional and biochemical profiles of the accessions growing in the Country. Assessment of the nutritional and phytochemical content of Physalis accessions growing in Kenya could support the utilization of the plants as sustainable resource for the development of biofortified foods and also promote their use as natural source of antioxidants. Molecular identification and characterization of *Physalis* species has majorly been done in Colombia and China (Chacón et al., 2016; Feng et al., 2016). Precise identification of Physalis species is crucial to ensure safe utilization especially for medicinal applications, like in any other medicinal plants; it is paramount to prevent improper use (Feng et al., 2016; Menzel et al., 1951). Molecular identification could also ensure the maintenance and conservation of *Physalis* genetic resources to prevent the loss/extinction of important species and accessions and also help in the development of breeding programs to create hybrids. For breeding purposes, information on accurate identification of the different species is fundamental. DNA barcoding is the most effective and emerging method of molecular identification of different species in plants.

1.4 Objectives

1.4.1 Main objective

The main objective of the study was to determine the mineral and phytochemical profiles of *Physalis* accessions and the genetic relationships of *Physalis* species using DNA barcoding.

1.4.2 Specific objectives

- 1. To determine the mineral composition, phytochemical content, antioxidant activity and identity of indigenous *Physalis* accessions from Sorget forest, Kericho County, Kenya.
- 2. To determine the identity and genetic diversity of *Physalis* accessions in Kenya using their DNA sequences and RNA secondary structural information of their ITS2 barcode.
- 3. To determine the identity and genetic diversity of *Physalis* accessions in Kenya using cpDNA gene sequences.

4. To investigate the species resolution ability of nuclear (ITS2) and chloroplast DNA (*rbcL*) loci in 64 accessions of *Physalis* collected in Kenya.

1.5 Null Hypotheses

- 1. *Physalis* accessions growing in Kenya are not rich in nutrients, minerals, phytochemicals and lack anti-oxidant activity.
- 2. *Physalis* species growing in Kenya cannot be discriminated based on sequences and RNA secondary structures of their ITS2 barcode.
- 3. *Physalis* species growing in Kenya cannot be discriminated based on cpDNA gene sequences.
- 4. *Physalis* species and their accessions are not genetically diverse and have low level of nucleotide polymorphism based on nuclear and cpDNA sequences.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 The Genus Physalis

Physalis is a genus that belongs to the Solanaceae (nightshade) plant family. *Physalis* was first described by Linnaeus in 1753. There are more than 90 known species of *Physalis* that grow in the temperate and tropical regions of the world (Zimmer *et al.*, 2019). Most species of *Physalis* are found in the Andes and America with few originating in Europe and Asia (Seleem and Nassar, 2021; Whitson and Manos, 2005). In China five *Physalis* species and two varieties have been identified (Chinese Academy of Sciences, 1978). In Mexico and China, *P. peruviana*, *P. pubescens*, *Physalis alkekengi* and *Physalis philadelphica* are extensively cultivated for their edible fruits which are rich in nutrients and phytochemicals that confer them with medicinal properties (Zamoras-Tavares *et al.*, 2015; Wei *et al.*, 2012).

Physalis species are considered annual or perennial flowering herbs that can also be woody at their base and are creeping plants (Zimmer *et al.*, 2019). The leaves of *Physalis* species have soft texture, are alternate, petioled and angled. Their flowers are mostly yellowish, whitish or blue with extra axillary pedicles. They have a bladder like calyx that is five-toothed and encloses yellowish-green berries that are pulpy in the inside with small, flat and rounded seeds (Figure 2.1.) (Bailey, 1949).



Figure 2.1. Plant morphology of *Physalis* accessions.A: represents a photograph of mature *Physalis* fruits; and B: represents a *Physalis* plant

2.2 Distribution and economic importance of Physalis

The plant being native to the Andes has been naturalized in other parts of the world such as Asian and African countries. The *Physalis* plants are mainly grown, consumed and exported for income in Colombia. The economic value of *Physalis* in Colombia is linked to the high demand for fruits in the European market (Álvarez-Flórez *et al.*, 2017; Ordoñez *et al.*, 2017). Other exporters of *Physalis* plants include Madagascar, New Zealand, Uganda, Australia, Zimbabwe and Kenya (Zhang *et al.*, 2013; Ramadan and Moersel, 2003). *Physalis* plants are considered important for income generation, as food and for medicinal purposes.

2.3 Nutritional profile of *Physalis* fruits

The nutritional profile of *Physalis* fruits has shown that they contain unique bioactive compounds. These compounds include withanolides, physalins, vitamins such as A, C, E, K and B complex, carbohydrate sugars and particularly rich in sucrose, glucose and fructose (Zhang et al., 2013; Ramadhan, 2011; Puente et al., 2011; Zhao, 2007). Sucrose levels are usually higher than glucose. Fructose is less than sucrose and glucose but is important for diabetic patients as a source of energy (Puente *et al.*, 2011). It is also rich in fiber such as pectin which is an intestinal regulator and is also used in the preparation of jams and jellies (Gironés-Vilaplana et al., 2014). Other studies have indicated that *Physalis* is a good source of polyunsaturated fatty acids which are essential fats. It has been noted to have 0.2% fatty acids of different types such as palmitic acid, palmitoleic acid, oleic acid, linoleic acid and gamma-linolenic acid (Rodrigues et al., 2009; Ramadhan and Morsel, 2003). Foods that have high linoleic acid content prevent the development of hypertension and cardiovascular diseases (Ramadhan and Morse, 2003). The fruit also contains phytosterols such as ergosterol (9.23 g/kg) and stigmasterol (6.23 g/kg) (Ramadhan and Morsel, 2003). Another study showed that the most abundant phytosterol is campesterol but the fruits also contain stigmasterols and sitosterols. The phytosterol content is thought to play an important role in the ability of the fruit to lower cholesterol levels (Puente et al., 2011). The leaves of Physalis angulata have a high concentration of fatty acids (Ogundajo et al., 2015). The ascorbic acid content of the fruit is higher compared to those of other common fruits (Rosa et al., 2023). However, the ascorbic acid level of Physalis is comparable to that of orange (50 mg/100ml) and strawberry (60 mg/100ml) fruits (Ramadan and Mörsel, 2003; Belitz and Grosch, 1999). P. peruviana in particular has a high amount of vitamins C, A and B complex (Puente et al., 2011).

Physalis plants have been studied for the presence of essential trace elements (minerals). *Physalis* contains phosphorus, zinc, iron, potassium, magnesium and calcium (Rodrigues *et al.*, 2009;

Musinguzi *et al.*, 2007). The iron content of *P. peruviana* was noted to be higher than in regular sources such as beans (Rodrigues *et al.*, 2009). These minerals are thought to be important for fruit health and also confer the fruit with some of its functional properties. Zinc for example is thought to be a non-enzymatic antioxidant and is thought to attribute to the anti-oxidant activity of the fruit even at low concentrations (Puente *et al.*, 2011).

2.4 Phytochemical profile of Physalis fruits

Phytochemical activity of *Physalis* has majorly been attributed to the presence of withanolides, physalins, phenolics, flavonoids and carotenoids (Puente et al., 2011; Wu et al., 2006). Withanolides are steroidal lactones that have biological properties such as insect repellant and anti-feedant, antitumor, anti-inflammatory, antibacterial, immune-modulatory and cytotoxic activity (Ahmad et al., 1999). Lan et al. (2009) demonstrated the presence of seventeen withanolides found in Physalis including withanolide E and 4-beta-hydroxy-withanolides that have anticancer activity (Lan et al., 2009). Carotenoids found in *Physalis* majorly include all-trans-beta-carotene as well as others such as 9-cis-beta-carotene and all-trans-alpha-cryptoxanthin (Puente et al., 2011). Physalins which are simply immunosuppressive substances are also found in *Physalis*. Those isolated include; physalins A, B, D and glycosides which have been credited with anti-cancer activity (Wu et al., 2004). Due to the high antioxidant properties, the fruit has been used in folk medicine to treat ailments such as malaria, asthma, dermatitis, hepatitis and rheumatism (Wu et al., 2004). Phytochemicals such as polyphenols and terpenes have been identified in P. minima, P. angulata and P. peruviana (Kasali et al., 2021; Ogundajo et al., 2015; Usaizan et al., 2014). Among the Malayali tribe in Kolli Hills of India the whole *P. peruviana* plant extract is used in the treatment of skin diseases (Anjalam *et al.*, 2016). Other Indian tribes such as Manjoor, Thiashola and Western Ghats use the seeds and leaves of P. peruviana to treat glaucoma and jaundice (Sharmila et al., 2014). Studies have shown that the fruit of *Physalis* also has antihelminthic properties as well as playing an important role in the strengthening of the optic nerve due to its high vitamin A content (Arun and Asha, 2007).

2.4 Genetic characterization of plants

Molecular characterization studies in plants help to identify and discriminate the species of plants, assess the genetic relatedness of species and describe their germplasm. Genetically diverse plants have better chances of survival in changing environmental conditions (Chacón *et al.*, 2016). Any information achieved from genetic diversity studies of natural and cultivated crops helps to identify variation in plants. This is essential for crop breeding programs and improves the value of crops

(Grandillo, 2014). This information also prevents loss of diversity as a result of the extinction of plant species due to the effects of climate change.

2.4.1 Use of molecular markers in genetic characterization of plants

The development and utilization of molecular markers to determine plant genetic diversity is important for molecular genetic studies (Idrees and Irshad, 2014). Markers majorly show polymorphism which can arise due to mutations in the genome loci (Amiteye, 2021). Plant molecular markers are used in the identification of cultivars, genetic diversity assessment and marker assisted crop breeding (Collard et al., 2005). The properties of good molecular markers include easy to use and rapid results, easily available, co-dominant inheritance, reproducible, highly polymorphic, recurrent occurrence in the genome and they should be selectively neutral to environmental changes (Idrees and Irshad, 2014). Genetic characterization and diversity can be assessed using dominant molecular markers, co-dominant molecular markers and DNA barcoding techniques. Some of the dominant molecular marker techniques include DNA amplified fingerprinting (DAF), inter-simple sequence repeats (ISSR), random amplified polymorphic DNA (RAPD) as well as amplified fragment length polymorphism (AFLP). Co-dominant molecular marker techniques include simple sequence repeats (SSR), sequence characterized amplified regions (SCARs), cleaved amplified polymorphic sequence (CAPS) as well as restriction fragment length polymorphism (RFLP) (Govindaraj et al., 2015). Co-dominant markers are preferred in genetic diversity studies over dominant markers because they show heterozygosity (Idrees and Irshad, 2014).

2.4.2 DNA barcoding in genetic characterization of plants

DNA barcoding is a novel technique that uses short regions on a DNA molecule to classify species (Hebert *et al.*, 2004). It is an important technique for understanding how to conserve the biodiversity of plants (de Vere *et al.*, 2015). DNA barcoding of plants is not only important in species discrimination but can also be used to assess intraspecific and interspecific variation during genetic diversity studies (Li *et al.*, 2015). DNA barcoding for assessment of genetic diversity requires the presence of individual plant barcodes studies to have successful genetic variation analysis (Li *et al.*, 2015).

Terrestrial plants have their DNA barcode markers in the coding regions of chloroplast and mitochondria, especially the part of the genes *rbcL* and *matK* DNA sequences (Li *et al.*, 2015). The ideal barcode locus for identification and discrimination of plants is still debatable as the

performance of each barcode differs among different genera of plants. The two chloroplast barcodes *rbcL* and *matK* are considered ideal loci for the identification of plants and were proposed as the preferred plant barcode loci by the Consortium for the Barcode of Life (CBOL) (CBOL Plant Working Group A, 2009). Although *rbcL* and *matK* are considered standard barcodes for plants they do not perform well in species discrimination due to their high rate of conservation within and between species (Li *et al.*, 2014). Their low sequence variation provides poorly resolved phylogenetic trees, which means they cannot discriminate species but can authenticate the plant genus of the plants (Li *et al.*, 2014). Other plant barcodes include chloroplast barcodes *psbA-trnH*, *atpF*, *atpH* and *ycf 1* (Chase *et al.*, 2005, Kress, 2005).

The mitochondrial DNA barcode cytochrome oxidase 1 (CO 1) can be used in the identification of both plant and animal species (Kress, 2005). The DNA barcode CO 1 is largely preserved across species that use oxidative phosphorylation for energy production (Hebert *et al.*, 2003). This barcode is rarely used in plant species discrimination due to low genetic variation associated with a low rate of mutation (Kress, 2005). It is however considered a standard barcode in the discrimination of animals (Yao *et al.*, 2010). In animals, mitochondrial genes are preferred in species discrimination due to their lack of introns (Yao *et al.*, 2010). Other mitochondrial barcodes for animals include *cytb*, 12S ribosomal ribonucleic acid (rRNA) and 16S rRNA (Yang *et al.*, 2018).

Nuclear barcodes for plants are ITS1 and ITS2 obtained from the ITS region (Yao *et al.*, 2010). ITS2 is considered a secondary barcode for the identification of plants and is preferred over the whole ITS region as it has a short length and high efficiency in PCR amplification (Han *et al.*, 2013; Chen *et al.*, 2010). It has been proposed that the ITS2 region be used as the standard barcode for phylogenetic analysis and species discrimination of plants (Zhao *et al.*, 2015; Chen *et al.*, 2010; Shultz and Wolf, 2009). This is due to its high interspecific and low intraspecific variation, available conserved regions for universal barcode design and ease of amplification (Yao *et al.*, 2010).

Differences in the efficiency of DNA barcodes can be demonstrated whereby in the study of the genus *Aquilaria* there was more genetic variation observed for the *matK* loci than *rbcL*, and this made species identification using *matK* more robust (Thitikornpong *et al.*, 2018). The barcode *matK* has also shown better species discrimination of the genus *Dioscorea* as compared to *rbcL* and *psbA*-*trnH* (Sun *et al.*, 2012). The *matK* barcode is considered strong but not perfect for the identification of plant species (Sun *et al.*, 2012). In another study for the species discrimination of the two genes (Ho

et al., 2021). A study on the discrimination of *Calligonum* species using four DNA barcodes (*rbcL*, *matK*, *psbA-trnH* and *trnLF*) showed an inability for any of the individual barcodes to discriminate species (Li et al., 2014). However, in a study of the same species, a combination of the three barcodes *rbcL*, *matK* and *trnLF* provided a slight improvement in species discrimination (Li et al., 2014). The barcode *psbA-trnH*, a non-coding chloroplast marker within the intergenic region, has effectively identified species rich genera *Pedicularis*, *Primula*, *Rhododendron* and *Parnassia* (Pang et al., 2012). A combination of *psbA-trnH* and ITS2 showed better species discrimination than the use of the *psbA-trnH* barcode alone (Pang et al., 2012). ITS2 has mostly shown low amplification and sequencing efficiency as compared to chloroplast barcodes but better resolution of species due to its high interspecific variation (Acharya et al., 2022; Tripathi et al., 2013). ITS2 can also help assess secondary structures for RNA which helps in understanding the mechanism of RNA molecules and its ability to demonstrate polyphyletic phylogeny can be used in genetic divergence studies (Acharya et al., 2022).

2.5 Molecular markers in identification and genetic characterization of *Physalis* plants

Physalis accessions have been characterized using different types of molecular markers such as SNPs, InDels, SSR markers and DNA barcoding (Ralte and Singh, 2021; Muraguri *et al.*, 2021; Feng *et al.*, 2016; Garzón-Martínez *et al.*, 2015; Simbaqueba *et al.*, 2011). Few studies have used SSR markers in the characterization of *Physalis* species (Feng *et al.*, 2023; Muraguri *et al.*, 2021; Simbaqueba *et al.*, 2011). A study has shown that identification of plants based on morphological characteristic is more reliable and authentic than the use of SSR markers (Yin *et al.*, 2023). This study indicated that SSR molecular markers cannot replace morphological markers but a combination of the two would be more accurate and reliable in plant variety identification (Yin *et al.*, 2023). Therefore, SSR markers are not very efficient in species discrimination but can provide robust data on genetic diversity of plants.

Physalis is categorized as an orphan fruit crop, therefore, there is very little information on its genetic diversity. It is important to understand the diversity of *Physalis* as this information will assist in developing crossbreeding strategies and conservation methods for the various species identified (Garzón-Martínez *et al.*, 2015). Genetic diversity of *Physalis* has been studied in Colombia where the plant mainly grows as a wild fruit and also cultivated for commercial purposes (Garzón-Martínez *et al.*, 2015; Chacón *et al.*, 2014). In Colombia, the genetic diversity of the *Physalis* was assessed using single nucleotide polymorphisms (SNPs) and InDels derived from immunity regulated genes

(IRG) and conserved ortholog set (COS) II markers. The studies demonstrated that there were moderate to high genetic diversity in P. peruviana and related taxa species in Colombia (Garzón-Martínez et al., 2015). Recommendations indicated a need to further analyze the genetic diversity of the fruit in other parts of the world where it is available (Garzón-Martínez et al., 2015). Other markers that have been used to assess diversity of *Physalis* include random amplified microsatellites (RAM) for genetic diversity studies of Colombian *Physalis* spp and showed high heterozygosity (Morilla-Paz et al., 2011). Molecular markers used in tomato characterization such as SSRs, InDels and COS have also been utilized in determining *Physalis* genetic diversity. However, due to the fact that Physalis and tomatoes are only related at the family level, high polymorphism detected (Garzón-Martínez et al., 2015). Genetic diversity of Physalis spp., from Indonesia has been assessed based on SSR markers and revealed high intraspecies variation amongst the Physalis accessions studied (Sadiya et al., 2021). The SSR markers have also been used to assess the genetic diversity of Physalis in Kenya and identified a high diversity amongst accessions studied (Muraguri et al., 2021). However, the species identity of the *Physalis* accessions used in the study was not known. In China, the recent use of SSR markers in assessment of genetic diversity of P. angulata has shown considerable diversity among the accessions within the species (Feng *et al.*, 2023). There are limited studies that have focused on assessing the genetic diversity of *Physalis* species and their accessions using DNA barcode genes. More work needs to be done on determining interspecific and intraspecific genetic diversity of Physalis accessions based on chloroplast and nuclear DNA barcodes. Genetic diversity of Physalis plants has also been assessed using morphological and physicochemical traits (Santos et al., 2022; Usaizan et al., 2018). Understanding the genetic diversity of plants is key in establishing proper breeding programs and ensuring conservation of rare and endangered species and cultivars.

2.6 DNA barcoding in species discrimination and genetic characterization of *Physalis* accessions

The identification of *Physalis* accessions and assessment of their genetic diversity based on DNA barcodes has not been widely studied. However, much of the work that has been done has shown that DNA barcodes have a high efficiency in species discrimination based on BLASTn analysis and phylogenetic analysis (Feng *et al.*, 2018; Feng *et al.*, 2016). DNA barcodes such as ITS2, *rbcL*, *matK* and *psbA-trnH* have been utilized in the characterization of *Physalis* accessions (Ralte and Singh, 2021; Rosario *et al.*, 2019; Feng *et al.*, 2018; Feng *et al.*, 2016). In one study the barcode *psbA-trnH* was able to facilitate the identification of *Physalis* accessions from China as *P. angulata*, *Physalis alkekengi* var. *franchetti*, *P. pubescens* and *P. peruviana* (Feng *et al.*, 2018). In another study of

Physalis accessions from China, the ITS2 RNA secondary structures facilitated the identification of *Physalis greenmanii*, *Physalis hintonii*, *P. alkekengi* and *P. alkekengi* var. *franchetti* (Feng *et al.*, 2016). DNA barcoding has been considered more robust in species discrimination of plants than other molecular markers. Combining two DNA barcode markers in species discrimination provides more robust species identification (Parmentier *et al.*, 2013).

2.6.1 DNA barcoding in species discrimination of *Physalis* accessions

Physalis accessions in China have been discriminated using the psbA-trnH barcode marker which showed high efficiency at discrimination based on BLASTn analysis and phylogenetic analysis (Feng *et al.*, 2018; Feng *et al.*, 2016). In a study by Feng et al. (2016), species like *P. greenmanii* and *P. hintonii* were identified. Furthermore, the identification of *Physalis* as an ethno-medicinal plant within the *Solanaceae* family has been documented based on ITS2 and *rbcL* genes (Ralte and Singh, 2021). Another study conducted in China utilized the ITS2 barcode to effectively identify *Physalis* accessions through BLASTn analysis and near distance methods (Feng *et al.*, 2016).

2.6.2 DNA barcodes in assessment of genetic diversity of Physalis accessions

Due to the status of *Physalis* as an orphan plant, few studies are focusing on its genetic diversity. Information on genetic diversity of *Physalis* plant would provide important details to breeders for selection parents for breeding programs and conservation of endangered species and accessions from extinction (Delgado-Bastidas *et al.*, 2019). Conservation of the species *Physalis peruviana* L. in Colombia entails the preservation of domesticated and wild type germplasms in research centers and Universities (Simbaqueba *et al.*, 2011). Molecular characterization of *Physalis peruviana* in Colombia has largely been done using SSR markers which are ideal in population genetics studies due to their high co-dominant and polymorphic inheritance (Juyó *et al.*, 2015). The intraspecific and interspecific genetic divergence of *Physalis* accessions in China has been studied with the results indicating that the accessions had higher interspecific divergence of *Physalis* accessions from the *psbA-trnH* barcode (Feng *et al.*, 2018). Intraspecific divergence of *Physalis* accessions from China was noted to be low using the ITS2 barcode (Feng *et al.*, 2016).

2.7 ITS2 RNA secondary structures in discrimination of plant species

The ITS2 barcode is a spacer nuclear gene in plants that has a high level of interspecific and intraspecific variation and can be used in species discrimination among various plant genera (Anaz *et al.*, 2021). This gene is important in ribosome synthesis and its secondary and tertiary structures are

crucial for this function (Zhang *et al.*, 2020). Despite its variation among species and its rapid evolution it must maintain specific RNA secondary structures that provide the functionality of the ribosome (Zhang *et al.*, 2020). The RNA secondary structure of the ITS2 gene can also facilitate species discrimination above the generic level and this makes ITS2 efficient in species discrimination (Coleman, 2003). ITS2 secondary structure comparison among plant species can also help divulge the level of divergence of genes within species and also provide visual differences of various plant species (Anaz *et al.*, 2021).

ITS2 gene sequences and RNA secondary structures have been used in species discrimination of genus *Achyranthes* with 100% success in correct identification of species (Singh *et al.*, 2020). ITS1 and ITS2 secondary structures have been used to successfully discriminate *Nepenthes* species with enhanced resolution (Saidon *et al.*, 2023). Therefore, the use of ITS2 secondary structure in species discrimination has been widely successful for different plant genera. ITS2 secondary structure discrimination for *Physalis* has not been widely studied but in the few studies done species discrimination was successful. The ITS2 secondary structures have been successfully used in discrimination of *Physalis* species from China such *P. greenmanii*, *P. alkekengi*, *P. hintonii* and *P. alkekengi* var. *franchetti* (Feng *et al.*, 2016). Identification of plants species using ITS barcode sequences and their secondary structures can therefore provide an efficient and robust analysis which can be used as a basis for the conservation and utilization of plant genetic resources. No study has been done to use the ITS2 RNA secondary structures to discriminate *Physalis* species in Kenya.

CHAPTER THREE

3.0 Determination of mineral composition, phytochemical content, antioxidant activity and identity of *Physalis* accessions from Sorget forest, Kericho County, Kenya

3.1 Introduction

Indigenous varieties adapted to a particular region are ideal resilient crops for climate change adaptation but are neglected and often lost due to the rapid domestication of commercial cultivars. Restoring such plant species would empower local farmers and provide huge economic and nutritional benefits. One such underutilized wild plant species is of the genus *Physalis* and belongs to the Nightshade (Solanaceae) family (Afroz et al., 2020). Physalis species are native to the Peruvian and Ecuadorian Andes region of South America; hence, it is referred to as the Peruvian gooseberry (Feng et al., 2016), although some are also native to Southeast Asia and Eurasia (Wei et al., 2012). Studies of Physalis in China have identified five species including P. alkekengi, P. angulata, P. pubescens, P. peruviana, and P. minima and two variants of P. alkekengi (Chinese Academy of Sciences, 1978). Physalis species such as P. philadelphica, P. peruviana, and P. pubescens are grown in various parts of the world (Sang-Ngern et al., 2016). Physalis fruits are exported from several countries including Colombia, Australia, New Zealand, Great Britain, Zimbabwe, Kenya, Egypt, South Africa, Madagascar, and South East Asia (Zhang et al., 2013; Ramadan and Moersel, 2003). The largest producer, consumer, and exporter of *Physalis* fruits is Colombia (Zhang et al., 2013). In Kenya, the fruits are seen in vast numbers as wild and self-propagating plants, commonly in farms during and after the harvesting of maize. Currently, there is growing commercial interest in this fruit crop because of its nutritional and pharmacological properties and health benefits. The key steps involved in the proper utilization of this indigenous plant species are accurate identification and authentication.

Taxonomic identification and morphological characterization are the most common methods of plant authentication, although they are limited by environmental or physiological factors and the developmental phase of the plant species (Menzel, 1951). Employing molecular tools such as DNA barcoding could be more successful in species identification. DNA barcoding requires a short universal DNA sequence that exhibits a sufficient level of variation to discriminate species (Barcaccia *et al.*, 2015, Hebert *et al.*, 2003). The proposed plant DNA core barcodes from the Consortium for the Barcode of Life (CBOL) Plant Working Group comprise the chloroplast gene large subunit of ribulose bisphosphate carboxylase (*rbcL*) and *matK* with the *psbA-trnH* intergenic sequence and internal transcribed spacer (ITS), and a nuclear gene as the supplement barcode (Kang *et al.*, 2017). Chloroplast DNA barcodes such as *matK* and *rbcL* have been used in many phylogenetic and plant species identification analyses (Feng *et al.*, 2018). The nuclear internal transcribed spacer 2 (ITS2) barcode has also been demonstrated to exhibit 100% species identification and discrimination statistics in plants due to its high intra- and interspecific divergence (Zhao *et al.*, 2018). Currently, there is lack of information on the genetic characterization of indigenous *Physalis* plants from the wild in Kenya.

The nutritional and phytochemical profiles of *Physalis* have been studied to a moderate level in the Andes (Ramadan and Moersel, 2007). The Physalis fruit contains fat and water-soluble vitamins (Bcomplex, C, A, E, and K), minerals (mainly phosphorus, magnesium, potassium, zinc, and calcium), sugars (e.g., sucrose, glucose, and fructose), fatty acids (palmitate, oleic, and gamma linoleic acid), phytosterols (sitosterol and stigmasterol), and fiber (pectin) (Puente et al., 2011; Ramadan and Moersel, 2003). The fruit pomace (skin and seed) contains 19.3% oil, 3.1% ash, 17.8% protein, 24.5% carbohydrates, and 28.7% crude fiber (Ramadan and Moersel, 2007). The phytochemicals found in *Physalis* include withanolides, physalins, carotenoids, phenolics, and flavonoids (Puente et al., 2011). A review study states that the most studied phytochemicals are the polyphenolics, which have antioxidant properties and many health-related benefits (Somani et al., 2015). The key polyphenolics include flavonoids, stilebenes, phenolic acids, coumarins, and tannins (Bayir et al., 2019). The *Physalis* plant's high content of vitamins, minerals, and antioxidant phytochemicals gives it medicinal properties such as anti-inflammatory activity and this has been specifically determined for P. alkekengi species (Hong et al., 2015). The characterization of the nutritional and bioactive properties of cultivated and wild fruits of *P. peruviana* growing in the northern Argentinian region identified several types of phytochemicals present in the plant, such as flavonoids and tannins (Bazalar Pereda et al., 2019). However, the mineral composition, phytochemical profile, and antioxidant activities of wild fruits of *Physalis* growing in Kenya have not yet been characterized.

The current study aimed to identify and assess the *rbcL* and ITS2 gene barcodes to discriminate indigenous *Physalis* accessions collected from the forest. The mineral and phytochemical content as well as antioxidant activities of ripe fruits were also evaluated to determine if they are nutrient-rich so that they could be used as sustainable resources for the development of biofortified crops and also promoted as a natural source of antioxidants.

3.2 Materials and methods

3.2.1 Sampling of plant material

Leaves and mature fruits of 10 *Physalis* plants were collected based on purposive sampling in April 2019 from different spots in Sorget forest in Londiani area of Kericho County, Kenya (Figure 3.1.). The area is located at an elevation of 2528 m above sea level and a latitude of 0.0684° S and a longitude of 35.5548° E (Appendix 1A).



Figure 3.1. Map showing the location of *Physalis* accessions sampling in Londiani, Kericho County, Kenya.

The collected *Physalis* plant samples were identified by the taxonomist Mr. Patrick Mutiso and the samples were preserved in the University of Nairobi herbarium in the Department of Biology (Codes of Voucher Specimens: KP/UON2019/001- KP/UON2019/010). Ten *Physalis* plants were sampled for their fruits and leaves based on the availability and ripeness of the fruits. The maturity of the fruits was assessed based on the color of the fruit. Ripe fruits had a yellow to orange color. The leaves were used for the molecular identification of the plant species, while the fruits were used for the study of the nutritive value and functional attributes. The collected leaf and fruit samples were wrapped with aluminum foil, kept in an ice box and transferred to the Molecular Biology Laboratory in the Department of Biochemistry, University of Nairobi. The leaf samples were kept at -80 °C prior to genomic DNA extraction. The fruit samples were utilized immediately upon arrival at the laboratory for the extraction of phytochemicals and the determination of the mineral content.

3.2.2 Molecular authentication of *Physalis* plants

3.2.2.1 Isolation of genomic DNA from leaves of Physalis accessions

Isolation of genomic DNA from leaves of *Physalis* accessions was performed using the cetyltrimethylammonium bromide (CTAB) method Dellaporta *et al.*, 1983). Ribonuclease A (RNase, 0.6 mg/mL) was added to the DNA accessions followed by incubation at 37 °C in a water bath for 30 min to eliminate any contaminating RNA. The integrity of the extracted genomic DNA was verified using 0.8% (*w/v*) agarose gel stained with ethidium bromide (0.5 μ g/mL) and viewed under UV transilluminator in Gel DocTM EZ Imaging System (BioRad, Hercules, CA, USA). DNA was stored at –20 °C until use in the molecular analysis.

3.2.2.2 Polymerase chain reaction (PCR) amplification and sequencing

Polymerase chain reaction (PCR) amplification was performed using the DNA barcoding primers *rbcL* and ITS2 (Table 3.1). DNA amplification was conducted using a One Taq[®] Hot start 2× master mix with standard buffer (New England Biolabs, Ipswich, MA, USA) following the manufacturer's instructions. Amplification was conducted in a Veriti, 96-well Thermal Cycler (Thermo Fischer Scientific, Waltham, MA, USA). Optimization was performed in order to acquire the best conditions for PCR amplification. The annealing temperature for both primers was optimized at the following temperatures: 50 °C, 51 °C, 52 °C, 54 °C, 56 °C, and 58 °C. The best optimum cycling conditions for both primers were used for the PCR amplification of the DNA samples (Table 3.1). The amplicons were confirmed using 1% agarose gel stained with ethidium bromide (0.5 μ g/mL) under a UV transilluminator in the Gel DocTM EZ Imaging System (BioRad, Hercules, CA, USA). Amplicons were cleaned using a gel clean up kit (Applied Biosystems, Thermo Fischer Scientific, Waltham, MA, USA) and sent for sanger sequencing at the University of Nairobi (UoN) Center of Excellence in HIV Medicine (CoEHM) using a 3730 s DNA analyzer (Thermo Fischer, Waltham, MA, USA).
Barcode Region	Primer Name	Primer Sequence (5' to 3')	PCR Conditions
ITS2	ITS2-F	CCTTATCATTTAGAGGAAGGAG	1 cycle of 94 °C 5 min;
			30 cycles of 94 °C 30 s,
	ITS2-R	TCCTCCGCTTATTGATATGC	58 °C 45 s, and 72 °C 1 min;
			72 °C 7 min
rbcL	rbcL-1-F	ATGTCACCACAAACAGAA	1 cycle of 94 °C 5 min;
			30 cycles of 94 °C 30 s,
	rbcL-74-R	TCGCATGTACCTGCAGTAGC	58 °C 45 s, 72 °C 1min;
			72 °C 7 min

 Table 3.1. Oligonucleotide primers used for PCR amplification and optimum PCR cycling conditions

3.2.2.3 Sequence and phylogenetic analysis

The sequences of each barcode were edited manually in the BioEdit software version 7.2.5.0 (Hall, 1999). The BioEdit software successfully recognized and opened the auto sequencer trace files for the sequenced ITS2 and *rbcL* genes from the *Physalis* accessions. In every instance of sequence editing the chromatogram trace was adjusted with the horizontal and vertical scale bars so as to observe the peaks of the trace. The editable notepad file comprising the sequence. The called bases on the chromatogram trace were then visualized and editing of the sequence for pseudobases was done by observing the color-coded peaks on the chromatogram trace below the pseudobase and replacing the pseudobase with the correct base. Edited sequences were then saved under the FAST All (FASTA) format in preparation for Basic Local Alignment Search Tool for nucleotides (BLASTn) analysis.

The edited sequences were compared with the available nucleotide sequences in the GenBank database. The sequences were blasted in the NCBI GenBank BLASTn database to determine the sequence homology with other deposited ITS2 and *rbcL* sequences (https://blast.ncbi. nlm.nih.gov/Blast.cgi accessed on 10 February 2023). The identification of *Physalis* species was based on the least expected value (E-value), highest query coverage, and similarity percentage. The obtained sequences were also assembled and aligned using the MUSCLE algorithm. Multiple sequence alignment (MSA) of ITS2 and *rbcL* sequences in this study and the reference sequences retrieved from the NCBI database was performed using the MUSCLE software version 3.8 (Edgar,

2004). This MSA was used in the preparation of a phylogenetic tree. The ITS2 and *rbcL* sequences were also aligned separately using MUSCLE, and viewed and trimmed on Jalview version 2.11.2.6 to obtain uniform sequence lengths (Troshin *et al.*, 2018; Troshin *et al.*, 2011). Two MSAs were prepared separately for ITS2 and *rbcL* sequences without use of their reference sequences and were used in the genetic diversity, nucleotide polymorphism, neutrality test, and automatic barcode gap discovery (ABGD) analysis. All MSAs attained were compressed using ESPript 3 (http://espript.ibcp.fr accessed on 12 February 2023) (Robert and Gouet, 2014). The ITS2 and *rbcL* sequences were submitted to NCBI GenBank through a web-based sequence submission tool and accession numbers were assigned.

Phylogenetic trees were constructed based on the Bayesian inference (BI) method using MrBayes version 3.2.7 (https://nbisweden.github.io/MrBayes/ accessed on 12 February 2023). Statistical analysis was performed using the posterior distribution of the model parameter, which was estimated using the Markov chain Monte Carlo (MCMC) method (Ronquist *et al.*, 2012; Ronquist and Huelsenbeck, 2003; Huelsenbeck and Ronquist, 2001). MCMC sampling was performed over 18,000,000 generations at a sampling frequency of 1000 and the first 25% (relburnin = yes burninfrac = 0.25) of samples were discarded when estimating the posterior probabilities of the trees. After 18,000,000 generations, the analysis was stopped when the average standard deviation of the split frequencies was less than 0.01 and tree parameters were summarized. The constructed phylogenetic trees were visualized and modified using the FigTree software version 1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/ accessed on 12 February 2023).

3.2.3 Analysis of genetic divergence

DNA divergence within *Physalis* accession populations based on ITS2 and *rbcL* sequences was determined using the DnaSP software version 6.12.03 (Kartartsev, 2011). The multiple sequence alignment (MSA) for *Physalis* accessions based on either the ITS2 or *rbcL* marker was uploaded into the software and various parameters for the divergence were determined. The number of polymorphic segregating sites (S), nucleotide diversity, and the total number of substitutions were assessed as outlined by the Jukes and Cantor algorithm on DnaSP.

3.2.4 Determination of genetic distance within Physalis accessions

Intraspecific genetic distances and the overall mean distance of *Physalis* accessions based on the ITS2 and *rbcL* sequences were determined using the Kimura 2 parameter (K2P) model with the gamma distribution and a gamma parameter of 0.27 using MEGA version 11.0 (Kumar *et al.*, 2018).

Sequence genetic distance was determined using multiple sequence alignments for *Physalis* accessions based on ITS2 and *rbcL* markers.

3.2.5 Nucleotide polymorphism

DNA polymorphisms of the ITS2 and *rbcL* sequences were assessed in all the *Physalis* accessions. The DNA sequence Polymorphism (DnaSP) software version 6.12.03 was utilized in the DNA polymorphism analysis for ITS2 and *rbcL* sequences of all *Physalis* accessions. The DNA polymorphism parameters determined were polymorphic segregating sites, singleton and parsimony informative sites, the nucleotide diversity, and the average number of nucleotide differences.

3.2.6 Tajima's neutrality tests

Tajima's neutrality test for both ITS2 and *rbcL* sequences of *Physalis* accessions were determined to estimate the frequency of mutations among species (Tajima, 1989). The Tajima's neutrality test determined the Tajima D value among the ITS2 and *rbcL* sequences of *Physalis* accessions using the MEGA 11.0 software (Tamura *et al.*, 2021; Nei and Kumar, 2000). The analysis involved nine and ten ITS2 and *rbcL* sequences of *Physalis* accessions, respectively. The codon positions included were 1st + 2nd + 3rd + noncoding for the *rbcL* gene sequences. All ambiguous positions were eliminated for each sequence pair (pairwise deletion option) in both the analysis based on ITS2 and *rbcL* genes, respectively. The MSAs utilized in this analysis were similar those utilized for genetic diversity and DNA polymorphism studies based on ITS2 and *rbcL* sequences.

3.2.7 Analysis of DNA barcoding gap and intraspecific distance

In order to delimit the *Physalis* species based on their intraspecific divergence within a population, the automatic barcode gap discovery (ABGD) method described by (Puillandre *et al.*, 2012) was utilized in this study. Multiple sequence alignments utilized in genetic diversity analysis were also utilized for the ABGD analysis of ITS2 and *rbcL* sequences of *Physalis* accessions. The ITS2 and *rbcL* multiple sequence alignments were separately inputted into the ABGD website (https://bioinfo.mnhn.fr/abi/public/abgd/abgdweb.html accessed on 17 February 2023) and the distance analysis was performed based on the K80 Kimura measure of distance. The default value for the relative gap width (X) was set at 1.5. Moreover, *p* values of intraspecific diversity of 0.001 and 0.1, respectively. Default settings were utilized for all other parameters.

3.2.8 Analysis of mineral content in ripe fruits

The analysis of macrominerals (calcium (Ca), magnesium (Mg), potassium (K), and sodium (Na)) and trace elements (iron (Fe), zinc (Zn), manganese (Mn), copper (Cu), lithium (Li), and nickel (Ni)) was performed according to the method described by (Hernández *et al.*, 2005). All the analyses were performed in triplicate. Each fruit sample (1 g) was digested in 5 mL of nitric acid, which was made up to 25 mL using distilled water. The mixture was heated on a hot plate until a third of the volume was left, which was filtered with Whatman filter paper No. 1. The filtrate was appropriately diluted and analyzed for mineral elements using an atomic absorption spectrophotometer (AAS) (Shimadzu, Kyoto, Japan). The wavelengths used for the analysis of each mineral were as follows: Ca-422.42 nm; Zn-213.52 nm; Cu-324.53 nm; Na-588.88 nm; Mg-285.04 nm; Fe-248.23 nm; K-766.74 nm; Ni-231.90 nm; Mn-27.03 nm; Li-670.85 nm. The results were expressed in ppm (1 ppm = 1 mg/L) of a sample of dry weight (DW). All the experiments were carried out three times with different fruit accessions.

3.2.9 Determination of phytochemical content

3.2.9.1 Estimation of total polyphenol content (TPC)

The estimation of phenol in fruit extracts was assayed using the Folin Ciocalteau method (Singleton *et al.*, 1999). In a test tube with 2.25 mL of 10% Folin Ciocalteau reagent, 1 mL of filtrate of ethanolic fruit extract was added, mixed thoroughly, and allowed to settle at 23 ± 2 °C for 5 min. To the mixture, 2.25 mL of sodium bicarbonate solution (60 g/L) was added, vortexed, and incubated at 23 ± 2 °C for 90 min. The absorbance was measured at 725 nm using a spectrophotometer (Shimadzu, Kyoto, Japan). A blank was prepared using the same method, but the fruit extract was replaced with sterile distilled water. A standard curve was used to determine the phenol content using gallic acid. All the experiments were carried out three times with different fruit accessions. The TPC was assessed as mg/mL of gallic acid equivalents per gram of fruit extract.

3.2.9.2 Estimation of Total Tannin Content (TTC)

The content of tannins in the fruit samples was assayed using the Folin Ciocalteau method (Singleton *et al.*, 1999). In a test tube, 0.25 mL of 10% Folin Ciocalteau reagent was added to 0.1 mL of ethanolic fruit extracts and vortexed. The mixture was allowed to settle at 23 ± 2 °C for 5 min, and then 1.25 mL of sodium hydroxide was added and the mixture was incubated at room temperature for 40 min. Absorbance was measured at 725 nm using a spectrophotometer. A blank was prepared using the same method, but the fruit sample was replaced with sterile distilled water. A standard curve was

then prepared for the estimation of the tannin content from *Physalis* fruits using tannic acid. All the experiments were carried out three times with different fruit accessions. The TTC was assessed as mg/mL of tannic acid equivalents per gram of fruit extract.

3.2.9.3 Estimation of total flavonoid content (TFC)

The determination of the flavonoid content in the fruit extracts was performed using the aluminum chloride (AlCl₃) colorimetric method (Chang *et al.*, 2002). In a test tube, 1 mL of ethanolic *Physalis* fruit extract was added to 4 mL of water and 0.3 mL of 5% sodium nitrate solution. The content was mixed thoroughly followed by the addition of 0.6 mL of aluminum chloride. The mixture was mixed thoroughly and incubated for 6 min at 23 ± 2 °C before the addition of 2 mL sodium hydroxide. A precipitate was formed on mixing, which was centrifuged and the absorbance of the supernatant was measured at 510 nm. A blank was prepared using the same method, but the fruit extract was replaced with sterile distilled water. A standard curve was prepared for the estimation of the flavonoid content using rutin. All the experiments were carried out three times with different fruit accessions. The TFC was assessed as mg/mL of rutin equivalents per gram of fruit extract.

3.2.10 Estimation of antioxidant activity

The antioxidant activity was measured using 2, 2-diphenyl-2-picrylhydrazyl (DPPH) and hydrogen peroxide radical scavenging in vitro assays. The DPPH radical scavenging (RS) assay was performed based on the radical degradation method described by Brand-Williams *et al.* (1995) with some modifications. The sample extracts (0.5 mL) were mixed with 0.1 mM DPPH radical solution (0.3 mL) prepared in an ethanol solution. Color change from deep violet to light yellow was observed and the absorbance was measured at 517 nm using a UV-Visible spectrophotometer after 100 min of reaction in the dark. The blank was prepared using 3.3 mL of ethanol and 0.5 mL of the sample. A control was prepared using 3.5 mL of absolute ethanol and 0.3 mL of the DPPH radical solution and the absorbance was measured. The percentage inhibition of the DPPH radical of the sample extract relative to the control was used to determine the antioxidant capacity using the equation:

$$AA\% = 100 - \left(\frac{Abs \, sample - Abs \, blank}{Abs \, control}\right) * 100$$

The hydrogen peroxide scavenging assay was performed using a method determined by Ruch *et al.* (1989) with a few modifications. In a test tube, 0.5 mL of the sample extract was mixed with 4 mL of 4 mM hydrogen peroxide solution prepared in 0.1 M phosphate buffer (pH 7.4). The mixture was incubated for 10 min at room temperature and the absorbance was measured at 230 nm using a UV-Visible spectrophotometer. A blank was prepared using phosphate buffer and sample extract. A control was prepared using phosphate buffer and hydrogen peroxide and the absorbance was

measured. The hydrogen peroxide radical scavenging (HRS) activity percentage was calculated using the equation:

$$HRS\% = \left(\frac{Abs \text{ control-Abs sample}}{Abs \text{ control}}\right) * 100$$

3.2.11 Statistical analysis

The results for the antioxidant activity, and mineral and phytochemical content of the *Physalis* accessions obtained were reported as mean \pm standard deviation (SD) using SPSS version 20 (IBM SPSS, 2010). All the measurements were performed in triplicate. One-way analysis of variance (ANOVA) was performed using the statistical software SPSS version 20 (IBM SPSS, 2010). The means from all analyses were separated by Tukey's HDS multiple comparisons test at $\alpha = 0.05$. Regression and correlation analysis was also performed to determine the impact of polyphenols on the antioxidant activity. Regression was analyzed using the statistical software SPSS version 20 IBM SPSS (2010) while correlation studies were analyzed using Microsoft excel version 2016.

3.3 Results

3.3.1 Amplification and sequencing success rate

The PCR amplification results in both ITS2 and *rbcL* regions achieved success rates of 100% (Table 3.2 and Appendix 1B and 1C). The lengths of the ITS2 and *rbcL* sequences were in the range of 301–663 bp and 520–733 bp, respectively. Images of the ITS2 and *rbcL* amplicons are indicated in Figure 3.2. and 3.3. respectively. The average lengths of ITS2 and *rbcL* sequences were 561 bp and 616 bp, respectively. The GC contents of the ITS2 and *rbcL* sequences were in the ranges of 60%–65.2% and 42.7%–43.9%, respectively. The average GC content of ITS2 sequences was 61.1%, which was significantly higher than that of the *rbcL* sequences (43.1%). The sequencing success rate was 99% and 100% for ITS2 and *rbcL* sequences, respectively (Table 3.2). Therefore, there were 9 sequences for the ITS2 genes and 10 sequences for the *rbcL* genes of *Physalis* accessions from Sorget forest studied.

Barcode Region	Samples Tested (n)	Number of Amplicons Produced	Number of Sequences Produced	Amplificatio n Efficiency (%)	Sequencing Efficiency (%)	Alignment Length (bp)	Mean Sequence Length (bp)	GC Content (%)
ITS2	10	10	9	100	99	663	561	61.1
rbcL	10	10	10	100	100	730	616	43.1

Table 3.2. Efficiency of PCR amplification and sequencing for *Physalis* accessions based on ITS2 and *rbcL* barcode genes



Figure 3.2. Image of PCR amplicons of *Physalis* accessions from Londiani based on the ITS2 marker.

The letter L in Figure 3.2 above represents the DNA ladder (1kb DNA ladder, Sigma Aldrich, St. Louis, Missouri, USA), 11i-110i represents the *Physalis* accessions amplicons based on ITS2 sequence amplification, NC represents the negative control for the experiment.



Figure 3.3. Image of PCR amplicons of *Physalis* accessions from Londiani based on the *rbcL* marker.

The letter L in Figure 3.3 above represents the DNA ladder, 11r-110r represents the *Physalis* accessions amplicons based on *rbcL* sequence amplification, NC represent the negative control for the experiment.

3.3.2 Species discrimination based on BLASTn analysis

According to the BLASTn analysis of ITS-2 sequences, seven of the nine *Physalis* accessions were identified as *P. purpurea*, and one was identified as *P. peruviana* and one as *Physalis aff philadelphica* (Table 3.3). The BLASTn analysis of *rbcL* sequences identified all the *Physalis* accessions as *P. minima* (Table 3.3). The percentage identity for the nine *Physalis* accessions based on ITS2 sequences ranged from 86.00 to 94.4%. The percentage identity for 10 *Physalis* accessions based on *rbcL* sequences ranged from 99.86 to 100%. Eight out of the ten *rbcL* sequences of *Physalis* accessions gave a 100% sequence similarity with *P. minima* (NC_048515.1 from the GenBank). Two accessions (OQ507154.1 and OQ507156.1) were also identified as *P. minima* (NC_048515.1 from the GenBank) with a similarity identity of 99.59 and 99.86%, respectively (Table 3.3).

Londiani 1	P. minima	NC_048515.1	0.0	100	OQ507152.1	-	-	-	-	-
Londiani 2	P. mimima	NC_048515.1	0.0	100	OQ507153.1	P. purpurea	MH763740.1	0.0	92.98	OQ372021.1
Londiani 3	P. minima	NC_048515.1	0.0	99.59	OQ507154.1	P. purpurea	MH763740.1	0.0	94.06	OQ372022.1
Londiani 4	P. minima	NC_048515.1	0.0	100	OQ507155.1	P. peruviana	AY665914.1	0.0	97.41	OQ372023.1
Londiani 5	P. minima	NC_048515.1	0.0	99.86	OQ507156.1	P. purpurea	MH763740.1	0.0	94.45	OQ372024.1
Londiani 6	P. minima	NC_048515.1	0.0	100	OQ507157.1	P. aff.	AY665868.1	2e-144	91.35	OQ372025.1
						philadelphica				
Londiani 7	P. minima	NC_048515.1	0.0	100	OQ507158.1	P. purpurea	MH763740.1	1e-148	86.00	OQ372026.1
Londiani 8	P. minima	NC_048515.1	0.0	100	OQ507159.1	P. purpurea	MH763740.1	0.0	93.07	OQ372027.1
Londiani 9	P. minima	NC_048515.1	0.0	100	OQ507160.1	P. purpurea	MH763740.1	0.0	88.96	OQ372028.1
Londiani 10	P. minima	NC_048515.1	0.0	100	OQ507161.1	P. purpurea	MH763740.1	0.0	90.16	OQ372029.1

Table 3.3. BLASTn analysis results for *Physalis* accessions based on ITS2 and *rbcL* markers.

3.3.3 Multiple sequence alignment

The multiple sequence alignment of combined ITS2 and rbcL gene sequences and retrieved sequences from the BLASTn analysis based on MUSCLE had a sequence length of 730 bp. The MSA is presented in Appendix 2A. A high rate of substitution mutations was noted for the ITS2 sequences, while very few substitutions, deletions, and insertion mutations were noted for the *rbcL* sequences. The MSA of ITS2 sequences of the nine Physalis accessions had a sequence length of 399 bp (https://espript.ibcp.fr/ESPript/temp/1397454355/0-0-1688383432-esp.pdf) (Figure 3.4). There was a high rate of substitution and deletion mutation within this MSA. A deletion point mutation was observed at position 9 of the MSA whereby, in *Physalis* accessions OQ372026.1 and OQ372023.1, the nucleotide thymine was deleted while all other accessions contained a thymine at this position (Figure 3.4). Another deletion point mutation was noted at position 46 of the MSA whereby guanine was deleted for the Physalis accessions OQ372023.1, OQ372026.1, OQ372027.1, and OQ372029.1 (Figure 3.4). These Physalis accessions also had a deletion macrolesion mutation of eight nucleotides from position 179 to 187. Both transition and transversion point mutations were also identified in the alignment. At position 107 of this MSA, there was a transition point mutation for the Physalis accession OQ372023.1, whereby guanine replaced adenine. A transversion point mutation was observed at position 119 for the Physalis accession OQ372023.1 whereby guanine replaced the thymine found on all other sequences. Insertion mutations were not identified on this MSA (Figure 3.4). The multiple alignment of rbcL sequences of 10 Physalis accessions had a sequence length of 614 bp (https://espript.ibcp.fr/ESPript/temp/1129027434/0-0-1688384286esp.pdf) (Figure 3.5). There were no deletions, insertions or substitution mutations noted in this MSA (Figure 3.5). All *Physalis* accessions had similar sequences with the key difference being the length of the sequences.

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00372028.1 00372021.1 00372024.1 00372022.1 00372025.1 00372025.1 00372023.1 00372023.1 00372027.1 00372029.1	GGCCACCTT GGCCACCTT GGCCACCTT GGCCACCTT GGCCACCTT GGCCACCCTT GGCCACCCTT GGCCACCCTT	ACCTGGAGG ACCCGGAGG ACCCGGAGG ACCCGGAGG ACCCGGAGG ACCCGGAGG ACCCGGAGT GCCCGGAGT	TTCGCTCGCC .CGCTCGCC TTCGCTCGCC TTCGCTCGCC TTCAGCCGAC TTCAGCCGAC TTCAGCCGAC TTCAGCCGAC	TCCCGCTCG TCCCGCTCG TCCCGCTCG TCCCGCTCG TCCCGCTCG ACGGCCAG ACGGCCAT ACGGCCAT	TCGGCCAGCA TCGGCCAGCA TCGGCCAGCA TCGGCCAGCA TCGGCCAGCA TCGGCCA.CC TCGGCCA.CG TCGGCCA.CG	GCCGCACGTG GCCGCACGTG GCCGCACGTG GCCGCACGTG GCCGCACGTG GCCGCACGTG GCCCCACACA GCACCACCACG GCACCACAACF GCACCACAACF	GCCGTCGCCTAC GCGGTCGCCTAG GCCGTCGCCTAG GCCGTCGCCTAG GCCGTCGCCTAG GTTGAGATTCAA GTTGAGATTCAA GTTGAGATTCAA GTTGAGATTCAA	CGACTAATG CGACTAACG CGACTAATG CGACTAACG CGACTAACG CCACTGACG CCACTGACG CCACTGACG CCACTGACG CCACTGACG
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0Q372028.1 0Q372021.1 0Q372024.1 0Q372025.1 0Q372025.1 0Q372025.1 0Q372025.1 0Q372027.1 0Q372027.1	170 GTCTCGCT GTGTTCGCT GTGTCGCT GTGCTCGCT GTGCTCGCT ATGCCTCGCT ATGCCTCGCT ATGCCTCGCT ATGCCTGCGT ATGCGTGCGT ATGCGTGCGT	18 CAAACACAA CAAACACAA CAAACACAA CAAACACAA CAAACACAA CACACCCA CACCCCCA CATCCCCA CATCCCCA	0, 19 ATGATCTCG ATGATCTCGG ATGATCTCGG ATGATCTCGG 	Q 2 CAACGCATA CAACGCATA CAACGCATA CACCGCATA CACCGCATA CACACGCTGC CAGACGTGC CAGACGTGC CAGACGTGC	0002 TCTCGGCTCT TCTCGGCTCT TCTCGGCTCT TCTCGGCTCT CCTCGACCTT CCTCGACCTT CCTCGACCTT	10 22 GCATCCATC GCATCCATCA CGCATCCATCA CGCATCCATCA CGCATCCATCA CGCATCCGCCA CGCTTCCGCCC CGCTTCCGCCC CGCTTCCGCCCA	0 230 AGAACGTAGCGA 360 AGAACGTAGCGA 360 AGAACGTAGCGA 360 AGAACGTAGCGA 360 CAAGCCTACCA 360 CAAGCCTICCAA 360 CAAGCGTICAAA 360 CAAGCGTICAAA 360 CAAGCGTICAAA 360 CAAGCGTICAAA 360	249 AATGCGATA AATGCGATA AATGCGATA AATGCGATA GACTCCAAG GACTCCAAG GACTCCATG GACTCCATG
0Q372028.1 0Q372021.1 0Q372024.1 0Q372025.1 0Q372025.1 0Q372025.1 0Q372023.1 0Q372027.1 0Q372027.1	2 5 6 C TT GGT G T G7 C TT AC G G 7 C TT C AC G G 7 G TT C AC G G 7	26 ATTGCAGAA ATTGCAGAA ATTGCAGAA ATTGCAGAA TTCCTGCAAT TCCTGCAAT TCCTGCAAT TCCTGCAAT	• 27 TCCAAATCGT TCCAAATCGT TCCAAATCGT T TCCAAATCGT TCCAAATCGT TCCAAATCGT TCCAAATCGT	C TACGTTCCG TACGTTCCG TACGTTCCG TACGTTCCG TACGTTACG TACGTTACG TACGTTACG	80, 2 AAGCCAGCGA AAGCCAGCGA AAGCCAGCGA AAGCCAGCGA AAGCCAACGA ATGCGAGCGA ATGCGAGCGA ATGCGAGCGA	90 30 GCTGCC GTCF GCTGCC GTCF GCTGCC GTCF ACTGCC GTCF GCTGCC GTCF GCTGCC GTCF	Q 31Q ITEGCACCCCCCG GCGCACCCCCCG GCGCACCCCCCG GCGCACCCCCCG GCCGCACCCCCCG GCCGCACCCCCCG GCGCACCCCCCG GCGCACCCCCCG	320 CCGCCCGCG CCGCCCGCG CCGCCCGCG CCGCCCGC
0Q372028.1 0Q372021.1 0Q372024.1 0Q372025.1 0Q372025.1 0Q372025.1 0Q372025.1 0Q372027.1	330 6C66C66A60 6C66C66A60 6C66C66A60 6C66C66A60 6C66C66A60 6C66C66A60	34 GTGGCCATC GTGGCCATC GTGGCCATC GTGGCCATC GTGGCCATC GCGGCCATC	0 35 GGCGGTCCTG GGCGGTCCTG GGCGGTCCTG GGCGGTCCTG GGCGGTCCTG GGCGGTCCTG GGCTGATCCTG GGCTACTCTG GGCGGTCTTGT CGCGGTCTTG	0 3 CCTGTCTGG CTGTCTGG CCTGTCTGG CTGTCTGG CCTGTCTGG CTGTCTGG CCTGCCAGG CCCGCCAGG CCCCCCCGCCCGG CCCCCCCGC	60 GTIGTATICT GTIG.AAICT GTIG.AAICT GTIG.AAICT GTIG.AAICC GTIGTAAICC GTCGTAGICG GTCGTAGICG	79 36 CCTGTGAGGCC CCTGTGGGGCC CCTGTGGGGCC CCTGTGGGCC CCTGTGGGCC CCGCCGGGCC CCGCCGGGCC	0 390 CCCCGGGATAACC CCCCGGAGAACCC CCCCGGAGAACCC CCCCGGAGAACCC CCCCGGAGAACCC	ITCGACGC CGACGC I.CGACGC I I ITCGACGC CTCGACGC TTC

Figure 2.4. Multiple sequence alignment for *Physalis* accessions based on ITS2 gene only



Figure 3.5. Multiple sequence alignment of *Physalis* accessions based on *rbcL* gene only

3.3.4 Physalis species identification based on phylogenetic analysis

The phylogram tree was constructed based on Bayesian inference and the combination of ITS2 and *rbcL* sequences. All the *Physalis* accessions were clustered together based on the *rbcL* gene sequences (Figure 3.6). The *Physalis rbcL* genes did not form clades with their reference sequences on the phylogram and there was no species discrimination. Therefore, the *Physalis rbcL* gene sequences species names (*P. minima*) indicated in the phylogram were based on the BLASTn analysis. Based on the ITS2 gene sequences, the *Physalis* accessions were identified with a percentage posterior probability of 100 as *P. purpurea* (Figure 3.6) and the sequences were deposited in GenBank with accession numbers OQ372021.1–OQ372029.1.



Figure 3.6. Phylogenetic tree generated by MrBayes for the *Physalis* accessions based on ITS2 and *rbcL* gene sequences

Different colors are used to represent *Physalis* accessions (experimental) as the variant species and reference sequences used in this study. Black represents the two clusters and sequences retrieved from GenBank for both ITS2 and *rbcL* genes. Blue represents *P. purpurea* sequences and red represents *P. minima* sequences. The values above the branches represent the percentage posterior probability statistic from the MrBayes phylogram.

3.3.5 Intraspecific divergence of Physalis accessions

DNA divergence was determined based on the number of polymorphic (segregating) sites (S), nucleotide diversity, and the total number of substitutions. Based on ITS2 gene sequences, nucleotide

diversity, the total number of nucleotide substitutions, and the number of polymorphic (segregating) sites were 0.27629, 134, and 124, respectively. There was no nucleotide diversity (0), nucleotide substitutions (0.00000), or polymorphic segregating sites (0) among the *Physalis* accessions based on *rbcL* gene sequences.

3.3.6 Genetic distance within *Physalis* accessions

The genetic distance within *Physalis* accessions based on ITS2 and *rbcL* gene sequences was assessed. The overall average genetic distance among the *Physalis* accessions based on ITS2 gene sequences was 1.67 ± 0.77 , while there was no genetic distance based on *rbcL* gene sequences. The mean average genetic distance within (intraspecific) *Physalis* species was 1.67 ± 0.84 and 0 based on ITS2 and *rbcL* gene sequences, respectively.

3.3.7 Nucleotide polymorphism and genetic diversity of *Physalis* accessions

There were 124 segregating sites identified with ITS2 gene sequences, while no segregating sites were recorded for the *rbcL* gene sequences (Table 3.4). The lack of segregating polymorphic sites within a population is an indication that all plants within this population are identical. The high number of polymorphic segregating sites for the ITS2 *Physalis* gene sequences is an indication that this gene is highly diverse among the *Physalis* accessions and has undergone differentiation. There were 21 singleton and 103 parsimony sites identified among the segregating sites of *Physalis* accessions based on the ITS2 gene sequences.

	ITS2			rbcL		
Polymorphic sites/Segregation sites (S)	124	Position in the gene	Variants	0	Positions in the gene	Variants
Singleton	21	49,58,90,107,116,117,118,119,120,125,138,139,144,158,162,164,172, 219,225,237,239	2	0		2
Parsimony informative sites	103	23,24,25,30,32,33,37,38,48,51,59,61,62,64,65,66,67,68, 69,71,7377,79, 81,82,84,85,88,91,93,94,95,97,99,100, 101,102,108,109,111,112,114, 126,129,132,136,140, 146,148,157,160,161,166,169,174,176,192, 193, 194,196,197,198,199,204,206,207,209,212,216,217,218,220,221,223, 227,228,229,230,232,234,235,240,241, 245,246,248,251,253,254, 255, 256,257,259 28,36,52,110,113,123,137,165,173,244	2	0		2 3
Nucleotide diversity (Pi)	0.2762	,9		0.00000	L	1
Average number of nucleotide differences (k)	61.889			0.000		
Sequence length (base pairs)	399			614		
Number of sequences	9			10		

Table 3.4. DNA polymorphism of *Physalis* accessions based on ITS2 and *rbcL* markers.

3.3.8 Tajima's neutrality test

Tajima's neutrality test was performed for both the ITS2 and *rbcL* gene sequences to assess the selection and nucleotide diversity of the *Physalis* accessions. The number of segregating sites (S) for ITS2 and *rbcL* were 180 and 0, respectively. The Tajima values of the *Physalis* accessions based on the ITS2 and *rbcL* gene sequences were 0.779171 and 0, respectively. The Tajima D of the ITS2 sequences indicated a negative selection pressure in the *Physalis* population. The nucleotide diversity of the ITS2 and *rbcL* sequences based on Tajima's test was 0.190894 and 0, respectively, indicating a variation in the ITS2 barcode region of *Physalis* accessions.

3.3.9 Genetic differences and barcoding gap analysis

Automatic barcode gap discovery (ABGD) results generated by the K80 Kimura measure of distance (K2P) based on the ITS2 gene sequences for *Physalis* accessions were used to assess the presence of a barcoding gap. The *rbcL* gene sequences for *Physalis* accessions were not able to provide results on barcoding as there was no variation in the sequences at an intraspecific and interspecific level. Based on the ITS2 gene sequences, all pairwise distances were ranked by increasing the distance values from 0.02 to 0.70 and three barcoding gaps were detected (Figure 3.7). The first and smallest barcode gap was observed between distances of 0.15 (15%) and 0.18 (18%) (Figure 3.7). The second and largest barcode gap was found between the distances of 0.22 (22%) and 0.44 (44%) (Figure 3.7). The third barcode gap was found between the distances of 0.59 (59%) and 0.70 (70%).



Figure 3.7. A histogram indicating the hypothetical distribution of pairwise differences of ITS2 gene sequences for nine *Physalis* accessions.

Low divergence is presumably intraspecific divergence, whereas higher divergence indicates interspecific divergence. The abbreviation nbr on the *y*-axis of the histogram stands for the number of pairwise comparisons. A, B and C represent the three barcode gaps identified.

3.3.10. Mineral analysis

The mineral content of *Physalis* accessions was determined for macro- and microminerals (Tables 3.5, 3.6, Appendix 3A and 3B). The highest macromineral content among the *Physalis* accessions was noted for potassium at a mean of 527.778 \pm 260.526, while the lowest was the magnesium content at a mean of 33.911 \pm 29.942 (Table 3.5). Sodium and calcium contents were at moderate levels in *Physalis* accessions with means of 377.46 \pm 147.193 and 128.121 \pm 20.976, respectively (Table 3.5).

Table 3.5. Macro-mineral content of fruits of *Physalis* accessions.

Data are expressed as mean \pm SD of three independent accessions. CV: coefficient of variation; CV: coefficient of variation; n = 3; means followed by single letters in a column differ significantly at a 5% level of significance.

Sample ID	ITS Accession Number in the GenBank	Ca (ppm)	Na (ppm)	K (ppm)	Mg (ppm)
L1	OQ507152.1	145.493 ± 6.087^{aa}	445.378 ± 51.116 ^{aa}	352.941 ± 24.758 ^{aa}	61.056 ± 93.957 ^{aa}
L2	OQ372021.1	58.700 ± 7.451 ^a	275.910 ± 18.080 ^{aa}	247.549 ± 8.947 ^{aa}	24.247 ± 20.009 ^{aa}
L3	OQ372022.1	121.803 ± 26.283 ^{aa}	175.070 ± 49.239 aa	497.549 ± 14.036 ^{aa}	13.604 ± 6.519^{aa}
L4	OQ372023.1	77.778 ± 2.618 ^{aa}	208.687 ± 81.942 ^{aa}	470.588 ± 11.725 ^{aa}	8.342 ± 6.455 ^{aa}
L5	OQ372024.1	81.132 ± 9.804 ^{aa}	263.306 ± 14.761 ^{aa}	811.275 ± 77.914 ^{aa}	71.532 ± 43.883 aa
L6	OQ372025.1	140.042 ± 26.804 ^{aa}	441.176 ± 21.091 ^{aa}	681.372 ± 37.395 ^{aa}	24.346 ± 22.820^{aa}
L7	OQ372026.1	131.447 ± 3.328 ^{aa}	456.583 ± 47.782 ^{aa}	450.981 ± 12.484 ^{aa}	19.381 ± 9.648 ^{aa}
L9	OQ372028.1	147.170 ± 23.966^{aa}	410.364 ± 25.673^{aa}	823.530 ± 24.961 ^{aa}	61.520 ± 48.887 ^{aa}
L10	OQ372029.1	133.962 ± 22.440^{aa}	380.952 ± 10.052 ^{aa}	414.216 ± 22.517 ^{aa}	21.169 ± 17.301 aa
	Mean	128.121 ± 20.976	377.46 ± 14.193	527.778 ± 26.526	33.911 ± 29.942
	CV	16.372%	39.000%	49.363%	88.296%

The micro-mineral content of *Physalis* accessions was also determined (Table 3.6). The highest micro-mineral content was noted for zinc at a mean of 24.364 ± 12.572 (Table 3.6). The lowest micro-mineral content was noted for lithium at a mean of 0.047 ± 0.024 (Table 3.6). A moderate micro-mineral content was noted for iron, manganese, copper, and nickel (Table 3.6).

Sample	Accession	Fe (nnm)	Zn (nnm)	Ni (nnm)	Cu (nnm)	Li (nnm)	Mn (nnm)
ID	Number	re (ppm)	zu (ppm)	ru (ppm)	Cu (ppm)	El (ppin)	tim (ppm)
L1	OQ507151.1	4.597 ± 3.081 ^{aa}	17.534 ± 3.369^{aa}	0.214 ± 0.000 ^{aa}	0.015 ± 0.006 ^{aa}	0.035 ± 0.022 ^{aa}	0.565 ± 0.258 ^{aa}
L2	OQ372021.1	6.398 ± 2.543 ^{aa}	7.618 ± 2.702 ^{aa}	0.166 ± 0.083^{aa}	0.158 ± 0.050 ^{aa}	$0.079 \pm 0.060^{\ aa}$	0.491 ± 0.205 ^{aa}
L3	OQ372022.1	5.806 ± 2.864 ^{aa}	8.538 ± 4.987 ^{aa}	0.357 ± 0.124 ^{aa}	0.270 ± 0.079 ^{aa}	0.019 ± 0.004 ^{aa}	1.139 ± 0.467 ^{aa}
L4	OQ372023.1	5.780 ± 2.215^{aa}	84.663 ± 37.191 ^a	1.048 ± 0.527 ^a	0.427 ± 0.413 ^{aa}	0.203 ± 0.091 ^a	0.954 ± 0.423 ^{aa}
L5	OQ372024.1	6.317 ± 1.391 ^{aa}	7.771 ± 0.176 ^{aa}	0.167 ± 0.109 ^{aa}	1.322 ± 0.468 ^{aa}	0.021 ± 0.013 ^{aa}	2.102 ± 0.135 ^{aa}
L6	OQ372025.1	6.129 ± 1.268 ^{aa}	35.276 ± 24.020 ^{aa}	0.428 ± 0.189 ^{aa}	1.809 ± 1.523 ^a	0.010 ± 0.008 ^{aa}	1.250 ± 0.074 ^{aa}
L7	OQ372026.1	6.640 ± 1.341 aa	7.311 ± 1.240^{aa}	0.476 ± 0.289 ^{aa}	1.089 ± 0.161 ^{aa}	$0.022 \pm 0.010^{\ aa}$	1.454 ± 0.158 ^{aa}
L9	OQ372028.1	8.145 ± 1.218 ^{aa}	37.270 ± 36.851 ^{aa}	0.929 ± 0.500 ^{aa}	1.072 ± 0.116 ^{aa}	0.014 ± 0.005 ^{aa}	1.954 ± 0.434 ^{aa}
L10	OQ372029.1	6.989 ± 0.492 ^{aa}	13.293 ± 2.609^{aa}	0.357 ± 0.124 ^{aa}	0.402 ± 0.522 ^{aa}	0.018 ± 0.000 ^{aa}	1.870 ± 0.181 ^{aa}
	Mean	6.311 ± 1.824	24.364 ± 12.572	0.460 ± 0.216	0.810 ± 0.371	0.047 ± 0.024	1.309 ± 0.482
	CV	28.902%	51.601%	46.957%	45.802%	51.064%	36.822%

 Table 3.6. Trace element content in fruits of *Physalis* accessions.

Data are expressed as mean \pm SD of three independent accessions. CV: coefficient of variation; CV: coefficient of variation; n = 3; means followed by single letters in a column differ significantly at a 5% level of significance.

3.3.11 Phytochemical content and *in vitro* antioxidant activity

Ripe fruits of *Physalis* accessions were assessed for phytochemicals (total phenolic acid, tannic acid, and flavonoid) and antioxidant activities (Table 3.7 and Appendix 3C). The phytochemical contents and antioxidant activities did not change significantly (p > 0.05) among the *Physalis* accessions (Table 3.7). The TPC of different *Physalis* accessions did not change considerably, ranging from 0.024 ± 0.025 to 0.092 ± 0.053 mg GAE/g DW (Table 3.7). *Physalis* accessions L1 and L5 recorded significantly higher TTC compared with the other eight accessions (Table 3.7). The TFC of the different *Physalis* accessions did not change significantly and ranged from 0.058 ± 0.034 to 0.152 ± 0.089 mg Rutin/g DW. Two different chemical assays (DPPH and HRS) were performed to assess the antioxidant activity of *Physalis* accessions (Table 3.7 and Appendix 3 D). The DPPH and HRS values obtained for the antioxidant property did not show significant differences (p > 0.05) among the different *Physalis* accessions ranged from 29.846 ± 13.537 to 97.344 $\pm 2.263\%$ and 8.696 ± 7.609 to 64.131 $\pm 9.962\%$, respectively (Table 3.7).

Sample	Accession	TPC (mg GAE/g	TTC (mg Tannic	TFC (mg Rutin/g		UDC4''4 0/
ID	Number	DW)	acid/g DW)	DW)	ДРРН К5 А %	HKS activity %
L1	OQ507152.1	0.092 ± 0.053 ^{aa}	0.158 ± 0.004 ^a	0.145 ± 0.073 ^{aa}	29.846 ± 13.537 ^a	64.131 ± 9.962 ^{aa}
L2	OQ372021.1	0.059 ± 0.040 ^{aa}	0.126 ± 0.045 ^{aa}	0.072 ± 0.020 ^{aa}	94.095 ± 0.182 ^{aa}	52.174 ± 9.962 ^{aa}
L3	OQ372022.1	0.024 ± 0.025 ^{aa}	0.099 ± 0.039 ^{aa}	0.070 ± 0.017 ^{aa}	75.862 ± 2.970 ^{aa}	30.435 ± 18.827 ^{aa}
L4	OQ372023.1	0.035 ± 0.026 ^{aa}	0.115 ± 0.067 ^{aa}	0.063 ± 0.040 ^{aa}	44.868 ± 6.556 ^a	6.159 ± 7.863 ^{aa}
L5	OQ372024.1	0.034 ± 0.008 ^{aa}	0.184 ± 0.015 ^a	0.096 ± 0.026 ^{aa}	67.539 ± 17.427 ^a	41.667 ± 12.120^{aa}
L6	OQ372025.1	0.081 ± 0.051 ^{aa}	0.047 ± 0.022 ^{aa}	0.071 ± 0.051 ^{aa}	73.088 ± 9.318^{aa}	59.420 ± 44.952 ^{aa}
L7	OQ372026.1	0.060 ± 0.016 ^{aa}	$0.049 \pm 0.039^{\ aa}$	0.058 ± 0.034 ^{aa}	95.045 ± 7.149 ^{aa}	53.623 ± 26.721 ^{aa}
L8	OQ372027.1	0.082 ± 0.011 ^{aa}	0.061 ± 0.023^{aa}	0.097 ± 0.069 ^{aa}	96.156 ± 3.924 ^{aa}	8.696 ± 7.609 ^{aa}
L9	OQ372028.1	0.060 ± 0.027 ^{aa}	0.041 ± 0.015 ^{aa}	0.128 ± 0.038 ^{aa}	97.344 ± 2.263^{aa}	62.319 ± 8.786 ^{aa}
L10	OQ372029.1	0.080 ± 0.071 ^{aa}	0.072 ± 0.016 ^{aa}	0.152 ± 0.089 ^{aa}	89.666 ± 16.692 ^{aa}	39.131 ± 20.738 ^{aa}
	Mean	0.061 ± 0.033	0.095 ± 0.029	0.095 ± 0.046	76.351 ± 8.002	41.776 ± 16.754
	CV	54.098%	30.526%	48.421%	10.481%	40.104%

Table 3.7. Phytochemical content and radical scavenging activities of *Physalis* accessions.

Data are expressed as the mean \pm SD of three independent accessions. CV: coefficient of variation; n = 3; TPC: total phenol content; TTC: total tannin content; TFC: total flavonoid content; DPPH RSA: 2, 2-diphenyl-2-picrylhydrazyl radical scavenging activity; HRSA: hydrogen peroxide radical scavenging activity. Means followed by a single letter in a column differ significantly at a 5% level of significance.

3.3.12 Correlation analysis between phytochemical contents and antioxidant activities

Correlation and regression studies were performed to assess the effect of each phytochemical content (phenolic acid, tannins, and flavonoids) on the radical scavenging activity of *Physalis* accessions (Table 3.8). DPPH radical scavenging was largely facilitated by the phenolic acid content, with a correction of r = 0.327, while flavonoids and tannins had a negative correlation (Table 3.8). Hydrogen peroxide radical scavenging was largely facilitated by phenolic acids and flavonoids at a correlation value of r = 0.3599 and 0.2877, while tannins had a negative correlation (Table 3.8). The regression analysis showed that all phytochemicals (phenolic acids, tannins, and flavonoids) had a linear relationship to the radical scavenging of DPPH and hydrogen peroxide radicals (Table 3.8).

Table 3.8. Correlation and regression analysis of phytochemical content and radical scavenging activity of *Physalis* accessions.

Polyphenol Content	Correlation Coefficient (r) for DPPH RSA	Correlation Coefficient (r) for HRSA	ANOVA (p Value) for Hypothesis Testing of Slope of Regression Line for DPPH RSA	ANOVA (p Value) for Hypothesis Testing of Slope of Regression Line for HRSA
Phenolics	0.327	0.3599	0.928	0.307
Tannins	-0.6316	-0.0374	0.050	0.918
Flavonoids	-0.1150	0.2877	0.752	0.420

3.4. Discussion

DNA barcoding is relatively fast in terms of species identification and discrimination (Chen *et al.*, 2010). DNA barcodes such as *rbcL*, *mat*K, *psbA-trnH*, and ITS2 are very efficient in identifying unknown plant species, with *ITS2* being among the best DNA barcodes for species identification and discrimination (Zhao *et al.*, 2018; Chen *et al.*, 2010). Based on BLASTn and the phylogenetic analysis of ITS2 and *rbcL* gene sequences, the *Physalis* accessions used in the current study were all confirmed to belong to the genus *Physalis*.

The results of this study showed that the used barcode regions have different abilities of species discrimination and identification. ITS2 was proposed as a core barcode for seed plants by the Consortium for the Barcode of Life (CBOL) Plant Working Group (China Plant BOL Group, 2011). It was clear that the *Physalis* accessions used in the current study were identified as *P. purpurea* based on ITS2 barcode. The phylogenetic tree was able to discriminate the *Physalis* accessions and had reliable clades with a posterior probability of 80%. Species discrimination based on the *rbcL* gene was not possible as there was no formation of clades on the Bayesian inference phylogenetic tree. The high conservation of the *rbcL* barcode gene in *Physalis* accessions makes it a less ideal candidate for DNA barcoding when compared to other barcode genes such as ITS2 (Ralte and Singh, 2021). The ability of ITS2 to emerge as a better barcode than *rbcL* is clearly supported in other studies on *Physalis* and other plants (Feng *et al.*, 2016; Zhao *et al.*, 2018; Chen *et al.*, 2010).

The *rbcL* barcode gene of *Physalis* accessions under study did not display genetic distance, diversity, or polymorphism. This is an indication that there were no genetic differences between the *Physalis* accessions used. Therefore, the *rbcL* barcode is highly conserved in some species of *Physalis*, which has also been reported in other studies (Xu *et al.*, 2021; Lee *et al.*, 2013). The ITS2 barcode gene exhibited genetic variation among the *Physalis* accessions with a notable nucleotide diversity of 0.27629. This has also been reported in the DNA barcoding and identification of Solanaceae plants (Ralte and Singh, 2021). The genetic distance observed among the *Physalis* accessions in this study based on ITS2 concurs with previous studies where the ITS2 barcode region showed high genetic variation due to its high mutation rate (Tan *et al.*, *et a*

2020). High intraspecies variation was observed based on the ITS2 sequences, supporting the successful identification of *Physalis* accessions using the ITS2 barcode region. The Tajima D value of *Physalis* accessions based on the ITS2 gene was 0.779171, indicating low-frequency mutations and balancing selection within the population (Korneliussen *et al.*, 2013). Three barcode gaps were identified for the ITS2 gene sequences among *Physalis* accessions using the ABGD method. The presence of barcode gaps is crucial for species delimitation and serves as the basis for plant species identification and discrimination (Collins and Cruickshank, 2013).

Commercial interest in plants of the genus *Physalis* has been rising worldwide due to its nutritional value, edible fruits, and the current and potential medicinal uses (Feng et al., 2016). The *Physalis* accessions were investigated for mineral content and the analysis revealed that *P*. purpurea fruits are rich in potassium, sodium, calcium, and magnesium, which concurs with reports from other studies on the wild edible fruits of Physalis (Musinguzi et al., 2007). Based on these findings, this fruit can be used as an alternative to the daily intake of minerals, which are essential for human health. Potassium is important for the function of the cardiovascular system in humans (Sica, 2002). Potassium/sodium balance is fundamental for the transmission of electrical impulses in the heart (Kowey, 2002). Magnesium is an important mineral in protein synthesis, oxidative phosphorylation, the regulation of body temperature and muscle contractions, and it is a cofactor for many enzymes (Jahnen-Dechent and Ketteler, 2012). Calcium is also another important element required for blood clotting, growth, bone formation, cell metabolism, and heart function (Berchtold et al., 2000; Ross et al., 2012). The Physalis fruits also contain trace elements including zinc, iron, copper, nickel, lithium, and manganese. Low levels of iron and nickel in *Physalis* have also been reported in other studies (Erkaya *et al.*, 2012; Musinguzi et al., 2007). Zinc is important in the catalytic activity of enzymes, cellular signaling, and facilitates the modification of the structures of DNA and RNA, proteins, and cellular membranes (Brown et al., 2001). Iron is an essential vitamin that is required in small amounts for DNA synthesis, oxygen transportation, and the electron transport chain (Abbaspour et al., 2014). Copper is also an essential element that is required in small amounts for facilitating lung elasticity, neurovascularization, the metabolism of iron, adequate growth, energy metabolism, reactive oxygen species detoxification, and cardiovascular integrity (Ruiz et al., 2021; National Research Council, 2000). The functions of nickel in animals are not well known

(Genchi *et al.*, 2020). However, in plants and bacteria it is required as a cofactor for the enzymes involved in growth and germination in plants (Genchi *et al.*, 2020). Lithium is an essential element in the physiological regulation of mood (Demling *et al.*, 2001). Manganese is required as a cofactor for enzymes that perform cholesterol, carbohydrate, and protein metabolism (National Research Council, 2001). The presence of minerals in plant accessions can be linked to their medicinal properties as well (Okwu, 2005). Our analyses show the potential of *P. purpurea* as an excellent mineral supplement in nutraceuticals. Though little attention is given to this wild fruit, our findings indicate a richness of nutrients and its potential application as a nutritional supplement.

The *Physalis* accessions were rich in phytochemicals such as phenols, tannins, and flavonoids, which have also been identified in the genus in other previous studies (Sathyadevi and Subramanian, 2015). The levels of these different types of phytochemicals were different in the Physalis accessions, an indication of the existence of different cultivars within P. purpurea. Variation in phytochemical secondary metabolites in plants, such as phenolic acid and flavonoids, have been linked to environmental stress during growth and development (Pant et al., 2021). Ecologically limiting factors like lighting, carbon dioxide, soil salinity, temperature, and soil fertility can affect the biochemical and physiological responses of plants and their secondary metabolite production (Li et al., 2020). Abiotic stressors lead to fluctuations in the chemical constituents of plants, selectively altering the content of secondary metabolites such as phytochemicals (Pant et al., 2021). Soil salinity, an abiotic stressor for plants, has been shown to cause the accumulation of secondary metabolites such as flavonoids in plants as a response to nutritional imbalance, decreased photosynthesis, and the uptake of nutrients (Banerjee and Roychoudhury, 2017). Flavonoid accumulation when plants are under stress due to the increased salinity of soils provides a curative effect for affected plants (Gengmao et al., 2015). The tannin and flavonoid contents were the highest among the phytochemicals identified in the Physalis accessions studied. Previous studies have found that phenols have the highest phytochemical content, followed by tannins, with flavonoids having the lowest content (Kasali et al., 2021; El-Beltagi et al., 2019). The concentration of phenols might have varied in this study as compared to others due to the geographical variations, environmental/abiotic stressors, the method of extraction of phenols, the sugars present, and the carotenoid and ascorbic acid contents (Pant et

al., 2021; Aryal *et al.*, 2019; Oszmiański *et al.*, 2018). The presence of phenols has been associated with antioxidant properties and, therefore, the ability to scavenge for free reactive oxygen species is facilitated by phytochemicals (El-Beltagi *et al.*, 2019; Sahoo *et al.*, 2013). According to the radical scavenging activity assays conducted, the fruit extracts of *Physalis* accessions scavenged free radicals such as DPPH and hydrogen peroxide due to the presence of phytochemicals. Phenolic and flavonoid contents in plants are important for their antioxidant properties, which allow them to scavenge reactive free radicals by donating hydrogen atoms to the free radicals (Amarowicz *et al.*, 2004).

Correlation studies of the polyphenol content and the ability of polyphenols to promote radical scavenging have shown a linear relationship between phenolic and flavonoid contents in relation to radical scavenging capacity (Shrestha and Dhillion, 2006). In this study, the correlation analysis showed a positive correlation between the phenolic content and the DPPH radical scavenging activity. However, a negative correlation was observed for the tannin and flavonoid contents (r = -0.1150) and the DPPH radical scavenging activity. This is an indication that the phenolic content of *P. purpurea* contributed more towards the DPPH radical scavenging activity than tannins and flavonoids. This concurs with similar studies on the role of phenolic content from the genus *Physalis* in DPPH radical scavenging (Karpagasundari and Kulothungan, 2014). Phenol and flavonoid contents showed a moderate correlation to the hydrogen peroxide scavenging capability. This concurs with other studies showing that phenol and flavonoid contents contribute towards hydrogen peroxide scavenging activity (Aryal et al., 2019). The presence of tannins in the Physalis accessions did not show any DPPH radical and hydrogen peroxide scavenging activities. However, tannic acid in other plant studies has been shown to have radical scavenging activity against DPPH radicals and hydrogen peroxide (Karpagasundari and Kulothungan, 2014; Gülçin et al., 2010).

3.5 Conclusions

The *Physalis* accessions used in the current study were identified as *P. purpurea* based on the ITS2 barcode region. The high genetic variation among the *Physalis* accessions based on the ITS2 sequences allowed for the clear identification of *Physalis* species as *P. purpurea*. There was no genetic variation among the *rbcL* sequences of *Physalis*, an indication that the gene is

relatively conserved. The study confirmed that the fruits of *P. purpurea* contained a high content of minerals, including calcium, sodium, magnesium, and potassium. The fruits were also rich in phenolic acids, tannins, and flavonoids, and exhibited antioxidant properties. The phenolic compounds and flavonoids were the major contributors to the radical scavenging activity of the *P. purpurea* fruits. Therefore, the underutilized *P. purpurea* can be used as an excellent source of antioxidants for the management of oxidative stress-induced human diseases.

CHAPTER FOUR

4.0 Molecular identification, genetic diversity and secondary structure predictions of *Physalis* species using ITS2 DNA barcoding

4.1 Introduction

The genus *Physalis* are well-known herbaceous plants which belong to the *Solanaceae* family. *Physalis* is native to the Andes of South America which includes countries such as Colombia, Peru and Ecuador (Simbaqueba *et al.*, 2011). The genus has several species that grow in the wild with only a few species under cultivation as food crops and ornamentals (Khan and Bakht, 2015). *Physalis* plant was initially consumed largely by the Inca people but later introduced to Africa and India after the entry of Christopher Colombus into the Americas (Popenoe *et al.*, 1990). *Physalis* species including *P. peruviana*, *P. alkengi*, *P. purpurea*, *P. pubescens* and *P. philadelphica* are widely cultivated worldwide for their nutritional, medicinal and economic value (Shenstone *et al.*, 2020; Yen *et al.*, 2010). These plants are rich in both nutrients (provitamin A, vitamins C, vitamin B complex, phosphorus and fiber) and phytochemicals such as phytosterols, polyphenols, saponins, peruvises, fisalins and withanolides (Petkova *et al.*, 2021; Golubkina *et al.*, 2018). Economic interest in *Physalis* fruits has been steadily increasing over the years with countries in South East Asia and others such as Colombia, Egypt, Kenya, Zimbabwe and South Africa being major exporters (Novoa *et al.*, 2006).

Precise identification of *Physalis* species in order to ensure safe utilization especially for medicinal applications - like in any other medicinal plants - is paramount to prevent improper use (Shinwari *et al.*, 2018). It is also important for the maintenance and conservation of *Physalis* genetic resources since most natural *Physalis* species are being destroyed and cleared to pave the way for alternative land use as well as urbanization (Feng *et al.*, 2016). This could lead to the loss/extinction of important species. The use of morphological identification of *Physalis* species is unreliable due to phenotypic similarities among the different species (Menzel, 1951). For example, *P. minima* are morphologically confused for *P. angulata* or *P. pubescens* due to similar phenotypic characters (Feng *et al.*, 2016). Moreover, morphological characters are affected by environmental and developmental factors resulting in inaccurate identification of species

(Buckley *et al.*, 1997). Molecular characterization using DNA markers such as simple sequence repeats (SSR) and random amplified microsatellites (RAM) have been used to comprehensively show genetic variability among genotypes (Muraguri *et al.*, 2021; Chacón *et al.*, 2016; Simbaqueba *et al.*, 2011). However, these approaches do not provide sufficient discriminating capacity for classifying the *Physalis* genotypes into different species. A simple and accurate method is necessary for foolproof identification and determination of genetic relationships between the different cultivars of *Physalis* species.

DNA barcoding is a reliable tool of choice for studying genetic relationships between plants for species identification and delineation. It uses short and standardized DNA sequences that exhibit a sufficient level of variation to discriminate among species (Barcaccia *et al.*, 2015; Hebert *et al.*, 2003). The chloroplast-plastid region DNA sequences (such as *matK*, *rbcL*, *psbA-trnH*, *ycf*) and a nuclear internal transcriber spacer (ITS) region with less interspecific barcode gaps have been proposed as potential plant barcodes (Elansary *et al.*, 2017). The ITS2 is a DNA spacer localized between the ribosomal 5.8S and 28S, in the chromosomal or corresponding polycistronic transcript region most commonly used for species discrimination studies (Lahaye *et al.*, 2008). DNA barcode, ITS2 has been proposed as an efficient barcode in the identification of medicinal plants (Chen *et al.*, 2010). It has been utilized in *Physalis* identification where it showed efficient species discrimination in comparison to chloroplast DNA barcodes due to its advantages such as small fragment length, good universality, high interspecific divergence and small intraspecific variation (Yao *et al.*, 2010). A study done on the identification of *Physalis* species using ITS2 in China showed that the barcode is effective in species identification (Feng *et al.*, 2016). ITS2 has also been used to identify *P. angulata* among *Solanaceae* plants (Ralte and Singh, 2021).

To date, there have been no reports on the identification of *Physalis* species both in the wild and those cultivated in Kenya. Molecular characterization using simple sequence repeat (SSR) markers made the assumption that only *P. peruviana* is present in Kenya (Muraguri *et al.*, 2021). The present study was therefore aimed at identifying and clarifying the phylogenetic relationships of *Physalis* species in Kenya using the sequence and structural information of ITS2 barcode gene. The ITS2 barcode-anchored species delimitation would be useful for genetic resource conservation as well as augmenting future breeding programs.

4.2 Materials and methods

4.2.1 Plant material and sample collection

Leaves of *Physalis* plants were randomly collected from eight Counties in Kenya namely Nyamira, Kiambu, Nakuru, Kajiado, Nyeri, Homa Bay, Elgeyo-Marakwet and Kericho (Figure 4.1 and Table 4.1). The samples were collected from April to June, 2019. The eight counties were selected based on the presence of *Physalis* germplasm. Geographical coordinates of locations and the number of *Physalis* plants sampled are presented in Table 4.1. Leaves were sampled in triplicates from 68 *Physalis* accessions (Appendix 1 A) based on availability as all plants were collected from the wild except for the samples from Elgeyo-Marakwet County which were collected from a *Physalis* plant farmer. The collection of *Physalis* leaf samples and storage in preparation for genomic DNA extraction was done as described in section 3.2.1.



Figure 4.1. Locations from the eight counties in Kenya where *Physalis* plants were sampled.

Table 4.1. Geographical coordinates and number of *Physalis* samples collected from each of the selected eight Counties in Kenya

No.	Main	Specific Location	Latitude	Longitudes	Number of leaf
	Location				samples
	(County)				collected
1.	Kericho	Londiani, Sorget	0.0684° S	35.5548° E	10
2.	Elgeyo-	Chebororwa	0.9487° N	35.4234° E	13
	Marakwet				
3.	Homa Bay	Ndhiwa	0.7299° S	34.3671° E	3
4.	Nyeri	Mukurweini	0.5609° S	37.0488° E	5
5.	Kajiado	Ongata Rongai	1.3939° S	36.7442° E	5
6.	Nakuru	Gilgil market	0.4923° S	36.3173° E	1
7.	Kiambu	Tigoni	1.1651° S	36.7065° E	17
		Thika	1.0388° S	37.0834° E	9
		Nyathuna	1.1859° S	36.6782° E	1
		Muguga	1.2551° S	36.6580° E	1
8.	Nyamira	Magwagwa	0.4830° S	35.0222° E	3

4.2.2 Molecular authentication of *Physalis* plants

4.2.2.1 Genomic DNA extraction

Physalis accessions genomic DNA extraction, purification, viewing and storage was carried out as described in section 3.2.2.1.

4.2.2.2 PCR amplification and sequencing

Polymerase chain reaction (PCR) amplification for internal transcribed spacer (ITS) of nuclear ribosomal DNA of *Physalis* accessions was performed using ITS2 primer. PCR amplification, purification of PCR products and sequencing was performed as described in section 3.2.2.2.

4.2.2.3 Sequence and Phylogenetic analysis

The ITS2 sequences achieved were manually curated using BioEdit version 7.0.5.3 software (Hall, 1999). Analysis of sequences in relation to curation of sequences, BLASTn analysis and preparation of multiple sequence alignments was performed as described in section 3.2.2.3. The two MSA prepared were for phylogenetic analysis and genetic diversity studies of *Physalis* based on ITS2 marker only. The first MSA was performed using the ITS2 sequences of 34 *Physalis* accessions from this study and seven *Physalis* ITS2 reference sequences (AY665886.1, MH763728.1, AY665905.1, AY665914.1, AY665903.1, AY665868.1 and MH763740.1) from NCBI database while the second was prepared using the ITS2 sequences of the 34 *Physalis* accessions only. The first MSA was used for phylogenetic analysis of *Physalis* accessions based on ITS2 marker while the second was utilized for the determination of genetic diversity, distance, polymorphism, neutrality and barcoding gap analysis of *Physalis* accessions based on ITS2 marker. A phylogenetic tree was prepared using the Bayesian inference method by MrBayes software version 3.2.7a (https://nbisweden.github.io/MrBayes/) as described in section 3.2.2.3 on 13th February 2023.

4.2.3 ITS2 secondary structure predictions

The RNA secondary structure predictions of the identified *Physalis* species were performed using the nucleotide sequences based on three species identified from the MrBayes phylogenetic tree, using rRNA database of *RNAfold* WebServer v2.4.18 (<u>http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi</u>) (Lorenz *et al.*, 2011; Gruber *et al.*, 2008; Mathews *et al.*, 2004). The secondary structures of the representative *Physalis* accessions used in the current study were generated. RNA secondary structures were predicated based on the minimum free energy prediction method.

4.2.4 DNA divergence between and within *Physalis* accession populations

DNA divergence between and within *Physalis* species identified from the MrBayes phylogenetic tree based on ITS2 sequences was determined using the DnaSP software version 6.12.03 (Kartavtsev *et al.*, 2011). The 34 ITS2 *Physalis* sequences were used to create a multiple sequence alignment (MSA). This MSA was uploaded and trimmed using Jalview software

version 2.11.2.0 to ensure uniform sequence lengths. The trimmed MSA was then used for DNA polymorphism analysis as described by Troshin *et al.* (2018, 2011). The edited MSA was then fed into the DnaSP software to assess divergence within and between *Physalis* species accessions.

DNA divergence between the three *Physalis* species identified was based on the analysis of nucleotide diversity (Pi), average nucleotide substitution per site between populations (Dxy) and number of nucleotide substitutions per site between populations (Da) as outlined by Jukes and Cantor algorithm on DnaSP. DNA divergence within each of the three *Physalis* species based on ITS2 gene was performed as described in section 3.2.3.

4.2.5 Determination of genetic distance between and within *Physalis* accessions

The interspecific, intraspecific and overall mean genetic distance of 34 *Physalis* accessions was calculated based on the ITS2 sequences using Kimura 2 parameter (K2P) with gamma distribution and a gamma parameter of 0.27 on the MEGA version 11 software (Kumar *et al.*, 2018). The MSA used in the genetic diversity analysis was uploaded into the MEGA 11.0 software and grouping of ITS2 *Physalis* sequences into the 3 identified species was performed. Genetic distance was then calculated between and within grouped species based on K2P model.

4.2.6 Determination of DNA polymorphism

Sequence polymorphism of the ITS2 sequences was determined for all the 34 *Physalis* accessions through the use of DNA Sequence Polymorphism (DnaSP) software and analysis performed according to the parameters described in section 3.2.5.

4.2.7 Tajima's neutrality test

Tajima's neutrality test was performed using MEGA 11.0 software (Tamura *et al.*, 2021). This test helped to determine the frequency of mutations and selection among the 34 *Physalis* accessions based on ITS2 sequences studied as described by Tajima *et al.*, (1989). All ambiguous positions were removed for each sequence pair (pairwise deletion option).

4.2.8 DNA barcoding gap analysis

The ITS2 MSA for the 34 *Physalis* sequences were uploaded to ABGD website (<u>https://bioinfo.mnhn.fr/abi/public/abgd/abgdweb.html</u> accessed on 17 February 2023) and distance analysis performed based on K80 Kimura measure of distance described in section 3.2.7.

4.3 Results

4.3.1 Amplification and sequencing success rate

The success rate of PCR amplification calculated as the percentage of samples expected band size in three attempts was 75% (Table 4.2 and Appendix 1 B). Some of the images of the *Physalis* accessions amplicons are represented in Figure 3.2., 4.2. and 4.3. Sequence recovery success rate of the ITS region was 67%. The lengths of the ITS2 sequences generated from *Physalis* accessions were in the range of 237 - 707 bp, with an average of 523 bp. The mean GC content was 61%, with a range of 55.1 - 66.9% (Table 4.2). All the sequences generated from the amplification of ITS2 barcode were successfully deposited into the GenBank database (Table 4.3).

Table 4.2. Efficiency of PCR amplification and sequencing for *Physalis* accessions based on

 ITS2 DNA barcode region.

Barcode Region	Samples Tested (n)	Number of Amplicons Produced	Number of Sequences Produced	Amplification Efficiency (%)	Sequencing Efficiency (%)	Alignment Length (bp)	Mean Sequence Length (bp)	GC Content (%)
ITS2	68	51	34	75	67	707	523	61

		hb2i	hb3i	norli	gmi	elini	e2ini	e3ini	e4ini	e5ini	eđini	e7ini
1000												
1000	Ξ	-										
200	Ξ											

Figure 4.2. PCR amplicons for ITS2 sequences of *Physalis* accessions from Homabay (hb2i and hb3i) Kajiado (nor1i), Nakuru (gmi) and Elgeyo-Marakwet counties (e1-e7ini).

The letter L in Figure 4.2 above represents the DNA ladder, hb2i-e7ini represents the *Physalis* accessions amplicons based on ITS2 sequence amplification.



Figure 4.3. PCR amplicons for ITS2 sequences of *Physalis* accessions from Kajiado (nor4i and nor5i), Elgeyo-Marakwet (c2i and c5i), Baringo (mmi), Nyeri (ny4i) and Nyamira (mw3i) counties.

The letter L in Figure 4.3 above represents the DNA ladder, nor4i-mw3i represents the *Physalis* accessions amplicons based on ITS2 sequence amplification.

4.3.2 Identification using BLASTn analysis

The ITS2 sequence of each sample was used to perform BLASTn analysis independently in order to retrieve top hits available in the database and filtered by pairwise identity. The BLASTn analysis results for the 34 *Physalis* accessions revealed that all sequences generated were of the targeted loci. BLASTn analysis of ITS2 sequences from this study identified all the 34 (100%) *Physalis* accession as *Physalis* species. The highest similarity recorded for the 34 ITS2 sequences was 99.37% for *P. peruviana* (AY665914.1) (Table 4.3). Based on ITS2 sequences, 23, 4, 3 and 2 accessions were found to be related to *P. purpurea*, *P. cordata*, *P. peruviana* and *P. aff. Philadelphica*, respectively. Additionally, one sample each was found to be related to *P. minimaculata* and *P. microcarpa* (Table 4.3).
	Sample ID	Species of Best BLAST match	GenBank accession number (of database)	Max score	E value	Percent identity (%)	Percent coverage (%)	GenBank accession number
1	Chebororwa C2iF	P. purpurea	MH763740.1	972	0.0	94.70	91	OQ371996.1
2	Chebororwa e2iniF	P. purpurea	MH763740.1	418	4e-112	89.86	82	OQ371999.1
3	Chebororwa e3iniF	P. purpurea	MH763740.1	963	0.0	94.26	91	OQ372000.1
4	Chebororwa e5iniF	P. purpurea	MH763740.1	760	0.0	89.35	87	OQ372002.1
5	Chebororwa e6iniF	P. purpurea	MH763740.1	937	0.0	93.75	93	OQ372003.1
6	Chebororwa e7iniF	P. purpurea	MH763740.1	965	0.0	94.27	90	OQ372004.1
7	Gilgil gmi	P. purpurea	MH763740.1	161	5e-35	81.98	70	OQ372005.1
8	Muguga DMiF	P. purpurea	MH763740.1	880	0.0	93.83	97	OQ372007.1
9	Mukurweini ny5iF	P. peruviana	AY665914.1	355	4e-93	88.82	54	OQ372008.1
10	Ndhiwa hb2iF	P. purpurea	MH763740.1	965	0.0	94.28	92	OQ372009.1
11	Ongata Rongai nor1iF	P. purpurea	MH763740.1	966	0.0	94.28	92	OQ372011.1
12	Ongata Rongai nor4iF	P. purpurea	MH763740.1	955	0.0	94.09	92	OQ372013.1
13	Ongata Rongai nor5iF	P. purpurea	MH763740.1	959	0.0	94.51	90	OQ372014.1
14	Tigoni T2iF	P. purpurea	MH763740.1	577	7e-160	91.79	95	OQ372017.1
15	Tigoni T9iF	P. purpurea	MH763740.1	750	0.0	92.22	96	OQ372019.1
16	Tigoni T11iF	P. purpurea	MH763740.1	150	9e-32	84.85	62	OQ372020.1
17	Londiani 2i	P. purpurea	MH763740.1	686	0.0	92.98	100	OQ372021.1
18	Londiani 3i	P. purpurea	MH763740.1	896	0.0	94.06	97	OQ372022.1

Table 4.3. BLASTn analysis results for the *Physalis* accessions based on ITS2 barcode gene.

19	Londiani 5i	P. purpurea	MH763740.1	948	0.0	94.45	93	OQ372024.1
20	Londiani 7i	P. purpurea	MH763740.1	540	1e-148	86.00	98	OQ372026.1
21	Londiani 8i	P. purpurea	MH763740.1	885	0.0	93.07	94	OQ372027.1
22	Londiani 9i	P. purpurea	MH763740.1	758	0.0	88.96	100	OQ372028.1
23	Londiani 10i	P. purpurea	MH763740.1	747	0.0	90.16	99	OQ372029.1
24	Chebororwa	P. cordata	AY665886.1	451	5e-122	87.78	81	OQ371997.1
	C5iF							
25	Chebororwa	P. cordata	MH763728.1	316	1e-81	82.24	95	OQ371998.1
	e1iniF							
26	Chebororwa	P. cordata	AY665886.1	407	1e-108	86.06	73	OQ372001.1
	e4iniF							
27	Ongata Rongai	P. cordata	AY665886.1	300	2e-76	82.00	86	OQ372012.1
	nor3iF							
28	Thika TK8iF	<i>P</i> .	AY665905.1	355	2e-93	88.51	94	OQ372015.1
		minimaculata						
29	Thika TK9iF	P. peruviana	AY665914.1	163	1e-35	80.36	80	OQ372016.1
30	Magwagwa	P. peruviana	AY665914.1	1147	0.0	99.37	92	OQ372006.1
	mw3iF							
31	Londiani 4i	P. peruviana	AY665914.1	1044	0.0	97.41	91	OQ372023.1
32	Tigoni T4iF	P.microcarpa	AY665903.1	250	1e-61	86.78	81	OQ372018.1
33	Londiani 6i	P. aff.	AY665868.1	425	2e-144	91.35	100	OQ372025.1
		philadelphica						
34	Nyathuna NKiF	P. aff.	AY665868.1	374	7e-99	90.00	91	OQ372010.1
		philadelphica						

4.3.3 Multiple sequence alignment

Delimited ITS2 sequences were used for MSA preparation (Appendix 2B and Figure 4.4). The MSA of the curated 34 ITS2 Physalis sequences and their seven reference sequences retrieved from BLASTn analysis had a sequence length of 707 bp. The MSA was compressed using **ESPript** 3 (http://espript.ibcp.fr) and is indicated in Appendix $2\mathbf{B}$ (https://espript.ibcp.fr/ESPript/temp/1101891838/0-0-1680467018-esp.pdf accessed on 17th February 2023). This alignment had a high rate of nucleotide substitutions among and between *Physalis* species studied. The substitution mutations entailed both transition and transversion point mutations. The MSA of only the 34 ITS2 Physalis sequences, prepared by MUSCLE, trimmed and viewed by Jalview had a sequence length of 533 bp. It was compressed using ESPript and is indicated in Figure 4.4 (https://espript.ibcp.fr/ESPript/temp/1035513530/0-0-1688384112-esp.pdf accessed on 17th February 2023). The latter MSA also showed substitution mutations of the transition type between species. For example, at position 116 of the alignment, most P. purpurea have an adenine nucleotide while the P. cordata and P. peruviana have a guanine nucleotide. The substitution at position 116 of the MSA indicates a transition mutation between species. On the other hand, at positions 130 and 138 of the MSA, all P. cordata have an adenine nucleotide while P. purpurea and P. peruviana species have a guanine at this position (Figure 4.4). This is an indication of transition mutations between species. An insertion mutation of 6 nucleotides is noted between nucleotide 89 and 90.

	1	10	20	30	40	50	60	70
OQ372005.1	AACAG	CTGCTGGG	TCGGGCGTACT	AAGTGCCGGA	AGGGCT <mark>G</mark> GCA <mark>G</mark>	CCGACCGGGCCA	GGGTTCGGC	CACGGCAC.
00372026.1	СТ	GG <mark>G</mark> TC <mark>G</mark> GG	Т <mark>С</mark> G <mark>С</mark> Т	AAGCGCCGGA	AGGGTCTGTCAG	CCGACACGGGCCAA	AGGGTCGGC	CACCGCCCG
00372023.1		. GGTCGGG	T <mark>C</mark> GG	. AGCGGCCG	GAGGGTCTGTCAG	CCGGCACGGGCGAC	GGGTTCGGC	CACGGCACG
0Q372027.1			AGTT	A <mark>AGCG</mark> CCGG	AGGTTCAGTCAG	CCGACACGGGCCAC	GGGTTCGGC	CACGGCACG
OQ372029.1	TACCC	CTGCTGGG	T C G C G T C G A C T	AAGCGCCGGA	AGGTTCAGTCAG	CCGACACGGGCCAC	GGGTTCGGC	CACGGCACG
0Q372020.1	GGTCA	TTGTCGAA	C C T G C T A A G <mark>C</mark> A	GAGCGACCC	CAAACCCGTTGA	ACATGGGAA	GGCTTCGCT	CGCICC
OQ372008.1	CG	CCCATGTG	A C C T G C G A G C A	G <mark>AGCG</mark> ACCC	GCGAACCTGTTTG	A A C A C C G G G G A G	G	G <mark>C</mark> G <mark>C</mark> T
0Q372016.1	GGTCA	TTGTCGAA	C <mark>C</mark> TGC.AAG <mark>C</mark> A	G <mark>AGCG</mark> ACCC	GCGAACCTGTTTG	AACACCGGGGAG	GCGTTCTT	CCCCCCCC
0Q371999.1								
0Q372006.1	GATCA	TTGTCGAA	C <mark>C</mark> TGC.AAG <mark>C</mark> A	G <mark>AGCG</mark> ACCC	GCGAACCTGTTTG	AACACCGGGGAG	GCGTTGGCT	CGCCTCCCC
0Q372018.1	AGTCA	TTGTCGAA	CCTGCTAAG <mark>C</mark> A	G <mark>AGCG</mark> ACCC	GCAAACCCGTTTG	AACACCGGGAAG	GCGTTCGCT	CGCCTCCCG
0Q372010.1					A T T C C G T G C G			
0Q372015.1	AGTCA	TTGTCGAA	CCTGCTAAGCA	GAGCGACCC	GC.AACCTGTTTG	AACACCGGGAAG	GCGTTCGCT	CCCCTCCCG
0Q372002.1	GGGTA	TGGTTTAA	CCGGCGAAGCA	GAGAGACAC	GCACACCCGTTTG	AACACCGGGAAG	GCGITCGCI	CCCCTCCCG
0Q372028.1	.GTCA	TTGTCGAA	C <mark>C</mark> TGCTAAG <mark>C</mark> A	GAGCGACCCG	GCAAACCCGTTTG	AACACTGGGAAG	GCGITCGCI	CCCCCCCCC
0Q371996.1	GGTCA	TTGTCGAA	C <mark>C</mark> TGCTAAG <mark>C</mark> A	GAGCGACCCG	GC.AACCCGTTTG	AACACCGGGAAG	GCGTTCGCT	CCCCCCCCC
00372019.1	GGTCA	TTGTCGAA	CCTGCTAAGCA	G <mark>AGCG</mark> ACCC	GCAAACCCGTTTG	AACACCGGGAAG	GCGTTCGCT	CCCCTCCCG
00372013.1	GATCA	TTGTCGAA	CCTGCTAAGCA	GAGCGACCCC	GCAAACCCGTTTG	AACACCGGGAAG	GCGTTCGCT	CCCCCCCCC
00372017.1	GGTCA	TTGTCGAA	CCTGCTAAGCA	G <mark>AGCG</mark> ACCC	GCAAACCCGTTTG	AACACCGGGAAG	GCGIICGCI	CGCCTCCCG
00372021.1							CGCI	CCCCTCCCG
0Q372025.1	GGTCA	TTGTCGAA	CCTGCTAAGCA	GAGCGACCCG	GCAAACCCGTTTG	AACACCGGGAAG	GCGITCGCI	CCCCTCCCG
00372014.1	GATCA	TTGTCGAA	CCTGCTAAGCA	GAGCGACCC	GCAAACCCGTTTG	AACACCGGGAAG	GCGITCGCI	CGCCTCCCG
00372022.1		· · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · ·	GCAAACCCGTTTG	AACACCGGGAAG	GCGIICGCI	CGCCTCCCG
00372011.1	GGTCA	TTGTCGAA	CCTGCTAAGCA	GAGCGACCCG	GCAAACCCGTTTG	AACACTGGGAAG	GCGTTCGCT	CGCCTCCCG
00372000.1	GGTCA	TTGTCGAA	CCTGCTAAGCA	GAGCGACCCG	GCAAACCCGTTTG	AACACTGGGAAG	GCGTTCGCT	CGCCTCCCG
00372004.1	GGTCA	TTGTCGAA	CCTGCTAGGCA	GAGCGACCCC	GCAAACCCGTTTG	. AACACCGGGAAG	GCGTTCGCT	
00372007.1	GGTCA	TTGTCGAA	CCTGCTAAGCA	GAGCGACCCC	GCAAACCCCGTTTG	. AACACCGGGAAG	GCGIICGCI	CGCCTCCCG
00372009.1	.GTCA	TTGTCGAA	CCTGCTAAGCA	GAGCGACCCC	CAAACCCCGTTIG	. AACACCGGGAAG	GCGTTCGCT	
00372024.1	GGTCA	TTGTCGAA	CCTGCTAAGCA	GAGCGACCCC	GCAAACCCGTTTG	AACACCGGGAAG	GCGTTCGCT	
00372003.1	.GTCA	TTGTCGAA	CCTGCTAAGCA	GAGCGACCCG	GCAAACCCGTTTG		GCGTTCGCT	CCCCTCCCC
00371998.1			• • • • • • • • • • •	· · · · · · · · · · ·		ACGICCCAGGCTAA	G	
00372012.1			· · · · · · · · · · · · · · ·		ACGITAA		GIACGUCAC	
00372001.1	•••••	TACAGGC	TITCITGGAGG	GAGIGI	ACACGTTCA	I AGGGACAGGGAGG	ACAGIGACO	I G G A G C G A C
00311331.1	CA	IAGACGG.	AGA	A A G C G A C G G G	3	A A C C C G G A G G A T	AU	

	8 Q	90	100 11	0 120	130
00372005.1	.,TGAGATCACCACCAC	, TGCC, GTGA	CGTCCGTCGACCT	TAGGCCACAGCAGCGA	TGGCCACGAA
00372026.1	TT.GAGATTCAACCACCAC	. TGCC. GTGA	CGTCCGTCGACCA	TTTAGGCCAACCACCA	GCCGCCCAACGGAAA.
00372023.1	TT.GAGATTCAACCACCAC	. T <mark>GC</mark> C. GTGA	CGTCCGTCGACCA	TTTAGGCCAGCCGCGC	GCTGCGCACGGGAG
0Q372027.1	TT.GAGATTCAACCACCAC	. TGCC. GTGA	CGTCCGTCGACCA	TTTAGGCCAACCACGA	GCCGCGCACGGAAG
0Q372029.1	TT.GAGATTCAACCACCAC	. TGCC. GTGA	CGTCCGTCGACCA	TTTAGGCCAACCACGA	GCCGCGCACGGAAG
00372020.1			CGCTCGTCGGC.		
OQ372008.1	TTGGTCCCTCGTCGGCGGCGGTC	GCGCGGGCGG	CGCCGGTCGCT	AACAACCCCGGCGCGG	A.CGCGCCTAGGA.TA
00372016.1	TCCCCCGGGCGGCGGTCGCGT	GTCCC.GT	CGCCAGTACAATC	CCCAACCCCGGAGCGG	ACCTCGCCAACTAATA
0Q371999.1			.GTCCTACGA	. TAAGACCCG CAG	AACGCCCAAGGAACT.
0Q372006.1	C C T G T C G G C C G G C G G T C G C G	GCGCG.GT	CGCCGGTCGACTA	ACGAACCCCGGCGCGG	AACGCGCCAAGGAATA
OQ372018.1	CTCGTCGGCCAGCAGCCGCACGT	GCGCG.GT	CGCCTAGCGACTA	ACGAACCCCGGCACGA	AACGCGCCAAGGAATA
OQ372010.1		GCGCG.GT	CGCCTAGCGACTA	ATGAACCCCGGCACGA	AACGCGCCAAGGAATA
OQ372015.1	CTCGTCGGCCAGCAGCCGCACGT	GCGCG.GT	CGCCTAGCGACTA	ACGAACCCCGGCACGA	AACGCGCCAAGGAATA
OQ372002.1	CTCGTCAGCCAGCAGCCGCACGT	GCGCG.GT	CGCCTAGCGACTA	A. GAACCCCGGCACGA	AACGCGCCAAGGAATA
0Q372028.1	CTCGTCGGCCAGCAGCCGCACGT	GCGCG.GT	CGCCTAGCGACTA	ATGAACCCCGGCACGA	AACGCGCCAAGGAATA
0Q371996.1	C T C G T C G G C C A G C A G C C G C A C G T	GCGCG.GT	CGCCTAGCGACTA	ACGAACCCCGGCACGA	AACGCGCCAAGGAATA
OQ372019.1	CTCGTCGGCCAGCAGCCGCACGT	GCGCG.GT	CGCCTAGCGACTA	ACGAACCCCGGCACGA	AACGCGCCAAGGAATA
OQ372013.1	CTCGTCGGCCAGCAGCCGCACGT	GCGCG.GT	CGCCTAGCGACTA	ACGAACCCCGGCACGA	AACGCGCCAAGGAATA
OQ372017.1	CTCGTCGGCCAGCAGCCGCACGT	GC <mark>GC</mark> G.GT	CGCCTAGCGACTA	ACGAACCCCGGCACGA	AACGCGCCAAGGAATA
0Q372021.1	CTCGTCGGCCAGCAGCCGCACGT	GC <mark>GC</mark> G.GT	CGCCTAGCGACTA	ACGAACCCCGGCACGA	AACGCGCCAAGGAATA
0Q372025.1	C T C G T C G G C C A G C A G C C G C A C G T	GC <mark>GC</mark> G.GT	CGCCTAGCGACTA	ACGAACCCCGGCACGA	AACGCGCCAAGGAATA
OQ372014.1	CTCGTCGGCCAGCAGCCGCACGT	GCGCG.GT	CGCCTAGCGACTA	ACGAACCCCGGCACGA	AACGCGCCAAGGAATA
0Q372022.1	CTCGTCGGCCAGCAGCCGCACGT	GC <mark>GC</mark> G.GT	CGCCTAGCGACTA	ACGAACCCCGGCACGA	AACGCGCCAAGGAATA
00372011.1	CTCGTCGGCCAGCAGCCGCACGT	GC <mark>GC</mark> G.GT	CGCCTAGCGACTA	ATGAACCCCGGCACGA	AACGCGCCAAGGAATA
0Q372000.1	CTCGTCGGCCAGCAGCCGCACGT	GC <mark>GC</mark> G.GT	CGCCTAGCGACTA	ATGAACCCCGGCACGA	AACGCGCCAAGGAATA
0Q372004.1	CTCGTCGGCCAGCAGCCGCACGT	GC <mark>GC</mark> G.GT	CGCCTAGCGACTA	ACGAACCCCGGCACGA	AACGCGCCAAGGAATA
0Q372007.1	CTCGTCGGCCAGCAGCCGCACGT	GC <mark>GC</mark> G.GT	CGCCTAGCGACTA	ACGAACCCCGGCACGA	AACGCGCCAAGGAATA
OQ372009.1	CTCGTCGGCCAGCAGCCGCACGT	GC <mark>GC</mark> G.GT	CGCCTAGCGACTA	ACGAACCCCGGCACGA	AACGCGCCAAGGAATA
0Q372024.1	CTCGTCGGCCAGCAGCCGCACGT	GC <mark>GC</mark> G.GT	CGCCTAGCGACTA	ATGAACCCCGGCACGA	AACGCGCCAAGGAATA
0Q372003.1	CTCGTCGGCCAGCAGCCGCACGT	GCGCG.GT	CGCCTAGCGACTA	ATGAACCCCGGCACGA	AACGCGCCAAGGAATA
0Q371998.1	· · · · · · · · · · · · · · · · · · ·			ACCGCAG	AACG.GCCAGGAAAT.
0Q372012.1	· • • • • • • • • • • • • • • • • • • •	GTGC	I G C I T T C C G G G C A	C. GACCCGG CCG	AACG.GCCAGAAACT.
0Q372001.1	GACGTTACACGAAAGCCTCCGT.	. TGCC. ACAG	CGACTTGCGTTCT	AAGAACCCGCAG	AACGCCCAAAAAACT.
0Q371997.1	TGGTCCGTTGTCGCCGCG	ACACC.GTTG	<u>CGTT</u> C <mark>CGAC</mark> CT	ACGAACCCGGCCG	AACGCGCAAGAACATA

		140	150	160	170	180	
00372005.1		. GCATACCGTC	CGCACT	CCCCGGTGCGCGAGGC	GGAGCGATC	TTATGC	
00372026.1		AGTTTCCCTCC	CGCACCACC.	. C C C G G T <mark>G</mark> C G C G A G G G	GG. GCGATG	CCATGCGTGG7	IGCCCA
0Q372023.1	<mark>G</mark> CC	AGTATCCGTCC	CGCGCC	. C C G C G C G C G C G C G C G C G C G	GG. GCGACG	CGATGCGTGA	GCCCA
0Q372027.1	GCC	AGTATCCGTCC	CGCAACGCG	. C C G C G G T <mark>G</mark> C G C G A G G G	GG. GCGATG	CGATGCGTGA7	GCCCA
OQ372029.1	GCC	TGTATCCGTCC	CGCAACGCG.	. C C G C G G T <mark>G</mark> C G C G A G G G	GG. GCGATG	CGATGCGTGA	GCCCA
0Q372020.1			CGCGCCGCCC	GTGGCGGT <mark>G</mark> CCTGCGA.		CTACG	A A C C C G
OQ372008.1	CTTAACC <mark>GA</mark> .	. GGCCCGCCCT	CGCGCCCCCC	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GGAG.TGCG	CCTCGCTTGA	ACAAAACGATC
OQ372016.1	CTTTGG. <mark>GA</mark> C	TGCCCCCCCC	C.CTCCCCG	GCCTCGTT <mark>G</mark> CGCGCGGT	GTAGCTGCG	ΤΤ	
0Q371999.1	GAC	GGGGCACCCC	CGCGCCTGT	.CCCGGGT <mark>G</mark> CCGGG	GA CIG	GTTCGCTGAA	CACAAAGAC
OQ372006.1	CTTAACC <mark>GA</mark> C	GGCCCGCCCCT	CGCGCCCCCC	cccccccccccccccccccccccccccccccccccccc	GGAGCTGCG	CCTCGCTIGA	ACACGACGAC
OQ372018.1	CTCGACC <mark>GA</mark> T	TGCACCCCCT	CGCGCCTTG	TCAC.AC <mark>G</mark> TGCGCTGG	GGAGCTGCC	CTTCGCTTGA	CACCC
0Q372010.1	CTCGACC <mark>GA</mark> T	GGCACACCCCT	CGCGCCTCG	CCACTGC <mark>G</mark> TGCGCGGG	GGAGCTGTG	CTTCGCTTGA	ACACA.ATGAC
0Q372015.1	CTCGACC <mark>GA</mark> T	GGCACACCCCT	CGCGCCTCG	CCACTGC <mark>G</mark> TGCGCGGG	GGAGCTGTG	CTTCGCTTGA	ACACAAATGAC
0Q372002.1	CTCGACC <mark>GA</mark> T	GGCACACCCCT	CGCGCCTCG	CCACTGC <mark>G</mark> TGCGCGGG	GGAGCTGTG	CTTCGCTTGA	ACACAAATGAC
0Q372028.1	CTCGACC <mark>GA</mark> T	GGCACACCCCT	CGCGCCTCG:	CCACTGC <mark>G</mark> TGCGCGGG	GGAGCTGTG	CTTCGCTTGA	ACACAAATGAC
0Q371996.1	CTCGACC <mark>GA</mark> T	GGCACACCCCT	CGCGCCTCG:	ICCACGGC <mark>G</mark> IGCGCGGG	GGAGCTGTG	ATTCGCTTGA	ACACAAATGAC
00372019.1	CTCGACC <mark>GA</mark> T	GGCACACCCCT	CGCGCCTCG	CCACTGC <mark>G</mark> TGCGCGGG	GGAGCTGTG	CTTCGCTTGA	ACACAAATGAC
0Q372013.1	CTCGACCGAT	GGCACACCCCT	CGCGCCTCG:	I C C A C G G C G T G C G C G G G	GGAGCTGTG	ATTCGCTTGA	ACACAAATGAC
00372017.1	CTCGACCGAT	GGCACACCCCT	CGCGCCTCG	I C C A C G G C G T G C G C G G G	GGAGCTGIG	CTTCGCTTGA	ACACAAATGAC
00372021.1	CTCGACCGAT	GGCACACCCCT	CGCGCCTCG.	TCCCGGCGTGCGCGGG	GG.ACTGIG	TT.CGCTTGAA	ACACAAATGA.
00372025.1	CTCGACCGAT	GGCACACCCCT	CGCGCCTCG.	I C CACGG C G T G C G C G G G	GGAGCTGTG	CTTCGCTTGA	ACACAAATGAC
00372014.1	CTCGACCGAT	GGCACACCCCT	CGCGCCTCG.	IC CACGG C <mark>G</mark> TG C G C G G G	GGAGCTGTG	CTTCGCTTGA	AACACAAATGAC
00372022.1	CTCGACCGAT	GGCACACCCCT	CGCGCCTCG.		GGAGCTGTG	CTTCGCTTGA	ACACAAATGAC
00372011.1	CTCGACCGAT	GGCACACCCCT			GGAGCTGTG	CTTCGCTTGA	ACACAAATGAC
00372000.1	CIUGACUGAI	GGCACACCCCT			GGAGCIGIG	CTICGCIIGA	ACACAAAIGAC
00372004.1	CICGACCGAI	GGCACACCCCT			GGAGCIGIG	CIICGCIIGA	ACACAAAIGAC
00372007.1	CICGACCGAI	CCCACACCCCT			CONCOTOTO	CTTCCCTTCAL	ACACAAAIGAC
00372009.1	CICGACCGAI	CCCACACCCCT			CCACCTCTC	CTTCGCTTGAL	ACACAAAIGAC
00372024.1	CTCCACCCAT	CCCACACCCCT	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		CCACCTCTC	CTTCCCTTCAL	ACACAAAIGAC
00371999 1	CICGACCGAI	CACCCCCCC	CCCCCCTCTCT		CCCTCT	CTTCCCTTCA	ACACAAAIGAC
00371998.1	AAC	CAGGCCGCCCT				CCCCCCCCCCA.	ACACAAIGCIC
00372001 1	С л л т	CACCCCCCCC			СССТАС	CTTCGCTGAAC	ACAAC AC
00371997 1		GAGGCCACCCT			GCCTAG	TT CACTO	ACACGAATGAC
02011991.1	••••••AAC	GUGGGGGGGCCI	GUACUU.			IICACIO	ACACOARIGAC

		190	2	00	210		22	o 230
0Q372005.1		GGA <mark>GC</mark> TO	GC <mark>TCAC</mark> TAI	GCTCGT	ATTGCG		, TCATTCCTT	GTTATGGTTTT
OQ372026.1		AGACGTO	GCCCCCGAC	CCTGGC	T <mark>TCG</mark> GGG	ACAAGCCTTCCAA	GACTCCAAGGTT	T A C <mark>G G G A</mark> T T C T G C A <mark>A</mark> T
0Q372023.1		AGACGTO	GCCTCGGC	CTTGGC	T <mark>TCG</mark> GGC	GCAAGCGTTCAAA	GACTCGATGGTT	C A C G G G A T T C T G C A A T
0Q372027.1	GGC	AGACGIO	GCCCCCGAC	CTTGGC	T <mark>TCG</mark> GGC	ACAAGCGTTCAAA	GACTCGATGGTT	CACGGGATTCTGCAAT
0Q372029.1	GGC	AGACGTO	GCCCCCGAC	CTTGGC	ITCGGGC	ACAAGCGTTCAA	GACTCGATGGTT	CACGGGATTCTGCAAT
00372020.1			. .		C	ACGAAC		
OQ372008.1	TCGGC	ACGGT	TCTCGGC	TCTCGC	ГССАТ	GAAAACGTATCGA	••••••••••••••••••••••••••••••••••••••	A C T G G T G G A T T G C A A T
0Q372016.1						G <i>F</i>	AATGAAATGATT	Τ
0Q371999.1	TCTCGGC	AAGGAT.	TCTCGGC	TCTCGC	A T C G A G A A G	ACGAGCG	AAATCGATACTT	GG <mark>TG</mark> GAATGCAGA
0Q372006.1	TCTCGGC	AACGGAT	ATCTCGGC	TCTCGC.	ATCGATG	AAGAACGTAGCGA	AATGCGATACTT	GGTGTGAATTGCAGAA
0Q372018.1	• • • • • • •		CTCGTI	TTTGGT	TTTGT			
00372010.1	TCTCGGC	AACGGAI	ATCTCGGC	TCTCGC.	ATCGATG	AAGAACTTATCGA	AATGCTATACTT	G G T G T G A A T T G C A G A A
00372015.1	TCTCGGC	AACGGAI	ATCTCGGC	TCTCAC	ATCGAT	TTGAACGTAGCGA	ACCGCGATA	
00372002.1	TCTCGGC	AACGGAI	ATCTCGGC	TCTCGC.	ATCGAT. G	AAGAACGTAGCGA	AATGCGATACTT	GGTGTGAATTGCAGAA
00372028.1	TCTCGGC	AACGGAI	ATCTCGGC	TCTCGC	ATCGATG	AAGAACGTAGCGA	AATGCGATACTT	GGTGTGAATTGCAGAA
00371996.1	TOTOGGO	AACGGAI	ATCTCGGC	TOTOGO	ATCGATG	AAGAACGTAGCGA	AATGCGATACTT	GGTGTGAATTGCAGAA
00372019.1		AACGGAI	AICICGGC	TOTOGO	AICGATG	AAGAACGIAGCGA	AATGCGATACIT	G G I G I G A A I I G C A G A A
00372013.1	TCTCGGC	AACGGAI	AICICGGC	TOTOGO	AICGAL.G	AAGAACGIAGCGA	AAIGCGAIACII	G G I G I G A A I I G C A G A A
00372017.1	TCTCGGC	AACGGAI	ATCICGGC	TCTCGC	ATCGAL.G	AAGAACGIAGCGA	AATGCGATACII	C C T C T C A A T T C C A C A A
00372021.1	TCTCGGC	AACGGAI	ATCICGGC	TCTCGC	ATCCAT C	AAGAACGIAGCGA	AATGCGATACII	CCTCTCAATTCCACAA
00372025.1	TCTCGGC	AACGGAI	ATCTCGGC	TCTCGC	ATCGAT G	AAGAACGIAGCGA	AATGCGATACTT	GETETEAATTECAGAA
00372022 1	TCTCGGC	AACGGAT	ATCTCGGC	TCTCGC	ATCGAT G	AAGAACGTAGCGI	AATGCGATACTT	GETETEAATTECAGAA
00372011 1	TCTCGGC	AACGGAT	ATCTCGGC	TCTCGC	ATCGAT G	AAGAACGTAGCGI	AATGCGATACTT	GETETEAATTECAGAA
00372000 1	TCTCGGC	AACGGAT	ATCTCGGC	TCTCGC	ATCGAT G	AAGAACGTAGCGA	AATGCGATACTT	GGTGTGAATTGCAGAA
00372004.1	TCTCGG	AACGGAT	ATCTCGGC	TCTCGC	ATCGAT. G	AAGAACGTAGCGA	AATGCGATACTT	GGTGTGAATTGCAGAA
00372007.1	TCTCGGC	AACGGAT	ATCTCGGC	TCTCGC	ATCGAT.G	AAGAACGTAGCGA	AATGCGATACTT	GGTGTGAATTGCAGAA
00372009.1	TCTCGGC	AACGGAT	ATCTCGGC	TCTCGC	ATCGATG	AAGAACGTACCGA	AATGCGATACTT	GGTGTGAATTGCAGAA
00372024.1	TCTCGGC	AACGGAT	ATCTCGGC	TCTCGC	ATCGATG	AAGAACGTAGCGA	AATGCGATACTT	G G T G T G A A T T G C A G A A
00372003.1	TCTCGGC	AACGGAT	ATCTCGGC	TCTCGC	ATCGATG	AAGAACGTAGCGA	AATGCGATACTT	G G T G T G A A T T G C A G A A
00371998.1	TCGC	AAGGAT.	. TCTCGGC	TCTCGC	ACGA	GAAGACGTAGCGA	ATCGAACT	GGTGTGAATGCAGA
00372012.1	TCGCGAT	GGAA	. TCTCGCC	TCGC	. TCGAGAGA	AGAAAGAAAACGA	ACTTGGGTGAT.	
0Q372001.1	TCTCGGC	ATG <mark>G</mark> AT.	TCTCGGC	T. TCGC	A.CGATG	AAGAACGTAGCGA	A.ATGCGATACTT	GGTGTGAATGCAGA
0Q371997.1	TCTCGGC	GAG <mark>GG</mark> AI	ATCTCGGC	T. TCGC	ТСGАG	AAGAACGTAGCGA	AATGCGATACTT	. GTGTGAATGCAGA

0Q372005.1			[• •	• • •			• • •				.C1	ΑT				• •	•••		• • •		• •	•••	• •	
00372026.1	TCACA	CCA	GT	AIC	GCZ	ATT1	CG	CT	ACG	CCA	AGO	CA	GAA	CC	GAA	AT 7	TCC	GG	CCC	AGA	GGO	CA	ΤΤΙ	TI	ΓTΤ	TCI	AAG	CG	A
00372023.1	TCACA	CCA	AGT.	AIC	GCI		CG	CT	ACG	CGA	TGO	GA	GAC	CC	GAG	AT	TCC	GG	CCG	AG.	AG		GTI	СС	GGT	TT	A A C	CG	A
00372029.1	TCACA	CCA	GT	ATC	GCZ		CG	СТ		CGA	TG	GA	GAC	cc	GAG	AT	TCC	GG		AG.	AG	r c	ATT	ТС	GGT	TT		CG	
0Q372020.1																		GG	ССА	AG.	Α.								. Т А
0Q372008.1	CCCTG	ACG	[CG	ATC	ΤTΟ	GACI	GA	ΤT	GCG	CCC	TTO	ТТ	тG <mark>С</mark>	GG	GGA	СТС	GCI	GG	ст.			••	· · ·	· • •				• •	
00372016.1		· · ·					· · ·	•••				· · ·			AG	TCA	CGF	AT	CAG	AG.	G.				•••	· ·			••••
00372006 1	TCCCG	TG.		AIC	GA.			G A	AAG	CAA	GI.			CG.				GG		AG.	GGG	A C	GIC		C TGC	CT		CA	
00372018.1	10000	1.04		HIC.	GAC															AG.	990						300		
0Q372010.1	TCCCG	TGA	ACC	ATC	TAC	TCI	TT	GA	ATG	CAA	GT:	GT	GCC	ĊG.	AAG	тс	TTA	ΤG	TTG	AG	GGO	CA	ĊĠI	C C 1	rgc	CTO	GG	T.	T C A
OQ372015.1																						•••		.					
00372002.1	TCCCG	TGA	ACC	AIC	GAO	STCI	TTT	GA	ACG	CAA	GT	GT	GCC	CG	AAG	CCA	ATTF	GG	TCG	AG.	GG	CA	CGI	Cl	rgc	CTO	GGG	CA	I C A
00371996 1	TCCCG	TGA.		AIC	GAC			GA	ACG	CAA	GI.	GT		CG.	AAG			GG	тсс	AG.	GGG	CΑ ~ Δ			ICC TCC		366		
00372019.1	TCCCG	TGA	ACC	ATC	GAO	GTCI	TTT	GA	ACG	CAA	GT	GT	GCC	CG	AAG	cci	TTZ	GG	clcg	AG.	GGG	CA	CGI	C	rgc	CT	GGC	CA	T C A
0Q372013.1	TCCCG	TGA	ACC	ATC	GAO	TCT	ТТ	GA	ACG	CAA	GT:	Г <mark>G</mark> Т	GCC	CG	AAG	CCI	TTA	GG	TCG	AG.	GGO	CA	CGI	CJ	ГGС	CTO	GG	CA	r c A
OQ372017.1	TCCCG	TGA	ACC	ATC	GAO	GTC1	TT	GA	ACG	CAA	GT	[GT	GCC	CG	AAG	CCI	ATT A	GG	Τ <mark>С</mark> G	AG.	GGO	СΑ	CGI	[T]	ГGС	TT	GG	CT	ГСТ
00372021.1	TCCCG	TGA	ACC	ATC	GAO	STCI	TT	GA	ACG	CAA	GT	GT	GCC	CG.	AAG		T T F	GG	TCG	AG.	GGO	CA	CGI		ГGС	CT	GGG		I C A
00372025.1	TCCC	TGA		АТС	C A C		· · ·				GT.	ст		C C			тт	c c		AG	àà	- 2			· · ·				
00372022.1	TCCCG	TGA	ACC	ATC	GAO	GTCI	TT	GA	ACG	CAA	GT	GT	GCC	CG	AAG		TTA	GG	TCG	AG.	GGG	CA	CGT	i C 1	rgc	CT	GGC	CA	
0Q372011.1	TCCCG	TGA	ACC	ATC	GAO	TC	TT	GA	ACG	CAA	GT:	Г <mark>G</mark> Т	GCC	CG	AAG	CCI	TTA	GG	TCG	AG.	GG	CA	CGI	CJ	rgc	CTO	GG	CA	I C A
0Q372000.1	TCCCG	ΤGΑ	ACC	ATC	GAO	TCI	TT	GΑ	ACG	CAA	GT	Γ <mark>G</mark> Τ	GCC	CG.	AAG	CCI	ATT A	GG	ΤCG	AG.	GGO	CA	CGI	СЛ	ГGС	CTC	GG	CA	C C A
00372004.1	TCCCG	TGA.	ACC	ATC	GAO	GTC1	TTT	GA	ACG	CAA	GT	ΓGΤ	GCC	CG.	AAG	CCI	ATTF	GG	TCG	AG.	GGO	CA	CGI		FGC	CTC	GGG	CA	I C A
00372007.1	TCCCG	TGA.		AIC	GAC	TC.		GA	ACG	CAA	GI.	GI		CG.	AAG			GG	TCG	AG.	GGG	CA N N			rgc	CTO	366		
00372024.1	TCCCG	TGA	ACC	ATC	GAO	GTCI	T T	GA	ACG	CAA	GT	GT	GCC	CG	AAG	cci	TTZ	GG	TCG	AG.	GGG	CA		C	IGC	CT	GGG	CA	
0Q372003.1	TCCCG	TGA	ACC	ATC	GAO	TCI	ТТ	GA	ACG	CAA	GT:	Г <mark>G</mark> Т	GCC	CG	AAG	CCI	TTA	GG	TCG	AG.	GGO	CA	ĊĠI	C D	ГĞĊ	CTO	GG	CA	ΓĊΑ
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Figure 4.4. Multiple sequence alignment (MSA) for 34 *Physalis* accessions based on ITS2 sequences.

4.3.4 Phylogenetic-based identification

The phylogenetic tree based on ITS2 sequences for the different *Physalis* species assigned each of the *Physalis* accessions to its related species (Figure 4.5). The 3 *Physalis* species namely *P. cordata* (OQ5372012.1, OQ371998.1, OQ372001.1 and OQ371997.1), *P. peruviana* (OQ372016.1, OQ372008.1 and OQ372006.1) and *P. purpurea* (OQ371996.1, OQ371999.1, OQ372000.1, OQ372002.1 – OQ372005.1, OQ372007.1, OQ372009.1 - OQ2011.1, OQ372013.1 - OQ372015.1, OQ372017.1, OQ372018.1 - OQ372029) formed independent clades with > 80% branch support (Figure 4.5), indicating that *Physalis* species could be successfully discriminated using ITS2 sequences. The phylogenetic analysis indicates that the *Physalis* accessions showed species variation with different percentage indices (Figure 4.5).



Figure 4.5. Phylogenetic tree derived from Bayesian inference analysis of the ITS2 gene of 34 *Physalis* sequences.

Plants from this study are presented in blue, red and green colors. Black color represents reference sequences for different *Physalis* species retrieved from GenBank after BLASTn analysis, red represents *P. peruviana*, blue represents *P. purpurea* and green represents *P. cordata*. Numbers above branches represent the percentage posterior probability statistic for the MrBayes phylogenetic tree.

4.3.5 ITS2 RNA secondary structures predictions

Besides the use of divergence of primary sequences of ITS2, variations in ITS2 secondary structures were also used to identify *Physalis* species. The ITS2 secondary structure predictions based on minimum free energy (MFE) is shown in Figure 4.6. The optimal secondary structure for *P. cordata* (OQ372001.1), *P. peruviana* (OQ372006.1) and *P. purpurea* (OQ371996.1) had minimum free energies of -204.90 kcal/mol, -312.90 kcal/mol and 266.90 kcal/mol with free energy of thermodynamic ensemble of -210.51 kcal/mol, -322.47 kcal/mol and -275.94 kcal/mol and the frequency of the MFE structure in the ensemble of 0.01%, 0.00% and 0.00%, respectively. The ensemble diversity for *P. cordata* (OQ372001.1), *P. peruviana* (OQ372001.1), *P. peruviana* (OQ372001.1), *P. peruviana* (OQ372006.1) and *P. purpurea* (OQ371996.1) was 136.00, 146.99 and 149.89, respectively.

The secondary structure of *P. cordata* (OQ372001.1 used as a representative) had 26 double helices, 26 loops and 2 single helices. The secondary structure of *P. peruviana* (OQ372006.1 used as a representative) had 39 double helices, 36 loops and 5 single helices. *Physalis* (OQ371996.1) was chosen as the representative accession for *P. purpurea* and the secondary structure had 43 double helices, 41 loops and 4 single helices. The secondary structure predictions showed variations among the 3 *Physalis* species. The predicted ITS2 secondary structures of the 3 *Physalis* species represented 3 different structures with a central ring and different helical orientations (Figure 4.6). The studied *Physalis* species showed a unique secondary structure that differed with the reference structure in two respects, the length of helices and the number of loops on their helices (Figure 4.6). The variation in helices length in the secondary structure of ITS2 was observed in different *Physalis* species (Figure 4.6). The loop number, position, size and angle from the centroid were distinguishable in all the three *Physalis* species. Besides the differences in the number of stems and rings, the shape and distribution of stem-loops in the secondary structure of the 3 *Physalis* species were notably different (Figure 4.6).



Figure 4.6. The predicted secondary structures of the ITS2 region of three *Physalis* species.

4.3.6 Genetic divergence analysis

4.3.6.1 DNA divergence between populations based on ITS2 sequences

Divergence between *Physalis* accessions in this study was determined by calculating the nucleotide diversity, average nucleotide substitutions per site between populations and number of net nucleotide substitutions per site between populations (Table 4.4). There were varying shared mutations among the *Physalis* accessions. The highest number of shared mutations at 11 was observed between *P. peruviana* and *P. cordata* populations. The lowest shared mutations at 3 were observed between *P. peruviana* and *P. purpurea*. The highest nucleotide diversity (0.36923) was obtained between *P. peruviana* and *P. peruviana* and *P. cordata* while the lowest nucleotide diversity (0.15062) was recorded between *P. peruviana* and *P. purpurea*. There were no fixed differences between *P. peruviana* and *P. purpurea* populations as well as between *P. purpurea* and *P. cordata* populations, which had the highest nucleotide diversity.

Population	Р.	Р.	<i>P</i> .	<i>P</i> .	Р.	<i>P</i> .
	peruviana	cordata	peruviana	purpurea	purpurea	cordata
	(P1)	(P2)	(P1)	(P2)	(P1)	(P2)
Polymorphic sites in each	37	33	7	16	17	8
population	57	55	/	10	17	0
Total number of	<i>4</i> 9		17		18	
polymorphic sites	12		17		10	
Average number of	24 000		3 464		3 796	
nucleotide differences	24.000		5.404		5.770	
Nucleotide diversity Pi (t)	0.36923		0.15062		0.16503	
Number of fixed differences	2		0		0	
Mutations polymorphic in						
population 1 (P1) but	32		4		17	
monomorphic in population	52				17	
2 (P2)						
Mutations polymorphic in	28		18		3	
P2 but monomorphic in P1	20		10		5	
Shared mutations	11		3		6	
Average number of						
nucleotide differences	25.750		4.284		4.185	
between populations						
Average nucleotide						
substitution per site between	0.39615		0.18626		0.18196	
populations (Dxy)						
Number of net nucleotide						
substitutions per site	0.04359		0.01383		0.00449	
between populations (Da)						

Table 4.4. DNA divergence between (interspecific) *Physalis* species populations based on ITS2

 sequences

4.3.6.2 DNA divergence within populations based on ITS2 sequences

DNA divergence within each population of the identified *Physalis* species was determined based on ITS2 sequences (Table 4.5). The highest nucleotide diversity was recorded within the *P. peruviana* population at 0.26324 despite this population having moderate number of polymorphic segregating sites at 80 and moderate number of nucleotide substitutions at 89 (Table 4.5). The lowest nucleotide diversity was recorded for *P. purpurea* population at 0.15883 and this corresponded to the lowest number of polymorphic segregating sites at 37 and lowest number of substitutions at 37. Moderate nucleotide diversity was recorded for *P. cordata* population at 0.17167 and this population had the highest number of polymorphic segregating sites (89) and number of nucleotide substitutions (102).

 Table 4.5. DNA divergence within (intraspecific) *Physalis* species populations based on ITS2

 sequences

Physalis species	P. peruviana	P. cordata	P. purpurea
Total number of sequences	3	4	27
Number of polymorphic (segregating) sites (S)	80	89	37
Nucleotide diversity Pi (Total)	0.26324	0.17167	0.15883
Nucleotide diversity Pi (JC- Total)	0.32423	0.19494	0.17848
Theta (Total)	0.27726	0.18545	0.26665
Total number of substitutions	89	102	37

4.3.7 Genetic distance between and within Physalis species based on ITS2 sequences

The overall average genetic distance among all *Physalis* accessions studied was determined to be 0.51 ± 0.04 . The highest genetic distance (0.703) was obtained between *P. cordata* and *P. peruviana* and the lowest genetic distance (0.050) was between *P. purpurea* and *P. peruviana* (Table 4.6).

Groups	P. purpurea	P. peruviana	P. cordata
P. purpurea		0.050	0.057
P. peruviana	0.571		0.071
P. cordata	0.633	0.703	

 Table 4.6. Mean genetic distance between (interspecific) Physalis species based on ITS2 sequences

The average intra-specific distance within each *Physalis* population was determined based on ITS2 sequences. The highest mean intraspecific distance (0.46 ± 0.05) was recorded within the *P*. *peruviana* with no significant difference with the intra-specific distance of *P*. *purpurea* (0.43 ± 0.05) . The lowest mean intra-specific distance was within the *P*. *cordata* population at 0.28 ± 0.03 .

4.3.8 Nucleotide polymorphism and neutrality tests

Eight polymorphic sites were identified for the ITS2 gene sequences of the 34 *Physalis* accessions used in this study (Table 4.7). The nucleotide diversity (Pi) of the gene sequences was 0.14810 (Table 4.7). The eight polymorphic sites had one singleton and seven parsimony informative site mutations (Table 4.7).

Polymorphic sites/ Segregation sites (S)	8	Position in the gene	Variants
Singleton	1	188	4
Parsimony informative sites	7	169	2
		171	2
		172	2
		183	2
		186	2
		189	2
		170	3
Nucleotide diversity (Pi)	0.14	810	
Average number of nucleotide differences (k)	1.77	7	
Sequence length (base pairs)	533		
Number of sequences	34		

Table 4.7. DNA polymorphism of *Physalis* accessions based on ITS2 marker

Tajima's neutrality test was performed on all 34 ITS2 sequences of *Physalis* accessions to establish selection of the species based on the Tajima D value and the nucleotide diversity. The number of segregating sites (S) and nucleotide diversity (π) was 464 and 0.155388, respectively. The Tajima D value obtained was -1.034267.

4.3.9 Genetic differences and barcoding gap analysis

Automatic barcode gap discovery (ABGD) results generated by the K80 Kimura measure of distance (K2P) based on the ITS2 gene sequences for *Physalis* accessions were used to assess the presence of a barcoding gap. Based on the ITS2 gene sequences, all pairwise distances were ranked by increasing the distance values from 0.00 to 1.36 and absence of barcoding gaps was detected (Figure 4.7).



Figure 4.7. A histogram indicating the hypothetical distribution of pairwise differences of ITS2 gene sequences for 34 *Physalis* accessions.

Low divergence is presumably intraspecific divergence, whereas higher divergence indicates interspecific divergence. The abbreviation nbr on the *y*-axis of the histogram stands for the number of pairwise comparisons. No barcode gaps were detected.

4.4 Discussion

Currently, there is a growing demand for *Physalis* species worldwide due to their nutritional and medicinal value (Shenstone *et al.*, 2020). *Physalis* species are widely diverse as there are more than 85 species of *Physalis* distributed throughout the world (Vargas *et al.*, 2001). Different *Physalis* species have different applications and therefore accurately identifying the *Physalis* plants using molecular genetics will enhance the quick and precise identification of species for utilization, genetic resource conservation and development of genetic breeding programs (Shenstone *et al.*, 2020; Feng *et al.*, 2016). Morphological identification is not reliable due to high phenotypic similarities among *Physalis* species (Whitson and Manos, 2005). It is therefore important to use molecular identification tools such as DNA barcoding in the identification of *Physalis* (Feng *et al.*, 2014). This study focused on the use of the DNA ITS2 region as a recognition tag to identify and discriminate *Physalis* species in Kenya.

The results from sequence characteristics, genetic distance, phylogenetic relationships and secondary structure analyses showed the remarkable potential of ITS sequences for distinguishing *Physalis* species. The potential to discriminate at the species level and ease of amplification makes ITS a favourable locus for the barcoding of plants (Pang et al., 2011; Li et al., 2010). Several researchers have demonstrated the usefulness of the nuclear ITS region as a DNA barcode for determining high levels of inter-specific genetic divergence among land plants (Mishra et al., 2017; Zhang et al., 2016). One of the most important criteria required for a successful DNA barcode is the presence of a high rate of PCR amplification and good quality sequences among the different target species. In this study, the use of the ITS2 barcode locus was successful as the PCR amplification and direct sequencing success rates were 75% and 67%, respectively. This compares to other reported studies whereby the amplification of the ITS2 gene gives a higher success rate than the sequencing (Kang et al., 2017; Zhang et al., 2015). Contrary to the present study, Feng et al. (2016) reported a 100% PCR amplification and sequencing success rate of ITS region in *Physalis* species. The amplification and sequencing success rate of ITS2 has been shown in other studies to be much lower compared to other barcoding genes such as *rbcL*, *matK* and *psbA-trnH* (Kang *et al.*, 2017; Huang *et al.*, 2015).

The ITS2 phylogenetic tree based on Bayesian inference revealed that the *Physalis* accessions were closely clustered together with the sequences of P. cordata, P. peruviana and P. purpurea chosen from the BLASTn search. The resultant phylogenetic tree identified and discriminated the *Physalis* accessions into three species namely *P. cordata*, *P. peruviana* and *P. purpurea*. Studies have shown that plant species identification based on BLASTn and phylogenetic tree analysis are reliable as long as the species under study have a reference dataset in the GenBank (Ross et al., 2008). This is the first report indicating the identification of P. purpurea and P. cordata from Physalis accessions in Kenya. This is an indication that the ITS2 region can accurately discriminate Physalis species and also identify new species that had not been previously reported in a particular region. ITS2 was able to effectively distinguish *Physalis* species and facilitate the identification of three *Physalis* species among the accessions studied. This supports previous studies that the ITS2 barcode has a higher discriminatory ability among species than other barcodes such as *rbcL* which tend to be highly conserved in different plant species (Li et al., 2017). In other studies, ITS2 has been identified as a promising DNA barcode due to its fast substitution rate and hence variability that provides satisfactory resolving power for closely related species (Zhang et al., 2015).

Although ITS2 nucleotide sequences are substituted at a fast rate, their secondary structures are largely conserved and can also be utilized in the identification of species (Feng *et al.*, 2016, Zhang *et al.*, 2015). The ITS2 sequence usually functions as a secondary structure in cells. In addition, the secondary structure contains genetic information that can be used for the classification and identification of plant species (Chen *et al.*, 2012). In this study, we explored the differences in ITS2 secondary structures between three species of the genus *Physalis*. The ITS2 secondary structure inherently gave a visual distinctiveness between the three *Physalis* species. In our study, the prediction of the secondary structures in the three *Physalis* species revealed diverse secondary structures with distinguishable loop numbers, positions and elevations from the centroid. The ITS2 secondary structures revealed the uniqueness of the generated DNA barcode sequences. These unique genetic structures at the conserved nuclear region of *Physalis* species can be used to develop species-specific markers for the identification of *Physalis* accessions.

The genetic diversity of *Physalis* accessions studied largely concurred with the phylogenetic and genetic distance analysis. Both genetic diversity and genetic distance indicated the relatedness of species and in this study, P. purpurea and P. peruviana seem to be closely related while P. peruviana and P. cordata seem to be more diverse. Genetic diversity within (intraspecific divergence) species is assessed to determine the diversity of a group of organisms within a species. The high nucleotide diversity within *P. peruviana* is an indication that genetic change is much higher in this species than other species identified in this study. Intraspecific variation is important for evolution, adaptation and competition seen within the same species that can over time lead to genetically distinct members of a population adapted to specified environmental conditions such as cultivars (O'Dell and Rajakaruna, 2011). This information concurs with a previous study that showed high genetic divergence within P. peruviana populations and even when compared to other related taxa (Garzón-Martínez et al., 2015). The ABDG analysis was able to show the general intraspecific divergence within the *Physalis* accessions in this study as well. The maximum intraspecific distance P_{max} based on the ITS2 gene was 0.1 an indication that there is divergence within *Physalis* species. Intraspecific divergence is important as it creates variation among a species and allows for better conservation of the species in different environments.

The nucleotide polymorphism showed that the 34 *Physalis* accessions had eight polymorphic sites, with one singleton and seven parsimony informative sites. Higher polymorphic sites are consistent with high genetic diversity, an indication that the gene analyzed was effective in discrimination of *Physalis* species. The Tajima D value for the 34 *Physalis* accessions in this study gave a negative value of -1.034267, an indication that the population had a negative selection and higher low frequency mutations that can help in the differentiation of the *Physalis* species (Carlson *et al.*, 2005). This study shows that ITS2 is an ideal candidate barcode for discrimination of *Physalis* species.

4.5 Conclusion

In the present study, ITS2 was found to possess a sufficient variable region between the different species and accessions for the determination of genetic divergence with high discriminatory ability. DNA barcode ITS2 was highly efficient in the identification and discrimination of

Physalis species. ITS2 was found to possess a sufficiently variable region between the different accessions and species for the determination of genetic divergence with high discriminatory ability. The *Physalis* accessions were identified and discriminated into three species namely *P. peruviana*, *P. purpurea* and *P. cordata*. Our study revealed significant variations in ITS2 secondary structure predictions that enhanced discrimination among the three identified *Physalis* species. This study provides insight into the scope of the development of species-specific primers for the discrimination of the three *Physalis* species. Understanding the RNA molecules would be useful for the selection of parents in trait-specific breeding strategies for *Physalis* improvement.

CHAPTER FIVE

5.0 Molecular identification and genetic diversity assessment of *Physalis* accessions using ribulose-1,5-bisphosphate carboxylase large (*rbcL*) DNA barcode

5.1 Introduction

Physalis genus is one of the key genera in the plant family of *Solanaceae* (Nightshade family) (Martínez, 1998). Various species of Physalis have been identified both morphologically and using molecular genetic analysis. *Physalis* species are found all around the world in tropical and temperate regions growing mostly as wild plants with a few countries such as Colombia taking up farming of *Physalis* for economical use (Chacón *et al.*, 2016). Few species of *Physalis* are native to countries in the regions of Americas and others have been introduced in Eurasia and Southeast Asia (Vdovenko et al., 2021; Feng et al., 2020). In China five species of Physalis have been identified and these include; P. minima, P. alkekengi, P. peruviana, P. pubescens and P. angulata (Chinese Academy of Sciences, 1978). Two variants of Physalis have also been identified in China and they include; Physalis angulata var. villosa and P. alkekengi var. franchetii (Chinese Academy of Sciences, 1978). P. peruviana L. is native to the Andes of South America (Cailes, 1952). In the United States the Physalis species Physalis grisea is usually cultivated while in Mexico the two Physalis species P. angulata L. and P. philadelphica Lam are cultivated (Vargas-Ponce at al., 2016). Physalis species grow in areas from sea level to elevations of about 3,000 metres, they can also be found in a wide array of different climates such as high humidity areas to deserts as well (Vargas-Ponce et al., 2016; Toledo, 2013). The three species of Physalis namely P. philadelphica, P. pubescens and P. peruviana are widely cultivated in different parts of the world, mostly for their edible fruits (Sang-Ngern et al., 2016).

Physalis is a plant with high content of antioxidants, minerals and vitamins hence possessing medicinal value. The fruits of some *Physalis* species are edible and have high nutritive and antioxidant value (Shenstone *et al.*, 2020; Puente *et al.*, 2011). *Physalis* species of pharmacological interest such as *P. cordata*, *P. minima*, *P. pubescens* and *Physalis pruinosa* have been shown to produce compounds such as flavonoids, physalins, withanolides and saponin with medicinal value (Shah and Bora, 2019; Lima *et al.*, 2014). The high number of diverse

metabolites produced by *Physalis* species could be an indication of their variability at the genetic level among the different species (Sandoval-Padilla *et al.*, 2022). Morphologically *Physalis* species appear similar and can be easily misidentified (Feng *et al.*, 2020). *Physalis* species are also morphologically similar to other plants of the Solanaceae family such as *N. physalodes* (Feng *et al.*, 2016). Traditional morphological identification has greatly been hampered by heritable variations in *Physalis* species as well as differences in growth environments (Vargas-Ponce *et al.*, 2011). The biologically active compounds with medicinal properties differ among the various species of *Physalis* that morphological look similar (Feng *et al.*, 2018). In order to prevent improper use of *Physalis* in medicinal application it is crucial that reliable identification of *Physalis* species is done.

DNA barcoding has proven reliable in the rapid and accurate identification of plant species using short nuclear and chloroplast genes of plants to assess sequence diversity (Feng et al., 2015). Widely used DNA barcodes in the identification of plant species are the chloroplast DNA sequences including ribulose bisphosphate carboxylase large (*rbcL*), maturase K (*matK*), and psbA-trnH (Feng et al., 2018). Specifically, rbcL has been shown to have a higher distinguishing potential of plant species than *matK* or a combination of the two genes in previous studies (Tran et al., 2021). Among the several plant barcodes that have been identified, rbcL is proposed as one of the ideal plant barcoding loci by the Consortium for Barcode of life (CBOL) (Tran et al., 2021). It is however important to note that the ideal loci for plant barcoding will differ depending on whether they are used to identify taxonomic groups or for species discrimination (Tran et al., 2021). It has been noted that there is more species variation of the chloroplast DNA barcode *matK* as compared to *rbcL* which seems to be more conserved (Thitikornpong *et al.*, 2018). Another study showed that DNA barcodes matK and psbA-trnH provided more rates of variable sites than rbcL which possessed more conservation sites (Li et al., 2017). Other studies, however, *rbcL* showed better species resolution of various plants studied as compared to *matK* (Fatima et al., 2019). This is a clear indication that the efficiency of a DNA barcode in species resolution can vary in different species of plants.

The objective of this study was to evaluate the efficiency of *rbcL* DNA barcode in the species discrimination of *Physalis* plants collected in various regions of Kenya. This is important as it

will promote genetic conservation and increase in breeding programs of *Physalis* which is considered an orphan plant and grows mostly in the wild. This could also open up a channel for the value addition, classification, protection and conservation of *Physalis* species and accessions in Kenya.

5.2 Materials and methods

5.2.1 Plant material

Leaves and fruits of *Physalis* plants were randomly picked from Baringo, Kericho, Nairobi, Elgeyo Marakwet, Nyeri, Kajiado, Homabay, Kiambu, Nakuru and Machakos counties of Kenya from April 2019 to January 2021 as indicated in Figure 5.1. The locations from where samples were collected including their geographical coordinates are indicated in Table 5.1 and Appendix 1 A. The collected *Physalis* plant samples were placed in zip lock bags and stored in a cool box, transported to the laboratory and identified by the taxonomist Mr. Patrick Mutiso and part of the samples were preserved in the University of Nairobi herbarium in the Department of Biology (Code of Voucher Specimen: KP/UON2019/001). Seventy-eight plants as indicated in Appendix 1 A were sampled for their leaves and fruits based on phenotypic characteristic and availability from the ten counties in Kenya. All *Physalis* plants collected were wild self-propagating plants except those from Elgeyo-Marakwet that were collected from a gooseberry farmer. The leaves were utilized in the extraction of DNA for molecular identification and *Physalis* species discrimination.



Figure 5.1. Map showing the location of *Physalis* sampling in 10 counties within Kenya.

Table 5.1. Geographical coordinates and number of samples picked from the various regions of

 Physalis sampling within 10 different counties in Kenya

No.	Main Location	Specific	Latitude	Longitude	Number of
		Location			samples
					collected
1.	Londiani	Sorget	0.0532° S	35.5548° E	10
2.	Elgeyo Marakwet	Chebororwa	0.9487° N	35.4234° E	13
3.	Homabay	Ndhiwa	0.7299° S	34.3671° E	3
4.	Baringo	Maji Mazuri	0.0076° S	35.6861° E	1
5.	Kajiado	Ongata Rongai	1.3939° S	36.7442° E	5
6.	Nyeri	Mukurweini	0.5609° S	36.0488° E	5
7.	Nakuru	Gilgil market	0.4923° S	36.3173° E	1
8.	Nairobi	Kilimani	1.2893° S	36.7869° E	4
		Valley Arcade	1.2907° S	36.7692° E	2
9.	Kangundo	Tala	1.2670° S	37.3201° E	4
10.	Kiambu	Tigoni	1.1651° S	36.7065° E	17
		Thika	1.0388° S	37.0834° E	9
		Kahuho	1.2082° S	36.6795° E	2
		Banana Hill	1.1760° S	36.7550° E	1
		Muguga	1.2551° S	36.6580° E	1

5.2.2 Molecular authentication of Physalis plants

5.2.2.1 Genomic DNA extraction

Physalis accessions genomic DNA was isolated, purified, viewed and stored as described in section 3.2.2.1.

5.2.2.2 Polymerase chain reaction and DNA sequencing

Polymerase chain reaction (PCR) amplification of *Physalis* accessions was done using DNA barcoding primer *rbcL* (Lledo *et al.*, 1998) presented in Table 3.1. PCR amplification, purification of PCR products and sequencing was performed as described in section 3.2.2.2.

5.2.2.3 Sequence and phylogenetic analysis

The sequences of *rbcL* gene for *Physalis* accessions attained were curated, subjected to BLASTn analysis, used to prepare MSAs and phylogenetic trees as described in section 3.2.2.3. The MSA for the construction of MrBayes phylogenetic tree was prepared using the 56 *Physalis rbcL* gene sequences that had successfully been sequenced and BLASTn generated reference sequences for *Physalis rbcL* accession sequences. The MSA for the genetic diversity, nucleotide polymorphism, neutrality test and Automatic Barcode Gap Discovery (ABGD) analysis was generated using the 56 *Physalis rbcL* gene sequences only.

5.2.3 Genetic divergence within *Physalis* population based on *rbcL* sequences

DNA divergence within *Physalis* accession was assessed based on *rbcL* marker using DnaSP software version 6.12.03 (Kartavstev, 2011). DNA divergence within *Physalis* population based on *rbcL* sequences was done as described in section 3.2.3.

5.2.4 Genetic distance assessment within *Physalis* population based on *rbcL* sequences

Intraspecific and overall genetic distance of *Physalis* accessions based on the *rbcL* marker only was determined as described in section 3.2.4 using the 56 *Physalis* accessions *rbcL* sequences.

5.2.5 Determination of nucleotide polymorphism

Sequence polymorphism of the barcoding region *rbcL* was screened in all the sequenced *Physalis* accessions using the multiple sequence alignment for the 56 *Physalis* accessions *rbcL* sequences only as described in section 3.2.5.

5.2.6 Tajima's neutrality test

A Tajima's neutrality test for *rbcL* sequences of *Physalis* accessions under study was done to determine the frequency of mutations among *Physalis* population and to determine the selection of the population (Tajima, 1989). The test assessed the Tajima D value among *rbcL* sequences and nucleotide diversity using MEGA 11.0 (Nei and Kumar, 2000; Tamura *et al.*, 2021). This analysis involved 56 *Physalis* accessions *rbcL* sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were 730 positions in the final dataset. Multiple sequence alignment used for this analysis was based on the 56 *rbcL* sequences only

5.2.7 Barcoding gap determination within *Physalis* accessions based on *rbcL* sequences

The multiple sequence alignment for the 56 *rbcL* sequences only was uploaded to ABGD website (<u>https://bioinfo.mnhn.fr/abi/public/abgd/abgdweb.html</u>) and distance analysis performed based on K80 Kimura measure of distance as described in section 3.2.7.

5.3 Results

5.3.1 Amplification and sequencing success rate of *Physalis* accessions based on the *rbcL* marker

A total of 64 DNA samples out of 78 *Physalis* accessions were successfully amplified (Table 5.2 and Appendix 1 C). Some of the *rbcL* amplicons are indicated in gel images (Figure 3.3. and 5.2). The amplification success rate was 82% (Table 5.2). The amplicons from the 64 accessions were sequenced of which sequences were obtained from 56 *Physalis* accessions. The sequencing success rate was 88%. The *rbcL* sequences of the 56 *Physalis* accessions had a length range of 463 - 854 bp and an average length of 690 bp. The range of GC content was 42.1 - 45.5 % with an average of 43.4% (Table 5.2).

Barcode	Samples	Number	of	Number	Percentage of	Percentage	Alignment	Mean	Mean
region	tested	amplicons		of	amplification	of	length (bp)	sequence	GC
	(n)	produced		sequences	efficiency	sequencing		length	content
				produced	(%)	efficiency		(bp)	(%)
						(%)			
rbcL	78	64		56	82	88	854	690	43.4

Table 5.2. Efficiency of PCR amplification and sequencing for *Physalis* accessions *rbcL* DNA barcode regions.



Figure 5.2. PCR amplicons for *rbcL* sequences of *Physalis* accessions from Nakuru, Kajiado and Elgeyo-Marakwet counties.

The letter L in Figure 5.2 above represents the DNA ladder, gmr-e7inr represents the *Physalis* accessions amplicons based on *rbcL* sequence amplification.

The nucleotide base frequencies of the four standard deoxyribonucleotides at various coding positions in the *Physalis* accessions for *rbcL* sequences is presented in Table 5.3. The most abundant deoxyribonucleotide was thymine while cytosine appeared the least in the *rbcL* sequences. It was noted that the GC content of the *rbcL* sequences was significantly lower than the AT content (Table 5.4).

Table 5.3. The nucleotide base frequencies of candidate nucleotide sequences at different coding positions in *Physalis* accessions.

Barcode region	Base c	ontents	(%)			
	Α	Т	G	С	AT	GC
rbcL	28.17	28.44	23.13	20.26	56.56	43.44

5.3.2 Identification of *Physalis* species based using BLASTn analysis based on *rbcL* sequences

The BLASTn analysis results for the *rbcL* sequences of 56 *Physalis* accessions that were successfully sequenced are presented in Table 5.4. All 56 (100%) of the *Physalis* accessions *rbcL* sequences were identified as *Physalis* species after BLASTn analysis. Eight out of the 56 *rbcL* sequences of *Physalis* accessions gave 100% similarity with GenBank database sequences. The eight *Physalis* accessions with 100% identity match in the GenBank include OQ507152.1, OQ507153.1, OQ507155.1, OQ507157.1, OQ507158.1, OQ507159.1, OQ507160.1 and OQ507161.1. All eight sequences of the *Physalis* accessions were identified as *P. minima* based on BLASTn analysis.

Sample ID	Species of Best	GenBank	Max	Е	Percent	Percent	GenBank
-	BLAST match	accession	scor	value	identity	coverage	accession
		number (of	e		(%)	(%)	number
		database)					
Chebororwa	P. peruviana	NC_026570.1	1136	0.0	94.90	99	OQ507163.1
C2r							
Chebororwa	P. peruviana	NC_026570.1	1347	0.0	99.33	99	OQ507164.1
C4r							
Chebororwa	P. virginiana	KT178121.1	739	0.0	95.46	100	OQ507165.1
C5r							
Chebororwa	P. minima	NC_048515.1	754	0.0	93.18	100	OQ507166.1
elinr							
Chebororwa	P. minima	NC_048515.1	1351	0.0	99.46	100	OQ507167.1
e4inr							
Chebororwa	P. minima	NC_048515.1	1424	0.0	98.28	99	OQ507168.1
ебinr							
Chebororwa	P. minima	NC_048515.1	1343	0.0	99.19	100	OQ507169.1
e7inr							
Chebororwa	P. minima	NC_048515.1	1253	0.0	98.19	100	OQ507170.1
e8inr							
Gilgil gmi	P. minima	NC_048515.1	1144	0.0	99.06	100	OQ507171.1
Maji mazuri	P. minima	NC_048515.1	798	0.0	92.20	99	OQ507176.1
mmr							
Valley	P. minima	NC_048515.1	1435	0.0	97.28	99	OQ507207.1
Arcade Vanr							
Kilimani	P. minima	NC_048515.1	1267	0.0	99.29	99	OQ507175.1
SHRr							
Kilimani	P. minima	NC_048515.1	1308	0.0	98.39	100	OQ507174.1
KL1							
Kilimani	P. minima	NC_048515.1	1280	0.0	98.75	99	OQ507173.1
ANRr							
Mukurweini	P. minima	NC_048515.1	1411	0.0	96.49	100	OQ507178.1
ny1r							
Mukurweini	P. angulata	NC_039457.1	1092	0.0	94.01	99	OQ507179.1
ny4r							
Mukurweini	P. angulata	NC_039457.1	1027	0.0	92.90	98	OQ507180.1
ny5r							
Ndhiwa hb2r	P. minima	NC_048515.1	1341	0.0	93.33	99	OQ507181.1
Ndhiwa hb3r	P. minima	NC_048515.1	1327	0.0	999.05	99	OQ507182.1
Ongata	P. peruviana	NC_026570.1	1303	0.0	95.47	99	OQ507183.1
Rongai nor3r							
Ongata	P. virginiana	KT178121.1	1050	0.0	91.10	99	OQ507184.1
Rongai nor4r							

 Table 5.4. BLASTn analysis results for the *Physalis* accessions based on *rbcL* barcode gene.

Ongata	P. peruviana	NC_026570.1	1323	0.0	98.92	99	OQ507185.1
Rongai nor5r	*						
Tala KTr	P. minima	NC_048515.1	1123	0.0	97.01	100	OQ507186.1
Banana Hill	P. minima	NC_048515.1	1192	0.0	96.28	99	OQ507162.1
JCBKr							
Kahuho KKr	P. minima	NC_048515.1	1016	0.0	99.82	100	OQ507172.1
Muguga	P. minima	NC_048515.1	845	0.0	98.74	100	OQ507177.1
DMr							
Thika TK2r	P. minima	NC_048515.1	1310	0.0	99.17	99	OQ507187.1
Thika TK3r	P. minima	NC_048515.1	1352	0.0	97.59	99	OQ507188.1
Thika TK4r	P. minima	NC_048515.1	1363	0.0	97.04	99	OQ507189.1
Thika TK6r	P. minima	NC_048515.1	1336	0.0	97.33	99	OQ507190.1
Thika TK7r	P. minima	NC_048515.1	1310	0.0	99.04	99	OQ507191.1
Thika TK8r	P. minima	NC_048515.1	1120	0.0	99.04	99	OQ507192.1
Thika TK9r	P. minima	NC_048515.1	1411	0.0	98.03	99	OQ507193.1
Tigoni T2r	P. minima	NC_048515.1	1053	0.0	98.31	100	OQ507194.1
Tigoni T4r	P. minima	NC_048515.1	1384	0.0	96.42	99	OQ507195.1
Tigoni T6r	P. minima	NC_048515.1	785	0.0	97.20	100	OQ507196.1
Tigoni T7r	P. minima	NC_048515.1	1315	0.0	98.14	93	OQ507197.1
Tigoni T8r	P. minima	NC_048515.1	963	0.0	98.89	99	OQ507198.1
Tigoni T9r	P. minima	NC_048515.1	1399	0.0	98.13	100	OQ507199.1
Tigoni T10r	P. minima	NC_048515.1	824	0.0	94.25	99	OQ50200.1
Tigoni T11r	P. minima	NC_048515.1	1330	0.0	99.32	98	OQ507201.1
Tigoni T12r	P. minima	NC_048515.1	985	0.0	99.27	100	OQ507202.1
Tigoni T13r	P. minima	NC_048515.1	1319	0.0	97.54	99	OQ507203.1
Tigoni T14r	P. minima	NC_048515.1	1371	0.0	98.70	99	OQ507204.1
Tigoni T16r	P. minima	NC_048515.1	1297	0.0	98.25	99	OQ507205.1
Tigoni T17r	P. minima	NC_048515.1	1376	0.0	98.34	97	OQ507206.1
Londiani L1r	P. minima	NC_048515.1	1011	0.0	100	100	OQ507152.1
Londiani L2r	P. minima	NC_048515.1	1136	0.0	100	100	OQ507153.1
Londiani L3r	P. minima	NC_048515.1	1338	0.0	99.59	100	OQ507154.1
Londiani L4r	P. minima	NC_048515.1	961	0.0	100	100	OQ507155.1
Londiani L5r	P. minima	NC_048515.1	1343	0.0	99.86	100	OQ507156.1
Londiani L6r	P. minima	NC_048515.1	1171	0.0	100	100	OQ507157.1
Londiani L7r	P. minima	NC_048515.1	1136	0.0	100	100	OQ507158.1
Londiani L8r	P. minima	NC_048515.1	1147	0.0	100	100	OQ507159.1
Londiani L9r	P. minima	NC_048515.1	1003	0.0	100	100	OQ507160.1
Londiani	P. minima	NC_048515.1	1116	0.0	100	100	OQ507161.1
L10r							_

5.3.3 Multiple sequence alignment

The multiple sequence alignment of curated *rbcL* sequences and their reference sequences from BLASTn analysis was prepared based on MUSCLE and had a sequence length of 854 bp (Appendix 2 C). The alignment was mostly conserved with few substitution point mutations, absence of deletion or addition (frameshift) point mutations and absence of macrolesions (Appendix 2 C). At position 130 and 131 of the MSA a transversion substitution point mutation was identified on *Physalis* accessions OQ507186.1 where cytosine was replaced with adenine (Appendix 2 C). All other accessions had a cytosine base at this position. Another transversion point mutation was identified for *Physalis* accession OQ507165.1 where thymine was replaced by cytosine as compared to all other accessions (Appendix 2 C). Another transition point mutation is identified at position 368 of the MSA on *Physalis* accession OQ507166.1 where guanine was replaced by adenine (Appendix 2 C).

A second MSA was prepared for the *rbcL* sequences only based on MUSCLE, trimmed and edited on Jalview for genetic diversity and polymorphism analysis. This multiple sequence alignment had a sequence length of 730 bp (https://espript.ibcp.fr/ESPript/temp/1947945090/0-0-1683720272-esp.pdf accessed on 17th February 2023) (Figure 5.3). These MSA had no macrolesion or frameshift point mutation (Figure 5.3). It was highly conserved with few substitution point mutations (Figure 5.3). At position 25, 26 and 29 of the MSA, *Physalis* accession OQ507186.1 had transversion point mutations where cytosine replaced adenine at positions 25 and 26 and adenine was replaced by cytosine at position 29 (Figure 5.3). A transition point mutation was seen on the MSA at position 39 where for the *Physalis* accession OQ507166.1 cytosine replaced thymine (Figure 5.3).

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00507183.1	GAGTAACT	CTCAACCTC	GAGTTCCA	CCTGAAGAAGCA	GEGECCECEE	TAGCTGCCGAAT
00507179.1	GAGTAACT	CTCAACCTC	GAGTTCCA	CCTGAAGAAGCA	GEGECCECEE	TAGCTGCCGAAT
00507180.1	GAGTAACT	CTRACTE	CAGTICCA	CCTGAAGAAGCA	GEGECCECEC	PAGCTGCCGAAT
00507176.1	GAGTAACT	CTCAACCTC	GAGTICCA	CCTGAAGAAGCA	GEGECCECEC	TAGCTGCCGAAT
00507165.1	GAGTAACT	CTCAACCTC	CAGTOCCA	CCTGAAGAAGCA	Geeeccecec	TAGCTGCCGAAT
00507163.1	GAGTAACT	CTCAACCTC	GAGTICCA	CCTGAAGAAGCA	GEGECCECEC	TAGCTGCCGAAT
00507183.1	GAGTAACT	CTCAACCTC	GAGTICCA	CCTGAAGAAGCA	GEGECCECEE	TAGCTGCCGAAT
00507196.1	GAGTAACT	CTCAACCTC	CAGTICCA	CCTGAAGAAGCA	Geeeccecee	PAGCTGCCGAAT
00507162 1	CACTAACT	CTTC A A CCTTC	CACTICCA	COTCALCALCO	CCCCCCCCCC	TACCTCCCCANT
00507177 1	CACTAACT	CTC A CCTC	CACTUCCA	COTCALCALCOL	cccccccccc	TAGCIGCCGAAT
00507196 1	CACTAACT	ATCOACCTC	CACTUCCA	COTCALCALCO	cccccccccc	TAGCTGCCCAAT
00507199 1	GAGTAACT	CTREALCOTE	CACTICCA	COTCALCALCO	ccccccccc	PACCTCCCCAAT
00507164 1	CACTAACT	CTCAACCTC	CACTICCA	CCTCAACAACCA	cccccccccc	TACCTCCCCAAT
00507195 1	CACTAACT	CTCAACCTC	CACTUCCA	COTCALCALCO	cccccccccc	TAGCTGCCCAAT
00507154 1	GAGTAACT	CTCAACCTC	CACTICCA	CCTCAAGAAGCA	ccccccccc	PACCTCCCCAAT
00507156.1	GAGTAACT	CTCAACCTC	CACTICCA	CCTGAAGAAGCA	GCCCCCCCCCC	TACCTCCCCAAT
00507167.1	GAGTAACT	CTCAACCTC	CAGTICCA	CCTGAAGAAGCA	GEGECCECEC	TACCTCCCCAAT
00507168.1	GAGTAACT	CTCAACCTC	GAGTICCA	CCTGAAGAAGCA	GEGECCECEC	TAGCTGCCGAAT
00507169.1	GAGTAACT	CTCAACCTC	GAGTICCA	CCTGAAGAAGCA	GEGECCECEE	TAGCTGCCGAAT
00507170 1	CACTAACT	CREARCERC	CACTOCA	CCTCAACAACCA	cecececec	TACCTCCCCANT
00507171.1	GAGTAACT	CTCACCTC	GAGTICCA	CCTGAAGAAGCA	GCCCCCCCCC	TAGCTGCCGAAT
00507173.1	GAGTAACT	CTCAACCTC	GAGTICCA	CCTGAAGAAGCA	GEGECCECEC	TAGCTGCCGAAT
00507174.1	GAGTAACT	CTCAACCTG	GAGTTCCA	CCTGAAGAAGCA	GEGECCECEE	TAGCTGCCGAAT
00507175.1	GAGTAACT	CTCAACCTG	GAGTTCCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
00507178.1	GAGTAACT	CTCACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
00507181.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
00507182.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
OQ507187.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
00507188.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
OQ507189.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
OQ507190.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
00507191.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
OQ507192.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
OQ507193.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
OQ507194.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GEGECCECEE	TAGCTGCCGAAT
OQ507195.1	GAGTAACT	CTCAACCTG	GAGTTCCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
OQ507197.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
OQ507199.1	GAGTAACT	CTCMACCTG	GAGTICCA	CCTGAAGAAGCA	Geeeccecee	TAGCTGCCGAAT
00507201.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
00507203.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
00507204.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	Geeeccecee	TAGCTGCCGAAT
00507206.1	GAGTAACT	CTCMACCTG	GAGTICCA	CCTGAAGAAGCA	Geeeccecee	TAGCTGCCGAAT
00507207.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
00507172.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GGGGCCGCGG	TAGCTGCCGAAT
00507202.1	GAGTAACT	CTCAACCTG	GAGTICCA	CCTGAAGAAGCA	GEGECCECEE	TAGCTGCCGAAT
00507205.1	GAGTAACT		GAGTICCA	CUTGAAGAAGCA	Geographic	TAGCTGCCGAAT
00507160.1	GAGTAACT		GAGTICCA	CUTGAAGAAGCA	Geographic	TAGCTGCCGAAT
00507155.1	CACTAACT		CACTUCCA	COTGAAGAAGCA	66666666666	TAGCTGCCGAAT
00507152.1	CACTAACT		CACTUCCA	COTCALGAAGCA		TAGCTGCCGAAT
00507153.1	CACTAACT	CTCNACCT6	CACTUCCA	CCTCAAGAAGCA	CCCCCCCCCCC	TACCTCCCCAAT
00507150 1	CACTAACT	CTC/ACCTC	CACTUCCA	CCTCAAGAAGCA	ccccccccc	TACCTCCCCAAT
00507150.1	CACTAACT		CACTUCCA	COTCALCARCO		TACCTCCCCLAT
00507161 1	CACTAACT	CTC/ACCTC	CACTUCCA	CCTCAAGAAGCA	CCCCCCCCCCC	TACCTCCCCAAT
0200/101.1				C C A C A C A C A C A		

	80	90	100	110	120	130
00507166.1	CTATION A COLOGIN	ON WEEK OF	ACTIGUATICA	CCGATGGACT	VACCO ACCURATE OF	ATCCTVACA
00507200.1	CTTCTACTGGT	CATEGACA	ACTGTATGGA	CCGATGGACT	ACCOST	ATCGTTACA
00507183.1	CTTCTACTGGT	CATEGACA	ACTGTATGGA	CCGATEGACT	ACCACTO	ATCGTTACA
00507179.1	CTTCTACTGGT	CATEGACA	ACTGTATGGA	CCGATGGACT	ACCAGTOTTO	ATCGTTACA
00507180.1	CTTCTACTGGT	CATEGACA	ACTGTATGGA	CCGATGGACT	ACCAGECTE	ATCGTTACA
00507176.1	CTTCTACTGGT	CATEGACA	ACTGTATGGA	CCGATEGACT	ACCACTO	ACCECTACA
00507165.1	CTTCTACTGGT	CATEGACA	ACTGTATGGA	CCGATEGACT	ACCACTO	ATCGTTACA
00507163.1	CTTCTACTGGT	CATEGACA	ACTGTATGGA	CCGATGGACT	TACCAGTCTT	ATCGTTACA
00507183.1	CTTCTACTGGT	CATGGACA	ACTGTATGGA	CCGATGGACT	TACCAGTCTT	ATCGTTACA
00507196.1	CTTCTACTGGT	CATGGACA	ACTGTATGGA	CCGATGGACT	ACCAGTCTT	ATCGTTACA
00507162.1	CTTCTACTGGT	CATEGACA	ACTGTATGGA	CCGATGGACT	ACCAGECTE	ATCGTTACA
00507177.1	CTTCTACTGGT	CATEGACA	ACTGTATGGA	CCGATGGACT	ACCAGECTE	ATCGTTACA
00507186.1	CTTCTACTGGT	CATGGACA	ACTGTATGGA	CCGATGGACT	TACCAGTCTTC	ATCGUTACA
00507198.1	CTTCTACTGGT	ACATGGACA	ACTGTATGGA	CCGATGGACTT	ACCAGTCTT	GATCGITACA
00507164.1	CTTCTACTGGT:	ACATGGACA	ACTGTATGGA	CCGATGGACT	FACCAGTCTTO	FAILCGI TACA
00507185.1	CTTCTACTGGT	ACATGGACA	ACTGTATGGA	CCGATGGACTI	FACCAGTCTTC	GATCGT TACA
00507154.1	CTTCTACTGGT	ACATGGACA	ACTGTATGGA	CCGATGGACTI	FACCAGTCTTC	GATCGITACA
00507156.1	CTTCTACTGGT	ACATGGACA	ACTGTATGGA	CCGATGGACTI	FACCAGTCTTC	FATCGITACA
00507167.1	CTTCTACTGGT:	ACATGGACA	ACTGTATGGA	CCGATGGACT	FACCAGTCTTC	GATCGTTACA
00507168.1	CTTCTACTGGT.	ACATGGACA	ACTGTATGGA	CCGATGGACT	FACC AGTCTT	GATCGTTACA
OQ507169.1	CTTCTACTGGT.	ACATGGACA	ACTGTATGGA	CCGATGGACT	FACCAGTCTTC	GATCGTTACA
00507170.1	CTTCTACTGGT:	ACATGGACA	ACTGTATGGA	CCGATGGACTI	FACCAGECTE	FATCGITACA
00507171.1	CTTCTACTGGT	ACATGGACA	ACTGTATGGA	CCGATGGACT	FACC AGTCTTC	GATCGT TACA
00507173.1	CTTCTACTGGT	ACATGGACA	ACTGTATGGA	CCGATGGACT	ГАСС <mark>А</mark> СТСТТО	GATCGTTACA
00507174.1	CTTCTACTGGT:	ACATGGACA	ACTGTATGGA	CCGATGGACTI	FACCAGTCTT	FATCGITACA
00507175.1	CTTCTACTGGT:	ACATGGACA	ACTGTATGGA	CCGATGGACT	FACCAGTCTT	GATCGITACA
00507178.1	CTTCTACTGGT.	ACATGGACA	ACTGTATGGA	CCGATGGACTI	PACCAGTCTTC	GATC GTTACA
00507181.1	CTTCTACTGGT.	ACATGGACA	ACTGTATGGA	CCGATGGACT	ACCAGTOTTO	SAUC GUTACA
00507182.1	CTTCTACTGGT	ACATGGACA	ACTGTATGGA	CCGATGGACTI	ACCAGNETER	SAUCGUTACA
00507187.1	CTTCTACTGGT	ACATGGACA	ACTGTATGGA	CCGATGGACT	ACCAGNETER	SAUCGUTACA
00507188.1	CTTCTACTGGT	ACATGGACA	A CTGTATGGA	CCGATGGACT		AUCGUTACA
00507189.1	CITCIACIGGI	ACATGGACA	ACTGIATGGA	CCGATGGACTI	ACCASICITE	ALCGITACA
00507190.1	CTTCTACTGGT	ACATGGACA	ACTGIAIGGA	CCGATGGACT	ACCASICITE	ALCGITACA
00507191.1	CITCIACIGGI CRECENCER	ACAT GGACA	ACTOTATOGA LONCELNCCL	CCGAIGGACII	ACCAGICITE	AUCCUTACA
00507192.1	CTTCTACTGGT	CATCCACA	ACTGTATGGA	CCCATCCACT	ACCACTCITC	AUCCUTACA
00507194.1	CTTCTACTGGT	CATEGACA	ACTGTATEGA	CCGATGGACT	ACCACTOT	ATCOUTACA
00507195.1	CTTCTACTGGT	CATEGACA	ACTGTATEGA	CCGATGGACT	ACCACTO	ATCGTTACA
00507197.1	CTTCTACTGGT	CATEGACA	ACTGTATGGA	CCGATGGACT	ACCAGTOTTO	ATCGUTACA
00507199.1	CTTCTACTGGT	CATGGACA	ACTGTATGGA	CCGATGGACT	TACCAGTCTT	ATCGUTACA
00507201.1	CTTCTACTGGT:	ACATGGACA	ACTGTATGGA	CCGATGGACTI	ACCAGTCTT	GATCGITACA
00507203.1	CTTCTACTGGT:	CATGGACA	ACTGTATGGA	CCGATGGACTI	ACCAGTCTT	GATCGITACA
00507204.1	CTTCTACTGGT	ACATGGACA	ACTGTATGGA	CCGATGGACT	FACCAGTCTTO	FAILCGITACA
00507206.1	CTTCTACTGGT:	ACATGGACA	ACTGTATGGA	CCGATGGACTI	ACCAGTOTTO	FAILCGITACA
00507207.1	CTTCTACTGGT:	ACATGGACA	ACTGTATGGA	CCGATGGACTI	FACCAGTCTT	GAUCGUTACA
00507172.1	CTTCTACTGGT	ACATGGACA	ACTGTATGGA	CCGATGGACTI	FACCAGTCTTC	FATCGTTACA
00507202.1	CTTCTACTGGT	ACATGGACA	ACTGTATGGA	CCGATGGACT	FACCAGTCTTC	GATCGITACA
00507205.1	CTTCTACTGGT:	ACATGGACA	ACTGTATGGA	CCGATGGACT	ACCAGTCTT	GATCGTTACA
00507160.1	CTTCTACTGGT.	ACATGGACA	ACTGTATGGA	CCGATGGACT	FACCAGTCTT	GATCGTTACA
00507155.1	CTTCTACTGGT.	ACATGGACA	ACTGTATGGA	CCGATGGACT	FACCAGTCTT	GATCGITACA
00507152.1	CTTCTACTGGT:	ACATGGACA	ACTGTATGGA	CCGATGGACT	PACCAGTCTTO	GATCGTTACA
00507153.1	CTTCTACTGGT.	ACATGGACA	ACTGTATGGA	CCGATGGACT	TACCAGTCTTC	ALC GUTACA
00507157.1	CTTCTACTGGT.	ACATGGACA	ACTGTATGGA	CCGATGGACT	VACCAGTOTTO	SAUC GUTA CA
00507158.1	CTTCTACTGGT.	ACATGGACA	ACTGTATGGA	CCGATGGACTI	ACCACTOTIC	SATCGITACA
00507159.1	CTTCTACTGGT.	ACATGGACA	ACTGTATGGA	CCGATGGACT	VACEAGTOTIC	SATC GITACA
00507161.1	1 45 10 1 45 V 1 46 1 1 1 1 5 V	THE BEACH THE P	ENGLISH SUCCES		U EMMAILS UM GU	7.1

	140	150	160	170	180	190
00507166.1	ANGEGEGATE	CT MCCCCCATC	GAGCGTGTT	SIMILE G MEAN	AAAGATCA	ATATATICETTATE
00507200.1	AAGGGCGATG	CTTCCGCATC	GAGCGTGTT	STITEGAGA	AAAGATCA	ATATATTCOTTATC
00507103 1	AACCCCCATC	CTACCCCATC	CACCETCTT	ann clo cloab	AAAGAGAC	ATATATTCCTTATC
00507170 1	AAGGGGGATG	CTNCCCCATC	CACCCECTE		A A A CATCA	37373776677376
00507100 1	AAGGGCGAIG	CTRCCGCATC	CACCOLCIN		A A A GATCA	
00507180.1	AAGGGCGAIG	CTACCGCATC	GAGCGIGIT	ST TGG AGAI	AAAGATCA	ATATATIGETTATE
00507176.1	AAGGGCGATG	CTACCGCATC	GAGCGIGIT		TATA GALCCA	
00507165.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STIGIAGAU	AAAAATCA	ATATATTGITTATA
00507163.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STTEGAGAI	AAAGACCA	ATATATTGCTTATG
00507183.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STTEGAGA	AAAGACCA	ATATATTGCTTATG
00250/196.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STILLE G MISAL	AAAGAICA	ATATATTGCTTATG
00507162.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STOLEG VEAT	AAAGATCA	ATATATTGETTATE
00507177.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STOLEG MEAT	AAAGATCA	ATATATTGOTTATC
00507186.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STILLE GAGAI	AAAGATCA	ATATATTGUTTATE
00507198.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST TIGG AGAI	AAAGATCA	ATATATTGOTTATG
00507164.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITEG AGAI	AAAGATCA	ATATATTGOTTATE
00507185.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITICG AGAI	AAAGATCA	ATATATTGETTATE
00507154.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITIGG AGAI	AAAGATCA	ATATATTGOTTATC
00507156.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITIGG AGAI	AAAGATCA	ATATATTGETTATE
00507167.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STUDG AGAI	AAAGATCA	ATATATTGETTATE
00507168.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITEG AGAI	AAAGATCA	ATATATTGOTTATE
00507169.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITIG G AGAI	AAAGATCA	ATATATTGOTTATC
00507170.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST TGG AGA /	AAAGATCA	ATATATTGCTTATG
00507171.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST TGG AGAI	AAAGATCA	ATATATTGCTTATG
00507173.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST T G G A GAJ	AAAGATCA	ATATATTGCTTATG
00507174.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST TGG AGAI	AAAGATCA	ATATATTGCTTATG
00507175.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STTGG AGA /	AAAGATCA	ATATATTGCTTATG
00507178.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST TGG AGA /	AAAGATCA	ATATATTGCTTATG
00507181.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST TGG AGAI	AAAGATCA	ATATATTGCTTATG
00507182.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST T G G A GAJ	AAAGATCA	ATATATTGCTTATG
00507187.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST TGG AGAI	AAAGATCA	ATATATTGCTTATG
OQ507188.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITIGIG AIGAI	AAAGATCA	ATATATTGOTTATG
OQ507189.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITIC G AGAI	AAAGATCA	ATATATTGOTTATG
002507190.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST T G G A GA I	AAAGATCA	ATATATTGCTTATG
00507191.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST TGG AGAI	AAAGATCA	ATATATTGCTTATG
00507192.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST T G G A GA /	AAAGATCA	ATATATTGCTTATG
00507193.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST T G G A G A I	AAAGATCA	ATATATTGCTTATC
00507194.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST TGG AGAI	AAAGATCA	ATATATTGCTTATG
00507195.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST TGG AGAI	AAAGATCA	ATATATTGCTTATC
00507197.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST TIGG AGAI	AAAGATCA	ATATATTGOTTATG
00507199.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	GTTTGG AGAI	AAAGATCA	ATATATTGOTTATE
00507201.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITEG AGAI	AAGATCA	ATATATTGOTTATG
00507203.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITIEG AGAI	AAAGATCA	ATATATTGOTTATG
00507204.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITIGG AGAI	AAAGATCA	ATATATTGCTTAT
00507206.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST T G G A G A I	AAAGATCA	ATATATTGCTTATG
00507207.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST TGG AGAI	AAAGATCA	ATATATTGOTTATG
00507172.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITIGG AGAI	AAAGATCA	ATATATTGOTTATG
00507202.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITIGIG AIGAI	AAAGATCA	ATATATTGOTTATC
00507205.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STILLEG AGAI	AAAGATCA	ATATATTGOTTATG
00507160.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STILLEG AGAI	AAGATCA	ATATATTGCTTATC
00507155.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STILLEG AGAI	AAGATCA	ATATATTGCTTATG
00507152.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITIGG AIGA J	AAAGATCA	ATATATTGCTTATG
00507153.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	ST TIGG AIGA /	AAAGATCA	ATATATTGCTTATC
00507157.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STILLEG ALEAT	AAGATCA	ATATATTGOTTATG
00507158.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	GTTGG AGAI	AAAGATCA	ATATATTGCTTATG
00507159.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	STITCG AGAI	AAAGATCA	A TA TA TTGCTTA TG
00507161.1	AAGGGCGATG	CTACCGCATC	GAGCGTGTT	GUILLE G A GA I	AAAGATCA	ATATATTGCTTATC

		200	210	220	23	30	240	250
	00507166.1	TAGOTTACO	G C CIVACIACIO	TITTTTAAA	SAAGETT	GTAC	T A AMA A	AAAGEGENALANAA
	00507200.1	TAGCTTACC	CTTTAGACC	TTTTTGAA	GAAGGG	CCGTTT	CAACAT	GTTTACTTCCATTT
	00507183.1	TAAGTTACC	CTTTAGACC	TTTTTGAA	AGGGTT	COTTA/	CCACAT	GTTTACTTCCTTTG
	00507179.1	TAGCTTACC	CTTTAGACC	TTTTGAA	GAAGGTT	GTT	CACCAC	GTTTACTTCCTTTG
	00507180.1	TAGCTTACC	CTTTAGACC	TTTTTGAA	AAGGTT	CCGTT/	CACCAC	GTTTACTTCCTTTG
	00507176.1	TACCTIVACO	CTTTAGACC	TTTTCAA	SAAGETO	GTT	CAACCT	GTTTACTTCCATTT
	00507165.1	TAGGTTACC	CTTTAGACC	TTTTTGAA	SAAGGTT	GTAI	CAACAT	GTTTACTTCCATTA
	00507163.1	TACCTIVACO	CTTTAGACC	TTTTCAA	AARCTO	GGTI	CACCAT	GTTTACTTCCTTTC
	00507183.1	TACCTIVACO	CTTTAGACC	TTTTCAA	SAACCT1	GTT	CACCAT	GTTTACTTCCTTTG
	00507196.1	TACCTTACC	CTTTAGACC	TTTTTGAA	AAGGTT	GTT	CANCAT	GTTTACTTCCATTG
	00507162 1	TACCHERACO	CTTWACACC	TTTTCAA	MARGT 1	GTT	CANDAT	GTTTAC THE ANTE
00007198.1 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00 77.00	00507177.1	TACCTTACC	CTTTACACC	TTTTTAAA	AARCTT	GTTZ	CANCAT	GTTTACHTCANTG
00507199.1 TAC TTACC TTACCCTTACACCTTATONA CALCULATIONAL CALCULATION CALCULATIONAL	00507196 1	TACCTTACC	CTTTACACC	TTTTTAAA	AARCT	CTT	CANDAT	CTTTNCHACOANTC
	00507198.1	TACCTUACO	CTTTAGACC	TTTTTCAA	AAGETT	GTT	CANDAT	GTTTACTCCATC
00507185.1 FACC TTACC CTTTACACCTTTTCAACCCTTTTCAACCCTTTTCAACCCGTTACCATCAACATGTTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACTTCAACGATGTTACT	00507164 1	TACCTTACC	CTTTACACC	TTTTTAAA	AAGGTT	GTT	CANDAT	GTTTAC CONTRACTS
00507154.1 7A G C TACC CTT TACACCTT ACACCTTT ACA CATCTTA CAA C	00507185.1	TACCTTACC	CTTTACACC	TTTTTCAA	AARCTT	GTT	CANCAT	GTTTACHACCANTC
00507156.1 7A GC TACC CTT TACACCTTTACACCTTTACACCTTTACACCTTTACACCAACATCTTACCTACCAACATCTTACCTCCATTACCTACCAACATCTTACCTCCATTACCTACCAACATCTTACCTCCCATTACCTACCAACATCTTACCTCCCATTACCTACCAACATCTTACCTCCCATTACCTACCAACATCTTACCTCCCATTACCTACCAACATCTTACCTACCAACATCTTACCTCCCATTACCTACCAACATCTTACCTCCCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCCTTAACTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAACATCTTACCTACCAAC	00507154.1	TACCTUACO	CTTTACACC	TTTTTCAA	AARCTT	GTT	CANDAT	GTTTACTCCATC
00507167.1 TAGC TTACC TTTAGACCTITITE ON CANGETTCC GTTACCANCHTGTTA CLOCATE 00507168.1 TACC TTACC TTAGACCTITITE ON CANGETTCC GTTACCANCHTGTTA CATGC 00507168.1 TACC TTACC TTAGACCTITITE ON CANGETTCC GTTACCANCHTGTTA CATGC 00507170.1 TACC TTACC TTAGACCTITITE ON CANGETTCC GTTACCANCHTGTTA CATGC 00507171.1 TACC TTACC TTAGACCTITITE ON CANGETTCC GTTACCANCHTGTTA CATGC 00507173.1 TACC TTACC CTTAGACCTITITE ON CANGETTCC GTTACCANCHTGTTA CATGC 00507173.1 TACC TTACC CTTAGACCTITITE ON CANGETTCC GTTACCANCHTGTAC CATGC 00507173.1 TACC TTACC CTTAGACCTITITE ON CANGETTCC GTTACCANCHTGTAC CATGC 00507178.1 TACC TTACC CTTAGACCTITITE ON CANGETTCC CTTACCATTACC CATGC 00507181.1 TACC TTACC CTTAGACCTITITE ON CANGETTCC CTTACCATTACC CATGC 00507182.1 TACC TTACC CTTAGACCTITITE ON CANGETTCC CTTACACATACTAC CATGCTITACCANCACACACATACTAC 00507181.1 TACC TTACC CTTAGACCTITITE ON CANGETTCC CTTACCATACACATACTAC CATGCTITACCANCACACACATACTAC CATGCTITACCANCACACACACATACTAC 00507182.1 TACC TTACC CTTAGACCTITITE ON CAN	00507156.1	TACCTUACO	CTTTAGACC	TTTTTCAA	AAGETT	GTT	CANDAT	GTTTACTCCATTC
00507169.1 TACCTTACC TTTAGACCTTTTOAL CALGETTC CTTACAACATGTTA CALGETTC CTTACCTTACCCTTACAACATGTTA CALGETTC CALGETTC CALGETTC CALGETTC CALACAACATGTTA CALCTTACCCTTACCCTTACAACATGTTA CALCTTACCCTTACAACATGTTA CALCTTACCCTTACCAACATGTTACAACAACATGTTA CALCTTACCCTTACAACATGTTACAACAACATGTTA CALCTTACCCTTACAACATGTTACAACAACATGTTA CALCTTACCCTTACAACATGTTACAACAACATGTTA CALCTTACCCTTACAACATGTTACAACAACATGTTA CALCTTACCCTTACAACATGTTACAACAACATGTTA CALCTTACCCTTACAACATGTTACAACAACATGTTA CALCTTACCCTTACAACATGTTACAACAACATGTTACAACAACATGTTA CALCTTACCCTTACAACATGTTACAACAACATGTTA CALCTTACCCTTACAACATGTTACAACAACATGTTACAACAACATGTTA CALCTTACCCTTACAACATGTTACAACAACATGTTACAACAACATGTTAACAACATGTTA CALCTTACCCTTACAACAACATGTTACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAACATGTTAACAACAA	00507167.1	TACCTTACC	CTTTACACC	TTTTTAAA	AAGETT	GTTZ	CANCAT	GTTTAC CONCEASTS
00507180.1 TACC TTACC	00507168.1	TACCTTACC	CTTTACACC	TTTTTCAA	AARCTT	GTT	CANCAT	GTTTACTCCATC
00507170.1 71 C TTACC CTTTAGACCTTTTTAA CAGGTTCG GTTAGCAACATGTTTA CTCCATG 00507171.1 72 C TTACC CTTTAGACCTTTTTAA CAGGTTCG GTTAGCAACATGTTTA CTCCATG 00507175.1 73 C TTACC CTTTAGACCTTTTTAA CAGGTTCG GTTACAACATGTTTA CTCCATG 00507175.1 74 C TTACC CTTTAGACCTTTTTAA CAGGTTCG GTTACAACATGTTTA CTCCATG 00507181.7 74 C TTACC CTTTAGACCTTTTTAA CAGGTTCG GTTACAACATGTTTA CTCCATG 00507182.1 74 C TTACC CTTTAGACCTTTTTAA CAGGTTCG GTTACAACATGTTTA CTCCATG 00507182.1 74 C TTACC CTTTAGACCTTTTTAA CAGGTTCG GTTACAACATGTTTA CTCCATG 00507187.1 74 C TTACC CTTTAGACCTTTTTAA CAGGTTCG GTTACAACATGTTTA CTCCATG 00507190.1 74 C TTACC CTTTAGACCTTTTTAA CAGGTTCG GTTACAACATGTTTA CTCCATG 00507191.1 74 C TTACC CTTTAGACCTTTTTAA CAACGTTCCCTTTTCAACAACATGTTTA CTCCATG 00507191.1 74 C TTACC CTTTAGACCTTTTTAA CAACGTTCCCTTTTCAACAACATGTTA CTCCATG 00507191.1 74 C TTACC CTTTAGACCTTTTTAA CAACGTTCCCTTTTCAACAACATGTTA CTCCATG 00507191.1 74 C TTACC CTTTAGACCTTTTTAA CAACGTTCCCTTTTCAACAACATGTTA CTCCATG 00507191.1 74 C TTACC CTTTAGACCTTTTTAACAACGTTCCCTTTTCAACAACATGTTA CTCCATG 00507191.1 74 C TTACC CTTTAGACCTTTTTAAACAACGTTACCACTTTTTAACAACATGTTA CTCCATG 00507191.1 74 C TTACC CTTTAGACCTTTTTAAACACGTTTTTAAACAACGTTACCAACATGTTA CTCCATGC	00507169 1	TACOTTACO	CTTTACACC	TTTTTAAA	AACCT	CTT	CANDAT	CTTTACH COARTC
00507171.1 TAGC CTTTAGACCTTTTTAAA CAGG TCG GTTAG CAA CATGTTTA CTTCAA TG 00507173.1 TAGC CTTACCCTTTAGACCTTTTTAAA CAGG TCG GTTAG CAA CATGTTTA CTTCAA TG 00507175.1 TAGC CTTACCCTTTTAGACCTTTTTAAA CAGG TCG GTTAG CAA CATGTTTA CTTCAA TG 00507175.1 TAGC CTTACCCTTTTAGACCTTTTTAAA CAGG TTCG GTTAG CAA CATGTTTA CTTCAA TG 00507178.1 TAGC CTTACCCTTTTAGACCTTTTTAAA CAGG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507182.1 TAGC CTTACCCTTTAGACCTTTTTAAA CAGG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507182.1 TAGC CTTACCCTTTAGACCTTTTTAAA CAGG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507182.1 TAGC CTTACCCTTTAGACCTTTTTAAA CAGG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507182.1 TAGC CTTACCCTTTAGACCTTTTTAAA CAGG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507189.1 TAGC CTTACCCTTTAGACCTTTTTAAA CAGG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507190.1 TAGC TTACCCTTTAGACCTTTTTAAA CAA GG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507190.1 TAGC TTACCCTTTAGACCTTTTTAAA CAA GG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507190.1 TAGC TTACCCTTTAGACCTTTTTAAA CAA GG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507190.1 TAGC TTACCCTTTTAGAACCTTTTTAAA CAA GG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507190.1 TAGC TTACCCTTTTAGAACCTTTTTAAA CAA GG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507190.1 TAGC TTACCCTTTTAGAACCTTTTTAAA CAA GG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507191.1 TAGC TTACCCTTTAGACCTTTTTAAAA CAA GG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507191.1 TAGC TTACCCTTTAGACCTTTTTAAAA CAA GG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507191.1 TAGC TTACCCTTTAGACCTTTTTTAAA CAA GG TTCG GTTAG CAA CATGTTTA CTTCCAA TG 00507191.1 TAGC TTACCCTTTAGACCTTTTTTAAAA CAA GG TTCCGTTAG CAA CATGTTTA CTTCCAA TG 00507191.1 TAGC TTACCCTTTAGACCTTTTTTAAA CAA GG TTCCGTTAG CAA CATGTTTA CTTCCAA TG 00507191.1 TAGC TTACCCTTTAGACCTTTTTTAAAA CAA GG TTCCGTTAG CAA CATGTTTA CTTCCAA TG 00507191.1 TAGC TTACCCTTTAGACCTTTTTTAAA CAA GG TTCCGTTAG CAA CATGTTTA CTTCCAA TG 00507191.1 TAGC TTACCCTTTAGACCTTTTTTAAAA CAA GG TTCCGTTAG CAA CATGTTTA CTTCCAA TG 00507191.1 TAGC TTACCCTTTAGACCTTTTTTAAAA CAA GG TTCCGTTAG CAA CATGTTTA CTTCCAA TG 005	00507170 1	TACC TRACC	CTT TACACC			CTT	CANDAT	CTTTNO CONTO
00507173.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CGTTACCAACATGTTTACTTCCATG 00507173.1 TAGC TTACC CTTTAGACCTTTTGAA CAGG TIC CGTTACCAACATGTTTACTTCCATG 00507178.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CGTTACCAACATGTTTACTTCCATG 00507181.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CGTTACCAACATGTTACTTCCATG 00507181.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CGTTACCAACATGTTACTTCCATG 00507181.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CGTTACCAACATGTTACTTCCATG 00507181.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CGTTACCAACATGTTACTTCCATG 00507189.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CGTTACCAACATGTTACTTCCATG 00507189.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CGTTACCAACATGTTACTTCCATG 00507189.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CGTTACCAACATGTTACTTCCATG 00507199.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CGTTACCAACATGTTACTTCCATG 00507199.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CG TTACCAACATGTTACTTCCATG 00507199.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CG TTACCAACATGTTACTTCCATG 00507159.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CG TTACCAACATGTTACTTCCATG 00507152.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CG TTACCAACATGTTACTTCCATG 00507152.1 TAGC TTACC CTTTAGACCTTTTTGAA CAGG TIC CG TTACCAACATGTTACTTCCATG 005	00507171.1	TAGOTTAGO	CTTRACACC	TTTTTCAA		CTT?	CARGAI	GITTROFF CONTG
00507175.1 TAGC TTACC CTTTAGACCTTTTTGAACAGG TTCCGTTACCAACATGTTTACTTCCATG 00507175.1 TAGC TTACC CTTTAGACCTTTTTGAACAAGG TTCCGTTACCAACATGTTTACTTCCATG 00507181.1 TAGC TTACC CTTTAGACCTTTTTGAACAAGG TTCCGTTACCAACATGTTACTTCCATG 00507182.1 TAGC TTACC CTTTAGACCTTTTTGAACAAGG TTCCGTTACCAACATGTTACTTCCATG 00507182.1 TAGC TTACC CTTTAGACCTTTTTGAACAAGG TTCCGTTACCAACATGTTACTTCCATG 00507182.1 TAGC TTACC CTTTAGACCTTTTTGAACAAGG TTCCGTTACCAACATGTTACTTCCATG 00507182.1 TAGC TTACC CTTTAGACCTTTTTGAACAAGG TTCCGTTACCAACATGTTACTTCCATG 00507189.1 TAGC TTACC CTTTAGACCTTTTTGAACAAGG TTCCGTTACCAACATGTTACTTCCATG 00507191.1 TAGC TTACC CTTTAGACCTTTTTGAACAAGG TTCCGTTACCAACATGTTACTTCCATG 00507191.1 TAGC TTACC CTTTAGACCTTTTTGAACAGG TTCCG TTACCAACATGTTACTTCCATG 00507191.1 TAGC TTACC CTTTAGACCTTTTTGAACAGG TTCCG TTA	00507172.1	TAGOTTAGO	CTTTRACA CO	TITITI CAA			LOCA AGA 1	GTTTROITCOATIG
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000071611 7.3 G 17.3 G	00507170 1	TAGOTTACC	CTTRACACC	TTTTTCAA TTTTTCAA		CTT?	CARGAT	GITTROFF CONTG
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00507182.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGGTTCC GTTAC CAAGATGTTTA CTTC GAATG 00507189.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGGTTCC GTTAC CAAGATGTTTA CTTC GAATG 00507189.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGGTTCC GTTAC CAAGATGTTTA CTTC GAATG 00507190.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGGTTCC GTTAC CAAGATGTTTA CTTC GAATG 00507191.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGGTTCC GTTAC CAAGATGTTTA CTTC GAATG 00507192.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGGTTCC GTTAC CAAGATGTTTA CTTC GAATG 00507193.1 TAGC TTACC CTTTAGACCTTTTTT GAAGAAGGTTCC GTTAC CAAGATGTTTA CTTC GAATG 00507204.1 TAGC TTACC CTTTAGACCTTTTTT GAAGAAGGTTCC GTTAC CAAGATGTTTA CTTC GAATG 00507204.1 TAGC TTACC CTTTAGACCTTTTTT GAAGAAGGTTCC GTTAC CAAGATGTTTA CTTC GAATG 00507205.1 TAGC TTACC CTTTAGACCTTTTTT GAAGAAGGTTCC GTTAC CAAGATGTTTA CTTC GAATG 00507155.1 TAGC TTACC CTTTAGACCTTTTTT GAAGAAGGTTCC GTTAC CAAGATGTTACTTA CTTC GAATG 00507155.1 TAGC TTACC C	00507102 1	TACOTTACC	CTTRACACC	TTTTTCAA		CTT/	CANDAT	GTTTACT CONTC
00507188.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TTC GTTAG CAACATGTTACTT C GATG 00507189.1 TAGC TTACC CTTTAGACCTTTTT GAAGAGGTTC GTTAG CAACATGTTACTT C GATG 00507191.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGGTTC GTTAG CAACATGTTACTT C GATG 00507101.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGGTC G GTTAG CAACATGTTACTT C GATG 00507201.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGGTC G GTTAG CAACATGTTACTT C GATG 00507201.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGGTC G GTTAG CAACATGTTACTT C GATG 00507201.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGGTC G GTTAG CAACATGTTACTT C GATG 00507201.1 TAGC TTACC CTTTAGACCTTTTT GAAGAGGTC G GTTAG CAACATGTTACTT C GATG 00507201.1 TAGC TTACC CTTTAGACCTTTTT GAAGAGGTC G GTTAG CAACATGTTACTT C GATG 00507201.1 TAGC TTACC CTTTAGACCTTTTT GAAGAGGTC G GTTAG CAACATGTTACTT C GATG 00507201.1 TAGC TTACC CTTTAGACCTTTTT GAAGAGGTC G GTTAG CAACATGTTACTT C GATG 00507201.1 TAGC TTACC CTTTAGACCTTTTT GAAGAGGTC G GTTAG CAACATGTTACTT C GATG 00507120.1 TAGC TTACC CTTTAGACCTTTTT GAAGAGGTC G GTTAG CAACATGTTACTT C GATG 00507150.1 TAGC TTACC CTTTAGACCTTTTT GAAGGTC G GTTAG CAACATGTTACTT C GATG 00507150.1 TAGC TTACC CTTTAGACCTTTTT GAAGGTC G GTTAG CAACATGTTACTT C GATG 00507150.1 TAGC TTACC CTTTAGACCTTTTT GAAGAGGTC G GTTAG CAACATGTTACTT C GATG 00507150.1 TAGC TTACC CTTTAGACCTTTTT GAAGAGGTC G GTTAG CAACATGTTACTT C GATG 00507150.1 TAGC TTACC CTTTAGACCTTTTT GAAGAGGTC G GTTAG CAACATGTTACTT C GATG 00507150.1 TAGC TTACC CTTTAGACCTTTTT GAAGAGGTC G GTTAG CAACATGTTACTT C GATG 0	00507107 1	TACOTTACC	CTTRACACC	TTTTTAAA	DARCET 1	CTT	CANDAT	CTTTACT CONTC
00507189.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TTC GGTTAG CAACATGTTTACTT CAATG 00507190.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TTC GGTTAG CAACATGTTTACTT CATTG 00507192.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507193.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507193.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507193.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507193.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507193.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507197.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507197.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507201.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507201.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507201.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507201.1 TAGC TTACC CTTTAGACCTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507201.1 TAGC TTACC CTTTAGACCTTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507201.1 TAGC TTACC CTTTAGACCTTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507201.1 TAGC TTACC CTTTAGACCTTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507202.1 TAGC TTACC CTTTAGACCTTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 005071201.1 TAGC TTACC CTTTAGACCTTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 005071201.1 TAGC TTACC CTTTAGACCTTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507150.1 TAGC TTACC CTTTAGACCTTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507151.1 TAGC TTACC CTTTAGACCTTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG 00507151.1 TAGC TTACC CTTTAGACCTTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG CATTG 00507151.1 TAGC TTACC CTTTAGACCTTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG CATTG 00507151.1 TAGC TTACC CTTTAGACCTTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG CATTG 00507151.1 TAGC TTACC CTTTAGACCTTTTTT GAA GAAGG TCC GTTAG CAACATGTTACTT CATTG CATTG 00	00507100 1	TACOTTACO	CTTTACACC	TTTTTAAA	A RET	CTT	CANDAT	CTTTACT COATC
00507190.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCC GTTAC CAAGATGTTTACTT CAATG 00507191.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCC GTTACCAAGATGTTTACTT CATTG 00507191.1 TAGC TTACC CTTTAGACCTTTTT GAAGAGG TTCC GTTACCAAGATGTTTACTT CATTG 00507191.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCC GTTACCAAGATGTTTACTT CATTG 00507201.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCC GTTACCAACATGTTTACTT CATTG 00507151.1 TAGC TTACC CTTTAGGACCTTTTT GAAGAAGG TTCC GTTACCAACATGTTTACTT CATTG 00507151.1 TAGC TTACC CTTTAGGACCTTTTT GAAGAGGTTCC GTTACCAACATGTTTACTT CATTG 00507151.1 TAGC TTACC CTTTAGGACCTTTTT GAAGAGGTTCC GTTACCAACATGTTTACTT CATTG 00507151.1 TAGC TTACC CTTTAGGACCTTTTT GAAGAGG	00507100 1	TACOTTACC	CTTTACACC	TTTTTAAA	AACCT	CTT	CANDAT	CTTTACT COATC
00507191.1 TAGC TTACC CT TTAGACCTTTTT GAAGAGG TTC GATLA CAACATGTTTA CTTC GATG 00507192.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC GATG 00507193.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC GATG 00507193.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC GATG 00507193.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC GATG 00507193.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC GATG 00507193.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC GATG 00507197.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC GATG 00507199.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC GATG 00507201.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC GATG 00507203.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC GATG 00507204.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC GATG 00507205.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC CATG 00507205.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC GATG 00507205.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC CATG 00507205.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC CATG 0050715.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTTA CTTC CATG 0050715.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTA CTTC CATG 0050715.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTA CTTC CATG 0050715.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTA CTTC CATG 0050715.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTA CTTC CATG 0050715.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TTC GATLA CAACATGTTA CTTC CATG 0050715.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TC CGTTAC CAACATGTTA CTTC CATG 0050715.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TC CGTTAC CAACATGTTA CTTC CATG 0050715.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TC CGTTAC CAACATGTTA CTTC CATG 0050715.1 TAGC TTACC CT TTAGACCTTTTT GAAGAAGG TC CGTTAC CAACATGTTA CTTC CATG 0050715.1 TA	00507100 1	TACC TRACC	CTT TACACC	TTTTT - 3 3		CTT	CANDAT	CTTTNO CONCEASTO
00507192.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAAGATGTTTACTTCCATG 00507193.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAAGATGTTTACTTCCATG 00507193.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAAGATGTTTACTTCCATG 00507193.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAAGATGTTTACTTCCATG 00507199.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAAGATGTTTACTTCCATG 00507199.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAAGATGTTTACTTCCATG 00507199.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAAGATGTTTACTTCCATG 00507203.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAAGATGTTTACTTCCATG 00507203.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAAGATGTTTACTTCCATG 00507203.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAAGATGTTTACTTCCATG 00507206.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAAGATGTTTACTTCCATG 00507207.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAAGATGTTTACTTCCATG 00507107.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAACATGTTTACTTCCATG 00507107.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAACATGTTTACTTCCATG 00507155.1 TAGC TTACC CTTTAGACCTTTTT GAAGAAGG TTCCGTTACCAACATGTTACTTCCATG 00507157.1 TAGC TTACC CTTTAGACCTTTTTT GAAGAAGG TTCCGTTACCAACATGTTACTTCCATG 00507157.1 TAGC TTACC CTT	00507190.1	TAGUTTACC	CTTTAGACC	TITITCAA TTTTTTCAA		GIT/	USCARDAT	GITTROITCOATIG
00507192.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507193.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507195.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507199.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507199.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507203.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507203.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507203.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507204.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507204.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507204.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507204.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507204.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507204.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507205.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507105.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507155.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507155.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507155.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507155.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507155.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507155.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507155.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507155.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507155.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507155.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507155.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507155.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507155.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCG	00507191.1	TACOTTACC	CTTRACA CO	TTTTTCAA		CTT?	CANDAT	GTTTNOTCONTIG
00507194.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTACTT CCATTG 00507195.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTACTT CCATTG 00507199.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTACTT CCATTG 00507199.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTTACTT CCATTG 00507201.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTTACTT CCATTG 00507203.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTTACTT CCATTG 00507204.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTTACTT CCATTG 00507207.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTTACTT CCATTG 00507207.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTTACTT CCATTG 00507172.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTTACTT CCATTG 00507172.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTTACTT CCATTG 00507155.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTTACTT CCATTG 00507155.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTACTT CCATTG 00507155.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTACTT CCATTG 00507155.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTACTT CCATTG 00507155.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTTACTT CCATTG 00507155.1 TAGC TFACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTTACTT CCATTG 00507155.1 TAGC TTACC CT TTAGACCTTTTT CAAGAAGGTTCC GTTACCAACATGTTTACTT CCATTG 00507157.1 TAGC TTACC CT TTAGACCTTTTTT CAAGAAGGTTCC GTTACCAACATGTTTACTT CCATTG 00507157.1 TAGC TTACC CT TTAGACCTTTTTT CAAGAAGGTTCC GTTACCAACATGTTTACTT CCATTG 00507157.1 TAGC TTACC	00507193 1	TACOTTACC	CTTRACACC	TTTTTAAA	A RET 1	CTT	CANDAT	CTTTACT CONTC
00507195.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507197.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507199.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507201.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507203.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507204.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507204.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507204.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507204.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507207.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507207.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507202.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507205.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507155.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507157.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507157.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507157.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507157.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507157.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507157.1 TAGCTTACCCTTTAGACCTTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG	00507194 1	TACOTTACO	CTTTACACC	TTTTTAAA	A RET	CTT	CANDAT	CTTTACT COATC
00507197.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTTC CATTG 00507199.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTTC CATTG 00507201.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTTC CATTG 00507203.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTTC CATTG 00507204.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTTC CATTG 00507206.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTTC CATTG 00507207.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTTC CATTG 00507107.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTTC CATTG 00507157.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTACTTC CATTG	00507195 1	TACOTTACC	CTTTACACC	TTTTTAAA	AACCT	CTT	CANDAT	CTTTACH COARTS
00507199.1 TAGC TTACC CTT TAGACCTT TOT GAAGAAGGTT CCGTTACCAACATGTTTACTT CCATTG 00507203.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTT CCATTG 00507204.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTT CCATTG 00507204.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTT CCATTG 00507205.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTT CCATTG 00507207.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTT CCATTG 00507205.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTT CCATTG 00507205.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTT CCATTG 00507160.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTT CCATTG 00507155.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTT CCATTG 00507155.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTT CCATTG 00507157.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTT CCATTG 00507157.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTTACTT CCATTG 00507157.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTACTT CCATTG 00507157.1 TAGC TTACC CTT TAGACCTT TTT GAAGAAGGTT CCGTTACCAACATGTTACTACCT CATTG	00507197.1	TACCTTACC	CTTTACACC	TTTTTAAA	AARCTT	GTT	CANCAT	GTTTACHTCANTG
00507201.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507203.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507204.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507206.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507207.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507202.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507202.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507202.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507203.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507203.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507160.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507153.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCCATG 00507153.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCCATG 00507153.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCCATG 00507153.1 TAGC TTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCCATG 00507153.1 TAGC TTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507153.1 TAGC TTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507153.1 TAGC TTACCCTTTAGACCTTTTTGAAGAAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507153.1 TAGC TTACCCTTTAGACCTTTTTGAAGAAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507153.1 TAGC TTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG	00507199.1	TACCTUACO	CTTTACACC	TTTTTCAA	AARCTT	GTT	CANDAT	GTTTACTCCATC
00507203.1 TAGC TTACC CTTTAGACCTTTTTGAAGAGGTTCCGTTACCAACATGTTTACTTCCATG 00507204.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507206.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507207.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507202.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507202.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507202.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507202.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507160.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507155.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507157.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507157.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507157.1 TAGC TTACC CTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507157.1 TAGC TTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507157.1 TAGC TTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507157.1 TAGC TTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507157.1 TAGC TTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507157.1 TAGC TTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACTTCCATG 00507157.1 TAGC TTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTACCTCCATG	00507201.1	TACCTUACO	CTTTAGACC	TTTTTCAA	AAGETT	GTT	CANDAT	GTTTACTCCATTC
00507204.1 TAGC TTACC CTITAGACCTTETTGAAGAGGTTCCGTTACCAACATGTTTACTTCCATG 00507206.1 TAGC TTACC CTITAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507207.1 TAGC TTACC CTITAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507207.1 TAGC TTACC CTITAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507202.1 TAGC TTACC CTITAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507202.1 TAGC TTACC CTITAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507202.1 TAGC TTACC CTITAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507105.1 TAGC TTACC CTITAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507155.1 TAGC TTACC CTITAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507155.1 TAGC TTACC CTITAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507155.1 TAGC TTACC CTITAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507155.1 TAGC TTACC CTITAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATG 00507153.1 TAGC TTACC CTITAGACCTTETTGAAGAAGGTTCCG	00507203.1	TACCTTACC	CTTTAGACC	TTTTTCAA	AAGGTT	GTT	CANCAT	GTTTACTTCCATTC
00507206.1 TAGC TTACC CTTTAGACCTTETTGAAGAGGTTCCGTTACCAACATGTTACTTCCATTG 00507207.1 TAGC TTACC CTTTAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507207.1 TAGC TTACC CTTTAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507202.1 TAGC TTACC CTTTAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507202.1 TAGC TTACC CTTTAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507205.1 TAGC TTACC CTTTAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507155.1 TAGC TTACC CTTTAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507153.1 TAGC TTACC CTTTAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507153.1 TAGC TTACC CTTTAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGC TTACC CTTTAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGC TTACC CTTTAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGC TTACC CTTTAGACCTTETTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGC TTACC CTTTAGACCTTE	00507204.1	TACCTTACC	CTTTAGACC	TTTTTCAA	AAGETT	GTT	CANCAT	GTTTACTTCCATTC
00507207.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507207.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507202.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507205.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507160.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507160.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507155.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507152.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507153.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507153.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGC TTACC CTT TAGACCTT TTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG	00507206 1	TACCTURACO	CTTTACACC	TTTTTAAA	NARET 1	CTT	CANDAT	CTTTNC CONCEASTC
00507172.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507202.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507205.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507160.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507155.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507152.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507153.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507153.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGC TTACC CTT TAGACCTT TTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG	00507207 1	TACOTTACO	CTTTACACC	TTTTTAAA	AACCT	CTT	CANDAT	CTTTACH COARTC
00507202.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507205.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507160.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507155.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507152.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507153.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507153.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507158.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507158.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507161.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG	00507172 1	TACOTTACO	CTTTACACC	TTTTTAAA	AACCT	CTT	CANDAT	CTTTACH COARTC
00507205.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507160.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507155.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507152.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507153.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507158.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGC TTACC CTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507161.1 TAGC TTACCCTT TAGACCTT TTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG	00507202.1	TACCTTACC	CTTTACACC	TTTTTAAA	AACCT	CTT/	CANDAT	CTTTAC CONCEASTS
00507160.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507155.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507152.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507153.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507158.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507161.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG	00507205.1	TAGOTTACO	CTTTACACC	TTTTTCAA	AAGET	GTT	CANCAT	GTTTACTOCCAPTC
00507155.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507152.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507153.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507158.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG	00507160.1	TAGOTTACO	CTTTACACC	TTTTTCAA	AAGETT	GTT	CANCAT	GTTTACTOCCANTO
00507152.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507153.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507158.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507161.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG	00507155.1	TAGOTTACO	CTTTACACC	TTTTTCAA	AAGETT	GTT	CANCAT	GTTTACTOCCANTC
00507153.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507157.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507158.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG	00507152 1	TAGCTTACC	CTTTAGACC	TTTTTGAA	AAGGTT	GTT	CAACAT	GTTTACTTCCAUTG
00507157.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507158.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507161.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG	00507153.1	TAGCTTACC	CTTTAGACC	TTTTTGAA	AAGGTT	GGTT	CAACAT	GTTTACTTCCATTG
00507158.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507161.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG	00507157.1	TAGCTTACC	CTTTAGACC	TTTTTGAA	SAAGGTT	CCGTT/	CAACAT	GTTTACTTCCATTG
00507159.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG 00507161.1 TAGCTTACCCTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG	00507158.1	TAGCTITACO	CTTTAGACC	TTTTTGAA	SAAGGTT	GGTT	CANCAT	GTTTACTTCCATTC
00507161.1 TAGCTTACCCTTTTAGACCTTTTTGAAGAAGGTTCCGTTACCAACATGTTTACTTCCATTG	00507159.1	TAGOTTACO	CTTTACACC	TTTTTCAA	ARETT	GTT	CANDAT	GTTTRCCCCAPTC
	00507161.1	TAGCTTACC	CTTTAGACC	TTTTTGAA	AAGGTT	CCGTT	CAACAT	GTTTACTTCCATTG
	260	270	280	290	300	310		
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00507166.1	AAGAAAGA	GTATTTAGGG	TAAAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GCGCTCTG	GGTCCCCAAC	ATCTCCGGAACC		
00507200.1	TAGGTAAT	GTATTTGGGGG	TAAAGCCCTGC	GCCCCCA	CCTCTGGAAG	AACTGCCAATCC		
00507183.1	TAGGGAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CTTCCGGAAG	ATCTGCGAATCC		
00507179.1	TAGGGAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTCCGAATCC		
00507180.1	TAGGGAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTCC GAATCC		
00507176.1	TAGGGAAT	GTATTTGGGT	TAAAGGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGCGAATCC		
00507165.1	GAGATAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCGA	CGTCTGGAAG	ATCTGCCAATCC		
00507163.1	TAGGGAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGCGAATCC		
00507183.1	TAGGGAAT	GTATTTGGTT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTCCGAATCC		
00507196.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCCGC	CTTCTCTA	CCCCCGGATI	ATCTGCGATTCC		
00507162.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGGTGTA	GUTCTCCAAG	ATCREGAATCC		
00507177.1	TAGG TAA T	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGCAAG	ATCTCCGAATCC		
00507186.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTCCAAG	ATCTCCGAATCC		
00507198.1	TAGG TAA T	GTATTTGGGT	CAAAGCCCTGC	GCGCTCTA	CGTCTCCAAG	ATCTCCGAATCC		
00507164.1	TAGGTAAT	GTATTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGCAAC	ATCTCCGAATCC		
00507185.1	TAGG TAA T	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGCAAG	ATCTCCGAATCC		
00507154.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTCCAAG	ATCTCCGAATCC		
00507156.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGGTGTA	CGTCTCCAA	ATCTGCGAATCC		
00507167.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGCGAATCC		
00507168.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGGTGTA	CGTCTCCAA	ATCTGCGAATCC		
00507169.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGCGAATCC		
00507170.1	TAGG TAA T	GTATTTGGGT	TAAAGCCCTCC	GCGCTCTA	GTCTCCA	ATCTCCGAATCC		
00507171.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTCC	GCGCTCTA	GTCTGGAAG	ATCTGCGAATCC		
00507173.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTCC	GCGCTCTA	GGTCTGGAAG	ATCTCCGAATCC		
00507174.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTCCAAG	ATCTGCGAATCC		
00507175.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGGTGTA	CGTCTCCAAG	ATCTCCGAATCC		
00507178.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGCGAATCC		
00507181.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGCGAATCC		
00507182.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTCC GAATCC		
00507187.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTCC GAATCC		
00507188.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTCCAAG	ATCTGCGAATCC		
00507189.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGC GAATCC		
00507190.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTCCAAG	ATCTGC GAATCC		
00507191.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTCGAAG	ATCTGCGAATCC		
00507192.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTCGAAG	ATCTGCGAATCC		
00507193.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGCGAATCC		
00507194.1	TAGGTAAT	GTATTTGGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGC GAATCC		
00507195.1	TAGG TAA T	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGC GAATCC		
00507197.1	TAGG TAA T	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGCGAATCC		
00507199.1	TAGG TAA T	GTATTTGGGT	TIAAAGCCCIIGC	GCGCTCTA	CGTCTGGAAG	ATCTGCGAATCC		
00507201.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGICIGGAAG	ATCTGCGAATCC		
00507203.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCIGC	GCGUTUTA	CGICIGGAAG	ATCTGCGAATCC		
00507204.1	TAGGTAAT	GTATTTGGGT.	TAAAGCCCTGC	GCGUTUTA	CGICIGGAAG	ATCIGCGAATCC		
00507206.1	TAGG TAA T	GTATTTGGGT	TTAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGCGAATCC		
00507207.1	TAGG TAA T	GTATTTGGGT	TIAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGCGAATCC		
00507172.1	TAGG TAA T	GTATTTGGGT	TIAAAGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGCGAATCC		
00507202.1	TAGG TAA T	GTATTTGGGT	TAANGCCCTGC	GCGCTCTA	CGTCTGGAAG	ATCTGCGAATCC		
00507205.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGCTCTA	CGICIGGAAG	ATCTGCGAATCC		
00507160.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCIGC	GCGUTUTA	CGICIGGAAG	ATCTGCGAATCC		
00507155.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCIGC	GCGCTCTA	CGICIGGAAG	ATCTGCGAATCC		
00507152.1	TAGGTAAT	GTATTTGGGT	THAAAGCCCIIGC	GCGUTUTA	CGICIGGAAG	ATCTGCGAATCC		
00507153.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCIGC	GCGGTGTA	CGICIGGAAG	ATCTGCGAATCC		
00507157.1	TAGGTAAT	GTATTTGGGT.	TAAAGCCCTGC	GCGGTGTA	CGICIGGAAG	ATCTGCGAATCC		
00507158.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCTGC	GCGETETA	GETCTGGAAG	ATCTGCGAATCC		
00507159.1	TAGGTAAT	GTATTTGGGT	TAAAGCCCIGC	GCGUTUTA	CGICIGGAAG	ATCTGCGAATCC		
00507161.1	THEG THAT	I SHOW HIGH GIRLET	A 17 V. LA LEINING THEIN	GCGINTINTA	ING TINTING A G	TIMENTINGAATIMA		

	320	330	340	350	360	370
00507166.1 (TGTTGCTTAT	ATTAAACT	TTCCAAGGT	CCCCC TCAT GCC	ATCCAAGTT	GAAAGAGATA
00507200.1 (TGTTGTTAT	ATTAAAAAT	TTCCAAGGG	CCGCCTCCCGGG	GTCCAAGTT	GAAAAAATA
00507183.1 (TGTTGCTTAT	GTTAAAACT	TTCCAAGGG	CCGCCTCATTGG	ATCCAAGTT	GAAAGAGATA
00507179.1 (TGTTGCTTAT	ATTAAAACT	TTCCAGGGT	CCGCCTCATGGG	ACCCAAGTG	AAAAGTGATA
00507180.1 (TGTTGCTTAT	ATTAAAACT	TTCCAGGGT	CCGCCTCATGGG	ACCCAAGTG	AAAAGTGATA
00507176.1 (TGTTGCTTAT	ATTAAAACT	TTCCAGGG	CCGCCCCTCTGG	ACCCAAGTT	GAGAGAGAAA
00507165.1 (TGTTGCTTAT	GTTAAAACT	TTTCAGGGT	CCGCCTCATGGG	Α	
OQ507163.1 (TGTTGCTTAT	GTTAAAACT	TTCCAGGGT	CCCCCTCATGGG	ACCCAAGTT	GAAAGAGAGA
OQ507183.1 (TGTTGCTTAT	GTTAAAACT	TTCCAGGGT	CCCCCTCATGCG	ACCCAAGTT	GAAAGAGAGA
OQ507196.1 (TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCGCCTCATGGG	AT	
00507162.1 (TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCGCCTCATGGG	ATCCAAGTT	GAAAGAGATA
00507177.1	TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCCCCTCATGGG	ATCCAAGTT	GAAAGAGATA
00507186.1	TGTTGCTTAI	ATTAAAACT	TTCCAAGGI	CCGCCTCATGGG	ATCCAAGIT	GAAAGAGATA
00507198.1	TGTTGC TTAT	ATTAAAACT		CCCCCTCATGEG	ATCCAAGIT	GAAAGAGATA
00507104.1 (GITAAAACT		COCCCTCATGES	ATCCAAGII	CARAGAGAIA
00507154 1	TOTTOCTAT	ATTAAAACT	TTCCAACCT	CCCCCTCATCCC	ATCCAAGTT	CANACACATA
00507156.1	TGTTGOTTAT	ATTAAAACT	TTCCAACCT	CCCCCTCATCCC	ATCCAAGTT	GAAAGAGATA
00507167.1	TGTTGGTTAT	ATTAAAACT	TTCCAAGET	COCOTOATGE	ATCCAAGTT	GAAAGAGATA
00507168.1	TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CECETEATGE	ATCCAAGTT	GAAAGAGATA
00507169.1	TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCCCCTCATGEC	ATCCAAGTT	GAAAGAGATA
00507170.1	TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CECETEATGE	ATCCAAGTT	GAAAGAGATA
00507171.1 (TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCGCCTCATGGG	ATCCAAGTT	GAAAGAGATA
00507173.1 0	TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCGCCTCATGGG	ATCCAAGTT	GAAAGAGATA
00507174.1 (TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCGCCTCATGGG	ATCCAAGTT	GAAAGAGATA
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00507178.1 (TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCCCCTCATGCG	ATCCAAGTT	GAAAGAGATA
00507181.1	TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCGCCTCATGGG	ATCCAAGTT	GAAAGAGATA
00507182.1	TGTTGCTTAT	ATTAAAACT	TTCCAAGGI	CCCCCTCATGCC	ATCCAAGTT	GAAAGAGATA
00507187.1	TGTTGCTTAT	ATTAAAACT	TTCCAAGGI	CCGCCTCATGGG	ATCCAAGTT	GAAAGAGATA
00507188.1 (TGTTGCTTAT	ATTAAAACT		COCCOTON TOGO	AICCAAGII ATCCAACTT	GAAAGAGAIA
00507189.1 (A TRAANCE			ATCCARGIT	CANAGAGAIA
00507191.1	TGIIGCIIAI	ATTAAAACT	PROGALOGI	COCCTCATORS	ATCCAAGIT	CANAGAGAIA
00507192.1	TGTTGGTTAT	ATTAAAACT	TTCCAAGET	CCCCCTCATCCC	ATCCAAGTT	GAAAGAGATA
00507193.1	TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCCCCTCATGCC	ATCCAAGTT	GAAAGAGATA
00507194.1 (TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCGCCTCATGGG	ATCCAAGTT	GAAAGAGATA
00507195.1 (TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCGCCTCATGGG	ATCCAAGTT	GAAAGAGATA
OQ507197.1 (TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCCCCTCATGGG	ATCCAAGTT	GAAAGAGATA
OQ507199.1 (TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCGCCTCATGGG	ATCCAAGTT	GAAAGAGATA
00507201.1	TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CEGECTEATGEG	ATCCAAGTT	GAAAGAGATA
00507203.1	TGTTGCTTAI	ATTAAAACT	TTCCAAGGI	CCGCCTCATGGG	ATCCAAGIT	GAAAGAGATA
00507204.1 (TGTTGC TTAT	ATTAAAACT			AICCAAGII	GAAAGAGATA
00507206.1	TGTTGUTTAI	ATTAAAACT ATTAAAAACT		COCCUTOATOGG	ATCCAAGII	CANAGAGAIA
00507172 1 (16116011A1	ATTAAAACT		COCCTCATOGG	ATCCAAGII	CANACAGATA
00507202.1	TGTTCOTTAT	ATTAAAACT	TTCCAACCT	CCCCCTCATCCC	ATCCAAGTT	GAAAGAGATA
00507205.1	TGTTGCTTAT	ATTAAAACT	TTCCAAGET	CEGECTEATGEC	ATCCAAGTT	GAAAGAGATA
00507160.1	TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CECECTEATGE	ATCCAAGTT	GAAAGAGATA
00507155.1	TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCCCCTCATGEC	ATCCAAGTT	GAAAGAGATA
00507152.1	TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCGCCTCATGGG	ATCCAAGTT	GAAAGAGATA
00507153.1 (TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCGCCTCATGGG	ATCCAAGTT	GAAAGAGATA
OQ507157.1 (TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCGCCTCATGGG	ATCCAAGTT	GAAAGAGATA
OQ507158.1 (TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCCCCTCATGCC	ATCCAAGTT	GAAAGAGATA
00507159.1 (TGTTGCTTAT	ATTAAAACT	TTCCAAGGT	CCCCCTCATGCG	ATCCAAGTT	GAAAGAGATA
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	380	390	400	410	420	430
00507166.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	ATGTACTATT	AAACCTAAA	TTGGGGTTAT
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00507183.1	AATTGAACA	ATTATGGCCGTC	CCCTGTTGGG	GTGTACTATT	AAACCTAAA	TTGGGTTTAT
00507179.1	AATTGAACA	AGTGTGGTCGCG	CCCTGTTGGG	GTGTACTATT	AAACCTAAAI	TTGGGGTTCT
00507180.1	AATTGAACA	GATGTGGTCGCG	CCCTGTTGGG	GTGTACTATT	AAACCTAAAI	TTGGGGTTCT
00507176.1	AATTGAACA:	TGTATGGCCGTC	CCCTGTTGGG	GTGTACTATT	AAACCTAAA)	TTGGGGTTTT
00507165.1						
00507163.1	AATTGAACA	AGTGGCGTCGTC	CCCTGTTGGG	GTGTACTATT	AACCTTAAA)	TTGGGGTTAT
00507183.1	AATTGAACA	AGTATGGCCGGC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA:	TTGGGGTTAT
00507196.1						
00507162.1	AATTGAACA	AGTTGGGTCGTC	CCCTGGTGGG	GATGTACTATT	AAACCTAAA	GTGGGGTTAT
00507177.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTTCTATT	AAACTTTTA:	FTGGGGTTA.
00507186.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA:	FTGGGGTTAT
00507198.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA:	FTGGGGTT T .
00507164.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT
OQ507185.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA1	FTGGGGTTAT
00507154.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA1	FTGGGGTTAT
00507156.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT
00507167.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT
00507168.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT
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00507171.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT
00507173.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT
00507174.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT
00507175.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT
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00507181.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT
00507182.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAAI	TTGGGGTTAT
00507187.1	AATTGAACA	AGTATEGTCETC	CCCTGTTGGG	SATGTACTATT	AAACCTAAAT	FTGGGGTTAT
00507188.1	AATTGAACA	AGTATEGTCETC	CCCTGTTGGG	SATGTACTATT	AAACCTAAA	TTGGGGTTAT
00507189.1	AATIGAACA	AGIAIGGIUGIU	CCCIGIIGGE	AIGIACIAII	AAAUUIAAA.	TIGGGGTTAL
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00507191.1	AATTGAACA	AGTATEGTUGTU	CCCTGTTGGG	SAIGIACIAII	AAACCIAAA	TIGGGGTTAT
00507192.1	AATTGAACA	AGIAIGGICGIC	CCCTGTTGGG	AIGIACIAII	AAACCIAAA:	TIGGGGTTAT
00507193.1	AATTGAACA	AGIAIGGIUGIU	CCCTGIIGGG	AIGIACIAII	ARACCIARA.	TTCCCCTTAT
00507194.1	AATTGAACA	AGIAIGGICGIC	CCCTGTTGGG	ATGIACIAII ATCIACIATI	AAACCIAAA:	TCCCCCTTAT
00507197.1	AATTCAACA	AGIAIGGICGIC	CCCTGTTGGG	ATCTACTATT	AAACCTAAA:	TCCCCTTAT
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00507201.1	AATTGAACA	AGTATEGTCETC	CCCTGTTGGG	ATGTACTATT	AAACCTAAA	TTGGGGTTAT
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00507204.1	AATTGAACA	AGTATEGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT
00507206 1	AATTGAACA	AGTATEGTCETC	CCCTGTTGGG	ATGTACTATT	AAACCTAAA	TTGGGGTTAT
00507207.1	AATTGAACA	AGTATEGTCETC	CCCTGTTGGG	ATGTACTATT	AAACCTAAA	TTGGGGTTAT
00507172.1	AATTGAACA	AGTATEGTCETC	CCCTGTTGG	SATGTACTATT	AAACCTAAA	TTGGGGTTAT
00507202.1	AATTGAACA	AGTATEGTCETC	CCCTGTTGG	ATGTACTATT	AAACCTAAA	TTGGGGTTAT
00507205.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	ATGTACTATT	AAACCTAAA	TTGGGGTTAT
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00507155.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT
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00507153.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT
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00507158.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT
00507159.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT
00507161.1	AATTGAACA	AGTATGGTCGTC	CCCTGTTGGG	GATGTACTATT	AAACCTAAA	TTGGGGTTAT

	440	450	460	470	480	490
00507166.1	CIGCIAAAA	ACCTCGGTAGA	GCTGTTTATG.	AATGTCTTCGC	GGTGTGGT	IGATITICCCA
00507183.1	CTECTAAAT	ACGAGAGTATT	CTGTTTACG	AATGTTTACGC	GGTGGAAC	GATTTTACCA
00507179.1	GTGCTAAAA	ACTACGAGAGA	GTTATTTATG	GATGTCTCCGC	GGTGGGAT	IGATTTTACCA
00507180.1	GIGCIAAAA	ACTACGAGAGT	GCTATTTATG	GATGTCTCCGC	GGTGGGAT	FGATTTTACCA
00507176.1	CIGCIAAAT	ACGACGGTATT	GATGTTTCGG	AATGTCTTCGC.	AATGGAATI	FGATTTTACCA
00507165.1						
00507163.1	CIGTIAAAA	AATACGGTAGA	GTTGTTGATG.	AATGTCTCCGC	GGTGGGAT	IGATITITACCA
00507183.1	CIGCIAAAA	ACTACGAGAGA	GCTGTTTATG	GATGTCTCCGC	GGTGGATT	IGATITIACCA
00507190.1	CTCCTAAAA	ACTACCCCAAA	CTOTTATO		COTOCACT	CATTTAACCA
00507177 1	CIGCIAAAA	ACTACGGGAAA	SCIGITIAIG.	AAIGICIICGC	GGIGGACI.	IGATITAACCA
00507186.1	CTECTAAAA	ACTACAGTAGA	SCIGTITATE	AATGTCTTCCC	GGGGGACT	GATTTTACCA
00507198.1						
00507164.1	CIGCIAAAA	ACTACGGTAGA	GCTGTTTATG	AATGTCTTCGC	GGTGGACT	IGATITIACCA
00507185.1	CIGCIAAAA	ACTACGGTAGA	GCTGTTTATG.	AATGTCTTCGC	GGTGGACT	FGATTTTACCA
00507154.1	CIGCIAAAA	ACTACGGTAGA	GCTGTTTATG	AATGTCTTCGC	GGTGGACT	IGATTTTACCA
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00507167.1	CIGCIAAAA	ACTACGGTAGA	SCTGTTTATG.	AATGTCTTCGC	GGTGGACT	IGATITITACCA
00507168.1	CIGCIAAAA	ACTACGGIAGA	SCIGITIAIG.	AAIGICIICGC	GGIGGACI.	IGATITIACCA FCATTTTACCA
00507170 1	CTCCTAAAA	ACTACGGTAGA	CTGTTTATG	ANTGICTICGC	GGTGGACT	CATTTTACCA
00507171.1	CTGCTAAAA	ACTACGGTAGA	SCIGITIAIG	AATGTCTTCGC	GGTGGACT	IGATITITCCA
00507173.1	CIGCIAAAA	ACTACGGTAGA	GCTGTTTATG	AATGTCTTCGC	GGTGGACT	IGATITITACCA
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00507187.1	CIGCIAAAA	ACTACGGIAGA	CTGTTTATG	AATGICIICGC	GGIGGACI.	CATTTTACCA
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00507203.1	CIGCIAAAA	ACTACGGTAGA	GCTGTTTATG	AATGTCTTCGC	GGTGGACT	TGATTTTACCA
00507204.1	CIGCIAAAA	ACTACGGTAGA	GCTGTTTATG.	AATGTCTTCGC	GGTGGACTI	FGATTTTACCA
00507206.1	CIGCIAAAA	ACTACGGTAGA	GCTGTTTATG.	AATGTCTTCGC	GGTGGACTI	FGATTTTACCA
00507207.1	CIGCIAAAA	ACTACGGTAGA	GCTGTTTATG.	AATGTCTTCGC	GGTGGACT	IGATTTTACCA
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00507202.1	CTGC					
00507205.1	CIGCIAAAA	ACTACGGTAGA	SCIGITIAIG.	AATGICIICGC	GGTGGACT	IGATITIACCA FCATETTACCA
00507155.1	CIGCIANAA	ACTACGGTAGA	SCIGITIATC	AATGTCTTC	GGIGGACI.	GATITIACCA
00507152.1	CIGCIAAAA	ACTACGGTAGA	GCTGTTTATG	AATGTCTTCGC	GGTGGACT	IGATITTACCA
00507153.1	CIGCIAAAA	ACTACGGTAGA	GCTGTTTATG	AATGTCTTCGC	GGTGGACT	IGATTTTACCA
00507157.1	CIGCIAAAA	ACTACGGTAGA	GCTGTTTATG	AATGTCTTCGC	GGTGGACT	TGATTTTACCA
OQ507158.1	CIGCIAAAA	ACTACGGTAGA	GCTGTTTATG.	AATGTCTTCGC	GGTGGACT	IGATTTTACCA
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00507161.1	CIGCIAAAA	ACTACGGTAGA	SCTGTTTATG.	AATGTCTTCGC	GGTGGACTI	IGATTTTACCA

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00507200.1					
00507183.1	AATTTGCTG	AGAACGTT	TCTTGCAACCI	TTTAGAAGTTG	GCGAGAACATTTCTATTTTT
OQ507179.1	AATATGATG	CGGACGTGI	ACTCACCACCA	TTTACGTGTTG	GAGAGATCGTTTCCGCTTTT
OQ507180.1	AATGTGAGA	AGAACTTGA	ACTCACCACCI	TTTGCGCGTTG	GAGAGATCGTTTCCGCTTTG
00507176.1	AATTTGATG	AGAACGTC <i>I</i>	ACTGGCAACCI	TTTAGAAGTTG	GAGAGATAGCTTCGGATTTT
OQ507165.1					
00507163.1	AAGATGATG	AGAACGCGG	ACTCCCAACCA	TTTACGTGTTG	GAGAGATCGTTTCGTCTCTT
00507183.1	AAGACAATG	AGAAACTG <i>I</i>	ACTCACAACCA	CTTTTGCGTTG	GAGAGATCGTTTCGTCTTTT
OQ507196.1					
OQ507162.1	AAGTGGATG	AGAACGTGI	ACTCCCAACCA	TTAATGCGTTG	GAGAGATCGTTTCGCCTTTT
OQ507177.1					
00507186.1	AACATGATG	AGAACGTGI	ACTCACCACCC	TCTATGCGTGG	GAGAGAACGGTTOTTCTTT
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00507185.1	AAGATGATG	AGAACGTGI	ACTCACAACCA	TTTATGCGTTG	GAGAGATCGTTTCGTCTTTT
00507154.1	AAGATGATG	AGAACGTGI	ACTCACAACCA	TTTATGCGTTG	GAGAGATCGTTTGGTCTTTT
00507156.1	AAGATGATG	AGAACGTGI	ACTCACAACCA	TTTATGCGTTG	GAGAGATCGTTTGGTCTTTT
00507167.1	AAGATGATG	AGAACGTG	ACTCACAACCA	TTTATGCGTTG	GAGAGATCGTTTGGTCTTTT
00507168.1	AAGATGATG	AGAACGTG	ACTCACAACCA	TTTATGCGTTG	GAGAGATCGTTTGGTCTTTT
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00507171.1	AAGATGATG	AGAACGTGI	ACTCACAACCA	TTTATGCTTTG	GAGAGATCGGTTQGTCTTTT
00507173.1	AAGATGATG	AGAACGTGI	ACTCACAACCA	TTTATGCGTTG	GAGAGATCGTTTGGTCTTTT
00507174.1	AAGATGATG	AGAACGTGI	ACTCACAACCA	TTTATGCGTTG	GAGAGATCGTTTGGTCTTTT
00507175.1	AAGATGATG	AGAACGTG	ACTCACAACCA	TTTATGCGTTG	GAGAGATCGTTTCGTCTTTT
OQ507178.1	AAGATGATG	AGAACGTG	ACTCACAACCA	TTTATGCGTTG	GAGAGATCGTTTCGTCTTTT
00507181.1	AAGATGATG	AGAACGTG	ACTCACAACCA	TTTATGCGTTG	GAGAGATCGTTTCGTCTTTT
00507182.1	AAGATGATG	AGAACGTG	ACTCACAACCA	TTTATGCGTTG	GAGAGATCGTTTCGTCTTTT
00507187.1	AAGATGATG	AGAACGTG	ACTCACAACCA	TTTATGCGTTG	GAGAGATCGTTTCGTCTTTT
00507188.1	AAGATGATG	AGAACGTG	ACTCACACCCA	TTTATGCGTTG	GAGAGATCGTTTCGTCTTTT
0050/189.1	AAGATGATG	AGAACGIGA	ACTCACAACAA	TITAIGCGIIG	GAGAGATCGTTTUGTCTTTT
00507190.1	AAGATGATG	AGAACGTG	ACTCACAACCA	TTTATGCGTTG	GAAAGATCGTTTCGTCTTTT
00507191.1	AAGATGATG	AGAACGTGA	ACTCACAACCA	TTTAIGCGTTG	GAGAGATCGTTTCGTCTTTT
00507192.1	AAGATGATG	AGAACGTGA	ACTCAAA		
00507193.1	AAGATGATG	AGAACGTG	ACTCACAACCA	TTTAIGCGTTG	GAGAGATCGTTTUGTCTTTT
00507194.1					
00507195.1	AAGATGATG	AGAACGIGA	ACTCACAACCA	TTTAIGCGIIG	GAGAGAICGIIIGGICIIII
00507197.1	AAGAIGAIGI	AGAACGIGA	ACTCACAACCA	TTTATGCGIIG	CACACATCCTTTCCTCTTTT
00507201 1	AAGAIGAIGA	AGAACGIGI	ACTCACAACCA	TTTATGCGIIG	CACACATCCTTTCCTCTTT
00507201.1	AAGATGATG	AGAACGIGI	ACTCACAACCA	TTTATGCGIIG	CACACATCCTTTCCTCTTT
00507204 1	AAGATGATG	ACAACGIGI	ACTCACAACCA	TTTNTCCCTTC	CAGAGATCGTTTCGTCTTTT
00507204.1	AACATCATC	ACAACCIC	ACTCACAACCA	TTTATCCCTTC	CACACATCOTTTCCTCTTT
00507200.1	AAGAIGAIGI	AGAACGIGA	ACTCACAACCA	TTTATGCGIIG	CACACATCOTTTCCTCTTTT
00507172 1	AAGAIGAIGI	AGAACGIGI	ACICACAACCA	TITALGOGIIG	GAGAGAICGIIIGGICIIII
00507202 1	AAGAIGAIGI	AGA			
00507202.1	AACATCATC	ACAACCTCI	ACTOACAACCA	TTTATCCCTTC	CACACATCCTTTCCTCTTTT
00507160 1	ANGATGATG	AGANCG101	NOTORORROOR		GROMORICOTTICUTUTIT
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00507157 1	AAGATGATG	AGAACGTCI	ACTCACAACCA	TTTATGCGTTC	GAGAGATCGTTTTCGTCTTTT
00507158 1	AAGATGATG	AGAACGTCI	ACTCACAACCA	TTTATGCGTTG	GAGAGATCGTTTCGTCTTTT
00507159 1	AAGATGATG	AGAACGTCI	ACTCACAACCA	TTTNTCCCTTC	CACACATCCTTTCCTCTTT
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0Q507181.1	A	T	G	С	Т	A	С	Т	G	С	
00507182.1	A	T	G	С	Т	A	С	Т	G	С	
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Figure 5.3. Multiple sequence alignment for 56 *Physalis* accessions only based on *rbcL* marker.

5.3.4 Phylogenetic analysis

The *rbcL* gene was not able to facilitate species discrimination based on the phylogenetic tree (Figure 5.4). There was no cladding of *Physalis* accessions with their representative reference

sequences from the GenBank database. It was therefore impossible to discriminate *Physalis* accessions based on their *rbcL* gene sequences and species names assigned were based on BLASTn analysis.



Figure 5.4. Phylogenetic tree generated by MrBayes for *Physalis* accessions based on *rbcL* marker.

Different colors were used to represent *Physalis* accessions and reference sequences. Black represents all reference sequences, orange represents *P. minima*, purple represents *P. peruviana*, pink represents *P. angulata* and blue represents *Physalis virginiana*. The names of species are based on BLASTn analysis as there was no discrimination of species based on the Phylogenetic tree.

There was no cladding of *Physalis* accessions with there reference sequences. The *Physalis* accessions also clustered with different reference sequences other than their counterparts for example the accessions identified as *P. peruviana* clustered with *P. angulata* and *P. minima* accessions and not with the *P. peruviana* reference sequence as was expected. This is an indication that the *rbcL* barcode was unable to effectively identify the *Physalis* accessions studied based on the phylogenetic analysis.

5.3.5 Genetic diversity within *Physalis* population based on *rbcL* marker

DNA divergence within the *Physalis rbcL* sequences was assessed by determining the number of polymorphic (segregating) sites (S), nucleotide diversity and total number of substitutions (Table 5.5). The nucleotide diversity was noted at 0.01333 among the *rbcL* sequences of the *Physalis* accessions.

Table 5.5.Poly	morphism and	l divergence	within	(intraspecific)	Physalis	species	based	on	rbcL
sequences									

Physalis species	Physalis species
Total number of sequences	56
Number of polymorphic (segregating) sites (S)	85
Nucleotide diversity Pi (Total)	0.01333
Theta (Total)	0.0.05959
Total number of substitutions	98

5.3.6 Genetic distance within *Physalis* population based on *rbcL* marker

The overall genetic distance was very low at 0.04 ± 0.0 . Average intraspecific distance of *Physalis* accessions was also determined as 0.04 ± 0.0 . The average intraspecific distance was found to be the same as the overall genetic distance within the *Physalis* accessions.

5.3.7 Nucleotide polymorphism

Eighty-five segregation sites (S) were identified within the *rbcL* genes of 56 *Physalis* accessions under this study (Table 5.6). The nucleotide diversity within these sequences was 0.01333. There were 66 singleton sites and 19 parsimony informative sites among the 85 identified segregating

sites (Table 5.6). The data form this section when compared to data for 10 Physalis accessions from one area as seen on table 3.4 indicated that when more Physalis accessions (56) from various areas are compared in their nucleotide diversity, some slight nucleotide diversity is observed as compared to fewer accessions from the same region where no diversity was observed.

Polymorphic sites/ Segregation	85	Positions in the gene	Variants
sites (S)			
Singleton	66	129,130,133,143,225,233,236,253,274,	2
		275,278,282,285,286,295,300,303,310,	
		311,312,324,327,329,332,336,337,341,	
		342,345,347,348,349,350,352,355,359,	
		367,368,375,377,383,391,392,395,398,	
		401,407,408,410,416,417,418,421,427,	
		438,439,443,455,462	
		339,361,380,388,393,397,457	3
Parsimony informative sites	19	304,333,338,343,357,364,378,415,432,	2
		446,449,458,459	
		284,346,360,365,400,403	3
Nucleotide diversity (Pi)	0.0	1333	
Average number of nucleotide	4.7′	72	
differences (k)			
Sequence length (base pairs)	730		
Number of sequences	56		

Table 5.6. DNA polymorphism of *Physalis* accessions based on *rbcL* sequences

5.3.8 Tajima's neutrality test

Tajima's neutrality test was conducted on 56 *Physalis rbcL* sequences to determine the population selection and nucleotide diversity. The Tajima D value of *Physalis rbcL* sequences

was -2.533533. The negative Tajima D value indicates an excess of rare low frequency variations that are associated with population growth and positive selection pressure.

5.3.9 Barcoding gap analysis based on *rbcL* sequences

Automatic Barcode Gap Discovery results generated by distance model Kimura 80 parameter (K80P) based on ITS2 sequences for *Physalis* accessions indicate the presence of two barcoding gaps. The presence of a barcode gap indicates that the interspecific divergence of *rbcL* genes is higher than their intraspecific divergence. Based on the *rbcL* gene sequences, all pairwise distances were ranked by increasing distance values from 0.02 - 0.14 and two barcoding gaps identified (Figure 5.5). The barcode gaps were the same size and the first barcode gap was observed between distances of 0.12 (12%) and 0.13 (13%) (Figure 5.5). The second barcode gap was evident between the distances of 0.13 (13%) and 0.14 (14%) (Figure 5.5).



Figure 5.5. A histogram indicating the hypothetical distribution of pairwise differences of *rbcL* gene sequences of 56 *Physalis* accessions

Low divergence is presumably intraspecific divergence, whereas higher divergence indicates interspecific divergence. The abbreviation nbr on the *y*-axis of the histogram stands for the number of pairwise comparisons. A, B and C represent barcode gaps.

5.4 Discussion

Physalis species are relatively similar when it comes to their morphological characteristics. The *Physalis* genus plants also tend to have morphological similarities to the Solanaceae family plants such as *N. physalodes* (Feng *et al.*, 2016). Due to these reasons, species identification by morphological characterization is not accurate for the *Physalis* genus. Molecular identification of plant species by DNA barcoding is accurate, reliable and rapid than the use of morphological features (Saddhe and Kumar, 2018). Studies on the identification of *Physalis* accessions in Kenya are very few with one key study focusing on the analysis of genetic diversity of *Physalis* accessions based on SSR markers, which did not discriminate the accessions into different *Physalis* species (Muraguri *et al.*, 2021).

In the present study, *rbcL* barcode amplification and sequencing success rates were 82% and 88%, respectively. This high rate of success in amplification and sequencing of the *Physalis* accessions *rbcL* barcode was expected and concurred with results from other studies where *rbcL* barcode was used in identification of species (Kang *et al.*, 2017; Huang *et al.*, 2015). According to studies done by Kang *et al.* (2017) and Huang *et al.* (2015) the amplification and sequencing success rates for *rbcL* gene were between 75.26% and 63.84 and 97.6% and 90.8%, respectively. The high amplification and sequencing success rate of the *rbcL* gene is proposed to be due to the high conservation of the gene as a result of low frequency mutations (Kang *et al.*, 2017).

In the phylogenetic analysis of *Physalis* accessions based on *rbcL* barcode, there was little information on the discrimination of species based on the constructed phylogenetic tree. Species discrimination was limited due to the inability of the *rbcL* barcodes to form clusters and clades with the reference database sequences based on BLASTn analysis. This is expected and has also been demonstrated in many other studies whereby species discrimination power of the *rbcL* barcode is usually the least among DNA barcoding markers (Kang *et al.*, 2017; Huang *et al.*, 2015; Tripathi *et al.*, 2013; Hollingsworth *et al.*, 2009). The identities provided for the different *Physalis* accessions on the phylogenetic tree are based on BLASTn analysis results as the phylogenetic tree was not able to efficiently discriminate the *Physalis* accessions into different *Physalis* species. A previous study by Hollingsworth *et al.* (2011) demonstrated that the low efficiency of *rbcL* in inter-specific divergence discrimination shows that the gene is not efficient

in species discrimination but is a good candidate in the identification of plants at the genus level (Hollingsworth *et al.*, 2011).

Physalis accessions could not be categorized into various species based on rbcL barcode and therefore genetic diversity and distance analysis focused on intra-species variation. There was low nucleotide diversity at 0.0133 and low genetic distance at 0.4 ± 0.0 among the rbcL sequences of the *Physalis* accessions used in this study. This data supports the findings on the inability of rbcL sequences to discriminate the *Physalis* accessions based on phylogenetic analysis. The sequences were relatively similar with a very low genetic distance and diversity and hence could not cluster effectively into different species due to the high rate of conservation of the barcode. Genetic distance is an estimate of the genetic distance of zero value observed in this study indicates that there is no genetic difference within species demonstrated that the accessions were of the same species. The very low genetic distance among the rbcL barcode sequences approaching zero is an indication that the gene was relatively conserved among these plants and could not be effectively used in their species discrimination. This has also been observed in other studies where rbcL barcode could not differentiate wild cinnamon and clove plants (Chandrasekara *et al.*, 2021; Nurhasanah *et al.*, 2019).

The Automatic Barcode Gap Discovery was able to show two small barcode gaps identified among the *Physalis* accessions based on *rbcL* barcode. This is an indication that the genetic divergence of *rbcL* barcode sequences of *Physalis* accessions was low and the *rbcL* barcode is relatively conserved in *Physalis*. The nucleotide polymorphism of *rbcL* barcode sequences of *Physalis* concurred with the Tajima neutrality test results which indicated a positive selection with a negative Tajima D value of -2.533533. Although 85 segregating sites were identified, the mutations were low frequency mutations associated with a positive selection as indicated by the negative Tajima D value. The *rbcL* barcode sequences of *Physalis* in this study had high singleton and parsimony informative sites among their 85 segregating sites. Sixty-six of the segregating sites were singleton mutations while 19 were parsimony sites. These are low frequency mutations and are associated with low nucleotide diversity based on the Tajima neutrality test (Carlson *et al*, 2005; Tajima, 1989).

5.5 Conclusion

The *rbcL* DNA barcode was effective in genus identification of the *Physalis* accessions but not discrimination of the different species. All 56 *Physalis* accessions used in this study were identified as the genus *Physalis*. The *rbcL* barcode sequences of the 56 *Physalis* accessions were highly conserved and phylogenetic tree analysis could not facilitate *Physalis* species discrimination. Low sequence divergence and low genetic distance among *rbcL* sequences of the *Physalis* accessions were also observed, indicating the *rbcL* barcode conserved among the accessions used in this study.

CHAPTER SIX

6.0 Comparative efficacy of ITS2 and *rbcL* DNA barcodes for identification and genetic diversity assessment of *Physalis* accessions in Kenya

6.1 Introduction

The genus *Physalis* has many species that grow in a wide array of habitats and ecologies, a common feature of the Solanaceae family (Ralte and Singh, 2021). This plant is native to the Andean region of South America with Colombia being the main producer and exporter (Cháves-Gómez et al., 2020). The economic value of Physalis in Colombia is linked to the high demand for fruits from mainly European countries (Álvarez-Flórez et al., 2017; Ordoñez et al., 2017). Other exporters of *Physalis* include Australia, New Zealand, Great Britain, Egypt, South Africa, Uganda, Zimbabwe, Kenya, Madagascar, and Southeast Asian countries (Barirega, 2014; Zhang et al., 2013; Ramadan and Moersel, 2003). Physalis are useful for income generation and have a wide range of nutritional and medicinal applications (Afroz et al., 2020; Barirega, 2014). Nutritionally, several *Physalis* species are rich in water- and fat-soluble vitamins (A, E, K, C and B-complex), minerals (magnesium, potassium, calcium and zinc), fatty acids (such as palmitate and linoleic acid), proteins and sugars (Puente et al., 2011; Ramadan and Moersel, 2003). The increased consumption of *Physalis* fruits has been associated with a decreased risk of chronic degenerative diseases (Reddy et al., 2010). The fruits are also rich in soluble solids, such as sugars like fructose, which are valuable for diabetic sugar control (Barirega, 2014). P. peruviana and *P. angulata* are rich in flavonoids, physaloids and other phytochemicals, and have been utilized in ethno-medicine. These phytochemicals have been applied in wound healing and the treatment of various ailments such as jaundice caused by hepatotoxicity, asthma, arthritis and hepatitis (Abdul-Nasir-Deen et al., 2020; Zhang and Tong, 2016; Arun and Asha, 2007). Phytochemicals like polyphenols have also contributed to the antioxidant, anti-inflammatory, antidiabetic, antihypertension and anticancer activities of Physalis crude extracts (Lan et al., 2009; Pinto et al., 2009; Franco et al., 2007; Wu et al., 2006). In addition, Physalis ixocarpa, commonly referred to as tomatillo, is a source of nutrients used in the preparation of sauces and salads (Shenstone et al., 2020). Due to the wide diversity of Physalis species and species-specific applications, there is a need to authenticate and discriminate the different *Physalis* species in particular regions for efficient utilization, genetic resource conservation, and effective utilization in breeding programs (Feng *et al.*, 2016).

The identification of *Physalis* species using morphological properties has resulted in misidentifications due to similarities in the phenotypic characteristics of the different species (Feng *et al.*, 2016). For example, *P. minima* and *P. pubescens* are morphologically similar, which presents a challenge in their differentiation using their phenotypic characteristics (Feng *et al.*, 2016). Morphological identification is also affected by the environmental/physiological factors, stage of growth and development of plants (Vargas-Ponce *et al.*, 2011; Menzel, 1951). The misidentification of *Physalis* species can lead to losses of genetic information due to a lack of genetic conservation (Feng *et al.*, 2018). Since the morphological identification of *Physalis* species has proven to be inefficient, there is a need to use robust and accurate means of species identification (Yu *et al.*, 2021). Molecular identification is more accurate as it is based on unique nucleotide sequences that are not affected by the morphological factors (Schindel and Miller, 2005). To this end, DNA barcoding is one of the molecular techniques that can be used to identify and specify species accurately (Qian *et al.*, 2022).

DNA barcoding is a rapid and reliable method of species identification and discrimination using short universal standardized DNA sequences (Saddhe and Kumar, 2018). It has been widely utilized and accepted in the identification of plants and animals as an effective taxonomic tool (Yu *et al.*, 2021; Dormontt *et al.*, 2018; Kress, 2005). Several DNA barcodes can be utilized in the identification of plants, based on the chloroplast-plastid (ribulose-1,5-bisphosphate carboxylase large (*rbcL*), maturase (*matK*), *psbA-trnH* among others) and nuclear ITS (internal transcriber spacer (ITS1) and (ITS2)) regions. However, factors such as universality, success in amplification and specificity variation need to be considered. These factors influence the efficiency of particular DNA barcodes in the identification of a DNA barcode (Li *et al.*, 2021). *rbcL* is one of the universal barcode genes that is ideal for plant species discrimination studies, due to its high amplification and low mutation rate (Kang *et al.*, 2017). The low level of mutation in the *rbcL* gene implies that it can be used in detailed studies on intra-species genetic and phylogenetic

variation (Nurhasanah *et al.*, 2019). In addition, it is also a commonly used DNA barcode because it is conserved across a wide range of plant species (Manzara and Gruissem, 1988). Conversely, the nuclear DNA barcode, ITS2 gene is considered the best marker for DNA barcoding due to its high species discrimination power, inter- and intra-species level diversity, and high success rate in amplification and sequencing in plants (Kang *et al.*, 2017). Therefore, this suggests the combination of chloroplast–plastids and nuclear regions as an efficient barcode tool to explore plant species discrimination (CBOL Plant Working Group *et al.*, 2009).

According to the available literature, no DNA barcoding study has been conducted on the *Physalis* species present in Kenya. Similarly, no study has been conducted to assess the genetic diversity among *Physalis* accessions. The current study aimed at identifying the Kenyan *Physalis* species using *rbcL* and ITS2 barcodes and assessing the efficiency of the two candidate DNA barcodes to identify *Physalis* species. In addition, the phylogenetic relatedness of *Physalis* species was determined using *rbcL* and ITS2 sequences.

6.2 Materials and methods

6.2.1 Study area and collection of plant samples

Leaves of the genus *Physalis* were randomly collected from different locations of Kericho, Elgeyo-Marakwet, Homa Bay, Nakuru, Kajiado, Nyeri and Kiambu Counties of Kenya (Figure 6.1). The leaves were purposively sampled based on the availability, as most of the samples were wild plants growing without human intervention except for those collected from Elgeyo-Marakwet from a farmer. Within specific locations of sampling in the different counties, leaves and ripe fruits were collected and labeled after being placed in collection bags. The collected *Physalis* plant samples were identified by the taxonomist Mr. Patrick Mutiso and the samples were preserved in the University of Nairobi herbarium in the Department of Biology (Codes of Voucher Specimens: KP/UON2019/001- KP/UON2019/064). A Global Positioning System (GPS) device was used to record the location where the samples were collected in different counties; the altitude of the location of sampling was also noted and the assigned species name based on morphological appearance was also recorded (Table 6.1 and Appendix 1 A). Leaves of sixty-four (64) *Physalis* plants were collected between April and June 2019 in triplicate in ziplock bags. Since it was difficult to identify the samples morphologically, each set of triplicate

plants was given a specific unique identification name based on the location at which they were collected, and a number (Appendix 1 A). Representative images of plants of some of the collected samples are presented in Figure 6.2. The samples were transported within 24 h post-sampling in a cool box with icepacks to the Department of Biochemistry at the University of Nairobi, and kept in the laboratory for genomic DNA extraction.



Figure 6.1. The locations of *Physalis* sampling sites in seven counties of Kenya and spatial distribution of the *Physalis* species discriminated based on ITS2 barcoding

Table 6.1. Geographical coordinates and number of samples picked from the various regions of

 Physalis sampling within seven different counties in Kenya

Serial	County	Location	Latitude	Longitude	No.	of
No.					samples	
					collected	
1.	Kericho	Londiani - Sorget	0.0684° S	35.5548° E	10	
2.	Elgeyo-	Chebororwa	0.9487° N	35.4234° E	13	
	Marakwet					
3.	Homa Bay	Ndhiwa	0.7299° S	34.3671° E	3	
4.	Nakuru	Gilgil market	0.4923° S	36.3173° E	1	
5.	Kajiado	Ongata Rongai	1.3939° S	36.7442° E	5	
6.	Nyeri	Mukurweini	0.5609° S	37.0488° E	5	
7.	Kiambu	Tigoni	1.1651° S	36.7065° E	17	
		Thika	1.0388° S	37.0834° E	9	
		Muguga	1.2551° S	36.6580° E	1	



Figure 6.2. Plant morphology of *Physalis* species

(A) *P. purpurea*—OQ372009.1; (B) *P. microcarpa*—OQ372018.1; (C) *P. purpurea*—OQ372013.1; (D) *P. purpurea*—OQ372019.1; (E) *P. purpurea*—OQ372020.1 and (F) *P. cordata*—OQ372012.1) in their natural habits. The *Physalis* species were discriminated based on their ITS2 barcode sequence. Morphological data for the *Physalis* accessions was not recorded. *Physalis* accessions were highly morphologically similar and environmental factors like soil salinity and pH, light exposure and carbon dioxide saturation can affect the physiological growth stages of the plants.

6.2.2 Molecular authentication of Physalis plants

6.2.2.1 Genomic DNA extraction

Physalis accessions genomic DNA was isolated, purified, viewed and stored as described in section 3.2.2.1.

6.2.2.2 PCR amplification and sequencing

Polymerase chain reaction (PCR) amplification was performed using ITS2 and *rbcL* DNA barcode markers presented in Table 3.1. PCR amplification, purification of PCR products and sequencing was performed as described in section 3.2.2.2.

6.2.2.3 Sequence alignment, phylogenetic and data analysis

The sequences of only 28 *Physalis* accessions that were successfully sequenced for both ITS2 and *rbcL* primers were used. The sequences of ITS2 and *rbcL* genes for *Physalis* accessions attained were curated, subjected to BLASTn analysis, used to prepare MSAs and phylogenetic trees as described in section 3.2.2.3. The MSA for the construction of MrBayes phylogenetic tree was prepared using the 28 *Physalis* ITS2 and *rbcL* gene sequences that had successfully been sequenced and BLASTn generated reference sequences for the two genes. Two MSAs were also prepared separately for ITS2 and *rbcL* sequences without use of their reference sequences and were used in the genetic diversity, nucleotide polymorphism, neutrality test, and automatic barcode gap discovery (ABGD) analysis.

6.2.3 Analysis of genetic divergence

The DNA divergence between *Physalis* accessions based on ITS2 sequences was assessed as described in section 4.2.4. DNA divergence within *Physalis* accessions based on ITS2 gene sequences was performed as described in section 3.2.3.

6.2.4 Determination of intraspecific and interspecific genetic distance

The intra- and interspecific genetic distances and overall mean distance of *Physalis* accessions based on the ITS2 sequences were determined as described in section 4.2.5. The intraspecific distance of *Physalis* accessions based on *rbcL* genes was determined as described in section 3.2.4.

6.2.5 Nucleotide polymorphism

Nucleotide polymorphism was assessed using the two MSAs for 28 *Physalis* accessions based on ITS2 and *rbcL* sequences as described in section 3.2.5.

6.2.6 Tajima's neutrality tests

Tajima's neutrality test for ITS2 and *rbcL* sequences was performed to assess the frequency of mutations among species and to determine selection in the populations (Tajima, 1989). Tajima's neutrality test was assessed using the MEGA 11.0 software (Tamura *et al.*, 2021). The analysis involved 28 nucleotide sequences for the DNA barcode gene sequences analyzed. The codon positions included were the 1st + 2nd + 3rd + Noncoding for the *rbcL* gene sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option) in both analyses based on ITS2 and *rbcL* genes. There were totals of 532 and 716 positions for the ITS2 and *rbcL* genes, respectively, in the final dataset.

6.2.7 Barcoding gap analysis

The ITS2 and *rbcL* multiple sequence alignments for the 28 *Physalis* accessions were separately uploaded to the ABGD website (https://bioinfo.mnhn.fr/abi/public/abgd/abgdweb.html accessed on 20 February 2023) and distance analysis performed based on K80 Kimura measure of distance as described in section 3.2.7.

6.3 Results

6.3.1 Success rates of PCR amplification and sequencing

The success rates of PCR amplification for ITS2 and *rbcL* were 77% and 84%, respectively, while the sequencing success rates were high for *rbcL* (89%) and moderate for ITS2 (65%) (Table 6.2). The lengths of the ITS2 sequences were in the range of 237–707 bp, with an average of 525 bp and mean GC content of 61%, with a range of 55.7–66.9%. Similarly, the lengths of the *rbcL* sequences were in the range of 463–854 bp, with an average of 690 bp and mean GC content of 43.4%, with a range of 42.1–45.5% (Table 6.1, Appendix 1B and C).

Table 6.2. Efficiency of PCR amplification and sequencing for *Physalis* accessions for ITS2 and *rbcL* barcodes.

Barcode region	Samples tested (n)	Number o amplicons produced	Number of sequences produced	% amplification efficiency	% sequencing efficiency	Alignment length (bp)	Mean sequence length (bp)	Mean GC content (%)
ITS2	64	49	32	77	65	841	525	61.00
rbcL	64	54	48	84	89	841	690	43.40

The nucleotide base frequencies at different coding positions in *Physalis* accessions for ITS2 and *rbcL* sequences are indicated in Table 6.3. The percentage GC contents of ITS2 sequences were significantly higher than those of *rbcL* sequences for the *Physalis* accessions used in this study.

Table 6.3. The nucleotide base frequencies of candidate nucleotide sequences at different coding positions in *Physalis* accessions.

Barcode Locus	Base Co	ontents (%	/ 0)			
	Α	Т	G	С	AT	GC
ITS2	19.42	19.39	29.78	31.41	39.00	61.00
rbcL	28.22	28.40	23.10	20.28	56.58	43.42

6.3.2 Species discrimination of Physalis accessions using BLASTn analysis

Species discrimination used a similarity-based approach based on BLASTn. The results show a high similarity of ITS2 and *rbcL* with other sequences in the GenBank by BLASTn sequence similarity searches. The percentage identity based on ITS2 loci ranged from 80.36 to 97.41%, and the *Physalis* species identified were *P. cordata*, *P. peruviana*, *P. microcarpa*, *P. aff. philadelphica*, *P. minimaculata* and *P. purpurea* (Table 6.4). None of the *Physalis* accessions had 100% identity based on ITS2 sequences for the BLASTn analysis. BLASTn analysis of the *rbcL* sequences identified that all 28 *Physalis* accessions belonged to the genus *Physalis*. Out of the 28 *Physalis* accessions, 7 had 100% identity as *P. minima*, while the rest had percentage identities ranging from 91.10 to 99.86 and were identified as *P. peruviana*, *P. virginiana*, *P. angulata* and *P. minima* (Table 6.4).

Sample ID		rbcL					ITS2			
	Species of	GenBank	E-	Percent	Accession	Species of	GenBank	E-	Percent	Accession
	best BLAST	Accession	value	identity	number	best BLAST	Accession	value	identity	Number
	match	number (of		(%)		match	Number (of		(%)	
		database)					database)			
Chebororwa	<i>P</i> .	NC_026570.	0.0	94.90	OQ507163.	P. purpurea	MH763740.1	0.0	94.70	OQ371996.
C2	peruviana	1			1					1
Chebororwa	<i>P</i> .	KT178121	0.0	95.46	OQ507165.	P. cordata	AY665886.1	5e-	87.78	OQ371997.
C5	virginiana				1			122		1
Chebororwa	P. minima	NC_048515.	0.0	93.18	OQ507166.	P. cordata	MH763728.1	1e-81	82.24	OQ371998.
elin		1			1					1
Chebororwa	P. minima	NC_048515.	0.0	99.46	OQ507167.	P. cordata	AY665886.1	1e-	86.06	OQ372001.
e4in		1			1			108		1
Chebororwa	P. minima	NC_048515.	0.0	98.28	OQ507168.	P. purpurea	MH763740.1	0.0	93.75	OQ372003.
ебin		1			1					1
Chebororwa	P. minima	NC_048515.	0.0	99.19	OQ507169.	P. purpurea	MH763740.1	0.0	94.27	OQ372004.
e7in		1			1					1
Gilgil gm	P. minima	NC_048515.	0.0	99.06	OQ507171.	P. purpurea	MH763740.1	5e-35	81.98	OQ372005.
		1			1					1
Muguga DM	P. minima	NC_048515.	0.0	98.74	OQ507177.	P. purpurea	MH763740.1	0.0	93.83	OQ372007.
		1			1					1
Mukurweini	P. angulata	NC_039457.	0.0	92.90	OQ507180.	P. peruviana	AY665914.1	4e-93	88.82	OQ372008.
ny5		1			1					1
Ndhiwa hb2	P. minima	NC_048515.	0.0	93.33	OQ507181.	P. purpurea	MH763740.1	0.0	94.28	OQ372009.
		1			1					1
Ongata	<i>P</i> .	NC_026570.	0.0	95.47	OQ507183.	P. cordata	AY665886.1	2e-76	86	OQ372012.
Rongai nor3	peruviana	1			1					1
Ongata	<i>P</i> .	KT178121.1	0.0	91.10	OQ507184.	P. purpurea	MH763740.1	0.0	94.09	OQ372013.
Rongai nor4	virginiana				1					1

Table 6.4. BLASTn analysis results for 28 *Physalis* accessions based on ITS2 and *rbcL* barcode gene

Ongata	<i>P</i> .	NC_026570.	0.0	98.78	OQ507185.	P. purpurea	MH763740.1	0.0	94.51	OQ372014.
Rongai nor5	peruviana	1			1					1
Thika TK8	P. minima	NC_048515.	0.0	99.04	OQ507192.	<i>P</i> .	AY665905.1	2e-93	88.51	OQ372015.
		1			1	minimaculata				1
ThikaTK9	P. minima	NC_048515.	0.0	98.03	OQ507193.	P. peruviana	AY665914.1	1e-35	80.36	OQ372016.
		1			1					1
Tigoni T2	P. minima	NC_048515.	0.0	98.31	OQ507194.	P. purpurea	MH763740.1	7e-	91.79	OQ372017.
		1			1			160		1
Tigoni T4	P.s minima	NC_048515.	0.0	96.42	OQ507195.	P. microcarpa	AY665903.1	1e-61	86.78	OQ372018.
		1			1					1
Tigoni T9	P. minima	NC_048515.	0.0	98.13	OQ507199.	P. purpurea	MH763740.1	0.0	92.22	OQ372019.
		1			1					1
Tigoni T11	P. minima	NC_048515.	0.0	99.32	OQ507201.	P. purpurea	MH763740.1	9e-32	84.85	OQ372020.
		1			1					1
Londiani 2	P. mimima	NC_048515.	0.0	100	OQ507153.	P. purpurea	MH763740.1	0.0	92.98	OQ372021.
		1			1					1
Londiani 3	P. minima	NC_048515.	0.0	99.59	OQ507154.	P. purpurea	MH763740.1	0.0	94.06	OQ372022.
		1			1					1
Londiani 4	P. minima	NC_048515.	0.0	100	OQ507155.	P. peruviana	AY665914.1	0.0	97.41	OQ372023.
		1			1					1
Londiani 5	P. minima	NC_048515.	0.0	99.86	OQ507156.	P. purpurea	MH763740.1	0.0	94.45	OQ372024.
		1			1					1
Londiani 6	P. minima	NC_048515.	0.0	100	OQ507157.	P. aff.	AY665868.1	2e-	91.35	OQ372025.
		1		1.0.0	1	philadelphica		144		1
Londiani 7	P. minima	NC_048515.	0.0	100	OQ507158.	P. purpurea	MH763740.1	le-	86.00	OQ372026.
		1			1			148		1
Londiani 8	P. minima	NC_048515.	0.0	100	OQ507159.	P. purpurea	MH763740.1	0.0	93.07	OQ372027.
		1			1					1
Londiani 9	P. minima	NC_048515.	0.0	100	OQ507160.	P. purpurea	MH763740.1	0.0	88.96	OQ372028.
		1			1					1
Londiani 10	P. minima	NC_048515.	0.0	100	OQ507161.	P. purpurea	MH763740.1	0.0	90.16	OQ372029.
		1			1					1

6.3.3 Multiple sequence alignments

The multiple sequence alignment (MSA) of cleaned ITS2 and *rbcL* sequences as well as their reference sequences from BLASTn analysis was prepared based on MUSCLE had a sequence length of 841 bp. The multiple sequence alignment was compressed using ESPript 3 (Appendix 2D) (https://espript.ibcp.fr/ESPript/temp/1032964064/0-0-1680466160-esp.pdf accessed on 15 February 2023). This MSA had a high rate of nucleotide substitutions, deletions and insertions among and between *Physalis* species based on the ITS2 marker (Appendix 2D). The MSA also shows a high rate of nucleotide sequence conservation among and between the *Physalis* species based on the *rbcL* marker with very few deletions, insertions and substitutions. Substitution transition mutations can be noted at positions 304 and 368 (Appendix 2D). At position 304, we see a transition substitution mutation for the *Physalis* accession OQ507184.1 whereby this sequence has an adenine, but all other *rbcL* sequences and reference sequences have a guanine. At position 368, there is another substitution point mutation for *Physalis* accession OQ507166.1, whereby guanine replaces an adenine base. A transversion point mutation is also noted at position 305 for the *Physalis* accession OQ507184.1, whereby a guanine replaces cytosine (Appendix 2D).

Other transversion point mutations are noted at positions 369 and 419 of the *Physalis* accession OQ507166.1, whereby adenine replaces thymine in both cases (Appendix 2D). An insertion macro-lesion is noted between positions 579 and 580 for *Physalis* accession OQ507166.1, whereby five nucleotides are inserted (Appendix 2D). A deletion macro-lesion is noted for *Physalis* accession OQ507184.1 between positions 530 and 536 whereby seven nucleotides are deleted (Appendix 2D).

The MSA of the 28 ITS2 sequences based on MUSCLE, trimmed and edited by Jalview version 1.11.2.0, had a sequence length of 532 bp. It was compressed using ESPript (Figure 6.3) (https://espript.ibcp.fr/ESPript/temp/1440398212/0-0-1688383904-esp.pdf accessed on 15 February 2023). This MSA has many substitutions, deletion and insertion mutations (Figure 6.3). The substitution mutations in this MSA are composed of transition and transversion point mutations (Figure 6.3). The MSA of 28 *rbcL* sequences based on MUSCLE, trimmed and edited

by Jalview, had a sequence length of 716 bp. It was compressed using ESPript (Figure 6.4) (https://espript.ibcp.fr/ESPript/temp/1848737578/0-0-1688384397-esp.pdf accessed on 15 February 2023). This MSA is relatively conserved and does not have any insertion or deletion mutations, but it has quite a high number of substitution point mutations; for example, at positions 40, 170, 171, 180, 181, and many others (Figure 6.4). The substitution mutations are composed of transition and transversion point mutations Figure 6.4). The sequence alignments reveal a wide dispersal of sequence similarity for ITS2 sequences and homologous sequences for *rbcL* sequences among the tested *Physalis* accessions.

00372005.1	i	10			20			зọ					4 0			50			5 Q
00372023 1	GGGGT	GTAGT		GTTA	AGCGGA	GG <mark>G</mark> .	.CTC	GCAG	CG.			ACCO	GGC	CAG	GGTI			GGCI	CCA
00372026.1	CGGGT	GCGGT	CGAGC	GCTA	AGCGGA	AGGG	TCTC	TCAG	CGA	c		ACG	GCC	AAA	GGGI	CGGG	CAC	CGCC	CA.
00372027.1			CGG.	CGCCTA	AGCGGA	AGGT	TCTO	TCAG	CGA	с с		ACGO	GCC	ACG	GGTI		CAC	GGCI GGCI	CCA
00372016.1	GGGAT	ATTGT	CGAAC	CTGCGA	AGCAGA	GCGA	cccc	CGAAG	CTG	TTTC	GAAC	ACCO	GGG	AGG	GTI	СТТ	CGC	CTCC	ССТ
00372008.1	GGCGGG	CCCATT	CG.AC CGAAC	CTGCGA CTGCTA	AGCAGA	GCGA GC <mark>G</mark> A		CAAA (TTTC TTG <i>I</i>	388C 4	ACGC ACA	GGA	GGG AAG	CGT1 GCT1	TGG	CCCC CCG.	тссс	ccc
00372018.1	CAGGTO	ATTGT	CGAAC	CTGCTA	AGCAGA	GCGA	CCCC	CAAA	CCCG	TTTC	GAAC	ACCO	GGA	AGG	GTI	CGC		CTCC	CGC
00372028.1	GATC	CATTGT	CGAAC	CTGCTA	AGCAGA	GCGA		CAAA	CCCG	TTTC	GAAC	ACT	GGA	AGG	CGTI	CGC		CTCC	CGC
00372019.1	GGGAT	CATTGT	CGAAC	CTGCTA	AGCAGA	GCGA		CAAA	CCG	TTTC	GAAC	ACCO	GGA	AGG	GTI			CTCC	CGC
00372003.1	.GGATC	CATTGT	CGAAC	CTGCTA	AGCAGA	GCGA	cccc	CAAA	CCCG	TTTC	GAAC	ACCO	GGA	AGG	CGTI	CGC		CTCC	CGC
OQ372007.1 OO371996.1	AGGAT	CATTGT	CGAAC	CTGCTA CTGCTA	AGCAGA	GC <mark>G</mark> A GC <mark>G</mark> A		CAAAC		TTTC TTTC	GAAC GAAC	ACCO	GGA	AGG	CGTI			CTCC	CGC
00372004.1	GGGAT	ATTGT	CGAAC	CTGCTA	GGCAGA	GC <mark>G</mark> A	cccc	CAAA	CCG	TTT	GAAC	ACCO	GGA	AGG	GTI	CGC	CGC	СТСС	CGC
0Q372014.1	GGAAT	ATTGT	CGAAC	CTGCTA	AGCAGA	GCGA	cccc	CAAAC	CCCG	TTTC	GAAC	ACCO	GGA	AGG	CGTI	CGC		CTCC	CGC
00372013.1	GGAATO	ATTGT	CGAAC	CTGCTA	AGCAGA	GCGA		CAAAO		TTTC	GAAC	ACCO	GGA	AGG	CGTI			CTCC	CGC
00372021.1																CGC	CGC	CTCC	CGC
00372025.1	GGGAT	CATTGT	CGAAC	CTGCTA	AGCAGA	GC <mark>G</mark> A	CCCC	CAAAC CAAAC		TTTC TTTC	GAAC GAAC	ACCO	GGGA	AGG	CGT1 CGT1			CTCC	CGC
00371998.1	. ACGTC	CCAGC	TAGAC		. GCAGA	ACGG	CCAC	GAAA											
00372997.1		CAT	AGGAC	GTGAAA	AGCAGO	A	.AC	GGAAG	CCCG	G		A	GAT	ACT	GGTO	CGT	GTC	GCCC	GC GA
00372012.1	· · · · .		· · · · · · ·	A C <mark>G T A A</mark>	.CTCGGG	AG <mark>G</mark> G	TAC	GCCAC	GTG	т		CCC	<mark>G</mark> AG	GGT	G <mark>CT</mark>	CTT	CCG	G G <mark>C I</mark>	∖ <mark>C</mark> G.
00372005 1	CGAAC			BO CACTT	OCCOTO	ACCT						CON	120	тсС		130	-	_	
00372023.1	CGAGA	GTTGAG	AACCA	CACTT	GCCGT	ACGT	CCGI	CGAC	CGC	TAGO	GCCA	GCC	CG		.CGC	TGC	GAGC	GCAC	GGG
0Q372026.1 0Q372027.1	.CAAA CAAGA	GTTGAG GTTGAG	AACCA AACCA	CACTT	GCCGTC	ACGT	CCG1 CCG1	CGACI	CAC CAC	TAGO TAGO	GCCA GCCA	ACCA ACCA	ACCA ACGA	G		CGA	GCC GGC	CAA GCA	CGGA
00372029.1	CAAGA	GTTGAG	AACCA	CACTT	GCCGT	ACGT	CCGI	CGACI	CAC	TAGO	GCCA	ACCA	CGA		GO	CGA	GGC	GCAC	GGA
00372008.1	TCGTC	GCGGG.	· · CGG	rcgcgc	GIGGC	GCGC	CGGI	CG CI	CAAC	AACO	CCCG	GCG	GGA		GCCI	AGG	ATAC	TTA	ACCG
00372020.1	TCGTC	GCCAG		CACGT	000000		 Стас	CGACI	гаас	GAAC		GGC	CGA		C G C		GAA	 ТАС1	GA
00372015.1	TCGTC	GCCAG	CAGCCO	GCACGT	GCGCG	TCGC	CTAC	CGACI	ГААС	GAA	cccc	GGCI	CGA	AAC	GCGC	CAA	GAA	TACI	CGA
OQ372028.1 OQ372019.1	TCGTC	GCCAG GCCAG	CAGCCO	GCACGT GCACGT	GCGCGG	TCGC TCGC	CTAC	CGACI	ГААТ ГААС	GAAC		GGC1 GGC1	CGA	A A C	GCGC GCGC	CAAC	GAA GAA	TACI TACI	CGA
00372024.1	TCGTC	GCCAG	CAGCCC	GCACGT	GCGCGG	TCGC	CTAC	CGACI	TAA T	GAAC		GGCI	CGA	AAC		CAA	GAA	TACI	CGA
00372007.1	TCGTC	GCCAG	CAGCCO	GCACGI	GCGCGG	TCGC	CTAC	CGACI	FAAC	GAAC	cccc	GGCI	CGA	AAC	GCGC	CAA	GGAA	TACI	CGA
0Q371996.1 00372004.1	TCGTC	GCCAG	CAGCCO	GCACGT GCACGT	GCGCGG	TCGC TCGC	CTAC	CGACI	ГААС ГААС	GAAC GAAC		GGCI	CGA	AAC AAC	GCGC	CAAC	GAA GAA	TACI	CGA CGA
00372009.1	TCGTC	GCCAG	CAGCCO	GCACGT	GCGCG	TCGC	CTAC	CGAC	TAAC	GAA	cccc	GGC1	CGA	AAC	GCGC	CAA	GAA	TACT	CGA
00372014.1	TCGTC	GCCAG	CAGCCO	GCACGI	GCGCGG	TCGC	CTAC	CGACI	LAAC LAAC	GAAC		GGCI	CGA	AAC		CAA	GAAGGAA	TACI	CGA
00372017.1	TCGTC	GCCAG	CAGCCO	GCACGT	GCGCGG	TCGC	CTAC	CGAC		GAAC		GGCI	CGA	AAC			GAA	TACI	CGA
	TCCTC			CACGT	GCGCG	TCGC	CTAC		FAAC	GAAC	cccc	GGC	CGA	AAC		CAA	GGAA	TACI	CGA
00372025.1	ICGIC	GCCAG	CAGCU					CGACI							GCGC			TACI	CGA
OQ372025.1 OQ372022.1 OQ371998.1	TCGTC	GCCAG GCCAG	CAGCCO	CACGT	GCGCG	TCGC	CTAC	CGACI	ГААС ГААС	GAGO	SCCG	GGCI	ICGA	A A C		CAA	GGAA		
OQ372025.1 OQ372022.1 OQ371998.1 OQ372001.1	TCGTC	GCCAG GCCAG		GCACGT CGTGT	GCGCGG GCCACA	TCGC GCGA	CTAC	CGAC	FAAC FAAC FAAG	GAGO		GGCI	CAG	AAC AAC			GGAA	TCAR	TGA
0Q372025.1 0Q372022.1 0Q371998.1 0Q372001.1 0Q372097.1 0Q372012.1	TCGTC C	GCCAG GCCAG	CAGCCC CAGCCC .CCTC .ACCG	GCACGT CCGTGT TTGCGT	GCGCGG GCCACA GGCCGA	GCGA T ACCGG	CTAC CTTC CCGA	CGAC CGAC CGTT CGAC GAAAC	FAAC FAAC FAAG SAAC F.AC			GGCI	CAG GCAG	AAC AAC AAC		CAAC	GGAA AAAC AACA	TCA TAA	AT <mark>GA</mark> AC <mark>GA</mark>
00372025.1 00372022.1 00371998.1 00372001.1 00372997.1 00372012.1	C	GCCAG GCCAG	AGCCC CAGCCC .CCTC .ACCG	GCACGT CCGTGT TTGCGT . ACCC	GCGCGC GCCACA GGCCGA	TCGC AGCGA T ACGG	CTTC CTTC CCGA	CGAC CGAC CGAC CGTT CGAC GAAAC	FAAC FAAC FAAG GAAC F.AC	GAGC AACC CCGC GAGC	GCCG GCC GCC.G	GGC 2	CAG	AAC AAC AAC		CAA AAA AAG	GGAA AAAC AACA	TCA TAA	ATGA AC <mark>GA</mark>
0Q372025.1 0Q372022.1 0Q371998.1 0Q372001.1 0Q372001.1 0Q372012.1	TCGTCC	GCCAG GCCAG		GCACGT CCGTGT TTGCGT . ACCC	GCGCGC GCCACA GGCCGA	GCGC GCGA T ACGG	CTTC CTTC CCGI CCAC	CGAC CGAC CGAC CGTT CGAC	FAAC FAAC FAAG SAAC F.AC		GCCG GCCG GCCG GCCG GCCG GCCG	GGC /	GCAG	AAC AAC AAC			GGAA AAAC AACA	TCA TAA	ATGA ACGA
00372025.1 00372022.1 00371998.1 00372001.1 00372001.1 00372012.1	C	GCCAG GCCAG		GCACGT CGTGT TTGCGT . ACCC	GCGCGC GCCACP GGCCGZ	TCGC GCGA T ACGG	CTAC CTTC CCGA	CGAC CGAC CGTT CGTT CGAC GAAAC	FAAC FAAC FAAG GAAC F.AC		GCCG GCC. GCC. GCC GCC GCC GCC GCC GCC G	GGC2	CAG G	AAC AAC AAC		CAA AAA AAG	GGAA AAAC AACA		ATGA ACGA
00372025.1 00372022.1 00371998.1 00372001.1 00372097.1 00372012.1	TCGTCC	3GCCAG 3GCCAG		GCACGT CCGTGT TTGCGT . ACCC	GCGCGC GCCACA GGCCGA	ICGC AGCGA ACGG	CTAC CTAC CCCGA CCCAC	CGAC CGAC CGTT CGAC AAAC	FAAC FAAC FAAG GAAC F.AC		170	GGC1	CAG	A A C A A C A A C A A C			GGAA AAAC AACA	TCA TAA	ATGA ACGA
0Q372025.1 0Q372022.1 0Q371998.1 0Q372001.1 0Q37297.1 0Q372012.1		GCCAG GCCAG		GCACGT TGCGTGT TGCGT . ACCC	GCGCGG GCCACA GGCCGA GGCCGA	150 GCGC	CTAC CTAC CCTAC CCAC	ICGAC CGAC CGAC CGAC CGAC CGAC CGAC CGAC	TAAC TAAC TAAG GAAC T.AC		170 GATCG	TTA:	GCC GCC GCC GCC	AAC AAC AAC 		CAA AAAG AAG	GGAA AAACA AACA 	TGC1	TGA CGA
0Q372025.1 0Q372022.1 0Q371998.1 0Q372001.1 0Q37297.1 0Q372012.1 0Q372012.1		.CATA		GCACGT TGCGTGT TGCGT GCCAC GCCAA GCCAC	GCGCCG	150 GT GT GT GT	GC G	IGGAC CGAC CGAT CGAC CGAC CGAC CGAC CGAG CCGAG CCGAG CCCAG	TAAC TAAC TAAG GAAC T.AC		179 GATC GATC GATC	TTA	GCC GCC GCC GCC GCC GCC GCC	AAC AAC AAC 		CAAC AAAG AAG AAG	AAACAAACAAACAAACAAACAAACAAACAAACAAACAA	TGCI	CGA
0Q372025.1 0Q372022.1 0Q37201.1 0Q37201.1 0Q372012.1 0Q372012.1 0Q372023.1 0Q372023.1 0Q372023.1 0Q372023.1		. CATA 		GCACGT CGTGT TTGCGT ACCC GCAA GCAAC GCAAC GCAAC		150 GCGC GCGC GCGC GCGC GCGC GCGC GCGC GC	GC G	160 CGAC CGAC CGAT CGAC ACGAC AAAC	TAAC TAAC TAAC GAAC T.AC GGGG GGGG GGGG GGGG GGGG GGGG GGGG G		170 GATC GATC GATG GATG	TTA CGA CCA CGA	GCC GCC GCC GCC GCC GCC GCC GCC GCC	AAC AAC AAC AAC TGA TGA TGA		CTC CAG CCAG CCAG CCAG CCAG	GGAA AAACA AACA AACA ACTA GCAG GCAG GCAG	TGC1 CCC1 CCC1 CCC1	TCG. TCGG TCGG TCGA
0Q372025.1 0Q372022.1 0Q37201.1 0Q37201.1 0Q37201.1 0Q37201.2 0Q37201.2 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37200.8	AGGCCI AGGCCI AGGCCI GGACTI GGACTI	GCCAG GCCAG 		GC ACGT CG TGT T GC GT CG CAC CG CAC GC AAC GC AAC CG CAAC CG CAAC			GCGC GCGC GCGC GGGGC AGGC AGGC TGCC	ICGAC: CCGAC: CCGTT: CCGTT: CCGACC SCGACC CCCAGC CCCAGC CCCAGC CCCAGC CCCAGC CCCAGC	GGGGG GGGGG GGGGGGGGGGGGGGGGGGGGGGGGGG		170 GCC G GCC GCC	TTA: CGA: CGA: CGA:	GCCG GCCG GCCG GCCG GCCG	AAC AAC AAC AAC AAC TGA TGA TGA TGA		CTC CAG CCAG CCAG CCAG CCAG CCAG CCAG	GGAA AAACA AACA AACA CTA GCAG GCAG GCAG	TGC1 CCC1 CCC1	ICG. ICGGA ICGA ICGA
0Q372025.1 0Q372022.1 0Q372001.1 0Q372012.1 0Q372012.1 0Q372012.1 0Q372023.1 0Q372023.1 0Q372026.1 0Q372026.1 0Q372028.1 0Q372008.1 0Q372008.1	AGGCCI AAGGCCI AAGGCCI GGACTI AGGCCC	CATA GCCAG		GCACGT CCGTGT TIGCGT CCGTGC CCGTC CCCA CCCA CCCA CCCA CC			GC G	16 CGACC CGACC CGACC CGTT CGACC CGAACC CGAACC CGCGAG CGCGAG CGCGAG CGCGAG CGCGAG CGCGAG CGCGAG CGCGAG CGCGAG			179 GCCG GCCG GCCG GCCG GCCG GATG GATG GATG	TTA: CGA: CGA: CGA: CGA:	GCC GCC GCC GCC GCC GCC GCC GCC GCC GCC	AAC AAC AAC AAC GGA TGA TGA TGA	GCTC GCCCC GCCCC GCCCC GCCC GCCC GCCC G	CTC CAG CCAG CCAG CCAG CCAG CCAG CCAG CC	AAACA AAACA AACA AACA AACA ACTA GCAG GCAG	TGCI	CGA CGA CGA CGA CGG CGA CGG CGA
0Q372025.1 0Q372027.1 0Q372001.1 0Q372001.1 0Q372012.1 0Q372012.1 0Q372023.1 0Q372023.1 0Q372026.1 0Q372026.1 0Q372026.1 0Q372026.1 0Q372026.1 0Q372016.1 0Q372015.1	AGGCCI AAGGCCI AAGGCCI GGACTI GGACTI CCGATI CCGATI	GCCCAG GCCAG GCCAG GCCAG GCCAG GCATAC AGTATC GCATATC GCACC GCACC		GCACGT CCGTGT TIGCGT TIGCGT CCCAA CCAA CCAA CCAA CCCAA CCCAA CCCAA CCCAA CCCAA CCCAA CCCAA CCCAA CCCAC CCCAC CCCCCC			GCGC GCGC GCGC GGGG AGGC AGGC CCGC CCGC	IGCGACC CGACC CGACC CGACC CGACC CGACC CGACC CGAGC CCGAGC CCGAGC CCGAGC CCGAGC CCGAGC CCGAGC CCGAGC CCGAGC CCGAGC CCGACC	CAAC TAAC TAAC TAAC TAAC TAAC TAAC TAAC		170 GATC GATC GATC GATC GATC GATC GATC GATC	TTA: CCA: CCA: CCA: CCA: CCA: CCA: CCA:		A A C A A C A A C A C		CTC CAG CCAG CCAG CCAG CCAG CCAG CCAG CC	AAACA AAACA AACA AACA AACA AACA AACA A	TGC1 CCC1 CCC1 CCC1 CCC1 CCC1	CGA CGA CGA CGA CGA CGA CGA
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TT AC GG GC GA - TT AC GG GC GC GC GC GC GC GC GC GC GC GC GC AC TC AC TG AC TG CG CG CG CG CG CG CG CG CG CG CG CG CG				GAAC(AACC AACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CAACC CA	AATCG AATCG GGCCCCG AATCG GGCCCCG AATCG GGCCCCG AATCG GGCCCGGG GGCCCCGGGGGGGGGG	TTA: CGA: CGA: CGA: CTTC CTTC CTTC CTTC CTTC CTTC CTTC CT		A A C A C	GCGCCC GCCCCC GCCCCC GCCCCCC GCCCCCC GCCCCCC	C A A A A A A A A A A A A A A A A A A A	GGA. CA AAACA L90 A GCAGGCAG GCAGGCAG GCAGGCAG GCAGGCAG GCAGGCAG	TGC1 TGC1 CCC1 CCC1 CCC1 CCC1 CCC1 CCC1	

			200															
0Q372005.1			TAT	ATTG	CGT.													
0Q372023.1	CCTAATGG	CTTCGGG	CGCAA	CTTG	CGTT	CAAA	G i	ACTC	GATG	GTTC	CACGG	GATTC	TGC.	ΑΑΤΤ	CACA	CCAA	GTAT	CGC
00372026.1	CCCTATGG	CTTCGGG	GACAA	CTTG	CCTTC	CCAA	G I	ACTC	CAAG	GTTI	ACGG	GATTC	TGC.	AATT	CACA	CCAA	GTAT	CGC
00372027.1	CCTAATGG	CTTCGGG	CACAA	CTTG	CGIT		G	ACTC	GATG	GTTC	ACGG	GATTC	TGC.	AATT	CACA	CCAA	GTAT	CGC
00372016 1	CLIANIGG		CACAA	TC	COTT		σ	1010	GAIG	GIIC	ACGG	GAIIC	I GC.	AAII	CACA	CCAA	GIAI	GC
00372008.1	CACGG	TTCTCGG	CTCTC	GCT.	CGAT	GAAA	ACGT	TCG	AAT	TGTA	CTGG	TGGAT	TGC	AATC	сстб	ACGT	CGAT	стт
00372020.1				.CTG	CGAC	FAC G	Α									A	CCCG	CAC
OQ372018.1																		
OQ372015.1	CAACGGAT	ATCTCGG	CTCTC	ACAT	CGAT	ΓTTG	Αi	A C G T	AGC	AACC	G <mark>C G</mark> A	ΤΑ						
00372028.1	CAACGGAT	ATCTCGG	CTCTC	GCAT	CGAT	GAAG	Α	ACGT	AGC	AAAI	GCGA	TACTT	GGT	GTGA	ATTG	CAGA	ATCC	CGT
00372019.1	CAACGGAT	ATCTCGG	CTCTC	GCAT	CGAT	GAAG	A	ACGT	AGCG	AAAI	GCGA		GGT	GTGA	ATTG	CAGA	ATCC	CGT
00372024.1	CAACGGAI	ATCTCCC	CTCTC	GCAI	CCAT	JAAG	A	ACGI CCT	AGCO	TAAA	GCGA	TACTT	CCT	GIGA	AIIG	CAGA	ATCC	COT
00372007.1	CAACGGAT	ATCTCG	CTCTC	GCAT	CGAT	GAAG	Α	CGT	AGC	AAAT	GCGA	TACTT	GGT	GIGA	ATTG	CAGA	ATCC	CGT
00371996.1	CAACGGAT	ATCTCGG	CTCTC	GCAT	CGAT	GAAG	Α	ACGT	AGC	AAAT	GCGA	TACTT	GGT	GTGA	ATTG	CAGA	ATCC	CGT
0Q372004.1	CAACGGAT	ATCTCGG	CTCTC	GCAT	CGAT	GAAG	Α	A C G T	AGC	AAAI	G <mark>CG</mark> A	ТАСТТ	G <mark>G</mark> Τ	GTGA	ATTG	CAGA	ATCC	CGT
OQ372009.1	CAACGGAT	ATCTCGG	CTCTC	GCAT	CGAT	GAAG	Αί	ACGT	AGC	AAAI	G <mark>CG</mark> A	ΤΑСΤΤ	GGΤ	GTGA	ATTG	CAGA	ATCC	CGT
00372014.1	CAACGGAT	ATCTCGC	CTCTC	GCAT	CGAT	GAAG	Α	ACGT	AGC	AAAI	GCGA	TACTT	GGT	GTGA	ATTG	CAGA	ATCC	CGT
00372013.1	CAACGGAT	ATCTCGG	CTCTC	GCAT	CGAT		A	ACGT	AGC	AAAI	GCGA	TACIT	GGI	GIGA	ATTG	CAGA	ATCC	CGT
00372021.1	CAACGGAT	ATCTCGG	CTCTC	GCAT	CGAT	CAAG	Δ	CGT	AGC	AAAI	GCGA	TACTT	GGT	GIGA	ATTG	CAGA	ATCC	CGT
00372025.1	CAACGGAT	ATCTCG	CTCTC	GCAT	CGAT	GAAG	Α	CGT	AGC	AAAT	GCGA	TACTT	GGT	GTGA	ATTG	CAGA	AT	
00372022.1	CAACGGAT	ATCTCGC	CTCTC	GCAT	CGAT	GAAG	Α	ACGT	AGC	AAAI	GCGA	TACTT	GGT	GTGA	ATTG	CAGA	ATCC	CGT
OQ371998.1	CAAGGA	TCTCGG	CTCTC	GCA.	CGA.	.G <mark>A</mark> A	G	A C G T	AGC	ΑΑΤΟ	GAAC	ΓGG <mark>T</mark> G	TGA.	ATG.		.CAG	ATCC	CGT
00372001.1	CATGGA	TTCTCGG	CTTCG	CA	CGAT	GAAG	A I	ACGT	AGC	AAT.	GCGA	TACTT	GGT	GTGA	ATG.	.CAG	ATCC	CGT
00372997.1	CGAGGGAT	ATCTCGG	ATCTC		CGCTC	GAG	AAGA	ACGT	AGCG	AAA1	GCGA	TACTT		GTGT	GAAT	GCAG	ATCC	CGT
02372012.1	ACACGARG	AICICOA		GCCT			<u>.</u>		••••			n <mark>n</mark> Gnn	A <mark>G</mark> A.	AAAC	GAAC	1199	GIGH.	
00372005 1			-												-			
00372023 1	ATTTCCCT	ACCTTCT	TCATC	GATG	CGAG		GAGA	LATC	CGTT	acco	AGAG	 TC	• • •	GTTC	GGTT	TCAA	GCGA	
00372026.1	ATTTCGCT	ACGITCI	TCCTC	CAAG	CCAG	AACC	GAAA	TATC	CGTI	GCCC	AGAG	GC		ATTT	GTTT	TCAA	GCGA	AGC
00372027.1	ATTTCGCT	ACGTTCT	TCATC	GATG	CGAG	AGCC	GAGA	TATC	CGTI	GCCC	AGAG	гс	A	TTTG	ΤΤΤΤ	TCAA	GCGAI	AGC
OQ372029.1	ATTTCGCT	ACGTTCI	TCATC	GATG	CGA <mark>G</mark>	AGCC	GAG <mark>A</mark>	ΓΑΤC	CGTI	GCCC	AGAG	гс	A	TTTG	тдтт	TCAA	GC GA I	AGC
00372016.1													: : :		· · · ·	$\cdot \cdot \cdot$	•••	
00372008.1	GACTGATT	GCGCCGI	TCTTT	GCGG	GGA.	• • • •							CTG	GCTG	GCTC	CCAC	GC	• • •
00372018 1	GAACGGCC	AAGAIAC	, ICACC	GA		• • • •							• • •				•••••	• • •
00372015.1																		
00372028.1	GAACCATC	GAGTCTI	TGAAC	GCAA	GTTG	F GCC	CGAA	GCCA	TTAG	GTCO	AGGG	CACGT	CTG	CCTG	GGCA	TCAC	TCAT	CGC
OQ372019.1	GAACCATC	GAGTCTT	TGAAC	GCAA	GTT <mark>G</mark>	Г <mark>С</mark> СС	CGAA	GCCA	TTAG	GCCC	AGGG	CACGT	СТG	CCTG	GGCA	TCAC	G C A T (CGC
OQ372024.1	GAACCATC	GAGTCTI	TGAAC	GCAA	GTT <mark>G</mark>	Г <mark>С</mark> СС	CGA <mark>A</mark>	GCCA	TTAG	GTCC	GAGGG	CACGT	СТG	CCTG	GGCA	TCAC	GCAT	CGC
00372003.1	GAACCATC	GAGTCTI	TGAAC	GCAA	GTTG	rgcc	CGAA	GCCA	TTAG	GTCC	GAGGG	CACGT	CTG	CCTG	GGCA	TCAC	GCAT	CGC
00371996 1	GAACCATC	GAGICII	TGAAC	GCAA	GIIG.		CGAA	JCCA	TTAG	GICC	AGGG	CACGI	CTG	CCTG	GGCA	TCAC	GCATC	
00372004.1	GAACCATC	GAGTCTT	TGAAC	GCAA	GTTG		CGAA	ICCA	TTAG	GTCC	AGGG	CACGI	CTG	CCTG	GGCA	TCAC	GCAT	
00372009.1	GAACCATC	GAGTCTT	TGAAC	GCAA	GTTG	TGCC	CGAA	GCCA	TTAG	GTCO	AGGG	CACGT	CTG	CCTG	GGCA	TCAC	GCAT	CGC
OQ372014.1	GAACCATC	GAGTCTI	TGAAC	GCAA	GTT <mark>G</mark>	Г <mark>G</mark> CC	CGAA	GCCA	TTAG	GTCC	AGGG	CACGT	СТG	CCTG	GGCA	TCAC	GCATO	CGC
00372013.1	GAACCATC	GAGTCTI	TGAAC	GCAA	GTT <mark>G</mark>	Г <mark>G</mark> CC	CGAA	GCCA	TTAG	GTCC	GAGGG	CACGT	СТG	CCTG	GGCA	TCAC	GCAT	CGC
00372017.1	GAACCATC	GAGTCTI	TGAAC	GCAA	GTTG	rgcc	CGAA	GCCA	TTAG	GTCG	AGGG	CACGT	TTG	CTTG	GGCT	TCTC	GCAT	CGC
00372021.1	GAACCAIC	GAGICII	IGAAC	GCAA	GIIG.	IGUU	CGAA	JUCA	TIAG	GICO	AGGG	CACGI	CIG	CCIG	GGCA	TCAC	GCAIG	GGC
00372022.1	GAACCATC	GAGTOTT	TGAAC	GCAA	GTTG	TGCC	CGAA	ACCA	TTAG	GTCC	AGGG	CACGT	CTG	CCTG	GGCA	TCAC	GCAT	GC
00371998.1	G.ACCATC	GAGTCT.		GAAG	CAAG	ГGGC	CCGA	ACCA	. TAG	GTCC	AGGG	CAG	TCG	CCTG	GGC.	TCAC	GCAT	CGC
0Q372001.1	GACCATC.	GATCI	T GAAC	GCAA	G.T <mark>G</mark>	г <mark>сс</mark>	CGAA	GCCA	TTAG	GTCC	GAGGG	CA.GT	СТG	CCTG	GGCA	TCAC	GCATO	CGC
0Q372997.1	GACCATC.	GATCI	TGAAC	GCAA	GTT <mark>G</mark>	г <mark>ссс</mark>	CGAA	GCCA	. TAG	GCCG	AGGG	CACGT	CT.	CCTG	GGCA	TCAC	GCAT	CGC
OQ372012.1	AGATCCCT	GACCACC	AGTTT	TAAG	CAAA	Γ <mark>G</mark> TG	CCCA	AAAC	CATA	GCCC	AGGG	CAG	ΤΤΤ	CCTG	GGCA	TCAC	GCAT	CGC
												2	10					
00372005 1										1			А Т т	ССтт				
00372023.1	G.CAGCTC	cccccc	CGCGC	CGCG	GA	. c <mark>g</mark> g	GGCG	CGAG	GGGG	GCCG	TCGG	T	TTT	ĊĊTT	GCGC	GCCG	 GG.Т(CGT
00372026.1	A.CAGTTC	CCCCGC	CTCGC	CGTG	GA.CO	GA <mark>G</mark> G	CCCG	AGG <mark>G</mark>	TGTG	CCAI	CGGC	TAGTT	ΑΤΤ	тсст	G			
0Q372027.1	A.CAGCTC	CCCCGCG	CACGC	CGTG	GA	.C <mark>G</mark> A	GGC <mark>G</mark>	CGA <mark>G</mark>	GGGG	TCCA	TCCG	T	СТТ	CCTT	GTGC	CCGG	GG.T(СGТ
00372029.1	ACCAGCTC	CCCCGCG	CACGC	CGTG	GGAC	G A <mark>G</mark> G	.GC <mark>G</mark>	A G G <mark>G</mark>	GIGI	GCCA	TCTG	CGAGT	ΑΤΤ	CCTT	G			•••
00372016.1																• • • •	· · · · ;	
00372008.1		GTCTAC	CTACC		T	3001	CCIG	3106	6666	GCAP	ICCAG	••••	CTT	TTTT	600.	• • • •	••••	366
00372018.1												č	CCT	CGTT				
0Q372015.1																		
00372028.1	ΑΤ	CGCCCC	CTCGC	CCTG	CACCO	GC <mark>G</mark> G	CGC <mark>G</mark>	Г Т G <mark>G</mark>	GGAG	GATA	CTGG	c	СТТ	CCGT	GCGC	CATC	GG.T(CGT
00372019.1	AT	CGCCCCC	CTCGC	CCTG	CACCO	G C <mark>G</mark> G	CGCG	r t g <mark>g</mark>	GGAG	GATA	CIGG	c	CTT	CCGT	GCGC	CATC	GG.TO	CGT
000000000000000000000000000000000000000	- T	CGCCCCC	CTCCC	CCTG	CACCO	a C G G	CGCG	TGG	GGAG	GATA	CTGG	· · · · c	CTT	CCGT	GCGC	CATC	GG.TO	GT
00372024.1	Δ		بالمراجع المراجع		CACCO			1100	GOAG	CATA	10100		CTT		CCCC	URIC	00.10	COL
0Q372024.1 0Q372003.1 0Q372007 1	AT AT		CTCCC	CCTC	C A (. (. ,	CCC	CGUN	1 1 1 4 4 4 4	GGAC	1 - A I - "	CTGG					CATC	GG T7	
OQ372024.1 OQ372003.1 OQ372007.1 OO371996.1	AT AT AT		CTCGC	CCTG	CACC	GC <mark>G</mark> G GC <mark>G</mark> C	CGCG	TGG	GGAG GGAG	GATA	CTGG CTGG		СТТ	CCGT	GCGC	CATC	GG.TO GG.TO	CGT
OQ372024.1 OQ372003.1 OQ372007.1 OQ371996.1 OQ372004.1	AT AT AT AT		CTCGC CTCGC CTCGC	CCTG CCTG CCTG	CACCO	G C <mark>G</mark> G G C <mark>G</mark> G G C <mark>G</mark> G	CGCG	ITG <mark>G</mark> ITG <mark>G</mark> ITG <mark>G</mark>	GGAG GGAG GGAG	GATA GATA GATA	ACTGG ACTGG ACTGG		CTT CTT	CCGT	GCGC GCGC	CATC	GG.T(GG.T(GG.T(CGT
0Q372024.1 0Q372003.1 0Q372007.1 0Q371996.1 0Q372004.1 0Q372009.1	AT AT AT AT AT		CTCGC CTCGC CTCGC CTCGC	CCTG CCTG CCTG CCTG	CACCO	G C <mark>G</mark> G G C <mark>G</mark> G G C <mark>G</mark> G G C <mark>G</mark> G	CGCG CGCG CGCG	I TGG I TGG I TGG I TG <mark>G</mark>	GGAG GGAG GGAG GGAG	GATA GATA GATA	CTGG CTGG CTGG CTGG			CCGT CCGT CCGT	GCGC GCGC GCGC	CATC CATC CATC CATC	GG.T(GG.T(GG.T(GG.T(CGT CGT CGT
0Q372024.1 0Q372003.1 0Q372007.1 0Q371996.1 0Q372004.1 0Q372009.1 0Q372014.1	AT AT AT AT AT AT		CTCGC CTCGC CTCGC CTCGC CTCGC	CCTG CCTG CCTG CCTG CCTG	CACCO	G C G G G C G G G C G G G C G G G C G G	CGCG CGCG CGCG CGCG	ITGG ITGG ITGG ITGG ITG <mark>G</mark>	GGAG GGAG GGAG GGAG	GATA GATA GATA GATA	CTGG CTGG CTGG CTGG CTGG			CCGT CCGT CCGT CCGT		CATC CATC CATC CATC	GG.T(GG.T(GG.T(GG.T(GG.T(CGT CGT CGT
0Q372024.1 0Q372003.1 0Q372007.1 0Q371996.1 0Q372004.1 0Q372009.1 0Q372014.1 0Q372013.1	AT AT AT AT AT AT AT		CTCGC CTCGC CTCGC CTCGC CTCGC	CCTG CCTG CCTG CCTG CCTG CCTG	CACCO	GCGG GCGG GCGG GCGG GCGG		FTGG FTGG FTGG FTGG FTGG	GGAG GGAG GGAG GGAG GGAG	GATA GATA GATA GATA GATA	CTGG CTGG CTGG CTGG CTGG		C T T C T T C T T C T T C T T C T T	CCGT CCGT CCGT CCGT CCGT		CATC CATC CATC CATC CATC CATC	GG.T GG.T GG.T GG.T GG.T	CGT CGT CGT CGT
0Q372024.1 0Q372003.1 0Q372007.1 0Q371996.1 0Q372004.1 0Q372009.1 0Q372014.1 0Q372013.1 0Q372017.1 0Q372017.1	AT AT AT AT AT AT AT AT		CTCGC CTCGC CTCGC CTCGC CTCGC CTCGC	CCTG CCTG CCTG CCTG CCTG CCTG	CACCO CACCO CACCO CACCO CACCO				GGAG GGAG GGAG GGAG GGAG	GATA GATA GATA GATA GATA	ACTGG ACTGG ACTGG ACTGG ACTGG ACTGG			CCGT CCGT CCGT CCGT		CATC CATC CATC CATC CATC	GG.T(GG.T(GG.T(GG.T(GG.T(GG.T(CGT CGT CGT CGT CGT
0Q372024.1 0Q372003.1 0Q372007.1 0Q372004.1 0Q372014.1 0Q372014.1 0Q372013.1 0Q372013.1 0Q372017.1 0Q372025.1	AT AT AT AT AT AT AT AT AT AT		CTCGC CTCGC CTCGC CTCGC CTCGC CTCGC CTCGC	CCTG CCTG CCTG CCTG CCTG CCTG CCTG	CACCO CACCO CACCO CACCO CACCO CACCO				GGAG GGAG GGAG GGAG GGAG	GATA GATA GATA GATA GATA GATA	ACTGG ACTGG ACTGG ACTGG ACTGG ACTGG ACTGG			CCGT CCGT CCGT CCGT CCGT		CATC CATC CATC CATC CATC CATC	GG.T(GG.T(GG.T(GG.T(GG.T(GG.T(GG.T(CGT CGT CGT CGT CGT
00372024.1 00372003.1 00372007.1 00372004.1 00372009.1 00372014.1 00372014.1 00372017.1 00372017.1 00372017.1 00372022.1	AT AT AT AT AT AT AT AT AT AT AT		CTCGC CTCGC CTCGC CTCGC CTCGC CTCGC CTCGC CTCGC	CCTG CCTG CCTG CCTG CCTG CCTG CCTG	CACCO CACCO CACCO CACCO CACCO CACCO CACCO				GGAG GGAG GGAG GGAG GGAG GGAG	GATA GATA GATA GATA GATA GATA GATA	ACTGG ACTGG ACTGG ACTGG ACTGG ACTGG ACTGG					CATC CATC CATC CATC CATC CATC	GG.T(GG.T(GG.T(GG.T(GG.T(GG.T(GG.T(CGT CGT CGT CGT CGT
Qq372024.1 Qq372003.1 Qq372007.1 Qq372007.1 Qq372004.1 Qq372009.1 Qq372014.1 Qq372014.1 Qq372013.1 Qq372017.1 Qq372021.1 Qq372025.1 Qq372022.1 Qq372022.1	AT AT AT AT AT AT AT AT AT AT			CCTG CCTG CCTG CCTG CCTG CCTG CCTG 	CACCO CACCO CACCO CACCO CACCO CACCO CACCO CACCO	50000 50000 50000 50000 50000 50000 50000 50000 50000 50000	CGCG CGCG CGCG CGCG CGCG CGCG CGCG CGC	ITGG ITGG ITGG ITGG ITGG ITGG ITGG ITGG	GGAG GGAG GGAG GGAG GGAG GGAG GGAG	GATA GATA GATA GATA GATA GATA GATA	CTGG CTGG CTGG CTGG CTGG CTGG CTGG					CATC CATC CATC CATC CATC CATC CATC	GG.TC GG.TC GG.TC GG.TC GG.TC GG.TC GG.TC GG.TC GG.TC	CGT CGT CGT CGT CGT CGT
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00372005.1						[. 🗔			1]		1			1.	G	TA	GG	TI	CT1	rcl	AT	TC	TT	AT	TC	ст.	
00372023.1	AGTC	GA	CC	G	CGI	ACO	GA	CC	GGC	CC	GG	CC	GA	CG	GG	CCT	TO	CCC	GG	GG	GT	TTO	CC	G	TG	GG	TI	TT	CGI	AC	AA	ΤТ	CC	TT	CCC	с.
0Q372026.1													. G	CO	CC	GTT	TO	GI	GC	CA	GG	GGI	TO	G	TA	TO	CC	TI	AG	GC	TA	CT	GA	CA	ACC	
00372027.1	AGTC	GC	TA	GO	CGI	ATO	GGG	GGO	TO	GCI	GG	GC	AA	CO	CC	CCT	TO	CCC	GG	CG	GT	I G C	GG	G	TAG	GG	TI	TIC	CG	AC	CC	GT	GG	TC	CAC	т.
00372029.1					0	GC	GI	TT	TTC	GI	G	ГС	TG	GG	TA	ATC	TO	TA	GG	CA	AG	IGG	CI	GG	TG	GG	TO	TZ	AC	GA	GC	GG	AA	TG	TTE	G.
OQ372016.1																					. G.	AAA	TO	A	TTT	AC	T	CAC	CGI	AA	TC	AG	AG	G.		
OQ372008.1	GGTT	AA	CC	A	r G C	GT	GGG	GCC	CAC	CC	G	. C	GG	CO	TO	GCT	A	TC	TG	CC	AG	GGG	CA	G	GGG	AI	CC	GI	ΓA	ГΤ	ΤG	ΤT	AG	GG	SAG	
OQ372020.1																			GG	ΤG	CT	GGG	TI	C	TTT	AI	CC	TI	ATZ	AC	ΤТ	CT	TC	ΤТ	TTT	ΤT
OQ372018.1																								. 1	TTT	GG	TI	[T]	r G	ГΤ	ΤТ	ΤT	CG	т.		
OQ372015.1																																				
OQ372028.1	GGAT	GG	CC	TI	AAA	AT	GA	GG	CCC	A	GG 2	ГС	GA	CG	GZ	ACG	T	TAT	TG	ΤA	GT	TTO	TO	G	ΓTG	AI	TO	TI	CAJ	AC	TC	ΤТ	GG	TG	SCC	т.
OQ372019.1	GGTT	GG	CC	TI	AAT	ГТ	5 A A	GG	CCC	CAI	G G	ГС	GA	CO	GA	ACG	T	AC	GT	ΑT	AG	I G G	A	G	CAG	AA	TI	Γ.								
OQ372024.1	GGTT	GG	CC	T	AAA	AT	GA	GC	CCC	CAI	G	ГС	GA	CG	GZ	ACG	TO	AC	GG	CA	AG	F GG	TO	G	TTG	AA	TO	CTC	CAL	AC	TC	ΤΤ	GG	ΤG	SCC	Τ.
OQ372003.1	GGTT	GG	CC	TA	AAA	AT	GGA	GC	CCC	CAI	G G	ГС	GA	CC	GI	ACG	T	AC	GG	CA	AG	I G G	TO	G	TTO	AA	TO	CTC	CAL	AC	TC	ΤТ	GG	ΤG	SCC	Τ.
OQ372007.1	GGTT	GG	CC	TI	AAA	AT	GGA	GC	CCC	CAI	GG:	ГС	GA	CO	GA	ACG	TO	AC	GG	CA	AG	IGG	TO	G	TTG	AA	TO	TI	CAL	AC	TC	ΤT	GG	TG	SCC	т.
OQ371996.1	GGTT	GG	CC	TI	AAA	ATC	GGA	GG	CCC	CAI	G G	ГС	GA	CC	GI	ACG	TO	AC	GG	CA	AG	F GG	TO	G	TTG	AA	T	CIC	CAL	AC	TC	ΓΤ	GG	TG	SCC	т.
0Q372004.1	GGTT	GG	CC	TA	AAA	ATC	GGA	GG	CCC	CAI	G :	ГС	GA	CG	GZ	ACG	T	AC	GG	CA	AG	I G G	TO	G	ΓΤG	AA	TO	TI	CAL	AC	TC	TT	GG	TG	SCC	т.
OQ372009.1	GGTT	GG	CC	TI	AAA	ATC	GGA	GG	CCC	A	G G	ГС	GA	CG	GA	ACG	TO	AC	GG	CA	AG	I G G	TO	G	TTG	AA	TO	CTC	CAL	AC	TC	ΓΤ	GG	TG	SCC	Τ.
OQ372014.1	GGTT	GG	CC	TI	AAA	ATC	GA	GC	CCC	CAI	G	ГС	GA	CC	GZ	ACG	TO	AC	GG	CA	AG	F GG	TO	G	TTG	AZ	TO	T	CAL	AC	TC	ΓΤ	GG	TG	SCC	Τ.
0Q372013.1	GGTT	GG	CC	T	AAA	ATC	GGA	GC	CCC	CAI	G G	ГС	GA	CC	GI	A C G	TO	AC	GG	CA	AG	I G G	TO	G	TTG	AP	TO	CIC	CAL	AC	TC	ΓΤ	GG	ΤG	SCC	Τ.
00372017.1		• •	• •	•	• • •	•••	• • •	• •	• • •	• •	• •	• •	• •	• •	• •		• •	• • •		• •	• •		•	•	• • •	• •		• • •	• •	• •	• •	• •	• •	• •	•••	• •
00372021.1	GGTT	GG	CC	TI	AAA	ATC	GGA	GC	CCC	A	G:	I C	GA	C G	GA	ACG	TO	AC	GG	CA	AG	r G G	T	G	TTG	A A	TO	T	CAL	AC	TC	ΓT	GG	т.	• • •	• •
00372025.1		• •	• •	•	• • •	• • •		• •		• •	•	• •		• •			• •					• • •	•	•		::	•	• • •		• •	• •	• •	• •	• •		• •
00372022.1	GGTT	GG	CC	11	AAA	ATC	GA	GGC	CCC	A	G.	I C	GA	CG	GA	ACG	TO	AC	GG	CA	AG	I G G	TO	G	TG	AA	TO	110	A	AC	TC	ΓT	GG	TG	JCC	т.
00371998.1	GG		CC	11	AAA	410	GF	GGC		A	G	I C	GA	CO	GA	ACG	TO	AC	GG	CA	AG	GGG	T	G	IIG	Α.	TU	10	A	AC	TC		GG	IG	300	1.
00372001.1	GGTT	GG	CC		AA.		GA	GGC	100	A	G		GA	CE	GE	ACG	TO	AC	GG	CA	AG	GGG	T	G		AP	TU	110	A	AC	IC		GG	IG	SCC	1.
00372997.1	GGCI	GG	CC	11	AAA	AIC	GA	GC		A	G.		GA	CC	GF	ACG	T	AC	66	CA	AG	IGG	T	10	TTC	AA	T		A	AC	1 C	II	GG	IG		• •
002372012.1	GGCI	GG	ru u	. 1 /	AAA	410	GP	190		, A (-0	τÇ	GA		GF	ACG	11.(AU	99	CA	AG	1966	T (9.0	116	PA P	110	- 1 (, A1	AC	TC	τI	GG	1 G	300	•••

Figure 6.3. Multiple sequence alignment for 28 Physalis accessions based on ITS2 marker.

00507166.1 00507184.1 00507180.1 00507180.1 00507185.1 00507185.1 00507185.1 00507185.1 00507185.1 00507185.1 00507187.1 00507187.1 00507187.1 00507189.1 00507189.1 00507159.1 00507159.1 00507159.1 00507159.1 00507159.1 00507159.1 00507159.1 00507159.1 00507159.1 00507153.1 00507153.1	ATGTCACCACAAACAGAGACTA ATGTCACCACAAACAGAGACTA ATGTCACCACAAACAGAGACTA ATGTCACCACAAACAGAGACTA ATGTCACCACAAACAGAGACTA ATGTCACCCCACAAACAGAGACTA ATGTCACCCCCACACAGAAACTA ATGTCACCCCACAAACAGAGACTA ATGTCACCCACAAACAGAGACTA ATGTCACCACAAACAGAGACTA ATGTCACCACAAACAGAGACTA ATGTCACCACAAACAGAGACTA ATGTCACCACAAACAGAGACTA ATGTCACCACAAACAGAGACTA ATGTCACCACAAACAGAGACTA ATGTCACCACAAACAGAGACTA ATGTCACCACAAACAGAGACTA ATGTCACCACAAACAGAGACTA	AAGCAAGCTIGGATCAAGCT AAGCAAGTITGGATCAAGCT AAGCAAGTITGGATCAAGCT AAGCAAGTITGGATCAAGCT AAGCAAGTITGGATCAAGCT AAGCAAGTITGGATCAAGCT AAGCAAGTITGGATCAAGCT AAGCAAGTITGGATCAAGCT AAGCAAGTITGGATCAAGCT AAGCAAGTITGGATCAAGCT AAGCAAGTITGGATCAAGCT AAGCAAGTITGGATCAAGCT AAGCAAGTITGGATCAAGCT AAGCAAGTITGGATCAAGCT AAGCAAGTITGGATCAAGCT AAGCAAGCTIGGATCAAGCT AAGCAAGCTIGGATCAAGCT AAGCAAGCTIGGATCAAGCT AAGCAAGCTIGGATCAAGCT	GGTGTTAAAGAGCACCAAATT GGTGTTAAAGAGCACCAAATT GGTGTTAAAGAGTACCAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GGTGTTAAAGAGTACAAATT GAATT AAATT AAATT AAATT AAATT GAATTAAGAGTACAAATT GATGTTAAAGAGTACAAATT	GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA GACTTATTATACTCCTGA
00507166.1		1 10 20 ATATTGGCAGCATTCCGAGT	30 40 AACTCCTCAACCTGGAGTTC	50 CACCTGAAGAAGCAGGGG
00507184.1	GTACCAAACCAAGGATACTGAT	ATATTGGCAGCATTCCGAG1	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG
00507180.1	GTACCAAACCAAGGATACTGAT	ATATTGGCAGCATTCCGAG1	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG
00507165 1	GTACCAAACCAA	ATATTGGCAGCATTCCGAG1	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGCGG
00507163.1	GTACCAAACCAAGGATACTGAT	ATATTGGCAGCATTCCGAG	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG
00507183.1	GTACCAAACCAAGGATACTGAT	ATATTGGCAGCATTCCGAG	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG
00507177.1	GTACCAAACCAAGGATACTGAT	ATATTGGCAGCATTCCGAGT	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG
00507185.1	GTACCAAACCAAGGATACTGAT	ATATTGGCAGCATTCCGAGT	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG
00507154.1	GIACCAAACCAAGGAIACIGAT	ATATTGGCAGCATTCCGAGT	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG
00507156.1	GIACCAAACCAAGGAIACIGAT	ATATTGGCAGCATTCCGAGT	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG
00507167.1	GIACCAAACCAAGGAIACIGAT	ATATTGGCAG <u>CATTCCGAG</u> T	AACTCCTCAACCTGGAGTTC	CACCTGAAG <u>AAGCAGGGG</u>
00507168.1	GTACCAAACCAAGGATACTGAT	ATATTGGCAGCATTCCGAGT	AACTCCTCAACCTGGAGT	CACCTGAAGAAGCAGGGG
00507169.1	GTACCAAACCAAGGATACTGAT	ATATTGGCAGCATTCCGAGT	AACTCCTCAACCTGGAGT	CACCTGAAGAAGCAGGGG
00507181.1	GTACCAAACCAAGGATACTGAT	A T A T T G G C A G C A T T C C G A G 1	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG
00507193.1	GTACCAAACCAAGGATACTGAT	A T A T T G G C A G C A T T C C G A G 1	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG
00507195.1	GTACCAAACCAA	A T A T T G G C A <u>G C A T T C C G A G 1</u>	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG
00507199.1	GTACCAAACCAAGGATACTGAT	ATATTGGCAGCATTCCGAGT	AACTCCTCAACCTGGAGTIC	CACCTGAAGAAGCAGGGG
00507201.1	GTACCAAACCAAGGATACTGAT	ATATTGGCAGCATTCCGAGT	AACTCCTCAACCTGGAGTIC	CACCTGAAGAAGCAGGGG
00507192.1 00507155.1	GTACCAAACCAAGGATACTGAT GTACCAAACCAAGGATACTGAT GTACCAAACCAA	ATATTGGCAGCATTCCGAG1 ATATTGGCAGCATTCCGAG1 ATATTGGCAGCATTCCCAG1	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG CACCTGAAGAAGCAGGGG CACCTGAAGAAGCAGCGGG
00507161.1 00507159.1	GTACCAAACCAAGGATACIGAT GTACCAAACCAAGGATACIGAT GTACCAAACCAAGGATACIGAT	ATATTGGCAGCATTCCGAG ATATTGGCAGCATTCCGAG	AACTCCTCAACCTGGAGTTC AACTCCTCAACCTGGAGTTC AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG CACCTGAAGAAGCAGGGG CACCTGAAGAAGCAG <u>GGG</u>
00507158.1	GTACCAAACCAAGGATACTGAT	ATATTGGCAGCATTCCGAGT	AACTCCTCAACCTGGAGT	CACCTGAAGAAGCAGGGG
00507157.1	GTACCAAACCAAGGATACTGAT	ATATTGGCAGCATTCCGAGT	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG
00507153.1	GTACCAAACCAAGGATACTGAT	A T A T T G G C A G C A T T C C G A G T	AACTCCTCAACCTGGAGTTC	CACCTGAAGAAGCAGGGG
00507171.1	GTACCAAACCAAGGATACTGAT	A T A T T G G C A G C A T T C C G A G T	AACTCCTCAACCTGGAGTT	CACCTGAAGAAGCAGGGG
00507194.1	GTACCAAACCAA	A T A T T G G C A G C A T T <u>C C G A G T</u>	AACTCCTCAACCTGG <u>AGT</u> TC	CACCTGAAGAAGCAGGGG
00507166 1	60 70 80	90, 100		
0Q507184.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA
0Q507180.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA
00507165.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA
00507163.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA
00507183.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTETTGATEGTTACAAA
00507177.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTETTGATEGTTACAAA
00507185.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTETTGAT <u>EGTTACAA</u> A
00507154.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA
00507156.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA
00507167.1 00507168.1	CCGCGGTAGCTGCCGAATCTTC CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA AGTCTTGATCGTTACAAA AGTCTTGATCGTTACAAA
0Q507181.1 0Q507193.1	CCGCGGTAGCTGCCGAATCTTC CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC TACTGGTACA <u>TGGACAACTC</u>	TATGGACCGATGGACTTACC TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA AGTCTTGATCGTTACAAA AGTCTTGAT <u>CGTTACAAA</u>
00507195.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA
	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA
00507201.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACT(TATGGACCGATGGACTTACC	AGTETTGATEGTTACAAA
00507192.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACT(TATGGACCGATGGACTTACC	AGTETTGATEGTTACAAA
00507155 1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACT(TATGGACCGATGGACTTACC	AGTETTGATEGTTACAAA
00507160.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA
00507161.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGAC <u>TTACC</u>	AGTCTTGATCGTTACAAA
00507159.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA
00507158.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA
0Q507157.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA
0Q507153.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA
00507194.1	CCGCGGTAGCTGCCGAATCTTC	TACTGGTACATGGACAACTC	TATGGACCGATGGACTTACC	AGTCTTGATCGTTACAAA

	140	150	160	170	180	190	200	210
00507166.1	GGGCGA		TCGAGCGT	TTGTTG <mark>GA</mark> G	AAAAGATCAATA	TATTGCTTA	T <mark>GTAGCTTAC</mark>	CCTTTAGACCTTTT
00507180.1	GGGCGA	IGCTACCGCA'	ICGAGCGI(GTTGTTG <mark>GA</mark> GI	AAAAAGAGACATA AAAAAGATCAATA	TATTGCTTA	TGTAGCTTAC	CCTTTAGACCTTTT
00507165.1	GGGCGA	IGCTACCGCA	ICGAGCGT(TTGTTGTAG	A G A A A A A A T C A A T A	TATTGTTA	TATAGGTTAC	CCTTTAGACCTTTT CCTTTAGACCTTTT
00507183.1	GGGCGA	IGCTACCGCA	ICGAGCGT	TTGTTGGAG	А <mark>АААА</mark> <mark>басса</mark> ата	TATTGCTTA	TGTAGCTTAC	CTT TAGACCTTTT
00507177.1	GGGCGA	IGCTACCGCA	ICGAGCGT(STTGTTG <mark>GA</mark> GI	A <mark>AAAAGATCA</mark> ATA AAAAAGATCAATA	TATTGCTTA	TGTAGCTTAC	CCTTTAGACCTTTT CCTTTAGACCTTTT
00507154.1	GGGCGA	IGCTACCGCA'	ICGAGCGI	GTTGTTG <mark>GA</mark> GI	AAAAGATCAATA	TATTGCTTA	TGTAGCTTAC	CTT TAGACCTTTT
00507156.1	GGGCGA	IGCTACCGCA	ICGAGCGT(TTGTTGGAG	A <mark>AAAA</mark> GATCAATA	TATTGCTTA	TGTAGCTTAC	CCTTTAGACCTTTT CCTTTAGACCTTTT
00507168.1	GGGCGA	IGCTACCGCA	ICGAGCGT	TTGTTGGAG	A <mark>AAAAG</mark> ATCAATA	TATTGCTTA	TGTAGCTTAC	CTT TAGACCTTTT
0Q507169.1 00507181 1	GGGCGA	IGCTACCGCA	ICGAGCGT(STTGTTG <mark>GA</mark> GI	AAAAAGATCAATA AAAAAGATCAATA	TATTGCTTA	TGTAGCTTAC	CCTTTAGACCTTTT CCTTTAGACCTTTT
00507193.1	GGGCGA	IGCTACCGCA'	TCGAGCGT	GTTGTTG <mark>GA</mark> G2	А <mark>АААА</mark> <mark>БАТСА</mark> АТА	TATTGCTTA	TGTAGCTTAC	C <mark>CTT</mark> TAGACCTTTT
0Q507195.1 00507199.1	GGGCGA	IGCTACCGCA'	ICGAGCGT(ICGAGCGT(STTGTTGGAG STTGTTGGAG	A A A A A G A T C A A T A A A A A A G A T C A A T A	TATTGCTTA TATTGCTTA	TGTAGCTTAC TGTAGCTTAC	C <mark>CTT</mark> TAGACCTTTT C <mark>CTT</mark> TAGACCTTTT
00507201.1	GGGCGA	IGCTACCGCA'	ICGAGCGT	GTTGTTG <mark>GA</mark> GJ	аааадатсаата	TATTGCTTA	TGTAGCTTAC	CCTTTAGACCTTTT
00507192.1	GGGCGA: GGGCGA:	IGCTACCGCA IGCTACCGCA	FCGAGCGT(FCGAGCGT(TTGTTGGAG TTGTTGGAG	A A A A A G A T C A A T A A A A A A G A T C A A T A	TATTGCTTA TATTG <mark>C</mark> TTA	TGTAGCTTAC TGTAGCTTAC	CCTTTAGACCTTTT CCTTTAGACCTTTT
00507160.1	GGGCGA	IGCTACCGCA	TCGAGCGT	TTGTTG <mark>GA</mark> G	A <mark>AAAA</mark> GATCAATA	TATTCCTTA	T <mark>GTAGC</mark> TTAC	C <mark>CTT</mark> TAGACCTTTT
00507159.1	GGGCGA	IGCTACCGCA'	ICGAGCGIC	GTTGTTGGAG	AAAAAGATCAATA AAAAAGATCAATA	TATTGCTTA	TGTAGCTTAC	CCTTTAGACCTTTT
00507158.1	GGGCGA	IGCTACCGCA	ICGAGCGT(GTTGTTG <mark>GA</mark> GI	A <mark>AAAA</mark> GATCAATA	TATTGCTTA	TGTAGCTTAC	C <mark>CTT</mark> TAGACCTTTT CCTTTAGACCTTTT
00507153.1	GGGCGA	IGCTACCGCA	CGAGCGT(STTGTTG <mark>GA</mark> G	AAAAAGATCAATA	TATTGCTTA	TGTAGCTTAC	CCTTTAGACCTTTT
00507171.1	GGGCGA	IGCTACCGCA	ICGAGCGT(STTGTTGGAG	A <mark>AAAA</mark> GATCAATA	TATTGCTTA	TGTAGCTTAC	CCTTTAGACCTTTT CCTTTAGACCTTTT
02507154.1	000001	locinecoen.	100400010					
	220	230	240	250	260	270	280	290
00507166.1	TAAAGA	AGGTTCCGTA	GCTAACAAA	AAGAGTTAC	ATAAAAGAAAGAG	TATTTAGGG	TTAAAGCCCG	GCGCGCTCTCCGTC
00507184.1	TGAAAAA	GGTTCCTTA	ACCCA <mark>CA</mark> TO	TTTACTTCC:	ITTGTAGGGAATG	TATTT <mark>G</mark> GGT	TTAAAGCCCT	GCGCGCTC <mark>TA</mark> C <mark>T</mark> TC
00507165.1	TGAAGA	AGGTICCGII	ACCAACACAC	STTTACTTCC:	ATTAGAGATAATG	TATTTGGGT	TTAAAGCCCCT	GCGCGCTC <mark>GA</mark> C <mark>G</mark> TC
00507163.1	TGAAGA)	AGGTCCCGGT	ACCACCATO	TTTACTTCC	ITTGTAGGGAATG	TATTTGGGT	TTAAAGCCCT	GCGCGCTC <mark>TA</mark> CGTC
00507177.1	TGAAGA	AGGTTCCGTT	ACCAACAT(STTTACTTCC	ATTGTAGGTAATG	TATTTGGT	TTAAAGCCCT	GCGCGCTCTACGTC GCGCGCTCTACGTC
00507185.1	TGAAGA	AGGTTCCGTT	ACCAACAT(TTTACTTCC	ATTGTAGGTAATG	TATTTGGGT	TTAAAGCCCT	GCGCGCTC <mark>TAC</mark> GTC
00507156.1	TGAAGA	AGGTTCCGTT		TTTACTTCC	ATTGTAGGTAATG	TATTTGGGT	TTAAAGCCCT	GCGCGCTC <mark>TA</mark> CGTC
00507167.1	TGAAGA	AGGTTCCGTT	ACCAACAT(ACCAACAT(TTTACTTCC	ATTGTAGGTAATC	TATTTGGGT	TTAAAGCCCT	GCGCGCTCTACGTC
00507169.1	TGAAGA	AGGTTCCGTT	ACCAACAT(TTTACTTCC	A T T G T A G G T A A T G	TATTTGGGT	TTAAAGCCCT	GCGCGCTC <mark>TA</mark> CGTC
00507181.1	TGAAGA/ TGAAGA/	AGGTTCCGTT	ACCAACAT(ACCAACAT(TTTACTTCC/	ATTGTAGGTAATG ATTGTAGGTAATG	TATTTGGGT	TTAAAGCCCT TTAAAGCCCT	GCGCGCTC <mark>TAC</mark> GTC GCGCGCTCTACGTC
00507195.1	TGAAGA	A <mark>GGT</mark> TCC <mark>GTT</mark>	А <mark>ССАА</mark> САТО	TTT <mark>ACTTC</mark> C	A <mark>TTGTAG</mark> GT <mark>A</mark> ATG	TATTT <mark>G</mark> GGT	TTAAAGCCCT	GCGCGCTC <mark>TA</mark> C <mark>G</mark> TC
00507201.1	TGAAGA/ TGAAGA/	AGGTTCCGTT	ACCAACATO ACCAACATO	TTTACTTCC	ATTGTAGGTAATG ATTGTAGGTAATG	TATTTGGGT	TTAAAGCCCT	GCGCGCTCTACGTC
00507192.1	TGAAGA/	AGGTTCCGTT	ACCAACAT(TTTACTTCC/	ATTGTAGGTAATG	TATTTGGGT	TTAAAGCCCT	GCGCGCTC <mark>TA</mark> C <mark>G</mark> TC
00507160.1	TGAAGA	AGGTICCGTT	ACCAACAT(STTTACTTCC	ATTGTAGGTAATG	TATTTGGGT	TTAAAGCCCT	GCGCGCTCTACGTC
00507161.1	T G A A G A I	AGGTICCGTT	ACCAA <mark>CA</mark> TO	TTTACTTCC	ATTGTAGGTAATG	TATTTGGGT	TTAAAGCCCT	GCGCGCTC <mark>TA</mark> CGTC
00507158.1	TGAAGA	AGGTTCCGTT		TTTACTTCC	ATTGTAGGTAATG	TATTTGGGT	TTAAAGCCCT	GCGCGCTCTACGTC
0Q507157.1 00507153.1	TGAAGA) TGAAGA)	AGGTTCCGTT	ACCAACAT(ACCAACAT(TTTACTTCC/	ATTGTAGGTAATG ATTGTAGGTAATG	TATTTGGGT	TTAAAGCCC <mark>T</mark> TTAAAGCCCT	GCGCGCTC <mark>TAC</mark> GTC GCGCGCTCTACGTC
00507171.1	TGAAGA	AGGTICCGTT.	ACCAACATO	TTTACTTCC	A T T G T A G G T A A T G	TATTTGGGT	TTAAAGCCCT	GCGCGCTC <mark>TA</mark> CGTC
00507194.1	TGAAGA	AGGTICCGTT	ACCAACAT	TTTACTTCC	ATTGTACGTAATC	TATTTGGGGT	TTAAAGCCC	GCGCGCTC <mark>TA</mark> C <mark>GTC</mark>
00507166.1	GGGAAG	310	320 COTGTTG	330 TTATATAA	340 AGCTTTCCAAGGI	CCGCCTCAT	360 GGATCCAAG	370 TTGAAAGAGATAAA
00507184.1	GGGAAG	ATCTGCGAAT	CCCTGTTG	TTAT <mark>G</mark> TTAA	AACTTTCCAAGG	CCGCCTCAT	TGGATCCAAG	TTGAAAGAGATAAA
00507180.1	TGGAAG TGGAAG	ATCTGCGAAT(ATCTGCCAAT)	CCTGTTGC CC <mark>GTGTTGC</mark>	TTATATTAA TTAT <mark>G</mark> TTAA	AACTTTCCAGGGT AACTTTTCAGGGT	CCGCCTCAT	GGGACCCAAG	IGAAAAGTGATAAA
00507163.1	TGGAAG	ATCTGCGAAT	CCCTGTTG	TTATGTTAA	ACTTTCCAGGG	CCGCCTCAT	GGGACCCAAG	TIGAAAGAGAGAAA
00507177.1	TGGAAG	ATCTGCGAAT	CCCTGTTGC	TTATATTAA	ACTTTCCAGGGI	CCGCCTCAT	GGGATCCAAG	TTGAAAGAGATAAA
00507185.1	TGGAAGA	ATCTGC GAAT	CC <mark>CTGTTG(</mark>	TTAT <mark>G</mark> TTAA	AACTTTCCAAGGI	CCGCCTCAT	G <mark>GGA</mark> TCCAAG	TTGAAAGAGATAAA
00507156.1	TGGAAG	ATCTGCGAAT	CCCTGTTGC	CTTAT <mark>ATTAA</mark>	A CTTTCCA AGGI	CCGCCTCAT	GGGATCCAAG	TIGAAAGAGATAAA
00507167.1	TGGAAG	ATCTGCGAAT	CCTGTTG	TTATATTAA	AACTTTCCAAGGI	CCGCCTCAT	GGGATCCAAG	TTGAAAGAGATAAA
00507169.1	TGGAAG	ATCTGCGAAT	CCCTGTTGC	TTATATTAA	AACTTTCCAAGG	CCGCCTCAT	GGGATCCAAG	TTGAAAGAGATAAA
00507181.1 00507193 1	TGGAAG	ATCTGCGAAT(CCCTGTTG	TTAT <mark>A</mark> TTAA TTATATTAA	A A C T T T C C A A G G I	CCGCCTCAT CCGCCTCAT	GGGATCCAAG	TTGAAAGAGATAAA
00507195.1	TGGAAG	ATCTGCGAAT	CC <mark>CTGTTG</mark>	TTAT <mark>A</mark> TTAA	A A C T T T C C A A G G I	CCGCCTCAT	GGGATCCAAG	TTGAAAGAGATAAA
00507199.1	TGGAAG) TGGAAG)	ATCTGCGAAT ATCTGCGAAT	CCTGTTGC	CTTATATTAA CTTAT <mark>ATTAA</mark>	A A C T T T C C A A G G I A A C T T T C C A A G G I	CCGCCTCAT CCGCCTCAT	GGGATCCAAG GGGATCCAAG	ITGAAAGAGATAAA ITGAAAGAGATAAA
00507192.1	TGGAAG	ATCTGCGA <mark>A</mark> T	CCCTGTTG	TTATA TTAA	AACTTTCCAAGGI	CCGCCTCAT	GGGATCCAAG	TTGAAAGAGATAAA
00507155.1	TGGAAG T <mark>GGAA</mark> G	ATCTGCGAAT(ATCTGCGAAT)	CCTGTTGC CCCTGTTGC	TTATATTAA TTAT <mark>ATTAA</mark>	AACTTTCCAAGGT AACTTTCCAAGGT	CCGCCTCAT	GGGATCCAAG GGGATCCAAG	IIGAAAGAGATAAA TTGAAAGAGATAAA
00507161.1	TGGAAG	ATCTGCGAAT	CCCTGTTG	TTATATAA	AACTTTCCAAGGI	CCGCCTCAT	GGATCCAAG	TTGAAAGAGATAAA
00507159.1	TGGAAGI	ATCTGCGAAT(CCCTGTTGC	CTTATATTAA CTTAT <mark>ATTAA</mark>	A CTTTCCAAGGI	CCGCCTCAT	GGGATCCAAG	IIGAAAGAGATAAA IIGAAAGAGATAAA
00507157.1	TGGAAG	ATCTGCGAAT	CCTGTTGC	TTATATTAA	ACTTTCCAAGG	CCGCCTCAT	GGATCCAAG	TTGAAAGAGATAAA
00507171.1	TGGAAG	ATCTGCGAAT(CCCTGTTGC	TTATATTAA	A CTTTCCA AGGI	CCGCCTCAT	GGGATCCAAG	I TGAAAGAGATAAA
00507194.1	TGGAAG	ATCTGCGAAT	CCCTGTTG	CTTAT <mark>A</mark> TTAAI	AACTTTCCAAGGI	CCGCCTCAT	GGGATCCAAG	TTGAAAGAGATAAA

	380	390	400	410	420	430	440	450
00507166.1 00507184.1 00507180.1	TIGAAC TIGAAC TIGAAC	AAGTATGGTCGT AATTATGGCCGT AGATGTGGTCGC	CCCCTGTTGG CCCCTGTTGG CCCCTGTTGG	GATGTACTAT GCTGTACTAT GCTGTACTAT	TAAACCTAAA TAAACCTAAA TAAACCTAAA	TIGGGGTTATC TIGGGTTIATC TIGGGGTTCTG	ТССТААААА ТССТАААТА ТССТААААА	CCTCGGTAGAGC CGAGAGTAITGC CTACGAGAGTGC
00507165.1 00507163.1 00507183.1	TTGAAC TTGAAC	AAGTGGCGTCGT	CCCCTGTTGG	GGTGTACTAT GATGTACTAT	ТААССТТАААТ ТАААССТАААТ	TGGGGTTATC	ТСТТААААА. ТССТААААА	ATACGGTAGAGT CTACGAGAGAGC
00507177.1 00507185.1 00507154.1	TIGAAC TIGAAC TIGAAC	AAGTATGGTCGT AAGTATGGTCGT AAGTATGGTCGT	CCCCIGTIGG CCCCIGTIGG CCCCIGTIGG	GATGTTCTAT GATGTACTAI GATGTACTAI	TAAACTTTTA TAAACCTAAA TAAACCTAAA	TTGGGGTTA TTGGGGTTATC TTGGGGTTATC	ТGСТААААА ТGСТААААА	CTACGGTAGAGC CTACGGTAGAGC
00507156.1 00507167.1 00507168.1	TTGAAC TTGAAC TTGAAC	AAGTATGGTCGT AAGTATGGTCGT AAGTATGGTCGT	CCCCTGTTGG	GATGTACTAT GATGTACTAT GATGTACTAT	TAAACCTAAA TAAACCTAAA TAAACCTAAA	TIGGGGTTATC TIGGGGTTATC TIGGGGTTATC	TGCTAAAAA TGCTAAAAA TGCTAAAAA	CTACGGTAGAGC CTACGGTAGAGC CTACGGTAGAGC
00507169.1 00507181.1 00507193.1	TTGAAC TTGAAC TTGAAC	AAGTATGGTCGT AAGTATGGTCGT AAGTATGGTCGT	CCCCIGTIGG CCCCIGTIGG	GATGTACTAT GATGTACTAT GATGTACTAT	TAAACCTAAA TAAACCTAAA TAAACCTAAA	TIGGGGTTATC TIGGGGTTATC TIGGGGTTATC	TGCTAAAAA TGCTAAAAA TGCTAAAAA	CTACGGTAGAGC CTACGGTAGAGC CTACGGTAGAGC
00507195.1 00507199.1 00507201.1	TTGAAC TTGAAC TTGAAC	AAGTATGGTCGT AAGTATGGTCGT AAGTATGGTCGT	CCCCTGTTGG	GATGTACTAT GATGTACTAT GATGTACTAT	TAAACCTAAA TAAACCTAAA TAAACCTAAA	TIGGGGTTATC TIGGGGTTATC TIGGGGTTATC	TGCTAAAAA TGCTAAAAA TGCTAAAAA	CTACGGTAGAGC CTACGGTAGAGC CTACGGTAGAGC
00507192.1 00507155.1 00507160.1	TTGAAC TTGAAC TTGAAC	AAGTATGGTCGT AAGTATGGTCGT AAGTATGGTCGT	CCCCIGTIGG CCCCIGTIGG CCCCIGTIGG	GAIGTACTAI GAIGIACIAI GAIGIACIAI	TAAACCTAAA TAAACCTAAA TAAACCTAAA	TIGGGGTIAIC TIGGGGTIAIC TIGGGGTIAIC	TGCTAAAAA TGCTAAAAA TGCTAAAAA	CTACGGTAGAGC CTACGGTAGAGC CTACGGTAGAGC
00507151.1 00507159.1 00507158.1	TTGAAC TTGAAC TTGAAC	AAGTATGGTCGT AAGTATGGTCGT AAGTATGGTCGT	CCCCIGIIGG CCCCIGIIGG CCCCIGIIGG	GATGTACTAT GATGTACTAT GATGTACTAT	TAAACCTAAA TAAACCTAAA TAAACCTAAA	TIGGGGTTATC TIGGGGTTATC TIGGGGTTATC	TGCTAAAAA TGCTAAAAA TGCTAAAAA	CTACGGTAGAGC CTACGGTAGAGC CTACGGTAGAGC
00507157.1 00507153.1 00507171.1	TTGAAC TTGAAC TTGAAC	CAAGTATGGTCGT CAAGTATGGTCGT CAAGTATGGTCGT	CCCCIGTIGG CCCCIGTIGG CCCCIGTIGG	GАТСТАСТАТ GАТСТАСТАІ GАТСТАСТАТ	TAAACCTAAA TAAACCTAAA TAAACCTAAA	TIGGGGTIAIC TIGGGGTIAIC TIGGGGTIAIC	TGCTAAAAA TGCTAAAAA TGCTAAAAA	CTACGGTAGAGC CTACGGTAGAGC CTACGGTAGAGC
00507194.1	<u>TIGAAC</u>	AAGTATGGTCGT	CCCCIGTIGG	GATGTACTAT	TAAACCTAAAT	TIGGGGTIATC	TGCTAAAAA	<u>CTACGGTAGAGC</u>
00507166.1	460 TGTTTA	470 TGAAIGTCTTCG	4 B O CGGTGTGGTT	490 GATTTTCCCA	500 AAGATGATGA	510 GAACGTG		
00507184.1 00507180.1 00507165.1	TGTTTA TATTTA	CGAATGTTTACG	CGGTGGAACT	GATITTACCA GATITTACCA	AATTTGCIGA	GAACGTTCTCI GAACITGAACI	TGCAACCTI CACCACCTI	TTAGAAGTTGGC TTGCGCGTTGGA
00507163.1 00507183.1 00507177.1	TGTTGA TGTTTA	TGAAIGICICCG TGGAIGICICCG	CGGTGGGATT	GATTTTACCA GATTTTACCA	AAGATGATGAC AAGACAATGAC	GAACGCGGACI GAAACTGAACI	CCCAACCAT	TTACGTGTTGGA TTTTGCGTTGGA
00507185.1 00507154.1 00507156.1	TGTTTA TGTTTA TGTTTA	TGAAIGICTICG TGAAIGICTICG TGAAIGICTICG	CGGTGGACTT CGGTGGACTT CGGTGGACTT	GATTTTACCA GATTTTACCA GATTTTACCA	AAGATGATGAC AAGATGATGAC AAGATGATGAC	GAACGTGAACI GAACGTGAACI GAACGTGAACI	CACAACCAT CACAACCAT CACAACCAT	TTATGCGTTGGA TTATGCGTTGGA TTATGCGTTGGA
00507167.1 00507168.1 00507169.1	TGTTTA TGTTTA TGTTTA	TGAAIGTCTTCG TGAAIGTCTTCG TGAAIGTCTTCG	CGGTGGACTT CGGTGGACTT CGGTGGACTT	GATTTTACCA GATTTTACCA GATTTTACCA	AAGATGATGAC AAGATGATGAC AAGATGATGAC	GAACGTGAACI GAACGTGAACI GAACGTGAACI	CACAACCAT CACAACCAT CACAACCAT	TTATGCGTTGGA TTATGCGTTGGA TTATGCGTTGGA
00507181.1 00507193.1 00507195.1	TGTTTA TGTTTA TGTTTA	TGAAIGICTICG TGAAIGICTICG TGAAIGICTICG	CGGTGGACTT CGGTGGACTT CGGTGGACTT	GATTTTACCA GATTTTACCA GATTTTACCA	AAGATGATGA AAGATGATGA AAGATGATGA	GAACGTGAACI GAACGTGAACI GAACGTGAACI	CACAACCAT CACAACCAT CACAACCAT	TTATGCGTTGGA TTATGCGTTGGA TTATGCGTTGGA
00507199.1 00507201.1 00507192.1	TGTTTA TGTTTA TGTTTA	TGAATGTCTTCG TGAATGTCTTCG TGAATGTCTTCG	CGGTGGACTT CGGTGGACTT CGGTGGACTT	GATTTTACCA GATTTTACCA GATTTTACCA	AAGATGATGAC AAGATGATGAC AAGATGATGAC	GAACGTGAACI GAACGTGAACI GAACGTGAACI	CACAACCAT CACAACCAT	TTATGCGTIGGA TTATGCGTIGGA
00507155.1 00507160.1 00507161.1	TGTTTA TGTTTA TGTTTA	TGAAIGICTIC TGAAIGICTICG TGAAIGICTICG	CGGTGGACTT	GATITTACCA GATITTACCA	AA	GAACGTGAACT	CACAACCAT	TTATGCGTTGGA
00507159.1 00507158.1 00507157.1	TGTTTA TGTTTA TGTTTA	TGAATGTCTTCG TGAATGTCTTCG	CGGTGGACTT CGGTGGACTT CGGTGGACTT	GATTTTACCA GATTTTACCA GATTTTACCA	AAGATGATGAC AAGATGATGAC AAGATGATGAC	GAACGTGAACI GAACGTGAACI GAACGTGAACI	CACAACCAT CACAACCAT CACAACCAT	TTATGCGTTGGA TTATGCGTTGGA TTATGCGTTGGA
00507153.1 00507171.1 00507194.1	TGTTTA TGTTTA TGTTTA	TGAATGTCTTCG TGAATGTCTTCG	CGGTGGACTT	GATITTACCA GATITTICCA	AAGATGATGA AAGATGATGA	GAACGTGAACT GAACGTGAACT	CACAACCAT	TTATGCGTTGGA TTATGCTTIGGA
-								
00507166.1 00507184.1	GAGAAC	ATTTCTATTTT	GTATGGAAGC	 ACT <mark>T</mark> TATAAA	GCACAGGCTG	AATTGGTAAA	ATAAGGTTA	CTGATICG
00507180.1 00507165.1 00507163.1	GAGATC GAGATC	GITICCGCTIIG	GCGCCGAAAC	ATTTTATAAA ACCTTATAAA	.GGTCAGGAGGA 	AACAAGGGAA GAACAGGTGGA	ATAAGA ATAGGGTTA	CTGATICG
00507183.1 00507177.1 00507185.1	GAGATC GAGATC	GITICGICTIII GITICGICTIII	ATGCCGAAGC	А G T T T A T A A A 	.GCACAGGCTGA	AAAGAGGTGAA AAACAGGTGAA	ATAAGGTTA ATAAGGTTA	CTGATTCG CTGATTCG
00507154.1 00507156.1 00507167.1	GAGATC GAGATC GAGATC	GITICGICTIIT GITICGICTIIT GITICGICTIIT	GIGCCGAAGC GIGCCGAAGC GIGCCGAAGC	АСТТТАТААА АСТТТАТААА АСТ <mark>Т</mark> ТАТААА	.GCACAGGCTG .GCACAGGCTG .GCACAGGCTG	AAACAGGIGAA AAACAGGIGAA AAACAGGIGAA	ATAAGGTTA ATAAGGTTA ATAAGGTTA	CTGATICG CTGATICG CTGATICG
00507168.1 00507169.1 00507181.1	GAGATC GAGATC GAGATC	GITTCGTCTTIT GITTCGTCTTTT GITTCGTCTTIT	GTGCCGAAGC GTGCCGAAGC GTGCCGAAGC	АСТТТАТААА АСТТТАТААА АСТТТАТААА	.GCACAGGCTG .GCACAGGCTG .GCACAGGCTG	AAACAGGTGAA AAACAGGTGAA AAACAGGTGAA	ATAAGGTTA ATAAGGTTA ATAAGGTTA	CTGATTCG CTGATTCG CTGATTCG
00507193.1 00507195.1 00507199.1	GAGATC GAGATC GAGATC	GITTCGTCTTTT GITTCGTCTTTT GITTCGTCTTTT	GTGCCGAAGC. GTGCCGAAGC. GTGCCGAAGC.	АСТТТАТААА АСТТТАТААА АСТТТАТААА	GCACAGGCTGA GCACAGGCTGA GCACAGGCTGA	AAACAGGTGAA AAACAGGTGAA AAACAGGTGAA	ATAAGGTTA ATAAGGTTA ATAACGTTA	CTGATICG CTGATICG CTGATICG
00507201.1 00507192.1 00507155 1	GAGATC	GITICGICTII	GTGCCGAAGC	ACT T TATAAA	GCACAGGCTG	AACAGGTGAA	ATAAGGTTA	CTGATICG
00507160.1	GAGATO	GITTCGTCTTTT	GIG					· · · · · · · · ·
00507158.1	GAGATO	GITICGICTIT	GTGCCGAAGC	ACTTACTTTATAAA	GCACAGGCTGA	AA	· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·
00507171.1 00507194.1	GAGATC	GGTTCGTCTTTT	GIGCCCAACC	ACTTTATAAA	GTACAGGCTG	AACAG	· · · · · · · · · · · · ·	• • • • • • • • • • • • • • • • • • •

Figure 6.4. Multiple sequence alignment for 28 *Physalis* accessions based on *rbcL* markers.

6.3.4 Species discrimnation of *Physalis* species based on phylogenetic analysis

A phylogenetic tree constructed using combined ITS2 and *rbcL* sequences yielded two major clusters from the BI phylogeny that were robust with 100% posterior probability values (Figure 6.5), with each of the clusters separated based on the ITS2 and *rbcL* nucleotide data matrix. The combination of the two genes on the same phylogenetic tree gave a clear perspective on the Physalis species discrimination efficiency of each gene. Species discrimination was only possible with the ITS2 marker, while the discriminatory power of *rbcL* was low and inefficient. The *rbcL* region showed the lowest level of genetic differentiation, with the species samples *P*. minima, P. peruviana, P. angulata and P. virginiana forming a distinct cluster (Figure 6.5). The nucleotide data matrix from *rbcL* reflects the close genetic relationships of these species (Figure 6.5). The nucleotide data matrix of ITS2 splits the Physalis accessions into three clades representing three Physalis species, namely, P. cordata (OQ5372012.1, OQ371998.1, OQ372001.1 and OQ371998.1), P. peruviana (OQ372016.1 and OQ372008.1) and P. purpurea (00371996.1, OO372003.1, OO372004.1, OQ372005.1, 00372007.1. 00372009.1. OQ372013.1, OQ372014.1, OQ372015.1, OQ372017.1, OQ372018.1- OQ372029) (Figure 6.5).

The clades formed by the ITS2 sequences show longer branch lengths among the *P. peruviana* species, with a posterior probability percentage of 94. The *P. cordata* species is associated with moderate branch lengths on the phylogenetic tree, with a posterior probability percentage of 89. The shortest branch lengths among the ITS2 sequences on the phylogenetic tree are those associated with *P. purpurea*, with a posterior probability percentage of 66.



Figure 6.5. Consensus Phylogenetic tree prepared by MrBayes for *Physalis* accessions based on a combination of ITS2 and *rbcL* DNA barcodes

Black represents different *Physalis* species reference sequences retrieved from GenBank after BLASTn analysis, green represents *P. cordata*, plum represents *P. peruviana*, blue represents *P. purpurea*, teal represents *P. virginiana*, purple represents *P. angulata* and orange represents *P. minima*. Numbers above branches indicate the posterior probability percentage statistic for the MrBayes phylogenetic tree. The length of the branches indicates the genetic divergence of the *Physalis* accessions as compared to their counterparts.

6.3.5 Genetic divergence analysis between and within *Physalis* species based on ITS2 sequences

The ITS2 sequence was the only barcode that could be used to differentiate the accessions into *Physalis* species which is necessary for interspecific genetic divergence analysis (Figure 6.5). The *rbcL* genes could not discriminate *Physalis* species and hence it was impossible to assess for interspecific genetic divergence based on this gene (Figure 6.5).

6.3.5.1 DNA divergence between populations based on ITS2 sequences

Varying shared mutations were observed between the *Physalis* populations (Table 6.5). The nucleotide diversity was highest (0.33208) between *P. peruviana* and *P. cordata* and the lowest (0.14821) between *P. cordata* and *P. purpurea*. The average number of nucleotide substitutions per site between populations ranged from 0.24621 to 0.38915. The number of net nucleotide substitutions per site between nucleotides ranged from 0.01299 to 0.12343 (Table 6.5). The total number of fixed (base) differences between populations was: six for *P. peruviana* and *P. cordata*, one for *P. peruviana* and *P. purpurea*, and zero for *P. cordata* and *P. purpurea* (Table 6.5). The number of fixed differences was determined from the total polymorphic sites between populations, and it was observed that the higher the number of polymorphic differences between populations was, the higher the fixed difference would be, and vice versa (Table 6.5).

 Table 6.5. DNA divergence between (interspecific) Physalis species populations based on ITS2 sequences.

Population	P. peruviana (P1)	P. cordata (P2)	P. peruviana (P1)	P. purpurea (P2)	P. purpurea (P1)	P. cordata (P2)		
Polymorphic sites in each population	14	21	12	18	2	4		
Total number of polymorphic sites	35		23	I	4	I		
Average number of nucleotide differences	17.600		6.351		0.889			
Nucleotide diversity Pi (t)	0.33208		0.18147		0.14821			
Number of fixed differences	6		1		0			
Polymorphic mutations in population 1 (P1) but monomorphic ones in population 2 (P2)	13		10		2			
Polymorphic mutations in P2 but monomorphic ones in P1	28		22		1			
Shared mutations	1		2		2			
Average number of nucleotide differences between populations	20.625		10.158		1.477			
Average nucleotide substitution per site between populations (Dxy)	0.38915		0.29026		0.24621			
Number of net nucleotide substitutions per site between populations (Da)	0.12343		0.03881		0.01299			
6.3.5.2 DNA Divergence within Populations Based on ITS2 Sequences

DNA divergence within each *Physalis* species was assessed using ITS2 sequences by determining the number of polymorphic (segregating) sites (S), the nucleotide diversity and the total number of substitutions (Table 6.6). The *rbcL* marker was not able to facilitate species discrimination and hence the analysis for genetic divergence was only performed on the ITS 2 gene sequences. The nucleotide diversity was highest (0.31250) and lowest (0.14898) within *P. peruviana* and *P. purpurea*, respectively (Table 6.6). The highest (101) and the lowest (26) total numbers of nucleotide substitutions were observed in *P. cordata* and *P. purpurea*, respectively. The numbers of polymorphic segregating sites were highest (83) and lowest (20) within *P. cordata* and *P. purpurea*, respectively (Table 6.6).

Physalis Species	P. peruviana	P. cordata	P. purpurea	
Total number of sequences	2	4	22	
Number of polymorphic (segregating) sites (S)	70	83	20	
Nucleotide diversity Pi (Total)	0.31250	0.18095	0.14898	
Nucleotide diversity Pi (JC-Total)	0.40425	0.20708	0.16609	
Theta (Total)	0.31250	0.19675	0.17396	
Total number of substitutions	70	101	26	

 Table 6.6. Polymorphism and divergence within (intraspecific) *Physalis* species based on ITS2 sequences.

6.3.6. Genetic distance between and within *Physalis* species based on ITS2 and *rbcL* sequences

The average inter-specific distance between *Physalis* species was determined based on the ITS2 gene sequences only because the *rbcL* marker was not able to facilitate species discrimination. The analysis showed that the highest mean genetic distance (1589.41) was between *P. purpurea* and *P. cordata* (Table 6.7). The lowest mean genetic distance (9.53) was between *P. cordata* and *P. peruviana* (Table 6.7).

Groups	P. purpurea	P. peruviana	P. cordata		
P. purpurea		198.92	1589.41		
P. peruviana	9.58		357.92		
P. cordata	21.99	9.53			

 Table 6.7. Mean genetic distance between (interspecific) *Physalis* species based on ITS2 sequences.

The average intra-specific distance within *Physalis* species was determined based on ITS2 sequences. The highest mean intraspecific distance was noted for *P. purpurea* (9.98 \pm 12.73), followed by *P. peruviana* (1.31 \pm 0.46), while the lowest mean intraspecific distance (0.72 \pm 0.13) was recorded for *P. cordata*. The divergence was higher within *P. purpurea* and lowest within *P. cordata*. The average intraspecific distance within *Physalis* accessions was also determined based on *rbcL* sequences. The intraspecific distance within *Physalis* species based on *rbcL* sequences was 0.03 \pm 0.00.

6.3.7. Nucleotide Polymorphism

In total, 4 segregation sites (S) were identified within the ITS2 sequences, while 59 segregation sites were identified within the *rbcL* gene sequences (Table 6.8). The nucleotide diversity (Pi) of ITS2 sequences was 0.15917, which is higher than that of *rbcL* sequences (0.01632) (Table 6.8). For the ITS2 sequences, the four polymorphic sites identified had 1 singleton and 3 parsimony informative bases, while the *rbcL* sequences had 48 singletons and 11 parsimony informative sites (Table 6.8).

	ITS2		rbcL				
Polymorphic Sites/Segregation Sites (S)	4	Position in the Gene	n Variants	59	Positions in the Gene	Variants	
Singleton	1	177	2	48	141,272,273,276,280,283,284,293,298, 301,308,309,310,322,325,327,331,334, 335,337,339,340,345,346,347,348,350, 353,357,365,366,373,375,376,386,395, 396,398,413,414,416,419,436,441,447, 457 344,359	2 3	
Parsimony informative sites	3	179 176 178	2 3 4	11	302,336,341,355,358,362,401,430,444 282,363	2 3	
Nucleotide diversity (Pi)	0.15917		0.01632				
Average number of nucleotide differences (k)		5.844					
Sequence length (base pairs)	532		716				
Number of sequences	28			28	28		

6.3.8 Tajima's neutrality tests

Tajima's neutrality test was conducted on the ITS2 and *rbcL* barcode sequences in order to establish the existence of a population selection based on the Tajima D value and nucleotide diversity. The Tajima D value of ITS2 sequences (0.870515) was higher compared to that of *rbcL* (-2.73462). The nucleotide diversity based on Tajima's test was also significantly higher for ITS2 sequences ($\pi = 0.176498$) compared to *rbcL* ($\pi = 0.067832$).

6.3.9 Barcoding gap analysis

The Automatic Barcode Gap Discovery (ABGD) results generated by the K80 Kimura measure of distance based on ITS2 and *rbcL* markers for *Physalis* accessions were used to determine the presence of a barcoding gap (Figure 6.6). The histogram ranked pairwise distances by increasing distance values from 0.02 to 1.28 and 0.02 to 0.14 for ITS2 and *rbcL* gene sequences, respectively (Figure 6.6). No barcode gap was detected via ITS2 ABGD analysis, while two barcode gaps were detected by the *rbcL* ABGD analysis (Figure 6.6). The first barcode gap for the *rbcL* gene sequence was detected between distances of 0.02 (2%) and 0.03 (3%), while the second barcode gap was between a distance of 0.12 (12%) and 0.13 (13%).



Figure 6.6. Histogram for the hypothetical distribution of pairwise differences of ITS2 and *rbcL* gene sequences for 28 *Physalis* accessions

A represents the histogram prepared using ITS2 genes while B represents the histogram prepared using *rbcL* genes

Low divergence is presumably intraspecific divergence, whereas higher divergence indicates interspecific divergence. The abbreviation nbr on the y-axis of the histogram stands for number of pairwise comparisons.

6.4 Discussion

DNA barcoding is a novel approach for identifying and discriminating species based on the nucleotide diversity of target/specific conserved sequences. Several studies have indicated that the DNA barcodes *rbcL* and ITS2, based on the chloroplast–plastid and nuclear regions, respectively, have been used to identify various plant families with similar morphological traits (Ralte and Singh, 2021). This study aimed at species discrimination in *Physalis* genotypes collected from different regions in Kenya by deploying both *rbcL* and ITS2 barcodes, and evaluated the efficiency of these markers in the barcoding of *Physalis* species. This is the first report to identify *Physalis* in Kenya using chloroplast–plastid and nuclear regions.

In previous studies, DNA barcoding markers, *rbcL*, *psbA-trnH* and ITS2 have been proven to be efficient in discriminating *Physalis* species from China and India (Ralte and Singh, 2021, Feng *et al.*, 2018, Feng *et al.*, 2016). These barcode genes were identified as potential candidates for the barcoding of *Physalis* plants. In the current study, the amplification was not universal because 16% and 23% of the samples did not amplify for *rbcL* and ITS2, respectively. Amplification failure can be attributed to DNA degradation during the transit of samples from the field to the laboratory. In addition, failures of DNA amplification and sequencing could also be linked to poor-quality DNA due to the presence of large amounts of secondary metabolites, such as phenolic compounds released during DNA isolation, which are common in *Physalis* species (Kang *et al.*, 2017, Medina-Medrano *et al.*, 2015).

The *rbcL* region of *Physalis* in this study was amplified more effectively compared to the ITS2 region. This concurs with previous studies, which showed higher amplification and sequencing success rate for *rbcL* compared to ITS2 (Kang *et al.*, 2017, Huang *et al.*, 2015). The high success rate of *rbcL* amplification is attributed to the high conservation of the gene and its low frequency rates of mutation (Kang *et al.*, 2017). Conversely, the lower amplification and sequencing success rate of the ITS2 barcode could be attributed to its incomplete concerted evolution

process, as reported in other species (Simeone *et al.*, 2013, Denk *et al.*, 2010, Abeysinghe *et al.*, 2009).

Basic Local Alignment Search Tool (BLAST) results have been used to identify the genus and facilitate species differentiation. Taxonomic assignments of *Physalis* accessions through BLASTn analyses against publicly available accessions in the databases did not give reliable results. This was probably because of the limited sequence data, since the available sequences in the databases mostly represent the most well-known and broadly studied species with a larger distribution, and to a lesser extent, species from insufficiently studied regions (Ross *et al.*, 2008). Therefore, much more information and richer databases are necessary for the reliable application of the BLAST analysis to the Kenyan *Physalis* species.

The levels of genetic discrimination of *Physalis* accessions based on genetic distances differed between the two DNA barcode regions. All rbcL sequences and their reference sequences from the database formed a distinct cluster with no differentiation of species, indicating low levels of genetic differentiation in the *Physalis* species. The nucleotide data matrix from the *rbcL* region reflects the close genetic relationships of these species. This indicates the inefficiency of using *rbcL* in discriminating plant species, and thus we consider this region to offer little information relevant to the taxonomic classification of *Physalis*. The inefficiency of *rbcL* in discriminating plant species compared to other barcodes has also been noted in other studies (Kang et al., 2017, Huang et al., 2015, Tripathi et al., 2013). Similar results were presented in other studies, where the phylogenetic tree-based method could not effectively identify species of plants based on *rbcL* sequences (Huang et al., 2015). A study that used over 10,000 rbcL sequences from the GenBank to identify plant species also came up with similar conclusions to this study-that rbcL can only discriminate at the genus level (Newmaster et al., 2006). Chloroplast rbcL had higher universality but narrow inter-specific genetic divergence, and its species discrimination power was restricted. It is recommended that when rbcL is used as a first-tier barcode in species discrimination, and a supplement barcode is also used to increase the efficiency of species discrimination due to the limitations of the *rbcL* barcode (Newmaster *et al.*, 2006).

However, the phylogenetic tree constructed based on ITS2 sequences demarcated the *Physalis* accessions into three distinct clades, with each representing a different *Physalis* species namely, *P. peruviana*, *P. cordata* and *P. purpurea*. This could be due to the fact that the ITS2 region possesses high interspecific and low intraspecific divergence (Chen *et al.*, 2010). The clades had varying branch lengths, an indication that there was a divergence of the ITS2 sequences among the identified *Physalis* species (Binet *et al.*, 2016). The branch lengths of the ITS2 sequences were much longer than those of the *rbcL* sequences, an indication that the ITS2 gene was more divergent, while the *rbcL* gene was more conserved among *Physalis* accessions. This concurs with the results of the genetic diversity studies, which showed a higher divergence among ITS2 as compared to *rbcL* sequences. The phylogenetic tree also showed longer branch lengths among the *P. peruviana* species, an indication that the two *P. peruviana* identified had a high intraspecific divergence. The more divergent the DNA barcode is, the better its ability to provide plant species discrimination among the targeted species (Kartavstev, 2011). Therefore, comparatively, the ITS2 sequences enabled better *Physalis* species discrimination based on Bayesian inference.

Higher nucleotide diversity was obtained for ITS2 compared to *rbcL*, an indication that the *rbcL* barcode is more conserved than ITS2. Therefore, the ITS2 barcode is useful to the interspecific divergence analysis of the *Physalis* accessions used in this study, which is also indicated by its ability to discriminate *Physalis* species. The interspecific divergence analysis of the ITS2 sequences in this study showed the highest nucleotide diversity between *P. peruviana* and *P. cordata* and the lowest between *P. cordata* and *P. purpurea*. One study postulated that a barcode has to exhibit high interspecific divergence to achieve the discrimination of species, especially amongst closely related sister species, while having low intraspecific variation (Rach *et al*, 2008). The current study showed that ITS2 was less conserved and possessed higher interspecific divergence than *rbcL*, indicating the level of species divergence among *Physalis* accessions used in this study.

Genetic distance is a measure of the genetic divergence between species or populations within a species (Beaumont *et al.*, 1998). This was significantly higher for the ITS2 barcode compared to that of *rbcL*. This is an indication that there is high genetic divergence and variation among

Physalis species based on the ITS2 barcode. Based on the genetic distance, ITS2 was able to discriminate Physalis accessions into various species. The highest and lowest intraspecific distances were obtained within the P. purpurea and P. cordata populations, respectively. The low genetic distance for *rbcL* sequences is also a confirmation that the barcode is highly conserved in *Physalis* accessions used in this study. The results of the nucleotide polymorphism analysis for the ITS2 and *rbcL* sequences concur with those of the nucleotide divergence analysis, where ITS2's nucleotide diversity was higher than that of *rbcL*. A higher number of singleton and parsimony mutations in the *rbcL* gene indicate higher low-frequency mutations, concurring with the Tajima D value confirming the high level of conservation of the *rbcL* barcode (Carlson et al., 2005, Tajima, 1989b). The nucleotide polymorphism of the ITS2 sequences showed fewer low-frequency mutations compared to rbcL, and this explains the higher divergence among ITS2 sequences. The Automatic Barcode Gap Discovery (ABDG) was also able to show the intraspecific divergence between ITS2 and *rbcL* sequences of *Physalis* accessions used in this study. The maximum intraspecific distance, P_{max}, was much higher at 0.1 for ITS2 than 0.0219 for *rbcL*. This is an indication that ITS2 is not only more divergent between species, but is also more divergent within species compared to *rbcL*, which is highly conserved between and within Physalis species.

An ideal DNA barcode has significantly smaller intraspecific than interspecific distances, with a clear boundary between the two, referred to as the DNA barcoding gap, which can help in the identification of species (Ge *et al.*, 2021; Meyer *et al.*, 2005). This study confirmed that *rbcL* is highly conserved in *Physalis* plants, as its maximum intraspecific distance based on the automatic barcode gap discovery (ABGD) analysis was $P_{max} = 0.0129$. On the other hand, for the ITS2 marker, the maximum intraspecific distance based on the ABGD analysis was $P_{max} = 0.1$. This confirms that *rbcL* sequences cannot be used to group the *Physalis* accessions into species, and were indeed unable to discriminate *Physalis* species. This has also been reported in studies of other plant species, such as cinnamon, where not only *rbcL* but also other chloroplast-based barcodes such as *matK* and the intergenic sequence *psbA-trnH* were unable to discriminate and identify species of cinnamon (Chandrasekara *et al.*, 2021). In other studies, *matK* and *psbA-trnH* have been shown to have better and higher potential as barcodes for the identification of tropical cloud forest trees than *rbcL* (Huang *et al.*, 2015). However, other studies have shown that *rbcL* is

useful in the species discrimination of yams (Kipkiror *et al.*, 2023). This suggests that *rbcL* species discrimination might differ from one genus of plants to another. The ITS2 sequences of the *Physalis* plants used in this study recorded high intraspecific divergence, as seen in the ABDG analysis ($P_{max} = 0.1$), probably due to its high variation. The ITS2 sequences were able to discriminate the *Physalis* accessions into three species, and the barcoding gap could be identified for all the three of these species. Their interspecific distance was much higher than that yielded by the ITS2 marker. The presence of a barcoding gap in different species is also an indication that ITS2 is an ideal candidate barcode for use in the discrimination of *Physalis* species and the determination of species diversity.

6.5 Conclusions

The results regarding sequence characteristics, genetic distance and phylogenetic relationships show that ITS2 is a reliable marker for use in the discrimination of *Physalis* species, whereby the accessions used were identified and discriminated into three species, namely, *P. purpurea*, *P. peruviana* and *P. cordata*. The ITS2 barcode was found to possess a sufficient variable region between the different species and accessions for the determination of genetic divergence with high discriminatory ability. These results expand our knowledge of genetic relationships that will benefit future crop improvement strategies in the areas of food, nutrition and therapeutics.

CHAPTER SEVEN

7.0 General discussion, conclusion and recommendations

7.1 General discussion

Physalis species contains nutritional and bioactive compounds of immense importance to public health and represents a potential ingredient for the development of functional foods and beverages. However, no study has reported the chemical composition, nutritional and antioxidant capacity of *Physalis* fruits in the wild and cultivated in Kenya. The lack of this information affects the production and utilization of this important fruit. Based on ITS2 barcode the *Physalis* accessions collected from Kericho County were identified as *P. purpurea* and were used for the analysis of macro-mineral and trace element content. The accessions of *P. purpurea* were found to be rich in both macrominerals (calcium, potassium, magnesium and sodium) and trace elements (zinc, copper, nickel, lithium and manganese). The results indicate that many of the macro- and micro-nutrients necessary for human health are found in *Physalis* fruits. The key phytochemicals identified in the fruits were phenolics, tannins and flavonoids and they facilitate the radical scavenging activity of DPPH radical and hydrogen peroxide.

Over the last decade, commercial *Physalis* plantations in Kenya have significantly increased and the farmers are concerned about the reliability and identity of the planting material. Among the challenges facing the production of planting material is the difficulty in precise identification of the *Physalis* species. A further confounding problem is the lack of discriminatory morphological features in plants of different *Physalis* species. DNA barcoding is a method that can effectively identify species according to the short DNA fragments information. The nuclear barcode, ITS2 has lower length variation and more common primer sites, which can better elucidate the genetic relationship between plant species. Several studies have also demonstrated that *rbcL* is effective and commonly used to identify plant species. Species identification based on the *rbcL* DNA barcode was successful for BLASTn analysis but species discrimination based on phylogenetic analysis was not possible based on the same barcode. Using BLAST algorithm on the NCBI database this study was able to identify all the *Physalis* accessions collected at the genus level, but none were identified at the species level. Despite *rbcL* barcode having high rate of amplification and sequencing among the *Physalis* accessions used in this study, it did not

facilitate the discrimination of *Physalis* species based on phylogenetic analysis as no clear grouping was observed. This concurs with previous studies in other plants where *rbcL* DNA barcode has been reported to have low efficacy in species discrimination of some plant families (Pei *et al.*, 2015; Li *et al.*, 2014).

Physalis species discrimination by BLAST algorithm on the NCBI database and phylogenetic analysis was effective based on ITS2 DNA barcode. The ITS2 barcode identified three *Physalis* species among the *Physalis* accessions collected in Kenya based on phylogenetic analysis. The three identified species were *P. cordata*, *P. peruviana* and *P. purpurea*. Therefore, ITS2 provided more robust species discrimination than the *rbcL* genes. Other studies have also confirmed the ability of ITS2 to identify and discriminate species (Zhang *et al.*, 2015). The combination of multi loci barcodes could improve the species discrimination and several studies have demonstrated the effectiveness (Tran *et al.*, 2021; Simeone *et al.*, 2013). In the current study, the combination of the two barcode regions failed to increase the *Physalis* species discrimination efficiency compared to the single barcode.

Nucleotide diversity and genetic distance of *Physalis* accessions was higher based on ITS2 barcode as compared to the *rbcL* DNA barcode. The nucleotide polymorphism of ITS2 and *rbcL* barcode sequences for the *Physalis* accessions used in this study was different. Although *rbcL* barcode sequences had higher nucleotide polymorphism than the ITS2 barcode, it did not provide better discrimination of *Physalis* species. Nucleotide polymorphisms observed in the *rbcL* barcode sequences of *Physalis* accessions were singleton mutations which are considered low frequency mutations (Carlson *et al.*, 2005). This explained why the low genetic diversity observed in the *rbcL* barcode despite the high nucleotide polymorphism.

7.2 Conclusions

(i) The study confirmed that the fruits of *P. purpurea* contained a high content of minerals, including calcium, sodium, magnesium, and potassium. The fruits were also rich in phenolic acids, tannins, and flavonoids, and exhibited antioxidant properties. The phenolic compounds and flavonoids were the major contributors to the radical scavenging activity of the *P. purpurea* fruits.

- (ii) DNA barcode ITS2 was highly efficient in the identification and discrimination of *Physalis* species. The *Physalis* accessions were identified and discriminated into three species namely *P. peruviana*, *P. purpurea* and *P. cordata*. Our study revealed significant variations in ITS2 secondary structure predictions that enhanced discrimination among the three identified *Physalis* species.
- (iii) The results regarding sequence characteristics, genetic distance and phylogenetic relationships show that *rbcL* identified the genus *Physalis* but could not discriminate the 56 accessions studied into different *Physalis* species indicating high conservation of *rbcL* gene. Low sequence divergence and low genetic distance among *Physalis* accessions based on *rbcL* gene was also noted, indicating the *rbcL* gene is mostly conserved among the accessions studied.
- (iv) The results regarding sequence characteristics, genetic distance and phylogenetic relationships show that ITS2 is a reliable marker compared to *rbcL* for use in the discrimination of *Physalis* species, whereby the accessions used were identified and discriminated based on the ITS2 gene into three species namely, *P. purpurea*, *P. peruviana* and *P. cordata*.

7.3 Recommendations

- (i) The underutilized *P. purpurea* was demonstrated to be an excellent source of minerals, phytochemicals and antioxidants and therefore there is need to exploit the accessions for the management of oxidative stress-induced human diseases.
- (ii) *Physalis* accessions identified can be utilized for genetic breeding to develop hybrids that are valuable to human nutrition and health.
- (iii)There is need to evaluate the efficiency of other DNA barcodes such as *matK*, *trnK* intron, *trnH-psdA* and *psbA-trnH* in species discrimination of *Physalis* plants. These DNA barcodes can be used to assess species discrimination, genetic diversity and nucleotide polymorphism of *Physalis* genus in Kenya.

- (iv) There is need for further studies to understand the use of RNA secondary structures for the selection of parents in trait-specific breeding strategies for *Physalis* improvement.
- (v) There is need for the development of species-specific DNA barcode for the discrimination of the three *Physalis* species identified in the current study as well as other *Physalis* species.

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APPENDICES

Appendix 1: *Physalis* accessions sample collection data, PCR and sequencing success rates for ITS 2 and *rbcL* genes

Appendix 1A: Table showing all sample collection areas and their geographical coordinates for *Physalis* accessions used in this study.

No.	Sample ID	County of sample	Specific	Latitude	Longitude
		collection	Location of		
			collection		
1.	Londiani L1	Kericho	Londiani-Sorget	0.0532° S	35.5548° E
2.	Londiani L2	Kericho	Londiani-Sorget	0.0532° S	35.5548° E
3.	Londiani L3	Kericho	Londiani-Sorget	0.0532° S	35.5548° E
4.	Londiani L4	Kericho	Londiani-Sorget	0.0532° S	35.5548° E
5.	Londiani L5	Kericho	Londiani-Sorget	0.0532° S	35.5548° E
6.	Londiani L6	Kericho	Londiani-Sorget	0.0532° S	35.5548° E
7.	Londiani L7	Kericho	Londiani-Sorget	0.0532° S	35.5548° E
8.	Londiani L8	Kericho	Londiani-Sorget	0.0532° S	35.5548° E
9.	Londiani L9	Kericho	Londiani-Sorget	0.0532° S	35.5548° E
10.	Londiani L10	Kericho	Londiani-Sorget	0.0532° S	35.5548° E
11.	Chebororwa C1	Elgeyo Marakwet	Chebororwa	0.9487° N	35.4234° E
12.	Chebororwa C2	Elgeyo Marakwet	Chebororwa	0.9487° N	35.4234° E
13.	Chebororwa C3	Elgeyo Marakwet	Chebororwa	0.9487° N	35.4234° E
14.	Chebororwa C4	Elgeyo Marakwet	Chebororwa	0.9487° N	35.4234° E
15.	Chebororwa C5	Elgeyo Marakwet	Chebororwa	0.9487° N	35.4234° E
16.	Chebororwa e1in	Elgeyo Marakwet	Chebororwa	0.9487° N	35.4234° E
17.	Chebororwa e2in	Elgeyo Marakwet	Chebororwa	0.9487° N	35.4234° E
18.	Chebororwa e3in	Elgeyo Marakwet	Chebororwa	0.9487° N	35.4234° E
19.	Chebororwa e4in	Elgeyo Marakwet	Chebororwa	0.9487° N	35.4234° E
20.	Chebororwa e5in	Elgeyo Marakwet	Chebororwa	0.9487° N	35.4234° E
21.	Chebororwa e6in	Elgeyo Marakwet	Chebororwa	0.9487° N	35.4234° E
22.	Chebororwa e7in	Elgeyo Marakwet	Chebororwa	0.9487° N	35.4234° E
23.	Chebororwa e8in	Elgeyo Marakwet	Chebororwa	0.9487° N	35.4234° E
24.	Ndhiwa hb1	Homabay	Ndhiwa	0.7299° S	34.3671° E
25.	Ndhiwa hb2	Homabay	Ndhiwa	0.7299° S	34.3671° E
26.	Ndhiwa hb3	Homabay	Ndhiwa	0.7299° S	34.3671° E
27.	Mukurweini ny1	Nyeri	Mukurweini	0.5609° S	37.0488° E
28.	Mukurweini ny2	Nyeri	Mukurweini	0.5609° S	37.0488° E
29.	Mukurweini ny3	Nyeri	Mukurweini	0.5609° S	37.0488° E
30.	Mukurweini ny4	Nyeri	Mukurweini	0.5609° S	37.0488° E
31.	Mukurweini ny5	Nyeri	Mukurweini	0.5609° S	37.0488° E
32.	Ongata Rongai nor1	Kajiado	Ongata Rongai	1.3939° S	36.7442° E
33.	Ongata Rongai nor2	Kajiado	Ongata Rongai	1.3939° S	36.7442° E
34.	Ongata Rongai nor3	Kajiado	Ongata Rongai	1.3939° S	36.7442° E
35.	Ongata Rongai nor4	Kajiado	Ongata Rongai	1.3939° S	36.7442° E
36.	Ongata Rongai nor5	Kajiado	Ongata Rongai	1.3939° S	36.7442° E
37.	Gilgil gm	Nakuru	Gilgil market	0.4923° S	36.3173° E
38.	Muguga DM	Kiambu	Muguga	1.2551° S	36.6580° E
39.	Thika TK1	Kiambu	Thika	1.0388° S	37.0834° E

40.	Thika TK2	Kiambu	Thika	1.0388° S	37.0834° E
41.	Thika TK3	Kiambu	Thika	1.0388° S	37.0834° E
42.	Thika TK4	Kiambu	Thika	1.0388° S	37.0834° E
43.	Thika TK5	Kiambu	Thika	1.0388° S	37.0834° E
44.	Thika TK6	Kiambu	Thika	1.0388° S	37.0834° E
45.	Thika TK7	Kiambu	Thika	1.0388° S	37.0834° E
46.	Thika TK8	Kiambu	Thika	1.0388° S	37.0834° E
47.	Thika TK9	Kiambu	Thika	1.0388° S	37.0834° E
48.	Tigoni T1	Kiambu	Tigoni	1.1651° S	36.7065° E
49.	Tigoni T2	Kiambu	Tigoni	1.1651° S	36.7065° E
50.	Tigoni T3	Kiambu	Tigoni	1.1651° S	36.7065° E
51.	Tigoni T4	Kiambu	Tigoni	1.1651° S	36.7065° E
52.	Tigoni T5	Kiambu	Tigoni	1.1651° S	36.7065° E
53.	Tigoni T6	Kiambu	Tigoni	1.1651° S	36.7065° E
54.	Tigoni T7	Kiambu	Tigoni	1.1651° S	36.7065° E
55.	Tigoni T8	Kiambu	Tigoni	1.1651° S	36.7065° E
56.	Tigoni T9	Kiambu	Tigoni	1.1651° S	36.7065° E
57.	Tigoni T10	Kiambu	Tigoni	1.1651° S	36.7065° E
58.	Tigoni T11	Kiambu	Tigoni	1.1651° S	36.7065° E
59.	Tigoni T12	Kiambu	Tigoni	1.1651° S	36.7065° E
60.	Tigoni T13	Kiambu	Tigoni	1.1651° S	36.7065° E
61.	Tigoni T14	Kiambu	Tigoni	1.1651° S	36.7065° E
62.	Tigoni T15	Kiambu	Tigoni	1.1651° S	36.7065° E
63.	Tigoni T16	Kiambu	Tigoni	1.1651° S	36.7065° E
64.	Tigoni T17	Kiambu	Tigoni	1.1651° S	36.7065° E
65.	Kahuho KK1	Kiambu	Kahuho	1.2082° S	36.6795° E
66.	Kahuho KK2	Kiambu	Kahuho	1.2082° S	36.6795° E
67.	Banana Hill JCBK	Kiambu	Banana Hill	1.1760° S	36.7550° E
68.	Tala KT1	Machakos	Tala	1.2670° S	37.3201° E
69.	Tala KT2	Machakos	Tala	1.2670° S	37.3201° E
70.	Tala KT3	Machakos	Tala	1.2670° S	37.3201° E
71.	Tala KT4	Machakos	Tala	1.2670° S	37.3201° E
72.	Kilimani KL1	Nairobi	Kilimani	1.2893° S	36.7869° E
73.	Kilimani KL2	Nairobi	Kilimani	1.2893° S	36.7869° E
74	Kilimani ANR	Nairobi	Kilimani	1.2893° S	36.7869° E
75.	Kilimani SHR	Nairobi	Kilimani	1.2893° S	36.7869° E
76.	Valley Arcade Van1	Nairobi	Kilimani	1.2907° S	36.7692° E
77.	Valley Arcade Van 2	Nairobi	Kilimani	1.2907° S	36.7692° E
78.	Maji Mazuri mm	Baringo	Maji Mazuri	0.0076° S	35.6861° E
					-

No	PCR amplicon ID	Sequencing	Sequence	GC content (%)
	-	success	length (base	
			pairs)	
1.	Londiani L1i	Not successful	N/A	N/A
2.	Londiani L2i	Successful	466	61.6
3.	Londiani L3i	Successful	602	62.1
4.	Londiani L4i	Successful	663	65.2
5.	Londiani L5i	Successful	656	61
6.	Londiani L6i	Successful	310	60
7.	Londiani L7i	Successful	511	60.3
8.	Londiani L8i	Successful	642	60.4
9.	Londiani L9i	Successful	624	59.6
10.	Londiani L10i	Successful	578	59.9
11.	Chebororwa C2i	Successful	679	61.1
12.	Chebororwa C5i	Successful	469	61.6
13.	Chebororwa e1ini	Successful	373	62.5
14.	Chebororwa e2ini	Successful	383	61.4
15.	Chebororwa e3ini	Successful	683	60.6
16.	Chebororwa e4ini	Successful	508	60.2
17.	Chebororwa e5ini	Successful	707	61
18.	Chebororwa e6ini	Successful	664	60.4
19.	Chebororwa e7ini	Successful	692	60.8
20.	Magwagwa mw3i	Successful	688	65.6
21.	Ndhiwa hb2i	Successful	676	60.8
22.	Ndhiwa hb3i	Not successful	N/A	N/A
23.	Mukurweini ny4i	Not successful	N/A	N/A
24.	Mukurweini ny5i	Successful	514	66.9
25	Gilgil gmi	Successful	274	59.5
26.	Nyathuna NKi	Successful	314	55.1
27.	Muguga DMi	Successful	595	61.7
28.	Thika TK1i	Not successful	N/A	N/A
29.	Thika TK2i	Not successful	N/A	N/A
30.	Thika TK3i	Not successful	N/A	N/A
31.	Thika TK4i	Not successful	N/A	N/A
32.	Thika TK5i	Not successful	N/A	N/A
33.	Thika TK6i	Not successful	N/A	N/A
34.	Thika TK7i	Not successful	N/A	N/A
35.	Thika TK8i	Successful	310	61
36.	Thika TK9i	Successful	272	62.5
37.	Tigoni T1i	Not successful	N/A	N/A
38.	Tigoni T2i	Successful	431	59.6
39.	Tigoni T4i	Successful	274	60.6
40.	Tigoni T6i	Not successful	N/A	N/A
41.	Tigoni T7i	Not successful	N/A	N/A
42.	Tigoni T8i	Not successful	N/A	N/A
43.	Tigoni T9i	Successful	545	60.4
44.	Tigoni T10i	Not successful	N/A	N/A
45.	Tigoni T11i	Successful	237	55.7
46.	Tigoni T12i	Not successful	N/A	N/A

Appendix 1B: Amplification and sequencing rates for the ITS2 barcode gene of *Physalis* accessions

47.	Tigoni T17i	Not successful	N/A	N/A
48.	Ongata Rongai nor1i	Successful	679	60.2
49.	Ongata Rongai nor3i	Successful	415	63.6
50.	Ongata Rongai nor4i	Successful	677	60.4
51.	Ongata Rongai nor5i	Successful	683	60.8

Appendix 1 C:	Amplification and seque	ncing rates for the	<i>rbcL</i> barcode	gene of Pl	hysalis
accessions					

No	PCR amplicon ID	Sequencing	Sequence	GC content
	1	success	length	%
			(base	
			pairs)	
1.	Londiani L1r	Successful	547	43.9
2.	Londiani L2r	Successful	615	43.3
3.	Londiani L3r	Successful	733	43.1
4.	Londiani L4r	Successful	520	43.1
5.	Londiani L5r	Successful	730	42.7
6.	Londiani L6r	Successful	634	43.1
7.	Londiani L7r	Successful	615	43.3
8.	Londiani L8r	Successful	621	42.8
9.	Londiani L9r	Successful	543	43.1
10.	Londiani L10r	Successful	604	43
11.	Chebororwa C2r	Successful	732	45.5
12.	Chebororwa C4r	Successful	745	43.5
13.	Chebororwa C5r	Successful	463	44.5
14.	Chebororwa e1inr	Successful	513	45.2
15.	Chebororwa e2inr	Not successful	N/A	N/A
16.	Chebororwa e3inr	Not successful	N/A	N/A
17.	Chebororwa e4inr	Successful	743	42.8
18	Chebororwa e6inr	Successful	815	43.2
19	Chebororwa e7inr	Successful	745	43.9
20.	Chebororwa e8inr	Successful	717	43.5
21.	Ndhiwa hb1r	Not successful	N/A	N/A
22.	Ndhiwa hb2r	Successful	745	43
23.	Ndhiwa hb3r	Successful	744	43
24.	Mukurweini ny1r	Successful	854	42.3
25.	Mukurweini ny3r	Not successful	N/A	N/A
26.	Mukurweini ny4r	Successful	724	44.8
27.	Mukurweini ny5r	Successful	712	44.7
28.	Gilgil gmr	Successful	637	42.9
29.	Maji Mazuri mmr	Successful	565	45.5
30.	Muguga DMr	Successful	475	44
31.	Thika TK1r	Not successful	N/A	N/A
32.	Thika TK2r	Successful	733	43.4
33.	Thika TK3r	Successful	792	43.2
34.	Thika TK4r	Successful	815	43.4
35.	Thika TK5r	Not successful	N/A	N/A
36.	Thika TK6r	Successful	789	43.5

37.	Thika TK7r	Successful	733	42.8
38.	Thika TK8r	Successful	626	43.1
39.	Thika TK9r	Successful	815	43.1
40.	Tigoni T2r	Successful	582	43.1
41.	Tigoni T4r	Successful	841	43.6
42.	Tigoni T6r	Successful	464	44.4
43.	Tigoni T7r	Successful	807	43.1
44.	Tigoni T8r	Successful	540	43.7
45.	Tigoni T9r	Successful	802	42.8
46.	Tigoni T10r	Successful	540	45
47.	Tigoni T11r	Successful	745	43.5
48.	Tigoni T12r	Successful	545	43.1
49.	Tigoni T13r	Successful	773	43.5
50.	Tigoni T14r	Successful	775	42.7
51.	Tigoni T16r	Successful	742	42.3
52.	Tigoni T17r	Successful	803	43.3
53.	Kahuho KK1r	Successful	553	42.9
54.	Banana Hill JCBK	Successful	729	44.2
55.	Tala KT1r	Successful	668	43.9
56.	Ongata Rongai nor3r	Successful	818	43.9
57.	Ongata Rongai nor4r	Successful	776	42.1
58.	Ongata Rongai nor5r	Successful	745	43.2
59.	Kilimani KL1r	Successful	744	43
60.	Kilimani KL2r	Not successful	N/A	N/A
61.	Kilimani SHRr	Successful	703	43.1
62.	Kilimani ANRr	Successful	722	42.5
63.	Valley Arcade Van 1	Successful	847	43.3
64.	Valley Arcade Van 2	Not successful	N/A	N/A

Appendix 2: Multiple sequences alignments for *Physalis* accessions.

Appendix 2 A: Multiple sequence alignment of indigenous *Physalis* accessions from Sorget Forest based on their ITS2 and *rbcL* gene sequences as well as their reference sequences based on BLASTn analysis (<u>https://espript.ibcp.fr/ESPript/temp/1818399141/0-0-1680464456-esp.pdf</u>)



	160	170	180	190		200	21	LĢ
KT178121.1*	AGGGGCCGCG	GT	AG <mark>CTGC</mark> GAA	TCTTCTACTG	GT <mark>AC</mark> ATG	GACAAC	I <mark>G</mark> TAT <mark>G</mark>	GACCGATGG
NC_026570.1* KT178120.1*	AGGGGCCGCG	GT	AGCIGCGAA:	ICTTCTACTG ICTTCTACTG	GTACATG GTACATG	GACAAC' GACAAC'	FGTATG FGTATG	GACCGATGG GACCGATGG
NC_048515.1*	AGGGGCCGCG	GT	AG <mark>C</mark> TG <mark>C</mark> CGAA	TCT <mark>T</mark> CTACTG	GT <mark>ac</mark> at <mark>g</mark>	GA <mark>C</mark> AAC'	Γ <mark>G</mark> TAT <mark>G</mark>	. <mark>GAC</mark> CGATGG
NC_048514.1*	AGGGGCCGCG	GT	AGCTGCCGAA	ICTTCTACTG	GTACATG	GACAAC	FGTATG	GACCGATGG
NC_039458.1*	AGGGGCCGCG		AGCTGCCGAA	ICT TCTACTG	GTACATG	GACAAC	GTATG.	GACCGATGG
NC_039457.1*	AGGGGCCGCG	GT	AGCTGCCGAA	ICT TCTACTG	GTACATG	GACAAC	I <mark>G</mark> TATG	GACCGATGG
00507152.1	AGGGGGCCGCG		AGCIGCCGAA	TCTTCTACTG	G	GACAAC	IGTATG	GACCGATGG
0Q507154.1	AGGGGCCGCG	GT	AG <mark>C</mark> TG <mark>C</mark> CGAA	TCT <mark>T</mark> CTACTG	GTA <mark>C</mark> AT <mark>G</mark>	GA <mark>C</mark> AAC	I <mark>G</mark> TATG	, <mark>GAC</mark> CGAT <mark>G</mark> G
00507155.1	AGGGGCCGCG	GT	AGCTGCCGAA	ICT CTACTG	GTACATG	GACAAC	FGTATG	GACCGATGG
00507157.1	AGGGGCCGCG	GT	AGCTGCCGAA	TCTTCTACTG	GTACATG	GACAAC	GTATG	GACCGATGG
00507158.1	AGGGGCCGCG	GT	AGCTGCCGAA	ICT TCTACTG	GTACATG	GACAAC	IGTATG	GACCGATGG
00507160.1	AGGGGGCCGCG	GI	AGCIGCCGAA	ICITCIACIG	G	GACAAC'	IGTATG	GACCGATGG
0Q507161.1	AGGGGCCGCG	GT	AG <mark>C</mark> TG <mark>C</mark> CGAA	ICT <mark>T</mark> CTACTG	3	GA <mark>C</mark> AAC'	Γ <mark>G</mark> TATG	. <mark>GAC</mark> CGAT <mark>G</mark> G
AY665903.1*	CGGGGGAGGCG.T	TCGCTC	GCCT.CCCCC	CCGTCGGCCG	GCGGTCG.CGCGTG	CGCGGT	CCCGGGC	GACTAACGA
AY665910.1*	CGGGGTGGCG.C	TCGC	GCCT.CCCCC	TCGTCGGCCG	GCGGTCG.CG <mark>C</mark> GTG	CGCGGT	GCCGGGC	GACTAACGA
AY665914.1*	CGGGGAGGCG.CC	GCTTTGGCTC	GCCTCCCCC		GCGGTCG.CG <mark>C</mark> GT <mark>G</mark>	CGCGGT	CCCGGTC	GACTAACGA
AY665879.1* AY665905.1*	CGGGGGAGGCG.C	TCGCTC		TCGTCGGCCG	CCGCTCG.CCCCGCG	CGCGGT	GCCGGTC	GACTAACGA
AY665886.1*	CGGGGAGGCG.C	GCGTTCGCTC	GC <mark>CT.C</mark> CCCC	ICG <mark>T</mark> CGTCCG	ACGGCCG.CG <mark>C</mark> GT <mark>G</mark>	CG <mark>C</mark> GGT	C <mark>G</mark> CCGTTC	C <mark>GAC</mark> TAACTC
MH763728.1*	CGGGGGAGGCG.CC	GCGTTCGCTC	GCCT.CCCCC	ICGTCGGCCG	GCTGTCG.CG <mark>C</mark> GT <mark>G</mark>	CGCGGT	GCCGATC	GACTAACTC
OQ372021.1		.CGCTC	GCCT.CCCGC	ICGTCGGCCA	GCAGCCG.CACGTG	CGCGGT	GCCTAGC	GACTAACGA
00372022.1	CGGGAAGGCG.T	TCGCTC	GCCT.CCCGC	ICG <mark>T</mark> CGGCCA	GCAGCCG.CA <mark>C</mark> GT <mark>G</mark>	CGCGGT	C G C C T A G C	GACTAACGA
00372023.1	CGGGGAAGGCG.T	TCGCCAC	GCCT.CCCGC	ICGTCGGCCA	GCAGCCG.CACGTG	CGCGGGT	GCCTAGC	GACTAATGA
00372025.1	CGGGAAGGCG.T	TCGCTC	GC <mark>CT.C</mark> CCGC	ICG <mark>T</mark> CGGCCA	GCAGCCG.C <mark>AC</mark> GT <mark>G</mark>	CG <mark>C</mark> GGT(C <mark>G</mark> C C T A G C	C <mark>GAC</mark> TAACGA
00372026.1	CAAAGGGTCG	GCC TCGGCCAC	CACCGCCACA/	AAGTTGAGAT SAGTTGAGAT	ICAACCACCACTTG ICAACCACCACTTG	CCGTGA	CGTCCGTC CGTCCGTC	GAC. ATGG
00372028.1	TGGGAAGGCGTT	TCGCTC	GC <mark>CT.C</mark> CCGC	TCGTCGGCCA	GCAGCCG.C <mark>AC</mark> GT <mark>G</mark>	CGCGGT	GCCTAGC	GAC TAATGA
00372029.1	G <mark>GGCC</mark> AC <mark>GGG</mark> .T	TCGGCCAC	GGCACCACAA	GAG <mark>T</mark> TGAGAT	ICAACCACC <mark>AC</mark> T <mark>TG</mark>	CCGTGA	GTCCGTC	GACATGG
	220	230	240	2	50	2	6 Q	270
: KT178121.1* NC_026570.1*	220 ACTTACCA	230 GTCTTGATCG GTCTTGATCG	240 TTACAAAGGG	2 	50 ATGC	Z TAC <mark>CGC</mark> TAC <mark>CGC</mark>	60 Atcga.go	270 GIGTIGTIG GIGTIGTIG
:: KT178121.1* NC_026570.1* KT178120.1*	ACTTACCA ACTTACCA ACTTACCA	230 GTCTTGATCG GTCTTGATCG GTCTTGATCG	240 TIACAAAGGG TIACAAAGGG TIACAAAGGG	2 	50 ATGC ATGC	TACCGC; TACCGC; TACCGC;	60 ATCGA.GC ATCGA.GC ATCGA.GC	270 GTGTTGTTG GTGTTGTTG GTGTTGTTG
KT178121.1* NC_026570.1* KT178120.1* NC_048514.1*	ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA	230 GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG	240 TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG	2 CG CG	50 ATGC ATGC ATGC ATGC	TACCGC; TACCGC; TACCGT; TACCGC; TACCGC;	60 ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC	279 GTGTTGTTG GTGTTGTTG GTGTTGTTG GTGTTGTTG
KT178121.1* NC_026570.1* KT178120.1* NC_048514.1* NC_048514.1* NC_070364.1*	220 ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA	230 GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG	240 TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG	2 	50 ATGC ATGC ATGC ATGC ATGC	Z TACCGC TACCGC TACCGC TACCGC TACCGC TACCGC	60 ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC	279 GTGTTGTTG GTGTTGTTG GTGTTGTTG GTGTTGTTG
KT178121.1* NC_026570.1* KT178120.1* NC_048515.1* NC_048514.1* NC_070364.1* NC_039458.1* NC_039458.1*	ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA	230 GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG	240 TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG	2 	50 ATCC ATCC ATCC ATCC ATCC ATCC ATCC	Z TACCGC TACCGC TACCGC TACCGC TACCGC TACCGC TACCGC	60 ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC	270 GTGTTGTTG GTGTTGTTG GTGTTGTTG GTGTTGTTG
KT178121.1* NC_026570.1* NC_048515.1* NC_048515.1* NC_048515.1* NC_070364.1* NC_039458.1* NC_039457.1*	ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA	230 GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG	240 TTACAAAGGC TTACAAAGGC TTACAAAGGC TTACAAAGGC TTACAAAGGC TTACAAAGGC TTACAAAGGC TTACAAAGGC	2 	5 Q AT G	Z TACCCC TACCCCT TACCCCC TACCCCC TACCCCC TACCCCC TACCCCC TACCCCC TACCCCC	60 ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC	
$\begin{array}{c} {\rm KT178121.1*}\\ {\rm NC_026570.1*}\\ {\rm KT178120.1*}\\ {\rm NC_048515.1}\\ {\rm NC_048515.14.1*}\\ {\rm NC_070364.1*}\\ {\rm NC_039457.1*}\\ {\rm QO507152.1}\\ {\rm QO507153.1}\\ {\rm QO507153.1}\\ {\rm QO507154.1} \end{array}$	220 ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA ACTTACCA	230 GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG GTCTTGATCG	240 TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG	2 	59 ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC	Z TACCGC TACCGC TACCGC TACCGC TACCGC TACCGC TACCGC TACCGC TACCGC	60 ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC	
$\begin{array}{c} {\rm KT178121.1*} \\ {\rm NC_026570.1*} \\ {\rm NT708120.1*} \\ {\rm NC_048515.1*} \\ {\rm NC_048514.1*} \\ {\rm NC_070364.1*} \\ {\rm NC_039457.1*} \\ {\rm Oq507152.1} \\ {\rm Oq507155.1} \\ {\rm Oq507155.1} \end{array}$	220 ACTTACCA	230 GTCTTGATG GTCTTGATG GTCTTGATG GTCTTGATG GTCTTGATG GTCTTGATG GTCTTGATG GTCTTGATG GTCTTGATG GTCTTGATG	240 TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG TTACAAAGGG	2 . C G . C	59 ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC	TACCGC TACCGC TACCGC TACCGC TACCGC TACCGC TACCGC TACCGC TACCGC TACCGC TACCGC	SO ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC	
KT178121.1* NC 026570.1* KT178120.1* NC 048515.1* NC 039458.1* NC 039458.1* NC 039458.1* Og507152.1 Og507155.1 Og507155.1 Og507155.1	220 ITAC	230 GTCTTGATG GTCTTGATG TCTTGATG TCTTGATG TCTTGATG GTCTTGATG GTCTTGATG GTCTTGATG GTCTTGATG GTCTTGATG GTCTTGATG GTCTTGATG	240 TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG TTACAAAGG	2 	50 ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC	TACCCCC TACCCCCC TACCCCCC TACCCCCCC TACCCCCCC TACCCCCCC TACCCCCCC TACCCCCCCC	SO ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC ATCGA.GC	
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$\begin{array}{c} k \pi 1 \ 7 8 1 2 1 \ . 1 \\ k \pi 1 \ 7 8 1 2 0 \ . 1 \\ k \pi 1 \ 7 8 1 2 0 \ . 1 \\ k \pi 1 \ 7 8 1 2 0 \ . 1 \\ k \pi 1 \ 7 8 1 2 0 \ . 1 \\ k \pi 1 \ 7 8 1 2 0 \ . 1 \\ k \pi 1 \ 7 8 1 2 0 \ . 1 \\ k \pi 2 \ 0 \ 8 3 1 \\ k \pi 2 \ . 1 \\ k \pi 2 \ 0 \ 8 3 1 \\ k \pi 2 \ . 1$	220 ITACCA TTACCA A CTACCA A CTACCA A CTACCA A CTACCA A CTACCA A CTACCA A CCCA CA CCCA CA CCCA CA	2 2 0 G T C T T G A T G G C C G G A A A G G C C C G G A A G G C C G G A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C G G A A A A G C C C C G C C C G C C C C C C C C G G A A A A G C C C C G C A A A A A G C C C C G C A A A A A G C C C C G C C C C C C C C C C C C C C C	240 T TACAAAGG G. T TACAAAGG T T TACAAAGG C T T TACAAAGG C T T TACAAAGG C T T T T T T T T T T T T T T T T T T T	2 	59 ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC ATGC AT		60 TICGA . GC TICGA . GC TI	
$\begin{array}{c} k \pi 1 78121 \\ NC_{\rm O} 26570. . . . \\ k \pi 1 78120. . . . \\ NC_{\rm O} 048515. . . . \\ NC_{\rm O} 049514. . . \\ NC_{\rm O} 039458. . . \\ NC_{\rm O} 039458. . . \\ NC_{\rm O} 039457. . . \\ Og507152. . . \\ Og507155. . . \\ Og507155. . . \\ Og507155. . . \\ Og507156. . . \\ Og507156. . . \\ Og507159. . . \\ Og507159. . . \\ Nc65890. . . \\ Nc66590. . . \\ Nc665910. . . \\ Nc6658914. . . \\ Nc6658914. . . \\ Nc6658914. . . \\ Nc665886. . . \\ Nc6658914. . . \\ Nc6658914. . . \\ Nc665895. . . \\ Nc6658914. . . \\ Nc665895. . . \\ Nc6658914. . . \\ Nc665895. . . \\ Nc665892. . . \\ Nc665892. . . \\ Nc6522. . . \\ Og372022. . \\ Og372022. . \\ Og372025. . \\ Og372027. . \\$	220 A TTACA A TTACC A CCC CC CCC CCC CCC CCC CCC CCC CCC CCC CCC	230 C T T T CAT C T T T CAT C C C C C CAA C C C C C C C CAA C C C C C C C CAA C C C C C C C C CAA C C C C C C C C CAA C C C C C C C C C C C C C C C C C C C	249 T T A C A A A G G C T T A C A A A G G C T T A C A A A G G C T T A C A A A G G C T T A C A A A G G C T A C A A A G G C G C C A G G A A G C C A G G A A G C C A A G G A A G C C C A G G A A A G C C C A G G A A G A A G C C C A G G A A G A A G C C C A G G A A G A A G C C C A G G A A G A A G C C C A G G A A G A A G C C C A G G A A G A A G C C C A G G A A G A A G C C C A G G A A G A A A A A A A A A A	2 	5.9 NTG		TCGA.G TCGGT.G TCGGT.G TCGGT.G TCGT.G TCGT.G TCGGT.G	
<pre>KT178121.1* NC 026570.1* KT178120.1* NC 048514.1* NC 048514.1* NC 039458.1* NC 039458.1* NC 039458.1* Og507153.1 Og507153.1 Og507155.1 Og507155.1 Og507155.1 Og507155.1 Og507155.1 Og507155.1 Og507157.1 Og507158.1 Og507158.1 A7665903.1* A7665903.1* A7665905.1* A7665905.1* A7665905.1* A7665905.1* A7665905.1* A7665905.1* A7665905.1* A7665905.1* A7665905.1* A7665905.1* Og372022.1 Og372022.1 Og372022.1 Og372022.1 Og372022.1</pre>	220 F TTACCA G TTACCA G TTACCA G TTACCA G TTACCA G TTACCA G CCCA G CCCA G CCCC G	230 T C T T G AT G T C T T G AT G C C T G AT G T C T G AT G C C C G G AA G C C C G C AA A G C C C A A C C AA G C C C A A C C AA A G C C C A A C C AA A G		2	50 TTG		50 TICGA.C TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGA.G TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C TICGT.C	

	280	290	300	310	320	330	340	350
KT178121.1*	GAGAAAAA <mark>G</mark> AT	CAATATATTG	CTTATGTAGC	TTACCCT	TTAGACCTTTTT	GA <mark>A</mark> GAA <mark>G</mark> GTT	CCGTTACCA	CATGTTAC
NC_026570.1*	GAGAAAAAGAT	CAATATATTG	CTTATGTAGC	TTACCCT	TTAGACCTTTTT	GAAGAAGGTT CAAGAAGGTT	CCGTTACCA	ACATGTTTAC
NC 048515.1*	GAGAAAAAGAT	CAATATATTG	CTTATGTAGC	TTACCCT	TTAGACCTTTTT	GAAGAAGGTT	CCGTTACCA	CATGITTAC
NC_048514.1*	GАGААААА <mark>G</mark> АТ	CAATATATTG	CTTATGTAGC	TTACCCT	T T <mark>A</mark> GAC <mark>C T T T</mark> T T	GA <mark>A</mark> GAA <mark>G</mark> GTT	C <mark>C</mark> GTTAC <mark>C</mark> A <i>I</i>	A <mark>C</mark> ATGT <mark>T</mark> TA <mark>C</mark>
NC_070364.1*	GAGAAAAAGAT	CAATATATTG	CTTATGTAGC CTTATGTAGC	TTACCCT	TTAGACCTTTTT TTAGACCCTTTTT	GAAGAAGGTT CAAGAAGGTT	CCGTTACCA	ACATGTTTAC
NC_039457.1*	GAGAAAAAGAT	CAATATATTG	CTTATGTAGC	TTACCCT	TTAGACCTTTTT	GAAGAAGGTT	CCGTTACCA	CATGTTTAC
00507152.1	GAGAAAAA <mark>G</mark> AT	CAATATATTG	CTTATGTAGC	TTACCCT	TT <mark>A</mark> GAC <mark>CTTT</mark> TT	GA <mark>A</mark> GAA <mark>G</mark> GTT	CCGTTACCA	A <mark>C</mark> ATGT <mark>T</mark> TA <mark>C</mark>
00507153.1	GAGAAAAAGAT	CAATATATTG	CTTATGTAGC CTTATGTAGC	TTACCCT	TTAGACCTTTTT TTAGACCCTTTTT	GAAGAAGGIT GAAGAAGGIT	COGTIACCAR	ACATGTTTAC
00507155.1	GAGAAAAAGAT	CAATATATTG	CTTATGTAGC	TTACCCT	TTAGACCTTTTT	GAAGAAGGTT	CCGTTACCA	CATGTTTAC
00507156.1	GAGAAAAAGAT	CAATATATTG	CTTATGTAGC	TTACCCT	TTAGACCTTTTT	GAAGAAGGTT	CCGTTACCA	ACATGTTTAC
00507157.1	GAGAAAAAGAT	CAATATATIG	CTTATGTAGC	TTACCCT	TAGACCTITI	GAAGAAGGII	CCGTTACCAR	CATGINIAC
0Q507159.1	GAGAAAAA <mark>G</mark> AT	CAATATATTG	CTTATGTAGC	TTACCCT	TTAGACCTTTTT	GA<mark>A</mark>GAA<mark>G</mark>GTT	CCGTTACCA	ACATGT <mark>T</mark> TAC
00507160.1	GAGAAAAAGAT	CAATATATTG	CTTATGTAGC	TTACCCT	TTAGACCTTTTT	GAAGAAGGIT CAACAACCIT	CCGTTACCAR	ACATGTTTAC
AY665903.1*	CGCG.GGGGAG	CTGCGCTTCG	CTTG	. AAACAC	GAACGACTCTCG	GCAACGGATA	TCTCGO	CTCTCGC
AY665868.1*	CGCG.GGG <mark>G</mark> AG	CTGTGCTTCG	CTTG	. AAACAC	GA <mark>A</mark> CGA <mark>CTCT</mark> CG	GC <mark>A</mark> ACG <mark>G</mark> ATA	T <mark>C</mark> T <mark>C</mark> GO	G <mark>C</mark> IC <mark>I</mark> CG <mark>C</mark>
AY665910.1*	CGCG.GGGGAC	CTGCGCTTCG.	ATCG	. AAACAC	GAACGACTCTCG	GCAACGGATA GCAACGGATA	TCTCGC	CTCTCGC
AY665879.1*	CGCG.GGGGAG	CIGCGCCICG	CTIG	. AAACAC	GAACGACTCTCG	GCAACGGATA	TCTCGC	CICICGC
AY665905.1*	CGCG.GGG <mark>G</mark> AC	CTGTGCTTCG	СТТG	. AAACAC	GAACGA <mark>CTCT</mark> CG	GC <mark>A</mark> ACG <mark>G</mark> ATA	T <mark>C</mark> T <mark>C</mark> GC	GCTCTCGC
AY665886.1* MH763728 1*	CGCG.GGGGAC	CIGIGCIICG	CTIG	AAACAC	GAACGACTCICG	GCAACGGATA CCAACGCATA	TCTCGC	SCICCGC
MH763740.1*	CGCG.GGG <mark>G</mark> AC	CTGCGCTTCA	CTTG	AAACAC	GAATGACTCTCG	GCAATGGATA	TCTCGC	CIC. ICGC
00372021.1	CGCG.GGG <mark>G</mark> A.	CTGTG.TTCG	CTTG	. AAACAC	AAATGA.TCTCG	GC <mark>A</mark> ACG <mark>G</mark> ATA	TCTCGC	CTCTCGC
00372022.1	GGCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GACGCGATG	CIIG	. ACGCCC	AAAIGACICICG AG	GCAACGGATA GCAGACGTGC	CCTCGC	GCTAATGGC
00372024.1	CGCG.GGG <mark>G</mark> AG	CTGTGCTTCG	CTTG	. AAACAC	AAATGACTCTCG	GCAACGGATA	TCTCGC	CTCTCGC
00372025.1	CCCC.CCC <mark>G</mark> AC	CTGTGCTTCG	CTIG	.AAACAC	AAATGACTCTCG	GCAACCGATA	TCTCGC	CICICGC
00372027.1	GGCGAGGGGGGGG	CGATGCGATG	CGTG	ATGCCC	AGIGCCCAG	GCAGACGIGC	CCLLLTCGA	CTAATGGC
00372028.1	CGCG.GGG <mark>G</mark> AG	CTGTGCTTCG	CTT G	. AAACAC	AA <mark>A</mark> TGA <mark>CTCT</mark> CG	GC <mark>A</mark> ACG <mark>G</mark> ATA	T <mark>C</mark> T <mark>C</mark> GO	G <mark>C</mark> ICICG <mark>C</mark>
00372029.1	G G C G A G G G <mark>G</mark> G	GATGCGATG	<u>CGT</u> G	. ATGCCC	A	GCAGACGTGC	С <mark>С</mark> Т <mark>С</mark> С <i>І</i>	CTAA T GG <mark>C</mark>
ደጣ178121 1*	360 T TC TAC	370 GT ANTGT ATT	380 TGGGTTTANA	390 GCC T C C	400 	410 TGGDD <mark>CD</mark> TCT	420 606 M C C C C	430
NC_026570.1*	TTCCATTGIAG	GTAATGTATT	TGGGTTTAAA	GCCCTGC	GCGCTCTACGTC	TGGAAGATCT	GCGAATCCCT	GTTGCTTAT
KT178120.1*	TTCCATTGTAG	GTAATGTATT	TGGGTTTAAA	GCCCTGC	GCGCTCTACGTC	TGGAA <mark>GA</mark> TCT	GCGAATCCCT	GTTGCTTAT
NC_048514.1*	TTCCATTGTAG	GTAATGTATT	TGGGTTTAAA	GCCCTGC	GCGCTCTACGTC	TGGAAGATCT	GCGAATCCCT	GTTGCTTAT
NC_070364.1*	T <mark>TC</mark> CATTGTAG	G T A <mark>A T G T A</mark> T T	TGGG <mark>T</mark> TTA <mark>A</mark> A	GCCCTGC	GCGCTCTACGTC	TGGAA <mark>GA</mark> TC <mark>T</mark>	GCGA <mark>A</mark> TCCC1	T <mark>GT</mark> TGCTT <mark>A</mark> T
NC_039458.1*	TTCCATTGTAG	GTAATGTATT GTAATGTATT	TGGGTTTAAA	GCCCTGC	CGCTCTACGTC	TGGAAGATCT TGGAAGATCT	GCGAATCCCT	GTTGCTTAT
00507152.1	TTCCATTGTAG	GTAATGTATT	TGGGTTTAAA	GCCCTGC	GCGCTCTACGTC	TGGAAGATCT	GCGAATCCCT	GTTGCTTAT
00507153.1	TTCCATTGTAG	GTAATGTATT	TGGGTTTAAA	GCCCTGC	GCGCTCTACGTC	TGGAA <mark>GA</mark> TCT	GCGAATCCCT	GTTGCTTAT
00507155.1	TTCCATTGTAG	GTAATGTATT GTAATGTATT	TGGGTTTAAA	GCCCTGC	GCGCTCTACGTC	TGGAAGATCT	GCGAATCCCT	GTTGCTTAT
00507156.1	T <mark>TC</mark> CATTGTAG	G T A <mark>A T G T A</mark> T T	TGGG <mark>T</mark> TTA <mark>A</mark> A	GCCCTGC	GCGCTCTACGTC	TGGAA <mark>GA</mark> TCT	GCGA <mark>A</mark> TCCC1	TGTTGCTT <mark>A</mark> T
00507157.1	TTCCATTGTAG	GTAATGTATT GTAATGTATT	TGGGTTTAAA	GCCCTGC	CGCTCTACGTC	TGGAAGATCT TGGAAGATCT	GCGAATCCCT	GTTGCTTAT
00507159.1	TTCCATTGTAG	GTAATGTATT	TGGGTTTAAA	GCCCTGC	GCGCTCTACGTC	TGGAA <mark>GA</mark> TCT	GCGAATCCCT	GTTGCTTAT
00507160.1	TTCCATTGTAG	GTAATGTATT	TGGGTTTAAA	GCCCTGC	GCGCTCTACGTC	TGGAA <mark>GA</mark> TCT	GCGAATCCCT	GTTGCTTAT
AY665903.1*	ATCGATGAAGA	GTAATGTATT ACGCAGC	RAAATGCGAT	ACTTGGT	GCGCTCIACGIC	GAAGATUT	GCAGAATCCC	GTGAACCA.
AY665868.1*	A <mark>TC</mark> CATCAACA	ACGTACC	GAAA <mark>T</mark> CCG <mark>A</mark> T	ACTTCCT	g T	<mark>ga</mark> att	GCACAATCC	GTGAACC <mark>A</mark> .
AY665910.1*	ATCGATGAAGA	ACGTAGC	GAAATGCGAT	ACTTGGT	GT	GAATT	GCAGAATCCC	GTGAACCA.
AY665879.1*	ATCGATGAAGA	ACGYAGC	GAAATGCGAT	ACTTGGT	GT	GAATT	GCAGAATCC	GTGAACCA.
AY665905.1*	A <mark>TC</mark> G AT GAAGA	ACGCAGC	GAAA <mark>T</mark> GCG <mark>A</mark> T	ACTTGGT	G T	<mark>ga</mark> att	GCAGAATCC	GTGAACCA.
AY665886.1* MH763729 1*	ATCGATGAAGA	ACGTAGC	GAAATGCGAT	ACTTGGT	ст	GAATT	GCAGAATCCC	GTGAACCA.
MH763740.1*	ATCGATGAAGA	ACGYAGC	GAAATGCGAT	ACTTGGT	GT	GAATT	GCAGAATCC	GTGAACCA.
00372021.1	ATCGATGAAGA	ACGTAGC	GAAATGCG <mark>A</mark> T	ACTTGGT	GT	<mark>да</mark> атт	GCAGAATCCC	GTGAACCA.
00372022.1	TTCGGCGCCAA	CTTGCGTTCA	GAAATGCGAT	ACTTGGT	GI	GAATTC	GCAGAATCCC TGCAATTCAC	GIGAACCA.
00372024.1	ATCGATGAAGA	ACGTAGO	GAAATGCGAT	ACTTGGT	GT	GAATT	GCAGAATCC	GTGAACCA.
00372025.1	ATCGATGAAGA	ACGTAGC	GAAATGCGAT	ACTTGGT	GT	GAATT	GCAGAAT	
00372027.1	TTCGGGGCACAA	CTTGCGTTCA.	AAGACICCAA	GGITIAC	G	GATTC	TGCAATTCAC	CACCAAGTA.
00372028.1	A <mark>TC</mark> GATGAAGA	ACGTAGC	GAAATGCG <mark>A</mark> T	ACTTGGT	GT	<mark>GA</mark> ATT	GCAGAATCC	GTGAACCA.
00372029.1	T <mark>TC</mark> GGGCACAA	CTTGCGTTCA.	A A G A <u>C</u> T C G <mark>A</mark> T	GGITCAC	G G	GATTC	TGCANTTCAC	CACCAAGT <mark>A</mark> .

KT178121.1*	440	450 4	460 470	480	490
	GTTAAAACTTTC	CAAGGTCCGCCTCZ	ATGGGATCCAAGTTGAA.	AGAGATAAATTGAA	
NC_026570.1*	GTTAAAACTTTC	CAAGGTCCGCCTCZ	ATGGGATCCAAGTTGAA	AGAGATAAATTGAA	CAA
NC 048515.1*	ATTAAAACTTTC	CAAGGTCCGCCTCZ	ATGGGATCCAAGTTGAA	AGAGATAAATTGAA	CAA
NC_048514.1*	ATTAAAACTTTC	CAAGGTCCGCCTCZ	ATGGGATCCAAGTTGAA.	AGAGATAAATTGAA	<mark>CA</mark> A
NC_070364.1*	ATTAAAACTTTC	CAAGGTCCGCCTCZ	A TGGGATCCAAGTTGAA.	AGAGATAAATTGAA	CAA
NC_039457.1*	ATTAAAACTTTC	CAAGGTCCGCCTCZ	ATGGGATCCAAGTTGAA	AGAGATAAATTGAA	CAA
00507152.1	ATTAAAACTTTC	CAAGGTCCGCCTCZ	ATGGGATCCAAGTTGAA.	AGAGATAAATTGAA	CAA
00507154.1	ATTAAAACTTTC	CAAGGICCGCCICA	ATGGGATCCAAGTTGAA	AGAGATAAATTGAA	CAA CAA
OQ507155.1	ATTAAAACTTTC	CAAGGTCCGCCTCZ	ATGGGATCCAAGTTGAA.	AGAGATAAATTGAA	CAA
00507156.1	ATTAAAACTITC	CAAGGTCCGCCTCZ	A TGGGA TCCAAGT TGAA. A TGGGA TCCA AGT TGAA	AG AGATAAATTGAA	CAA
OQ507158.1	ATTAAAACTTTC	CAAGGTCCGCCTC	ATGGGATCCAAGTTGAA	AGAGATAAATTGAA	
00507159.1	ATTAAAACTTTC	CAAGGTCCGCCTCZ	ATGGGATCCAAGTTGAA.	AGAGATAAATTGAA	CAA
OQ507161.1	ATTAAAACTITC	CAAGGTCCGCCTCA	AIGGGATCCAAGTIGAA	AGAGATAAATTGAA	CAA
AY665903.1*	. TCGAGTCTTTGAAC	CAAGTTGCGCCCG7	AAGCCAT.TAGGCCGAG	GGCACGTCTG.CCTGGG	
AY665868.1* AY665910.1*	. TCGAGTCTTTGAAC	GCAAGTTGCGCCCG# GCAAGTTGCGCCCG#	AAGCCAT.TAGGCCGAG	GCACGICIG.CCIGGG	CGTCAC
AY665914.1*	. TCGAGTCTTTGAAC	CAAGTTGCGCCCGZ	AAGCCAT.TAGGCCGAG	GGCACGTCTG.CCTGGG	CGT <mark>CA</mark> C
AY665879.1*	. TCGAGTCTTTGAAC	CAAGTTGCGCCCG7	AAGCCAT. TAGGCCGAG	GCACGTCTG.CCTGGG	CGTCAC
AY665886.1*	TCGAGTCTTTGAAC	CAAGTTGCGCCCGZ	AAGCCAT. TAGGCCGAG	GGCACGTCTG.CCTGGG	CGTCAC
MH763728.1*	.TCGAGTCTTTGAAC	CANGTTGCGCCCGZ	AAGCCAT. TAGGCCGAG	GCACGTCTG.CCTGGG	CGT <mark>CA</mark> C
MH/63/40.1* 00372021.1	. TCGAGTCTTTGAAT	CAAGTTGTGCCCGZ	AAGCCAT.TAGGTCGAG	GCACGICIG.CCIGGG	CATCAC
0Q372022.1	. TCGAGTCTTTGAAC	CAAGTTGTGCCCG7	AAGCCAT. TAGGTCGAG	GGCACGTCTG.CCTGGG	CAT <mark>CA</mark> C
00372023.1	. TCGCATTTCGCTAC	GTTCTTCATCG	ATGCGAGAGCCGAG	ATATCCGTTG.CCGAGAGTC	GTTCGTGTTTCAA
00372025.1					
00372026.1	. TCGCATTTCGCTAC	TTCTTCCTCC7	AAGCCAGAACCGAA	ATATCCGTTG.CCCAGAGGC	ATTTGTTTTTCAA
00372028.1	. TCGAGTCTTTGAAC	CAAGTTGTGCCCGZ	AAGCCAT. TAGGTCGAG	GGCACGTCTGCCCTGGG.	CATCAC
OQ372029.1	. TCGCATTTCGCTAC	GTTCTTCATCG	ATGCGAGAGCCGAG	ATATCCGTTG.CCGAGAGTC	A T T T G T G T T T C A A
V7170101 1*				E10 E20	
NC_026570.1*	GIA.166106100		r		530
KT178120.1*	GIA. TGG TCGTCC	c		IGITG.GGATGIACIAITAA IGITG.GGATGIACIAITAA	530 ACCTAAATTGGGG ACCTAAATTGGGG
NO 040515 1*	GTA.TGGTCGTCC			TGTTG.GGATGTACTATTAA IGTTG.GGATGTACIATTAA IGTTG.GGATGTACIATTAA	530 ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG
NC_048515.1* NC 048514.1*	GIA.TGG.TCGTCC GIA.TGG.TCGTCC GIA.TGG.TCGTCC GIA.TGG.TCGTCC			TGTTG.GGATGTACTATTAA IGTTG.GGATGTACTATTAA IGTTG.GGATGTACTATTAA IGTTG.GGATGTACTATTAA IGTTG.GGATGTACTATTAA	530 ACCTAAATTGGGG ACCTAAATTGGGG ACCTAAATTGGGG ACCTAAATTGGGG
NC_048515.1* NC_048514.1* NC_070364.1*	GIA.TGGTCGTCC' GIA.TGGTCGTCC' GIA.TGGTCGTCC' GIA.TGGTCGTCC' GIA.TGGTCGTCC'			TGTTG, GGATGTACTATTAA IGTTG, GGATGTACTATTAA IGTTG, GGATGTACTATTAA IGTTG, GGATGTACTATTAA IGTTG, GGATGTACTATTAA IGTTG, GGATGTACTATTAA IGTTG, GGATGTACTATTAA	530 ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG
NC_048515.1* NC_048514.1* NC_070364.1* NC_039458.1* NC_039457.1*	GTA.TGGTCGTCC GTA.TGGTCGTCC GTA.TGGTCGTCC GTA.TGGTCGTCC GTA.TGGTCGTCC GTA.TGGTCGTCC GTA.TGGTCGTCC GTA.TGGTCGTCC			IGTTG.GGATGTACTATTAA IGTTG.GGATGTACTATTAA IGTTG.GGATGTACTATTAA IGTTG.GGATGTACTATTAA IGTTG.GGATGTACTATTAA IGTTG.GGATGTACTATTAA IGTTG.GGATGTACTATTAA IGTTG.GGATGTACTATTAA	530 ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG
NC_048515.1* NC_048514.1* NC_070364.1* NC_039458.1* NC_039457.1* OQ507152.1	GTM.HGG.,ICGTCC GTA.HGG.,ICGTCC GTA.HGG.,ICGTCC GTA.HGG.HCGTCC GTA.HGG.ICGTCC GTA.HGG.ICGTCC GTA.HGG.ICGTCC GTA.HGG.ICGTCC			I GITGI GGATGIACITATIAA I GITGI GGATGIACITATIAA I GITGI GGATGIACIATIAA I GITGI GGATGIACIATIAA I GITGI GGATGIACIATIAA I GITGI GGATGIACIATIAA I GITGI GGATGIACIATIAA I GITGI GGATGIACIATIAA I GITGI GGATGIACIATIAA	530 ACCTAAATTGGGG ACCTAAATTGGGG ACCTAAATTGGGG ACCTAAATTGGGG ACCTAAATTGGGG ACCTAAATTGGGG ACCTAAATTGGGG ACCTAAATTGGGG ACCTAAATTGGGG
NC_048515.1* NC_048514.1* NC_070364.1* NC_039458.1* NC_039457.1* OQ507152.1 OQ507153.1 OQ507154.1	GTA.TGG.TCGTCC' GTA.TGG.TCGTCC' GTA.TGG.TCGTCC' GTA.TGG.TCGTCC' GTA.TGG.TCGTCC' GTA.TGG.TCGTCC' GTA.TGG.TCGTCC' GTA.TGG.TCGTCC' GTA.TGG.TCGTCC' GTA.TGG.TCGTCC' GTA.TGG.TCGTCC'			10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10110.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.000 10100.0000 10100.0000 10100.0000 10100.0000 10100.0000 10100.0000 10100.0000 10100.0000 1010000 1010000 1010000 10100000 1010000000 10100000000	530 ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG
NC_048515.1* NC_048514.1* NC_070364.1* NC_039458.1* NC_039457.1* OQ507152.1 OQ507153.1 OQ507154.1 OQ507155.1	GTA. TGG. TCGTCC'			IGTTG GGATGTACTATTAA IGTTG GGATGTACTATTAA IGTTG GGATGTACTATTAA IGTTG GGATGTACTATTAA IGTTG GGATGTACTATTAA IGTTG GGATGTACTATATAA IGTTG GGATGTACTATATAA IGTTG GGATGTACTATATAA IGTTG GGATGTACTATTAA IGTTG GGATGTACTATATAA	530 ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG
NC_048515.1* NC_048514.1* NC_070364.1* NC_039458.1* NC_039458.1* NC_039457.1* 02507152.1 02507153.1 02507155.1 02507155.1 02507156.1 02507156.1	GTA TIGG . ICGTCC GTA TIGG . ICGTCC GTA TIGG . ICGTCC GTA . TGG . ICGTCC GTA . TGG . ICGTCC GTA . TGG . ICGTCC GTA TIGG . ICGTCC			IGTTG GGATGTACTATTAA IGTTG GGATGTACTATTATA IGTTG GGATGTACTATTATA IGTTG GGATGTACTATTATA IGTTG GGATGTACTATATATA IGTTG GGATGTACTATATATA IGTTG GGATGTACTATATATA IGTTG GGATGTACTATATATATA IGTTG GGATGTACTATATATATA IGTTG GGATGTACTATATATATA IGTTG GGATGTACTATATATATA IGTTG GGATGTACTATATATATA	530 ACCTAAATIGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGG ACCTAAATIGGG ACCTAAATIGGG ACCTAAATIGGG ACCTAAATIGGG ACCTAAATIGGG ACCTAAATIGGG ACCTAAATIGGG ACCTAAATIGGGG
$\begin{array}{c} NC_048515.1*\\ NC_048514.1*\\ NC_039458.1*\\ NC_039457.1*\\ Q507152.1\\ Q507153.1\\ Q507155.1\\ Q507155.1\\ Q507155.1\\ Q507156.1\\ Q507158.1 \end{array}$				I 0 110 GGA TG TA CT ATTAAA I 0 110 GA TG TA CT ATATAAA	530 AC TAAATIG GG AC TAAATIG GG
$\begin{array}{c} NC = 0.48515, 11*\\ NC = 0.048514, 1*\\ NC = 0.0364, 1*\\ NC = 0.0364, 1*\\ NC = 0.03645, 1*\\ OQ507152, 1\\ OQ507155, 1\\ OQ507156, 1\\$	GTA TIGG . TCGTCC GTA . TGG . TCGTCC . TCGTC . TCGTCC . TCGTC . TC			I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A TT AA I G T TG G G A TG T A CT A T	530 AC T A A AT T G G G AC T A A AT T G G G AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C AC T A A T T G G G C
$\begin{array}{c} NC = 0.485.15.1 \\ NC = 0.0485.14.1 \\ NC = 0.0364.1 \\ NC = 0.039458.1 \\ NC = 0.039458.1 \\ OQ507152.1 \\ OQ507153.1 \\ OQ507153.1 \\ OQ507154.1 \\ OQ507156.1 \\ OQ507156.1 \\ OQ507158.1 \\ OQ507159.1 \\ OQ507159.1 \\ OQ507160.1 \\ OQ507161.1 \\ \end{array}$	GTA TIGG . TCGTCC GTA TIGG . TCGTCC GTA TIGG . TCGTCC GTA . TIGG . TCGTCC			I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG G G A TG T A CT A TT A A I G T TG	530 ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG ACCTAAATIGGGG
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$\begin{array}{c} NC_{-}0.485.15_{-}1*\\ NC_{-}0.485.14_{-}1*\\ NC_{-}0.3945.14_{-}1*\\ NC_{-}0.39457_{-}1*\\ Og507152_{-}1\\ Og507152_{-}1\\ Og507155_{-}1\\ Og507155_{-}1\\ Og507155_{-}1\\ Og507155_{-}1\\ Og507156_{-}1\\ Og507156_{-}1\\ Og507160_{-}1\\ Og507160_{-}1\\ Ay66590_{-}1*\\ Ay665868_{-}1*\\ Ay66580_{-}1*\\ \end{array}$			CGCG	I I I I I I G A I G I A CI A I T I A A I G I I G G A I G I A CI A I T I A A I G I I G G A G A I G I A CI A I T I A A I G I I G G A G A I G I A CI A I T I A A I G I I G G A G A I G I A CI A I T I A A I G I I G G A G A I G I A CI A I T I A A I G I I G G A G A I G I A CI A I T I A A I G I I G G A G A I G I A CI A I T I A A I G I I G G A G A I G I A CI A I T I A A I G I I G G A G A I G I A CI A I T I A A I G I I G G A G A I G I A CI A I T A A I G I I G G A G A I G I A CI A I T A A I G I I G G A G A I G I A CI A I T A A I G I I G G A G A I G I A CI A I T A A I G I I G G A G A I G I A CI A I T A A I G I I G G A G A I G I A CI A I T A A I G I I G G A G A I G I A CI A I T A A I G I I G G A G A I G I A CI A I T A A I G I I G G A G A I G I A CI A I T A A I G I I G G A G A I G I A CI A I T A A I G I I G G A G A I G A CI A CI A I T A A I G I I G G G A G A I G A CI A CI A I T A A I G I I G G G A G A I G A CI A CI A I T A A I G I I G G G A G A G A CI A CI A A I T A A I G I I G G G G A C A CI A CI A A I T A A I G I I G G G G A C A CI A CI A I T A A I G I G G G G G A C A CI A CI A I T A	530 AC TA A A TI G GG AC TA A A TI G GG
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$\begin{array}{c} NC_{\rm O} d\bar{e} 515 1 i *\\ NC_{\rm O} 04 8514 1 *\\ NC_{\rm O} 070 364 1 *\\ NC_{\rm O} 039 458 1 *\\ NC_{\rm O} 039 457 1 *\\ 0 050 71 52 1\\ 0 050 71 52 1\\ 0 050 71 55 1\\ 0 050 71 55 1\\ 0 050 71 55 1\\ 0 050 71 55 1\\ 0 050 71 50 1\\ 0 050 71 50 1\\ 0 050 71 50 1\\ 0 30 71 50 1\\ 0 30 71 50 1\\ 1 3 Y66 55 10 1\\ 3 Y66 55 10 1\\ 3 Y66 55 90 5 1 *\\ 3 Y66 55 88 1 *\\ \end{array}$	$\begin{array}{c} {\rm GTA} & \ . \ . \ . \ . \ . \ . \ . \ . \$	CC CC CC CC CC CC CC CC CC CC CC CC CC	CGCG GGGCC TTC CGCCC GCG GGCC GCG GGCC GCG GGCC CCC GGCC CCC GGCC CCC GGCC	I I I I I I I G A I G I A C I A I I A A A I G I I A C I A I I A I A A A A A A A A A A A A A A	530 ACCTAAATIGGG ACTAAATIGGGG ACTAAATIGGGG ACTAAATIGGGG ACTAAATIGGGG ACTAAATIGGGG ACTAAATIGGGG ACTAAATIGGG ACTAAATIGGG ACTAAATIGGG ACTAAATIGGG ACTAAATIGGG ACTAAATIGGG ACTAAATIGGG ACTAAATIGGG ACTAAATIGGG ACTAAATIGGG ACTAAATIGGG ACTAAATIGGG CACTAAATIGGG CACTAAATIGGG CACTAAATIGGG CACTAAATIGGG CACTAAATIGGG CACTAAATIGGG CACTAAATIGGG CACTAAATIGGG CACTAAATIGGG CACTAAATIGGG CACTAAATIGGG CACTAAATIGGG CACTAATIGGG CATCCGT . CCC CCCCCGT . CCC CCCCCGT . CCC CCCCCGT . CCC CCCCCGT . CCC
$\label{eq:constraints} \begin{split} & \text{NC}_{-0.46515} = 1.1 \\ & \text{NC}_{-0.47516} = 1.1 \\ & \text{NC}_{-0.37456} = 1.1 \\ & \text{NC}_{-0.37457} = 1.1 \\ & \text{O}_{5071155} = 1.1 \\ & \text{O}_{5071155} = 1.1 \\ & \text{O}_{5071155} = 1.1 \\ & \text{O}_{5071156} = 1.1 \\ & \text{O}_{5071160} = 1.1 \\ & \text{O}_{5071160} = 1.1 \\ & \text{AY665203} = 1.1 \\ & \text{AY66203} = 1.1 \\$	GTA TGG TCGTCC GTA TGG TCGTCCC GTA TGG TCGTCCC		CGCG	I T T G G G A T G T A (T A T A T A A A A G A G A G A T G T A (T A T A T A A A A G A G A G A G A C A A T A A A A A A A A A A A A A A A	530 CITAANTIGEGG ACTAANTIGEGG ACTAACGGTCCC CTCCCCTCCC CCTCCCCTCCC CCTCCCCTCCCC
$\begin{array}{c} NC_{\rm c} 0.48515_{\rm c} 1*\\ NC_{\rm c} 0.48515_{\rm c} 1*\\ NC_{\rm c} 0.39345_{\rm c} 1*\\ NC_{\rm c} 0.39457_{\rm c} 1*\\ 0.0507153_{\rm c} 1\\ 0.0507155_{\rm c} 1\\ 0.050715_{\rm c} 1$	GTA IGG . ICGTCC GTA IGG . ICGTCCC GTA IGG . ICGTCC GTA IGG . ICGTCC GCA ICGCGTCGCCC GCA ICGCCC GCA ICGCCCC GCA ICGCCCC GCA ICGCCCC GCA ICGCCCCCCCC CCA ICGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	C C C C C C C C C C C C C C C C C C C	CGCG	TG TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG TA CT ATT AA I G TTG . GGA TG GA CT AT ATT AA I G TTG . GGA TG GA CT AT ATT AA I G TTG . GGA CG CG . A TA CT GG I G C CG . GGA CG G . A TA CT G G I G C CG . GGA CG G . A TA CT G G I G C CG . GGA CG G . A TA CT G G I G C CG . GGA CG G . A TA CT G G I G C CG . GGA CG G . A TA CT G G I G C CG . GGA CG G . A TA CT G G I T C CG . GGA CG G . A TA CT G G I T C CG . GGA CG G . A TA CT G G I T C CG . GGA CG G . A TA CT G G I T C CG . GGA CG G . A TA CT G G I T C CG . GGA CG G . A TA CT G G I T C CG . GGA CG G . A TA CT G G I T C CG . GGA CG G . A TA CT G G I T C CG . GGA CG G . A TA CT G G I T C CG . GGA CG G . A TA CT G G I T C CG . GGA CG G . A TA CT G G I T C CG . GGA CG G . A TA CT G G I T C CG . GGA CG G . A TA CT G G I T C CG . GGA CG G . A TA CT G G I T C CG . GGA CG G . A TA CT G G I T C CG . GGA CG CG . A TA CT G G I T C CG . GGA CG CG . A TA CT G G I T C CG . GGA CG CG . A TA CT G G I T C CG . GGA CG CG . A TA CT G G I T C CG . GGA CG CG . A TA CT G G I T C CG . GGA CG CG . A TA CT G G I T C CG . GGA CG CG . A TA CT G G I	530 AC TAAATTGG GG AC TAAATTGG GG CAC CC CT . CC CC CC CC T . CC CC CC CC C C CC CC CC CC CC CC CC CC
NC 048515 1* NC 048515 1* NC 048514 1* NC 039457.1* 02507152.1 02507152.1 02507155.1 02507155.1 02507155.1 02507155.1 02507155.1 02507157.1 02507157.1 02507157.1 02507150.1 AY665503.1* AY665503.1* AY665590.1* AY665590.1* AY665595.1* AY665281.1* MH763728.1* MH763728.1*	GTA : IGG . ICGTCC GTA : IGG . ICGTCCC GTA : IGG . ICGTCC GTA : IGG . ICGTCC GCA : ICGCCCC GCA : ICGCCCC GCA : ICGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		CACCS	TITE GGATGITACTATTAA TGTTG GGATGITACTATATAA TGTTG GGATGITACTATATAA TGTTG GGATGITACTATATAA TGTTG GGATGITACTATATAA TGTTGC GGATGITACTACTATATAA TGTTGC <	530 ACT TAAATIG GG ACT TAAATIG GG ACT TAAATIG GG ACT TAAATIG GG ACT AAATIG GG CT CC GT . CC CC CC CGT . CC CC CC CG C . CC CC CC CC CG C . CC CC CC CC CG . CC CC CC CC CC CC CC . CC CC CC CC CC CC . CC CC CC
$\label{eq:constraints} \begin{array}{l} \text{NC} & 0.485.15 & 1.* \\ \text{NC} & 0.485.14 & 1.* \\ \text{NC} & 0.039.45.1.* \\ \text{NC} & 0.39.457.1.* \\ \text{Og507155.1} \\ \text{Og507155.1} \\ \text{Og507155.1} \\ \text{Og507155.1} \\ \text{Og507155.1} \\ \text{Og507156.1} \\ \text{Og507156.1} \\ \text{Og507156.1} \\ \text{Og507156.1} \\ \text{Og507160.1} \\ \text{Og507160.1} \\ \text{Og507160.1} \\ \text{AY665903.1}* \\ \text{AY665590.1}* \\ \text{AY665686.1}* \\ \text{MH763720.1} \\ \text{Og372022.1} \\ \text{Og372022.1} \\ \text{Og372022.1} \\ \text{Og372022.1} \\ \end{array}$	$\begin{array}{c} \exists A \\ \exists A \\ \exists G \\ G \\ \exists A \\ \exists G \\ G \\ G \\ T \\ A \\ \exists G \\ G \\ G \\ T \\ A \\ \exists G \\ G \\ G \\ G \\ T \\ A \\ \exists G \\ G \\ G \\ G \\ T \\ A \\ \exists G \\ G \\ G \\ G \\ T \\ A \\ \exists G \\ G \\ G \\ G \\ G \\ A \\ G \\ G \\ G \\ G \\ A \\ G \\ G \\ G \\ G \\ G \\ A \\ G		CGCG CGCG CCCC CCCC CCCC CCCC CCCC CCCC	I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I	530 AC TA A ATT G G G AC T A A ATT G G G AC T A A ATT G G G AC T A A ATT G G G AC T C C C G T . C C G C C C C C C T . C C G C C C C C C T . C C G C C C C C C T . C C G C C C C C C T . C C G C C T C C C T . C C G C C T C C C T . C C G C C T C C C T . C C G C C T C C C T . C C G C C T C C C T . C C G C C T C C C T . C C G C C T C C C T . C C G C C T C C C T . C C G C C T C C C T . C C G C C T C C C T . C C G C C T C C C T . C C G C C T C C C T . C C G C C T C C C T . C C G C C C T C C C G T . C C G C C C T C C C G T . C C G C C C C C C C C C C C C C C C C
$\begin{array}{c} NC_{-}0.485.15_{-}1*\\ NC_{-}0.485.15_{-}1*\\ NC_{-}0.394.57_{-}1*\\ NC_{-}0.394.57_{-}1*\\ OQ507155_{-}1\\ OQ50716_{-}1\\ AY66590_{-}1*\\ AY66590_{-}1*\\ AY66590_{-}1*\\ AY66597_{-}1*\\ AY66597_{-}1*\\ AY66590_{-}1*\\ AY6690_{-}1*\\ AY6690_{-}1*$	GTA IGG . ICGTCC GTA IGG . ICGTCCC GTA IGG . ICGTCC GTA IGG . ICGTCC GTA IGG . ICGTCC GCA ICGCCTCCCC CCA ICGCCTCCCCC CCA ICGCCTCCCCC CCA . ICGCCTCCCCC CCA . ICGCCTCCCCCC CCA . ICGCCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		CCCG CGCCCC CCCG CGCCC CCCG CGCCCCC CCCG CGCCCCCCCC	I TTG. GGA TGT A CT ATTAA I G TG G GGA TGA CT A CT ATTAA TATA I G TG G GGA TGA CT A CT ATTAA TATA I G TG G GGA CGA CGA CA ATA CTATA TAA	530 AC TAAATIG GG AC TAATIG GG CT TAATIG GG CT TAATIG GG AC TAATIG GG CT TCC GT
$\begin{array}{c} NC_{0} \ de515 \ 1*\\ NC_{0} \ de515 \ 1*\\ NC_{0} \ de581 \ 1*\\ NC_{0} \ de581 \ 1*\\ NC_{0} \ de581 \ 1*\\ Op5071551 \ 1\\ Op5071601 \ 1\\ Op5071601 \ 1\\ Op5071601 \ 1\\ AY6659031 \ 1*\\ AY6659101 \ 1*\\ AY665911	GTA IGG ICGTCC GTA IGG ICCTCCC GTA IGG ICCTCCCC GTA IGG ICCTCCCCCC GTA IGG ICCTCCCCCCCC GTA IGG ICCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CC	CGCG	TG TG .GGA TG TA CT ATTAA IG TG .GGA CG A CT ACTATAA IG TG .GGA CG A CT ACTACTAA IG CT .GGA CG A CT ACTATAA IG TG .GGA CG A CT ACTATAA IG TG .GGA CG A CT ACTATAA IG TG .GGA CG A CT ACTACTACTAA IG CC .GGA CG A CT ACTACTACTAA IG CC .GGA CG A CT ACTACTACTAA IG CC .GGA CG CC .AT ACTG CG IG CC .GGA CG CC .GGA CG .AT ACTG CG IG CC .GGA CG CC .GGA CG .AT ACTG CG IG CC .GGA CG CC .GGA CG .AT ACTG CG IG CC .GGA CG CC .GGA CG .AT ACTG CG IG C	530 AC TAAATT GC GC AC TAAATT GC GC CC CC CC T. CC CC CC TC CC CT. CC CC CC CC CC CT. CC CC CT. CC CC CC CT. CC CT. CC CC CT. CC CT. CC CC CT. CC CC CT. CC CC CT. CC CC C
$\begin{array}{c} NC_{0} = 648518 - 1 \times \\ NC_{0} = 048514 - 1 \times \\ NC_{0} = 070364 - 1 \times \\ NC_{0} = 039457 - 1 \times \\ OSO71554 - 1 & OSO71552 - 1 & OSO71554 - 1 & OSO72024 - 0SO72024 - 1 & OSO72024 - 0SO72024 - 0SO72024 - 0SO7204 -$	GTA, TGG, TCGTCC GTA, TGGC GTCGCC GTA, TGGC GTCGCC GTA, TGGC GTCGCC GTA, TGGCCC GTA, TGGCCC GCA, TCGCCC GCA, TCGCCC GCA, TCGCCC GCA, TCGCCCC GCA, TCGCCCC GCA, TCGCCCC GCA, TCGCCCCCCC GCA, TCGCCCCCCCC GCA, TCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	C C C C C C C C C C C C C C	2000	TG TG .GGA TG TA CT ATTAA TG TG .GGA CG .GA TG CT ACTATAA TG TG .GGA CG .GA TG CT ACTAA TG TG .GGA CGG .GA TG CT ACTAA TG TG .GGA CGG .GA TG CT ACTAA TG TG .GGA CGG .GA TG CT CT ATTAA TG CT .GGA CGG .GA TG CT CT ATTAA TG CT .GGA CGG .GA TG CT CT ATTAA TG CT .GGA CGG .GA TG CT	530 ACT TAANT IG GG ACT TAANT IG GG CT CCCCT CC CCCCCT CC CCCCCCT CC CCCCCCT CC CCCCCCT CC CCCCCCT CC CCCCCCT CC CCCCCCT CC CCCCCCT CC CCCCCCT CC CCCCCCT CC CCCCCCT CC CCCCCCT CC CCCCCCT CC CCCCCCT CC CCCCCCT CC CCCCCCT CC CCTCCCCT CC CCTCCCCT CC CCTCCCCT CC CCTCCCCT CC CCTCCCCT CC CCTCCCCT CC CCTCCCCT CC CCTCCCCT CC CCTCCCCT CC CCTCCCCT CC CC CCCCCCT CC CC CCCCCCCT CC CC CCCCCCCT CC CC CCCCCCCT CC CC CCCCCCT CC CC CCCCCCT CC CC CCCCCCCT CC CC CCCCCCCT CC CC CCCCCCCT CC CC CCCCCCCT CC CC CCCCCCCT CC CC CCCCCCC CC CC CCCCCCCT CC CC CCCCCCCT CC CC CCCCCCC CC CC CCCCCCC CC CC CCCCCCC CC CC CCCCCCC CC CC CCCCCCC CC CC CC CC CC CC CC CC CC

	540	550	5 G O	570	580
KT178121.1* NC_026570.1*	TTATCTGCT	ААААА <mark>СТА</mark> ААААА <mark>СТА</mark>	CGGTA <mark>GAGC</mark> CGGTA <mark>GAGC</mark>	TGTTTATGA . TGTTTATGA .	
KT178120.1* NC 048515.1*	TTATCTGCT	ААААА <mark>СТА</mark> ААААА <mark>СТА</mark>	CGGTA <mark>GAGC</mark> CGGTA <mark>GAGC</mark>	TGTTTATGA.	ATGICITCGCG
NC_048514.1*	TTATCTGCT	ААААА <mark>СТА</mark>	CGGTA <mark>GAGC</mark> CGGTA <mark>GAGC</mark>	TGTTTATGA.	ATGTCTTCG
NC_039458.1*	TTATCTGCT	AAAAACTA	CGGTAGAGC	TGTTTATGA.	ATGICITCGCG
00507152.1	TTATCTGCT	AAAAACTA	CGGTAGAGC	TGTTTATGA.	ATGICTICGCG
OQ507153.1 OQ507154.1	TTATCTGCT	ААААА <mark>СТА</mark> ААААА <mark>СТА</mark>	CGGTA <mark>GAGC</mark> CGGTA <mark>GAGC</mark>	TGTTTATGA.	ATGICTICGCG
00507155.1	TTATCTGCT	ААААА <mark>СТА</mark>	CGGTA <mark>GAGC</mark> CGGTAGAGC	TGTTTATGA.	ATGTCTTC.
00507157.1	TTATCTGCT	АААААСТА	CGGTAGAGC	TGTTTATGA.	ATGTCTTCGCG
00507159.1	TTATCTGCT	AAAAACIA	CGGTA <mark>GAGC</mark>	TGTTTATGA.	ATGICITCGCG
OQ507160.1 OQ507161.1	TTATCTGCT	ААААА <mark>СТА</mark> ААААА <mark>СТА</mark>	CGGTA <mark>GAGC</mark> CGGTA <mark>GAGC</mark>	TGTTTATGA . TGTTTATGA .	ATGICITCGCG
AY665903.1* AY665868.1*	CCATCGGCA.CGCG.	GCIGGC <mark>CIA</mark>	AATGC <mark>GAGC</mark> AATGC <mark>GAGC</mark>	CCGCGTCGACGG.	ACGTCACGGCAAGTG
AY665910.1*	CTAGCAGCG.CGCG	GCTGGCCTA	AATGC GAGC	CCGCGTCGACGG.	ACGTCACGGCAAGTG
AY665879.1*	CTCGCAGCG.CGCG	GCTGGCCTA	AATGCGAGC	CCGCGTCGACGG.	ACGICACGGCAAGIG
AY665886.1*	CTCTCAGCG.CGCG	GCTGGCCTA GCTGGC <mark>CT</mark> A	AATGC <mark>GAGC</mark> AATGC <mark>GAGC</mark>	CCACGICGACGG.	ACGTCACGGCAAGTG
MH763728.1* MH763740.1*	CTCTCAGCG.CGTG CCATCGGCT.CGTG	GCTGGC <mark>CTA</mark> GTTGGC <mark>CTA</mark>	AATGC <mark>GAGC</mark> AATGT <mark>GAGC</mark>	CCACGTCGACGG.	ACGTCACGGCAAGTG
00372021.1	CCATCGGCTCCGTG		AATGA <mark>GAGC</mark>	CCATGTCGACGG.	ACGTCACGGCAAGTG
00372023.1	CGTTCCGCGCCGGGGT	CGTTAGTCGA	CCGGCGACC	GCGCACGCGCGA.	
0Q372024.1 0Q372025.1	CCATCGGCT.CGIG	GTTGGCCTA	AATGT <mark>GAGC</mark>	CCATGICGACGG.	
OQ372026.1 OQ372027.1	CCATCGGTCTAGTT CCATCCGTCGAG			TCGTGCCCGGGGT	TCGTTAGTCGCTAGGCGACCG.CGCACGTG
00372028.1	CCATCGGCT.CGTG	GAIGGC <mark>CIA</mark>	AATGT <mark>GAGC</mark>	CCATGTCGACGG.	ACGTCATTGITTTAGTTT
			00000	1.0010101000001	
	590 60	00 61	o 6	20 630	640 650
KT178121.1* NC_026570.1*	GTGGACT.TGATTTTA GTGGACT.TGATTTTA	CAAAGATGAT CAAAGATGAT	GAGAACGTO GAGAACGTO	AACTCACAACCAT AACTCACAACCAT	TTATGCGTTGGAGAGATC.GTTTCTGCT TTATGCGTTGGAGAGATC.GTTTCGTCT
KT178120.1*	GTGGACT. TGATTTTA	CAAAGATGAT	GAGAACGTO	AACTCACAACCAT	TTATGCGTTGGAGAGATC.GTTTCGTCT
NC_048514.1*	GIGGACT. TGATTITA	CAAAGATGAT	GAGAACGTO	AACTCACAACCAT	TTATGCGTTGGAGAGATC.GTTTCGTCT
NC_070364.1* NC_039458.1*	GTGGACT.TGATTTTA(GTGGACT.TGATTTTA)	CCAAAGATGAT CCAAAGATGAT	GAGAACGTO GAGAACGTO	AACTCACAACCAT AACTCACAACCAT	TTATGCGTTGGAGAGATC.GTTTCGTCT TTATGCGTTGGAGAGATC.GTTTCGTCT
NC_039457.1* 00507152.1	GTGGACT.TGATTTTA(GTGGACT.TGATTTTA)	CCAAAGATGAT CCAAAGATGAT	GAGAACGTG GAGAACGTG	AACTCACAACCAT AACTCACAACCAT	TTATGCGTTGGAGAGATC.GTTTCGTCT TTATGCGTTGGAGAGATC.GTT
00507153.1	GTGGACT. TGATTTTA	CAAAGATGAT	GAGAACGTO	AACTCACAACCAT	TTATGCGTTGGAGAGATC.GTTTCGTCT
00507155.1					
00507157.1	GIGGACT.TGATTTTA	CAAAGATGAT CAAAGATGAT	GAGAACGIG GAGAACGIG	AACTCACAACCAT	TTATGCGTTGGAGAGAGATC.GTTTCGTCT
OQ507158.1 OQ507159.1	GTGGACT.TGATTTTA	CCAAAGATGAT CCAAAGATGAT	GAGAACGTO GAGAACGTO	AACTCACAACCAT AACTCACAACCAT	TIATGCGTTGGAGAGATC.GTTTCGTCT TIATGCGTTGGAGAGATC.GTTTCGTCT
00507160.1	GTGGACT. TGATTTTA	CAAA	GAGAACGTO		TTAT COGTTOCACACATC CTTTCCTCT
AY665903.1*	GIGGTIG AACCI	CAACTCTCGT	GGTGCCGTG	GCCGAACCCG	TCGCCCGCGTC.GGCTGATG.GACCCTTCA
AY665910.1*	GTGGTTGGATCT	CAACTCTCTT	GGTGCCGTG	GCCGAACCCG	TCGCCCGCGTC.GGCTGCGA.GACCCTTCC
AY665914.1* AY665879.1*	GTGGTTGAATCT GTGGTTGGATCT	CAACTCTCGT CAACTCTCGT	GGTGCCGTG GGTGCCGTG	GCCGAACCCG GCCGAACCCG	TCGCCCGTGCC.GGCTGACA.GACCCTTCC TCGCCCGCGTC.TGCTGACA.GACCCTTCC
AY665905.1*	GIGGTIG. AAICI.	CAACTCTCTT	GGAGCCGTC	GCCGAACCCG	TCGCCCGTGTC.GGCTGTGA.GACCCTTCC
MH763728.1*	GTGGTTGAATCT	CAACTCTCTT	GGTGCCGTG	GCCGAACCCG	TCGCCCGTGTC.GGCTGCGA.GACCCTTCC
00372021.1	GIGGTIG AAICI	CAACICITGI	GGT		
00372022.1	GGGGGGAG	CAACICITGI		AGCGAACGCC	TICCCGGGTTCAAACGGGTTTGCGGGTC
0Q372024.1 0Q372025.1	GIGGTIGAAICI	CAACTCTTGT	GGTGC <mark>CGTG</mark>	GCCGAACCCG	TGGCCCGTGTC.GGCTGACA.GAACCTCCG
00372026.1		CGCGTTTCGT	G	CCAG	GGGTTCG
00372028.1	GTGGTTGTTATTCT	CAACTCTTGT	GGTGCCATC	GGCCGAATCCCGC	GGGCCCGTGTCGGGCTGACATAAACCTTCC
OQ372029.1	GIGGCIGCIGGGICIA	CGAGCG	G G G A A T G T I	AGCGAACICC	TTCCCCG
	660 670	680	690	700	710 720 730
KT178121.1*	TTTGTGCCGAAGCA	TTTATAAAG	CACAGGCT	GAAA.CAGGTGA	AATCAAAGGGCATTACTTGAATGCTACTG
KT178120.1*	TTTGTGCCGAAGCA	TTTATAAAG	CACAGGCT	GAAA.CAGGIGA	AATCAAAGGGCATTACTTGAATGCTACTG
NC_048515.1* NC_048514.1*	T T T G T G C C GAAG CA T T T G T G C C GAAG CA	CTTTATAAAG CTTTATAAAAG	CACAGGCT	GAAA.CAGGTGA GAAA.CAGGTGA	A A T C A A A G G G C A T T A C T T G A A T G C T A C T G A A T C A A A G G G C A T T A C T T G A A T G C T A C T G
NC_070364.1*	TTTGTGCCGAAGCA	TTTATAAAG	CACAGGCT	GAAA.CAGGTGA	AATCAAAGGGCATTACTTGAATGCTACTG
NC_039457.1*	TTTGTGCCGAAGCA	TTTATAAAG	CACAGGCT	GAAA.CAGGIGA	ATCAAAGGGCATTACTTGAATGCTACTG
00507152.1	TTTGTGCCGAAGCA				
00507154.1	T T T G T G C C G A A G C A	CTTTATA <mark>A</mark> AG	CACAGGCT	GAAA.CAGGTGA	AATCAAAGGGCATTACTTGAATGCTACTG
00507156.1	TTTGTGCCGAAGCA	TTATAAAG	CACAGGCT	GAAA.CAGGTGA	AATCAAAGGGCATTACTTGAATGCTACTG
OQ507157.1 OO507158.1	T T T G T G C C G A A G C A T T T G T G C C G A A G C A	CTTTATAA		AGCA.CAGGCTG	AAA
00507159.1	T T T G T G C C G A A G C A	CTTTATA <mark>A</mark> A.			
00507161.1	TTTGTG				
AY665903.1*	T GCGCTTAGGCG	TCCGACC	GCGACCCC.	AGGT.CAGGCGG	SATT
AY665910.1*	G GCGCTTAGGCG	TCCGACC	GCGACCCC	AGGT.CAGGCGG	GATC
A1005914.1* AY665879.1*	G., GCGCTTAGGCG	CTCCGACC	GCGACCCC.	AGGI.CAGGCGG(AGGI.CAGGCGG(GATT
AY665905.1* AY665886 1*	G. GCGCTTAGGCG	TCCGACC	GCGACCCC.	AGGT.CAGGCGG	GATT
MH763728.1*	G GCGCTTAGGCG	TCCGACC	GCGACCCC	AGGT.CAGGCGG	GATT
MH763740.1* OQ372021.1	G. GCGCTTAGGCG	JITCGACC	GCGACCCC.	AGGT.CAGGTGG	AATT
00372022.1	GGTGCGCTTAGGCG	CTT. CGACC	GCGACCCC	AGGTGCAGGTGG	AAT
00372024.1	GCGCTTAGGCG	CTCGACCA	GCGACCCA	GICIGG	SATTTTCG
OQ372025.1 OQ372026.1	TTAATCO	TAGGCTACO	GIGACACO	T	
00372027.1	GCTCTGCTTAGCAG	GTTT.CGACA	ATGAACCT	TCCG.CATGGTC	ACCT
00372028.1	GGCGITTTTTAGGCC	GITCCACCC	JCGTACCC	•••••	

Appendix 2 B: Multiple sequence alignment (MSA) for ITS2 sequences of the *Physalis* accessions as well as reference sequence (<u>https://espript.ibcp.fr/ESPript/temp/1101891838/0-0-1680467018-esp.pdf</u>)

		i	10	20	зo
AY665914.1*			GGAAGGA <mark>TCA</mark> TT	.GTCGAAACCTGC	.GAAGCAGAGCG
AY665886.1*			GGAAGGA <mark>TCA</mark> TT	.GTCGAAACCTGC	. TAAG CAGAGCG
MH763728.1*		CTGC	GGAAGGA <mark>TCA</mark> TT	.GTCGAAACCTGC	. TAAG CAGAGCG
MH763740.1*		CTGC	GGAAGGA <mark>TCA</mark> TT	.GTCGAAACCTGC	. TAAG CAGAGCG
00371996.1		TCTATGTCGAACG	CGCAGGATCATT	.GTCGAAACCTGC	.TAAGCAGAGCG
00371997.1				.66AC6	.IGAGAAAGCG
00371999 1				GTCCTA	CGATAAG
00372000.1		TCCTTGGGACTGC	GGCAGGATCATT	GTCG AACCTGC	TAAG CAGAGCG
00372001.1			TGAGAGGGA	.GTGTACACGTTC	ATAGGGACAGGGAGG
OQ372002.1			CGGGAGGGGGTATG	GATTTAAACCGGC	GGAAGCAGAGAG
0Q372003.1		TCGTTGTGACTGC	GGTGG.A <mark>TCA</mark> TT	.GTCG.AACCTGC	. TAAG CAGAGCG
00372004.1	GAGGACT	ICGIGGCGACCIGC	GGCAGGA <mark>TCA</mark> TT	.GTCG.AACCTGC	. TAGG CAGAGCG
00372005.1		GGAAGCAGC	TGACTGGGG <mark>TC</mark> GG.	.GTCGTAGTGT	CTAAGTGCCGGAGGG
00372006.1	CACATACT	CTAGTEGAACTEC		GTCG AACCTGC	.GAAGCAGAGCG
00372008 1		argratracaero	TCGTACCGCCCAT	GGICGARACCIGC	CAG CAGAGOG
00372009 1	100T	TCGTAGTGACTGC	GGAGG TCATT	GTCG AACCTGC	TAAG CAGAGOG
00372010.1				CCGIGC	.TATGCA
00372011.1		TCCTAGGTACTGC	GGTAGGA <mark>TCA</mark> TT	.GTCG.AACCTGC	. TAAG CAGAGCG
0Q372012.1			ACGT TAACT		CGGGAGG
OQ372013.1	CACG	TICTTTGCGACTC	GGAGGAA <mark>TCA</mark> TT	.GTCG.AACCTGC	. TAAG CAGAGCG
00372014.1	CTGCCGTTT	CCCTAGCGACTCC	GGCGGAATCATT	. GTCGAAACCTGC	. TAAG CAGAGCG
00372015.1	CTCCGTT	TCGTAGTGACCT	GCGGAGGTCATT	.GTCGAAACCTGC	. TAAG CAGAGCG
00372010.1		GGIIICCGIAGGIGACC	TCCCCACCATCATT	CTCCANACCIGC	TAAG. CAGAGOG
00372018 1	CAT	AAGGTTTCGTTGGTGACC	CTGCGGAGGTCATT	GTCGAAACCTGC	TAAG CAGAGCG
00372019.1		CGTTAGTGACCTG	CGGAGGATCATT	GTCGAAACCTGC	TAAG. CAGAGCG
0Q372020.1		TAGGTTTCTTAGTGACC	TGCGGAGGA <mark>TCA</mark> TT	. GTCGAAACCTGC	. TAAG CAGAGCG
0Q372021.1					
OQ372022.1					
00372023.1			GGG <mark>TC</mark> GCG	. GTCGGAGCGCCT	.AACGCCGGAGG
00372024.1	GAAGTCGTAACAAGGTTTCCA	TAGGTGAACCTGC	GGAAGGA <mark>TCA</mark> TT	.GTCGAAACCTGC	. TAAG CAGAGCG
00372025.1	• • • • • • • • • • • • • • • • • • • •		GAAGGATCATT	GTCG AACCIGC	TAAG. CAGAGCG
00372026.1				ACCCCCT	TAAGCGCCGGAAGG
00372028.1			GATCATT	GTCG AACCTGC	TTAAGCAGAGCG
0Q372029.1			TGACTGGGGTCGCG	.GTCGAGCGC	CTAAGCGCCGGAAGG
	4ọ 5ọ 6ọ	7 <u>0</u>	8	10	ọ 11 ọ
AY665914.1*	40 ACCCGCIGAACCTIGTTTIGAACA	70 C <mark>CGGG</mark> GAGGCGCGCT.T	80, 90 TGGCTCGCCTCCCC	10 CCTCGTCGG	o 110 CCGCGGTCG.CGCG
AY665914.1* AY665886.1*	40, 50, 60, ACCCGCGAACCIGIIIGAACA ACCCGCGAACCIGIIIIGAACA	79 C <mark>CGGGGAGGCGCGCT.I</mark> C <mark>CGGG</mark> GAGGCGCGCG.I	80 TGGCTCGCCTCCCC TCGCTCGCCT.CCC	10 CCTCGTCGG CCTCGTCGT	9 119 CCGGCGGTCG.CGCG CCGACGGCCG.CGCG
AY665914.1* AY665886.1* MH763728.1*	40 50 60 ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTTGAACA	79 CCGGGGAGGCGCGCT.T CCGGGGAGGCGCGCGCT CCGGGGAGGCGCGCGCG	80, 90 TGGCTCGCCTCCCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC	10 CCTCG.ICGG CCTCG.ICGT CCTCG.ICGG	• 11• CCGGCGGTCG.CGCG CCGACGGCCG.CGCG CCGGCTGTCG.CGCG
AY665914.1* AY665886.1* MH763728.1* MH763740.1* 0037196.1	40 50 60 ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTTGAACA ACCCGCAAACCTGTTTGAACA	79 CCGGGAGCGCGCCT.T CGGGGAGGCGCGCGCT CGGGGAGGCGCGCGCT CCGGGGAGGCGT	80 90 TGGCTCGCCTCCCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC	CCTCGTCGG CCTCGTCGT CCTCGTCGG CCTCGTCGG CCTCGTCGG	0 110 CCGECGETCG.CGCG CCGACGECCG.CGCG CCGCTGTCG.DGCC CCGCCGCCG.CGCC CCGCCGCCCC.CACC
AY665914.1* AY665886.1* MH763728.1* MH763740.1* OQ371996.1 OQ371997.1	40 50 60 ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTTGAACA ACCCGCAACCTGTTTGAACA ACCCGCAACCTGTTTGAACA ACCCGCAACCTGTTTGAACA	79 CCGGCGAGGCGCGCGT.T CCGGGGAGGCGCGCGGT CCGGGGAGGCGCGCGGT CCGGGGAGGGCG.T CCGGGAAGGCG.T	80 90 TGGCTCGCCTCCCC TCGCTCGCCTCCCC TCGCTCGCCTCCCC TCGCTCGC	10 CCTCGTCGG CCTCG.TCGG CCTCG.TCGG CCTCG.TCGG CCTCG.TCGG	9 119 CCGGCGGTCG.CGCG CCGACGGCCG.CGCG CCGGCGCCG.CGCC CCGGCGCCG.CGCC CCAGCGCCG.CACCG
AY665914.1* AY665886.1* MH763728.1* MH763740.1* OQ371996.1 OQ371998.1	40 50 60 ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTGAACA ACCCGCGAACCTGTTGAACA ACCCGCGAACCTGTTGAACA ACCCGCAACCTGTTGAACA ACCCGCAACCCGTTGAACA ACCCGCAAACCTGTTGAACA ACCCGCAACCCGTTGAACA ACCCGCAACCCGTTGAACA	70 CCGGGGAGGCGCGCGT CCGGGGAGGCGCGCGGT CCGGGGAGGCGCGCGGT CCGGGGAGGCGGGGT ACGGGAAGGCGGGT	80 90 TGGCTCGCCTCCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC	10 CCTCGTCGG CCTCGTCGG CCTCGTCGC CCTCGTCGC GAGGATACTGG GAGGATACTGG	0 110 CCGECGGTCG.CGCC CGCC CCGCCGCCG.CGCC CGCC CCGCCGCCG.CGCC CGCC CCGCCGCCG.CACC CACC TCCGTTGTCCCCCC CCCC .GACGTCCCA
A¥665914.1* A¥665886.1* MH763728.1* MH763740.1* OQ371996.1 OQ371997.1 OQ371999.1	40 50 60 ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTGAACA ACCCGCGAACCTGTTTGAACA ACCCGCTGAACCTGTTTGAACA ACCCGCAAACCTGTTTGAACA ACCCGCAAACCTGTTGAACA ACCCGCAAACCTGTTGAACA ACCCGCAACCGTTGAACA ACCCGCAAACCGGTTGAACA ACCCGCAACCGGTTGACA ACCCGCAAACCGGTTGAACA ACCCGCAACCGGTTGAACA ACCCGCAAACCGGTTGAACA ACCCGCAACGGTTGAACA	70 CCGGGGAGGCGCGCGCT. CCGGGGAGGCGCGCGCG CCGGGAGGGCG.T CCGGGAAGGCG.T ACGGCAAC	80 90 TGGCTCGCCTCCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC	10 CCTCGTCGG CCTCGTCGG CCTCGTCGG CCTCGTCGG GCTCGTCGG GAGGATACTGG	0 110 CCGGCGGTCG.CGCG CGCG CCGCCGCCG.CGCG CCGCG CCGCCGCCG.CGCG CCGCG CCGCCGCCG.CGC CCCGC CCGTTGTCGCCG.CGCG CCGTTGTCGCCG.CGCG
A¥665914.1* MH763728.1* MH763740.1* OQ371996.1 OQ371997.1 OQ371997.1 OQ371999.1 OQ372000.1	49 59 69 ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTTGAACA ACCCGCCAACCTGTTTGAACA ACCCGCAACCGTTTGAACA ACCCGCAACCGTTTGAACA ACCCGCAACCGTTTGAACA ACCCGCAACCGTTTGAACA ACCCGCAACCGTTTGAACA ACCCGCCAACCGCGTTTGAACA ACCCGCAACCGCGTTGAACA ACCCGCAACCGCGTTGAACA	79 CCGGCGAGGCGCGCGT CCGGGGAGGCGCGCGGT CCGGGGAGGCGCGCGGT CCGGGGAGGGCGT CCGGGGAAGGCGT 	80, 90 TGGCTCGCCTCCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC TCGCTCGCTCCCT.CCC TCGCTCGCTCCCT.CCC TCGCTCGCCT.CCC	10 CCTCGTCGG CCTCGTCGG CCTCGTCGG CCTCGTCGG CGTCGTCGG CAGGATACTGG 	9 119 CCGGCGGTCG.CGCG CGCG CCGGCGCGCG.CGCG CGCGCG CCGCGCGCG.CGCG CGCGCG CCGCGCGCG.CGCG CGCGCG CCGTTGTGCGCCGCG CGCGCG CCGTGTGTGCGCCGCG CGCGCG CCGTGTGTGCGCCGCG CGCGCG CCGTGTGTGCGCCGCG CCCA CCGCGCGCG CCCA CCGCGCGC CCCA
AY665914.1* AY665886.1* MH763728.1* OQ371996.1 OQ371996.1 OQ371998.1 OQ371999.1 OQ37200.1 OQ372001.1 OQ372001.1	49 50 60 ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTTGAACA ACCCGCAACCTGTTTGAACA ACCCGCAACCTGTTTGAACA ACCCCGCAACCTGTTTGAACA ACCCCGCAACCCGTTTGAACA ACCCCGCAACCCGTTTGAACA ACCCCGCAACCCGTTGAACA ACCCCGCAACCCGTTTGAACA ACCCCGCAACCCGTTGAACA ACCCCGCAACCCGTTTGAACA ACCCGCAACCAACA ACCCCGCAACCTGGAGCGACCAC ACCCGCAACA	70 CCGGGGAGGCGCGCGT CCGGGGAGGCGCGCGT CCGGGGAGGCGCGCGGT CCGGGGAGGGCGT ACGGGAAGGCGT 		10 CCTCGTCGG CCTCGTCGG CCTCGTCGG CCTCGTCGG GAGGATACTGG 	9 119 CCGGCGGTCG.CGCC CGCC CCGCCGCCG.CGCC CGCC CCGCCGCCG.CGCC CGCC CCGCCGCCG.CGCC CGCC CCGCGCCG.CGCC CGCC CCGCGCCG.CGCC CGCC CCGCGCCG.CGCC CGCC CCGCGCCC CGCC CCGCGCCC CGCC CCGCCCC CCCC CCGCCCC CGCC CCCCCC CGCC CCCCC CGCC
A¥665914.1* A¥665886.1* MH763728.1* MH763740.1* OQ371996.1 OQ371998.1 OQ371999.1 OQ372001.1 OQ372001.1 OQ372002.1	40 50 60 ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTGAACA ACCCGCGAACCTGTTTGAACA ACCCGCAACCTGTTTGAACA ACCCGCAAACCCGTTTGAACA ACCCGCAACCGTTTGAACA ACCCGCAACCCGTTTGAACA ACCCGCAACCCGTTGAACA ACCCGCAACCCGTTTGAACA ACCCGCAACCCGTTGAACA ACCCGCAACCCGTTTGAACA ACCAGCACCGTTTGAACA ACCAGCACCGTTTGAACA ACCGCGACACCCGTTTGAACA	79 CCGGGGAGGCGCGCGCT.T CCGGGGAGGCGCGCGCGT CCGGGAGGCGCGCGCGT CCGGGAAGGCGT ACGGGAACGCGT CCGGGAACGCGT CCGGGAACGCGT CCGGGAAGGCGT	80 90 TGGCTCGCCTCCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC 	10 CCTCGTCGG CCTCGTCGG CCTCGTCGG CCTCGTCGG GAGGATACTGG CCTCCTCGG AGGAAGACTCCT CCT.CCCCG. CCG CCT.CCG.TCGG CCT.CCG.TCGG	0 110 CCGGCGGTCG.CGCC CGCC CCGCGCCGCCG.CGCC CGCC CCGCCGGCCG.CGC CCCC CCGCCGCCGCCG.CCC CCCC GACGTCCCA CCCA GACGCC.CCCCCCCCCCCCCCCCCCCCCCCC CCCA GACGTCCCA CCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
AY665914.1* AY665886.1* MH763728.1* Q371996.1 Q371997.1 Q371997.1 Q372000.1 Q372000.1 Q372002.1 Q372002.1 Q372002.1 Q372002.1	40 50 60 ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTTGAACA ACCCGCAACTGTTTGAACA ACCCGCAACCTGTTTGAACA ACCCGCAACCTGTTGAACA ACCCGCAACCCGTTTGAACA ACCCGCAACCCGTTTGAACA ACCCGCAACCCGTTTGAACA ACCCGCAAACCCGTTTGAACA ACCCGCAAACCCGTTTGAACA ACCCGGAACACCGTTTGAACA ACCCGCAAACCCGTTTGAACA ACCACGCACACCGTTTGAACA ACCCGCAAACCCGTTTGAACA ACCCGCGAAACCCGTTTGAACA	79 CCGGGAAGCGCGCGCT CCGGGGAAGCGCGCGCG CCGGGGAAGC CCGGGAAG CCGGGAAC CCGGGAAC CCGGGAAC CCGGGAAG CCGGGAAG CCGGGAAG CCGGGAAG CCGGGAAG CCGGGAAG CCGGGAAG CCGGGAAG CCGGGAAG CCGGGAAG CCGGGAAG CCGGGAAG CCGGCAAC CCGGCAAC CCGGCAAC CCGGCAAC CCGCGCAAC CCGCGCAAC CCGCGCAAC CCGCGCAAC CCGCGCAAC CCGCGCAAC CCGCCCAC CCGCCCAC CCGCCCAC CCGCCCAC CCGCCCAC CCGCCCCCCCCCC	80, 90 TGGCTCGCCT.CCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC TCGCTCGCCT.CCC TCGCTCGCTC.CCC 	10 CCTCGTCGG CCTCGTCGG CCTCGTCGG CCTCGTCGG CGGAGATACTGG CCTCGTCGG CCTCGTCGG CCTCGTCGG CCTCGTCGG CCTCGTCGG CCTCGTCGG	9 119 CCGGCGGTGG.CGCG CGCG CCGGCGCGCG.CGCG CGCGCGCG CCGCGCGCG.CGCG CCCGCG CCGTGCGCG.CACG CACGC CCGTGCGCG.CACG CCCA CCGCGCGCG.CACG CCCA CCACCAGCCG.CACG CACGC CCACCAGCCG.CACG CACGC CCACGAGCCG.CACG CACGC CCACGAGCCG.CACG CACA CCACGAGCCG.CACG CACA
AY665914.1* AY665886.1* MH763728.1* 0Q371996.1 0Q371997.1 0Q371998.1 0Q372000.1 0Q372000.1 0Q372000.1 0Q372002.1 0Q372003.1 0Q372005.1	40 50 60 ACCCGCGAACCTGTTTGAACA ACCCGCGAACCTGTTTGAACA ACCCGCAACCTGTTTGAACA ACCCGCAAACCTGTTTGAACA ACCCGCAACCTGTTTGAACA ACCCCGCAACCCGTTTGAACA ACCCGCAAACCCGTTTGAACA ACCCGCAACCCGTTTGAACA ACCCCGCAACCCGTTGAACA ACCCGCAAACCCGGTTGAACA ACCCGCAAACCCGGTTGAACA ACCCGCAAACCCGTTGAACA ACCCGCAAACCCGGTTGAACA ACCAGCACCGGTTGAACA ACCCGCAAACCCGTTTGAACA ACCCGCAAACCCGTTTGAACA ACCCGCAAACCCGTTTGAACA ACCCGCAAACCCGTTTGAACA ACCCGCAAACCCGTTTGAACA ACCCGCAACCGGTTGAACA ACCCGCAAACCCGTTTGAACA ACCCGCAAACCCGTTTGAACA ACCCGCGAACCGGCCAC ACCCGCAACCGGTTTGAACA	70 CCGGGGAGGCGCGCGT CCGGGGAGGCGCGCGT CCGGGGAGGCGCGCGT CCGGGGAGGGCGT ACGGGAACGCGT CTGCGAAGGCGT CCGGGAAGGCGT CCGGGAAGGCGT CCGGGAAGGCGT	80 90 TGGCTCGCCTCCC TCGCTCGCCTCCC TCGCTCGCCTCCC TCGCTCGCCTCCC TCGCTCGCCTCCC TCGCTCGCCTCCC ACCCAAACGCTTAC TCGCTCGCCTCCC TCGCTCGCCTCCC TCGCTCGCCTCCC TCGCTCGCCTCCC TCGCTCGCCTCCCC TCGCTCGCCTCCCC TCGCCCCGCCC	10 CCTCGTCGG CCTCGTCGG CCTCGTCGG CCTCGTCGG GAGGATACTGG CGTCGG CCTCGTCGG ACGAAAGAGTCCT GCTCGTCAG GCTCGTCAG GCTCGTCAG GCTCGTCGG ACGA.CGTCGG	0 110 CCGGCGGTCG.CGCC CGCC CCGGCGCCG.CGCC CGCC CCGCCGCCCC.CGCC CGCC CCGCCCCC.CCCC CGCC CCGCCCC.C.CCCC CCCC CCGCCCCC.CCCC CCCC CCGCCCCC.CCCCC CCCC CCACCCCC.CCCCC CACC CCACCAGCCCG.CACC CACC CCACCAGCCCG.CACC CCACC CCAGCAGCCCG.CACC CCACC CCAGCAGCCCG.CACC CCACC CCAGCAGCCCG.CACC CCACC CCAGCAGCCCG.CACC CCACC CCAGCAGCCCG.CACC CCACC
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A1003914.1*	.190909109	CCGGICGAC	1	AACGAACCCCGG	GGG	AACGCGCCAA	GGAATACTI	AACCGACG
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MH763728.1*	. TGCGCGGTCG	CCGATCGAC	T	AACTCACCCCGG	C G <mark>C G</mark> G <mark>7</mark>	AACGCGCCAA	GGAATACTG	AACCGATG
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003/1990.1	.160606106	CUIAGCGAC	1	AACGAACCCCGG	CACGA	AACGCGCCAAG	GGAAIACIC	GACCGAIG
OQ371997.1	ACACCGTTG	CGTTCCGAC		CTACGAACCCGGC	С	AACGCGCAAG	AAC <mark>ATA</mark> .	AACG
00371998.1	. G G				C A G	AACG.GCCAG	GAAATA	ACG
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00372000.1	.TGCGCGGTCG	CCTAGCGAC	T	TAATGAACCCCGG	CACGA	AACGCGCCAA	GGAATACTC	GACCGATG
00372001.1	. TGCCACAGCG	ACTIGCGTI		CCGGGCTAAG	AACCCGCAG	AACGCCCAAA	AA <mark>ACT</mark>	CAATG
00372002 1	TCCCCCTCC	CCTACCAAC	Т	AA CAACCCCCC	CACC	ARCCCCCAA	CONTACTO	CACCATC
00372002.1	.190909109	CCIAGCGAC	1	AA. GAACCCCGG	CACGAZ	ANCOCOCCAN	JGAAIACIC	GACCOALG
00372003.1	TGCGCGGTCG	CCTAGCGAC	T	AATGAACCCCGG	CACGA	AACGCGCCAA	GGAATACTC	GACCGATG
00372004.1	. TGCGCGGTCG	CCTAGCGAC	T	AACGAACCCCGG	CACGA	AACGCGCCAA	GGAATACTC	GACCGATG
00372005 1	TACCATANCA	TCCGTCGAC		тесс	CTCACTTAC	CCACACACCAC	CCA TC	CCCACCAA
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003/2006.1	.TGCGCGGTCG	CUGGTCGAC	 T	AACGAACCCCGG	CGCGG/	AACGCGCCAA	GGAATACTI	AACCGACG
00372007.1	.TGCGCGGTCG	CCTAGCGAC	T	AACGAACCCCGG	CACGA	AACGCGCCAA	GGAATACTC	GACCGATG
00372009 1	CCTCCCCCCC	CCCCTCCCT		AACAACCCCCCC	CCCC C	ACCCCCCTA	CCA TACT	AACCCACC
00572008.1	.0919909909		• • • • • • • • • • <u>•</u>	AACAACCCCCGG		ACGCGCCIA	JON. INCII	nncconoo
00372009.1	TGCGCGGTCG	CCTAGCGAC	T	AACGAACCCCGG	CACGA	AACGCGCCAA	GGAATACTC	GACCGATG
00372010.1	TTGCGCGGTCG	CCTAGCGAC	T	AATGAACCCCGG	CACGA	AACGCGCCAA	GGAATACTC	GACCGATG
00372011 1	TCCCCCCTCC	CCTACCAC	Т	AATCAACCCCCC		ACCCCCAN	CONTACTO	CACCATC
00572011.1	.1969669169		±	AAIGAACCCCGG	CAC 9 A2	ACGCGCCAR	JONNINCIC	GUCCOULO
00372012.1	TACGAGGCCG	C C		•••••				
00372013.1	.TGCGCGGTCG	CCTAGCGAC	T	AACGAACCCCGG	CACGA	AACGCGCCAA	GGAATACTC	GACCGATG
00372014 1	TCCCCCTCC	CCTACCAS	тт	AACCAACCCCCC		ACCCCCCAN	CONTACTO	CACCATC
00572014.1	.190909109	CCIAGCGAC	<u>+</u>	ANCOANCCCCGG		ACGCGCCAR	GGARIACIC	GACCOAIG
00372015.1	.receceeTCG	CCTAGCGAC	T	AACGAACCCCGG	CACGA	AACGCGCCAA	GGAATACTC	GACCGATG
OQ372016.1	. TGTCCCGTCG	CCAGTACAA	T	CCCCAACCCCGG	AG <mark>CG</mark> G <mark>2</mark>	ACCTCGCCAA	CTAATACT	TGGGACTG
00372017 1	Tececeter	CCTACCAR	т	AACGAACCCCCC	CACC	AACGCGCCAA	GGAATACTC	GACCGATC
00372010 1						N C C C C C C C C C C C C C C C C C C C		Ch C C C A T T
003/2018.1	Tececette	CUTAGCGAC	T	AACGAACCCCGG	CACGA/	AACGCGCCAAG	GGAATACTC	GACCGAIT
OQ372019.1	. TGCGCGGTCG	CCTAGCGAC	T	AACGAACCCCGG	CACGA	AACGCGCCAA	GGAATACTC	GACCGATG
00372020 1	CCCCCCTCCCC	GTGCCTGCCAC		TACCAACCC C		AACG GCCAA	с атастс	ACCGACT
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003/2021.1	.IGCGCGGTCG	CUTAGCGAC	• • • • • • • • • T	AACGAACCCCGG	САСБА/	AACGCGCCAA	GGAATACTC	GACCGAIG
OQ372022.1	. TGCGCGGTCG	CCTAGCGAC	<i>.</i> T	AACGAACCCCGG	CACGA	AACGCGCCAA	GGAATACT <mark>C</mark>	GACCGATG
00372023 1	TGCCGTGACG	TCCGTCGAC	GCGGGGCTCGC	ATTTAGGCCAGC	CGCGCGCTGC	CGAGCGCACG	GGAG	GCCA
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00372024.1	.1969666666	CUIAGCGAC	1	AAIGAACCCCGG	CACGA/	AACGUGUUAA	GGAAIACIC	GACCGAIG
OQ372025.1	. TGCGCGGTCG	CCTAGCGAC	. T	AACGAACCCCGG	CACGA/	AACGCGCCAA	GGAATACT <mark></mark> C	GACCGATG
00372026.1	TGCCGTGACG	TCCGTCGAC	ATGGGCTCAC	ATTTAGGCCAAC	CACCAGCCT	ATGGCCCAAC	GGAA	AGGCA
00272027 1	TCCCCTCACC	TCCCTCCAC	ATCCCCTCAC	ATTTACCCAAC	CACCACCCC	TCCCCCACC	C A A C	CCCA
00072027.1	. IGCCOIGACG		VIGGGCICVC	ATTINGGCCARC.		AIGGCGCACG		
003/2028.1	.TGCGCGGTCG	CUTAGCGAC	 T	AATGAACCCCGG	CACGA/	AACGCGCCAA	GGAATACTC	GACCGAIG
OQ372029.1	. TGCCGTGACG	TCCGTCGAC	ATGGGCTCAC	CATTTAGGCCAAC	CACGAGCCG	ATGGCGCACG	GAAG	GCCT
	180 1	90 20	0 2	210 22	0 2:	30 24	4 0	250
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AY665914.1* AY665886.1*	180 1 GCCCGCCCCT GCCTGGCCCTC	90 20 GCGCCCCGTC GCGCCCCGTC	0 2 GCGGCGC.GC GCGGCGC.GC	210 22 CGCG.GGGGAGCT	0 2: GCGCCTCGC GTGCTTCGC	30, 24 FTGAAACACG FTGAAACACG	4 9 A A C G A A C G	250 ACTCTCGG ACTCTCGG
AY665914.1* AY665886.1* MH763728.1*	180 1 GCCCGCCCCTC GCCTGGCCCTC	90 20 GCGCCCCGTCC GCGCCCCGTCC GCGCCCCGTCC	Q 2 GCGGCGC.GC GCGGCGC.GC	210 22 GCCG.GGGGAGCTC GCCG.GGGGACCTC	0 2: GCGCCTCGCC GTGCTTCGCC	30, 2 ITGAAACACG ITGAAACACG ITGAAACACG	4 0 AACG AACG	250 ACTCTCGG ACTCTCGG
A¥665914.1* A¥665886.1* MH763728.1*	180 1 GCCCGCCCCTC GCCTGGCCCTC GCCTGGCCCTC	90 20 GCGCCCCGTCC GCGCCCCGTCC GCGCCCCGTCC	Q GCGCCGC GC GCGGCCGC GC GCGGCCGC GC GCGGCCGC GC	210 22 CGCG.GGGGAGCT CGCG.GGGGACCT CGCG.GGGGACCT	• 2: GCGCCTCGC: GTGCTTCGC: GTGCTTCGC:	30 2 , ITGAAACACG ITGAAACACG ITGAAACACG	4 0 A A C G A A C G A A C G	250 ACTCTCGG ACTCTCGG ACTCTCGG
AY665914.1* AY665886.1* MH763728.1* MH763740.1*	180 1 GCCCGCCCTC GCCTGGCCCTC GCCTGGCCCTC GTCTGGTCCTG	90 20 GCGCCCCGTCC GCGCCCCCGTCC GCGCCCCCGTCC GCGCCCCGTCC GCGCCCCATCC	0 2 CCGCCGC .GC GCGGCCGC .GC GCGGCCGC .GC GCGGCCGC .GC	210 22 GCCG.GGGGAGCT GCCG.GGGGACCT GCCG.GGGGACCT GCCG.GGGGACCT	9 2: GCGCCTCGC: GTGCTTCGC: GTGCTTCGC: GCGCTTCAC:	30, 2 ITGAAACACG ITGAAACACG ITGAAACACG	4 0 AACG AACG AACG AACG	250 ACTCTCGG ACTCTCGG ACTCTCGG ACTCTCGG
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AY665914.1* AY665886.1* MH763728.1* MH763740.1* OQ371997.1 OQ371997.1 OQ371999.1 OQ37299.1 OQ372000.1	180 1 GCCCGCCCTC GCCTGGCCTC GCTGGCCTC GCACACCCCT AGGCCACCCTC A.GCCCCCCCTC CACCCCCC	90 20 GCGCCCCCTCC GCGCCCCTCC GCGCCCCTCC GCGCCTCCCCCC GCACCC GCGCCTCTCC GCGCCTCTCCC GCGCCTCTCC	0 2 GC GG CG C GC	210 22 GGG.GGGGAGCT GGG.GGGGACCT GGG.GGGGACCT GGG.GGGGACCT GGGCGGGGGCT GGGGCCT 	9 2: GCGCCTCGC GTGCTTCGC GCGCTTCAC GCGCTTCAC GTCACTG. GT.CTTCGC GT.CTTCGC GTCCTCGC	30 2 TTGAAACACG TTGAAACACG TTGAAACACG TTGAAACACA AACACG TTGA.ACACA TGAACACAAA	40 AACG AACG AATG AATG A.TG G AATG	250 ACTCTCGG ACTCTCGG ACTCTCGG ACTCTCGG GCTCTCGG ACTCTCGG ACTCTCGG ACTCTCGG
AY665914.1* AY665886.1* MH763728.1* MH763740.1* OQ371996.1 OQ371997.1 OQ371998.1 OQ371999.1 OQ372000.1 OQ372001.1	180 1 GCCCGGCCCTC GCCTGGCCCTC GTCTGGTCCTC GCCTGGCCCCTC AGGCCACCCCTC AGGCCGCCCTC CACCCCCC GCACACCCCTC ATGCCCCC	90 20 GCGCCCCCTCC GCGCCCCCTCC GCGCCCCATCC GCGCCCCATCC GCGCCTCCTCC GCGCCTCCTCC GCGCCTCTCC GCGCCTCCTCC GCGCCTCCTCC	0 2 GC GG CG C GC GC GG CG C GC AC GG CG C GC CG GG CG CG GG CG CG CG CG CG CG CG CG CG CG CG CG CG CG CG CG CG br>CG CG CG CG CG CG CG CG CG CG CG CG CG CG CG CG CG CG CG CG CG CG	210 22 GCCG. GGGGAGCTI GCCG. GGGGACCTI GCCG. GGGGACCTI GCCG. GGGGACCTI GCCG. GGGGACCTI GCCG. GGGGACCTI GCCG. GGGGACCTI GCCG. GGGGCCTIA GCGG. GGGGCCTIA GGGGCCTIA GGGGCCTIA GGGGCCTIA GGGGCCTIA GCGG. GGGCCTIA GCGGCCTIA GGGCCTIA GGGCGCTIA GGGCCTIA GCGGCCTIA GGGCCTIA GCGCA GGGCCTIA GCGCA <td< th=""><th>Q 22 GCGCCTCGC GTGCTTCGC GCGCTTCACT GTGATTCGC GTTCACTG. .TGGTTCGC GTCCTTCGC GTCCTTCGC GTCCTTCGC</th><th>30 2 ITGAAACACG ITGAAACACG ITGAAACACCG ITGAAACACA AACACA ITGAACACAAA ITGAACACAAA ITGAACACAAA</th><th>4 Q AACG AACG AATG AATG G AATG A A</th><th>250 ACTCTCGG ACTCTCGG ACTCTCGG ACTCTCGG ACTCTCGG GCTCTCCG ACTCTCGG ACTCTCGG</th></td<>	Q 22 GCGCCTCGC GTGCTTCGC GCGCTTCACT GTGATTCGC GTTCACTG. .TGGTTCGC GTCCTTCGC GTCCTTCGC GTCCTTCGC	30 2 ITGAAACACG ITGAAACACG ITGAAACACCG ITGAAACACA AACACA ITGAACACAAA ITGAACACAAA ITGAACACAAA	4 Q AACG AACG AATG AATG G AATG A A	250 ACTCTCGG ACTCTCGG ACTCTCGG ACTCTCGG ACTCTCGG GCTCTCCG ACTCTCGG ACTCTCGG
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	260	270	280	290	300	310	320	ззо
AY665914.1*	CAACGGATAT	CICGGCICIC	GCATCGATGAA GCATCGATGAA	GAACGTAGCGAAA	TGCGATACTTG	GTGTGAATTO	CAGAATCCCGTG	AAC AAC
MH763728.1*	CAACGGATAT	CICGGCICIC	GCATCGATGAA	GAACGTAGCGAAA	TGCGATACTTG	GIGIGAATIC	CAGAATCCCGTG	AAC
OQ371996.1	CAACGGATAT	CICGGCICIC	GCATCGATGAA	.GAACGTAGCGAAA .GAACGTAGCGAAA	TGCGATACTIG	GIGIGAAIIC	CAGAAICCCGIG	AAC
0Q371997.1 00371998.1	CGAGGGATAT CAA.GGAT.T	CICGGCII	.CGCTCGAG <mark>AA</mark> GCA.CGAGA	GAACGTAGCGAAA	TGCGATACTT.	GIGIGAA.IC GIGIGAA.IC	CAGA. TCCCGTG	AC AC
00371999.1	CAAGGATT	CTCGGCTCTC	GCATCGAGA	AGACG.AGCGAAA	T.CGATACTTG	GTG. GAATO	CAGA. TCCCGTG	AC
00372001.1	CAT GGATAT	CICGGCICIC CICGGCI.IC	GCA.CGATGAA	.GAACGIAGCGAAA .GAACGIAGCGA.A	TGCGATACTIG	GIGIGAAIIC GIGIGAA.TO	CAGA. TCCCGIG	.AC
OQ372002.1 OO372003.1	CAACGGATAT CAACGGATAT	CTCGGCTCTC CTCGGCTCTC	GCATCGATGAA GCATCGATGAA	.GAACGTAGCGAAA .GAACGTAGCGAAA	TGCGATACTTG	G T G T G A A T T C G T G T G A A T T C	CAGAATCCCGTG CAGAATCCCGTG	A A C A A C
00372004.1	CAACGGATAT	CICGGCICIC	GCATCGATGAA	GAACGTAGCGAAA	TGCGATACTTG	GTGTGAATTO	CAGAATCCCGTG	AAC
00372006.1	CAACGGATAT	CTCGGCTCTC	GCATCGATGAA	GAACGTAGCIGCI	TGCGATACTTG	GTGTGAATTC	CAGAATCCCGTG	AAC
OQ372007.1 OQ372008.1	CAACGGATAT CACGGTT	CTCGGCICTC CTCGGCICTC	GCATCGATGAA GC.TCGATGAA	.GAACGTAGCGAAA . AACGTATCGAA	TGCGATACTTG TGTG.TACTG.	GIGIGAAIIC GIGGAIIC	CAGAATCCCGTG	AAC .GA
00372009.1	CAACGGATAT	CICGGCICIC	GCATCGAT <mark>G</mark> AA	GAACGTAGCGAAA	TGCGATACTTG	GTGTGAATTC	CAGAATCCCGTG	AAC
00372011.1	CAACGGATAT	CTCGGCTCTC	GCATCGATGAA	GAACGTAGCGAAA	TGCGATACTTG	GTGTGAATTC	CAGAATCCCGTG	AAC
OQ372012.1 OQ372013.1	CAACGGATAT	. TGGAATCTC CTCGGCTCTC	GCCTCGCTCGA GCATCGATGAA	.GAGAAGAAAGAAA .GAACGTAGCGAAA	ACGAACTTGG .TGCGATACTTG	GTGATO GTGTGAATTO	CAGATCCCTGAC CAGAATCCCGTG	CAC AAC
00372014.1	CAACGGATAT	CICGGCICIC	GCATCGAT <mark>G</mark> AA ACATCGATTTT	GAACGTAGCGAAA	TGCGATACTTG	GTGTGAATTG	CAGAATCCCGTG	AAC
00372016.1	· · · · · · · · · · · · · · · · · · ·				TGAAATGATTT			
OQ372017.1 OQ372018.1	CAACGGATAT	CICGGCICIC	GCATCGATGAA	GAACGTAGCGAAA	TGCGATACTTG	GTGTGAATTO	CAGAATCCCGTG	AAC
00372019.1	CAACGGATAT	CTCGGCICTC	GCATCGATGAA	.GAACGTAGCGAAA	TGCGATACTTG	GTGTGAATTC	CAGAATCCCGTG	AAC
00372021.1	CAACGGATAT	CTCGGCTCTC	GCATCGATGAA	GAACGTAGCGAAA	TGCGATACTTG	GTGTGAATTO	CAGAATCCCGTG	AAC
0Q372022.1 0Q372023.1	CCTAATGGCT	TCGGGCGCAA	GCATCGATGAA CTIGCGTTCAA	.GAACGTAGCGAAA .AG <mark>AC</mark> TCGAT <mark>G</mark> GTT	CACGGGATACTTG	G T G T G A A T T C G C A A T T C A C A	CCAGAATCCCGTG CCAAGTATCGCA	A A C T T T
00372024.1	CAACGGATAT	CICGGCICIC	GCATCGAT <mark>G</mark> AA GCATCGATGAA	GAACGTAGCGAAA	TGCGATACTTG	GIGIGAAIIC GIGIGAAIIC	CAGAATCCCGTG	AAC
00372026.1	CCCTATGGCT	TCGGGGACAA	CTIGCCTICCA	AGACTCCAAGGTT	TACGGGATTCT	GCAATTCACA	CCAAGTATCGCA	ΤΤΤ
0Q372027.1 0Q372028.1	CAACGGATAT	CTCGGCTCTC	GCATCGAT <mark>G</mark> AA	.GAACGTAGCGAAA	TGCGATACTTG	GTGTG <mark>AATT</mark> CACF	CAGAAGTATCGCA CAGAATCCCGTG	A A C
00372029.1	<u>CCT</u> AATGGCT	TCGGGCACAA	CTIGCGTTCAA	AGACTCGATGGTT	CACGGGATTCT	GCAATTCACA	CCAAGTATCGCA	ΤΤΤ
	340	350	360	370	380	390 a armanda	400	
AY665914.1* AY665886.1*	340 CATCGAGTCT CATCGAGTCT	350 TTGAACGCAA TTGAACGCAA	360 GTIGCGCCCGA GTIGCGCCCGA	370 AGCCATTAGGCCG AGCCATTAGGCCG	380 AGGGCACGTCT AGGGCACGTCT	390 G.CCTGGGCG G.CCTGGGCG	400 TCACGCA . TCGC TCACGCA . TCGC	G T <mark>C</mark> G T <mark>C</mark>
AY665914.1* AY665886.1* MH763728.1* MH763740.1*	340 CATCGAGTCT CATCGAGTCT CATCGAGTCT CATCGAGTCT	350 TTGAACGCAA TTGAACGCAA TTGAACGCAA TTGAATGCAA	360 GTIGCGCCCGA GTIGCGCCCGA GTIGCGCCCGA GTIGTGCCCGA	370 AGCCATTAGGCCG AGCCATTAGGCCG AGCCATTAGGCC AGCCATTAGGCC	380 AGGGCACGTCT AGGCACGTCT AGGCACGTCT AGGCACGTCT	390 G.CCTGGGCC G.CCTGGGCC G.CCTGGGCC G.CCTGGGCC	400 TCACGCA.TCGC TCACGCA.TCGC TCACGCA.TCGC	GTC GTC GTC
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OQ372028.1	GCCCCCC	TCGCCC	TGCACC	GC	GGCG	GCGT	TGC	GGGZ	ACO	GGTF	ATAC	TGG	ССТЗ	CC C	GTG	CGC	CAT	CGG	ст.	CGTG
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AY665914.1* AY665886.1* MH763728.1* MH763740.1* OQ371996.1 OQ371999.1 OQ371999.1	480 GCTGGCC GCTGGCC GCTGGCC GTTGGCC GCTGGCC GCTGGCC GTTGGCC	49 CT . AAAT CT . AAAT CT . AAAT CT . AAAT CT . AAAT CT . AAAT CT . AAAT	GCGAG GCGAG GTGAG GTGAG GTGAG GCGAG GTGAG GTGAG	500 CCCGCGT CCCACGT CCCACGT CCCATGT CCCACGT CCCACGT .CCCACGT	CGAC CGAC CGAC CGAC CGAC CGAC CGAC	60000000000000000000000000000000000000	510 ACG ACG ACG ACG ACG ACG ACG ACG	. TC7 . TC7 . TC7 . TC7 . TC7 . TC7 . TC7 . TC7	a a a			52 CAA CAA CAA CAA CAA CAA CAA CAA	GTG GTG GTG GTG GTG GTG GTG GTG	TG TG TG TG TG TG TG TG	G TT G TT G TT G TT G TT G TT G TT G TT	5	3 0 GAA GAA GAA GAA GAA GAA GAA		CAA CAA CAA CAA CAA CAA CAA	540. TTTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
AY665914.1* AY665886.1* MH763728.1* OQ371996.1 OQ371998.1 OQ371998.1 OQ371999.1 OQ372000.1	480 GCTGGCC GCTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC	49 2T. AAAT 2T. AAAT 2T. AAAT 2T. AAAT 2T. AAAT 2T. AAAT 2T. AAAT 2T. AAAT 2T. AAAT	GCGAG GCGAG GCGAG GTGAG GTGAG GCGAG GCGAG GTGAG GTGAG	500 CCCACGTC CCCACGTC CCCACGTC CCCATGTC CCCATGTC CCCACGTC CCCACGTC .CCCAGTC .CCCAGTC	CGAC CGAC CGAC CGAC CGAC CGAC CGAC CGAC		510 ACG ACG ACG ACG ACG ACG ACG ACG ACG	. TC2 TC2 TC2 TC2 TC2 TC2 TC2 TC2 TC2 TC2	A			CAA CAA CAA CAA CAA CAA CAA CAA CAA	GTG GTG GTG GTG GTG GTG GTG GTG GTG		G G G G G G G G G G G G G G G G G G G	5	3 0 GAA GAA GAA GAA GAA GAA GAA GAA		CAA CAA CAA CAA CAA CAA CAA	540. CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
AY665914.1* AY665886.1* MH763728.1* MH763740.1* Q371996.1 Q371999.1 Q371999.1 Q371999.1 Q372000.1 O372001.1	480 GCTGGCC GCTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC	49 CT . AAAT CT . AAAT	GCGAG GCGAG GTGAG GTGAG GTGAG GCGAG GTGAG GTGAG GTGAG GTGAG	500 CCCGCGT CCCACGT CCCACGT CCCATGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT	CGAC CGAC CGAC CGAC CGAC CGAC CGAC CGAC		510 ACG ACG ACG ACG ACG ACG ACG ACG	. TCP . TCP . TCP . TCP . TCP . TCP . TCP . TCP . TCP				52 CAA CAA CAA CAA CAA CAA CAA CAA	9 3 3 3 3 5 5 5 5 5 5 5 5		G G G G G G G G G G G G G G G G G G G	5	39 GAA GAA GAA GAA GAA GAA GAA GAA		CAA CAA CAA CAA CAA CAA CAA	540. CONTRACTOR
AY665914.1* AY665886.1* MH763728.1* OQ371996.1 OQ371997.1 OQ371999.1 OQ372000.1 OQ372000.1 OQ372000.2	480 GCTGGCC GCTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC	49 T. AAAT T. AAAT T. AAAT T. AAAT T. AAAT T. AAAT T. AAAT T. AAAT	GCGAG GCGAG GCGAG GTGAG GTGAG GCGAG GCGAG GTGAG GTGAG GTGAG GTGAG GTGAG	500 CCCACGTG CCCACGTG CCCACGTG CCCATGTG CCCACGTG CCCACGTG CCCACGTG CCCACGTG CCCACGTG CCCACGTG	CGAC CGAC CGAC CGAC CGAC CGAC CGAC		510 ACG ACG ACG ACG ACG ACG ACG ACG ACG	. TCP . TCP . TCP . TCP . TCP . TCP . TCP . TCP . TCP . TCP				52 CAA CAA CAA CAA CAA CAA CAA CAA CAA CA	9 3 3 3 3 3 3 4 5 5 5 5 5 5 5 5		G TT G TT G G TT G G TT G G G TT G G G G	5	30 GAA GAA GAA GAA GAA GAA GAA CAA		CAA CAA CAA CAA CAA CAA CAA	540. CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
AY665914.1* AY665886.1* MH763728.1* MH763740.1* QQ371996.1 QQ371998.1 QQ371999.1 QQ372000.1 QQ372000.1 QQ372000.1 QQ372000.1 QQ372000.1	480 GCTGGCC GCTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC	49 T. AAAT T. AAAT T. AAAT T. AAAT T. AAAT T. AAAT T. AAAT T. AAAT T. AAAT T. AAAT	CCCAG GCCAG GCCAG GTCAG GTCAG GCCAG GCCAG GCCAG GCCAG GCCAG GCCAG GCCAG GCCAG GCCAG GCCAG GCCAG GCCAG	500 CCCCCCCCC CCCACGT CCCACGT CCCATGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT	CGAC CGAC CGAC CGAC CGAC CGAC CGAC CGAC		510 ACG ACG ACG ACG ACG ACG ACG ACG ACG	. TC7 TC7 TC7 TC7 TC7 TC7 TC7 TC7 TC7				52 CAA CAA CAA CAA CAA CAA CAA CAA CAA CA	C G T G G G G G G G G G G G G G G G G G	T G G G G G G G G G G G G G G G G G G G	G T T T T T T T T T T T T T T T T T T T	5 TGG	30 GAA GAA GAA GAA GAA GAA GAA GAA		CAA CAA CAA CAA CAA CAA CAA	540. 00000000000000000000000000000000000
AY665914.1* AY665886.1* MH763728.1* MH763740.1* OQ371996.1 OQ371999.1 OQ371999.1 OQ37200.1 OQ372000.1 OQ372002.1 OQ372002.1	480 GCTGGCC GCTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC	49 CT. AAAT CT. AAAT CT. AAAT CT. AAAT CT. AAAT CT. AAAT CT. AAAT CT. AAAT CT. AAAT CT. AAAT	C CCCAC CCCAC GCCAC GTCAC GCCAC GCCAC GTCAC GTCAC GTCAC GTCAC GTCAC GTCAC GTCAC	500 CCCCCCT CCCACCT CCCACCT CCCACCT CCCACCT CCCACCT CCCACCT CCCACCT CCCACCT CCCATCT CCCATCT CCCATCT CCCATCT	CGAC CGAC CGAC CGAC CGAC CGAC CGAC CGAC		510 ACCGGACCGGACCGGACCGGACCGGACCGGACCGGACC	. TC7 TC7 TC7 TC7 TC7 TC7 TC7 TC7 TC7 TC7				52 CAA CAA CAA CAA CAA CAA CAA CAA CAA CA	••••••••••••••••••••••••••••••••••••••			5 	GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA		CAA CAA CAA CAA CAA CAA CAA CAA	540. 00000000000000000000000000000000000
AY665914.1* AY665886.1* MH763740.1* Q371996.1 Q371997.1 Q371999.1 Q372001.1 Q372001.1 Q372001.1 Q372003.1 Q372003.1 Q372004.1 Q372005.1	480. GCTGGCC GCTGGCC GCTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC	49 T. AAAT T. AAAT T. AAAT T. AAAT T. AAAT T. AAAT T. AAAT T. AAAAT T. AAAA T. AAAT T. AAAT	Ç CCAC. CCAC. CCAC. CTCAC. CTCAC. CTCAC. CCCAC. CCCAC. CTCAC. CTCAC. CTCAC. CTCAC. CTCAC. CTCAC. CTCAC. CTCAC.	500 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CGAC CGAC CGAC CGAC CGAC CGAC CGAC CGAC		510 ACCG ACCG ACCG ACCG ACCG ACCG ACCG ACC	. TCP TCP TCP TCP TCP TCP TCP TCP TCP TCP				52 CAA CAA CAA CAA CAA CAA CAA CAA CAA CA	9 G T G G G G T G G G G G G G G G G G G G G G G G G G	GTG: GTG: GTG: GTG: GTG: GTG: GTG: GTG:	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	5 TGG	3 GAA GAAA GAAA GAAA GAA GAA GAA		CAA CAA CAA CAA CAA CAA CAA CAA CAA CAA	540.00000000000000000000000000000000000
AY665914.1* AY665886.1* MH763728.1* MH763740.1* OQ371996.1 OQ371999.1 OQ37200.1 OQ372000.1 OQ372000.1 OQ372002.1 OQ372002.1 OQ372003.1 OQ372003.1 OQ372003.1	480 GCTGGCC GCTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC	49 CT. AAAT CT. AAAT CT. AAAT CT. AAAT CT. AAAT CT. AAAT CT. AAAT CT. AAAT CT. AAAT CT. AAAT	CCGAG. CCGAG. CCGAG. CCGAG. CCGAG. CCGAG. CCGAG. CTGAG. CTGAG. CTGAG. CCGAG. CCGAG. CTGAG. CCGAG. CCGAG. CCGAG. CCGAG.	500 CCCGCGT CCCACGT CCCACGT CCCATGT CCCATGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCATGT CCCATGT CCCATGT CCCATGT	CGAC CGAC CGAC CGAC CGAC CGAC CGAC CGAC		510 ACCG ACCG ACCG ACCG ACCG ACCG ACCG ACC	. TCP . TCP				52 CAA CAA CAA CAA CAA CAA CAA CAA CAA CA		5 T G G 5 T G 5	GTT GTT GTT GTT GTT GTT GTT GTT GTT GTT	5 	3 0 GAAA GAAA GAAA GAAA GAAA GAAA GAAA GA		CAA CAA CAA CAA CAA CAA CAA CAA CAA CAA	540.00000000000000000000000000000000000
AY665914.1* AY665886.1* MH763740.1* OQ371997.1 OQ371998.1 OQ371999.1 OQ372001.1 OQ372001.1 OQ372001.1 OQ372003.1 OQ372003.1 OQ372005.1 OQ372006.1	480 G CTGGCC G CTGGCC G CTGGCC G TTGGCC G TTGCC G TTGCCC G TTGCCCC G TTGCCCC G TTGCCCCC G TTGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	49 T. AAAT T. AAAT	9 C CCAC. C TCAC. C CCAC. C CCCAC. C CCCAC. C CCCAC. C CCCAC. C CCCAC. C CCCCCCCCC. C CCCCCCCCCC. C CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	500 CCCGCGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT	CGAC CGAC CGAC CGAC CGAC CGAC CGAC CGAC		510 ACCG ACCG ACCG ACCG ACCG ACCG ACCG ACC	. TC2 TC2 TC2 TC2 TC2 TC2 TC2 TC2 TC2 TC2			· · · · · · · · · · · · · · · · · · ·	52 CAA CAA CAA CAA CAA CAA CAA CAA CAA CA	9 37 37 37 37 37 37 37 37 37 37	5 T G (5 T G	GITT GITT GITT GITT GITT GITT GITT GITT	5 	3 QAAA GAAA GAAA GAAA GAAA GAAA GAAA GAA		CAA CAA CAA CAA CAA CAA CAA CAA CAA CAA	54.0.0000000000000000000000000000000000
AY665914.1* AY665886.1* MH763728.1* OQ371996.1 OQ371997.1 OQ371999.1 OQ372000.1 OQ372000.1 OQ372002.1 OQ372002.1 OQ372002.1 OQ372004.1 OQ372005.1 OQ372007.1	480 GCTGGCC GCTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC	49 T. AAAT T. AAAT	C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C	500 CCCGCGT CCCACGT CCCACGT CCCATGT CCCATGT CCCACGT CCCACGT CCCACGT CCCACGT CCCATGT CCCATGT CCCATGT CCCATGT CCCATGT CCCATGT	CGAC CGAC CGAC CGAC CGAC CGAC CGAC CGAC		519 ACG ACG ACG ACG ACG ACG ACG ACG ACG ACG	- TC7 - TC7				52 CAA CAA CAA CAA CAA CAA CAA CAA CAA CA	9 3 3 5 6 3 3 5 7 6 3 5 7 6		GTTT GTTT GTTT GTTT GTTT GTTT GTT GTT G	5 	3 9 GAAA GGAAA GGAA GGAA GAAA GAAA GAAA G		CAA CAA CAA CAA CAA CAA CAA CAA CAA CAA	540. CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
AY665914.1* AY665886.1* MH763728.1* MH763740.1* OQ371996.1 OQ371999.1 OQ372000.1 OQ372001.1 OQ372001.1 OQ372001.1 OQ372003.1 OQ372004.1 OQ372005.1 OQ372006.1 OQ372008.1	480 GCTGGCC GCTGGCC GCTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC	49 CT. AAAT T. AAAT	9 CCGAG. GCGAG. GCGAG.<	500 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CGAC CGAC CGAC CGAC CGAC CGAC CGAC CGAC		510 ACG ACG ACG ACG ACG ACG ACG ACG ACG ACG	. TCP . TCP				52 CAA CAA CAA CAA CAA CAA CAA CAA CAA CA	9 3 3 3 3 5 5 5 5 5 5 5 5		GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITT GITTT GITTT GITT GITT GITT GITT GIT	5	30 GAAAG GAAAG GAAAG GAAAG GAAAG GAAAG GAAAG GAAAG GAAC TAAG		CAA CAAACCAAA CAAACCAAA CCAAACCAAA CCAAACCCAA CCAAACCCAA CCAAACCCAA CCAAACCCAA CCAAACCCAAACCCAA	540. 0.000000000000000000000000000000000
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AY665914.1* AY665886.1* MH763728.1* MH763740.1* OQ371996.1 OQ371999.1 OQ372000.1 OQ372001.1 OQ372001.1 OQ372002.1 OQ372003.1 OQ372005.1 OQ372006.1 OQ372006.1 OQ372008.1 OQ372009.1 OQ372001.0	480 GCTGGCC GCTGGCC GCTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC GTTGGCC	49 CT . AAAT T . AAAT 	• • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • • •	500 CCCGCGCGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCATGT CCCATGT CCCATGT CCCATGT CCCATGT CCCATGT CCCATGT	CGAC CGAC CGAC CGAC CGAC CGAC CGAC CGAC		510 ACG ACG ACG ACG ACG ACG ACG ACG ACG ACG	- TCP - TCP	A			52 CAA CAA CAA CAA CAA CAA CAA CAA CAA CA	7 3 3 3 3 3 3 3 3		GTTT GTTT GTTTT GTTTT GTTTT GTTTT GTTT GTTT GTTT GTTT GTTT GTTT GTTT	5	30 GAAAAG GAAAAG GAAAAG GAAAA GAAAAG GAACA GAACA GAACA GAACA		CAA CAAA CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC CAAAC	540.00000000000000000000000000000000000
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TC / TC /				52 CAAA CAAA CAAA CAAA CAAA CAAA CAAA CA		GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GITTTTTTT GITTTTTTT GITTTTTTT GITTTTTT GITTTTTT GITTTTT GITTTT GITTTT GITTTT GITTTT GITTTT GITTTT GITTTT GITTTT GITTTT GITTTT GITTTT GITTTT GITTTTT GITTTTT GITTTTT GITTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTT GITTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTT GITTTTTTTT	5	3 GAAAAAAAGAAAAGAAAAAAAAAAAAAAAAAAAAAAA	нинининининининининининининининининини	CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	540. CHTHHHCUTHHHCUTHHHCUTHHCUTHU CECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
AY665914.1* AY665886.1* MH763728.1* MH763728.1* Q371996.1 Q371997.1 Q371999.1 Q372000.1 Q372000.1 Q372001.1 Q372002.1 Q372003.1 Q372005.1 Q372005.1 Q372005.1 Q372005.1 Q372007.1 Q372010.1 Q372010.1 Q372010.1 Q372011.1 Q372012.1 Q372012.1 Q372015.1 Q372015.1 Q372015.1 Q372015.1 Q372015.1 Q372015.1 Q372015.1 Q372015.1 Q372015.1 Q372015.1 Q372021.1 Q372021.1 Q372021.1 Q372022.1 Q372022.1 Q372022.1 Q372022.1 Q372022.1 Q372022.1 Q372022.1 Q372022.1 Q372025.1 Q372025.1 Q372026.1 Q372027.1		49 21. AAAT 21. AAAT 21	C C G C G C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C	500 CCCCCCT CCCCCCT CCCCCCT CCCCCCT CCCCCCC	CGAC CGAC CGAC CGAC CGAC CGAC CGAC CGAC		510 ACCG ACCG ACCG ACCG ACCG ACCG ACCG ACC	- TC 7 - TC 7				52 CAA CAA CAAA CAAA CAAA CAAA CAAA CAAA			GITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	5	3 GAAAAAAAAGAAAGAAAGAAA. GGAAAAAAAGAAAGGAACA. GGAAAAAAGAAAGGAAA. GGAAAAAGAAAGGAAA. GGAACAA. GGAACAA. GGAACAA. GGAACAA. GGAACAA. GGAACAA. GGAACAA. GGAACAA. GGAACAA. GGAACAA. GGAACAA. GGAACAA. GGAACAA. GGAACAA. GGAACAA. GGAACAA. GGAACAA. GGAACAAAAAAAAGAA. GGAACAAAAAAAAAGAA. GGAACAAAAAAAAAGAA. GGAACAAAAAAAAAA	НОС НООННИИ СТОРИИ НИКИ СТОРИИ СТОРИИ СТОРИИ СТОРИИ ССССССССССССССССССССССССССССССССССС	CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	540 HUTCHTHTHTT
AY665914.1* MH763728.1* MH763740.1* 0Q371997.1 0Q371999.1 0Q372000.1 0Q372001.1 0Q372001.1 0Q372001.1 0Q372003.1 0Q372005.1 0Q372006.1 0Q372005.1 0Q372006.1 0Q372007.1 0Q372010.1 0Q372010.1 0Q372011.1 0Q372012.1 0Q372013.1 0Q372015.1 0Q372015.1 0Q372015.1 0Q372015.1 0Q372015.1 0Q372015.1 0Q372015.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q37202.1 0Q3720.2 0 0 0 0 0 0 0 0 0 0 0 0 0		49 T. AAAT T. AAAT	C C C G C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C C	500 CCCGCGCGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCATGT CCCATGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCACGT CCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCATGT CCCCCCCCCC	CGAC CGAC CGAC CGAC CGAC CGAC CGAC CGAC		5 1 C G ACCG ACCG ACCG ACCG ACCG ACCG ACCG	- TC 7 - TC 7				52 CAAA CAAA CAAA CAAA CAAA CAAA CAAA CA		GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	5	3 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	нничничничничничничничничничничничничнич	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	540. CHANNERCHENNENNENNENNENNENNENNENNENNENNENNENNENN

	550	560	570 58	0 590	600
AY665914.1*	CGT.GGTGCCG.	. TGGCCGAACCCGTCG.		ACAGACCCTTCCG.	.GCGCTTAGGCGCTCC
AY665886.1*	CTT.GGTGCCG.	. TGGCCGAACCCGTCG.	CCCGTGTC.GGCTG	CGAGACCCTTCCG.	.GCGCTTAGGCGCTCC
MH763728.1*	CTT.GGTGCCG.	.TGGCCGAACCCGTCG.	CCCGTGTC.GGCTG	CGAGACCCTTCCG.	.GCGCTTAGGCGCTCC
MH763740.1*	TGT.GGTGCCG.	. TGGCCGAACCCGTGG.	.CCCGTGTC.GGCTG	ACAGAACCTTCCG.	.GCGCTTAGGCGCTTC
00371996.1	TGT.GGTGCCG.	. IGGCCGAACCCGIGG.		ACAGAACCITCCCG	.GCGCTTAGGCGCTTC
00371997.1	CTT.GGTGC		••••••		
00371999 1	TGT CGTCCCGT	с			
00372000.1	TGT.GGTGCCG.	TGGCCGAACCCGTGG		ACAGAACCTTCCG.	.GCGCTTAGGCGCTTC
00372001.1	CTT.GGTGCCG.	. TGG			
00372002.1	TGTGGGTGCCGG	TGGGCCGAACCCGTGG	CCCGGTGTC.GGCTG	GAACATAAACCTTTCCG	GGCGCTTTAGGGCGGCTTC
OQ372003.1	TGT.GGTGCCG.	. TGGCCGAACCCGTGG.	.CCCGTGTC.GGCTG	ACAGAACCTTCCGG	CGCTTAGCGCTTC
00372004.1	TGT.GGTGCCG.	. TGGCCGAACCCGTGG.	.CCCGTGTC.GGCTG	ACAGAACCTTTCCG	.GCGCTTAGGCGCTTC
0Q372005.1	TTTATTCAT.	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •
00372006.1	CGI.GGIGCCG.	. TGGCCGAACCCGTCG.		ACAGAUCUIICCG.	.GUGCTIAGGCGUTUU
00372009 1		.IGGUUGAAUUUGIGG.		ACAGAACCIIICCG	
00372009 1	TGT GGTGCCG	TGGCCGAACCCGTGG	CCCGTGTC GGCTG	ACA GAACCTTCCG	GCGCTTAGG CGCTTC
00372010.1					
00372011.1	TGT.GGTGCCG.	.TGGCCGAACCCGTGG.		ACAGAACCTTCCG.	.GCGCTTAGGCGCTTC
OQ372012.1	CTT.GGTGCCG.				
OQ372013.1	TGT.GGTGCCG.	. TGGCCGAACCCGTGG.	.CCCGTGTC.AGCTG	ACAGAACCTTCCG.	.GCGCTTAGGCGCTTC
00372014.1	TGT.GGTGCCG.	. IGGCCGAACCCGIGG.		ACAGAACCTTCCGG	CGCTTAGCGCTTC
00372015.1	••••••••				
00372016.1					
00372018.1	сст				
00372019.1					
00372020.1	СТТ				
0Q372021.1	TGT.GGT				
00372022.1	TGT.GGTGCCG.	.TGGCCGAACCCGTGG.	CCCGTGTC.GGCTG	ACAGAACCTTTCGG	TGCGCTTAGGCGCTTC
00372023.1	GTT.GGTTTCG.		ACAATGATCCTTCC	GCAGGTTCACCTATCGA	AACCTTTGTTAC
00372024.1	TGT,GGTGCCG,	. IGGCCGAACCCGIGG.		ACAGAACCICCG	.GCGCTTAGGCGC.TC
00372025.1	CGT GACACCT				
00372027 1	GAA COTTCCGC	ATGGTCACCTACGGGA	ACTTTTGTT	TTGAACTTCCTC	
00372028.1	TOT COTOCO	TEEECCENNTCCCCCCC	COCCETETCOCCECT	ACA TAAACCTTCCCC	COTTTTACC CCCTTC
	101.0010CCA.	TGGGCCGVUICCCGCGC	3666661616666616	ACH. INAACCIICCGG	COTTTTINGOC. CCCTIC

	610	620	630
AY665914.1* AY665886.1* MH763728.1* MH763740.1* OQ371996.1 OQ371997.1 OQ371998.1	GACCGCGACCCC GACCGCGACCCC GACCGCGACCCC GACCGCGACCCC GACCGCGACCCC	AGGTCAGO AGGTCAGO AGGTCAGO AGGTCAGO AGGT.CAO	GCGGGATT CGGGATT GCGGATT GTGGAATT GTGGAATT GTGGAATTACCCGCTGAGTTTAAGCATATCAATAGGCGGAGGGA
00371999.1 00372000.1 00372001.1 00372002.1 00372003.1 00372004.1	GACCGCGACCCCC. GAACCGGCGACCCCCC GA.CGCGACCCA GACCGCGACCCC.	AGGTGCAGG AGGGTGCAGG GGTC AGGTCAG	GTGGAAATTTACCCGCTGAGTTTAAGCATATCAATAAGGCGGGAGGGAA GTGGGAATTTAACCCCGGGCTTGAAGGTTTTAATGCCCATAA AGGTGATTACCCGCTGAGTTAAGCATAATGAATAGC GTGGAAATTACCCCGCTGAGTTTAAGCCATATCAATAAGCGGGAAGGAA
0Q372006.1 0Q372006.1 0Q372007.1 0Q372008.1 0Q372009.1 0Q372010.1 0Q372011.1	GACCGCGACCCC GTGGATCCGT GACCGCGACCCC GACCGCGACCCC.	ATTTGTTATAG	GGGGATTACCCGCTGAGTTTAAGCATATCAATAAGCGGGAGGAA GGGAGA GGTGGAATTACCCGCTGAGTTTAAGCATATCAATAAGGCGGGAGGAAA GGTGGAATTACCCGCTGAGTTTAAGCATATCAATAAGCGGGAGGAAA
00372012.1 00372013.1 00372014.1 00372015.1 00372016.1 00372017.1	GACCGCGACCCC GACCGCGACCCC	AGGTC2	AGTEGRATTACCCGCTGAGTTTAAGCATATCAATAAGCCGGAGGAA AGTEGRATTACCCGCTGAGTTTAAGCATATCAATAAGCCGGAGGAAA
OQ372018.1 OQ372019.1 OQ372020.1 OQ372022.1 OQ372022.1 OQ372022.1 OQ372023.1 OQ372024.1 OQ372025.1	GACCGCGACCCC. GAACTGGGGCCTTCTT GACC.GCGACCCA.	AGGTGCA TTAAGGGATA GTCT	GGTGGAATTACCCCGCTGAGTT AGG GGGATTTTCG
00372026.1 00372027.1 00372028.1 00372029.1	CACCCGCGTACCCC	· · · · · · · · · · · · · · · · · · ·	

Appendix 2 C: Multiple alignment sequence for *Physalis* accessions gene sequence as well as reference sequences from BLASTn analysis based on *rbcL* marker (https://espript.ibcp.fr/ESPript/temp/1694482275/0-0-1680468378-esp.pdf).

	1	10	20	30	40	50	60	70
KT178121.1*	ATGTCAC	CACAAACA	GAGACTAAAG	AAGTGTT	GGATTCAAGGCTG	GTGT <mark>TAAAG</mark> A	GTACAAAI	TGACTTATTATACT
NC_026570.1*	ATGTCAC	CACAAACA	GAGACTAAAG	AAGTGTT	<mark>G</mark> G A T T C A A G G <mark>C</mark> T <mark>G</mark>	G T G T <mark>T A A A G</mark> A	G T <mark>A</mark> C A A A I	TGACTTATTATACT
NC_048515.1*	ATGTCAC	CACAAACA	GAGACTAAAG	AAGTGTT	<mark>G</mark> G A T T C A A G G <mark>C</mark> T <mark>G</mark>	G T G T <mark>T A A A G</mark> A	G T <mark>A C A A A T</mark>	TGACTTATTATACT
NC_039457.1*	ATGTCAC	CACAAACA	GAGACTAAAG	CAAGTGTT	<mark>G</mark> GATTCAAGG <mark>C</mark> T <mark>G</mark>	GTGT <mark>TAAAG</mark> A	GTACAAAI	TGACTTATTATACT
00507152.1		• • • • • • • •	• • • • • • • • • • •		• • • • • • • • • • • •			
00507153.1	ATCTORC				· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·	CTACAAAI	IGACIIAIIAIACI TCACTTATTATACI
00507154.1	AIGICAC	CUCACACA	GAAACIAAAG	AAGIGII	GGAIICAAGGCIG	GIGIIAAAGA	GIACAAAI	TGACIIAIIAIACI TGACTTATTATACT
00507156.1	ATGTCAC	CACAAACA	GAAACTAAAG	AAGTGTT	GATTCAAGGCTG	GTGTTAAAGA	GTACAAAT	TGACTTATTATACT
00507157.1								TGACTTATTATACT
OQ507158.1							AAAI	TGACTTATTATACT
OQ507159.1							AAAT	TGACTTATTATACT
OQ507160.1							.	TGACTTATTATACT
OQ507161.1							AAAT	TGACTTATTATACT
00507162.1	ATGTCAC	CACAAACA	GAGACTAAAG	GAGTGCT	GGATCCAATGCTG	GTGTTAAAGA	GTACAAAI	TGACTTATTATACT
00507163.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGTATT	GGATACAAGGCTG	GTGTTAAAGA	GTACAAAI	TGACTTATTATACT
00507165 1	ATGICAC	CACAAACA	CACACIAAAG	GAGIGII NACTOOT	GCATICAAGGGGGG	GIGIIAAAGC CTCTTAAAGCA	GIACAAAI CTACAAAT	TGACIIAIIAIACI TCACTTATTATACI
00507166 1	AIGICAC	CACAAACA	GAGACIAAAG	ANGIGUI	GGACACCAGICIG	GIGIIAAAGA	GINCANAI	IGACITATIATACI
00507167.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGTGTT	GATCAAAGACTG	ATGTTAAAGA	GTACAAAT	TGACTTATTATACT
00507168.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGTGTT	GGATGCATGGGTG	GTGCTAAAGA	GTACAAAT	TGACTTATTATACT
OQ507169.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGTGTG	G G A T T C A G G G <mark>C</mark> C G	GCGC <mark>TAAAG</mark> C	GTACAAAI	TGACTTATTATACT
OQ507170.1	ATGTCAC	CACAAACA	GAGACTAAAG	CAGTGTT	<mark>G</mark> CATTGAAGG <mark>C</mark> TC	g t g c <mark>g a a a g</mark> a	G T <mark>A</mark> C A A A I	TGACTTATTATACT
OQ507171.1							AAA1	TGACTTATTATACT
00507172.1							AAAI	TGATTTATTATACT
00507173.1							TTAAT	TGAATTATTATACT
00507175 1	ATGICAC	CACAAACA	GAGACTAAAG	AATCICT	GGGATCATGGCTG	GIGITAAAGA	GIACAAAI	TGACITATIATACT
00507176 1								IGACITATIATACI
00507177.1								GACTAATTACACT
00507178.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGTGTT	GCATTCGAGGCTG	GCATTAAAGT	GTACAAAI	TGACTTATTATACT
00507179.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGTGTT	GCATTGAACGCTG	GTGTTAAAGA	GICCAAAI	TGACTTATTATACT
OQ507180.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGTGTT	<mark>G</mark> C A T T G A A C G <mark>C</mark> T <mark>G</mark>	G T G T <mark>T A A A G</mark> A	GTCCAAAI	TGACTTATTATACT
OQ507181.1	ATGTCAC	CACAAACA	GAGACTAAAG	CAAGTGTT	<mark>G</mark> G A T G C A A A G <mark>C</mark> T <mark>G</mark>	GAGC <mark>TAAAG</mark> T	G Т <mark>А</mark> СААА І	TGACTTATTATACT
OQ507182.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGTGGT	<mark>G</mark> GACACAAGT <mark>C</mark> T <mark>G</mark>	AGCT <mark>TAAAG</mark> A	GTACAAAT	TGACTTATTATACT
00507183.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGCATG	GGATTCAAAGCTG	GTGTTAAAGA	GTCAAAAI	TGACTTATTATACT
00507184.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGCATT	GGATTCAAAGCTG	GIGITAAAGA	GCACAAAI	TGACTTATTATACT
00507186 1	ATGICAC	CACAAACA	GAGACIAAAGO	CCCTTTT	GCATCAGICIG	GTGTTAAAGC	GIACAAAI	TGACIIAIIAIACI
00507187.1	ATGTCAC	CACAAACA	GAGACTAAAG	CAGTGCT	GGATTCATGGCTG	GTGTTAAAGA	GTACAAAT	TGACTTATTATACT
00507188.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGCGTT	GGTTTCATGCTG	GTGTTAAAGA	GTACAAAI	TGACTTATTATACT
OQ507189.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGTATT	<mark>G</mark> GGTTCAAGG <mark>C</mark> T <mark>G</mark>	G T G T <mark>T A A A G</mark> A	GTACAAAI	TGACTTATTATACT
OQ507190.1	ATGTCAC	CACAAACA	GAGACTAAAG	GCGTTTT	<mark>G</mark> G G A T C A A G G <mark>C</mark> T <mark>G</mark>	g t g t <mark>t a a a g</mark> a	GTACAAAI	TGACTTATTATACT
OQ507191.1	ATGTCAC	CACAAACA	GAGACTAAAG	CAACCATT	<mark>G</mark> G A G T C C A G A <mark>C</mark> T <mark>G</mark>	A T G T <mark>T A A A G</mark> A	G T <mark>А</mark> СААА Т	TGACTTATTATACT
00507192.1	ATGTCAC	CACAAACA	GAGACTAAAG	GAGGTTT	GGGATCATGG <mark>C</mark> TG	GTGTTAAAGA	GTACAAAI	TGACTTATTATACT
00507193.1	ATGTCAC	CACAAACA	GAGACTAAAG	GCTTGTT	GGATCCAAGGCTG	GTGTTAAAGA	GTACAAAI	TGACTTATTATACT
00507194.1	ATGTCAC	CACAAACA	GAGACTAAAG	AGATGIT	GGGTTCAAIGCTG	GIGIIAAAGA	GIACAAAI	TGACTTATTATACT
00507196 1	ATGICAC	CACAAACA	GAGACIAAAG	CCTTGTT	GGATTCAAGGCIG	GIGIIAAAGA	GIACAAAI	TGACITATIATACI
00507197.1	ATGTCAC	CACAAACA	GAGACTAAAG	AACCGTT	GGAATCAAGGCTG	GTGTTAAAGA	GTACAAAT	TGACTTATTATACT
00507198.1	ATGTCAC	CACAAACA	GAGACTAAAG	AGCAGIT	GGATTTCAGGCTG	GTGTTAAAGA	GTACAAAI	TGACTTATTATACT
OQ507199.1	ATGTCAC	CACAAACA	GAGGCTAAAG	AACTATT	GGATTCAAGGCTG	GTGTTAAAGA	GTACAAAI	TGACTTATTATACT
OQ507200.1	ATGTCAC	CACAAACA	GAGACTAAAG	GAGTGTT	<mark>G</mark> GATTCAAGG <mark>C</mark> T <mark>G</mark>	G T G T <mark>T A A A G</mark> A	GIACAAAI	TGACTTATTATACT
OQ507201.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGCGTT	<mark>G</mark> G A T T T C A T G <mark>C</mark> T <mark>G</mark>	G T G T <mark>T A A A G</mark> A	GTACAAAI	TGACTTATTATACT
00507202.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGAGTT	GGAATTAATG <mark>C</mark> TG	GTGT <mark>TAAAG</mark> A	GIACAAAI	TGACTTATTATACT
00507203.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGTGCC	GAGTTTAAGGCAG	GTGTTAAAGA	GIACAAAI	TGACTTATTATACT
00507204.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGGGTT	GGGTTCAACG <mark>C</mark> TG	GIGITAAAGA	GIACAAA'I	IGACTTATTATACT
00507205.1	ATGTCAC	CACAAACA	GAGACTARAC	AAGCGTT	GGGACAATCCTC	GTGTTAAACA	GTACAAAT	TGACIIAIIAIACT TGACTTATTATACT
00507207.1	ATGTCAC	CACAAACA	GAGACTAAAG	AAGCGTT	GGAGATAAGGCTG	GTGTTAAAGA	GTACAAAT	TGACTTATTATACT

KT178121.1* CCTGAGTACCAAACCAAGGATACTGAT ATATTGGCAGCATTACCGAGTAACTGCTGAACTGCTGAACTACGACTGAAGAACAACGACTGAAGAACAAGAACGAAC		8 Q	эö	100	110	120	130	140	150
NC_02570.1* CTCGAGTACCAAACCAAGGATACTGAT ATATTGGCAGCATTACCGAGTAACTGCT ACCTCGAGAGAACGACCGAACGAACGAACGAACGACCGAGAGAACGACG	KT178121.1*	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
NC_04815.1* CTGAGTACCAAACCAAGGATACTGAT ATATTGGGAGCATTCGAGTAACTGC GACTGGAGT CCACTGAAGAA 00507153.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGGAGCATTCGAGTAACTGC GACTGGAGT CCACTGAAGAA 00507155.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGGAGCATTCGAGTAACTGC GACTGGAGT CCACCTGAAGAA 00507155.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGGAGCATTCGGAGTAACTGC GACTGGAGT CCACCTGAAGAA 00507155.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGGAGCATTCGGAGTAACTGC GACTGGAGT CCACCTGAAGAA 00507155.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGGAGCATTCGGAGTAACTGC GACTGGAGT CCACCTGAAGAA 00507155.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGGAGCATTCGGAGTAACTGC GACTGGAGT CCACCTGAAGAA 00507156.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGGAGCATTCCGAGTAACTGC GACTGGAGT CCACCTGAAGAA 00507158.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGGAGCATTCCGAGTAACTGC GACTGGAGT CCACCTGGAAGAA 00507159.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGGAGCATTCCGAGTAACTGC GACTGAGAGT CCACCTGAAGAA 00507179.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGGAGCATTCCGAGTAACTGC GACTGGAGT CCACCTGAAGAA 00507179.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGGAGCATTCCGAGTAACTGC GACTGGAGT CCACCTGAAGAA 00507179.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGGAGCATTCCGAGTAACTGC GACTGAGGT CCACCTGAAGAA 00507179.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGGAGCATTCCGAGTAACTGC GACTGAGAGT CCACCTGAGAGT CCACCTGAAGAA 00507179.1 CCTGAGTACCAAACCAAGGATA	NC_026570.1*	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
NC_03917.1 * CT GAGTA CCAAACCAAGGA TA CT GA. TA ATT GGC AGCAT TC GAGTA CT GA CT TG GAGT T CCAAGGA T CCGAGT T CCAAGTA CT GAGT T CCAAGTA CT	NC_048515.1*	CCTGAGTAC	CCAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACT <mark>CCTC</mark> A	ACCTGGAGT	CCACCTGAAGAA
00507151	NC_039457.1*	CCTGAGTAC	CCAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA.	ACCTGGAGT	CCACCTGAAGAA
0489/135.1 CLEAR INCLARED AND CARGENT CLEAR CATTERED ACCATTERED AT A THE GED ACCATENCE CARGENTAL CONCERNENT OF A CONCERNENT AND	00507152.1				ATATTGGC	AGCATTCCGAG	TAACTCCTCA.	ACCTGGAGT	CCACCTGAAGAA
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00001161 CCTGAGTACCAAACCAAGGATACTGATATTGACAATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGATATATTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGATATATTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGATATATTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGATATATTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGATATTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGATATTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGATATTTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGATATTTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGATATTTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGATATTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGATATTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGATATTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGATATTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTCCCAACCAAGGATACTGATATTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTCCCAACCAAGGATACTGATATTGTGATATTGGCAGCAATTCCGAGTAACTCCTG ACCTGGAGTCCCAACCAAGGATACTGATATTGTGATATTTGGGCAGCATTCCGAGTAACTCCTG	00507154.1	COTGAGIAC	CAAACCAAG	GATACIGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
00507187.1 CCTGAGTACCAAGGATACTGAT NATTGGCAGGATTCCGAGTAACTCCTG ACCTGGAGT CCACCTGAAGTA 00507189.1 CCTGAGTACCAAACCAAGGATACTGAT NATTGGCAGGATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGAT NATTGGCAGGATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGAT NATTGGCAGGATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGAT NATTGGCAGGATTCCGAGTAACTCCTG ACCTGGAGTACCAAACCAAGGATACTGAT NATTGGCAGCATTCCGAGTAACTCCTG ACCTGGAGTCCCAACCAAGGATACTGAT NATTGGCAG	00507156 1	CCTGAGIAC	CAAACCAAG	GATACIGAT	ATATTGGC	ACCATTCCCAC	TAACTCCTCA	ACCTGGAGI	CCACCTGAAGAA
00507159.1 CCTGAGTACCAAGGATACTGATATATTGGAGGATTCCGATTACTGATCTCGA ACCTGGATTCCAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCAAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCAAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCAAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCAAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCAAACCAAGGATACTGATATTTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCAAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCAAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCAAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCAAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCCAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCCAAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCCAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCCAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCCAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCCAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCCAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCCAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCCAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCTG ACCTGGATTCCCAACCAAGGATACTGATATTGGCAGGATTCCGCAGTACTCCGAGTAACTCCTG ACCTGGATTCCCAACCAAGGATACTGATATTGGCAGGATTCCGAGTAACTCCGAGTAACCCGAGTACCGAGTTCCGAGTAACTCGAGTAACTGATATTGGCAGGATTCCGAGTAACTCCGAGTAACCCAAGGATTCCGAGTAACCGAGTTCCGAGTAACTCGAGTAACTGATATTGGCAGGATTCCGAGTAACTCGAGTACCGAGTTCCGAGTAACCCGAGTACCGAGTTCCGAGTAACTCGAGTAACCGAGGATTCCGAGTAACCCGAGTACCGAGTTCCGAGTAACCCGAGTACCGAGTTCCGAGTAACCGAGGATTCCGAGTAACCGAGGATTCCGAGTAACCGAGTTCCGAGTAACCGAGGATTCCGAGTAACCGAGGATTCCGAGTAACCGAGGATTCCGAGTAACCGAGGATTCCGAGTAACCGAGTTCCGAGTAACCGAGGATTCCGAGTAACCGAGTTCCGAGTAA	00507157.1	CCTGAGTAC	CAAACCAAG	GATACIGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
0507199.1 CCTGAGTACCAAGCATACTAA TANTGCACGATTCCCAAGTAACTCAAGGATACTAA TANTGCACGATTCCAAGTAACTCAAGGATACTAA 0507161.1 CCTGAGTACCAAGCATACTAA TANTGCACGATTCCGAGTAACTCA CCAACCTGAGGATT 0507161.1 CCTGAGTACCAAGCATACTAA TANTGCACGATTCCGAGTAACTCA CCAACCTGAGGATT 0507163.1 CCTGAGTACCAAACCAAGGATACTGA TANTGCACGATTCCGAGTAACTCC CCAACCTGAGGATT 0507165.1 CCTGAGTACCAAACCAAGGATACTGA TANTGCACGACTTCCGAGTAACTC CCAACCTGAGGAT 0507165.1 CCTGAGTACCAAACCAAGGATACTGA TANTGCACGACTTCCGAGTAACTC CCAACCTGAGGAT 0507167.1 CCTGAGTACCAACCAAGGATACTGA TANTGCACGACTTCCGAGTAACTC CCAACCTGAGGAT 0507167.1 CCTGAGTACCAACCAAGGATACTGA TANTGCACGACTTCCGAGTAACTC CCAACCTGGAGT 0507167.1 CCTGAGTACCAACCAAGGATACTGA TANTGCACGACTTCCGAGTAACTC CCAACCTGGAGT 05071761.1 CCTGAGTACCAACCAAGGATACTGA TANTGCACGACTTCCGAGTAACTC CCAACCTGGAGT 0507172.1 CCTGAGTACCAACCAAGGATACTGA TANTGCACGACTTCCGAGTAACTC CCAACCTGGAGT 0507173.1 CCTGAGTACCAACCAAGGATACTGA TANTGCACGCATTCCGAGTAACTC CCAACCTGGAGT 0507174.1 CCTGGAGTACCAAACCAAGGATACTGA<	00507158.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
02507160.1 CCTGAGTACCAAGCATACTAA TATTGGCACGATTCCGAGTAACTC CAACCTGAAGAT 02507162.1 CCTGAGTACCAAGCATACTGA TATTGGCACGATTCGCAGTAACTC CGACGTGCCGACT 02507163.1 CCTGAGTACCAAGCATACTGA TATTGGCACGATTCGCAGTAACTC 02507164.1 CCTGAGTACCAAGCATACTGA TATTGGCACGATTCGCAGTAACTC 02507165.1 CCTGAGTACCAAGCATACTGA TATTGGCACGATTCGCAGTAACTC 02507165.1 CCTGAGTACCAAGCATACTGA TATTGGCACGATTCGCAGTAACTC 02507165.1 CCTGAGTACCAAGCATACTGA TATTGGCACGATTCGGAGTAACTC 02507165.1 CCTGAGTACCAAGCATACTGA TATTGGCACGATTCGGAGTAACTC 02507165.1 CCTGAGTACCAAGCATACTGA TATTGGCACGATTCGGAGTAACTC 02507165.1 CCTGAGTACCAAGCATACTGA TATTGGCACGATTCGGAGTAACTC 02507165.1 CCTGGAGTACCAAGCATACTGA TATTGGCACGATTCGGAGTAACTC 02507165.1 CCTGGAGTACCAAGCATACTGA TATTGGCACGATTCGGAGTAACTC 02507175.1 CCTGGAGTACCAAGCATACTGA TATTGGCACGATTCCGAGTAACTC 02507171.1 CCTGGAGTACCAAGCATACTGA TATTGGCACGATTCCGAGTAACTC 02507173.1 CCTGGAGTACCAAGCATACTGA TATTGGCACGATTCCGAGTAACTC 02507173.1 CCTGGAGTACCAAGCATACTGA TATTGGCACGATTCCGAGTAACTC 02507173.1 CCTGGAGTACCAAGCATACTGA TATTGGCACGATTCCGAGTAACTC 02507175.1 CCTGGAGTACCAAGCATACTGA 02507176.1 CCTGGAGTACCAAGCATACTGA 02507176.1 CCTGGAGTACCAAGCATACTGA 02507176.1 CCTGGAGTACCAAGCATACTGA 02507176.1 CCTGGAGTACCAAGCATACTGA 02507176.1 CCTGGAGTACCAAGCATACTGA 02507176.1 CCTGGAGTACCAAGCATACTGA 02507176.1 CCTGGAGTACCAAGGATACTGA 02507176.1 CCTGGAGTACCAAGGATACTGA 02507176.1 CCTGGAGTACCAAGGATACTGA 02507176.1 CCTGGAGTACCAAGGATACTGA 02507176.1 CCTGGAGTACCAAGGATACTGA 02507180.1 CCTGGAGTACCAAGGATACTGA 0250718	0Q507159.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
09507161.1 CCTGAGTACCAAGCAAGGATACTGA TA'ATTGGCACGATTCCGAGTAACT C'GAACTGGAGTT CCACCTGAAGAA 09507163.1 CCTGAGTACCAAACGAAGGATACTGA TA'ATTGGCACGATTCGGAGTAACT C'GAACTGGAGT CCACCTGAAGAA 09507165.1 CCTGAGTACCAAACGAAGGATACTGA TA'ATTGGCACGATTCGGAGTAACT C'GAACTGGAGT CCACCTGAAGAA 09507167.1 CCTGAGTACCAACGAAGGATACTGA TA'ATTGGCACGATTCGGAGTAACT C'GAACTGGAGT CCACCTGAAGAA 09507167.1 CCTGAGTACCAAGGATACTGA TA'ATTGGCACGATTCGGAGTAACT C'GAACTGGAGT CCACCTGAAGAA 09507167.1 CCTGAGTACCAAGGATACTGA TA'ATTGGCACGATTCGGAGTAACT C'GAACTGGAGT CCACCTGAAGAA 09507170.1 CCTGAGTACCAAGGATACTGA TA'ATTGGCACGATTCGGAGTAACT C'GAACTGGAGT CCACCTGAAGAA 09507170.1 CCTGAGTACCAAGGATACTGA TA'ATTGGCACGATTCGGAGTAACT C'GAACTGGAGT CCACCTGAAGAA 09507170.1 CCTGAGTACCAAGGATACTGA TA'ATTGGCACGATTCCGAGTAACT C'GAACTGGAGT CCACCTGAAGAA 09507171.1 CCTGAGTACCAAGGATACTGA TA'ATTGGCACGATTCCGAGTAACT C'GAACTGGAGT CCACCTGAAGAA 09507171.1 CCTGAGTACCAAGGATACTGA TA'ATTGGCACGATTCCGAGTAACT C'GAACTGGAGT CCACCTGAAGAA 09507171.1 CCTGAGTACCAAGGATACTGA TA'ATTGGCACGATTCCGAGTAACT C'GAACTGGAGTT CCACCTGAAGAA 09507171.1 CCTGAGTACCAAGGATACTGA TA'ATTGGCACGATTCCGAGTAACT C'GAACTGGAGTT CCACCTGAAGAA 09507171.1 CCTGAGTACCAAGGATACTGA TA'ATTGGCACGATTCCGAGTAACT C'GAACTGGAGTT CCACCTGAAGAA 09507171.1 CCTGAGTACCAAGGATACTGA TA'ATGGCACGATTCCGAGTAACT C'GAACTGGAGTT CCACCTGAAGAA 09507171.1 CCTGAGTACCAAGGATACTGA TA'ATGGCACGATTCCGAGTAACT C'GAACTGGAGTT CCACCTGAAGAA 09507171.1 CCTGAGTACCAAGGATACTGA TA'ATGGCACGATTCCGAGTAACT C'GAACTGGAGTT CCACCTGAAGAA 09507171.1 CCTGAGTACCAAGGATACTGA TA'ATGGCACGATTCCGAGTAACT C'GAACTGGAGTT CCACCTGAAGAA 09507171.1 CCTGAGTACCAAACCAAGGATACTGA TA'ATGGCACGATTCCGAGTAACT C'GAACTGGAGTT CCACCTGAAGAA 09507171.1 CCTGAGTACCAAGGATACTGA TA'ATGGCACGATTCGGAGTAACT C'GAACTGGAGTT CCACCTGAAGAA 09507181.1 CCTGGAGTACCAAGGATACTGA TA'ATGGCACGATTCGGAGTAACT C'GAACTGGAGTT CCACCTGAAGAA 09507181.1 CCTGGAGTACCAAGGATACTGA TA'ATGGCACGATTCGGAGTAACT C'GAACTGGAGTT CCACCTGAAGAA 09507181.1 CCTGGAGTACCAAGGATACTGA TA'ATGGCACGATTCGGAGTAACT C'GAACTGGAGTT CCACCTGAAGAA 09507181.1 CCTGGATACCAAGGATACTGA TA'ATGGCACGATTCGGAGTAACT C'GA	OQ507160.1	CCTGAGTAC	CCAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACT <mark>CC</mark> TCA	ACCTGGAGT	CCACCTGAAGAA
09507162.1 CCTGAGTACCAACCAAGGATACTGA 09507163.1 CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCTGAAGGAT CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCTGAAGGAT CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCTGAGATACTGA CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCTGAGATACTGA CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCTGAGATACTGA CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCTG CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCTG CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCTG CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCTG CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCTG ACCTGGAGT CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCTG ACCTGGAGT CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCCTG ACCTGGAGT CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCCTG ACCTGGAGT CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCCTG ACCTGGAGT CCTGAGTACCAAGCAAGGATACTGA TATTGCAAGCATTCCGAGTACCCTG ACCTGGAGT CCTGAGTACCAAACCAAGGATACTGA TATTGCGACGATTCCGAGTAACCCTC ACCTGGAGT CCTGAGTACCAAACCAAGGATACTGA TATTGCGACGATTCCGAGTAACCCTC ACCTGGGAGT CCTCGGGAGT CCTGAGTACCAAACCAAGGATACTGA TATTGCGACGATTCCGAGTAACCCTC ACCTGGGAGT CCTCGGGAGT CCTCGGAGT CCTGAGTACCAAACCAAGGATACTGA TATTGGCACGATTCCGAGTAACCTCTC ACCTGGGAGT CCTCGGGAGT CCTCGGGAGT CCTCGGAGT CCTGAGTACCAAACCAAGGATACTGA TATTGGCACGATTCCGAGTAACCTCTC ACCTGGGAGT CCTGGGAGT CCTGAGTACCAAACCAAGGATACTGA TATTGCGACGATCCTCG ACCTGGGAGT CCTGGGAGT CCTGAGTACCAACCAAGGATACTGA TATTGCGACGATCCCTG ACCTGGGAGT CCTGGGAGT CCTGAGTACCAACCAAGGATACTGA TATTGCCACGATTCCGAGTACCTCTC ACCTGGGAGT CCTGGGAGT CCTGGGAGT CCTGGAGTACCAACCAAGGATACTGA TATTGCGACGATTCCGAGTACCTCCTG ACCTGGGAGT CCTGGGAGT CCTGGAGTACCAACCAAGGATACTGA TATTGCGACGATTCCGAGTACCTCTC ACCTGGGAGT CCTGGGAGT CCTGGAGTACCAACCAAGGATACTGA TATTGCGACGATTCCGAGTACCTCTC ACCTGGGAGT CCTGGGAGT CCTGGAGTACCAACCAAGGATACTGA TATTGCGACGATTCCGAGTAACCTCTC ACCTGGAGT CCTGGAGTACCAACCAAGGATACTGA TATTGCCACGATACCAACCTGGAGTACCACCAGGATACCCTC ACCTGGAGT CCTGGAGTACCAACCAAGGATACTGA TATTGCCACGATACCAACCTGGAGTA	OQ507161.1	CCTGAGTAC	CCAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
00507163.1 CCTGACTACCAAGCAAGGATACTGA TATHTGCAAGCATTCCGAGTAACTCCTGAAGCTGCAGCTGCACGTAAGAA 00507165.1 CCTGACTACCAAGCAAGGATACTGA TATHTGCAAGCATTCCGAGTAACTCCTGAAGCA 00507165.1 CCTGACTACCAAGCAAGGATACTGA TATHTGCAAGCATTCCGAGTAACTCCTGAAGCA 00507165.1 CCTGACTACCAAGCAAGGATACTGA TATHTGCAAGCATTCCGAGTAACTCCTGAAGCA 00507165.1 CCTGACTACCAAGCAAGGATACTGA ATATTGCAAGCATTCCGAGTACCCTGAGACATCCGAGAGAAGTCCGAGTAAGTCCTGAAGA 00507169.1 CCTGAGTACCAAGCAAGGATACTGA ATATTGCAAGCATTCCGAGTACCCTGAGCATCCGAGGAGCCCTGGAGT CCTGAGTACCAAGCAAGGATACTGA ATATTGCAAGCATTCCGAGTACCCTGAGCATCCGAGTAACTCCTGAAGCA 00507179.1 CCTGAGTACCAAGCAAGGATACTGA ATATTGCAAGCATTCCGAGTACCCTGAGCATCCGAGGAGCCCTGGAGT CCTGAGTACCAAGCAAGGATACTGA ATATTGCAAGCATTCCGAGTACCCTGAGCATCCGAGGAGCCCTGGAGT CCTGAGTACCAAGCCAAG	OQ507162.1	CCTGAGTAC	CCAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA.	ACCTGGAGT	CCACCTGAAGAA
00201151.1 CCTGAGTACCAAGCAAGGATACTGA 02501151.1 CCTGAGTACCAAGCAAGGATACTGA 02501171.1 CCTGAGTACCAAGCAAGGATACTGA 02501173.1 CCTGAGTACCAAGCAAGGATACTGA 02501173.1 CCTGAGTACCAAGCAAGGATACTGA 02501173.1 CCTGAGTACCAAGCAAGGATACTGA 02501175.1 CCTGAGTACCAAGCAAGGATACTGA 02501181.1 CCTGAGTACCAAGCAAGGATA	00507163.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
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0200167.1 CCTGGATACCAALCAAGGATACTGA TATTGGCAGGATACTGATAGTGC CGACCTGAGGT CCCTGGAGTACCAACCAAGGATACTGA TATTGGCAGGATACTGACGATAGTGC CGACCTGGAGGT CCCTGAGGTACCAACCAAGGATACTGA TATTGGCAGGATAGTGC CGACCTGGAGGT CCCTGAGGTACCAACCAAGGATACTGA TATTGGCAGGATAGTGC CGACCTGGAGGT CCCTGAGGAGGT CCCTGAGGAGT CCCTGAGGAGT CCCTGAGGAGGT CCCTGAGGAGGT CCCTGAGGAGT	00507166 1	CUIGAGIA	CAAACCAAG	GATACIGAT	ATATIGGC	AGCATTCCGAG	TAACICCICA	ACCTGGAGI	CCACCTGAAGAA
0 0 0 0 0 0 0 0 0 0 0 0 0 0	00507167 1	CCTGAGTAC	CABACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
00001169.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACT CTC CACTGGAGTTCCACCGCGAGTACCAGAGATACTGATATATTGGCAGCATTCCGAGTAACT CCTGAGTACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACT CCTGAGTACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACT CCTGAGTACCAAGGATACTGATATATATGGCAGCATTCCGAGTAACT CCTGAGTACCAAGGATACTGATATATATGGCAGCATTCCGAGTAACT CCTGAGTACCAAGGATACTGATATATATGGCAGCATTCCGAGTAACT CCTGAGTACCAAGGATACTGATATATATGGCAGCATTCCGAGTAACT CCTGAGTACCAAGGATACTGATATATATGGCAGCATTCCGAGTAACT CCTGAGTACCAAGGATACTGATATATATGGCAGCATTCCGAGTAACT CCTGAGTACCAAGGATACTGATATATATGGCAGCATTCCGAGTAACT CCTGAGTACCAAGGATACTGATATATATGGCAGCATTCCGAGTAACT CCTGAGTTCCACCTCAAGGATACTGATATATATGGCAGCATTCCGAGTAACT CCTGAGTTCCACCTCAAGGATACTGATATATATGGCAGCATTCCGAGTAACT CCTGAGTTCCACCCTCAAGGATACTGATATATATGGCAGCATTCCGAGTAACT CCTGAGTTCCACCTCAAGGATACTGATATATTGGCAGCATTCCGAGTAACT CCTGAGTTCCACCCAAGGATACTGATATATATGGCAGCATTCCGAGTAACT CCTGAGTTCCACCCCTCAAGGATACTGATATATTGGCAGCATTCCGAGTAACT CCTGAGTTCCACCCCCCTCAAGGATACTGATATATTGGCAGCATTCCGAGTAACT CCTGAGTTCCACCCAAGGATACTGATATATTGGCAGCATTCCGAGTAACT CCTGAGTTCCACCCAAGGATACTGATATATTGGCAGCATTCCGAGTAACT CCTGAGGTTCCACCCCCCCCCCAAGGATACTGATATATAT	00507168.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
00507170.1 CCTCAGTACCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCACCTGAAGA 00507171.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCACCTGAAGA 00507172.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCACCTGAAGA 00507173.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCACCTGAAGA 00507176.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCACCTGGAGT 02507177.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCACCTGGAGT 02507177.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCACCTGGAGT 02507178.1 CCTGAGTACCAAACCAAGGATACTGATATATATGGCAGCATTCCGAGTAACTCC CCACCTGAAGA 02507178.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCACCTGAAGA 0250718.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCACCTGAACA	00507169.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
02507171.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAAGAA 02507173.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAAGAA 02507175.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAAGAA 02507176.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAACAA 02507180.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAACAA 02507182.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAACAA 02507184.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAACAA 02507184.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAACAA 02507185.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAACAA 02507186.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAACAA 02507187.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAACAA 02507187.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAACAA 02507187.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAACAA 02507187.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAACAA 02507197.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAACAA 02507197.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAACAA 02507197.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC TCAACCTGGAGT CCACCTGAACAA 02507197.1 CCTGAGTACCAAACCAAGGATACTGATATATTG	OQ507170.1	CCTGAGTAC	CCAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
09507172.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTC CTG AACCTGAGGT CCACCTGAAGAA 09507173.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTC CTG AACCTGAGGT CCACCTGAAGAA 09507175.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTC CTG AACCTGAGGT CCACCTGAAGAA 09507176.1	OQ507171.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACT <mark>CC</mark> TCA	ACCTGGAGT	CCACCTGAAGAA
00507173.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTC CTGAACCTGGAGT 00507175.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTC CTGAACCTGGAGT 00507175.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTC CTGAACCTGAAGT 00507176.1	OQ507172.1	CCTGAGTAC	CCAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
00001174.1. CUTGACTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGACTAACTC TCAACCTGGACT TCCACCTGAAGAA 00507176.1	00507173.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA.	ACCTGGAGT	CCACCTGAAGAA
0Q507175.1 CCTGAGTACCAAACCAAGGATACTGATATTGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507177.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507179.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507180.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507181.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507182.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507184.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTCCACCTGAAGAA Q507185.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTCCCACCTGAAGAA Q507186.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTCCCACCTGAAGAA Q507186.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTCCCACCTGAAGAA Q507186.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507186.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507187.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507189.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507191.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507191.1 CCTGAGTACCAAACCAAGGATACTGATATTATGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507192.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507193.1 CCTGAGTACCAAACCAAGGATACTGATATTATTGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507194.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507195.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507196.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507197.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCT CAACCTGGAGTTCCACCTGAAGAA Q507197.1 CCTGAGTACCAA	00507174.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA.	ACCTGGAGT	CCACCTGAAGAA
02007177.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA 02007178.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA 02007180.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA 02007181.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA 02007182.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA 02007183.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA 02007184.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA 02007185.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA 02007185.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA 02007187.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA 02007187.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA 02007187.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA 02007189.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA 02007190.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA 02007191.1 CCTGAGTACCAAACCAAGGATACTGA TATATTGGCAGCATTCCGAGTAACTCC TGAACCTGGAGTT CCACCTGAAGAA	00507176 1	CUIGAGIA	CAAACCAAG	GATACIGAT	ATATTGGC	AGCATTCCGAG		ACCTGGAGT	CCACCTGAAGAA
00507178.1 CCTGAGTACCAAAGCATACTGAT ATATTGGCAGCATTCCGAGTAACT CCTCAACCTGGAGT CCACCTGAAGAA 00507179.1 CCTGAGTACCAAAGCATACTGAT ATATTGGCAGCATTCCGAGTAACT CCTCAACCTGGAGT CCACCTGAAGAA 0050718.1 CCTGAGTACCAAAGCATACTGAT ATATTGGCAGCATTCCGAGTAACT CCTCAACCTGGAGT CCACCTGAAGAA 0050718.1 CCTGAGTACCAAAGCATACTGAT ATATTGGCAGCATTCCGAGTAACT CCTCAACCTGGAGT CCACCTGAAGAA 0050718.1 CCTGAGTACCAAAGCAAAGGATACTGAT ATATTGGCAGCATTCCGAGTAACT CCTCAACCTGGAGT CCACCTGAAGAA 0050718.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGCAGCATTCCGAGTAACT CCTCAACCTGGAGT CCACCTGAAGAA 0050719.1 CCTGAGTACCAAACCAAGGATACTGAT ATATTGGCAGCATTC	00507177 1	сставатьс		сатастсат	ATATTGGC	ACCATTCCCAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
00507179.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGTA00507180.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGTA00507181.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507182.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507183.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507184.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCAACCTGAAGAA00507185.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCAACCTGAAGAA00507186.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCAACCTGAAGAA00507187.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCAACCTGAAGAA00507189.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507190.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507192.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507192.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507193.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCAACCTGAAGT00507193.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCAACCTGAAGAA00507193.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCCCAAACCTGGAGTTCCAACCTGAAGAA00507193.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCCCAAACCTGGAGTTCCAACCTGAAGAA00507193.1CCTGAGTACCAAACCAAGGATACTGATATATT	00507178.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
0507180.1CCTGAGTACCAAACCAAGGATACTGAT ATATTGGCAGCATTCCGAGTAACTCC CCGACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCTGAAGAA OQ507188.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCTGAAGAA OQ507192.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC CCAACCTGGAGTTCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCC <b< th=""><th>00507179.1</th><th>CCTGAGTAC</th><th>CAAACCAAG</th><th>GATACTGAT</th><th>ATATTGGC</th><th>AGCATTCCGAG</th><th>TAACTCCTCA</th><th>ACCTGGAGT</th><th>CCACCTGAAGAA</th></b<>	00507179.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
00507181.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCACCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507182.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507183.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507183.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507183.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507185.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507187.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507188.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507198.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507191.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507192.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507193.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507194.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507197.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507197.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCACCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507197.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCACCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507197.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCACCATTCCGAGTAACTCCTCA	OQ507180.1	CCTGAGTAC	CCAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
00507182.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGTA00507183.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507183.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507183.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507183.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507183.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507183.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507190.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507191.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCACTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507192.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCACTTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507193.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCACTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507194.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCACTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCACTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507196.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCACTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507199.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCACTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507199.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507199.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507199.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCACCATTCCGAGTAACTCCTC	OQ507181.1	CCTGAGTAC	CCAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACT <mark>CC</mark> TCA	ACCTGGAGT	CCACCTGAAGAA
00507183.1CCTGAGTACCAAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCCACCTGAAGAA00507185.1CCTGAGTACCAAAGCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507185.1CCTGAGTACCAAAGCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507187.1CCTGAGTACCAAAGCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507188.1CCTGAGTACCAAAGCAAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507189.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507190.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507191.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507192.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507193.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCAACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCACCATTC	00507182.1	CCTGAGTAC	CCAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
00507184.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTGAACCTGGAGTTCCACCTGAAGAA00507185.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507187.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507188.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507189.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507190.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507191.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507192.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507193.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCCACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507197.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507198.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507199.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507199.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCCT	00507183.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA.	ACCTGGAGT	CCACCTGAAGAA
0Q507185.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTAATGCACCTGGAGTTCCACCTGAAGAA 0Q507187.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTAATGCACCTGGAGTTCCACCTGAAGAA 0Q507188.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507189.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507190.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507191.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507193.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507193.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507193.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507193.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507194.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507195.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCACCTGAAGAA 0Q507197.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCACCTGAAGAA 0Q507199.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCACCTGAAGAA 0Q507199.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCACCTGAAGAA 0Q507199.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCACCTGAAGAA 0Q507200.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCACCTGAAGAA 0Q507201.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCACCTGAAGAA 0Q507203.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCACCTGAAGAA 0Q507204.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCACCTGAAGAA 0Q507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCACCTGAAGAA 0Q507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCACCTGAAGAA 0Q507205.1 CCTGAGTACCAAACCAAGGATA	00507184.1	CUTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA.	ACCTGGAGT	CCACCTGAAGAA
00507187.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGAACCTGGAGTTCCACCTGAAGAA 00507188.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507190.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCACCTGAAGAA 00507190.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCACCTGAAGAA 00507193.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCACCTGAAGAA 00507193.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCACCTGAAGAA 00507194.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCACCTGAAGAA 00507195.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCACCTGAAGAA 00507196.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCACCTGAAGAA 00507197.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCCACCTGAAGAA 00507198.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCCACCTGAAGAA 00507199.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCACCTGAAGAA 00507199.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCCACCTGAAGAA 00507199.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCCACCTGAAGAA 0050720.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCCACCTGAAGAA 0050720.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCCACCTGAAGAA 0050720.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCCACCTGAAGAA 0050720.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCCACCTGAAGAA 0050720.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCCACCTGAAGAA 0050720.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCCACCTGAAGAA 0050720.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCCACCTGAAGAA 0050720.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCCACCTGAAGAA 0050720.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGAGAGTCCCAC	00507185.1	CCTGAGIAC	CAAACCAAG	GATACIGAT	ATATTGGC	AGCATTCCGAG	ТААСТССТСА	ACCTGGAGT	
OQ507188.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCCCTGAACCTGGAGTTCCCACCTGAAGAAOQ507189.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCCCTGAACCTGGAGTTCCACCTGAAGAAOQ507191.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCCCTGAACCTGGAGTTCCACCTGAAGAAOQ507192.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCCCTGACCTGGAGTTCCACCTGAAGAAOQ507193.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCCCTGACCTGGAGTCCACCTGAAGAAOQ507194.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCCCTGACCTGGAGTCCACCTGAAGAAOQ507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTCCACCTGAAGAAOQ507196.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTCCACCTGAAGAAOQ507197.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507198.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507101.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTCCACCTGAAGAAOQ507201.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTCCACCTGAAGAAOQ507203.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507204.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATAC	00507187.1	CCTGAGTAC	CAAACCAAG	GATACIGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
OQ507189.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCCCCCAACCTGGAGTTCCCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGTACCAAGGATCCGAGTACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGTACCAAGGATCCGAGTACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGTACCAAGGATCCGAGTACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGTACCAAGGATCCGAGTACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGTACCAAGGATCCGAGTACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGTACCAAGGATCCGAGTACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGTACCAAGGATCCGAGTACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGTACCAAGGATCCGAGTACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGTACCAAGGATCCGAGTACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGTACCAAGGATCCGAGTACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGTCCCACCTGAAGAAOQ507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGCTCCACCTGAAGAAOQ507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGCTCCACCTGAAGAAOQ507196.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTGAACCTGGAGTTCCACCTGAAGAAOQ507197.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTGAACCTGGAGTTCCACCTGAAGAAOQ507199.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507201.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507202.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507203.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507203.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCCAACCTGGAGTTCCA	00507188.1	CCTGAGTAG	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
OQ507190.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTGAGTCCCCCTGAAGGATCCGATATATTGGCAGCATTCCGAGTAACTCCTGAGTCCCCCCGAGTACCAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507192.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507193.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507194.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTCCACCTGAAGAAOQ507196.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTCCACCTGAAGAAOQ507197.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507198.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507200.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507201.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507203.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507204.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCCGAGTAACTCCTCGACCTGAGGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCCGAGTAACTCCTCGACCTGAGGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCCGAGTAACTCCTCGACCTGGAGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATA	OQ507189.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
00507191.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507192.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507193.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507194.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507196.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507196.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507196.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507199.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCCACCTGAAGAA00507199.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTG	OQ507190.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
00507192.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGGATTCCGAGTAACTCCTGAACCTGGAGTTCCACCTGAAGAA00507193.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507194.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507196.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507197.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507197.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507197.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA00507197.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCCACCTGAAGAA00507197.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGAGGATCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGAGGTTCCACCTGAAGAA0050720.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGAG	OQ507191.1	CCTGAGTAC	CCAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACT <mark>CCTC</mark> A	ACCTGGAGT	CCACCTGAAGAA
OQ507193.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGGCTAACTCCTCAACCTGGAGTICCACCTGAAGAAOQ507194.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAAOQ507195.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAAOQ507196.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAAOQ507198.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAAOQ507199.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAAOQ507199.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAAOQ507201.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAAOQ507202.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAAOQ507203.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAAOQ507203.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAAOQ507204.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGAGGTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTC	00507192.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA.	ACCTGGAGT	CCACCTGAAGAA
00507194.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTGAACCTGGAGTTCCACCTGAAGAA 00507196.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507197.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507199.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507199.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507200.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507201.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507203.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507203.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507203.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507203.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507203.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507203.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA	00507193.1	CCTGAGTAC	CCAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA.	ACCTGGAGT	CCACCTGAAGAA
0Q507196.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507197.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507198.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507199.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507200.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507201.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507202.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507203.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507204.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCCACCTGAAGAA0Q507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507205.1CCTGAGTACCAAACCAAGGATACTGATATATGCCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507205.1CCTGAGTACCAAACCAAGGATACTGATATATGCCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA0Q507205.1CCTGAGTACCAAACCAAGGATACTGATATATGCCAGCATTCCGAGTAACTCCTCAACCTGAGAGAA0Q507205.1CCTGAGTACCAAACCAAGGATACTGATATATGCCAGCATTCCGAGTAACTCCTCAACCTGAGAGAA <th>00507194.1</th> <th>CCTGAGIAC</th> <th>CAAACCAAG</th> <th>GATACIGAT</th> <th>ATATTGGC</th> <th>AGCATTCCGAG</th> <th>TAACTCCTCA</th> <th>ACCTGGAGT</th> <th>CCACCTGAAGAA</th>	00507194.1	CCTGAGIAC	CAAACCAAG	GATACIGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
00507197.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507199.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCACCTGAAGAA 00507200.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCACCTGAAGAA 00507201.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCACCTGAAGAA 00507202.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCACCTGAAGAA 00507203.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTCCACCTGAAGAA 00507204.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507204.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 00507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA	00507196 1	CCTGAGIAC	CARACCARG	GATACIGAT	ATATTGGC	ACCATTCCCAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
OQ507198.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCCTGAACCTGGAGTTCCACCTGAAGAAOQ507199.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507200.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507201.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507202.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507203.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507204.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507207.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507207.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507207.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGAGGATCCACCTGAAGAA	00507197.1	CCTGAGTAC	CAAACCAAG	GATACIGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
OQ507199.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507200.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507201.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507202.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507203.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507204.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507207.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCCACCTGAAGAAOQ507207.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGAGGTTCCACCTGAAGAAOQ507207.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGAGGTTCCACCTGAAGAAOQ507207.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGAGTTCCCACCTGAAGAA	00507198.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
OQ507200.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507201.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507202.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507203.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507204.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507205.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507206.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAAOQ507207.1CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCCACCTGAAGAA	0Q507199.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
0Q507201.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGGATACTCCGCAGTAACTCCCTGAACCTGGAGTTCCACCTGAAGAA 0Q507202.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507203.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507204.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507206.1 CCTGAGTACCAAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA 0Q507207.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA	OQ507200.1	CCTGAGTAC	CCAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCC <mark>TC</mark> A	ACCTGGAGT	CCACCTGAAGAA
00507202.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAA 00507203.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAA 00507204.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAA 00507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAA 00507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAA 00507206.1 CCTGAGTACCAAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAA 00507207.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTICCACCTGAAGAA	OQ507201.1	CCTGAGTAC	CCAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
Op507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTTGGCAGCATTCCGGAGTAACTCCTGAACCTGGGGTTCCACCTGAAGAA Op507204.1 CCTGAGTACCAAACCAAAGGATACTGATATATTGGCAGCATTCCGGAGTAACTCCTCAACCTGGGGTTCCACCTGAAGAA Op507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA Op507206.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGAGCTGCACCTGGAGTACCACCTGAAGAA Op507206.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGAGGTCCACCTGGAGAA Op507207.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA	00507202.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA.	ACCTGGAGT	CCACCTGAAGAA
00507204.1 CCTGAGTACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTGAACCTGGAGTTCCACCTGAAGAA 00507205.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGAGCTGGAGTTCCACCTGAAGAA 00507206.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCGAGGTCCACCTGAAGAA 00507207.1 CCTGAGTACCAAACCAAGGATACTGATATATTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCCACCTGAAGAA	00507203.1	COTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA.	ACCTGGAGT	CCACCTGAAGAA
0Q507206.1 CCTGAGTACCAAGGATACTGATATATTGGCAGCAGTACTCCGAGTAACTCCTGAGGTGCCCCTGAAGGA 0Q507207.1 CCTGAGTACCAAGGATACTGATATATTGGCAGCAGTACTCCGAGTAACTCCTGAAGGAGTCCCCCTGAAGAA	00507204.1	CCTGAGIAC	CAAACCAAG	GATACIGAT	ATATTGGC	ACCATTCCCAC	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
00507207.1 CCTGAGTACCAAACCAAGGATACTGATATTGGCAGCATTCCGAGTAACTCC	00507206.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA
	OQ507207.1	CCTGAGTAC	CAAACCAAG	GATACTGAT	ATATTGGC	AGCATTCCGAG	TAACTCCTCA	ACCTGGAGT	CCACCTGAAGAA

	160	170	180	190	200	210	220	230
KT178121.1*	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTGI	TATGGACCGAT	GGACTTACCA	GTCTTGAT
NC 026570.1*	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
NC 048515.1*	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
NC 039457.1*	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507152.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT	ACTGGTACAT	GGACAACTGT	TATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507153.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
0Q507154.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT	ACTGGTACAT	GGACAACTGI	TATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507155.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507156.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507157.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507158.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT	ACTGGTACAT	GGACAACTGI	TATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507159.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507160.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTGI	FATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507161.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507162.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTG	FATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507163.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACC <mark>A</mark>	GTCTTGAT
OQ507164.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507165.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT	ACTGGTACAT	GGACAACTGI	TATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507166.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT.	ACTGGTACAT	GGACAACTGI	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507167.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507168.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507169.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507170.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507171.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507172.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT.	ACTGGTACAT	GGACAACTG	PATGGACCGAT	GGACTTACCAC	GTCTTGAT
00507174 1	GCAGGGGGCCG	GCGGTAGCTGC	CGAATCTTCT.	ACTGGTACAT	GGACAACTGI	TATEGACCEAT	GGACTTACCAC	GTCTTGAT
00507175 1	GCAGGGGCCG	GEGETAGETGE	CGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCAC	GTCTTGAT
00507176 1	GCAGGGGCCG		CGAAICIICI.	ACTOGIACAI	GGACAACIG	TATGGACCGAT	GGACITACCA	GICIIGAI
00507177 1	CAGGGGCCC	CCCTACCTCC	CGAATCTTCT	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507178 1	GCAGGGGCCG	CGGTAGCIGC	CGAATCTTCT	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507179 1	GCAGGGGCCG	CCGTACCTC	CGAATCTTCT	ACTOGTACAT	GGACAACTCI	TATGGACCGAT	GACTTACCA	GTCTTGAT
00507180.1	GCAGGGGCCG	CGGTAGCTGC	CGAATCTTCT	ACTEGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507181.1	GCAGGGGCCG	CGGTAGCTGC	CGAATCTTCT	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507182.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507183.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507184.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507185.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT	ACTGGTACAT	GGACAACTGI	TATGGACCGAT	GGACTTACC A	GTCTTGA <mark>T</mark>
OQ507186.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTGI	TATGGACCGAT	GGACTTACC <mark>A</mark>	GTCTTGAT
OQ507187.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACC <mark>A</mark>	GTCTTGAT
00507188.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507189.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507190.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA(GTCTTGAT
00507191.1	GCAGGGGGCCG	GCGGTAGCTGC	CGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCAC	GTCTTGAT
00507192.1	GCAGGGGCCG	CGGTAGCIGC	CGAATCIICI	ACTGGTACAT	GGACAACIGI	TATGGACCGAT	GGACTIACCA	GICIIGAI
00507194 1	CACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CCCTACCTCC	CGARCTTCT	ACTECTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTCAT
00507195 1	GCAGGGGCCG	CCGTACCTCC	CGAATCTTCT	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507196 1	GCAGGGGCCG	CGGTAGCTGC	CGAATCTTCT	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507197.1	GCAGGGGCCG	CGGTAGCTGC	CGAATCTTCT	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507198.1	GCAGGGGCCG	GCGGTAGCTGC	CGAATCTTCT	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507199.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT	ACTGGTACAT	GGACAACTGI	TATGGACCGAT	GGACTTACCA	GTCTTGAT
00507200.1	GCAGGGGCCC	GCGGTAGCTGC	CGAATCTTCT.	ACTGGTACAT	GGACAACTGT	TATGGACCGAT	GGACTTACCC	GTCTTG <mark>A</mark> T
OQ507201.1	GCAGGGGCCC	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTGI	TATGGACCGAT	GGACTTACCA	GTCTTGA <mark>T</mark>
OQ507202.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507203.1	GCAGGGGCCC	GCGGTAGCTGC	CGAATCTTCT.	ACTGGTACAT	GGACAACTG	TATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507204.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTGI	TATGGACCGAT	GGACTTACC <mark>A</mark>	GTCTTGAT
OQ507205.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTGT	TATGGACCGAT	GGACTTACCA	GTCTTGAT
OQ507206.1	GCAGGGGCCG	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTGT	TATGGACCGAT	GGACTTACC A	GTCTTGA T
OQ507207.1	GCAGGGGCCC	GCGGTAGCTGC	CCGAATCTTCT.	ACTGGTACAT	GGACAACTGI	TATGGACCGAT	GGACTTACCA	GTCTTGAT

	2	40	250	260	270	28	ò	290	300	310
KT178121.1*	CGTT	ACAAAGGG	GATGCT	ACCGCATCGA	GCGTGTTGTT	GGA <mark>GA</mark> A	ΑΑΑ <mark>G</mark> ΑΤCΑ	ATATATT	GCTTATGT	AGCTTACCCT
NC_026570.1*	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GA <mark>GA</mark> A	AAA <mark>G</mark> ATCA	ATATATT	G <mark>CTTAT</mark> GI	AGC <mark>TTACC</mark> CT
NC_048515.1*	CGTT.	ACAAAGGG	CGATGCT	A C C G C A T C G A	GCGTGTTGTT	GGA <mark>GA</mark> A	AAAG <mark>A</mark> TCA	ATATATTO	GCTTATGI	'AGC <mark>TTACC</mark> CT
NC_039457.1*	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GGA <mark>GA</mark> A	AAAG <mark>A</mark> TCA	ATATATTO	GCTTATGI	AGCTTACCCT
00507152.1	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GA GA A	AAAGATCA	ATATATTO	GCTTATGI	AGCTTACCCT
00507153.1	CGIT	ACAAAGGGG	CATGCT	ACCGCATCGA	GCGTGTTGTT	GAGAA	AAAGATCA	ATATATTO	GUTTATGI	AGCTTACCCT
00507154.1	CGTT.	ACAAAGGGG	CATGCT	ACCGCATCGA	CCCTCTTCTT		AAAGAICA	ATATATIC		AGCTTACCCT
00507156 1	CGTT	ACAAAGGGG	CATCOT	CCCCATCCA	CCCTCTTCTT	CACAA	AAAGAICA	ATATATIC	CTTATCT	AGCTTACCCT
00507157 1	CGTT	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GAGAA	AAAGATCA	ATATATT	CTTATCT	AGCTTACCCT
00507158.1	CGTT	ACAAAGGG	GATGCT	CCGCATCGA	GCGTGTTGTT	GAGAA	AAAGATCA	ATATATT	CTTATGT	AGCTTACCCT
00507159.1	CGTT.	ACAAAGGG	GATGCT	CCGCATCGA	GCGTGTTGTT	GA GA A	AAAGATCA	ATATATT	GCTTATGI	AGCTTACCCT
OQ507160.1	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GA <mark>GA</mark> A	ΑΑΑ G <mark>Α</mark> ΤСΑ	ATATATT	GCTTATGT	AGC TTACC CT
OQ507161.1	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GGA <mark>GA</mark> A	AAA G <mark>A</mark> TCA	ATATATTO	GCTTATGI	AGC <mark>TTACC</mark> CT
OQ507162.1	CGTT.	ACAAAGGG	CGATGCT	A C C G C A T C G A	GCGTGTTGTT	GA <mark>GA</mark> A	AAA <mark>G</mark> ATCA	ATATATT	G <mark>CTTAT</mark> GI	'AGC <mark>TTACC</mark> CT
OQ507163.1	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GGA <mark>GA</mark> A	AAAGACCA	ATATATTO	GCTTATGI	'AGCTTACCCT
OQ507164.1	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GGA GA A	AAAGATCA	ATATATT	GCTTATGT	AGCTTACCCT
00507165.1	CGTT.	ACAAAGGG	CATGCT	ACCGCATCGA	GCGTGTTGTT	STAGAG	AAAAATCA	ATATATTO	STTTATA1	AGGTTACCCT
00507167.1	CGIT.	ACAAAGGGG	CATGCT	ACCGCATCGA	GCGTGTTGTT	GGAGAA	AAAGATCA	ATATATTO	CTTATG1	AGCTTACCGC
00507168 1	CGTT	ACAAAGGG	CATCCT	CCCCATCCA	CCCTCTTCTT	CACAA	AAAGATCA	ATATATIC	CTTATCT	AGCTTACCCT
00507169.1	CGTT	ACAAAGGG	GATGOT	ACCGCATCGA	GCGTGTTGTT	GAGAA	AAAGATCA	ATATATT	CTTATGT	AGCTTACCCT
00507170.1	CGTT	ACAAAGGG	GATGCT	CCGCATCGA	GCGTGTTGTT	GA GA A	AAAGATCA	ATATATT	CTTATGT	AGCTTACCCT
00507171.1	CGTT	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GA <mark>GA</mark> A	AAAGATCA	ATATATT	GCTTATGT	AGCTTACCCT
0Q507172.1	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GA <mark>GA</mark> A	ΑΑΑ <mark>G</mark> ΑΤCΑ	ATATATTO	GC TTAT GT	AGC <mark>TTACC</mark> CT
OQ507173.1	CGTT.	ACAAAGGG	CGATGCT	A CCGCATCGA	GCGTGTTGTT	GGA <mark>GA</mark> A	AAA G <mark>A</mark> TCA	ATATATT	G <mark>C T T A T</mark> G I	AGC <mark>TTACC</mark> CT
OQ507174.1	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GGA <mark>GA</mark> A	AAAG <mark>A</mark> TCA	ATATATTO	GCTTATGI	'AGC <mark>TTACC</mark> CT
00507175.1	CGTT.	ACAAAGGG	GATGCT	ACCGCATCGA	GCGTGTTGTT	GGA GA A	AAAGATCA	ATATATTO	GCTTATGI	AGCTTACCCT
00507176.1	CGGT	ACAAAGGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GGAGAA	AAAGACCA	ATATATTO	GUTTATGI	AGCTTACCCT
00507178 1	CGIT.	ACAAAGGGG	CATGCT	ACCGCATCGA	CCCTCTTCTT	CACAA	AAAGAICA	ATATATTO	CTTATG1	AGETTACCET
00507179 1	ССТТ	ACAAAGGG	CATCOT	CCGCATCGA	CCGTGTTGTT	GACAA	AAAGATCA	ATATATT	CTTATCT	AGCTTACCCT
00507180.1	CGTT	ACAAAGGG	GATGCT	ACCGCATCGA	GCGTGTTGTT	GAGAA	AAAGATCA	ATATATT	GTTATGT	AGCTTACCCT
00507181.1	CGTT	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GA <mark>GA</mark> A	AAAGATCA	ATATATT	GCTTATGI	AGCTTACCCT
OQ507182.1	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GA <mark>GA</mark> A	ΑΑΑ <mark>G</mark> ΑΤCΑ	ATATATTO	GCTTATGT	AGC <mark>TTACC</mark> CT
OQ507183.1	CGTT.	ACAAAGGG	CGATGCT	A CCGCATCGA	GCGTGTTGTT	GGA <mark>GA</mark> A	AAA <mark>G</mark> ACCA	ATATATT	G <mark>CTTAT</mark> GI	'AGC <mark>TTACC</mark> CT
OQ507184.1	CGTT.	ACAAAGGG	CGATGCT	A C C G C A T C G A	GCGTGTTGTT	GGG <mark>GA</mark> A	AAA <mark>G</mark> AGAC	ATATATTO	GCTTATGI	'AAG <mark>TTACC</mark> CT
00507185.1	CGTT.	ACAAAGGG	GATGCT	ACCGCATCGA	GCGTGTTGTT	GGA GA A	AAAGATCA	ATATATTO	GCTTATGI	AGCTTACCCT
00507186.1	CGTT	ACAAAGGGG	GATGCT	ACCGCATCGA	GCGTGTTGTT	GGAGAA	AAAGATCA	ATATATTO	GUTTATGI	AGCTTACCCT
00507188 1	CGIT	ACAAAGGGG	CATGCT	CCCCATCGA	CCGTGTTGTT	CACAA	AAAGAICA	ATATATTC	CTTATG1	AGETTACCET
00507189 1	ССТТ	ACAAAGGG	CATCOT	CCGCATCGA	CCGTGTTGTT	GACAA	AAAGATCA	ATATATT	CTTATGT	AGCTTACCCT
00507190.1	CGTT	ACAAAGGG	GATGCT	CCGCATCGA	GCGTGTTGTT	GAGAA	AAAGATCA	ATATATTO	GCTTATGT	AGCTTACCCT
0Q507191.1	CGTT.	ACAAAGGG	CGATGCT	CCGCATCGA	GCGTGTTGTT	GAGAAA	ΑΑΑGΑΤCΑ	ATATATT	GCTTATGI	AGCTTACCCT
OQ507192.1	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GGA <mark>GA</mark> A	AAA <mark>G</mark> ATCA	ATATATTO	GCTTATGI	AGC <mark>TTACC</mark> CT
OQ507193.1	CGTT.	ACAAAGGG	CGATGCT	A CCGCATCGA	GCGTGTTGTT	GA <mark>GA</mark> A	AAA G <mark>A</mark> TCA	ATATATT	GC <mark>TTAT</mark> GI	'AGC <mark>TTACC</mark> CT
00507194.1	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GGA <mark>GA</mark> A	AAAGATCA	ATATATTO	GCTTATGI	AGC TTACC CT
00507195.1	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GGA GA A	AAAGATCA	ATATATTO	GCTTATGI	AGCTTACCCT
00507196.1	CGTT.	ACAAAGGGG	GATGCT	ACCGCATCGA	GCGTGTTGTT	GAGAA	AAAGATCA	ATATATTO	CTTATG1	AGCTTACCCT
00507198 1	CGTT	ACAAAGGGG	CATCCT	CCGCATCGA	CCGTGTTGTT	CACAA	AAAGAICA	ATATATIC	CTTATCT	AGCTTACCCT
00507199.1	CGTT	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GAGAA	AAAGATCA	ATATATT	GCTTATGT	AGCTTACCCT
OQ507200.1	CGTT	ACAAAGGG	GATGCT	CCGCATCGA	GCGTGTTGTT	GA <mark>GA</mark> A	AAAGATCA	ATATATT	CTTATGT	AGCTTACCCT
OQ507201.1	CGTT	ACAAAGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GA <mark>GA</mark> A	<mark>ааа</mark> датса	ATATAT	GCTTATGI	AGC <mark>TTACC</mark> CT
OQ507202.1	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GA <mark>GA</mark> A	ΑΑΑ <mark>G</mark> ΑΤCΑ	ATATATTO	GCTTATGI	AGC <mark>TTACC</mark> CT
00507203.1	CGTT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GGA <mark>GA</mark> A	AAAG <mark>A</mark> TCA	ATATATTO	GC TTAT GI	'AGC <mark>TTACC</mark> CT
00507204.1	CGTT.	ACAAAGGG	GATGCT	ACCGCATCGA	GCGTGTTGTT	GGA <mark>GA</mark> A	AAA G <mark>A</mark> TCA	ATATATTO	GCTTATGT	AGC TTACC CT
00507205.1	CGIT.	ACAAAGGG	CGATGCT	ACCGCATCGA	GCGTGTTGTT	GGA <mark>GA</mark> A	AAAGATCA	ATATATTO	CTTATGI CTTATGI	AGCTTACCCT
00507208.1	CCTT	ACAAAGGGG	CATCOT	ACCCCATCCA	CCCTCTTCTT	GAGAAA	AAAGATCA	ATATATT		AGCTTACCCT
02001201.1	CGTT.	RCAAAGGGG	GAIGCI	CCGCAICGA	GCGIGIIGII	GAGAA	IN THE OWNER OF A	AIAIAII		ACCLIACCUL

	320	330	340	350	360	370	380	390
KT178121.1*	TAGACCTTTTT	GAAGAAGGTT	CC GTTA <mark>C</mark> CAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCTG
NC_026570.1*	T AGACCTTTTT	G <mark>AA</mark> G <mark>A</mark> A <mark>GG</mark> T I	CC GTTA <mark>C</mark> CAA	CATGTTT <mark>A</mark> C	TTC <mark>C</mark> ATTGTAG	GT <mark>A</mark> AT <mark>GTATTT</mark>	G <mark>GGTTTAA</mark> AG	CCCTG
NC_048515.1*	TAGACCTTTTT	G <mark>AA</mark> G <mark>A</mark> A <mark>GG</mark> TI	CC GTTA <mark>C</mark> CAA	CATGTTT <mark>A</mark> C	TTCCATTGTAC	G T <mark>A A T G T A T T T</mark>	G <mark>G</mark> GT T T AA AG	CCCTG
NC_039457.1*	TAGACCTTTTT	G <mark>AA</mark> G <mark>A</mark> A <mark>GG</mark> TI	CC GTTA <mark>C</mark> CAA	CATGTTT <mark>A</mark> C'	TTC <mark>C</mark> ATTGT A C	G T <mark>A A T G T A T T T</mark>	G <mark>G</mark> GT T T AA AG	CCCIG
00507152.1	TAGACCTTTTT	G AA GAAGGTI	CC GTTA <mark>C</mark> CAA	CATGTTT <mark>A</mark> C:	TTCCATIGIAC	GTAATGTATTT	GGGTTTAAAG	CCCTG
00507153.1	TAGACCTTTTT	GAAGAAGGT I	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCTG
00507154.1	TAGACCTTTTT	GAAGAAGGTI	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCTG
00507155.1	TAGACCTTTTT	GAAGAAGGTI	CCGTTACCAA	CATGTTTAC:	TTCCATTGTAG	GTAATGTATTT	GGGTTTAAAG	CCCIG
00507155.1	THAGACCTTTTT	GAAGAAGGII	CCGITACCAA	CAIGIIIAC	TTCCATIGIAC	GTAAIGTATTT	GGGITIAAAG	
00507157.1	TRGACCITIT	GAAGAAGGII	CCGTTACCAA	CATGITIAC	TICCATIGIAG	GTAAIGIAIII CTAATCTATTT	CCCTTTAAAG	CCCIG
00507158.1	TTAGACCITIT	CAACAACCTT	CCCTTACCAA	CATCTTTAC	TTCCATIGIAG	CTARTGIAIII	CCCTTTAAAG	CCCTC
00507160 1	TTAGACCTTTTT	GAAGAAGGTT	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCTG
00507161.1	TAGACCTTTTT	GAAGAAGGTT	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCTG
00507162.1	TTAGACCTTTTT	GAAGAAGGTT	CCGTTACCAA	CATGTTTAC	TTCCATTGTAG	GTAATGTATTT	GGGTTTAAAG	CCCTG
00507163.1	TTAGACCTTTTT	GAAGAAGGTC	CCGGTACCAC	CATGTTTAC	TTCCTTTGTAG	GGAATGTATTT	GGGTTTAAAG	CCCTG
0Q507164.1	TTAGACCTTTTT	G <mark>AA</mark> G <mark>A</mark> AGGTI	<mark>сс</mark> дтта <mark>с</mark> саа	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	G <mark>GGTTTAA</mark> AG	CCCTG
00507165.1	TAGACCTTTTT	G <mark>AA</mark> G <mark>AAGG</mark> TI	CC GTAA <mark>C</mark> CAA	CATGTTT <mark>A</mark> C'	TTCCATTAGAG	A T <mark>A A T G T A T T T</mark>	G <mark>G</mark> GT <mark>TTAA</mark> AG	CCCTG
OQ507166.1	CTAGACCTTTTT	A <mark>AA</mark> G <mark>A</mark> A <mark>GG</mark> TI	CC GTAG <mark>C</mark> TAA	C <mark>AAAAAG</mark> AG	TTA <mark>CA</mark> TAAA <mark>A</mark> G	AA <mark>A</mark> GA <mark>GTATT</mark>	A <mark>GGGTTAA</mark> AG	CCCGG
OQ507167.1	TAGACCTTTTT	G <mark>AA</mark> G <mark>A</mark> A <mark>GG</mark> TI	CC GTTA <mark>C</mark> CAA	CATGTTT <mark>A</mark> C:	TTC <mark>C</mark> A <mark>T</mark> TGT <mark>AC</mark>	G T <mark>A A T G T A T T T</mark>	G <mark>GGTTTAA</mark> AG	CCCTG
OQ507168.1	TAGACCTTTTT	G <mark>AA</mark> GA <mark>AGG</mark> TI	CCGTTA <mark>C</mark> CAA	CATGTTT <mark>A</mark> C	T T C C A T T G T A G	G T A A T G T A T T T	G <mark>GGTTTAA</mark> AG	CCCTG
OQ507169.1	TTAGACCTTTTT	G AA G A AGGTI	CC GTTA <mark>C</mark> CAA	CATGTTT <mark>A</mark> C	TTCCATTGTAG	G T A A T G T A T T T	GGGTTT AA AG	CCCTG
00507170.1	TTAGACCTTTTT	GAAGAAGGTI	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGG T T T A A A G	CCCIG
00507171.1	TAGACCTTTTT	GAAGAAGGTI	CCGTTACCAA	CATGTTTAC	TTCCATTGTAG	GTAATGTATTT	GGGTTTAAAG	CCCIG
00507172.1	TAGACCTTTTT	GAAGAAGGTI	CCGITACCAA	CATGITIAC:	TTUCATIGIAG	GTAAIGTATTT GTAAIGTATTT	GGGTTTAAAG	CCCIG
00507174 1	TAGACCTTTTT	GAAGAAGGTT	CCGITACCAA	CAIGITIAC	TTCCATIGIAC	GTAAIGTATTT GTAATGTATTT	GGGITIAAAG	
00507175 1	TAGACCITITT	GAAGAAGGII	CCGITACCAA	CAIGIIIAC	TTCCATIGIAG	GTAAIGTATTT CTAATCTATTT	CCCTTTAAAG	CCCTG
00507176 1	TTAGACCITIT	GAAGAAGGII	CCGTTACCAA	CATGITIAC	TTCCATIGIAG	GIAAIGIAIII	GGGTTTAAAG	CCCTC
00507177 1	TTAGACCTTTTT	GAAGAAGGTT	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCTG
00507178.1	TTAGACCTTTTT	GAAGAAGGTT	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCTG
00507179.1	TAGACCTTTTT	GAAGAAGGTT	CCGTTACCAC	CACGTTTAC	TTCCTTTGTAG	GGAATGTATTT	GGGTTTAAAG	CCCTG
00507180.1	TTAGACCTTTTT	GAAGAAGGTI	CC GTTA <mark>C</mark> CAC	CACGTTTAC	TTCCTTTGTAG	GGAAIGTATTT	GGGTTTAAAG	CCCTG
00507181.1	TTAGACCTTTTT	G <mark>AA</mark> G <mark>A</mark> AGGTI	ССGТТА <mark>С</mark> САА	CATGTTTAC	TTCCATTGTAG	GTAATGTATTT	G <mark>GGTTTAA</mark> AG	CCCTG
OQ507182.1	TAGACCTTTTT	G <mark>AA</mark> G <mark>A</mark> A <mark>GG</mark> T I	CC GTTA <mark>C</mark> CAA	CATGTTT <mark>A</mark> C	TTCCATTGTAC	G T <mark>A A T G T A T T T</mark>	G <mark>G</mark> GT <mark>TTAA</mark> AG	CCCTG
OQ507183.1	T AGACCTTTTT	G <mark>AA</mark> G <mark>A</mark> A <mark>GG</mark> TI	CCGTTACCAC	CATGTTT <mark>A</mark> C:	TTC <mark>CT</mark> TGTAC	GG <mark>A</mark> AT <mark>GTATTT</mark>	G <mark>GTTTTAA</mark> AG	CCCTG
OQ507184.1	TAGACCTTTTT	G <mark>AA</mark> AAGGGTI	CCTTAA <mark>C</mark> CCA	C A T G T T T <mark>A</mark> C '	TTCCTTTGTAC	G G <mark>A A T G T A T T T</mark>	G <mark>G</mark> GT TTAA AG	CCCTG
OQ507185.1	TAGACCTTTTT	G <mark>AA</mark> GA <mark>AGG</mark> TI	CC GTTA <mark>C</mark> CAA	CATGTTT <mark>A</mark> C'	TTCCATTGTAG	GT <mark>AATGTATTT</mark>	G <mark>GGTTTAA</mark> AG	CCCTG
00507186.1	TTAGACCTTTTT	GAAGAAGGTI	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCIG
00507187.1	TAGACCTTTT	GAAGAAGGTI	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCIG
00507188.1	TAGACCTTTTT	GAAGAAGGTI	CCGTTACCAA	CATGTTTAC:	TTCCATTGTAG	GTAATGTATTT	GGGTTTAAAG	CCCIG
00507189.1	TAGACCTTTTT	GAAGAAGGII	CCGITACCAA	CAIGITIAC	TTCCATIGIAC	GTAAIGTATTT	GGGITIAAAG	
00507191 1	TTACACCTTTTT	GAAGAAGGII	CCGTTACCAA	CATGTTTAC	TTCCATIGIAC	GTAAIGIAIII	GGGTTTAAAG	
00507192 1	TTAGACCTTTTT	GAAGAAGGTT	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATCTATT	GCGTTTAAAG	CCCTC
00507193.1	TTAGACCTTTTT	GAAGAAGGTT	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCTG
00507194.1	TTAGACCTTTTT	GAAGAAGGTT	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCTG
00507195.1	TAGACCTTTTT	GAAGAAGGTI	CC GTTA <mark>C</mark> CAA	CATGTTTAC	TTCCATTGTAG	GTAATGTATTT	GGGTTTAAAG	CCCTG
OQ507196.1	TAGACCTTTTT	G <mark>AA</mark> G <mark>A</mark> AGGTI	CC GTTA <mark>C</mark> CAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCCG
0Q507197.1	T AGACCTTTTT	G <mark>AA</mark> G <mark>A</mark> A <mark>GG</mark> TI	CC GTTA <mark>C</mark> CAA	CATGTTT <mark>A</mark> C	TTC <mark>C</mark> ATTGT A C	GTAATGTATTT	G <mark>G</mark> GT <mark>TTAA</mark> AG	CCCTG
OQ507198.1	TAGACCTTTTT	G <mark>AA</mark> G <mark>A</mark> A <mark>GG</mark> T I	CC GTTA <mark>C</mark> CAA	CATGTTTAC	TTCCATTGTAC	G T <mark>A A T G T A T T T</mark>	GGGTTCAAAG	CCCTG
OQ507199.1	TAGACCTTTTT	G AA G A A <mark>GG</mark> TI	CC GTTA <mark>C</mark> CAA	CATGTTT <mark>A</mark> C	TTC <mark>C</mark> ATTGT <mark>A</mark> G	GT <mark>A</mark> AT <mark>GTATTT</mark>	G <mark>G</mark> GT T T AA AG	CCCTG
OQ507200.1	TAGACCTTTTT	G AA G A AGGCI	CC GTT TC CAA	C ATGTTT <mark>A</mark> C	TTCCATTTTAC	GT <mark>A</mark> AT <mark>GTATTT</mark>	GGGGTTAAAG	CCCTG
00507201.1	TAGACCTTTTT	GAAGAAGG T I	CCGTTACCAA	CATGTTT <mark>A</mark> C:	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCTG
00507202.1	TAGACCTTTTT	GAAGAAGGTI	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCIG
00507203.1	TTAGACCTTTTT	GAAGAAGGTI	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCIG
00507204.1	TAGACCTTTTT	GAAGAAGGTI	COGTTACCAA	CATGTTTAC.	TTCCATTGTAG	GTAAIGTATTT GTAATGTATTT	GGGITTAAAG	CCCTG
00507205.1	TTAGACCTTTTTT	GAAGAAGGTI	CCGTTACCAA	CAIGIIIAC	TTCCATIGIAG	GTAAIGTATTT CTAATCTATTT	GGGITIAAAG	CCCIG
00507207.1	TAGACCTTTTT	GAAGAAGGTT	CCGTTACCAA	CATGTTTAC	TTCCATTGTAC	GTAATGTATTT	GGGTTTAAAG	CCCTG

		400			410		420		4	30		440			450		46	i o	
KT178121.1*	CGCG <mark>C</mark> T	CTAC	GTC	IGGA	AG <mark>A</mark> :	T <mark>CTGC</mark> G	AATC	СТ	GTTGC	TAT	GTTAA	AAC	TTT	CAA	GGT	CCGC	Т <mark>С</mark> АТ	G <mark>G</mark>	ATCCAA
NC_026570.1*	CGCG <mark>C</mark> T	СТАС	G T C	IGGA	AG <mark>A</mark> :	ICTGCG	AATC	СТ	GTTGC	TTAT	GTTAA	AAC	ттт	CAA	GGT	CCGC	CT <mark>C</mark> AI	G <mark>G</mark> C	ATCCAA
NC_048515.1*	CGCGCT	CTAC	GTC	IGGA	AGA.	TCTGCG	AATCO	CI	GTTGC	TTAT	ATTAA	AAC	TTTO	CAA	IG G T	CCGC	CTCA1	GGG	ATCCAA
NC_039457.1*	СССССТ	CTAC	GIC.	TGGA	AGA. AGA		AAICC		GTTGC GTTGC	TTAT. TTAT	ATTAA ATTAA	AC	TTTC	CAA	GGT	CCGC	TCAT		AICCAA
00507153.1	CGCGCT	CTAC	GTC	TGGA	AGA	TCTGCG	AATC	сī	GTTGC	TTAT	ATTAA	AC	TTT	CAA	GGT	CCGC	TCAT	GGG	ATCCAA
00507154.1	CGCGCT	CTAC	GTC	IGGA	AGA	CTGCG	AATC	Сī	GTTGC	TTAT	ATTAA	AAC	TTTC	CAA	GGI	CCGC	TCAT	GGG	ATCCAA
OQ507155.1	CGCG <mark>C</mark> T	CTAC	G T <mark>C</mark> 3	T GGA	A G <mark>A</mark> (Г <mark>СТGС</mark> G	AATC	CI	GTTG <mark>C</mark>	TTAT	ATTAA	A A C	T T T 🤇	CAA	GGT	CCGC	СТ <mark>С</mark> АТ	'G <mark>G</mark> (ATCCAA
OQ507156.1	СССС <mark>С</mark> Т	CTAC	G T <mark>C</mark> :	IGGA	A G <mark>A</mark> :	I <mark>CTGC</mark> G	AAT <mark>C</mark>	CI	'GTTG ^C	TTAT	ATTAA	AAC	TTT	CAA	GGI	CCGC	CT <mark>C</mark> AT	G <mark>G</mark>	ATCCAA
00507157.1	CGCGCT	CTAC	GTC	IGGA	AGA:	ICTGCG	AATCO	CI	GTTGC	TTAT.	ATTAA	AAC	TTT	CAA	GGT	CCGC	CTCAI	GGG	ATCCAA
00507158.1	CGCGCT	CTAC	GIC.	IGGA	AGA:		AATCO	C I	GTTGC	TTAT.	ATTAA	AAC	TTTC		GGI		ATCA1	GGGC	ATCCAA
00507160 1	CGCGCT	CTAC	GTC	TGGA	AGA	гстаса	AATCO	\widetilde{c}	GTTGC	TTAT	ATTAA	AC	TTT	CAA	GGT	CCGC	TCAT	GGC	ATCCAA
00507161.1	CGCGCT	CTAC	GTC	TGGA	AGA	TCTGCG	AATC	čт	GTTGC	TTAT	ATTAA	AC	TTTO	CAA	GGI	CCGC	TCAT	GGG	ATCCAA
0Q507162.1	CGCGCT	CTAC	GTC	IGGA	AG <mark>A</mark> :	ICTGCG	AATC	СТ	GTTGC	TTAT	ATTAA	AAC	ттт	CAA	GGT	CCGC	стсат	G <mark>G</mark> G	ATCCAA
OQ507163.1	CGCGCT	CTAC	GTC	I GGA	A G <mark>A</mark> (Г <mark>СТБС</mark> Б	AATC	СТ	GTTGC	TAT	G <mark>TTAA</mark> i	AAC	ттт (CAG	GGT	CCGC	CT <mark>C</mark> AI	G <mark>G</mark> G	ACCCAA
00507164.1	CGCGCT	CTAC	GTC	IGGA	AG <mark>A</mark> :	[CTGCG	AATC	СТ	GTTGC	TAT	G T T A A J	AAC	TTT	CA A	GGI	CCGC	CTCAT	GGG	ATCCAA
00507165.1	CGCGCT	CGAC	GTC	IGGA	AGA:	ICTGCC	AATC	GI	GTTGC	TAT	GTTAA	AAC	TTTI	CAG	GGI	CCGC	TCAI	GGC	Α
00507166.1	CGCGCI		GTC	GGGA	AGA:	ICIGCG	GAAC		GTTGC	TTAT.	ATTAA	AGC	TTTO	CAA	G G I	CCGC		GGG	ATCCAA
00507169 1	CCCCCT	CTAC	GIC.	TGGA	AGA.		AAICO		GTTGC	TTAT.	ATTAA	AAC	T T T C		G G T	CCGC	TOAT	GGG	ATCCAA
00507169 1	CCCCCT	CTAC	GTC	TCCA	AGA		AATC			TTAT	ATTAA	AC	TTTC	CAA	C C T	CCGC	TCAT	a c c	ATCCAA
00507170.1	CGCGCT	CTAC	GTC	TGGA	AGA	ICTGCG	AATC	CI	GTTGC	TTAT	ATTAA	AC	TTTC	CAA	GGT	CCGC	TCAT	GGG	ATCCAA
00507171.1	CGCGCT	CTAC	GTC	IGGA	AGA	ICTGCG	AATC	Сī	GTTGC	TTAT	ATTAA	AAC	тттс	CAA	GGT	CCGC	тсат	GGG	ATCCAA
OQ507172.1	CGCGCT	CTAC	GTC:	IGGA	AG <mark>A</mark> :	I <mark>CTGC</mark> G	AATC	СТ	GTTGC	TTAT	ATTAA	AAC	тттс	CAA	GGT	CCGC	TCA1	G <mark>G</mark> G	ATCCAA
OQ507173.1	CGCGCT	CTAC	GTC	IGGA	A G <mark>A</mark> (Г <mark>СТБС</mark> Б	AATC	СТ	GTTGC	TTAT	ATTAA	A A C	T T T 🤇	CA A	GGT	CCGC	T <mark>C</mark> A I	G <mark>G</mark> C	ATCCAA
00507174.1	CGCGCT	CTAC	GTC	IGGA	A G <mark>A</mark> :	ICTGCG	AATC	CI	GTTGC	TTAT	ATTAA	AAC	TTTC	CAA	GGI	CCGC	CT <mark>C</mark> AI	GGG	ATCCAA
00507175.1	CGCGCT	CTAC	GTC	IGGA	AGA:		AATCO	CI	GTTGC	TTAT	ATTAA	AAC	TTTO	CAA	G G I	CCGC	TCAT	GGG	ATCCAA
00507177 1	CCCCCT	CTAC	GIC.	TGGA	AGA.		AATCO		GTTGC	TTAT.	ATTAA	AC	T T T T	CAG	GGI	CCGC			ACCCAA
00507178 1	CGCGCI	CTAC	GTC.	TGGA	AGA. AGA		AAICC		GTTGC	TTAT.	ATTAA	AC	T T T C		GGT		TCAT		AICCAA
00507179.1	CGCGCT	CTAC	GTC	TGGA	AGA	TCTGCG	AATC	čī	GTTGC	TTAT	ATTAA	AC	TTTC	CAG	GGT	CCGC	ТСАТ	GGC	ACCCAA
00507180.1	CGCGCT	CTAC	GTC	IGGA	AGA	ICTGCG	AATC	CI	GTTGC	TTAT	ATTAA	AAC	TTTC	CAG	GGT	CCGC	TCAT	GGG	ACCCAA
OQ507181.1	CGCGCT	стас	GTC	IGGA	A G <mark>A</mark>	r <mark>ctgc</mark> g	AATC	СТ	GTTGC	TTAT	ATTAA	AAC	ттт	CAA	GGT	CCGC	Т <mark>С</mark> АТ	G <mark>G</mark>	АТССАА
OQ507182.1	CGCGCT	CTAC	GTC	IGGA	AG <mark>A</mark> :	г <mark>стсс</mark> с	AATC	CI	GTTGC	TTAT	A T T A A i	AAC	TTT	CAA	GGT	CCGC	CT <mark>C</mark> AI	G <mark>G</mark> C	ATCCAA
00507183.1	CGCGCT	CTAC	GTC	IGGA	A G A :	ICTGCG	AATC	Ст	GTTGC	TTAT	GTTAA	AAC	TTT	CAG	GGI	CCGC	ТСАТ	GGG	ACCCAA
00507184.1	CGCGCT	CTAC	TTCC	GGGA	AGA:	TCTGCG	AATCO	IC I	GTTGC	TTAT	GTTAA	AAC	TTTO		GGG	CCGC		TGO	ATCCAA
00507186 1	CGCGCI	CTAC	GIC.	TCCA	AGA.		AAICC		GTTGC	TTAT	ATTAA ATTAA	AAC	T T T T			CCGC			AICCAA
00507187 1	CGCGCT	CTAC	GTC	TGGA	AGA'		AATC		GTTGC	TTAT	ATTAA	AC	TTT	CAA	GGT	CCGC	TCAT		ATCCAA
00507188.1	CGCGCT	CTAC	GTC	IGGA	AGA	CTGCG	AATC	Сī	GTTGC	TTAT	ATTAA	AAC	TTTC	CAA	GGT	CCGC	TCAT	GGC	ATCCAA
OQ507189.1	CGCGCT	CTAC	GTC:	IGGA	AG <mark>A</mark> :	r <mark>ctgc</mark> g	AATC	СТ	GTTGC	TTAT	ATTAA	AAC	TTTC	CAA	GGT	CCGC	тсат	G <mark>G</mark> G	АТССАА
OQ507190.1	CGCGCT	CTAC	GTC	IGGA	AG <mark>A</mark> :	Г <mark>СТGС</mark> G	AAT <mark>C</mark>	CI	GTTGC	TTAT	A TTAA	A A C	тттс	CA A	GGT	CCGC	TCAT	G <mark>GC</mark>	ATCCAA
OQ507191.1	CGCGCT	CTAC	GTC	IGGA	AGA	[CTGCG	AATC	CI	GTTGC	TTAT	ATTAA	AAC	TTT	CAA	GGT	CCGC	ТСАТ	GGC	ATCCAA
00507192.1	CGCGCT	CTAC	GTC	IGGA	AGA:	ICIGCG	AATCO	CI	GTTGC	TTAT	ATTAA	AAC	TTTO	CAA	GGI	CCGC	CTCAI	GGG	ATCCAA
00507193.1	CGCGCI	CTAC	GIC.	IGGA	AGA.		AAICO		GTTGU	TTAT.	ATTAA	AAC	TTT		GGI			GGG	AICCAA
00507195 1	CCCCCT	CTAC	GTC	TGGA	AGA:		AATC		CTTCC	TTAT	ATTAA	AC	TTTC	CAA	GGT	CCGC	TCAT		ATCCAA
00507196.1	CCTTCT	CTAC	CCC	GGA	TTA	ICTGCG	ATTC	сī	GTTGC	TTAT	ATTAA	AC	TTTC	CAA	GGT	CCGC	TCAT	GGG	AT
00507197.1	CGCGCT	CTAC	GTC	IGGA	AG <mark>A</mark> :	TCTGCG	AATC	СТ	GTTGC	TTAT	ATTAA	AAC	тттс	CAA	GGT	CCGC	тсат	GGG	АТССАА
OQ507198.1	CGCGCT	CTAC	GTC	I GGA	AG <mark>A</mark> :	Г <mark>СТGС</mark> G	AATC	СТ	GTTGC	TTAT	ATTAA	AAC	ттт	CAA	GGT	CCGC	C T <mark>C</mark> A T	G <mark>G</mark> C	ATCCAA
OQ507199.1	CGCG <mark>C</mark> T	CTAC	GTC	IGGA	A G <mark>A</mark> (I <mark>CTGC</mark> G	AATC	СТ	GTTGC	TTAT	ATTAA	AAC	TTT	CAA	.GGT	CCGC	TCA1	G <mark>G</mark> C	ATCCAA
00507200.1	CGCCCC	CCAC	CTC	IGGA	AGA	ACTGCC	AATC	CI	GTTGT	TTAT	ATTAA	AAA	TTT	CAA	GGG	CCGC	ICCC	GGC	GTCCAA
00507201.1	CGCGCI	CTAC	GTC	IGGA	AGA:		AATC		GTTGC	TTAT.	ATTAA	AAC	TTT(CAA	GGT	CCGC	TCAT	GGG	ATCCAA
00507202.1	CCCCCT	CTAC	GIC.	TCCA	AGA.		AAICO		GTTGC	TTAT.	ATTAA	AC	T T T ()		GGT	CCGC	т с А Т		ATCCAN
00507204.1	CGCGCT	CTAC	GTC	TGGA	A GA	гстесе	AATC	\mathbf{c}_{1}	GTTGC	TTAT	ATTAA	AAC	TTT	CAA	GGT	CCGC	TCAT	GCC	ATCCAA
00507205.1	CGCGCT	CTAC	GTC	IGGA	AGA	CTGCG	AATC	Сī	GTTGC	TTAT	ATTAA	AAC	TTT	CAA	GGI	CCGC	TCAT	GGC	ATCCAA
00507206.1	сссст	CTAC	GTC	IGGA	AGA	ICTGCG	AATC	CI	GTTGC	TTAT	ATTAA	AAC	TTT	CAA	GGT	CCGC	TCAT	G <mark>G</mark>	ATCCAA
OQ507207.1	CGCGCT	CTAC	GTC:	IGGA	AG <mark>A</mark> :	T <mark>CTGC</mark> G	AATC	СТ	GTTGC	TTAT	ATTAA	AAC	TTT	CAA	GGT	CCGC	ТСАТ	G <mark>G</mark> C	ATCCAA

	470	480	490	500	510	520	530	540
KT178121.1*	GTTGAAAG	AGATAAATTGA.	ACAAGTAT	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
NC 026570.1*	GTTGAAAG	AGATAAATTGA	ACAAGTAT	GGTCGTCCCC	TGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
NC 048515 1*	GTTGAAAG	ΔGΔΤΔΔΔΤΤGΔ	ACAAGTAT	GGTCGTCCCC	TGTTGGGATGT	ΔΟΤΔΤΤΔΔΔ	CCTAAATTGG	GGTTATCTGCT
NC 039457 1*	GTTGAAAG	ACATAAATTCA	ACAAGTAT	GGTCGTCCCC	FGTTGGGATGT	АСТАТТАЛА	CCTABATTGG	GGTTATCTGCT
00507152 1	GTTGAAAG	ACATAAATTCA	ACAACTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTABATTCC	GGTTATCTCCT
00507152.1	CTTCADAC	AGATAAATIGA.	ACAACTA1	COTCOTCOCC	FOTTOGGGAIGI	ACTATTAAA	CCTABATTCC	COTTATOIGOI
00507153.1	GIIGAAAGA	AGATAAATIGA.	ACAAGIAI	GGICGICCCC.	CTTCCCATCT	ACTATIAAA	COTANATIGG	GGIIAICIGCI
00507154.1	GIIGAAAGA	AGATAAATIGA.	ACAAGIAI	GGICGICCCC.	IGIIGGGAIGI	ACTATIAAA	CCIAAAIIGG	GGITAICIGCI
00507155.1	GIIGAAAGA	AGATAAATIGA.	ACAAGIAI	GGICGICCCC.	IGIIGGGAIGI	ACTATIAAA	CCIAAAIIGG	GGIIAICIGCI
00507156.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCIGCT
OQ507157.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGICGICCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507158.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAT	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507159.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507160.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507161.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
00507162.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTTO	GGTCGTCCCC	FGGTGGGATGT	ACTATTAAA	CCTAAAGTGG	GGTTATCTGCT
00507163.1	GTTGAAAG	AGAGAAATTGA.	ACAAGTGO	CGTCGTCCCC	FGTTGGGGTGT	ACTATTAAC	CTTAAATTGG	GGTTATCTGTT
00507164.1	GTTGAAAG	AGATAAATTGA	ACAAGTAT	GGTCGTCCCC	TGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
00507165 1								
00507166 1	GTTGAAAG	асатаааттса	асаастал	GGTCGTCCCC	гаттаааатат	астаттала	сставаттсе	GGTTATCTCCT
00507167 1	CTTCAAAC	ACATAAAIICA.	ACAACIAI	COTCOTCCCC	CTTCCCATCT	ACTATTAAA	CCTABATTCC	COTTATCIOCI
00507169 1	GIIGAAAGA	NGATAAATIGA.	ACAAGIAI	GGICGICCCC.	CTTCCCATCT	ACTATIAAA	CCIAAAIIGG	GGIIAICIGCI
00507168.1	GIIGAAAGA	AGATAAATIGA.	ACAAGIAI	GGICGICCCC.	IGIIGGGAIGI	ACTATIAAA	CCTAAATIGG	GGTTATCIGCT
00201169.1	GIIGAAAGA	AGATAAATIGA.	ACAAGIAI	GGICGICCCC.	IGIIGGGAIGI	ACTATIAAA	CCIAAAIIGG	GGITAICIGCI
0050/1/0.1	GITGAAAGA	AGATAAATTGA.	ACAAGTAI	GGICGICCCC.	IGIIGGGAIGI	ACTATTAAA	CCTAAATTGG	GGTTATCIGCT
00507171.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507172.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507173.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	T G T T G G G A T G T	АСТАТТААА	CCTAAATTGG	GGTTATCTGCT
OQ507174.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507175.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
00507176.1	GTTGAGAG/	AGAAAAATTGA.	ACATGTAT	GGCCGTCCCC	FGTTGGGGTGT	ACTATTAAA	CCTAAATTGG	GGTTTTCTGCT
00507177.1	GTTGAAAG/	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	IGTTGGGATGT	TCTATTAAA	CTTTTATTGG	GGTTA
00507178.1	GTTGAAAG	AGATAAATTGA	ACAAGTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
00507179.1	GTGAAAAG	TGATAAATTGA	ACAAGTGT	GGTCGCGCCC	TGTTGGGGTGT	ACTATTAAA	CCTAAATTGG	GGTTCTGTGCT
00507180 1	GTGAAAAG	TGATAAATTGA	ACAGATGI	GETCGCGCCC	TGTTGGGGTGT	ACTATTAAA	CCTAAATTGG	GGTTCTGTGCT
00507181 1	GTTGAAAG	ΔΟΔΤΔΔΔΤΤΟΔ	ACAAGTAT	GGTCGTCCCC	FGTTGGGATGT	ΔΟΤΔΤΤΔΔΔ	CCTAAATTGG	GGTTATCTGCT
00507182 1	GTTGAAAG	ACATAAATTCA	ACAACTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTABATTGG	GGTTATCTGCT
00507193 1	CTTCAAAC	ACACAAATTCA	ACAACTA1		LGIIGGGAIGI FCTTCCCATCT	ACTATIAAA	CCTANATICC	COTTATOIGCI
00507194 1	CTTCAAAC	AGAGAAAIIGA.	ACAAGIAI ACAATTAI		CTTCCCCTCT	ACTATTAAA	CCTAAATTCC	GGIINICIGCI CTTTNTCTCCT
00507185 1	CTTCANAC	AGAIAAAIIGA. ACATAAATIGA	ACAAIIAI	GGCCGICCCC.	IGIIGGGGIGI FETTECCATET	ACTATIAAA	CCIAAAIIGG	GITTAICIGCI
00507185.1	GIIGAAAGA	AGAIAAAIIGA. AGAEDDDDEEGD	ACAAGIAI	GGICGICCCC.	IGIIGGGAIGI	ACTATIAAA	CCIAAAIIGG	GGIIAICIGCI
00507108.1	GIIGAAAGA	AGATAAATIGA.	ACAAGIAI	GGICGICCCC.	IGIIGGGAIGI	ACTATIAAA	CCIAAAIIGG	GGIIAICIGCI
00201181.1	GIIGAAAGA	AGATAAATIGA.	ACAAGIAI	GGICGICCCC.	IGIIGGGAIGI	ACTATTAAA	CCIAAATIGG	GGITAICIGCI
00507188.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC.	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
00207189.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC.	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507190.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507191.1	GTTGAAAGA	AGATAAATTGA.	АСААСТАЛ	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507192.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507193.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507194.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAT	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507195.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507196.1								
00507197.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
00507198.1	GTTGAAAG	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	IGTTGGGATGT	АСТАТТААА	CCTAAATTGG	GGTTT
00507199.1	GTTGAAAG	AGATAAATTGA	ACAAGTAT	GGTCGTCCCC	FGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
00507200.1	GTTGAAAA	AAATAAATTGA	ACAAAAA	GGCCGCCCCC	CGTTGGGATGG	ACTATTAAA	CCCAAATCGG	AGTTT
00507201 1	GTTGAAAG	AGATAAATTGA	ACAAGTAT	GETCETCCCC	TGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTCCT
00507202 1	GTTGAAAG	ΔGΔΤΔΔΔΤΤCΛ	ΔΟΔΔΩΤΑΙ	GGTCGTCCCC	TGTTGGGATGT	Δάτδττδλλ	CCTABATTCC	GGTTATCTCC
00507202.1	CTTCAAAC	ACATAAAIIGA.	ACAACIAI	COTCOTCCCC.	TGTTGGGGAIGI	ACTATIANA ACTATTANA	CCTABATTCC	COTTATOIGO
00507203.1	GIIGAAAGA	ΑΘΑΙΑΑΑΙΙΘΑ. ΛΟλΠλλλΠΠΟλ	ACAAGIAI ACAACTAT		LGIIGGGAIGI FCTTCCCAMOM	ACTATIAAA XOTXTTXXX	COTAAAIIGG	COTTAICIGUE
00507204.1	GIIGAAAGA	AGAIAAAITGA.	ACAAGIAI	GGICGICCCC.	IGIIGGGATGT	ACTATIAAA	CCIAAAIIGG	GGITAICIGCT
00201205.1	GIIGAAAGA	AGAIAAATTGA.	ACAAGTAI	GGICGTCCCC	LGIIGGGATGT	ACTATTAAA	CCIAAATTGG	GGIIATUTGUT
00507206.1	GTTGAAAGA	AGATAAATTGA.	ACAAGTAI	GGTCGTCCCC	LGTTGGGATGT	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT
OQ507207.1	GTTGAAAGA	AGATAAATTGA.	<u>ACAAGTAI</u>	GGTCGTCCCC	<u>rgttgggatgt</u>	ACTATTAAA	CCTAAATTGG	GGTTATCTGCT

	550	560	570	580	590	600	610	620
KT178121.1*	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	STCTTCGCGG:	FGGACTTGATT	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
NC_026570.1*	AAAAACTA	CGGTAGAGCTGT	TTATGAATG	GTCTTCGCGG:	[GGACTTGATT	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
NC_048515.1*	AAAAACTA	CGGTAGAGCTGT	TTATGAATG	GTCTTCGCGG	[GGACTTGATT]	TTACCAAAGAT	GATGAGAA	CGTGAACTCA
NC_039457.1*	AAAACTA	CGGTAGAGCTGT	TTATGAATO	STCTTCGCGG	FGGACTTGATT	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
0Q507152.1	AAAACTA	CGGTAGAGCTGT	TTATGAATG	STCTTCGCGG:	FGGACTTGATT	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
OQ507153.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATG	STCTTCGCGG	[GGACTTGATT]	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
OQ507154.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	GTCTTCGCGG	[GGACTTGATT]	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
OQ507155.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	STCTTC				
00507156.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	STCTTCGCGG	FGGACTTGATT	ITACCAAAGAI	GATGAGAA	CGTGAACICA
00507157.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	STCITCGCGG	IGGACTTGATT	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
00507158.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATG	STCTTCGCGG	IGGACTTGATT	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
00507159.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATG	STCTTCGCGG:	IGGACTTGATT IGGACTTGATT	FTACCAAAGA1	GATGAGAA	GIGACICA
00507160.1	AAAAACIA	CGGIAGAGCIGI	TTATGAATG		IGGACIIGAII	I I ACCAAA		
00507161.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	TCTTCGCGG.	IGGACITGATI	TTACCAAAGAT	GATGAGAA	CGTGAACICA
00507162.1	AAAAACIA	CORDONATION	TCATGAAL	TCTTCGCGG.	LGGACIIGAII FCCCATTCATT	TACCAAAGIG	GAIGAGAA	CCCCAACICC
00507163.1	AAAAAAIA	COTAGAGIIGI	TGAIGAAIG	STOTUCGUGG.	LGGGAIIGAII	I I ACCAAAGA I	GAIGAGAA	CECEGACICE
00507164.1	AAAAACIA	GGIAGAGCIGI	TIAIGAAIG	SICIICECEE.	IGGACIIGAII	TIACCAAAGAI	GAIGAGAA	GIGAACICA
00507166 1							CATCACAA	
00507167 1	AAAAACCI	COTAGAGCIGI	TTATCAALC	TCTTCGCGG.	LGIGGIIGAII FCCACTTCATT	TTACCAAAGAI	CATCACAA	CTCAACTCA
00507168 1	AAAAACTA	CGETAGAGCIGI	TTATCAATC	TCTTCGCGG.	LGGACIIGAII FGGACTTGATT	TTACCAAAGAI	CATCACAA	CETENACICA
00507169 1		CGGTAGAGCIGI	TTATGAAIG	STOTICGCGG:	IGGACIIGAII IGGACTTGATT	TTACCANAGAI	GATGAGAA	COTGAACTCA
00507170 1	AAAAACTA	CGETAGAGCICI	TTATGAATG	TCTTCGCGG	EGGACTTGATT'	TTACCAAAGAT	GATGAGAA	CIGIGAACICA
00507171 1	ΔΔΔΔΔΟΤΔ	CGGTAGAGCTGT	TTATGAATG	TCTTCGCGG	IGGACTTGATT'	TTTCCAAAGAT	GATGAGAA	CGTGAACTCA
00507172.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	TOTTOGOGG	IGGACTTGATT'	TTACCAAAGAT	GATGAGA.	
00507173.1	AAAAACTAG	CGGTAGAGCTGT	TTATGAATO	TCTTCGCGG	GGACTTGATT	TTACCAAAGAT	GATGAGAA	CGTGAACTCA
00507174.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATC	TCTTCGCGG	GGACTTGATT	TTACCAAAGAT	GATGAGAA	CGTGAACTCA
00507175.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	TCTTCGCGG	GGACTTGATT	ITACCAAAGAT	GATGAGAA	CGTGAACTCA
00507176.1	AAATACGA	CGGTATTGATGT	TTCGGAATO	GTCTTCGCAA:	GGAATTGATT	ITACCAAATTI	GATGAGAA	CGTCAACTGG
0Q507177.1								
OQ507178.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	STOTTOGOGGI	FGGACTTGATT	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
OQ507179.1	AAAAACTA	CGAGAGAGTTAT	TTATGGATO	STCTCCGCGG:	r g g g a t t g a t t '	ITACCAAATAT	GATGCGGA	CGTGAACTCA
OQ507180.1	AAAAACTA	CGAGAGTGCTAT	TTATGGATO	GTCTCCGCGG:	I G G G A T T G A T T '	ITACCAAAIGI	GAGAAGAA	CTTGAACTCA
OQ507181.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATG	GTCTTCGCGG	IGGACTTGATT'	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
OQ507182.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATG	STCTTCGCGG:	[GGACTTGATT]	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
OQ507183.1	AAAAACTA	CGAGAGAGCTGT	TTATGGATO	STCTCCGCGG:	I G G A <mark>T</mark> T T G A T T '	TTACCAAAGAC	CAATGAGAA	ACTGAACTCA
OQ507184.1	AAATACGA	GAGTATTGCTGT	TTACGAATO	GTTTACGCGG	[GGAACTGATT]	ITACCAAATTI	GCTGAGAA	CGTTCTCTTG
00507185.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	STCTTCGCGG	IGGACTTGATT	ITACCAAAGAI	GATGAGAA	CGTGAACICA
OQ507186.1	AAAAACTAG	CAGTAGAGCTGT	TTATGAATO	STCTTCCCGG	GGACTTGATT	ITACCAAACAI	GATGAGAA	CGTGAACTCA
00507187.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	GTCTTCGCGG:	[GGACTTGATT]	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
00507188.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATG	STCTTCGCGG	[GGACTTGATT]	ITACCAAAGA1	GATGAGAA	CGTGAACTCA
00507189.1	AAAAACTA	CGGTAGAGCTGT	TTAIGAATO	STCTTCGCGG.	IGGACTTGATI'	TTACCAAAGAT	GATGAGAA	CGTGAACICA
00507190.1	AAAAACIA	COTAGAGUIGI	TTAIGAALU	STOTICGUGG.	LGGACIIGAII Eccactecate	I I ACCAAAGA I	GAIGAGAA	CUCACICA
00507191.1	AAAAACIA	CCTACAGCIGI	TTATGAALG	STUTTUGUGG.	LGGACIIGAII ECCACTTCATT	TTACCAAAGAI	GAIGAGAA	CETCAACICA
00507192.1	AAAAACIA	CCTACACCICI	TTATCAALC	STOTICGCGG.	LGGACIIGAII FCCACTTCATT	TTACCARAGAI	CATCACAA	CTCAACICA
00507194 1	AAAAACTA	CGGIAGAGCIGI	TTATCAATC	TCTTCGCGG.	GGACIIGAII	IIACCAAAGAI	GAIGAGAA	GIGNACICA
00507195 1	AAAAACTA	COTACACCICI	TTATCAATC	TCTTCCCCC	CCACTTCATT'	ттассаласат	CATCACAA	CTCAACTCA
00507196 1		50011101100101	1111011110		l'dono i toni i	1 1710 Ommoni	. on rondini,	5010mmc1cm
00507197 1	АААААСТА	CGETAGAGETET	TTATGAATO	TOTTOGOGG	IGGACTTGATT'	ттассавадат	GATGAGAA	GTGAACTCA
00507198.1							. on i on dini.	
00507199.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATG	STCTTCGCGG	IGGACTTGATT'	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
00507200.1								
00507201.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	STCTTCGCGG	GGACTTGATT	TTACCAAAGAT	GATGAGAA	CGTGAACTCA
00507202.1								
OQ507203.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	STOTTOGOGG:	GGACTTGATT'	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
OQ507204.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	STCTTCGCGG	rggacttgatt'	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
OQ507205.1	AAAAACTA	CGGTAGAGCTGT	TTATGAATO	STOTTOGOGG	IGGACTTGATT'	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
OQ507206.1	AAAACTA	CGGTAGAGCTGT	TTATGAATO	GTCTTCGCGG:	IGGACTTGATT'	ITACCAAAGAI	GATGAGAA	CGTGAACTCA
OQ507207.1	AAAAACTA	<u>CGGTAGAGCTGT</u>	TTATGAATO	<u>STCTTCGCGG</u>	<u>IGGACTTGATT</u>	<u>ITACCAAAGAI</u>	GATGAGAA	CGTGAACTCA

	630	640	650	660	670	680	690	700
KT178121.1*	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	GCTTTT	GTGCCGAAGCAC	TTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
NC_026570.1*	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	STCTTT	gtgccgaa <mark>g</mark> cac	TTTATAAAGCAC.	AGGCTGAAAC	CAGGTGAA
NC_048515.1*	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	STCTTT	GTGCCGAA <mark>G</mark> CAC	TTTATAAA GCAC	AGGCTGAAAC	CAGGTGAA
NC_039457.1*	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	4 K C T T T T	GTGCCGAA <mark>G</mark> CAC	CTTTA <mark>TAAA</mark> GCAC	AGGCTGAAAC	CAGGTGAA
OQ507152.1	CAACCATTTAT	GCGTIGGAGAGA	TCGTT					
OQ507153.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	STCTTTT	GTGCCGAA <mark>G</mark> CAC	TT		
OQ507154.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	STCTTT	G T G C C G A A <mark>G</mark> C A C	CTTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
00507155.1						•••••		
00507156.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTCC	STCTTTT	GTGCCGAAGCAC	TTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
00507157.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTCC	STCTTTT STCTTTT	GTGCCGAAGCAC	TTTATAAAGCAC	AGGCIGAAA.	
00507158.1	CAACCAITTAT	GUGIIGGAGAGA	TCGTTTCC	STCIIII	GTGCCGAAGCAC			
00507159.1	CAACCAITIAT	GUGIIGGAGAGA	.10611100	5101111	GIGUUGAAGUAU	, IIIAIAAA		
00507161 1	CAACCATTTAT	CONTRONONON	TCGTTTC		стс			
00507162 1	CAACCATTAAT	GCGIIGGAGAGA GCGIIGGAGAGA	TCGTTTC		GCGCCGAAGCAC	TTTCTAAACCCC	ACCCTCTTAC	TCCTCAA
00507163 1	CAACCATTTAC	GTGTTGGAGAGA	TCGTTTC	STCTCTT	GTGCCGAAGCAC	CTTATAAAGCAC	AGGTTGGAAC	AGGTGGA
00507164.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	STOTITT	GTGCCGAAGCAC	TTTATAAAGCAC	AGGCTGAAAC	LAGGTGAA
00507165.1								
00507166.1								
0Q2507167.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	STCTTT	gtgccgaa <mark>g</mark> cac	TTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
00507168.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	GTCTTT	GTGCCGAA <mark>G</mark> CAC	TTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
002507169.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	GT CTTTT	GTGCCGAA <mark>G</mark> CAC	TTTA <mark>TAAA</mark> GCAC	AGGCTGAAAC	CAGGTGAA
OQ507170.1	CCACCATTTAT	GCGTTGGAGAGA	TCGTTTC	GTCTTT	T T G C C G A A <mark>G</mark> C A C	TTTA <mark>TAAA</mark> GCAC	CAGCTGAAAC	CGGGGAAA
OQ507171.1	CAACCATTTAT	GCTTTGGAGAGA	TCGGTTC	GTCTTT	GTGCCCAA <mark>A</mark> CAC	CTTTA <mark>TAAA</mark> GTAC	AGGCTGAAAC	CAG
OQ507172.1								
OQ507173.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	STCTTTT	G T G C C G A A <mark>G</mark> C A C	CTTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
00507174.1	CAACCATTTAT	GCGTIGGAGAGA	TCGTTTC	STCTTTT	GTGCCGAAGCAC	CTTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
00507175.1	CAACCATTTAT	GCGTIGGAGAGA	TCGTTTCC	JTCTTTT	GTGCCGAAGCAC	CTTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
00507176.1	CAACCTTTTAG	AAGTTGGAGAGA	TAGCTTCC	3GATTTT	GTGCCGAAA	••••		•••••
00507170.1			TOOTTTO					
00507179 1	CAACCAITIAI	GUGIIGGAGAGA CTCTTCCACACA	TCCTTTC		GIGUUGAAGUAU	TTTATAAAGCAC	AGGUIGAAAC	CCCCCAA
00507180 1	CCACCATITAC	CCCTTCCACACA	TCCTTTC		CCCCCCAAACAC	TTTATAAACCAG	ACCACCAAAC	CAGGGGAA
00507181 1	CAACCATTTAT	GCGIIGGAGAGA	TCGTTTC		GTGCCGAAGCAC	TTTATAAAGGIC	AGGCTGAAAC	CAGGGGAA
00507182.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	TCTTT	GTGCCGAAGCAC	TTTATAAAGCAC	AGGCTGAAAC	LAGGTGAA
00507183.1	CAACCACTTT	GCGTTGGAGAGA	TCGTTTC	TCTTT	ATGCCGAAGCAG	TTTATAAAGCAC	AGGCTGAAAC	GAGGTGAA
00507184.1	CAACCTTTTAG	AAGTIGGCGAGA	ACATTTC	TTTTTA	GTATGGAAGCAC	TTTATAAAGCAC	AGGCTGAAAI	TGGTAAA
0Q507185.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	STCTTT	GTGCCGAA <mark>G</mark> CAC	TTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
00507186.1	CCACCCTCTAT	GCGT <mark>G</mark> GGAGAGA	ACGGTTC	TTTTCT	GTGCCGA			
OQ507187.1	CAACCATTTAT	GCGTIGGAGAGA	TCGTTTC	T C T T T T	GTGCCGAA <mark>G</mark> CAC	TTTA <mark>TAAA</mark> GCAC	AGGCTGAACC	CAAGTGAA
OQ507188.1	CACCCATTTAT	GCGTTGGAGAGA	TCGTTTC	G T C T T T T	GTGCCGAA <mark>G</mark> CAC	TTTA <mark>TAAA</mark> GCAC	AGGCTGAAAC	CAGGTGAA
OQ507189.1	CAACAATTTAT	GCGTTGGAGAGA	TCGTTTC	GTCTTT	GTGCCGAA <mark>G</mark> CAC	CTTTA <mark>TAAA</mark> GCAC	AGGCTGAACC	CAAGTGAA
OQ507190.1	CAACCATTTAT	GCGTTGGAAAGA	TCGTTTC	STCTTT	GGGGCAAAGCAC	CTTTATAAAGCAA	AGGCTGAAAC	CAGGTGAA
00507191.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	STCTTT	gtgccgaa <mark>g</mark> cac	CTTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
00507192.1	AA							
00507193.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	STCTTTT	GTGCCGAAGCAC	TTTATAAAGCAC.	AGGCTGAAAC	CAGGTGAA
00507194.1						····		
00507195.1	CARCCATTIAT	GCGIIGGAGAGA	.10611100	5101111	GIGCCGAAGCAC	TITATAAAGCAC	AGGCIGAAAC	AGGIGAA
00507197 1	CAACCATTTAT	CCGTTCCACACA	TCGTTTC		GTGCCGANCCAC	TTTATAAACCAC	ACCCTCAAAC	DCCTCAA
00507198 1	CARCCATITAT	OCCITOCACACA	10011100		OIUCCUARUCAC	IIIAIAAAOCAC	AUDUIDAAAU	AUGIOAN
00507199.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	TCTTTT	GTGCCGAAGCAC	TTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
00507200.1								
00507201.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	STCTTT	GTGCCGAAGCAC	TTTATAAAGCAC	AGGCTGAAAC	AGGTGAA
00507202.1								
00507203.1	CAACCATTTAT	GCGTIGGAGAGA	TCGTTTC	STCTTTT	GTGCCGAAGCAC	TTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
OQ507204.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	G T C T T T T	gtgccgaa <mark>g</mark> cac	TTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
OQ507205.1	CAACCATTTAT	GCGTIGGAGAGA	TCGTTTC	T C T T T T	gtgccgaa <mark>g</mark> cac	TTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
OQ507206.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	G T C T T T T	GTGCCGAA <mark>G</mark> CAC	TTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA
OQ507207.1	CAACCATTTAT	GCGTTGGAGAGA	TCGTTTC	GT <u>CTTT</u>	<u>GTGCCGAA</u> GCAC	CTTTATAAAGCAC	AGGCTGAAAC	CAGGTGAA

	710	720	730	740	750	760	770 780
KT178121.1*	ATCAAAGGGCAT	TACTTGAATG	CTACTGCAGGTA	CATGCGAAGA	AATGATCAAA	AGAGCTGTAT	TTGCTAGAGAATTG
NC_026570.1*	ATCAAAGGGCAT	TACTTGAATG	CTACTGCAGGTA	CATGCGAAGA	AATGATCAAA	AGAGCTGTAT	TTGCTAGAGAATTG
NC_048515.1*	ATCAAAGGGCAT	TACTIGAAIG	LIACIGCAGGIA CTACTGCAGGTA	CATGCGAAGA	AAIGAICAAA AATGATCAAA	AGAGCIGIAI. AGAGCTGTAT'	TIGCIAGAGAAIIG TIGCIAGAGAAIIG
OQ507152.1							
OQ507153.1							
00507154.1	ATCAAAGGGCAT	FACTTGAATG	CTACTGCAG				• • • • • • • • • • • • • • • •
00507156.1	ATCAAAGGGCAT	TACTTGAATG					
OQ507157.1							
OQ507158.1	• • • • • • • • • • • • •						
00507159.1							
OQ507161.1							
00507162.1	ATCCAAGGGCAT	TACTTTTATG	CTTTA				
00507163.1	ATCAAGGAGCAT	TACTTGGATG(CTTCGGCC				
00507165.1	AICAAAGGGCAI	IACIIGAAIG	LACIGCAGGIA	CAIGCGAAA.			
OQ507166.1							
OQ507167.1	ATCAAAGGGCAT	TACTTGAATG	CTACTGCAGGTA	CATGCGA			
00507168.1	ATCAAAGGGCAT	TACTTGAATG	CTACTGCAGGTA	CATGCGAAGA	ΑΑΤΑΤΤĊΑΑΑ	AGAGGTGTCT	TTGCCAGGGAATTG
00507170.1	ATCAAAGGGCAT	TACIIGAAIG	LACIGCAGGIA	CAIGCGAAG.			
OQ507171.1							
OQ507172.1							
00507173.1	ATCAAAGGGCAT	TACTTGAATG	CTTCTGCATGTA	CATGCGAAAA	ACTGATTAAA	AGAGCTGTAT	CTGCGAGACAATTG
00507175.1	ATCAAAGGGCAT	TACTTGAATG	CTACIGCAGIIA	CTTGCCAAGA	CGTGATCAAA	ATAGCAG	
OQ507176.1							
00507177.1							
00507178.1	ATCAAAGGGCAT ATCAAAGGGTAT	FACTIGAATG(FACTGCAATG	CTACTGCAGTTA	CATGCGAAGA	AACTATTAAA	AGGGCTGTCT	TTGATAGAGAACGG
00507180.1	ATTGAAGTAT						
OQ507181.1	ATCAAAGGGCAT	FACTTGAATG	CTACTGCAGGTA	CATGCAAAA.			
00507182.1	ATCAAAGGGCAT	TACTTGAATG	CTACTGCAGGTA	CATTGCAA			
00507183.1	ATCAAAGGGGGGT	TACTIGAAIG	LIACIGCAGGIA TTACTGCAGGTA	CCGGCGAAGA	AAIGAICAAA AATGAGTAAA	AGAGCIGIAI	TTAGTAGAGAATIG
OQ507185.1	ATCAAAGGGCAT	TACTTGAATG	CTACTGCAGGTA	CATGGCAAA.			
OQ507186.1							
00507187.1	ATCAAAGGGCAT	FACTTGGATG(CTATCCGTG				
00507189.1	ATCACAGGGCAT	TACTGGAATG	CATTGCAGGTA	CATTCCAAGA	ATTGGCCAAG	AGAAATGTTC'	TTGCGAGAGAATTG
OQ2507190.1	ATCAACGCGCAT	TACTTGAATG	CTACTGCAGTTA	CCTGCGAAGA	AATGGCCAAA	TGGGCTGTAT	TTGTAAGAGAACTG
OQ507191.1	ATCAAAGGGCAT	TACTTGAATG	CTACTGAGT				
00507192.1	ATCAAAGGGCAT	TACCTGAATG		CATECGAAGA	AATGATCAAG	AGTTCTATAT	TTGCTAGAGAATTG
OQ507194.1							
OQ507195.1	ATCAAAGGGCAT	TACTTGGATG	CTACTGCAGGTG	CACTTGAAGA	ACTATTCAAA	AGAGCTTCTT	TTGCCACGGAATTG
OQ507196.1	 TTCAACCCATAC						
00507198.1	IICAACGCAIAC	IGCIIGAAIG(LIACIGCAGICA	CAIGCGAAGA	AGCGAICAIG	IIIICCCIAC	ACACAAGAAAACCG
OQ507199.1	ATTCAACGGCAT	TACTTGAATG	CTACTGCAGTTA	CATGGGAAGA	AATTCTCAAA	AGAGCTCTAT	TCACTAGAGAATTG
00507200.1							
00507201.1	ATCAAAGGGCAT	IACTTGGATG	CIACTGCAGGTC	CAGGGGGAA.		•••••	• • • • • • • • • • • • • • • •
oQ507203.1	ATCAAAGGGTAC	 FACTTGAATG(CTATTGCAGGCA	CTCGCGAAGA	GATCATCTGG	AGAGAGGTAT	TTGCTGC
OQ507204.1	ATCAAAGGGCAT	FACTTGAATG	CTACTGCAGTTA	CATGCGAAAA	CATGGTCAAA	AGTGTTGAAT	TIGCTACAT
00507205.1	ATCAAAGGGCAT	TACTTGAATG	CTACTGCAGGTA	CATGCGAAGA	GATGCTTAAA	AACGCTGTAT	TIGCTTTAGCATIG
00507208.1	ATCAAAGGGCAT	TACIIGAAIG	CIACIGUAGIIC CIACIGCAGGTA	CAIGCGAAGA	AAIGAICAAA AATTTTCAAA	AGAGCCCTAT	TIGCGAGAGACIIG TIGAGAGAGAAACG
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	79 Q	800	810	820	830	34 Q	850
KT178121.1* NC_026570.1* NC_048515.1*	GGCGTTCCGATCGTAA GGCGTTCCGATCGTAA GGCGTTCCGATCGTAA	TGCATGACTA TGCATGACTA TGCATGACTA	CTTAACGGGG CTTAACGGGGG CTTAACGGGGG	GGATTCACCGC GGATTCACCGC GGATTCACCGC	AAATACTAGC AAATACTAGC AAATACTAGC	ITGGCTCATI ITGGCTCATI ITGGCTCATI	CATTGCCG CATTGCCG CATTGCCG
00507152.1	GGCGIICCGAICGIAA			JGAIICACCGC	AAAIACIAGC	LIGGCICAII	AIIGCCG
OQ507153.1							
OQ507154.1							
OQ507155.1							
OQ507156.1							
00507157.1							
00507158.1					• • • • • • • • • • •		
00507160 1							
00507161.1						<i></i> 	
0Q507162.1							
OQ507163.1							
OQ507164.1							
00507165.1							
00507166.1	• • • • • • • • • • • • • • • • • • •	• • • • • • • • • •			• • • • • • • • • •		• • • • • • • •
00507169 1		 	····				
00507169 1	GGCGIICCGGICGIAA	TATAIGACCA	CIIAACGII.				
00507170.1							
OQ507171.1							
00507172.1							
OQ507173.1	G						
00507174.1							
00507175.1							•••••
00507177 1					• • • • • • • • • • •		• • • • • • • •
00507178 1	GGTATTCCAATTATAA	TTTATGACTA	TTCCAAGGGG	GATTCACCAC	AAATACTAGC	ГТАТСТСАТС	ATTACCG
00507179.1							
OQ507180.1							
OQ507181.1							
OQ507182.1							
00507183.1	GGCGTTCCGATCGTAA	TGCATTACAA	CTTAACGGGG	AA			• • • • • • • •
00507184.1	••••••	• • • • • • • • • •			• • • • • • • • • • •		• • • • • • • •
00507186 1							
00507187.1						 	
00507188.1	GGCCTTCCGGTA						
OQ507189.1	GGCGTTCCCAGCGTAA	TGCATAACTG	CTTACCGAG.				
OQ507190.1	GGCGTTGCG						
00507191.1							• • • • • • • •
00507192.1		 TCTATCACTA	 				
00507193.1	CGCGCICCIGICGIGA	IGIAIGAGIA	CITARCIIC.				
00507195.1	GGGGTTCCGGTCGAAA	CGGATGAGCA	CTTGATGGGG	GGTTTCACTAC	AAACACTAGC'	гтт <u>б</u>	
00507196.1							
0Q507197.1	ACCTCTTTTTGTGTAG	TACGTGATGA	A				
OQ507198.1							
OQ507199.1	CGCGTTCCGATCGTAA	.TGGATG					
00507200.1							
00507202 1					• • • • • • • • • • •		• • • • • • • •
00507203 1						• • • • • • • • • • •	
00507204.1							
OQ507205.1	ATCGTTCCAATTATAA	TGCATA					
OQ507206.1	GGCGCTCTGGTTGTGA	TTGATGC					
OQ507207.1	GGCGTTGTGGGCGTAA	TGCATGTCTT	GTTAACGGGG	GGATTCATTGC	TAATACTAGG	FTGGCTCATG	3

Appendix 2 D:Multiple alignment sequence for ITS2 and *rbcL Physalis* accessions gene sequence as well as reference sequences. (<u>https://espript.ibcp.fr/ESPript/temp/1032964064/0-0-1680466160-esp.pdf</u>)

	i 10	p 20	30		40	50	စေ	7 <u>0</u>	
KT178121.1*	ATGTCACCA	CAAACAGAGACI	TAAAGCAAGT	. GTT	GGATTCAAGGC	TGGTGT	FAAAGAGTAC	AAATTGACTTAT	TATACTC
NC_026570.1*	ATGTCACCAC	CAAACAGAGACI	FAAAGCAAGT	. GTT	<pre>GGATTCAAGGC</pre>	TGGTGT	FAAAGAGTAC	AAATTGACTTAT	TATACTC
NC_039457.1*	ATGTCACCAC	CAAACAGAGACI	FAAAGCAAGT	.GTT	GGATTCAAGGC	CIGGIGI	FAAAGAGTAC	AAATTGACTTAT	TATACTC
NC_070364.1*	ATGTCACCAC	CAAACAGAGACI	FAAAGCAAGT	. GTT	GGATTCAAGGC	CIGGIGI	FAAAGAGTAC	AAATTGACTTAT	TATACTC
NC_039458.1*	AIGICACCAC		TAAAGCAAGT	GTT	CGATTCAAGGC	TGGIGI.	ΙΑΑΑGΑGΙΑΟ ΓδδδςδςΤδς	AAAIIGACIIAI	TA. IACIC
NC 048515.1*	ATGTCACCA	CAAACAGAGACI	TAAAGCAAGT	GTT	GGATTCAAGGC	TGGIGI	TAAAGAGTAC	AAATTGACTTAT	TA. TACIC
0Q507153.1								AAATTGACTTAT	TATACTC
0Q507154.1	ATGTCACCC	CACACAGAAACI	TAAAGCAAGT	. <mark>G T</mark> T	<pre>GATTCAAGGC</pre>	TGGTGT	FAAAGAGTAC	AAATTGACTTAT	TATACTC
00507155.1								AAATTGACTTAT	TATACTC
00507156.1	ATGTCACCAC	CAAACAGAAACI	FAAAGCAAGT	. GTT	<pre>GGATTCAAGGC</pre>	CTGGTGT	FAAAGAGTAC	AAATTGACTTAT	TATACTC
00507157.1	• • • • • • • • • •					• • • • • •		AAATTGACTTAT	TATACIC
00507159 1	• • • • • • • • • •						•••••	AAATTGACTTAT	TA TACIC
00507160.1								AAATTGACTTAT	TA. TACTC
0Q507161.1								AAATTGACTTAT	TATACTC
OQ507163.1	ATGTCACCAC	CAAACAGAGACI	FAAAGCAAGT	. A T T	<mark>G</mark> GATACAAGGC	TGGTGT	FAAAGAGTAC	A A A T T G A <mark>C T</mark> T A T	T <mark>A</mark> TACTC
00507165.1	ATGTCACCAC	CAAACAGAGACI	FAAAGCAAGT	. GCT	<pre>GGACACCAGTC</pre>	CIGGIGI	FAAAGAGTAC	AAATTGACTTAT	TATACTC
00507166.1	ATCTCACCA(· · · ·					
00507168 1	AIGICACCA		TAAAGCAAGT	CTT	GGAICAAAGAC	TGAIGI.	TAAAGAGIAC	AAAIIGACIIAI	TA. TACIC
00507169.1	ATGTCACCA	CAAACAGAGACI	TAAAGCAAGT	GTG	GGATTCAGGGC	CGGCGC	TAAAGCGTAC	AAATTGACTTAT	TA. TACTC
0Q507171.1								AAATTGACTTAT	TATACTC
OQ507177.1								AAATTGA <mark>CT</mark> AAT	T <mark>A</mark> CACTC
00507180.1	ATGTCACCAC	CAAACAGAGACI	TAAAGCAAGT	.GTT	<pre>GCATTGAACGC</pre>	CTGGTGT	FAAAGAGTCC	AAATTGA <mark>CT</mark> TAT	TATACTC
00507181.1	ATGTCACCA	CAAACAGAGACI	TAAAGCAAGT	. GTT	GGATGCAAAGC	CIGGAGC	FAAAGTGTAC	AAATTGACTTAT	TATACTC
00507183.1	ATGTCACCAC	CAAACAGAGACI	TAAAGCAAGC	ATG	GGATTCAAAGC	TGGTGT	FAAAGAGTCA	AAATTGACTTAT	TA. TACTC
00507185 1	ATGTCACCAC	CAAACAGAGACI	TAAAGCAAGC	G A T	GGCATCAAGC	TGAGCT	TAAAGAGCAC	AAATTGACTTAT	
00507192.1	ATGTCACCA	CAAACAGAGACI	TAAAGCGAGG	. T T T	GGGATCATGGC	TGGTGT	TAAAGAGTAC	AAATTGACTTAT	TA. TACTC
0Q507193.1	ATGTCACCAC	CAAACAGAGACI	FAAAGCGCTT	. СТТ	<pre>GATCCAAGGC</pre>	TGGTGT	FAAAGAGTAC	AAATTGACTTAT	T <mark>A</mark> TACTC
OQ507194.1	ATGTCACCAC	CAAACAGAGACI	ΓΛΑΑGCΑGΑΤ	. G T T	<pre>GGTTCAATGC</pre>	CTGGTGT	ΓΑΛΑGΑGΤΑC	<mark>λλλ</mark> ΤΤGΛ <mark>СΤ</mark> ΤΑΙ	Υ <mark>Λ</mark> ΤΛCTC
0Q507195.1	ATGTCACCAC	CAAACAGAGACI	TAAAGCACAT	. GTT	GGATTCATGGC	TGGTGT	TAAAGAGTAC	AAATTGACTTAT	TATACTC
00507199.1	ATGTCACCAC	CAAACAGAGGCI	TAAAGCAACT	ATT	GGATTCAAGGC	TGGTGT	FAAAGAGTAC	AAATTGACTTAT	TA. TACTC
AY665903 1*	AIGICACCA	CTGCGG	AGGATCATT	GTC	GGATIICAIGC	JGGIGI.	IAAAGAGIAC	AAACCTGCTAAG	CA. IACIC
AY665868.1*		CTGCGGA	AGGATCATT	GIC	G			AAACCTGCTAAG	GCA
AY665914.1*		CTGCGGA	AAGGATCATT	. <mark>С</mark> ТС	G			AAACCTGCGAAG	GC <mark>A</mark>
AY665905.1*		CTGCGG <i>A</i>	AAGGATCATT	.GTC	G			AAACCTG <mark>C</mark> GAAG	GC <mark>A</mark>
AY665886.1*	• • • • • • • • • •	CTGCGGA	AAGGATCATT	.GTC	G	• • • • • • •		AAACCTGCTAAG	CA
MH/03/28.1*	• • • • • • • • • •	СІССССА	AAGGAICAII AAGGATCATT	CIC CTC	С			AAACCIGCIAAC	CA
00371996.1		AACGCGG	CAGGATCATT	GTC	G		 	AAACCTGCTAAG	
00371997.1			CATA	GGAC	G				A
OQ371998.1				. <mark>G</mark> A C	G			TCCCAGG <mark>CT</mark> A <mark>A</mark> G	GAC
00372001.1	GGGCTTTCT	ITGAGAGGGAGI	GTACACGTT	CATA	G			G G <mark>A</mark> C A G G G A G G A	CATGTGACC
00372003.1	•••••	CTGCGG	STGGATCATT	. GTC	G	• • • • • •		AA.CCTGCTAAG	CA
00372004.1	• • • • • • • • • •		AGGAICAII	стс	G			AA.CCIGCIAGG	CA
00372007.1		CGGGAA <i>i</i>	GGGATCATT	GGTC	G			AAACCTGCTAAG	GC <mark>A</mark>
0Q372008.1		GTCGTAG	GCGGCCCAT.	. GTC	G			ACCTG <mark>C</mark> .GAG	GC <mark>A</mark>
OQ372009.1		GACTGCO	GGAGGTCATT	.GTC	G			. AACCTG <mark>CT</mark> AAG	GC <mark>A</mark>
00372012.1	• • • • • • • • • •			· · · ·				ACGTTAACTCGG	GA
00372013.1	• • • • • • • • • •	CIUGGA	AGGAAICAIT	CTC	G			AACCIGCIAAG	CA
00372015.1		ACCTGC	GAGGTCATT	GTC	G			AAACCTGCTAAG	
00372016.1			GAGGATCATT	GTC	G		 	AAACCTGCGAAG	GCA
0Q372017.1		CCTGCGG	GAGGATCATT	.GTC	G			AAACCTGCTAAG	GC <mark>A</mark>
OQ372018.1		CCTGCC	GGAGGTCATT	.GTC	G			AAACCTG <mark>CT</mark> AAG	GC <mark>A</mark>
00372019.1	• • • • • • • • • •	CCTGCGC	GAGGATCATT	. GIC	G	• • • • • •		AAACCTGCTAAC	CA
00372020.1	• • • • • • • • • •	CCTGCGG	BAGGATCATT	. GTC	6	• • • • • •		AAACCTGCTAAC	, C <mark>A</mark>
00372022.1								••••••••••••••••	
00372023.1				GTC	G		 		GCCTAACG
00372024.1		CTGCGG7	AAGGATCATT	. GTC	G			AAACCTGCTAAG	GCA
00372025.1		G <i>A</i>	AAGGATCATT	.GTC	G			AA.CCTG <mark>CT</mark> AAG	GC <mark>A</mark>
00372026.1	• • • • • • • • • •			. GTC	G	• • • • • •		AGCG <mark>CTAA</mark> G	cgc
00372027.1	• • • • • • • • •			стс		• • • • • •		ACCTCCTTAAC	
00372029.1			GAICAII	стс	G			AGCGCCTAAG	CGC
		 .							

	во	90	100	110		120	i i	1	30	1	40			
KT178121.1*	ĊТ	GAGTACCAAACCAA	GGATAC <mark>TGA</mark>	TATATTG	GCAG	CATTO	CGAC	TAAC	TCCT	CAACCT	G		AGT <mark>TC</mark>	CACC
NC_026570.1*	CT	AGTACCAAACCAA	GGATACTGA	TATATTG	GCAG	CATTO	CGAC	TAAC	TCCT	CAACCT	G		AGTTC	CACC
NC_039457.1*	CTO	FAGTACCAAACCAA	GGATACTGA	TATATTG	G A G	CATTO	CGAC	JTAAC	TCCT	CAACCT	GG		AGTTC	CACC
NC 039458.1*	CTC	AGTACCAAACCAA	GGATACTGA	TATATTG	GCAG	CATIC	CGAC	GTAAC	TCCT	CAACCT	GG		AGTIC	CACC
NC_048514.1*	СТ	SAGTAC <mark>C</mark> AAA <mark>C</mark> C <mark>AA</mark>	GGATAC <mark>TGA</mark>	T A T A T T <mark>G (</mark>	GCAG	САТТС	C <mark>C G</mark> A (G T A A <mark>C</mark>	TCCT	CAA <mark>CC</mark> T	G G		AGT <mark>TC</mark>	CACC
NC_048515.1*	CTO	GAGTACCAAACCAA	GGATACTGA	TATATTG	GCAG	CATTO	CGA	GTAAC	TCCT	CAACCT	GG	•••••	AGTTC	CACC
00507154.1	CTC	AGTACCAAACCAA	GGATACIGA	TATATIG	GCAG	CATIC	CGAC	JI AAC	TCCT	CAACCT	GG		AGIIC	CACC
OQ507155.1	CT	GAGTACCAAACCAA	GGATAC <mark>TGA</mark>	TATATTG	GCAG	CATTO	CGAO	TAA C	TCCT	CAACCT	G G		AGTTC	CACC
00507156.1	CT	AGTACCAAACCAA	GGATACTGA	TATATTG	GCAG	CATTO	CGAO	TAAC	TCCT	CAACCT	G		AGTTC	CACC
00507157.1	CTC	AGTACCAAACCAA	GGATACTGA	TATATIG	CAG	CATTO	CGAU	TAAC	TCCT	CAACCT	G		AGITO	CACC
0Q507159.1	CTC	GAGTACCAAACCAA	GGATACTGA	TATATTG	GCAG	CATTO	CGAO	TAAC	TCCT	CAACCT	G		AGTTC	CACC
00507160.1	CT	AGTACCAAACCAA	GGATAC <mark>TGA</mark>	TATATTG	GCAG	CATTO	CGAO	G T A A C	TCCT	CAACCT	G G		AGTTC	CACC
00507161.1	CTO	GAGTACCAAACCAA	GGATACTGA	TATATTG	CAG	CATTO	CGAC	JTAAC	TCCT	СААССТ	GG	• • • • • • • •	AGTTC	CACC
00507165.1	CTC	AGTACCAAACCAA	GGATACTGA	TATATTG	GCAG	CATTO	CGAC	GTAAC	TCCT	CAACCT	GG		AGTCC	CACC
002507166.1				. A T A T T <mark>G</mark> (GCAG	САТТС	C <mark>C G</mark> A (G <mark>T</mark> AA <mark>C</mark>	TCCT	C A A <mark>C C</mark> T	G G		AGT <mark>TC</mark>	CA <mark>CC</mark>
00507167.1	CTC	SAGTACCAAACCAA	GGATACTGA	TATATTG	GCAG	CATTO	CGA	GTAAC	TCCT	CAACCT	GG		AGTTC	CACC
00507169.1	CTC	AGTACCAAACCAA	GGATACIGA	TATATIG	GCAG	CATIC	CGAC	GTAAC	TCCT	CAACCT	GG		AGTTC	CACC
0Q507171.1	СТ	GAGTACCAAACCAA	GGATAC <mark>TGA</mark>	TATATTG	GCAG	CATTO	CGAO	TAAC	TCCT	CAACCT	G G		AGTTC	CACC
00507177.1	CT	AGTACCAAACCAA	GGATACTGA	TATATTG	GCAG	CATTO	CGAC	TAA C	TCCT	CAACCT	G		AGTTC	CACC
00507180.1	CTC	AGIACCAAACCAA	GGATACIGA	TATATIG	CAG	CATIC	CGAU	TAAC	TCCT	CAACCI	66 66		AGIIC	CACC
oQ507183.1	CTC	GAGTACCAAACCAA	GGATACTGA	TATATTG	CAC	CATTO	CGAC	TAAC	TCCT	CAACCT	G		AGTTC	CACC
OQ507184.1	СТ	GAGTACCAAACCAA	GGATAC <mark>TGA</mark>	TATATT <mark>G</mark>	GCAG	CATTO	CGAO	G T A A <mark>C</mark>	TCCT	СААССТ	G G		AGT <mark>TC</mark>	CA <mark>CC</mark>
00507185.1	CTC	GAGTACCAAACCAA	GGATACTGA	TATATTG	GCAG	CATTO	CGAC	GTAAC	TCCT	CAACCT	GG	•••••	AGTTC	CACC
00507193.1	CTC	AGTACCAAACCAA	GGATACTGA	TATATTG	GCAG	CATIC	CGAC	GTAAC	TCCT	CAACCT	GG		AGTTC	CACC
OQ507194.1	СТ	GAGTACCAAACCAA	GGATAC <mark>TGA</mark>	TATATTG	GCAG	CATTO	CGAO	G T A A C	TCCT	CAACCT	G G		AGTTC	CACC
00507195.1	CTC	SAGTACCAAACCAA	GGATACTGA	TATATTG	GCAG	CATTO	CGAC	JTAAC	TCCT	CAACCT	GG		AGTTC	CACC
00507201.1	CTC	AGTACCAAACCAA	GGATACIGA	TATATIG	GCAG	CATIC	CGAU	JIAAC	TCCT	CAACCI	G		AGIIC	CACC
AY665903.1*		AGCGACCCGCGAA	CTTGTTTGA	ACACCGG	GAG	G	CG	TCG <mark>C</mark>	TCGC	ст.ссс	cc		CCGTC	GG <mark>CC</mark>
AY665868.1*		SAGCGACCCGCGAA	CCCGTTTGA	ACACTGG	GGAG		CG.(TCGC	TCGC	CICCCC	cc		TCGTC	GGCC
AY665914.1* AY665905 1*		AGCGACCCGCGAA	CCTGTTTGA	ACACCGG	GAG	GCGCG	CC	TTCCC	TCGC	CTCCCC CT CCC			TCGTC	GGCC
AY665886.1*	Ģ	GAGCGACCCGCGAA	CCTGTTTGA	ACACCGG	GAG	GCGCG	CG.	TCGC	TCGC	CT.CCC	cc		TCGTC	GTCC
MH763728.1*	•••	GAGCGACCCGCGAA	CCTGTT <mark>TGA</mark>	ACACCG <mark>G</mark>	GGAG	GCGCG	CG.	Γ <mark>Τ</mark> СG <mark>С</mark>	TCGC	ст.ссс	cc		TCGTC	GG <mark>CC</mark>
MH763740.1*		GAGCGACCCGCAAA	CCTGTTTGA	ACACCGG	GAG	••••	CG	TCGC	TCGC	CT.CCC		•••••	TCGTC	GCCC
00371997.1		AGCGAC	A	GCAACGG	GAA.						GGAGG.		ATACT	GGTC
002371998.1														
00372001.1	TG	SAGCGACGACGCAA	ACGGTTACA	CGAAAGA	3Τ						• • • • • • •		CCTCC	CICC
00372004.1		AGCGACCCGCAAA	CCCGTTTGA	ACACCGG	GAAG		CG.		TCGC	CT.CCC	GC		TCGTC	GGCC
0Q372005.1	1	T AG TG	TCTAA	GTGCCG <mark>G</mark> A	A G <mark>G G</mark>									Ст
00372007.1	•••	GAGCGACCCGCAAA	CCCGTTTGA	ACACCGG	GAAG		CG 1	TCGC	TCGC	CT.CCC	GC	•••••	TCGTC	GGCC
00372009.1	0	GAGCGACCCGCAAA	CCCGTTTGA	ACACCGG	GAG			TCGC	TCGC	CT.CCC	GC		TCGTC	GGCC
OQ372012.1	6	GGTACGCCAC	CGT	GTCCCGG	A G G G	TGCTO	CTTT	TCCGG	GCAC	GACCCG	GC		CGAAC	GGCC
00372013.1	•••	SAGCGACCCGCAAA	CCCGTTTGA	ACACCGG	GAAG		CG.I	TCGC	TCGC	ст.ссс	GC	• • • • • • • •	TCGTC	GGCC
00372014.1		BAGCGACCCGCAAA	CCCGTTTGA	ACACCGG	JAAG LAAG		CG		TCGC	ст.ссс ст.ссс	GC	•••••	TCGTC	GGCC
00372016.1		GAGCGACCCGCGAA	CCTGTTTGA	ACACCGG	GAG		ĊG.	TCTT	TCGC	CTCCCC	TC		CGCCT	GCCC
00372017.1	G	SAGCGACCCGCAAA	CCCGTT <mark>TGA</mark>	ACACCGG	G A A G	G	CG.1	TCG <mark>C</mark>	TCGC	ст.ссс	GC		TCG <mark>TC</mark>	G G <mark>C C</mark>
00372018.1	6	SAGCGACCCGCAAA	CCCGTTTGA	ACACCGG	SAAG	· · · · G	CG	TCGC	TCGC	CT.CCC	GC		TCGTC	GGCC
00372020.1		AGCGACCCGCAAA	CCCG.TTGA	ACATGGG	AAGG	c		TCGC	TCGC	T.CCC	G C		TCGTC	GGC.
00372021.1								cg <mark>c</mark>	TCGC	ст.ссс	GC		TCG <mark>TC</mark>	GG <mark>CC</mark>
00372022.1		GAGGGTGTGTGAG	CCCGTTTGA	ACACCGG	JAAC	••••	CG I	TCGC	TCGC	CT.CCC	C		TCGTC	GGCC
00372024.1		AGCGACCCGCAAA	CCCGTTTGA	ACACCGG	AAG		CG.	TCGC	TCGC	CT.CCC	GC	STIGAGA.	TCGTC	GGCC
OQ372025.1		GAGCGA <mark>C</mark> CCG <mark>CAAA</mark>	CCCGTT <mark>TGA</mark>	ACACCGG	G A <mark>A G</mark>	c	CG	TCGC	TCGC	ст.ссс	GC		TCGTC	GG <mark>CC</mark>
00372026.1	CG	AAGGGTCTGTCAG	CCGACACGG	GCCAAAG	3		· · · · ·	GTCGG	CCAC	CG.CCC	AC.AAAC	STTGAGA	TCAAC	CACC
00372027.1	UG G	CAGCGACCCGCAAA	CCCGTTTGA	GCUAUG <mark>G</mark> Acactg <mark>g</mark>			ССТ		TCGC	GGCACC CT.CCC	ACAAGA(GC	JIIGAGA'.	TCGTC	GGCC
00372029.1	CG	AAGGTTCTGTCAG	CCGACACGG	GCCACGG	3			TCGG	CCAC	GGCACC	ACAAGAC	STTGAGAT	TCAAC	CACC

1	L 5 0		160		170		180	190		200	210		220
KT178121.1*	Т	GAAGAAG	CAG	G <mark>G</mark> .	CCGCGGTA		GAA	TCTTCTACTGG	ТАСАТ	GGACAAC	TGTATGGACCGA	ΓG	GACTT
NC 026570 1*	T	GAAGAAG	CAG	GG	CCGCGGTAG	стесс	GAA	TCTTCTACTGG	TACAT	GGACAAC	TGTATGGACCGA	r G	GACTT
NC 039457 1*	Ť	CAACAAC	CACC		CCCCCTAC		CAA	TCTTCTACTCC	TACAT	CCACAAC	TCTATCCACCCA		CACTT
NC_039457.1*		GAAGAAG	. CAGO				GAA	TCTTCTACTGG	TACAT	OGACAAC	TGTATOGACCOA	10	GACII
NC_070364.1*	Т	GAAGAAG	CAGC	5 G G . I	CCGCGGTAG	CTGCC	GAA	TETTETACTEG	T A C A T	GGACAAU	TGTATGGACCGA	rG	GACTT
NC_039458.1*	Т	GA <mark>AG</mark> AAG	.CAGC	GGG.(C CGCGGTA	G CTGCC	GAA	TCTTCTACTGG	ГАСАТ	GGACAAC	TGTATGGACCGA	ΓG	GACTT
NC_048514.1*	Т	GAAGAAG	CAGO	GG <mark>G</mark> .(CCGCGGTA	G CTGCC	GAA	TCTTCTACTGG	ТА <mark>СА</mark> Т	GGACAAC	TGTATGGACCGA	ΓG	GACTT
NC 048515.1*	Т	GAAGAAG	CAGO	GG.	CCGCGGTA	CIGCC	GAA	TCTTCTACTGG	ГАСАТ	GGACAAC	TGTATGGACCGA	ΙG	GACTT
00507153.1	Т	GAAGAAG	CAGO	GG.	CCGCGGTAG	CIGCC	GAA	TCTTCTACTGG	гасат	GGACAAC	TGTATGGACCGA	ΓG	GACTT
00507154 1	Т	GAAGAAG	CAGO	GG I	CCCCCCTA	стесс	GAA	TCTTCTACTGG	ТАСАТ	GGACAAC	TGTATGGACCGA	r G	GACTT
00507155.1	- -	CARCAAC	C A C		CCCCCCTAC			TOTTOTACTOO		CCACAAC	TCTATCCACCCA		CACTT
00507155.1	-	GAAGAAG						TOTTOTACIGG		GGACAAC	TOTATOGACCOA	· · · · · · ·	GACII
00507156.1	1	GAAGAAG	CAGO		CCGCGGIAG		GAA	ICIICIACIGG	IACAI	GGACAAC	IGIAIGGACUGA	1G	GACII
00507157.1	т	GAAGAAG	. CAGO	GG.	CCGCGGTAG	CIGCC	GAA	TCTTCTACTGG	T A C A I	GGACAAC	TGTATGGACCGA	Г G	GACTT
OQ507158.1	Т	GAAGAAG	CAGO	GGG.(CCGCGGTA	G CTGCC	GAA	TCTTCTACTGG	ГА <mark>СА</mark> І	GGACAAC	TGTATGGACCGA	ΓG	GACTT
00507159.1	Т	GAAGAAG	CAGO	GG.	CCGCGGTA	G CTGCC	GAA	TCTTCTACTGG	ГА <mark>СА</mark> Т	GGACAAC	TGTATGGACCGA	ΓG	GACTT
00507160.1	Т	GAAGAAG	CAGO	GG.	CCGCGGTA	CTGCC	GAA	TCTTCTACTGG	ТАСАТ	GGACAAC	TGTATGGACCGA	ΓG	GACTT
00507161 1	T	GAAGAAG	CAGO	GG (CCCCCCTA	стасс	GAA	TCTTCTACTGG	ТАСАТ	GGACAAC	TGTATCCACCCA	r G	GACTT
00507163 1	Ť	CAACAAC	CACC		CCCCCCTA		GAA	TCTTCTACTCC	тасат	GGACAAC	TGTATCCACCCA		CACTT
00507165.1	- 1 T	CARCAAC			CCCCCCTAC			TOTTOTACIOG		CCACAAC	TOTATOGACCOA	· · · · · · ·	CACTI
00507165.1	1	GAAGAAG	. CAGO				GAA	ICTICIACIGG		GGACAAC	TGTATGGACCGA	16	GACII
00507166.1	Т	GAAGAAG	. CAGO	GG.	CCGCGGTAG	CTGCC	GAA	TCTTCTACTGG	TACAT	GGACAAC	TGTATGGACCGA	r G	GACTT
OQ507167.1	Т	GAAGAAG	.CAGO	GG <mark>G</mark> .(CCGCGGTAC	G CTGCC	GAA	TCTTCTACTGG	ГАСАТ	GGACAAC	TGTATGGACCGA	Г G	GACTT
OQ507168.1	Т	GAAGAAG	CAGO	GG <mark>G</mark> .(CCGCGGTA	G CTGCC	GAA	TCTTCTACTGG	Т А <mark>С А</mark> Т	GGACAAC	TGTATGGACCGA	ΤG	GACTT
00507169.1	Т	GAAGAAG	CAGO	GGG.	CCGCGGTA	G CIGCC	GAA	TCTTCTACTGG	ГА <mark>СА</mark> Т	GGACAAC	TGTATGGACCGA	ΙG	GACTT
00507171 1	т	GAAGAAG	CAGO	GG	CCGCGGTA	CTGCC	GAA	TCTTCTACTGG	тлслт	GGACAAC	TGTATGGACCGA	r G	GACTT
00507177 1	Ť	GAAGAAG			CCCCCCTA		CAA	TCTTCTACTCC	тасат	GGACAAC	TGTATGGACCGA	T G	GACTT
00507100 1	- 1 T	CARCAAC			CCCCCCTAC			TOTTOTACTOG		CCACAAC	TOTATOGACCOA	· · · · · ·	CACTT
00507180.1	1	GAAGAAG	CAGO		CCGCGGIAG		GAA	ICIICIACIGG		GGACAAC	TGIAIGGACCGA	1 G	GACII
00201181.1	т	GAAGAAG	CAGO	GG.	CCGCGGTAG	CIGCC	GAA	TETTETACTGG	TACAT	GGACAAC	TGTATGGACCGA	I G	GACTT
OQ507183.1	Т	GAAGAAG	. CAGO	GGG.(CCGCGGTAG	G CTGCC	GAA	TCTTCTACTGG	T A <mark>C A</mark> T	GGACAAC	TGTATGGACCGA	ΓG	GACTT
OQ507184.1	Т	GAAGAAG	CAGO	GGG.(CCGCGGTA	G CTGCC	GAA	TCTTCTACTGG	ГА <mark>СА</mark> Т	GGACAAC	TGTATGGACCGA	ΙG	GACTT
00507185.1	Т	GAAGAAG	CAGO	GGG.	CCGCGGTA	G CTGCC	GAA	TCTTCTACTGG	ГА <mark>СА</mark> Т	GGACAAC	TGTATGGACCGA	ΓG	GACTT
00507192.1	Т	GAAGAAG	CAGO	GG.	CCGCGGTAC	crgcc	GAA	TCTTCTACTGG	ТАСАТ	GGACAAC	TGTATGGACCGA	r G	GACTT
00507193 1	T	GAAGAAG	CAGO	C C	CCCCCCTA	стасс	GAA	TCTTCTACTGG	ТАСАТ	GGACAAC	TGTATGGACCGA	r G	GACTT
00507194 1	Ť	CAACAAC	CACC		CCCCCCTAC		CAA	TCTTCTACTCC	тасат	CCACAAC	TCTATCCACCCA	· · · · · · · · · · · · · · · · · · ·	CACTT
00507194.1		CARCARO	CACC		CCCCCCTAC		CAA	TETTETACIGO		CCACAAC	TOTATOGACCOA	· · · · · ·	CACII
00507195.1	1	GAAGAAG.	. CAGO		CCGCGGTAG		GAA	ICIICIACIGG	IACAI	GGACAAC	IGIAIGGACCGA	1 G	GACII
00201133.1	Т	GAAGAAG	CAGO	- G G . I	CCGCGGTAG	CIGCC	GAA	TUTTUTACIGG	TACAT	GGACAAC	TGTATGGACCGA	I G	GACIT
OQ507201.1	Т	GAAGAAG	.CAGO	GGG.(CCGCGGTA	G CTGCC	GAA	TCTTCTACTGG	T A <mark>C A</mark> T	GGACAAC	TGTATGGACCGA	ΓG	GACTT
AY665903.1*	G	GCGGTC <mark>G</mark>	. <mark>C</mark> G C C	GTG.	.CGCGGTC	C.CGGGC	GAC	TAACGA <mark>AC</mark> CCC	G G <mark>C</mark> G C	GGAACGC	GCCAAGGAATAC	ΓG	AACCG
AY665868.1*	G	GCGTCC <mark>G</mark>	CGC	EC <mark>G</mark> .	.CGCGGTC	C.CGGGC	GAC	TAACGAACCCC	GG <mark>C</mark> GC	GGAACGC	GCCAAGGAATAC	ΓG	AACCG
AY665914.1*	G	GCGGTCG	CGCC	GTG.	.CGCGGTC	C.CGGTC	GAC	TAACGAACCCC	GGCGC	GGAACGC	GCCAAGGAATAC	гт	AACCG
AY665905 1*	Ĝ	GCGGTCG	CGCC	TG	CGCGGTCG		GAC	TAACGAACCCC	GGCGC	GGAACGO	GCCAAGGAATAC	r G	AACCG
AV665886 1*	c	ACCECCE		TC.	Cecesto		GAC	TAACTCACCCC			CCCAACCAATAC	гс	AACCG
MU762720 1+	2				CCCCCTCC		CAC	TAACTCACCCC		CCARCO	CCCAACCAATAC		n n c c c
MR/03/20.1*	G			516.		C.CGAIC	GAC	TAACICACCCC		GGAACGC	GCCAAGGAATAC	L G	AACCG
MH/63/40.1*	G	GCGGCCG		51G.	CGCGGTCG		GAC	TAACGAACCCC	GGCGC	GAAACGU	GCCAAGGAATAC	IC	AACIG
00311336.1	А	GCAGCCG	. CACC	ΞIG.	. CGCGGTCG	GC.CTAGC	GAC	TAACGAACCCCC	GGCAC	GAAACGC	GCCAAGGAATAC	r C	GACCG
OQ371997.1	С	GTTGTCGC	.CGCC	ACA	C <mark>CG</mark> TT <mark>G</mark> CG1	T.CCGAC	GAC	TA.CGA <mark>AC</mark> CCG	GC <mark>C</mark> .	. GAACGC	GCA <mark>A</mark> GAACATAA	АС	
OQ371998.1									<mark>C</mark> GC	AGAACG.	GCCAGGAAATAA	с	
00372001.1	G	TGTGCCA	CAGO	GAC	TTGCGTTC.	CGGGC	TAA	GAACC	CGC	AGAACG	CCAAAAAACTC.		. AATG
00372003.1	А	GCAGCCG	CACO	TG.	.CGCGGTC	C.CTAGC	GAC	TAATGAACCCC	GGCAC	GAAACGC	GCCAAGGAATAC	гс	GACCG
00372004 1	Δ	CACCC	CACC	TG	CGCGGTCG	CTAGO	GAC	TAACGAACCCC		GAAACGO	GCCAAGGAATAC	r C	GACCG
00372005 1	G	CACCC	. • . • .					111100111100000	0000110	Acces	CCCAC	•••••	011000
00372003.1	7				CCCCCTC				$\cdot \cdot $			· · · · ·	
003/2007.1	A	GCAGCCG	. CACC	516.		C.CIAGO	GAC	TAACGAACCCC	GGCAC	GAAACGC	GCCAAGGAATAC	1	GACCG
00372008.1	G	GCGGICG	. CGCC	-166			CGC	TAAC.AACCCC	GGCGC	GGA.CGC	GCCTAGGA.TAC	11	AACCG
0Q372009.1	A	GCAGCCG	.CACC	GΤG.	.CGCGGTCG	GC.CTAGC	GAC	TAACGA <mark>AC</mark> CCC	G G <mark>C A</mark> C	GAAACGC	GCCAAGGAATAC	ΓC	GACCG
0Q372012.1	А	GAAACTA			.CGAGGCC	G							
OQ372013.1	Α	GCAGCCG	CACO	GTG.	.CGCGGTCG	GC.CTAGC	GAC	TAACGA <mark>AC</mark> CCC	GG <mark>CA</mark> C	GAAACG	GCCAAGGAATAC	ΙC	GACCG
00372014.1	А	GCAGCCG	CACO	ΞTG.	.CGCGGTC	C.CTAGC	GAC	TAACGAACCCC	GG <mark>CA</mark> C	GAAACGC	GCCAAGGAATAC	гс	GACCG
00372015.1	А	GCAGCCG	CACO	TG	CGCGGTCG	C. CTAGC	GAC	TAACGAACCCC	GGCAC	GAAACGC	GCCAAGGAATAC	гс	GACCG
00372016 1	G	CCCCCCCCT		TC	TCCCGTCG	C CACTA	CAA	TCCCCAACCCC	CCACC	GGACCTC	GCCAACTAATAC	TTTCC	GACTO
00272017 1	2				CCCCCTCC	C CTACC	CAC	TAACCAACCCC		CAAACCC	CCCARCCARTAC		CACCC
00372017.1	A	GCAGCCG	. CACC	31G.		C.CIAGO	GAC	TAACGAACCCC	GGCAC	GAAACGC	GCCAAGGAATAC	L C	GACCG
00372018.1	А	GCAGCCG	CACC	51G.	.CGCGGTCG	C.CIAGC	GAC	TAACGAACCCC	GGCAC	GAAACGC	GCCAAGGAATAC	I C	GACCG
00372019.1	Α	GCAGCC <mark>G</mark>	CAC	έΤ <mark>Γ</mark> .	.CGCGGTCG	GC.CTAGC	GAC	TAACGA <mark>AC</mark> CCC	G G <mark>C A</mark> C	GAAACG	GCC <mark>AAGGA</mark> ATAC	rc	GACCG
OQ372020.1	•		. <mark>C</mark> G C (GCCG	C <mark>C G T G G C G</mark> O	T G <mark>C</mark> C T G <mark>C</mark>	GAC	TA.CGA <mark>AC</mark> CC.	.G <mark>CA</mark> C	GAA	· · · · · · · · · · · · 		
OQ372021.1	Α	GCAGCCG	CAC	GT <mark>G</mark> .	.CGCGGTC	C.CTAGC	GAC	TAACGA <mark>AC</mark> CCC	GG <mark>CA</mark> C	GAAACG	GCCAAGGAATAC	[C	GACCG
00372022.1	A	GCAGCCG	CACO	GTG.	.CGCGGTC	C.CTAGC	GAC	TAACGAACCCC	GGCAC	GAAACGC	GCCAAGGAATAC	гс	GACCG
00372023 1	Д	CTTGCCGTG	CGTO	dG	TCGACGCG	G. CTCCC	ATT	TAGGCCAGCCG	GGCGC	TGCGAG	GCACGGGA		GGCCA
00372024 1	7			TC	Cecesto	CCTACC	GNC	TAATGAACCCC		GAAACCC	GCCAAGGAATAC	r	GACCO
00272024.1	A		CAC				CAC	TAALGAACCCC		CAAACGC	GOGAAGGAATAC		CACCO
00372023.1	A	GUAGUUG	CAUC				GAU	TAACGAACCCC		GAAACG	GCCAAGGAAIAC	1 • • • C	GAUCG
003/2026.1	А	GITIGCCGTGI	AU GII (- CIGI -	ICGACATG	G C T C A C	АТТ	IAGGCCAACCA	UCAGC	CTATGGC	CCAACGGAAAG.		•••
00372027.1	Α	CITT IGCCIGT GI	ACGTO	CG.	T <mark>CGACATG</mark>	G.CTCAC	ATT	TAGGCCAACCA	UGAGC	CGATGGC	GC.AC <mark>GGA</mark> AGGC		
OQ372028.1	Α	GCAGCC <mark>G</mark>	CAC	ΞΤ <mark>G</mark> .	.CGCGGTCG	C.CTAGC	GAC	TAATGA <mark>AC</mark> CCC	G G <mark>C A</mark> C	GAAACG	GCC <mark>A</mark> A <mark>GGA</mark> ATAC	ΓC	GACCG
OQ372029.1	Α	CTTGCCGTGF	ACGT(CC <mark>G</mark> .	T <mark>C G A C A T G</mark>	G.CTCAC	ATT	TAGGCCAACCA	CGAGC	CGATGG	GCACGGAAGGCC	Γ	

	230	240	250	260	270	280	290	300
KT178121.1*	ACCAGTCTTGA	ICGTTACAAA	GGGCGATGCT	ACCGCATCG	. AGCGTGTT	G T T G <mark>G</mark> A G A A A A A G A	ΑΤ <mark>Ϲ</mark> ΑΑΤΑΤΑΤΊ	GCTTATGTA
NC_026570.1*	ACCAGTCTTGA	ICGTTACAAA	GGGCGATGCT	ACCGCATCG	. AGCGTGTT	GTTG <mark>G</mark> AGAAAAG	ATCAATATAT	GCTTATGTA
NC_039457.1*	ACCAGTCTTGA	FCGTTACAAA	GGGCGATGCT	ACCGCATCG	. AGCGTGTT	GTTGGAGAAAAG/	АТСААТАТАТТ	GCTTATGTA
NC_070364.1*	ACCAGTOTTGA	TCGTTACAAA	GGGCGATGCT	ACCGCATCG	AGCGTGTT	GTTGGAGAAAAG	ΑΤΟΑΑΤΑΤΑΤΑΤΑΤΑ	GCTTATGTA
NC 048514.1*	ACCAGTCTTGA	ICGITACAAA	GGGCGATGCI	ACCGCATCG	AGCGTGTT	GTTGGAGAAAAG	ATCAATATATI	GCTTATGTA
NC_048515.1*	ACCAGTCTTGA	ICGITACAAA	G GG <mark>C</mark> GATG <mark>C</mark> I	ACCGCATCG	. AGCGTGTT	GTTG <mark>G</mark> AGAAAAG	A T C A A T A T A T I	GCTTATGTA
OQ507153.1	ACCAGTCTTGA	ICGTTACAAA	<mark>g</mark> g g <mark>c</mark> g a t g <mark>c t</mark>	ACCGCATCG	. AGCGTGTT	GTTG <mark>G</mark> AGAAAAG	<mark>Α</mark> Τ <mark>Ϲ</mark> ΑΑ <mark>Τ</mark> ΑΤΑ <mark>Τ</mark> Ί	GCTTATGTA
00507154.1	ACCAGTCTTGA	ICGTTACAAA	GGGCGATGCI	ACCGCATCG	. AGCGTGTT	GTTG <mark>G</mark> AGAAAAG	ATCAATATAT	GCTTATGTA
00507155.1	ACCAGTCTTGA	ICGITACAAA	GGGCGATGCI	ACCGCATCG	. AGCGTGTT	GTTGGAGAAAAG	ATCAATATATI	GCTTATGTA
00507157 1	ACCAGICIIGA.	ICGIIACAAA	GGGCGATGCT	ACCGCATCG	AGCGIGII	GTTGGAGAAAAG	ATCAATATAT	GCTTATGIA
00507158.1	ACCAGTCTTGAT	ICGITACAAA	GGGCGATGCI	ACCGCATCG	.AGCGTGTT	GTTGGAGAAAAAG	ATCAATATATI	GCTTATGTA
0Q507159.1	ACCAGTCTTGA	ICGTTACAAA	GGGCGATGCI	ACCGCATCG	. AGCGTGTT	GTTG <mark>G</mark> AGAAAAAG	ATCAATATATI	GCTTATGTA
OQ507160.1	ACCAGTCTTGA	ICGTTACAAA	<mark>g</mark> gg <mark>c</mark> gatg <mark>ct</mark>	ACCGCATCG	. AGCGTGTT	GTTG <mark>G</mark> AGAAAAAG	<mark>ΑΤ</mark> C Α Α Τ Α Τ Α Τ Τ	GCTTATGTA
00507161.1	ACCAGTCTTGA	ICGTTACAAA	GGGCGATG <mark>C</mark> T	ACCGCATCG	. AGCGTGTT	GTTG <mark>G</mark> AGAAAA <mark>G</mark>	ATCAATATAT	GCTTATGTA
00507163.1	ACCAGTCTTGA:	FCGTTACAAA FCGTTACAAA	GGGCGATGCT	ACCGCATCG	.AGCGTGTT	GTTGGAGAAAAGA	ACCAATATATT	GCTTATGTA
00507166 1	ACCAGICIIGA	ICGITACAAA	GGGCGATGCT	ACCGCATCG	AGCGTGTT	GTTGGAGAAAAA	ATCAATATATAT	GCTTATGTA
00507167.1	ACCAGTCTTGA	ICGITACAAA	GGGCGATGCI	ACCGCATCG	AGCGTGTT	GTTGGAGAAAAAG	ATCAATATATI	GCTTATGTA
OQ507168.1	ACCAGTCTTGA	TCGTTACAAA	GGGCGATGCT	ACCGCATCG	. AGCGTGTT	GTTGGAGAAAAG	ATCAATATAT	GCTTATGTA
OQ507169.1	ACCAGTCTTGAT	ICGTTACAAA	<mark>G</mark> G G <mark>C</mark> G A T G <mark>C T</mark>	ACCGCATCG	. AGCGTGTT	G T T G <mark>G</mark> A G A A A A A <mark>G</mark> J	<mark>Α</mark> Τ <mark>Ϲ</mark> ΑΑ <mark>Τ</mark> ΑΤΑ <mark>Τ</mark> Ί	GCTTATGTA
OQ507171.1	ACCAGTCTTGA:	ICGITACAAA	G G G <mark>C</mark> G A T G <mark>C I</mark>	ACCGCATCG	. AG <mark>CGTG</mark> TT	<mark>G T T G G</mark> Λ <mark>G</mark> Λ Λ Λ Λ Λ <mark>G</mark> Ι	<mark>ΛΤ</mark> ΟΛΛΤΛΤΛΤΊ	GCTTATGTA
00507177.1	ACCAGTCTTGA	ICGITACAAA	GGGCGATGCI	ACCGCATCG	. AGCGTGTT	GTTGGAGAAAAG	ATCAATATATI	GCTTATGTA
00507180.1	ACCAGICIIGA.	ICGIIACAAA	GGGCGAIGCI	ACCECATCE	AGCGIGII	GIIGGAGAAAAAG GTTCCACAAAAAG	AICAAIAIAI ATCAATATATAT	GCTTAIGIA
00507183.1	ACCAGICIIGA	ICGITACAAA	GGGCGATGCT	ACCGCATCG	AGCGTGTT	GTTGGAGAAAAAG	ACCAATATAT	GCTTATGTA
OQ507184.1	ACCAGTCTTGA	ICGTTACAAA	GGGCGATGCI	ACCGCATCG	. AGCGTGTT	GTTG <mark>G</mark> GGAAAAAG	AGACATATATI	GCTTATGTA
OQ507185.1	ACCAGTCTTGA:	ICGTTACAAA	<mark>g</mark> gg <mark>c</mark> gatg <mark>c</mark> 1	ACCGCATCG	. AGCGTGTT	GTTG <mark>G</mark> AGAAAA <mark>G</mark> J	<mark>Α</mark> Τ <mark>Ϲ</mark> ΑΑΤΑΤΑΤΊ	GCTTATGTA
OQ507192.1	ACCAGTCTTGA:	ICGTTACAAA	G G G C G A T G <mark>C 1</mark>	ACCGCATCG	. AG <mark>CGTG</mark> TT	GTTG <mark>G</mark> AGAAAAG	ΑΤ <mark>С</mark> ААТАТАТ	GCTTATGTA
00507193.1	ACCAGTCTTGA	ICGITACAAA	GGGCGATGCI	ACCGCATCG	.AGCGTGTT	GTTGGAGAAAAG	ATCAATATAT1	GCTTATGTA
00507194.1	ACCAGICIIGA.	ICGIIACAAA	GCCCCATCCT	ACCECATCE	ACCOLOT	GTTCCACAAAAAG	ΑΙ CΑΑΙΑΙΑΙ	CCTTAIGIA
00507199.1	ACCAGICITGA	ICGITACAAA	GGGCGATGCT	ACCGCATCG	AGCGTGTT	GTTGGAGAAAAAG	ATCAATATAT	GCTTATGTA
00507201.1	ACCAGTCTTGA	ICGTTACAAA	GGGCGATGCT	ACCGCATCG	. AGCGTGTT	GTTGGAGAAAAG	ATCAATATAT	GCTTATGTA
AY665903.1*	ΑΤ	G	GCCTGCCC <mark>C</mark> T	CG <mark>CGC</mark> CCCG	. T T <mark>C G C G</mark> G C	GCGCGCGGGG	A G <mark>C</mark> T G C G C T T C	GCTTGAAAC
AY665868.1*	A T	• • • • • • • • • • • • • • • • • • •	GCCIGCCC <mark>C</mark> I	CGCGCCCCG	.IC <mark>CGCG</mark> GC	GCGCGCGGGG	AGCIGIGCIIC	GCTTGAAAC
AY665914.1*	AC	G	GCCCGCCCC	CGCGCCCCG	. ICCGCGGC	GCGCGCGGGGG	AGCIGCGCCIC	GCTTGAAAC
A1005905.1* AV665886 1*	A 1	••••••••••••••••••••••••••••••••••••••	GCCTGGCCCT		TCCCCCCCCC		ACCTGTGCTTC	CCTTGAAAC
MH763728.1*	A T	G	GCCTGGCCCT	CGCGCCCCG	.TCCGCGGC	GCGCGCGGGGG	ACCIGIGCIIC	GCTTGAAAC
MH763740.1*	АТ	G	GTCTGGTC <mark>C</mark> I	CG <mark>CGC</mark> CCCA	. TCCGCGGC	GCGCGCGGGG	ACCTGCGCTTC	ACTTGAAAC
OQ371996.1	ΑΤ	G	GCA <mark>C</mark> ACCC <mark>C</mark> I	CGCGCCTCG	. TCCACGGC	GTGCGCGGGG	A G <mark>C</mark> T G T G A T T C	GCTTGAAAC
00371997.1		G	AGGCCACCCI	CGCACCC	.TCCG.GGC	GTGCGCGGGG.	CCTAGITO	CACTGAAC
00372001 1		G	AGGCCGCCCI	CCTCTCCCC	. GCCGCGGC		CCCTTCCTTC	CCT CAAC
00372003.1	AT	G	GCACACCCC	CGCGCCTCG	TCCACTGC		AGCTGTGCTTC	GCTTGAAAC
OQ372004.1	ΑΤ	G	GCACACCC	CGCGCCTCG	.TCCACTGC	GTGCGCGGGG	AGCTGTGCTTC	GCTTGAAAC
00372005.1		G	<mark>g</mark> tt <mark>c</mark> ggccac	G G <mark>C A C</mark> C A C G				
00372007.1	ΑΤ	G	GCACACCCC	CGCGCCTCG	. TCCACTGC	GTGCGCGGGG	AGCTGTGCTTC	GCTTGAAAC
00372008.1		A	GGCCCGCCCI	CGCGCCCCG	.ICCGCGGC	GCGCGCGGGGG	AG.IGCGCCIC	GCTTGAAAC
00372009.1	A 1	•••••	GUACAUUUU	CTCCCCCCC	TECECEEC		AGCIGIGUII(GAAC
00372013.1	AT	G	GCACACCC	CGCGCCTCG	. TCCACGGC	GT. GCGCGGGGG	AGCIGIGATIC	GCTTGAAAC
00372014.1	ΑΤ	G	GCACACCC	CGCGCCTCG	. TCCACGGC	GTGCGCGGGG	AGCTGTGCTTC	GCTTGAAAC
OQ372015.1	ΑΤ	G	GCA <mark>C</mark> ACCC <mark>C</mark> I	CGCGCCTCG	. TCCACTGC	GTGCGCGGGG	AGCTGTGCTTC	GCTTGAAAC
00372016.1				CCCTCCCCG	. GCCTCGTT	GCGCGCGGTGT	AGCTGCGTT	
00372017.1	AT	G	GCACACCCCT	CGCGCCTCG	. ICCACGGC	GT. GCGCGGGGGG	AGCIGIGCIIC	GCTTGAAAC
00372019 1	A T	I G	GCACACCCCT	CGCGCCTCG	TCCACTGC	GT GCGCGGGGGG	AGCTGTGCTTC	GCTTGAAAC
OQ372020.1					.GCCAAGAT	AC		
OQ372021.1	ΑΤ	G	GCACACCC	CGCGCCTCG	.TCC.CGGC	GTGCGCGGGG	A.CTGTG.TTC	GCTTGAAAC
OQ372022.1	ΑΤ	G	GCA <mark>C</mark> ACCC <mark>C</mark> T	CGCGCCTCG	. TCCACGGC	GTGCGCGGGGG	AGCTGTGCTTC	GCTTGAAAC
00372023.1	GT	• • • • • • • • • • <u>•</u>	ATCCGI	CCCGCCAAG	cccccccccc	GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GGCGACGCGAT	GCGTGACGC
00372024.1	A 1	•••••G	GCACACCCCT	CACACCTCC	. ICCACGGC	GT. GCGCGGGGGG	AGCIGIGCIT	GCTTGAAAC
00372026.1	•••••••	G	CAGTTTCCCT	CCCGCACCA	CCCCCCCGGT	GCAGGGCGAGGGG	GGCGATGCCAT	GCGTGGTGC
00372027.1		A	GTATCCGTCC	CGCAACGCG	CCGCGGT	GCAGGGCGAGGG	GGCGATGCGAT	GCGTGATGC
OQ372028.1	ΑΤ	G	GCA <mark>C</mark> ACCC <mark>C</mark> I	CGCGCCTCG	. TCCACTGC	GTGCGCGGGG	AGCTGTGCTTC	GCTTGAAAC
OQ372029.1			GTATCCGT	CCCCCAACG	C G C <mark>C G</mark> C <mark>G</mark> G T	GCAGGGCGAGGG	GGCGATGCGAT	GCGTGATGC

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KT178121.1*	GCTTA	CCCTTTAGAC	CTTTTT.	. G <mark>a</mark> aga <mark>a</mark>	GGTTC	<mark>C G</mark> T T A	CCAA	<mark>C A T</mark> G T	TTACTTCCATTC	TAGGT <mark>AA</mark> T	<mark>G T A</mark> T T T G G G	ΤΤΤΑΑ
NC_026570.1*	GCTTA	CCCTTTAGAC	CTTTTT.	GAAGAA	GGTTC	CGTTA	CCAA	CATGT	TTACTTCCATTC	TAGGTAAT TAGGTAAT	GTATTTGGG	ΤΤΤΑΑ ΤΤΤΑΛ
NC_070364.1*	GCTTA	CCCTTTAGAC	CTTTTT.	. GAAGAA	GGTTC	CGTTA	CCAA	CATGT	TTACTTCCATTC	TAGGTAAT	GTATTTGGG	TTTAA
NC_039458.1*	GCTTA	CCCTTTAGAC	CTTTTT.	.GAAGAA	GGTTC	CGTTA	CCAA	CATGT	TTACTTCCATTC	TAGGT <mark>AA</mark> T	G T A T T T G G G	ΤΤΤΑ
NC_048514.1*	GCTTA	CCCTTTAGAC	CTTTTT.	GAAGAA	GGTTCC	CGTTA	CCAA	CATGT	TTACTTCCATT(TTACTTCCATT(TAGGTAAT TAGGTAAT	GTATTTGGG	ΤΤΤΑΑ ΤΤΤΑΑ
0Q507153.1	GCTTA	CCCTTTAGAC	CTTTTT.	. GAAGAA	GGTTC	CGTTA	CCAA	CATGT	TTACTTCCATTC	TAGGTAAT	GTATTTGGG	TTTAA
00507154.1	GCTTA	CCCTTTAGAC	CTTTTT.	. G <mark>A</mark> A <mark>G</mark> AA	GGTTC	CGTTA	CAA	CATGT	TTACTTCCATTC	TAGGT <mark>AA</mark> T	GTATTTGGG	ΤΤΤΑ <mark>Α</mark>
0Q507155.1	GCTTA	CCCTTTAGAC	CTTTTT.	GAAGAA	GGTIC(CGTTA	CCAA	CATGT	TTACTTCCATT(GTAGGTAAT	GTATTTGGG	ΤΤΤΑΑ ΤΤΤΔΑ
00507157.1	GCTTA	CCCTTTAGAC	CTTTTT.	. GAAGAA	GGTTC	CGTTA	CCAA	CATGT	TTACTTCCATTC	TAGGTAAT	GTATTTGGG	TTTAA
OQ507158.1	GCTTA	CCCTTTAGAC	CTTTTT.	.G <mark>A</mark> AGA <mark>A</mark>	GGTTC	CGTTA	ССАА	CATGT	TTACTTCCATTC	TAGGT <mark>AA</mark> T	<mark>G T A</mark> T T T G G G	ΤΤΤΑ <mark>Α</mark>
OQ507159.1	GCTTA	CCCTTTAGAC	CTTTTT.	GAAGAA	GGTTC	CGTTA	CCAA	CATGT	TTACTTCCATT(GTAGGTAAT TAGGTAAT	GTATTTGGG	TTTAA
00507161.1	GCTTA	CCCTTTAGAC	CTTTTT.	. GAAGAA	GGTTC	CGTTA	CCAA	CATGT	TTACTTCCATT	TAGGTAAT	GTATTTGGG	TTTAA
OQ507163.1	GCTTA	CCCTTTAGAC	С <mark>СТ</mark> ТТТТ.	. G <mark>A</mark> A <mark>G</mark> AA	GGTCC	<mark>C G</mark> G T A	CAC	<mark>C A T</mark> G T	TTACTTCCTTTC	T A G G G <mark>A A</mark> T	<mark>G T A</mark> T T T G G G	ТТТА <mark>А</mark>
00507165.1	GGTTA	CCCTTTAGAC	CTTTTT.	. GAAGAA	GGTIC	CGTAA	CCAA	CATGT	TTACTTCCATT	GAGATAAT	GTATTTGGG	TTTAA
00507167.1	GCTTA	CCCTTTAGAC		. GAAGAA	GGTTC	CGIAG	CCAA	CAAAA. CATGT	AGAGIIACAIAA TTACTTCCATT(AAGAAAGA TAGGTAAT	GTATTTGGG	GIIAA TTTAA
OQ507168.1	GCTTA	CCCTTTAGAC	CTTTTT.	GAAGAA	GGTTC	CGTTA	CCAA	CATGT	TTACTTCCATTC	TAGGTAAT	GTATTTGGG	ΤΤΤΑΑ
00507169.1	GCTTA	CCCTTTAGAC	CTTTTT.	. GAAGAA	GGTTC	CGTTA	CCAA	CATGT	TTACTTCCATTC	TAGGTAAT	GTATTTGGG	TTTAA
00507171.1	GCTTA	CCCTTTAGAC	CTTTTT.	GAAGAA	GGTTCC	CGTTA	CCAA CCAA	CATGT	TTACTTCCATTC TTACTTCCATTC	TAGGTAAT	GTATTTGGG GTATTTGGG	ΤΤΤΑΑ ΤΤΤΔΔ
00507180.1	GCTTA	CCCTTTAGAC	CTTTTT.	. GAAGAA	GGTTC	CGTTA	CCAC	CACGT	TTACTTCCTTTC	TAGGGAAT	GTATTTGGG	TTTAA
OQ507181.1	GCTTA	CCCTTTAGAC	CTTTTT.	. G <mark>A</mark> A <mark>G</mark> A <mark>A</mark>	3 G <mark>T</mark> T C <mark>(</mark>	<mark>C G</mark> T T A	ССАА	CATGT	TTACTTCCATTC	TAGGT <mark>AA</mark> T	<mark>G T A</mark> T T T G G G	ΤΤΤΑ <mark>Α</mark>
OQ507183.1	GCTTA	CCCTTTAGAC	CTTTTT.	. GAAGAA	GGTTC	CGTTA	CCAC	CATGT	TTACTTCCTTTC	TAGGGAAT	GTATTTGGT	TTTAA
00507185.1	GCTTA	CCCTTTAGAC		. GAAGAA	GGTTC	CGTTA	CCAA	CATGT	TTACTTCCATTC	TAGGGAAT	GTATTTGGG	TTTAA
OQ507192.1	GCTTA	CCCTTTAGAC	CTTTTT.	. GAAGAA	GGTTC	CGTTA	CCAA	CATGT	TTACTTCCATTC	T A G G T <mark>A A</mark> T	<mark>G T A</mark> T T T G G G	ТТТА <mark>А</mark>
00507193.1	GCTTA	CCCTTTAGAC	CITTTI.	. GAAGAA	GGTTC	CGTTA	CCAA	CATGT	TTACTTCCATTC	TAGGTAAT	GTATTTGGG	TTTAA
00507194.1	GCTTA	CCCTTTAGAC	CTITIT.	GAAGAA	GGTTCC	CGTTA	CCAA	CATGT	TTACTICCATIC TTACTICCATIC	TAGGTAAT	GTATTTGGG	ΤΤΤΛΛ ΤΤΤΑΑ
0Q507199.1	GCTTA	CCCTTTAGAC	CTTTTT.	GAAGAA	GGTTC	CGTTA	CCAA	CATGT	TTACTTCCATTC	TAGGTAAT	GTATTTGGG	TTTAA
OQ507201.1	GCTTA	CCCTTTAGAC	CTTTTT.	. GAAGAA	GGTTC	CGTTA	CCAA	CATGT	TTACTTCCATTC	TAGGTAAT	GTATTTGGG	ΤΤΤΑΑ
AY665868 1*	ACGAA	CGAC1	CICEGC.	AACGGA	TATCT TATCT	CGGCT	CTCG	САТ САТ.		TGAAGAAC	GCAGCRAAA GTAGCGAAA	TGCGA
AY665914.1*	ACGAA	CGAC1	CTCGGC.	AACGGA	TATCT	CGGCT	CTCG	CAT	CGA	TGAAGAAC	GTAGCGAAA	TGCGA
AY665905.1*	ACGAA	CGAC1	CTCGGC.	. A <mark>A</mark> C <mark>G</mark> G <mark>A</mark>	ΓΑΤΟΤ	CGGCT	CTCG	CAT	CG7	TGAAG <mark>AA</mark> C	GCAGCGAAA	TGCG <mark>A</mark>
A1665886.1* MH763728 1*	ACGAA	CGAC1	CICEGC.	AACGGA	TATCT	CGGCT	CTCG	САТ САТ	CGA	TGAAGAAC	GTAGCGAAA	TGCGA
MH763740.1*	ACGAA	TGAC1	CTCGGC.	AATGGA	TATCT	CGGCT	CTCG	CAT		TGAAGAAC	GYAGCGAAA	TGCGA
00371996.1	ACAAA	TGAC1	CICGGC.	. A A C G G A	ΓΑΤΟΤ	CGGCT	CTCG	CAT	CGZ	TGAAGAAC	GTAGCGAAA	TGCGA
OQ371997.1	ACGAA	TGACI	CICGGC.	CAAGGGA	TATCTO TATCTO	CGGCT	. TCG	C	TCC	GAGAAGAAC	GTAGCGAAA	TGCGA
00372001.1	ACAAG		CTCGGC.	ATGGA	T.TCT	CGGCT	. TCG	CA	C G A	TGAAGAAC	GTAGCGAA.	TGCGA
OQ372003.1	ACAAA	TGAC1	CTCGGC.	. A <mark>a</mark> c <mark>g</mark> g a	ГАТСТ	С <mark>С</mark> СТ	CTCG	CAT	CG#	TGAAG <mark>AA</mark> C	GTA GCGAAA	TGCGA
00372004.1	ACAAA	TGACI	CICEGC.	AACGGA	TATCT	CGGCT	CTCG	CAT	CGA	TGAAGAAC	GTAGCGAAA	TGCGA
00372007.1	ACAAA	TGACI	CTCGGC.	AACGGA	TATCT	ссст	C TCG	CAT	C G Z	TGAAGAAC	GTA GCGAAA	TGCGA
OQ372008.1	AAAC	GAI	CTCGGC.	<mark>A</mark> C <mark>G</mark> GT	T CT	CGGCT	CTCG	СТ	CG7	TGAA. <mark>AA</mark> C	GTATCGAA.	
00372009.1	ACAAA	TGACT	CICGGC.	AACGGA	ATCT	CGGCT	CICG	CAT	CGA	TGAAGAAC	GTAGCGAAA	TGCGA
00372013.1	ACAAA	TGACT	CTCGGC.	AACGGA	TATCT	CGGCT	CTCG	CAT		TGAAGAAC	GTAGCGAAA	TGCGA
OQ372014.1	ACAA <mark>A</mark>	TGACI	CICGGC.	. A <mark>A</mark> C <mark>G</mark> G <mark>A</mark>	ГАТСТ	<mark>С G</mark> G C T	СТСG	CAT	CG7	TGAAG <mark>AA</mark> C	<mark>g t a</mark> g c g a a a	TGCGA
00372015.1	ACAAA	TGAC1	CICGGC.	. AAC <mark>G</mark> GA	F A T C T (CGGCT	СТСА	CAT	CG1	TTTTGAAC	GTAGCGAAC	CGCGA
00372017.1	ACAAA	TGAC1	CTCGGC.	AACGGA	TATCT(ссст	CTCG	CAT	C G #	TGAAGAAC	GTAGCGAAA	TGCGA
0Q372018.1												
00372019.1	ACAAA	TGAC1	CICGGC.	. AACGGA	Г А <mark>Т</mark> С Т (CGGCT	CTCG	CAT	CG#	TGAAGAAC	GTA GCGAAA	TGCGA
00372021.1	ACAAA	TGAI	CTCGGC.	AACGGA	IATCT	CGGCT	C C T C G	CAT	C G A	TGAAGAAC	GTAGCGAAA	TGCGA
0Q372022.1	ACAAA	ТСАСТ	CTCCGC.	. A A C G G A	ГАТСТ	СССТ	CTCG	CAT	C C Z	TGAAG <mark>AA</mark> C	<mark>CTA</mark> GCGAAA	TGCG <mark>A</mark>
00372023.1	CCAGG	CAGACGTGCC		TAATGG.	CTT	CGGGC	GCAA	CTTG.		TCAAAGAC	TCGATGGTT	CACGG
00372025.1	ACAAA	TGACT	CTCGGC.	AACGGA	TATCT	CGGCT	CTCG	CAT		TGAAGAAC	GTAGCGAAA	TGCGA
00372026.1	C <mark>C</mark> A G G	CAGACGTGCC	CTCGACCO	CTATGG.	CTT	<mark>C G</mark> G G G	ACAA	CTTG.		TCCAAGAC	TCCAAGGTT	TACGG
00372027.1	CCAGG	CAGACGIGCO	CTCGACC	TAATGG.	CIIC	CGCGC	ACAA	CTTG.	CG1	TCAAAGAC	TCGATGGTT	CACGG
00372029.1	CCAGG	CAGACGTGCC	CICGACC	TAATGG.	CIT	CGCGC	ACAA	CTTG.		TCAAAGAC	TCGATGGTT	CACGG

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KT178121.1*	AGCCCTGCGCG	CTC <mark>TAC</mark> G	TCTGGAAGATCI	GCGAATCCCTG		TTATGTTA	AAACTTTCCAAGG
NC_026570.1*	AGCCCTGCGCG	CTC <mark>TA</mark> CG	T C T G <mark>G</mark> A A G <mark>A</mark> T C I	GCGAATCCCTG		ТТАТ GТТА	<mark>A</mark> A A C T T <mark>T C C A</mark> A <mark>G G</mark>
NC_039457.1*	AGCCCTGCGCG	CTC <mark>TAC</mark> G	TCTGGAAGATCI	GCGAATCCCTG	T <mark>TGC</mark>	ΤΤΑΤΑΤΤΑ	AAACTTTCCAAGG
NC_070364.1*	AGCCCTGCGCG	CTCTACG	TCTGGAAGATCT	GCGAATCCCTG	TTGC	TTATATTA	AAACTTTCCAAGG
NC_039456.1*	AGCCCTGCGCG	CICIACG	TCTGGAAGAICI	GCGAATCCCTG	ттсс	11A1AIIA ТТАТ АТТА	AAACIIICCAAGG
NC_048515.1*	AGCCCTGCGCG	CTCTACG	TCTGGAAGATCT	GCGAATCCCTG	TTGC	TTAT A TTA	AAACTTTCCAAGG
00507153.1	AGCCCTGCGCG	CTCTACG	TCTGGAAGATCT	GCGAATCCCTG		ΤΤΑΤΑΤΤΑ	AAACTTTCCAAGG
OQ507154.1	AGCCCTGCGCG	CTCTACG	TCTGGAAGATCT	GCGAATCCCTG		ΤΤΑΤ <mark>Α</mark> ΤΤΑ	AAACTTTCCAAGG
OQ507155.1	AGCCCTGCGCG	CTC <mark>TAC</mark> G	T C T G <mark>G</mark> A A G <mark>A</mark> T C T	GCGAATCCCTG		ΤΤΑΤ <mark>Α</mark> ΤΤΑ	A A A C T T T C C A A G G
00507156.1	AGCCCTGCGCG	CTCTACG	TCTGGAAGATCI	GCGAATCCCTG	T <mark>T G C</mark>	TTATATTA	AAACTTTCCAAGG
00507157.1	AGCCCTGCGCG	CTCTACG	TCIGGAAGATCI	GCGAATCCCTG.	TTGC	TTATATTA	AAACTITCCAAGG
00507159 1	AGCCCTGCGCG	CTCTAC G	TCTGGAAGATCT	GCGAATCCCTG	ттес.	ТТАТАТТА ТТАТ АТТА	AAACTTTCCAAGG
00507160.1	AGCCCTGCGCG	CTCTACG	TCTGGAAGATCI	GCGAATCCCTG	TTGC	TTATATTA	AAACTTTCCAAGG
OQ507161.1	AGCCCTGCGCG	CTC <mark>TAC</mark> G	TCTGGAAGATCT	GCGAATCCCTG	T T G C	ΤΤΑΤΑΤΤΑ	AAACTTTCCAAGG
OQ507163.1	AGCCCTGCGCG	CTC <mark>TAC</mark> G	TCTGGAAG <mark>A</mark> TCT	GCGAATCCCTG		ТТАТ GTTA	A A A C T T <mark>T C</mark> C A G <mark>G G</mark>
00507165.1	AGCCCTGCGCG	CTCGACG	TCTGGAAGATCT	GCCAATCCGTG	T <mark>TGC</mark>	ТТАТ GTTА	AAACTTTTCAGGG
00507166.1	AGCCCGGCGCG	CTCTGCG	TCGGGAAGATCI	GCGGAACCCTG	TTGC	TTATATTA	AAGCTTTCCAAGG
00507168 1	AGCCCTGCGCG	CICIACG	TCTGGAAGATCT	GCGAATCCCTG.	IIGC TTGC	ТТАТАТТА ТТАТ АТТА	AAACIIICCAAGG
00507169.1	AGCCCTGCGCG	CTCTACG	TCTGGAAGATCT	GCGAATCCCTG	TTGC	TTATATTA	AAACTTTCCAAGG
0Q507171.1	AGCCCTGCGCG	CTC <mark>TAC</mark> G	TCTGGAAGATCT	GCGAATCCCTG	TGC	ΤΤΑΤΑΤΤΑ	AAACTTTCCAAGG
0Q507177.1	AGCCCTGCGCG	СТС <mark>ТА</mark> СG	T C T G <mark>G</mark> A A G <mark>A</mark> T C I	GCGAATCCCTG		ΤΤΑΤ <mark>Α</mark> ΤΤΑ	A A A C T T T C C A A G G
OQ507180.1	AGCCCTGCGCG	CTC <mark>TAC</mark> G	T C T G <mark>G</mark> A A G <mark>A</mark> T C I	GCGAATCCCTG		ΤΤΑΤ <mark>Α</mark> ΤΤΑ	AAACTTTCCAGGG
OQ507181.1	AGCCCTGCGCG	CTCTACG	TCTGGAAGATCI	GCGAATCCCTG	TTGC	TTATATTA	AAACTTTCCAAGG
00507183.1	AGCCCTGCGCG	CICIACG	TCCCCCAAGAICI	GUGAAICCCIG.		TTALGIIA	AAACITICCAGGG
00507185.1	AGCCCTGCGCG	CTCTACG	TCTGGAAGATCT	GCGAATCCCTG	TTGC	TTATGTTA	AAACTTTCCAAGG
00507192.1	AGCCCTGCGCG	CTCTACG	TCTGGAAGATCT	GCGAATCCCTG	TTGC	TTAT <mark>А</mark> ТТА	AAACTTTCCAAGG
OQ507193.1	AGCCCTGCGCG	СТС <mark>ТА</mark> СG	T C T G G A A G A T C T	GCGAATCCCTG		ТТАТ <mark>А</mark> ТТА	AAACTTTCCAAGG
OQ507194.1	AGCCCTGCGCG	CTC <mark>TAC</mark> G	T C T G <mark>G</mark> A A G <mark>A</mark> T C T	GCGAATCCCTG		ΤΤΑΤ <mark>Α</mark> ΤΤΑ	<mark>A</mark> A A C T T <mark>T C</mark> C <mark>A</mark> A <mark>G G</mark>
00507195.1	AGCCCTGCGCG	CTCTACG	TCTGGAAGATCT	GCGAATCCCTG		TTATATTA	AAACTTTCCAAGG
00507199.1	AGCCCTGCGCG	CTCTACG	TCIGGAAGATCI	GCGAATCCCTG	TTGC	TTATATTA	AAACTTTCCAAGG
AV665903 1*	TACTTCCTCTC	AATTCCACAA	TCCCCCTCAACCA	TCGACTCTTTG	A A C G C A A C T T G C G C	CCGN AGCC	ATTACCCCCACCC
AY665868.1*	TACTTGGTGTG	AATTGCAGAA	TCCCGTGAACCA	TCGAGTCTTTG	ACGCAAGTTGCGC	CCGAAGCC	ATTAGGCCGAGGG
AY665914.1*	TACTTGGTGTG	AAT <mark>T</mark> G <mark>C</mark> AGAA	TCCCGTGAACCA	TCGAGTCTTTG	AACGCAAGTTG <mark>CGC</mark>	CCGA <mark>A</mark> GCC	ATTAGGCCGAGGG
AY665905.1*	TACTTGGTGTG	AAT <mark>T</mark> G <mark>C</mark> AGAA	TCCCGTGAACCA	TCGAGTCTTTG2	A A C G C A A G T T G <mark>C G C</mark>	CCGA <mark>A</mark> GCC	A T T A G G C <mark>C </mark> G A G <mark>G G</mark>
AY665886.1*	TACTTGGTGTG	AAT <mark>TGC</mark> AGAA	TCCCGTGAACCA	TCGAGTCTTTG	ACGCAAGTTG <mark>CGC</mark>	CCGAAGCC	ATTAGGCCGAGGG
MH763728.1*	TACTTGGTGTG.	A A T T G C A G A A A A T T G C A G A A	TCCCGTGAACCA	TCGAGTCTTTGA	AACGCAAGTTGCGC	CCGAAGCC	ATTAGGCCGAGGG
MH/03/40.1^	TACTIGGIGIG	AAIIGCAGAA AATTGCAGAA	TCCCGTGAACCA	TCGAGICIIIGA	AALGCAAGIIGIGC	CCGAAGUU	ATTAGGICGAGGG
00371997.1	TACTT GTGTG	AA.TGCAG.A	TCCCGTG.ACCA	TCGA. TCTTG	ACGCAAGTTGTGC	CCGAAGCC	A. TAGGCCGAGGG
OQ371998.1	. AACTGGTGTG	AA.TG <mark>C</mark> AG.A	TCCCGTG.ACCA	TCGAGTCT	GAAGCAAGTGGC	CCGAACCA	TAGGTCGAGGG
OQ372001.1	TACTTGGTGTG	AA. <mark>T</mark> G <mark>C</mark> AG.A	TCCCGTG.ACCA	TCGA TCTTG	AACGCAAGT.G <mark>TGC</mark>	CCGA <mark>A</mark> GCC	A T T A G G <mark>T C</mark> G <mark>A</mark> G <mark>G G</mark>
0Q372003.1	TACTTGGTGTG.	AAT <mark>T</mark> G <mark>C</mark> AGAA	TCCCGTGAACCA	TCGAGTCTTTG2	ACGCAAGTTG <mark>TGC</mark>	CCGAAGCC	ATTAGGTCGAGGG
00372004.1	TACTTGGTGTG.	AATTGCAGAA ACCT	TCCCGTGAACCA	TCGAGTCTTTG	AACGCAAGTTGTGC	CCGAAGCC	ATTAGGTCGAGGG
00372007 1	TACTTCCTCTC	ACGI	TCCCCTCAACCA	TCGACTCTTTC	ACCCAACTTCTCC	CCGA ACCC	ATTACCTCCACCC
00372008.1	TGTG	TACTGGTGGA	TTGC	AATCCCTG	ACGTCGATCTTGA	CTGATTGCGCC	GTTCTTTGCGGGG
OQ372009.1	TACTTGGTGTG	AAT <mark>T</mark> G <mark>C</mark> AGAA	TCCCGTGAACCA	TCGAGTCTTTG	AACGCAAGTTG <mark>TGC</mark>	CCGA <mark>A</mark> GCC	ATTAGGTCGAGGG
OQ372012.1	CTT <mark>G</mark> G <mark>G</mark> T <mark>G</mark>	A <mark>T</mark> G <mark>C</mark> AGAT	CCCT <mark>GA</mark> CCA	CCAGTTTT	.AAGCAAAT.G <mark>TGC</mark>	CCAA <mark>A</mark> ACC	A T A G C C G A G G G
00372013.1	TACTTGGTGTG.	A A T <mark>T G C</mark> A G A A	TCCCGTGAACCA	TCGAGTCTTTG/	AACGCAAGTTG <mark>TGC</mark>	CCGA <mark>A</mark> GCC	A T T A G G <mark>T C</mark> G A G G G
00372014.1	TACTTGGTGTG.	AATTGCAGAA	TCCCGTGAACCA	TCGAGTCTTTG	AACGCAAGITG <mark>TGC</mark>	CCGAAGCC	ATTAGGTCGAGGG
00372016 1	ТА			• • • • • • • • • • • •	· · · · · · · · · · · · · · · · · · ·		ACGAATCAGAGG
00372017.1	TACTTGGTGTG	AATTGCAGAA	TCCCGTGAACCA	TCGAGTCTTTG	AACGCAAGTTGTGC	CCGAAGCC	ATTAGGTCGAGGG
0Q372018.1							
OQ372019.1	TACTTGGTGTG	AAT <mark>T</mark> G <mark>C</mark> AGAA	TCCCGTGAACCA	TCGAGTCTTTG2	AACGCAAGTTG <mark>TGC</mark>	CCGA <mark>A</mark> GCC	A T T A G G C <mark>C </mark> G A G <mark>G G</mark>
OQ372020.1				CCGAGTCTAC.	· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · ·	
00372021.1	TACTTGGTGTG	AATTGCAGAA	TCCCGTGAACCA	TCGAGTCTTTGA	AACGCAAGTTG <mark>TGC</mark>	CCGAAGCC	ATTAGGTCGAGGG
00372022.1	CATTCTCCAAT	TCACACCAGAA	TATCCCATTTCC	CTACGTTCTTC	ACGUAAGIIG <mark>TGU</mark> ATCGATGCGAGAGAG	CGAG ATAT	CCGTTCCCCACCC
00372024.1	TACTTGGTGTG	AATTGCAGAA	TCCCGTGAACCA	TCGAGTCTTTG	ACGCAAGTTGTGC	CCGAAGCC	ATTAGGTCGAGGG
0Q372025.1	TACTTGGTGTG	A A T T G C A G A A	Τ				
OQ372026.1	GATTCTGCAAT	T C A <mark>C</mark> C A A G	TATCGCATTTC	CTACGTTCTTC	CTCCAAGCCAG <mark>AAC</mark>	CGAA <mark>A</mark> TAT	C C G T T G C <mark>C</mark> A G A <mark>G</mark>
00372027.1	GATTCTGCAAT	TCACACCAAG	TATCGCATTTC	CTACGTTCTTC	ATCGATGCGAG <mark>AGC</mark>	CGAGATAT	CCGTTGCCGAGAG
00372028.1	TACTTGGTGTG	AATTGCAGAA	TCCCGTGAACCA	TUGAGTOTTTG	ACGCAAGTTG <mark>TGC</mark>	CCAC ATAT	ATTAGGTCGAGGG
JU2012023.1	GALLCIGCAAL	ICACALCAAG	TUTUUUATITI		1 CONTROCA CAC	CONGMIAI	OCGTTOCCGROAG

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Km178121 1*	TCCCC		ATCC	ATCOAA	CTTC	AACACA	TAAA	ттс		сааст	ATCO	TCCT	CCC		CT			C A C	TA
K11/0121.1"				AICCAA	G I I G	AAAGAGA	IAAA		nn'	CANGI	AIGO					GIIG	JGAI	G_AC	IA
NC_026570.1*	TCCGC	CT	CATGGG	ATCCAA	GTTG	AAAGAGA	TAAA	TTG	A A	CAAGI	ATGO	TCGT	CCC.			GTTG	G G A T	GIAC	TA
NC_039457.1*	TCCGC	CT	CATGGO	ATCCAA	GTTG	AAAGAGA'	ΤΑΑΑ΄	ΤΤG	A A	CAAGI	ATGG	TCGT	CCC.		CI	GTTG	GGAT	GTAC	ТΑ
NC 070364.1*	TCCGC	ст	CATGGO	ATCCAA	GTTG	AAAGAGA'	TAAA	ттс	AA	CAAGT	ATGO	TCGT	ccc.		CT	GTTG	GGAT	GTAC	ТΑ
NC 039458 1*	TCCCC	СТ	ATCC	ATCCAA	CTTC	A A A C A C A'	TAAA	TTC	77	CAACT	ATCO	TCCT	CCC.		CT	CTTC	CAT	COAC	TΛ
NC_039430.1*	TCCCCC			A I COAA	0110	NANGAGA			20		AIGO						O A I		10
NC_048514.1*	TCCGC	СТ	CATGGG	ATCCAA	GTTG	AAAGAGA	TAAA	TTG	j A A (CAAGI	ATGO	TÇGT	ccc.			GTTG	GGAT	GTAC	ТΑ
NC_048515.1*	TCCGC	СТС	CATGGO	ATCCAA	GTTG	AAAGAGA'	TAAA	ΤΤG	AA	CAAGI	ATGG	TCGT	CCC.		CI	GTTG	GGAT	GTAC	ТΑ
00507153.1	TCCGC	ст с	CATGGO	ATCCAA	GTTG	AAAGAGA'	TAAA	TTG	AA	CAAGI	ATGO	TCGT	CCC.		СТ	GTTG	GGAT	GTAC	TΑ
00507154 1	TCCCC	CT (ATCC	ATCCAA	GTTG	AAAGAGA	TAAA	ттс	D D	CAAGT	ATGO	TCGT	CCC		C T	GTTG	CAT	C A C	TΔ
00507154.1	TCCGC			A TOONA		ABBCBCB					n r G G							O D A C	T 2
00201122.1	TCCGC		AIGGO	AICCAA	GIIG	AAAGAGA	IAAA	116	AA	CAAGI	AIGG	TCGT			· · · CI	GIIG	JGAI	G_AC	1 A
OQ507156.1	TCCGC	CT	CATGGO	ATCCAA	GTTG.	AAAGAGA'	TAAA	ΤΤG	AA(CAAGI	ATGG	TCGT	CCC.			GTT <mark>G</mark>	GGAT	GTAC	ТΑ
00507157.1	TCCGC	СТ	CATGGO	ATCCAA	GTTG	AAAGAGA	TAAA	TTG	AA	CAAGI	ATGG	TCGT	CCC.		CI	GTTG	GGAT	GTAC	ТΑ
00507158 1	TCCCC	СТ	ATCC	ATCCAA	GTTG	AAAGAGA	ΤΑΑΑ	ттс		CAACT	ATGO	TCGT	CCC		СТ	GTTG	GAT	GTAC	ТΑ
00507150.1	TOOOC			A TOONA	O T T O	ANNONON					A TOO								T 3
00307139.1	TUCGU		AIGGO	AICCAA	GIIG	AAAGAGA	IAAA	110	AA	CAAGI	AIGG	TCGI	CCC.		CI	GIIG	GAI	G_AC	1 A
OQ507160.1	TCCGC	CT	CATGGO	GATCCAA	GTTG	AAAGAGA'	TAAA	ΤΤG	JAA (CAAGI	ATGG	TCGT	CCC.		C1	GTTG	GGAT	GTAC	ТΑ
00507161.1	TCCGC	СТ	CATGGO	ATCCAA	GTTG	AAAGAGA'	TAAA	TTG	AA	CAAGI	ATGO	TCGT	CCC.		CI	GTTG	GGAT	GTAC	ΤA
00507163 1	TCCCC	CT	ATCC	ACCCAA	GTTG	AAAGAGA	CAAA	ттс	2 2	CAACT	'eeco	TCGT	CCC		СТ	GTTG	CCT	CAR	тδ
00507105.1	TOCOC			ACCORA	0110	AAAGAGAG	JAAA	110		CAROI	00000	1001					3001	0 - AC	1 17
00201162.1	TCCGC	CT C	CATGGG				A .	• • •	•••							• • • •			• •
OQ507166.1	TCCGC	CTC	CATGGO	JATCCAA	GTTG	AAAGAGA'	TAAA	TTG	A A	CAAGI	ATGG	TCGT	CCC.		CI	GTTG	GGAT	GTAC	ТΑ
00507167.1	TCCGC	СТ	CATGGO	ATCCAA	GTTG	AAAGAGA'	TAAA	TTG	AA	CAAGI	ATGO	TCGT	ccc.		CI	GTTG	GGAT	GTAC	ΤA
00507168 1	TCCCC	СТ	ATGGO	ATCCAA	GTTG	AAAGAGA	TAAA	ттс	AA	CAAGT	ATGO	TCGT	ccc		. CT	GTTC	GAT	GTAC	ТΔ
00507100.1	TCCCCC				O T T O											GTTG			
00201109.1	TUCGO	<u> </u>	AIGGO	AICCAA	GIIG	MAAGAGA	IAAA	116	AA	CAAGI	ALGO	TOGT				GIIG	JGAT	- AC	1 A
OQ507171.1	TCCGC	CT	TGGG	ΑΤС <mark>СΛ</mark> Λ	GTTG	ΛΛΛGΛGΛ	ΤΛΛΛ	TTG	jΛΛ	CAAGI	ΛTGG	TCGT	CCC.		CI	GTT <mark>G</mark>	GΛT	GIVC	ТΛ
00507177.1	TCCGC	СТ	CATGGO	ATCCAA	GTTG.	AAAGAGA'	TAAA	TTG	AA	CAAGI	ATGG	TCGT	CCC.		CI	GTTG	GGAT	GITC	ТΑ
00507180 1	TCCCC	СТ	ATGGO	ACCCAA	GTGA	AAAGTGA	TAAA	ттс	AA	CAGAT	GTGG	TCGC	GCC		Ст	GTTC	GGGT	GTAC	ΤA
00507191 1	TCCCC			ATCONA	CTTC		T 7 7 7	TTC		0 3 3 6 7		TCCT				CTTC	CAT		T 7
00307181.1	TUCGU		AIGGO	AICCAA	GIIG	AAAGAGA	IAAA	110	AA	CAAGI	AIGG				· · · CI	GIIG	GAI	G_AC	IA
OQ507183.1	TCCGC	CT	CATGGO	ACCCAA	GTTG	AAAGAGA	GAAA	ТТС	JAA (CAAGI	ATGG	C C G G	ccc.		C1	GTTG	GGAT	GTAC	ТΑ
OQ507184.1	GCCGC	CT	CATTGO	ATCCAA	GTTG	AAAGAGA'	TAAA	TTG	AA	CAATI	ATGG	GCCGT	CCC.		CI	GTTG	GGGT	GTAC	ΤA
00507185.1	TCCCC	ст.	CATGGO	ATCCAA	GTTG	AAAGAGA	TAAA	ттс	AA	CAAGT	ATGO	тсст	CCC.		СТ	GTTG	GAT	GTAC	ТΑ
00507192 1	TCCCC	CT C	CATCO	ATCCAA	CTTC	A A A C A C A '	T A A A	TTC		0 0 0 0 1	NTCC	TCCT	CCC.			CTTC	CAT	C	TA
00007192.1	TCCGC		AIGGO	AICCAA	G I I G	AAAGAGA			- A A	CAAGI	AIGO					GIIG	JGAI	G_AC	1 1
0020/193.1	TUCGC		CATGGO	ATCCAA	GIIG	AAAGAGA	TAAA	116	AA	CAAGI	AIGO	TCGT	000.			GIIG	JGAT	GLAC	TA
OQ507194.1	TCCCC	CT	CATGGO	CATCCAA	CTTG	AAAGAGA'	ΤΑΑΑ΄	TTC	AA	CAAGI	ATGO	TCCT	CCC.		CI	CTTC	GCAT	GTAC	ТΑ
00507195.1	TCCGC	СТ	CATGGO	ATCCAA	GTTG	AAAGAGA'	TAAA	TTG	AA	CAAGI	ATGO	TCGT	ccc.		CI	GTTG	GGAT	GTAC	ТΑ
00507199 1	TCCCC	CT	ATCC	ATCCAA	CTTC	AAAGAGA	TAAA	ттс	2 2	CAACT	ATCO	TCGT	CCC		СТ	GTTG	CAT	CAC	TΔ
00507199.1	TCCCCC			ATCOAR	C T T C	AAAGAGA					AIGO								10
00507201.1	ICCGC		AIGGO	AICCAA	GIIG	AAAGAGA	IAAA	110	AA	CAAGI	AIGO		CCC.		••••	GIIG	JGAI	G_AC	1 A
AY665903.1*	CACGT	CTG.C	CCTGGG	GCGTCAC	GC		A.	TCG	CG	ICGCC	сссс	TCGC	ccc.		GC	CCCG	GGGG	GCGT	СG
AY665868.1*	CACGT	CTG.C	CCTGGG	CGTCAC	GC		A.'	TCG	CG	ICGCC	CCCC	TCGC	CCC.			T	IGGG	GCGT	CG
AY665914 1*	CACGT	CTG (CTGG	CGTCAC	GC		Δ	тсс	CG	TCGCC	CCCC	TCGC	CCC		GC	GCCG	GGG	GCTT	GG
AV665005 1*	CACCT			CCTCAC	čč			TCC	CC.	TCCCC		TCCC	CTC			ATCC		CCCT	CC
A1665905.1*	CACGI			GICAC	66		A .	IUG	CG	TCGCC		TCGC	CIC.			AICG	6666	GCGI	GG
AY665886.1*	CACGI	CTG.C	CCTGGG	GTCAC	GC		A . '	TCG	CG	ICGCC	CCCC	TCGC	ccc.		GC	CACTG	GGGG	GCGT	СG
MH763728.1*	CACGT	CTG.C	CCTGGG	CGTCAC	GC		A . '	TCG	CG	ICGCC	сссс	TCGC	CCC.		GC	CACTG	CGGG	GCGT	CG
MH763740.1*	CACGT	CTG.	CCTGGG	CATCAC	GC		Α.	TCG	CA	TCGCC	cccc	TCGC	сст.		GC	ACCG	CGGC	GCKT	ΤG
00371996 1	CACCT	CTC	CTCCC	CATCAC	C C		7	TCC	C A	TCCCC	0000	TCCC	CCT			ACCC	000	CCCT	TC
00371330.1	CACGI			CATCAC	00		•••••••									ACCO			10
00311331.1	CACGI		CIGGG	CATCAC	GC		A.	TCG	CG	ICGCC	CCCCC	TCCC	CCC.		GC	GGI <mark>G</mark>	666	GAGT	СG
OQ371998.1	CA.GT	[<mark>CG</mark> (CCTGGC	C. TCAC	GC		A.'	TCC	C.	ICGCC	сссс	TCGC	CCT.		GC	GGC <mark>G</mark>	C <mark>G</mark> G.	GAGT	ΤG
00372001.1	CA.GT	CTG.C	CCTGGC	CATCAC	GC		A . '	TCG	CG	ICGCC	cccc	TCGC	ccc.		GC	GGTG	CGG.	GAGT	CG
00372003 1	CACCT		CTCCC	CATCAC	CC		Δ.	тсс	C A	TCGCC	cccc	TCCC	ССТ		GC	ACCO	CCC	CCGT	TG
00373004 1	CACCT			CATCAC						10000		Taca	CCT					CCCT	TC
00372004.1	CACGI			CATCAC	60		. A .	1 C C	CA	LCGCC		1060	CC1.			ACCG		GCGI	10
00372005.1	CACAG	GCAGCO	GATGGC	CCACGAA	GC		A.		•••	. TACC	GTCC	GCAC	TCC.		CC	GGT <mark>G</mark>	CGGC	GAG.	. G
0Q372007.1	CACGT	CTG.C	CCTGGG	GCATCAC	GC		A . '	TCG	CA'	TCGCC	сссс	TCGC	CCT.		GC	CACCG	CGGC	GCGT	ΤG
00372008.1	ACTG.		GCTGGC	TCCCAC	GC			TC.		cc	CCCG	CCGG	CCG.			GCTG	GGA	CGTC	ΤG
00372009 1	CACCT	СТС	CTCC	CATCAC	c c			TCC	C A	TCCCC		TCCC	CCT.			ACCC	CCC	CCGT	TC
00372009.1	CACGI			CAICAC	GC		•••									ACCO		0001	10
00372012.1	CA.GI	L I I C	CIGGGG	CATCAC	60		A .	TCC	CG	TCGCC		TCGC	ccc.		•••GC	GGIG	GGGG	GAGT	СG
OQ372013.1	CACGI	CTG.C	CCTGGG	CATCAC	GC		A . '	TCG	GCA.	ICGCC	сссс	TCGC	CCT.		GC	CACCG	CGGC	GCGT	ΤG
00372014.1	CACGT	CTG.C	CCTGGG	CATCAC	GC		A . '	TCG	CA'	ICGCC	CCCC	TCGC	CCT.		GC	CACCG	CGGC	GCGT	ΤG
00372015.1																			
00272016 1								· · · ·	1.1.										111
00072010.1					· · · ·		•••	:::::::::::::::::::::::::::::::::::::::								· · ·			
00372017.1	CACGI	urig.(TIGGG	JUTICIC	60		A . '	TCC	CA	TCGCC	.0000	T C C C	\cdots			· · ·	• • • •		• •
OQ372018.1									1.			C	CCT.						
00372019.1	CACGT	CTG.	CCTGGG	CATCAC	GC.		. A.	TCC	CA	ICGCC	cccc	TCGC	CCT.		GC	ACCG	CGGC	GCGT	ΤG
00372020 1			CTAC						1701		0.0	CCCT	ССТ						
00372021.1					· · · ·		•••	:::::::::::::::::::::::::::::::::::::::	::				CCT.		••••				· ·
00372021.1	CACGI	1016.0		CATCAC	60		A .	TCC	CA	TCCCC		TCGC	CCI.		•••GC	ACCG	- 6 6 C	GCGT	IG
00372022.1	CACGT	CTG.	CTGGC	CATCAC	GC		A.'	TCC	CA'	TCGCC	0000	TCGC	CCT.		GC	ACCG	GGC	GCGT	ΤG
OQ372023.1	TCG	1	TTCGTC	TTTCAA	GC		. GAG	GCC	CA	GC.TC	CCCC	GCGC	GCG.		co	GCGG	ACGG	GGCG	CG
00372024 1	CACGT	CTG	CTGGG	CATCAC	GC		A	тсс	CA	TOGOC	cccc	TCGC	ССТ		GC	ACCG	GGC	GCGT	TG
00372025 1					- · · ·		· · ·		~~~										1
00372023.1	· : : : ·		· · · · · ·	:::::	· · · ·		•••	::::	· ·			· · · ·				• • • •	•••••	:	· ·
00372026.1	. GCAT	TGT	TTTCZ	AGCGAA	GC		A.	ÇΑG	TT	recce	GCGC	TLC C C	CGT.				GG	ACGA	GG
OQ372027.1	TCATT	TGTG	TTTT	AGCGAA	GC		A.	CAG	CT	ccccc	GCGC	ACGC	CGTG	GACGA	GGCGC	GA. <mark>G</mark>	GGT	GTGC	СΑ
00372028.1	CACGT		CCTGGG	CATCAC	ΤС		A T	TCG	CA	ICGCC	cccc	TCGC	CCT.		GC	ACCG	GGC	GCGT	ΤG
00372029 1	TCA		TTGTO	TTTCAA	c c		G	AAC	CA	CAGO	TCCC	CCCC	GC		20	GCCC	TGGG	ACGA	GG
02312023.1	· · · ·		11010	· · · · · · · ·	<u>v</u>		••••••			CCR9C			<u> </u>		· · · · · · ·		1000	n c G A	99

		530	540	55 Q	560	570		
KT178121.1*	T	. <mark>A</mark> AA	T <mark>TGG</mark> GGTTATCTG	CTAAAAACTA	CGGTAGAGCTGT	TTATG	AAT <mark>G</mark> TCTT	
NC_026570.1*	TTAAACCI	. AAA	TTGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCTGT	TTATG	AATGTCTT	•
NC_039457.1*	ТТАААССЛ	. AAA	TTGGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCTGT	TTATG	ААТСТСТТ ААТСТСТТ	•
NC 039458.1*	TTAAACC1	. AAA	TTGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCIGI	TTATG	AATGTCTT	
NC_048514.1*	TTAAACCI	. AAA	TTGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCTGT	TTATG	AATGTCTT	
NC_048515.1*	ТТАА <mark>АС</mark> СТ	. <mark>AAA</mark>	T T G G G G T T A T C T G	CTAAAAACTA	CGGTAGAGCTGT	TAT <mark>G</mark>	ААТ <mark>G</mark> Т <mark>С</mark> ТТ	
00507153.1	TTAAACC1	. A A A	TTGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCTGT	TTATG	AATGTCTT	•
00507154.1	ТТАААССІ	. AAA	TTGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCTGT	TTATG	AAIGICII	•
00507156.1	TTAAACCT	AAA	TTGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCTGT	TTATG	AATGTCTT	
0Q507157.1	ТТАА <mark>АС</mark> СТ	. <mark>AAA</mark>	T T G G G G T T A T C T G	CTAAAAACTA	CGGTAGAGCTGT	TAT <mark>G</mark>	AAT <mark>G</mark> T <mark>C</mark> TT	
OQ507158.1	TTAAACCI	. AAA	TTGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCTGT	TTATG	AAT <mark>GTC</mark> TT	• •
OQ507159.1	TTAAACCI	. AAA	TTGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCTGT	TTATG	AATGTCTT	• •
00507161.1	TTAAACCI	. A A A	TTGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCIGI	TTATG	AATGTCTT	
0Q507163.1	TTAACCT1	. AAA	TTGGGGTTATCTG	TTAAAAAATA	CGGTAGAGTTGT	TGATG	AATGTCTC	
OQ507165.1			• • • • • • • • • • • • • • • • • • •					
00507166.1	TTAAACCI	. AAA	TTGGGGTTATCTG	CTAAAAACCT	CGGTAGAGCTGT	TTATG	AATGTCTTCGCGG	3.
00507168 1	ТТАААССІ	. AAA	TTCCCCTTATCIC	CIAAAAACIA	CGGIAGAGCIGI	TTATC	AAIGICII	•
00507169.1	TTAAACC1	AAA	TTGGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCIGI	TTATG	AATGTCTT	
0Q507171.1	T	. <mark>A A A</mark>	T T C C G G T T A T C T G	CTAAAAACTA	CGGTAGAGCTGT	TAT <mark>C</mark>	ААТ <mark>С</mark> ТТ	
00507177.1	ΤΤΑΑΑСΤΊ	. TTA	T T G G					• •
OQ507180.1	TTAAACCI	. AAA	TTGGGGTTCTGTG	CTAAAAACTA	CGAGAGTGCTAT	TTATG	GATGTCTC	•
00507181.1	Т ТАЗАССТ	· AAA	TTGGGGTTAICIG	СТАААААСТА	CGAGAGAGCIGI	TTATG	GATGTCTC	•
00507184.1	TTAAACCI	AAA	TTGGGTTTATCTG	CTAAATACGA	GAGTATTGCTGT	TTACG	AATGTTTA	
OQ507185.1	ТТАА <mark>АС</mark> СТ	. <mark>AAA</mark>	T TGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCTGT	TAT <mark>G</mark>	AAT <mark>G</mark> T <mark>C</mark> TT	
00507192.1	TTAAACC1	. AAA	TIGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCTGT	TTATG	AATGTCTT	• •
00507193.1	TTAAACC1	AAA	TTGGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCTGT	TTATG	AATGTCTT	• •
00507195.1	TTAAACCI	. AAA	TTGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCIGI	TTATG	AATGTCTT	
0Q507199.1	TTAA <mark>AC</mark> CT	. AAA	TTGGGGTTATCTG	CTAAAAACTA	CGGTAGAGCTGT	TTATG	AAT <mark>G</mark> TCTT	
OQ507201.1	TTAA <mark>AC</mark> CI	. <mark>AAA</mark>	T T G G G G T T A T C T G	CTAAAAACTA	CGGTAGAGCTGT	TTATG	AAT <mark>G</mark> TCTT	
AY665903.1*	TGGGACGG	. ATA	CTGGC		C	TCCCG	IGC <mark>GCC</mark> ATCGGCA	7.
AI003808.1* AV665914 1*	C C C C C C C C C C C C C C C C C C C	ΔΤΔ	CTGGC			TCCCG		,. :
AY665905.1*	CGGGACGG	. A T A	CTGGC		C	TCCCG	TGCGCTCGCAGCO	3
AY665886.1*	CGGG <mark>AC</mark> GC	. <mark>A T A</mark>	CTGGC		C	TCCC <mark>G</mark>	TGC <mark>G</mark> CTCTCAGCC	3.
MH763728.1*	CGGGACGC	. A T A	CTGGC		C	TCCCC	TGCGCTCTCAGCC	j.
MH763740.1*	CGGGACGC	. АТА ЛТЛ	CTGGC		C	TTCCG	TGYGCCATCGGC1	
00371997.1	T	ATA	CTGGC		C	TCCCG	TGCGCTCGAAGAC	; ;
OQ371998.1	T	T A	C T G		C	TCCCG	T.CGCCAAAGAT.	
00372001.1	TGAG <mark>A</mark> TGC	T <mark>A</mark>	C T G		C	TCCCG	TGC <mark>G</mark> C <mark>C</mark> GAAGAG.	• •
00372003.1	CGGGACGC	. A T A	CTGGC	• • • • • • • • • •	C	TTCCG	IGC <mark>GCC</mark> ATCGGCI	
00372004.1	G GGAGCGA	· . A I A			••••••	TCTTA	TGC	•
00372007.1	CGGGACGG	ATA	C <mark>TGG</mark> C		C	TTCCG	TGCGCCATCGGCT	ſ.
OQ372008.1	CCTCCTGGTCAGGGGTGG	.CA <mark>A</mark>	CCAGC		G	GCCC <mark>G</mark>	cgc <mark>g</mark> g	
00372009.1	CGGGACGG	. ATA	CTGGC		C	TTCCG	IGC <mark>GCC</mark> ATCGGCT	
00372012.1	TGGGATGC	. АГА лтл	CTGGC	• • • • • • • • • •	C	TCCCG	TGCGCTCGAAGAG	j.
00372014.1	CGGGACGC	. ATA	CTGGC		C	TTCCG	TGCGCCATCGGCI	ŕ.
0Q372015.1								
OQ372016.1			• • • • • • • • • • • • •					• •
OQ372017.1		• • • • • • • • • •	• • • • • • • • • • • • • •				• • • • • • • • • • • • • • •	•
00372018.1	C GGGACGO	 АТА	CTGGC		 ۲	TTCCG	TGC <mark>GCC</mark> ATCGGCI	r
00372020.1	· · · · · · · · · · · · · · · · · · ·				T	TTTTG	GGT <mark>G.</mark>	
00372021.1	C	. АТА	C <mark>TGG</mark> C		C	ТТСС <mark>G</mark>	ТGC <mark>G</mark> C <mark>С</mark> АТСGGCТ	C
00372022.1	ç	. A T A	CTGGC		<u></u> C	TTCCG	IGC <mark>GCC</mark> ATCGGCT	
00372023.1	AGGGGCGG	GCCG	TUGGT		TAAGTAT	TTCCTT	JGCGCGTTCCGCG	эC
00372025.1	C	. A 1 A				TICCG	I GCGCCAICGGCI	•
00372026.1	CCCGAGGO				· · · · · · · · · · · · · ·	G	TGT <mark>G</mark> C <mark>C</mark> ATCGGTC	żт
00372027.1	TCCGTCGZ	GTA	TTC		c	TTGG <mark>G</mark>	CGC <mark>G</mark> TTTCGIGCC	2.
00372028.1	CGGGACGG	TATA	CTGGC		C	TTCCG	I GCGCCATCGGCT	
00312029.1	UGUG <mark>A</mark> IGO	GGIGIGCCAI	. C <u>I G I</u> C		GAGTATTCC	TLLCG	CGCGTHTTCGTGI	. C

58	io 590	600	610	620	630	640	1
KTT178121 1*	CCCCCTCCACTT	CATTTACCAAAC	ATCATCACAA	CCTCAAC	TCACAACCA	TTTATCC CTT	CC
NE 006530 1+	COCOGIOGACIT	. GATITIACCAAAC	ATGATGAGAA		TOACAACC .A		00
NC_026570.1*	CGCGGTGGACTT	.GATITTACCAAAG	ATGATGAG <mark>AA</mark>	CGTGAAC	TCACAACC.A	GTT	GG
NC_039457.1*	CGCGGTGGACTT	.GATITTACCAAAG	ATGATGAG <mark>AA</mark>	CGTGAAC	TCACAACC.A		GG
NC 070364.1*	CGCGGTGGACTT	. GATITTACCAAAG	ATGATGAGAA	CGTGAAC	TCACAACC.A	GTT	GG
NC 039458 1*	CCCCCCCCCCTT	GATTTTACCAAAG	ATGATGAGAA	GTGAAC	TCACAACCA	TTTATCC GTT	' G G
NC_049514_1*	CCCCCCCCCCTC	CATTTRACCANAC	ATCATCACA A	CCTCARC	TCACAACCA		00
NC_048514.1^	CGCGGIGGACII	. GATITIACCAAAG	AIGAIGAGAA	GIGAAC	ICACAACC.A		99
NC_048515.1*	CGCGGTGGACTT	. GATITITACCAAAG	ATGATGAG <mark>AA</mark>	CGTGAAC	TCACAACC.A	GTT	ĢG
OQ507153.1	CGCGGTGGACTT	. GATITIACCAAAG	ATGATGAG <mark>AA</mark>	CGTGAAC	TCACAACC.A	GTT	GG
00507154.1	CGCGGTGGACTT	GATTTTACCAAAG	ATGATGAGAA	CGTGAAC	TCACAACCA	TTTATGC GTT	GG
00507155 1							
00007100.1							
00307136.1	CGCGGIGGACII	.GAIIIIACCAAAG	AIGAIGAGAA	GIGAAC	ICACAACC.A	••••••••••••••••••••••••••••••••••••••	66
OQ507157.1	CGCGGTGGACTT	.GATTTTACCAAAG	ATGATGAG <mark>AA</mark>	CGTGAAC	TCACAACC.A	GTT	GG
00507158.1	CGCGGTGGACTT	.GATTTTACCAAAC	ATGATGAG <mark>AA</mark>	CGTGAAC	TCACAACC.A		GG
00507159.1	CCCCCTCCACTT	GATTTTACCAAAC	ATGATGAGAA	CGTGAAC	TCACAACCA	GTT	GG
00507160 1	CCCCCTCCACTT			00100			00
00007100.1	COCOOTGOACTT				· · · · · · · · · · · · · · · · · · ·		· ·
0020/101.1	CGCGGTGGACTT	.GATITIACCAAAG	ATGATGAG <mark>AA</mark>	CGIGAAC	ICACAACC.A	GII	GG
OQ507163.1	CGCGGTGGGATT	,GATTTTACCAAAG	ATGATGAG <mark>AA</mark>	CGCGGAC	TCCCAACC.A		GG
00507165.1							
00507166 1	TGTGGTTGATTT	ТСССАААС	ATGATGAGAA	GTG			
00507167 1	CCCCCTCCACTT		A T C A T C A C A A		TCACAACCA		<u> </u>
00507107.1	CGCGGIGGACII	. GATITIACCAAAG	AIGAIGAGAA	GIGANC	ICACAACC.A		G G
00201168.1	CGCGGTGGACTT	.GATITIACCAAAG	ATGATGAG <mark>AA</mark>	CGTGAAC	TCACAACC.A	GTT	GG
OQ507169.1	CGCGGTGGACTT	. GATITTACCAAAG	ATGATGAG <mark>AA</mark>	CGTGAAC	TCACAACC.A		GG
00507171.1	CGCGGTGGACTT	.GATTTTTCCAAAG	ATGATGAG <mark>AA</mark>	CGTGAAC	TCACAACC.A	TTTATGCTTT	GG
00507177.1	1						
00507190 1	CCCCTCCATT		CTCACAACAA		TCACCACCT	TTTCCCC CTT	00
00307180.1	CGCGGTGGGATT	. GATITIACCAAAI	GIGAGAAGAA		TCACCACC.I		GG
0020/181.1	CGCGGTGGACTT	.GATITTACCAAAC	ATGATGAG <mark>AA</mark>	CGTGAAC	TCACAACC.A	GTT	GG
OQ507183.1	CGCGGTGGATT	.GATTTTACCAAAG	ACAATGAG <mark>AA</mark>	ACTGAAC	TCACAACC.A		GG
00507184.1	CGCGGTGGAACT	.GATITTACCAAAI	TTGCTGAG <mark>AA</mark>	CGTTCTC	TIGCAACC		AG
00507185 1	CGCGGTGGACTT	GATTTTACCAAAG	ATGATGAGAA	GTGAAC	TCACAACC A	TTTATCC GTT	GG
00507192 1	CCCCCTCCACTT	CATTTTACCAAAC	ATCATCACAA	CTCAAC	тсада		00
00007192.1	COCGOTGOACTT	.GATITIACCAAAG	ATGATGAGAA	COTGAAC			
002507193.1	CGCGGTGGACTT	. GATITTACCAAAG	ATGATGAG <mark>AA</mark>	CGTGAAC	TCACAACC.A	GTT	GG
OQ507194.1	CGC					· · · · · · · · · · · · · · · · · · ·	• •
OQ507195.1	CGCGGTGGACTT	. GATTTTACCAAAG	ATGATGAG <mark>AA</mark>	CGTGAAC	TCACAACC.A	GTT	GG
00507199.1	CGCGGTGGACTT	. GATITIACCAAAG	ATGATGAGAA	CGTGAAC	TCACAACC.A	GTT	GG
00507201 1	CCCCCTCCACTT	GATTTTACCAAAA	ATGATGAGAA	CCTCAAC	TCACAACC A	TTTATCC CTT	'GG
AV665002 1+	CCCCCCCCCC		nii oni onomi	TCCCACC	CCCCCTCC A		
A1005903.1*				TGCGAGC	CCGCGICG.A		9.9
A1002808.1*	CCCCCCLCCCCCC	. A	AA	IGCGAGC	CCACGICG.A	CGG <mark>ACG</mark> TCAC	GG
AY665914.1*	CGCGGCTGGCCT	. A	AA	TGCGAGC	CCGCGTCG.A	CGGACGTCAC	. G G
AY665905.1*	CGCGGCTGGCCT	. A	<mark>AA</mark>	TGCGACC	CCACGTCG.A	CAC	GG
AY665886.1*	CGCGGCTGGCCT	. A	ΑΑ	TGCGAGC	CCACGTCG.A	CAC	GG
MU763728 1*	CETEECTEECCT	λ	7.7	TCCCACC	CCACCTCCA	CCCACCT CAC	C C
MR703720.1*				TOCOACC	CCACGICG.A		00
MH/63/40.1*	COLOCITOCCCL	. A	AA	IGIGAGU	CCAIGICG.A		GG
00371996.1	CGTGGTTGGCCT	. A		IGTGAGC	CCATGTCG.A	CGGACGTCAC	. G G
OQ371997.1	CGCGGCTGGCCT	. A	AA	TGCGAGC	CCACGTCG.A	CAC	. G G
00371998.1	CGTG TGGCCT	. A		TGCGAGC	CCACGICG.A	CAC	GG
00372001 1	CGCGGTTGGCCT		ΔA	ACCARC	CCACGTCG A	CGGACGT CAC	GG
00372002 1	COTCOTTCCCCT	· · · · · · · · · · · · · · · · ·		TOTOACC	CCATCTCC A	CCCACCT CAC	00
00372003.1			· · · · · · · · · · · · · · · · · · ·	IGIGAGC	CCAIGICG.A		GG
00372004.1	CGIGGIIGGCCI	. A	AA	IGIGAGC	CCAIGICG.A	CGG <mark>A</mark> CGICAC	GG
OQ372005.1	CGGAGCTGCTC.		AC	TATGCTC	GTATATTG	CGTCATTCCT	ΤG
00372007.1	CGTGGTTGGCCT	AA	AA	TGTGAGC	CCATGTCG.A	CAC	GG
00372008.1	AGGGGTTAACCA	ΓΤ	GG	TGCGGCC	ACCCCCCG	CGTGCTACTC	TG
00372009 1	CGTGGTTGGCCT	λ	77	TGTGAGC	CCATCTCCA	CGGACGT CAC	e c
00373013 1	CCCCCCCCC	7		TCCCACC	CONTOU A		.00
00372012.1	COCGOCIGOCCI	· A · · · · · · · · · · · · · ·		IGCGAGC	CCACGICG.A		66
00372013.1	CGTGGTTGGCCT	. A		TGTGAGC	CCATGTCG.A	CGG <mark>ACG</mark> TCAC	. G G
OQ372014.1	CGTGGTTGGCCT	. A	AA	TGTGAGC	CCATGTCG.A	CGGACGTCAC	. G G
00372015.1							
00372016 1							
00372017 1							• •
00072017.1			· · · · · · · · · · · · · ·		• • • • • • • • • •	· · · · · · · · · · · · · · · · · · ·	· ·
003/2018.1	Celli I I I GGI I I I				: :: ::: : - · · · · ·	· · · · · · · · · · · · · · · · · · ·	· ·
OQ372019.1	CGTGGTGGTCCT	. A	AT	TGTAAGC	CCATGTCG.A	CGGACGTCAC	GT
OQ372020.1	CTCGGTTTCTTT			ATC	CTATACTC		
00372021.1	CGTGGTTGGCCT	. A	Δ Δ	TGAGAGC	CCATGTCG .A	CAC	GG
00372022 1	COTO OTTO COOT	λ	λ λ	TCTCACC	CCATCTCC A	CCCACCT	i c c
00272022.1		····	Deceese and			CCCCCCACCACCACCACCACCACCACCACCACCACCACC	20
003/2023.1	COGGGGTTCGTTA	GICGACCGGCG	ACCECECACE		GCCGGCCG.ACGA	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	66
0Q372024.1	C G T G G T T G G C C T	. A	AA	TGTGAGC	CCATGTCG.A	CGGACGTCAC	GG
OQ372025.1	· · · · · · · · · · · ·						
00372026.1	AGTTATTTCCTG	. 		. 	lg cg ttt c g. .		GG
00372027 1	CGGGGTTCGTTA		ст	GCTAGG	CGACCGCGCA	CGTGCGGGCTGCT	GC
00372028 1	CATEGATEGOCT	λ		TGTGACC	CCATGTCG A	CCCACCT CAT	T C
00072020.1	CG1GGA1GGCC1				on a coor		
00372029.1	TGGGGTTTCATT		A T	UTCTAGG	CIACCGCT		. 🗉 G
		650	6 6	o.	670	680	
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KT178121.1*	A	GAGATCG	TTTCTCCTT	TTGT	CCGAAGC	ACTTTATAAAGCACAGG	
NC_026570.1*	A	GA <mark>G</mark> ATCG	TTTCGTCTT	ΤΤGΤ	CCGAAGC	ACTTTATAAAGCACAGG	
NC_039457.1*	A	GAGATCG	TTTCNKCTT	ΤΤGΤ	CCGAAGC	ACTTTATAAAGCACAGG	
NC_070364.1*	A	GAGATCG	TTTCGTCTT	TTGT	CCGAAGC	ACTTTATAAAGCACAGG	
NC_039458.1*	· · · · · · · · · · · · · · A	GAGATCG	TITCGTCTT		CCGAAGC	ACTITATAAAGCACAGG	
NC_048515 1*	А Д	GAGAICG	TTTCGTCTT		CCGAAGC	ACTITATAAAGCACAGG ACTITATAAAGCACAGG	
00507153.1	A	GAGATCG	TTTCGTCTT	TTGT	CCGAAGC	ACTT	
00507154.1	A	GAGATCG	TTTCGTCTT	TTGT	CCGAAGC	ACTITATAAAGCACAGG	
OQ507155.1							
00507156.1	A	GAGATCG	TTTCGTCTT	ΤΤGΤ	CCGAAGC	ACTTTATAAAGCACAGG	
00507157.1	A	GAGATCG	TITCGTCTT	TTGT	CCGAAGC	ACTTTATAAAGCACAGG	
00507158.1	A	GAGAICG	TITCGICIT	TIGI			
00507160 1		GAGAICG	CATTTACC	1161			
00507161.1	A	GAGATCG	TTTCGTCTT	ттст			
0Q2507163.1	A	GAGATCG	TTTCGTCTC	TIGTG	CCGAAGC	ACCTTATAAAGCACAGG	
OQ507165.1							
00507166.1							
00507167.1	A	GAGATCG	TTTCGTCTT	TIGTG	CCGAAGC	ACTTTATAAAGCACAGG	
00507168.1	A	GAGAICG	TTTCCTCTT		CCGAAGC	ACTITATAAAGCACAGG	
00507171.1	A	G AGATCG	GTTCGTCTT	ттст	CCCAAAC	ACTITATAAAGCACAGG	
00507177.1							
OQ507180.1	A	GAGATCG	TTTCCGCTT	Τ	GCGCCGA		
OQ507181.1	A	GA <mark>G</mark> ATCG	TTTCGTCTT	ΤΤGΤ	CCGAAGC	ACTTTATAAAGCACAGG	
00507183.1	A	GAGATCG	TTTCGTCTT	ΤΤΑΤ	CCGAAGC	AGTTTATAAAGCACAGG	
00507184.1	AAGTTG	GCGAGAA	CATTTCTATTT	TTGTA	TGGAAGC	ACTITATAAAGCACAGG	
00507185.1	A	GAGAICG	IIICGICII	1101	CCGAAGC	ACTITATAAAGCACAGG	
00507193.1		G AGATCG	TTTCGTCTT	ттат	CCGAAGC	ACTTTATAAAGCACAGG	
00507194.1							
0Q507195.1	A	GAGATCG	TTTCGTCTT	ΤΤGΤ	CCGAAGC	ACTTTATAAAGCACAGG	
OQ507199.1	A	GAGATCG	TTTCGTCTT	ТТСТС	CCGAAGC	ACTTTATAAAGCACAGG	
OQ507201.1	A	GAGATCG	TITCGTCTT	TIGT	CCGAAGC	ACTTTATAAAGCACAGG	
A1003903.1*	CAAGIG		AACCICAACIC		GIGUUGI.GGUUG.	AACCCGICGCCCGCG	
AY665914.1*	CAAGTG	G	AATCTCAACTC	TCGT	GTGCCGT.GGCCG	AACCC. GTCGCCCGTG	
AY665905.1*	CAAGTG	G	AATCTCAACTC	тстт	GAGCCGT,GGCCG	AACCCGTCGCCCGTG	
AY665886.1*	CAAGTG	G	AATCTCAACTC	тстт	GIGCCGI.GGCCG	AACCCGTCGCCCGTG	
MH763728.1*	CAAGTG	GT <mark>G</mark> GTTG	AATCTCAACTC	TCTTC	GTGCCGT.GGCCG	AACCCGTCGCCCGTG	
MH763740.1*	CAAGTG	GTGGTIG	AATCTCAACTC	TTGT	GIGCCGI.GGCCG	AACCCGTGGCCCGTG	
00371996.1	CAAGTG	GTGGTTG	AATCTCAACTC	TTGTG	GIGCCGI.GGCCG	AACCCGTGGCCCGTG	
00371998 1	CAAGIG	G TGGTTG	ATCTCAACTC		GIGCCGT		
00372001.1	CAAGTG	GTGGTIG	AATCTCAACTC	TCTT	GTGCCGTGG		
00372003.1	CAAGTG	GTGGTIG	AATCTCAACTC	ΤΤGΤ	GTGCCGT.GGCCG	AACCCGTGGCCCGTG	
OQ372004.1	CAAGIG	GT <mark>G</mark> GTT <mark>G</mark>	AATCTCAACTC	ΤΤGΤ	GTGCCGT.GGCCG	AACCCGTGGCCCGTG	
00372005.1		TATGG	TTTTCATTC	TTTT	.ATTCAT		
00372007.1	CAAGIG	GTGGTIG	AATCTCAACTC	TIGT	GIGCCGI.GGCCG	AACCCGIGGCCCGIG	
00372008.1	GIICCICACCAGUG	C TCCTTC	AICCGIAILIG		GEGGAGA	AACCC GIGGCCCGIG	
00372012.1	CAAGTG	GTGGTTG	AATCTCAACTC	ТСТТ	GTGCCG		
0Q372013.1	CAAGIG	GTGGTTG	AATCTCAACTC	TTGTG	GTGCCGT.GGCCG.	AACCCGTGGCCCGTG	
OQ372014.1	CAAGIG	GT <mark>G</mark> G T TG	AATCTCAACTC	TIGTG	GTGCCGT.GGCCG	AACCCGIGGCCCGIG	
OQ372015.1		· · · · · · · · <mark>· ·</mark> · · · · ·					
00372016.1		· · · · · · · · · · · · · · · ·					
00372018 1		······································	· · · · · · · · · · · · · · · · · · ·	 тсст			
00372019.1		GAGGTAG	AATT				
00372020.1			TTCTTCTTT	тстт			
00372021.1	CAAGTG	GTGGTTG	AATCTCAACTC	ΤΤGΤ	GT		
00372022.1	CAAGTG	GTGGTTG	AATCTCAACTC	TTGT	GTGCCGT.GGCCG	AACCCGTGGCCCGTG	
00372023.1	GTTCAAACG	GGITIGCGGGICG	CTCTGCTT	TGTT	GTTTCGA		
00372024.1	CAAGTG	G	AATCTCAACTC	1 1 G I 6	GIGUUGT.GGCCG	AACCCGIGGCCCGIG	
00372026 1			AATCCCTAG		СТАСССТ		
00372027.1	CCGACTAGCGGGAG	GTGAGCG.	AACGCCCTTCC	CGGTTTCAAAC	GGTTTGCGGGGTC	GCTCTGCTTAGCAGGTT	
OQ372028.1	TTTTAGTTT	GTGGTTGTT	ATTCTCAACTC	ΤΤGΤ	GTGCCATGGGCCG	AATCCCGCGGGGCCCGTG	
OQ372029.1	GGTCTACGAGCG	GGGAATGTTAGC <mark>G</mark>		Сттс		cccg	

	690	700	710	720	730	740	750 760
KT178121.1* NC_026570.1* NC_039457.1* NC_070364.1* NC_039458.1* NC_048514.1* NC_048515.1* 0C507153.1	CTG. CTG CTG CTG CTG CTG CTG CTG	AAACAGGTGAAATC AAACAGGTGAAATC AAACAGGTGAAATC AAACAGGTGAAATC AAACAGGTGAAATC AAACAGGTGAAATC AAACAGGTGAAATC	AAAGGGCATTA AAAGGGCATTA AAAGGGCATTA AAAGGGCATTA AAAGGGCATTA AAAGGGCATTA AAAGGGCATTA	ACTTGAATGCT/ ACTTGAATGCT/ ACTTGAATGCT/ ACTTGAATGCT/ ACTTGAATGCT/ ACTTGAATGCT/ ACTTGAATGCT/ ACTTGAATGCT/	ACTGCAGGTAC ACTGCAGGTAC ACTGCAGGTAC ACTGCAGGTAC ACTGCAGGTAC ACTGCAGGTAC ACTGCAGGTAC	ATGCGAAGA ATGCGAAGA ATGCGAAGA ATGCGAAGA ATGCGAAGA ATGCGAAGA ATGCGAAGA	AATGATCAAAAGAG AATGATCAAAAGAG AATGATCAAAAGAG AATGATCAAAAGAG AATGATCAAAAGAG AATGATCAAAAGAG AATGATCAAAAGAG
00507154.1	СТ	AAACAGGTGAAATC	AAAGGGCATTA	ACTTGAATGCT/	ACTGCAG		• • • • • • • • • • • • • • •
00507156.1	СТ	AAACAGGTGAAATC	AAAGGGCATTA	ACTTGAATGCT/	АСТБ		· · · · · · · · · · · · · · · · · · ·
OQ507157.1 OQ507158.1	СТ	AAA	CCGAAGCACT				
00507159.1 00507160 1		G A A	CCGAAGCACT	ITATAAA			
00507161.1							
00507165.1 00507165.1	11	GAACAGGIGGAAIC	AAGGAGCAII <i>.</i>	ACTIGGAIGCI.			· · · · · · · · · · · · · · · · · ·
OQ507166.1 OO507167.1	ст	AAACAGGTGAAATC	AAAGGGCATTA	ACTTGAATGCTA	ACTGCAGGTAC	ATGCGA	
00507168.1	СТ	AAACAGGTGAAATC	AAAGGGCATT	ACTTGAATGCTA	ACTGCAGGTAC	ATGCGAAGA	AATATTCAAAAGAG
00507171.1	CT	AAACAGGIGAAAIC AAACAG				AIGCGAAG.	· · · · · · · · · · · · · · · · · ·
OQ507177.1 00507180.1				TATAAAGGTCA	AGGAGGAAACA	AGGGAAATT	 GAAGTAT
00507181.1	СТ	AAACAGGTGAAATC	AAAGGGCATT	ACTTGAATGCT	ACTGCAGGTAC	ATGCAAAA.	
00507184.1	CTG	AAATTGGTAAAATC	AAAGGGGGGTTA	ACTTGAATTTT	ACTGCAGGTAC	CGGCGAAGA	AATGAGTAAAAGAG
OQ507185.1 OQ507192.1	СТ	AAACAGGTGAAATC 	AAAGGGCATT <i>i</i>	ACTTGAATGCT/	АСТБСАББТАС	ATGGCAAA.	
00507193.1 00507194 1	СТ	AAACAGGTGAAATC	AAAGGGCATTA	ACCTGAATGCTA	ACTGCAGGTAC	ATGCGAAGA.	AATGATCAAGAGTT
00507195.1	СТ	AAACAGGTGAAATC	AAAGGGCATT	ACTTGGATGCT	ACTGCAGGTGC	ACTTGAAGA	ACTATTCAAAAGAG
0Q507199.1 0Q507201.1	СТ	AAACAGGTGAAATI AAACAGGTGAAATC	AAAGGGCATTA	ACTIGAAIGCIA ACTIGGAIGCIA	ACTGCAGTTAC	AIGGGAAGA.	AATTCTCAAAAGAG
AY665903.1* AY665868.1*	TC.GGCTGATG.G. TC.GGCTTACA.G.	ACCCTTCATGCG ACCCTTCCGGCG	CTTAGGCGCT(CTTAGGCGCT)	CCGACCGCGA	ACCCCAGGTCA ACCCCCAGGTCA	GGCGGGGATT	
AY665914.1*	CC.GGCTGACA.G	ACCCTTCCGGCG	CTTAGGCGCT	CCGACCGCGA	ACCCCAGGTCA	GGCGGGGATT	
AY665886.1*	TC.GGCTGCGA.G	ACCCTTCCGGCG	CTTAGGCGCT	CCGACCGCG/	ACCCCAGGICA	GGCGGGGATT	· · · · · · · · · · · · · · · · · ·
MH763728.1* MH763740.1*	TC.GGCTGCGA.G. TC.GGCTGACA.G.	ACCCTTCCGGCG AACCTTCCGGCG	CTTAGGCGCT(CTTAGGCGCT)	CCGACCGCG# ICGACCGCG#	ACCCCAGGTCA ACCCCAGGTCA	GGCGGGGATT GGTGGAATT	
00371996.1 00371997 1	TC.GGCTGACA.G	AACCTTCCCG.GCG	CTTAGGCGCT	ICGACCGCG#	ACCCCAGGTCA	GGTGGAATT	
00371998.1							
00372001.1 00372003.1	TC.GGCTGACA.G.	AACCTTCCGGCGC.		ICGA.CGCGA	ACCC.AGGTCA	GGTGA	· · · · · · · · · · · · · · · · · ·
0Q372004.1 00372005.1	TC.GGCTGACA.G	AACCTTTCCG.GCG	CTTAGGCGCT	ICGACCGCG/	ACCCCAGGTCA	GGTGGAAA.	
00372007.1	TCGGGCTGACA.G	AACCTTTCCG					
00372009.1	TC.GGCTGACA.G	AACCTTCCGGCG	CTTAGGCGCT	ICGACCGCG/	ACCCCAGGTCA	GTGGAA	
0Q372012.1 0Q372013.1	TC.AGCTGACA.G.	AACCTTCCGGCG	CTTAGGCGCT	ICGACCGCG/	ACCCCAGGTCA	GTGGAA	
00372014.1	TC.AGCTGACA.G.	AACCTTCCGGCGC.	TTAGCGCT	ICGACCGCG/	ACCCCAGGTCA	GTGGAA	
00372016.1							
OQ372017.1 OQ372018.1		· · · · · · · · · · · · · · · · · ·				· · · · · · · · · · ·	· · · · · · · · · · · · · · · · · ·
0Q372019.1 00372020.1							
00372021.1						ACCTCCAN	• • • • • • • • • • • • • • •
00372023.1	CAATG	ATCCTTCCGCAG	GTT(CACCTATCGAA	ACC		· · · · · · · · · · · · · · · · · ·
0Q372024.1 0Q372025.1	TC.GGCTGACA.G	AACCTCCGGCG	CTTAGGCGCT	CGACCGCG/	ACCCAGTCTGG	GATTTTCG.	
00372026.1	тс слеллте	ACACCT	CATGGTCACC	TACGGGAAAC			
00372028.1	TCGGGCTGACATA	AACCTTCCGGCGTT	TTTAGGCCCCC	ITCCACCCGCG	FACCCC		· · · · · · · · · · · · · · · · · · ·
00372029.1							

	770	780	790	800	810	820	830	840
KT178121.1*	CIGIATITGCIAGAGA	ATTGGGCGTT	CCGATCGTAAI	GCATGACTAC	TTAACGGGGG	GGATTCACCG	CAAATACTAG	сттбб
NC_026570.1*	CTGTATTTGCTAGAGA	ATTGGGCGTT	CCGATCGTAAI	GCATGACTAC	TTAACGGGGG	GGATTCACCG	CAAATACTAG	CTTGG
NC_039457.1*	CTGTATTTGCTAGAGA	ATTGGGCGTT	CCGATCGTAAI	I GCATGACTAC	TTAACGGGGG	GGATTCACCG	CAAATACTAG	CTTGG
NC_070304.1*	CTGTATTTGCTAGAGA	ATTGGGCGTT	CCGATCGTAAI	IGCATGACIAC	TTAACGGGGG	GGATICACCG	CAAATACTAG	CTTGG
NC_048514.1*	CTGTATTTGCTAGAGA	ATTGGGCGTT	CCGATCGTAAT	GCATGACTAC	TTAACGGGGG	GGATTCACCG	CAAATACTAG	CTTGG
NC_048515.1*	CIGTATIIGCIAGAGA	ATTGGGCGTT	CCGATCGTAAT	IGCATGACTAC	TTAACGGGGG	GGATTCACCG	CAAATACTAG	CTTGG
00507153.1					• • • • • • • • •			• • • • •
00507155.1								
OQ507156.1								
00507157.1								
00507159.1								
OQ507160.1								
00507161.1								
00507165 1	••••••	• • • • • • • • • • •			• • • • • • • • • •		• • • • • • • • • • •	• • • • •
00507166.1								
OQ507167.1								
00507168.1	GTGTCTTTGCCAGGGA	ATTGGGCGTT	CCGGTCGTAAI	TATATGACCAC	TTAACGTT.			
00507171 1					• • • • • • • • • •			
OQ507177.1								
OQ507180.1								
00507181.1								
00507183.1	CIGINIIIGIINGAGA	AIIGGGCGII	CCGAICGIAAI	LGCATIACAAC	I I AACGGGGG			
00507185.1								
OQ507192.1								
OQ507193.1	CTATATTTGCTAGAGA	ATTGCGCGCT	CCTGTCGTGAI	IGTATGAGTAC	TTAACTTC.		•••••	• • • • •
00507195.1	CTTCTTTTGCCACGGA	ATTGGGGGTT	CCGGTCGAAAC	GGATGAGCAC	TTGATGGGG	GGTTTCACTA	CAAACACTAG	CTTTG
OQ507199.1	CTCTATTCACTAGAGA	ATTGCGCGTT	CCGATCGTAAI	GGATG				
OQ507201.1								
AY665903.1* AY665868 1*	•••••						• • • • • • • • • • •	• • • • •
AY665914.1*								
AY665905.1*								
AY665886.1*					• • • • • • • • •	• • • • • • • • • • •	• • • • • • • • • •	
MH763740.1*								
OQ371996.1								
00371997.1								
00372001 1								
00372003.1								
OQ372004.1								
00372005.1								
00372008.1								
OQ372009.1								
00372012.1								
00372013.1	•••••				• • • • • • • • • •		• • • • • • • • • • •	• • • • •
00372015.1								
OQ372016.1								
00372017.1								
00372018.1	•••••				• • • • • • • • • •		•••••	• • • • •
00372020.1								
00372021.1								
00372022.1								
00372024.1								
00372025.1				· · · · · · · · · · · · ·				
00372026.1								
00372027.1	• • • • • • • • • • • • • • • • • • • •							
00372029.1								· · · · ·

Appendix 3: Tables for ANOVA and Tukey's HSD post hoc analysis of mineral content, phytochemical content and radical scavenging activity of indigenous *Physalis* accessions

A	opendix	3 A	: Table	for o	ne wav	ANO	VA ar	nd p	ost hoc	analy	sis o	of macro	-minera	als of	indig	genous .	Phy	salis :	accessior	ns.
	1				_											_	~			

Accession	Accession	ANOVA	ANOVA	ANOVA	ANOVA	Tukey's	Tukey's	Tukey's	Tukey's
name (I)	name (J)	p-value	p-value	p-value	p-value	HSD p-	HSD p-	HSD p-	HSD p-
		of Ca	of Na	of K	of Mg	value of	value of	value of	value of
		content	content	content	content	Ca	Na	Κ	Mg
						content	content	content	content
OQ507152.1	OQ372021.1	0.050	0.509	0.380	0.435	0.027	0.973	1.000	0.963
	OQ372022.1					0.976	0.744	1.000	0.865
	OQ372023.1					0.136	0.850	1.000	0.790
	OQ372024.1					0.176	0.960	0.724	1.000
	OQ372025.1					1.000	1.000	0.937	0.964
	OQ372026.1					0.999	1.000	1.000	0.928
	OQ372028.1					1.000	1.000	0.698	1.000
	OQ372029.1					1.000	1.000	1.000	0.943
OQ372021.1	OQ507152.1					0.027	0.973	1.000	0.963
	OQ372022.1					0.193	0.999	0.987	1.000
	OQ372023.1					0.994	1.000	0.994	1.000
	OQ372024.1					0.983	1.000	0.488	0.867
	OQ372025.1					0.044	0.977	0.775	1.000
	OQ372026.1					0.091	0.961	0.997	1.000
	OQ372028.1					0.024	0.994	0.462	0.960
	OQ372029.1					0.074	0.999	0.999	1.000
OQ372022.1	OQ507152.1					0.976	0.744	1.000	0.865
	OQ372021.1					0.193	0.999	0.987	1.000
	OQ372023.1					0.604	1.000	1.000	1.000
	OQ372024.1					0.692	1.000	0.950	0.702
	OQ372025.1					0.995	0.759	0.998	1.000

	OQ372026.1			1.000	0.704	1.000	1.000
	OQ372028.1			0.965	0.854	0.939	0.859
	OQ372029.1			1.000	0.922	1.000	1.000
OQ372023.1	OQ507152.1			0.136	0.850	1.000	0.790
	OQ372021.1			0.994	1.000	0.994	1.000
	OQ372022.1			0.604	1.000	1.000	1.000
	OQ372024.1			1.000	1.000	0.924	0.607
	OQ372025.1			0.205	0.862	0.996	1.000
	OQ372026.1			0.363	0.818	1.000	1.000
	OQ372028.1			0.119	0.930	0.909	0.783
	OQ372029.1			0.310	0.970	1.000	1.000
OQ372024.1	OQ507152.1			0.716	0.960	0.724	1.000
	OQ372021.1			0.983	1.000	0.488	0.867
	OQ372022.1			0.692	1.000	0.950	0.702
	OQ372023.1			1.000	1.000	0.924	0.607
	OQ372025.1			0.259	0.964	1.000	0.869
	OQ372026.1			0.442	0.944	0.900	0.799
	OQ372028.1			0.155	0.989	1.000	1.000
	OQ372029.1			0.382	0.997	0.843	0.826
OQ372025.1	OQ507152.1			1.000	1.000	0.937	0.964
	OQ372021.1			0.044	0.977	0.775	1.000
	OQ372022.1			0.995	0.759	0.998	1.000
	OQ372023.1			0.205	0.862	0.996	1.000
	OQ372024.1			0.259	0.964	1.000	0.869
	OQ372026.1			1.000	1.000	0.992	1.000
	OQ372028.1			1.000	1.000	1.000	0.961
	OQ372029.1			1.000	1.000	0.980	1.000
OQ372026.1	OQ507152.1			0.999	1.000	1.000	0.928
	OQ372021.1			0.091	0.961	0.997	1.000
	OQ372022.1			1.000	0.704	1.000	1.000
	OQ372023.1			0.363	0.818	1.000	1.000
	OQ372024.1			0.442	0.944	0.900	0.799

	OQ372025.1			1.000	1.000	0.992	1.000
	OQ372028.1			0.998	1.000	0.882	0.924
	OQ372029.1			1.000	1.000	1.000	1.000
OQ372028.1	OQ507152.1			1.000	1.000	0.698	1.000
	OQ372021.1			0.024	0.994	0.462	0.960
	OQ372022.1			0.965	0.854	0.939	0.859
	OQ372023.1			0.119	0.930	0.909	0.783
	OQ372024.1			0.155	0.989	1.000	1.000
	OQ372025.1			1.000	1.000	1.000	0.961
	OQ372026.1			0.998	1.000	0.882	0.924
	OQ372029.1			1.000	1.000	0.822	0.939
OQ372029.1	OQ507152.1			1.000	1.000	1.000	0943
	OQ372021.1			0.074	0.999	0.999	1.000
	OQ372022.1			1.000	0.922	1.000	1.000
	OQ372023.1			0.310	0.970	1.000	1.000
	OQ372024.1			0.382	0.997	0.843	0.826
	OQ372025.1			1.000	1.000	0.980	1.000
	OQ372026.1			1.000	1.000	1.000	1.000
	OQ372028.1			1.000	1.000	0.822	0.939

A	A							T-1	T 1 ?-	T 1	T 1 ?.	T 1	T 1 ?-
Accession	Accession	ANOVA	ANOVA	ANOVA	ANOVA	ANOVA	ANOVA	Tukey's	Tukey's	Tukey's	Tukey's	Tukey's	Tukey's
name (1)	name (J)	p-value	P-value	p-value	p-value	p-value	p-value	HSD p-	пзD р-	HSD p-	HSD p-	HSD p-	нзD р-
		of Fe	of Zn	OI IN1	orCu	OF L1	of Mn	value of					
		content	content	content	content	content	content	Fe	Zn	N1	Cu	L1	Mn
0.0.5051.50.1	0.0000001.1	0.501	0.000	0.005	0.001		0.1.10	content	content	content	content	content	content
OQ507152.1	0Q3/2021.1	0.691	0.002	0.007	0.021	0.000	0.140	0.967	0.999	1.000	1.000	0.871	1.000
	OQ372022.1	-						0.997	1.000	0.999	1.000	1.000	0.988
	OQ372023.1	_						0.998	0.011	0.036	0.999	0.001	0.999
	OQ372024.1	_						0.974	0.999	1.000	0.305	1.000	0.298
	OQ372025.1							0.987	0.963	0.987	0.050	0.995	0.965
	OQ372026.1							0.934	0.999	0.956	0.572	1.000	0.868
	OQ372028.1							0.462	0.934	0.098	0.594	0.998	0.416
	OQ372029.1							0.858	1.000	0.999	1.000	1.000	0.493
OQ372021.1	OQ507152.1	-						0.967	0.999	1.000	1.000	0.871	1.000
-	OQ372022.1							1.000	1.000	0.994	1.000	0.584	0.975
	00372023.1							1.000	0.003	0.024	1.000	0.017	0.997
	00372024.1							1.000	1.000	1.000	0.313	0.630	0.248
	00372025.1							1.000	0.711	0.957	0.052	0.420	0.939
	00372026.1							1.000	1.000	0.897	0.583	0.643	0.813
	00372028.1							0.972	0.636	0.066	0.604	0.487	0.354
	00372029.1							1.000	1.000	0.994	1.000	0.564	0.425
00372022.1	00507152.1	-						0.997	1.000	0.999	1.000	1.000	0.988
	00372021.1	-						1.000	1.000	0.994	1.000	0.584	0.975
	00372023.1	-						1.000	0.003	0.120	1.000	0.000	1.000
	00372024.1	-						1.000	1.000	0.994	0.434	1.000	0.813
	003720251							1 000	0 744	1 000	0.082	1 000	1 000
	00372026.1							1.000	1,000	1.000	0.723	1.000	1.000
	00372028.1							0.872	0.671	0.286	0.744	1.000	0.912
	00372020.1	-						0.072	1,000	1.000	1,000	1.000	0.912
00372023 1	00507152.1							0.998	0.011	0.036	0.000	0.001	0.950
00312023.1	00372021 1	4						1.000	0.011	0.030	1.000	0.001	0.777
	002720221.1	4						1.000	0.003	0.024	1.000	0.017	1.000
	00372022.1	4						1.000	0.003	0.120	1.000	0.000	1.000
	UQ372024.1							1.000	0.003	0.024	0.630	0.000	0.646

Appendix 3 B: Table for one way ANOVA and Tukey's HSD post hoc analysis of micro-minerals of indigenous Physalis accessions

										1
	OQ372025.1				1.000	0.103	0.205	0.149	0.000	1.000
	OQ372026.1				1.000	0.003	0.287	0.885	0.000	0.995
	OQ372028.1				0.865	0.129	1.000	0.899	0.000	0.782
	OQ372029.1				0.997	0.006	0.120	1.000	0.000	0.848
OQ372024.1	OQ507152.1				0.974	0.999	1.000	0.305	1.000	0.298
	OQ372021.1				1.000	1.000	1.000	0.313	0.630	0.248
	OQ372022.1				1.000	1.000	0.994	0.434	1.000	0.813
	OQ372023.1				1.000	0.003	0.024	0.630	0.000	0.646
	OQ372025.1				1.000	0.716	0.957	0.978	1.000	0.891
	OQ372026.1				1.000	1.000	0.897	1.000	1.000	0.975
	OQ372028.1				0.964	0.642	0.066	1.000	1.000	1.000
	OQ372029.1				1.000	1.000	0.994	0.597	1.000	1.000
OQ372025.1	OQ507152.1				0.987	0.963	0.987	0.050	0.995	0.965
	OQ372021.1				1.000	0.711	0.957	0.052	0.420	0.939
	OQ372022.1				1.000	0.744	1.000	0.082	1.000	1.000
	OQ372023.1				1.000	0.103	0.205	0.149	0.000	1.000
	OQ372024.1				1.000	0.716	0.957	0.978	1.000	0.891
	OQ372026.1				1.000	0.699	1.000	0.832	1.000	1.000
	OQ372028.1				0.938	1.000	0.442	0.815	1.000	0.959
	OQ372029.1				1.000	0.887	1.000	0.136	1.000	0.980
OQ372026.1	OQ507152.1				0.934	0.999	0.956	0.572	1.000	0.868
	OQ372021.1				1.000	1.000	0.897	0.583	0.643	0.813
	OQ372022.1				1.000	1.000	1.000	0.723	1.000	1.000
	OQ372023.1				1.000	0.003	0.287	0.885	0.000	0.995
	OQ372024.1				1.000	1.000	0.897	1.000	1.000	0.975
	OQ372025.1				1.000	0.699	1.000	0.832	1.000	1.000
	OQ372028.1				0.989	0.624	0.565	1.000	1.000	0.995
	OQ372029.1				1.000	1.000	1.000	0.864	1.000	0.999
OQ372028.1	OQ507152.1				0.462	0.934	0.098	0.594	0.998	0.416
	OQ372021.1				0.972	0.636	0.066	0.604	0.487	0.354
	OQ372022.1				0.872	0.671	0.286	0.744	1.000	0.912
	OQ372023.1				0.865	0.129	1.000	0.899	0.000	0.782
	OQ372024.1				0.964	0.642	0.066	1.000	1.000	1.000
	OQ372025.1				0.938	1.000	0.442	0.815	1.000	0.959
	OQ372026.1				0.989	0.624	0.565	1.000	1.000	0.995
	OQ372029.1	1			0.998	0.834	0.286	0.878	1.000	1.000
OQ372029.1	OQ507152.1	1			0.858	1.000	0.999	1.000	1.000	0.493
	OQ372021.1				1.000	1.000	0.994	1.000	0.564	0.425

OQ372022.1			0.998	1.000	1.000	1.000	1.000	0.950
OQ372023.1			0.997	0.006	0.120	1.000	0.000	0.848
OQ372024.1			1.000	1.000	0.994	0.597	1.000	1.000
OQ372025.1			1.000	0.887	1.000	0.136	1.000	0.980
OQ372026.1			1.000	1.000	1.000	0.864	1.000	0.999
OQ372028.1			0.998	0.834	0.286	0.878	1.000	1.000

Appendix 3 C: Table for ANOVA and Tukey's HSD post hoc analysis of phytochemical content of indigenous *Physalis* accessions.

Accession	Accession	ANOVA	ANOVA	ANOVA	Tukey's	Tukey's	Tukey's
name (I)	name (J)	p-value	p-value	p-value	HSD p-	HSD p-	HSD p-
		of	of tannic	of	value of	value of	value of
		phenolic	acid	flavonoid	phenolic	tannic	flavonoid
		acid	content	content	acid	acid	content
		content			content	content	
OQ507152.1	OQ372021.1	0.159	0.000	0.253	0.945	0.970	0.760
	OQ372022.1				0.265	0.521	0.731
	OQ372023.1				0.484	0.850	0.628
	OQ372024.1				0.449	0.991	0.968
	OQ372025.1				1.000	0.018	0.742
	OQ372026.1				0.958	0.021	0.554
	OQ372027.1				1.000	0.051	0.972
	OQ372028.1				0.958	0.011	1.000
	OQ372029.1				1.000	0.111	1.000
OQ372021.1	OQ507152.1				0.945	0.970	0.760
	OQ372022.1				0.931	0.990	1.000
	OQ372023.1				0.994	1.000	1.000
	OQ372024.1				0.991	0.527	1.000
	OQ372025.1				0.995	0.178	1.000
	OQ372026.1				1.000	0.205	1.000
	OQ372027.1				0.993	0.391	1.000
	OQ372028.1				1.000	0.118	0.933
	OQ372029.1				0.997	0.626	0.664
OQ372022.1	OQ507152.1				0265	0.521	0.731
	OQ372021.1				0.931	0.990	1.000
	OQ372023.1				1.000	1.000	1.000
	OQ372024.1				1.000	0.115	1.000
	OQ372025.1				0.466	0.675	1.000
	OQ372026.1				0.913	0.724	1.000
	OQ372027.1				0.442	0.917	1.000
	OQ372028.1				0.912	0.534	0.917
	OQ372029.1				0.496	0.990	0.632
OQ372023.1	OQ507152.1				0.484	0.850	0.628
	OQ372021.1				0.994	1.000	1.000
	OQ372022.1				1.000	1.000	1.000
	OQ372024.1				1.000	0.308	0.998
	OQ372025.1				0.722	0.339	1.000
	OQ372026.1				0.991	0.381	1.000
	OQ372027.1				0.698	0.628	0.997
	OQ372028.1				0.990	0.237	0.850

	OQ372029.1		0.751	0.847	0.526
00372024.1	00507152.1		0.449	0.991	0.968
	00372021.1		0.991	0.527	1.000
	00372022.1		1.000	0.115	1.000
	00372023.1		1.000	0.308	0.998
	00372025.1		0.687	0.002	1.000
	00372026.1		0.986	0.003	0.994
	00372027.1		0.662	0.006	1.000
	OQ372028.1		0.986	0.001	0.998
	OQ372029.1		0.717	0.015	0.931
OQ372025.1	OQ507152.1		1.000	0.018	0.742
-	OQ372021.1		0.995	0.178	1.000
	OQ372022.1		0.466	0.675	1.000
	OQ372023.1		0.722	0.339	1.000
	OQ372024.1		0.687	0.002	1.000
	OQ372026.1		0.997	1.000	1.000
	OQ372027.1		1.000	1.000	1.000
	OQ372028.1		0.997	1.000	0.923
	OQ372029.1		1.000	0.995	0.644
OQ372026.1	OQ507152.1		0.958	0.021	0.554
	OQ372021.1		1.000	0.205	1.000
	OQ372022.1		0.913	0.724	1.000
	OQ372023.1		0.991	0.381	1.000
	OQ372024.1		0.986	0.003	0.994
	OQ372025.1		0.997	1.000	1.000
	OQ372027.1		0.996	1.000	0.993
	OQ372028.1		1.000	1.000	0.793
	OQ372029.1		0.998	0.997	0.455
OQ372027.1	OQ507152.1		1.000	0.051	0.972
	OQ372021.1		0.993	0.391	1.000
	OQ372022.1		0.442	0.917	1.000
	OQ372023.1		0.698	0.628	0.997
	OQ372024.1		0.662	0.006	1.000
	OQ372025.1		1.000	1.000	1.000
	OQ372026.1		0.996	1.000	0.993
	OQ372028.1		0.996	0.999	0.999
	OQ372029.1		1.000	1.000	0.938
OQ372028.1	OQ507152.1		0.958	0.011	1.000
	OQ372021.1		1.000	0.118	0.933
	OQ372022.1		0.912	0.534	0.917
	OQ372023.1		0.990	0.237	0.850
	OQ372024.1		0.986	0.001	0.998
	OQ372025.1		0.997	1.000	0.923
	OQ372026.1		1.000	1.000	0.793
	OQ372027.1		0.996	0.999	0.999

	OQ372029.1		0.998	0.975	1.000
OQ372029.1	OQ507152.1		1.000	0.111	1.000
	OQ372021.1		0.997	0.626	0.664
	OQ372022.1		0.496	0.990	0.632
	OQ372023.1		0.751	0.847	0.526
	OQ372024.1		0.717	0.015	0.913
	OQ372025.1		1.000	0.995	0.664
	OQ372026.1		0.998	0.997	0.455
	OQ372027.1		1.000	1.000	0.938
	OQ372028.1		0.998	0.975	1.000

Appendix 3 D: . Table for one way ANOVA and Tukey's HSD post hoc analysis of DPPH RSA and HRSA of indigenous *Physalis* accessions.

Accession	Accession	ANOVA	ANOVA	Tukey's	Tukey's
name (I)	name (J)	p-value of	p-value	HSD p-	HSD p-
		DPPH	of HRSA	value of	value of
		RSA		DPPH	HRSA
				RSA	
OQ507152.1	OQ372021.1	0.000	0.013	0.000	0.999
	OQ372022.1			0.000	0.579
	OQ372023.1			0.692	0.052
	OQ372024.1			0.004	0.924
	OQ372025.1			0.001	1.000
	OQ372026.1			0.000	1.000
	OQ372027.1			0.000	0.071
	OQ372028.1			0.000	1.000
	OQ372029.1			0.000	0.869
OQ372021.1	OQ507152.1			0.000	0.999
	OQ372022.1			0.452	0.937
	OQ372023.1			0.000	0.203
	OQ372024.1			0.082	1.000
	OQ372025.1			0.277	1.000
	OQ372026.1			1.000	1.000
	OQ372027.1			1.000	0.261
	OQ372028.1			1.000	1.000
	OQ372029.1			1.000	0.998
OQ372022.1	OQ507152.1			0.000	0.579
	OQ372021.1			0.452	0.937
	OQ372023.1			0.027	0.887
	OQ372024.1			0.986	0.999
	OQ372025.1			1.000	0.750
	OQ372026.1			0.387	0.910
	OQ372027.1			0.317	0.937
	OQ372028.1			0.252	0.646
	OQ372029.1			0.777	1.000
OQ372023.1	OQ507152.1			0.692	0.052
	OQ372021.1			0.000	0.203
	OQ372022.1			0.027	0.887
	OQ372024.1			0.198	0.512
	OQ372025.1			0.054	0.091
	OQ372026.1			0.000	0.174
	OQ372027.1			0.000	1.000
	OQ372028.1			0.000	0.065
	OQ372029.1			0.001	0.606

OQ372024.1	OQ507152.1		0.004	0.924
	OQ372021.1		0.082	1.000
	OQ372022.1		0.986	0.999
	OQ372023.1		0.198	0.512
	OQ372025.1		0.999	0.981
	OQ372026.1		0.065	0.999
	OQ372027.1		0.049	0.606
	OQ372028.1		0.036	0.953
	OQ372029.1		0.222	1.000
OQ372025.1	OQ507152.1		0.001	1.000
	OQ372021.1		0.277	1.000
	OQ372022.1		1.000	0.750
	OQ372023.1		0.054	0.091
	OQ372024.1		0.999	0.981
	OQ372026.1		0.229	1.000
	OQ372027.1		0.182	0.122
	OQ372028.1		0.140	1.000
	OQ372029.1		0.574	0.958
OQ372026.1	OQ507152.1		0.000	1.000
	OQ372021.1		1.000	1.000
	OQ372022.1		0.387	0.910
	OQ372023.1		0.000	0.174
	OQ372024.1		0.065	0.999
	OQ372025.1		0.229	1.000
	OQ372027.1		1.000	0.226
	OQ372028.1		1.000	1.000
000270007.1	OQ372029.1		0.999	0.995
OQ3/2027.1	0050/152.1		0.000	0./1
	00372021.1		1.000	0.261
	00372022.1		0.317	0.937
	00372023.1		0.000	1.000
	00372024.1		0.049	0.000
	00372025.1		0.182	0.122
	00372020.1		1.000	0.220
	00372028.1		1.000	0.087
00372028 1	00507152.1		0.998	1.000
0Q372028.1	003720211		1,000	1.000
	00372021.1		0.252	0.646
	00372022.1		0.232	0.040
	00372023.1		0.000	0.003
	00372025.1		0.030	1 000
	003720261		1 000	1,000
	00372027.1		1.000	0.087
	00372029.1		0.992	0.910
	525,2027.1		0.772	0.710

OQ372029.1	OQ507152.1		0.000	0.869
	OQ372021.1		1.000	0.998
	OQ372022.1		0.777	1.000
	OQ372023.1		0.001	0.606
	OQ372024.1		0.222	1.000
	OQ372025.1		0.574	0.958
	OQ372026.1		0.999	0.995
	OQ372027.1		0.998	0.699
	OQ372028.1		0.992	0.910