VARIATIONS IN THE S SEGMENT OF RIFT VALLEY FEVER VIRUS WITH SPECIAL REFERENCE TO THE NONSTRUCTURAL NSS CODING REGION

BY

SUSAN CLAIRE AITKEN

DISSERTATION SUBMITTED IN FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE

MAGISTER SCIENTIAE

(VIROLOGY)

DEPARTMENT OF VIROLOGY, SCHOOL OF PATHOLOGY FACULTY OF HEALTH SCIENCES, UNIVERSITY OF THE WITWATERSRAND

SUPERVISOR: DR HAB. JANUSZ T. PAWESKA SPECIAL PATHOGENS UNIT, NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES OF THE NATIONAL HEALTH LABORATORY SERVICE

JULY 2008

Dedication

I dedicate this work to my late grandmother who was always so proud of every one of my achievements, but who sadly did not see the completion of this project. She was an incredible lady that lived every day of her life to the fullest up until the last. She is sadly missed but will live on forever in our hearts.

Neva Aitken

12/07/1919 - 18/07/2007

Acknowledgements

I would like to extend my gratitude to my supervisor Dr hab. Janusz T. Paweska and Mrs. Antoinette Grobbelaar for their unconditional support, advice and proficient insight during the course of my research. Their guidance through numerous challenges associated with certain aspects of my project have aided me in expanding my academic knowledge and propensity for troubleshooting, subsequently enabling me to achieve a thoroughly successful and enjoyable project.

Furthermore, I would like to thank the members of the National Institute for Communicable Diseases, Special Pathogens Unit (NICD-SPU) for their continuous technical support throughout this project. I also wish to express my sincere thanks to the NICD-SPU for financial support, providing laboratory equipment and instructions, and for supplying isolates of Rift Valley fever virus for this project.

I would also like to thank the CLS team at the Medical School of the University of the Witwatersrand and Mr. Peter Coetzee from the Polio Research Laboratory at the National Institute for Communicable Diseases for their assistance in sequencing.

Declaration

I, Susan Claire Aitken (0200154E), am a student registered for the degree of Master of Science, in the year 2008. On submittal of my MSc thesis, I do hereby declare the following:

- I confirm that the MSc dissertation submitted for assessment for the above course is my own unaided work except where I have explicitly indicated otherwise.
- I have followed the required conventions in referencing the findings and ideas of others.
- I have not submitted the MSc work for any degree or examination at any other university.
- I understand that the University of the Witwatersrand may take disciplinary action against me if there is a belief that this is not my own unaided work or that I have failed to acknowledge the published findings or ideas in my writing.

Abstract

Rift Valley fever virus (RVFV) is a *Phlebovirus* member of the *Bunyaviridae* family and it is the causative agent of Rift Valley fever (RVF), a mosquito-borne viral zoonotic disease that poses a significant threat to domestic ruminants and human health in Africa. The RVFV is an encapsulated, negative-sense, single-stranded RNA virus with a tripartite segmented genome, containing L (large), M (medium) and S (small) segments. The S segment codes for two proteins, namely the nucleocapsid (N) protein and non-structural protein (NSs). There is evidence that the NSs protein is involved in virulence by blocking the expression of the interferon beta (IFN- β) promoter. It has been recently demonstrated that the SAP30-NSs-YY1 multiprotein complex represses the IFN- β promoter. Consequently, the interferon expression is blocked, allowing virus to replicate.

A total of 45 isolates of RVFV recovered over a period of 53 years in 14 African countries, Madagascar and Saudi Arabia were characterized by full sequencing of the S segment of the virus. This data was added to another 27 strains of RVFV available on GenBank for phylogenetic analysis using MEGA4, giving a total of 72 strains analyzed. Alignments were made of the entire S segment, the NSs gene, the N gene, and their deduced amino acid sequences. The laboratory strains, clone 13, MP12 and Smithburn, were also included in the alignments.

Two isolates were passaged ten times through two different amplification systems to asses the potential for sequence variation to occur in the original material through routine laboratory manipulations. Sequencing data was generated from the virus RNA present in the original clinical specimens and from the extracted RNA from the tenth passage of virus in each amplification system. The results showed 100% homology for each respective isolate, demonstrating that the RVFV S segment remained stable during ten serial passages in different propagation systems.

Phylogenetic analysis was conducted on the naturally occurring RVFV strains (n = 72) and the findings indicate that circulating strains are compartmentalized and belong to one of three major lineages, namely Egyptian, western African, and central, eastern and southern African. The strains clustered in the Egyptian lineage had an average p-distance of 1.0%, the western African strains 0.9%, and the central, southern and eastern African strains 2.0%. The overall average p-distance was 2.5%, with a range from 0 to 4.1%. For the N gene, the range was from 0 to 4.2%, with an average of 2.2%. For the N protein, the range was from 0 to 2%, with an average of 0.2%. The NSs gene had a range of 0 to 4.6%, with an average of 2.4%. The NSs protein had a range of 0 to 3.8%, with an average of 1.7%. The intergenic region (IGR) had a range of 0 to 9.2%, with an average of 4.8%.

Results of the study suggest that RVF outbreaks can result from either the rapid spread of a single strain over vast distances or from an increased activity of a strain circulating at an endemic level within an area/region during prolonged dry periods.

Sequencing alignment showed that the length of the S segment ranged from 1690 to 1692 nucleotides. This difference in length was due to insertions and deletions found in the IGR, which is also the region with the most sequence divergence (4.8%). Both the NSs and N genes had neither insertions nor deletions, and were both found to be stable, though the NSs gene was slightly more variable than the N gene (2.5% versus 2.2%)

The deduced amino acid sequences of the NSs protein were considerably more variable than that of the N protein (1.7% versus 0.2%). Alignment of the NSs protein demonstrated that the 5 cysteine residues at positions 39, 40, 150, 179 and 195, are highly conserved among the isolates analyzed. These residues are important for conservation of the three-dimensional structure of the protein and the formation of filamentous structures observed in cells infected with natural strains of RVFV. The NSs protein is now implicated as the major factor of virulence and that its pathogenicity is associated with the blocking of interferon production. Therefore, any amino acid changes that result in changes to the filamentous structure of the NSs protein might impact on the binding kinetics between the NSs protein, SAP30 (Sin3A Associated Protein 30) and YY1 (Yin Yang-1). There were 6 amino acid changes in the NSs-SAP30 binding domain, with one being unique to the live-attenuated Smithburn vaccine strain.

Generated sequencing data contributes to global phylogenetic characterization of RVFV isolates and molecular epidemiology of the virus. In addition, findings of this study will further aid investigation on reassortment events occurring between strains of RVFV and genetically related viruses, the role of the NSs protein in the replicative cycle of the virus, the pathogenic effects of the NSs protein within the RVFV-infected host cells, and might help to identify molecular basis of RVFV virulence.

Table of Contents

Dedication.	ii
Acknowledgements	iii
Declaration	iv
Abstract	v
Table of contents	vii
List of figures	xi
List of tables	xii
Abbreviations	xiii
Chapter 1: Introduction	1
1.1. Family <i>Bunyaviridae</i>	1
1.1.1 Genus Phlebovirus	1
1.1.1.1 The Rift Valley fever virus	2
1.2. Vectors and transmission	3
1.3. The outbreak history of Rift Valley fever	5
1.4. The Rift Valley fever virus genome	12
1.5. Virus replication and transcription	14
1.5.1 Replication	14
1.5.2 Transcription	16
1.6. The nucleocapsid gene and protein	17
1.7. The non-structural gene and protein	17
1.8. Strains of Rift Valley fever virus	20
1.9. Aims and objectives	23
Chapter 2: Materials and Methods	24
2.1. Culture of Vero cells	24
2.2. Propagation of Rift Valley fever viral isolates in Vero cells	25
2.2.1. Passaging of Rift Valley fever viral isolates in Vero cells	26
2.2.2. Passaging of Rift Valley fever viral isolates in mice	26
2.3. Extraction of RNA from infected tissue culture	28
2.4. RT-PCR of extracted RNA using primers targeting the S RNA segment	28

2.4.1.	Primer design	
2.4.2.	Reverse transcription	
2.4.3.	Polymerase chain reaction	
2.5. Automat	ed sequencing of the S segment RT-PCR product	
2.5.1.	Primer design	31
2.5.2.	Cycle sequencing	32
2.5.3.	Sequencing	32
2.6. Analysis	of the sequencing data	33
Chapter 3: R	esults	34
3.1. Sequenci	ng analysis of the Rift Valley fever virus S segment	34
3.1.1. 5'	and 3' non-coding regions	36
3.1.2. T	he intergenic region	
3.1.3. T	he NSs gene and protein	
3.1.4. T	he N gene and protein	
3.2. Phylogen	y	41
3.2.1. T	he S RNA segment phylogeny	41
3.2.2. T	he N gene and protein phylogeny	45
3.2.3. T	he NSs gene and protein phylogeny	49
Chapter 4: D	iscussion	54
Chapter 5: R	eferences	59
Chapter 6: A	ppendix	72
6.1. Preparation	on of reagents	72
6.1.1. EN	IEM	72
6.1.2. PB	S	72
6.1.3. TB	E buffer	72
6.2. Routine l	aboratory methodologies	73
6.2.1. RN	A extraction using QIAamp kit	73
6.2.2. 1.2	% Agarose gel	74
6.2.3. PC	R product clean-up using the Wizard® SV gel and PCR cle	an-up system
		74

6.2.4. Isopropanol purification of cycle sequencing product	75
6.3. Full S RNA sequencing data	76
6.4. Protein amino acid alignment	119
6.4.1. N protein amino acid alignment	119
6.4.2. NSs protein amino acid alignment	125
6.5. Supplementary strain data	131
6.6. Evolutionary relatedness of two passaged strains of Rift Valley fever via	rus132
6.7. Ethics clearance certificate	133

List of Figures

Figure 1. Virions of Rift Valley fever virus
Figure 2. Abortions in sheep caused by Rift Valley fever virus infection5
Figure 3. Haemorrhagic state in human, cause by Rift Valley fever virus infection
6
Figure 4. Settlement of nomadic pastoralist in Kenya
Figure 5. Flooded areas in Garissa district in North-eastern Provine of Kenya, an
epicentre of Rift Valley fever outbreak in Kenya, 2006-20079
Figure 6. A map showing the distribution of the 2007 Rift Valley fever outbreak
in Kenya10
Figure 7. A diagrammatic cross-section representing a virus belonging to the
Bunyaviridae family
Figure 8. A schematic representation of the Rift Valley fever virus S segment
ambisense coding strategy15
Figure 9. The consensus sequence for the Rift Valley fever virus S segment in the
viral sense
Figure 10. The consensus amino acid sequence for the Rift Valley fever virus NSs
protein
Figure 11. The consensus amino acid sequence for the Rift Valley fever virus N
protein
Figure 12. Evolutionary relationship of S RNA segment of 72 strains of Rift
Valley fever virus
Figure 13. Evolutionary relationship of the N gene of 72 strains of Rift Valley
fever virus
Figure 14. Evolutionary relationship of the N protein of 72 strains of Rift Valley
fever virus
Figure 15. Evolutionary relationship of the NSs gene of 72 strains of Rift Valley
fever virus
Figure 16. Evolutionary relationship of the NSs protein of 72 strains of Rift
Valley fever virus

Figure 17. The complete nucleotide sequence alignment of the S segment of the
45 strains of Rift Valley fever virus sequenced in this study
Figure 18. The deduced N protein amino acid alignment of the 45 strains of Rift
Valley fever virus generated in this study119
Figure 19. The deduced NSs protein amino acid alignment of the 45 strains of
Rift Valley fever virus generated in this study125
Figure 20. Evolutionary relationship of 2 passaged strains of Rift Valley fever
virus

List of Tables

Table 1.	Identification, origin, year of isolation, source and accession numbers	of 45
	Rift Valley fever virus strains analyzed in the study	27
Table 2	. Primer sequences for the amplification of Rift Valley fever virus S	RNA
	segment	28
Table 3.	Primer sequences for the sequencing of the Rift Valley fever virus S seg	gment
		31
Table 4.	Average p-distances within the 16 genotypes A-P	41
Table 5.	Supplementary strain data	129

Abbreviations

ATF2	Activating transcription factor 2	
ВНК	Baby hamster kidney	
BUNV	Bunyamwera virus	
BSL	Biosafety level	
CAR	Central African Republic	
CDC	Centre for Disease Control	
CPE	Cytopathic effect	
DNA	Deoxyribonucleic acid	
DNase	Deoxyribonuclease	
dNTP	Deoxyribonucleotide triphosphate	
dsRNA	Double-stranded RNA	
DTT	1,4-Dithiothreitol	
EDTA	Ethylenediaminetetracetic acid	
ELISA	Enzyme-linked immunosorbent assay	
EM	Electron micrograph	
EMEM	Eagles minimum essential medium	
FCS	Foetal calf serum	
G1	Glycoprotein 1	
G2	Glycoprotein 2	
HDAC-3	Histone deacetylase 3	
IFN	Interferon	
IgM	Immunoglobulin M	
IGR	Intergenic region	
IRF3	Interferon regulatory factor 3	
LACV	La Crosse virus	
L RNA	Large RNA segment	
ME	Minimum evolution	
MEGA	Molecular Evolutionary Genetics Analysis (software)	
M-MuLV-RT	Moloney murine leukaemia virus reverse transcriptase	
M RNA	Medium RNA segment	

mRNA	Messenger RNA
NCoR	Nuclear receptor corepressor
NCR	Non-coding region
NICD	National Institute for Communicable Diseases
N protein	Nucleocapsid protein
NJ	Neighbourhood joining
NK-кВ	Nuclear factor kB
NSm	Non-structural protein/gene of the M RNA segment
NSs	Non-structural protein/gene of the S RNA segment
PBS	Phosphate buffered saline
PTV	Punta Toro virus
RVF	Rift Valley fever
RVFV	Rift Valley fever virus
RNA	Ribonucleic acid
RNA pol II	RNA polymerase II
RNase	Ribonuclease
RNP	Ribonucleoprotein
RT-PCR	Reverse transcription polymerase chain reaction
SAP30	Sin3A associated protein 30
SFSV	Sandfly fever Sicillian virus
SMB	Suckling mouse brain
SNS	Smithburn neurotropic strain
SPU	Special Pathogens Unit
S RNA	Small RNA segment
SSHV	Snowshoe Hare virus
Taq	Thermus aquaticus
TBE	Tris-borate-ethylenediaminetetracetic acid EDTA buffer
TFIIH	RNA polymerase II transcription factor H
Tgo	Thermococcus gorgonarius
Tm	Melting temperature
TOSV	Toscana virus
TSWV	Tomato Spotted Wilt virus
Ts	Transition
Tv	Transversion

UUKV	Uukuniemi virus
UV-vis	Ultraviolet-visible
YY1	Ying Yang

Chapter 1: Introduction

1.1. Family Bunyaviridae

The family *Bunyaviridae* is comprised of more than 300 viruses, which are categorized into five genera: *Orthobunyavirus*, *Hantavirus*, *Nairovirus*, *Tospovirus* and *Phlebovirus* (Nichol *et al.* 2005). Members of the *Bunyaviridae* family are enveloped and have a tripartite segmented, single-stranded RNA genome of negative or ambisense polarity (Brigden *et al.* 2001; Swanepoel and Coetzer 2004). Within the *Bunyaviridae* family there are viruses which are associated with severe human diseases, including Crimean-Congo haemorrhagic fever virus (*Nairovirus*), California encephalitis virus (*Orthobunyavirus*), Sin Nombre Hanta virus (*Hantavirus*) and Rift Valley fever virus (*Phlebovirus*) (Bishop and Shope 1979; Bi *et al.* 2008).

1.1.1. Genus Phlebovirus

The genus *Phlebovirus* is composed of two serogroups, the Sandfly fever viruses and the tick-transmitted uukuviruses (Murphy *et al.* 1995). The name *Phlebovirus* originates from the disease known as phlebotomous fever, which is caused by members of the Sandfly fever Sicilian (SFS) viruses transmitted by phlebotomous insects (Bishop and Shope 1979). Rift Valley fever virus (RVFV) (Figure 1), a member of the Sandfly fever group of *Phleboviruses*, is the causative agent of Rift Valley fever (RVF), an acute febrile disease predominantly affecting domestic ruminants in Africa and Madagascar, and is characterized by an increased mortality among newborn animals, abortion in pregnant animals, necrotic hepatitis and a hemorrhagic state (Swanepoel and Coetzer 2004).

Large outbreaks of the disease in sheep, cattle and goats occur at irregular intervals of several years when exceptionally heavy rains favour the breeding cycle of mosquitoes, the vectors of RVFV transmission. Transmission to humans usually occurs through contact with tissues and bodily fluids of infected and aborted animals, and less frequently through mosquito bites. Infected individuals often develop only mild febrile illness, but complications do occur in a small proportion of patients and

include ocular sequelae, encephalitis and fatal haemorrhagic disease (Swanepoel and Coetzer 2004; Ikegami *et al.* 2005b).

RVFV has a broad host range. The hosts most susceptible to disease are young domestic ruminants, including lambs, sheep, calves, some species of wild animals e.g. camels and buffalo, and various species of mice (Swanepoel and Coetzer 2004). Studies with different species of laboratory rodents have shown that the susceptibility to infection and the severity of clinical symptoms vary between the different species (Peters and Slone 1982; Anderson and Peters 1988; Ritter *et al.* 2000). There are a number of animals which can become infected with RVFV without developing clinical symptoms of the disease, including a wide range of wildlife species which might play a role in inter-epidemic maintenance of RVFV (Findlay 1931; Evans *et al.* 2007).

1.1.1.1. The Rift Valley fever virus

RVFV has the morphological and physiochemical properties typical of a member of the family *Bunyaviridae*. It is a negative-sense, single-stranded RNA virus with a tripartite segmented genome. The three segments are identified as large (L), medium (M) and small (S). Each genome segment is contained within a separate nucleocapsid and is associated with a transcriptase enzyme. The genome segments are concealed within a spherical virus particle measuring 90 to 100 nm in diameter, which is surrounded by an envelope containing glycoprotein surface projections (Von Bonsdorff and Pettersson 1975; Bishop *et al.* 1980). The L, M and S RNA segments have molecular weights of 2.7, 1.7 and 0.6 x 10^6 respectively, which forms 1 to 2% of the weight of the virus particle (Rice *et al.* 1980).



Figure 1: Virions of Rift Valley fever virus. Picture courtesy of Mike Lecatsas and Monica Birkhead, National Institute for Communicable disease, Electron Micrograph Unit (NICD-EMU).

1.2. Vectors and transmission

The Aedes, Anopheles, Culex, Eretmapoites and Mansonia mosquitoes have been shown to be capable of transmitting RVFV under laboratory conditions (Hoogstraal *et al.* 1979; Zeller *et al.* 1997; Mellor and Leake 2000). RVFV can persist in nature for several years in infected mosquito eggs and then re-emerge following rainfall, which facilitates hatching of mosquito eggs (Le May *et al.* 2004). Environmental conditions that support massive proliferation of mosquitoes increase the possibility of a RVF outbreak to occur. It has been shown that the flooding of isolated grassland depressions, called *dambos*, plays a key role in the generation of epizootics of RVF in Kenya (Davies 1975). This is further supported by the finding that floodwater-breeding aedine mosquitoes, which breed in *dambos*, are capable of transmitting RVFV transovarially (Davies 1975; Linthicum *et al.* 1985). During winter the eggs of aedine mosquitoes lie dormant, along with the RVFV which was transovarially passed on from the parent mosquito. These eggs are capable of surviving prolonged time

periods in dried mud. When the *dambos* flood during heavy rainfalls, transovarially infected *Aedes* mosquitoes hatch and the adult mosquitoes transmit the virus to livestock, where the virus amplifies to high titres and serves as a source of infection for other culicines and anopheline mosquitoes, which act as epizootic vectors. Biting flies such as midges, phlebotomids, stomoxids and simulids could possibly serve as mechanical transmitters of infection (Swanepoel and Coetzer 2004). Outbreaks occurring in arid countries in north and west Africa are independent of rainfall, and are dependent on mosquito vectors which breed in dams and rivers, but not the floodwater *Aedes* mosquitoes (Swanepoel and Coetzer 2004).

Activities that involve contact with infected animals are associated with an increased risk of human infection and include herding, milking, slaughtering, skinning, and the sheltering of animals within the home (Jouan *et al.* 1989; Woods *et al.* 2002). These activities are not limited to the rural setting, but also affect people in professional environments such as abattoir workers and veterinarians. Infected meat sold wholesale is unlikely to be a source of infection for humans as it has been shown that the virus cannot survive below pH 6.00; and meat generally falls to pH 6.00 or less during processing. It has, however, been postulated that unpasteurized milk from an infected animal might serve as a source of infection (Swanepoel and Coetzer 2004). Furthermore, RVFV is present in the nasopharyngeal secretions of infected humans (Abdel-Wahab *et al.* 1978) and can be transmitted by the respiratory tract under experimental conditions (Francis and Magill 1935; Miller *et al.* 1963; Brown *et al.* 1981).

1.3. The outbreak history of Rift Valley fever

The initial sign of an impending outbreak is observed as an increase in the incidences of mortality and abortions in domestic and wild ruminants such as sheep, goats, cattle, buffalo and camels (Figure 2). The demise of domestic animals is generally followed by increased reports of acute febrile illness and sporadically fatal haemorrhagic-like disease in humans (Figure 3) (Meegan 1979). Exact sources of outbreaks in humans are often difficult to establish, whilst some infections are not even reported. This is often attributed to the nomadic lifestyles (Figure 4) of infected individuals in some African countries (Jouan *et al.* 1989), cultural factors which make collection of specimens for laboratory confirmation difficult, as well as limited access to medical facilities (Siam *et al.* 1980).



Figure 2. Abortions in sheep caused by Rift Valley fever virus infection. Picture courtesy of Dr JT Paweska NICD-SPU.



Figure 3. Haemorrhagic state in a human, caused by Rift Valley fever virus infection. A Rift Valley fever patient with petechial rash and ecchymoses. Picture courtesy of Dr JT Paweska NICD-SPU.



Figure 4. Settlement of nomadic pastoralist in Kenya. Rift Valley fever is often diagnosed in pastoralists who have handled infected animals. Picture courtesy of Dr JT Paweska NICD-SPU.

The disease now known as Rift Valley fever was first recognized in sheep in the Rift Valley in Kenya at the turn of the 19th century, but the causative agent was only isolated in 1930 following an outbreak of "enzootic hepatitis" on a sheep farm near Naivisha in the Rift Valley region in Kenya. The outbreak was severe and within seven weeks 3,500 lambs and 1,200 ewes were reported to have died of acute necrosis of the liver (Daubney *et al.* 1931). Over the next four decades epizootics tended to occur in association with population-explosions of floodwater-breeding aedine mosquitoes following heavy rains (Swanepoel and Coetzer 2004).

Large outbreaks affecting livestock occurred in Kenya in 1930-31, 1968 and 1978-79, and lesser outbreaks at irregular intervals in the intervening years. A major epizootic, which caused an estimated 500,000 abortions and 100,000 deaths of sheep, occurred in South Africa in 1950-51; a second major, and more widespread outbreak caused extensive losses of sheep and cattle in 1974-76, while lesser outbreaks were recorded in 1952-53, 1955-59, 1969-71 and 1981 (Swanepoel and Coetzer 2004). Severe outbreaks occurred predominantly in the sheep farming areas of southern Namibia during 1955 and 1974-76. Extensive outbreaks of the disease in southern Africa occurred in areas dominated by cattle farming, in Zimbabwe during 1955, 1957, 1969-70 and 1978, in Mozambique during 1969, and in Zambia during 1973-74, 1978 and 1985. In addition, evidence of the occurrence of the infection was recorded in many other southern and east African countries (Swanepoel and Coetzer 2004).

It was noted from the original investigations in Kenya that febrile illness in humans accompanied outbreaks of disease in livestock, and that some patients experienced transient loss of visual acuity, but the occurrence of serious ocular sequelae was first recognized during the 1950-51 epizootic in South Africa (Weiss 1957). The potential lethality of the virus for man was recognized after seven deaths from encephalitis and/or haemorrhagic fever with necrotic hepatitis occurred during the 1974-76 RVF epizootic in South Africa (van Velden *et al.* 1977).

During 1973 and 1976, outbreaks of RVF affecting livestock were reported in Sudan (Swanepoel and Coetzer 2004). These epizootics were followed in 1977-78 by a major outbreak which occurred along the Nile delta and valley in Egypt, causing an unprecedented number of human infections and deaths, as well as numerous deaths and abortions in livestock, water buffalo and camels. Estimates of the number of human infections ranged from 18,000 to more than 200,000, with at least 598 mortalities resulting from encephalitis and/or haemorrhagic fever (Meegan 1979). Compared to other outbreaks, the Egyptian epidemic was characterized by an increase in the occurrence of encephalitic, ocular and fatal haemorrhagic-like diseases (Meegan *et al.* 1979). The subsequent Egyptian outbreak occurred during 1993, and resulted in an estimated 600 to 1,500 human infections occurring within the Aswan governate (CDC 1994). During this outbreak an increase in ocular disease was noted (Arthur *et al.* 1993).

Prior to the 1970s, the presence of the virus circulation in the west African countries was known from serosurveillance studies. In 1987 a severe epizootic was reported in the Senegal River basin of southern Mauritania and northern Senegal. In Mauritania alone an estimated 224 human patients died of the disease, and there was a high rate of abortion in sheep and goats (Digoutte and Peters 1989; Jouan *et al.* 1989; Karlen 1996). The virus has remained endemic to the region and was responsible for a substantial outbreak in 1998, as well as several smaller outbreaks (Zeller *et al.* 1997; Nabeth *et al.* 2001).

From October 1997 to February 1998, a large outbreak of RVF occurred in northeastern Kenya and Somalia; outbreaks of the disease also occurred in Tanzania (CDC 1998; Woods *et al.* 2002). There were heavy losses of livestock and an estimated 500 human deaths. This particular outbreak was one of the largest in eastern Africa following the discovery of the virus in 1930, with approximately 89,000 infected individuals and 250 deaths (Porter 1999). Several ruthless outbreaks were recognised again in East Africa following heavy rainfall and flooding in 2006-07 (Figure 5), first in the North Eastern Province of Kenya in November 2006, and by the end of January 2007 in the coastal, central, Rift Valley and eastern Provinces (Figure 6). A total of 684 human cases of the disease were reported, with a recorded death rate of 20%. In Somalia, Tanzania and Sudan the disease resulted in a total of 756 cases and a reported 34% death rate. The high death rate recorded in the recent outbreaks in East Africa were, however, estimated only from a number of cases which were diagnosed mainly based on clinical symptoms (Anonymous 2007a; Anonymous 2007b). Small outbreaks of RVF were recognized in north-eastern South Africa during 1999 and 2008 (Paweska *et al.* 2008), and in central Madagascar and the Comoros Islands during 2008 (Eloit 2008; Rakotosamimanan 2008).



Figure 5. Flooded areas in Garissa district in North-eastern Province of Kenya, an epicentre of RVF outbreak in Kenya, 2006-2007. Picture courtesy of Dr JT Paweska NICD-SPU.



* As of January 25, 2007.

Figure 6. A map showing the distribution of the 2007 Rift Valley fever outbreak in Kenya. Included are the number and percentage of reported RVF cases (n = 404) by district which occurred between November 2006 and January 2007 (CDC 2007).

The first documentation of RVF outside the African mainland occurred in Madagascar during 1979, where the virus was isolated from mosquitoes captured in the primary rainforest of Perinet (Mathiot *et al.* 1984). The virus was found to have genetic similarity to an isolated virus of Egyptian lineage. Although there was no outbreak of RVF in humans, antibodies to the virus were found in some of the Madagascan inhabitants (Saluzzo *et al.* 1989). The virus re-emerged in Madagascar during 1991 when the first documented infection of human and livestock occurred. Genetic typing showed that the 1991 isolate differed from the 1979 virus strain and that it was not related to the Egyptian lineage, indicating the presence of at least two separate strains of RVFV in Madagascar (Morvan *et al.* 1991; Morvan *et al.* 1992).

In September 2000, RVF broke out simultaneously in south-west Saudi Arabia and adjoining Yemen following heavy rains on the inland mountain range (Jupp et al. 2002; Al-Hazmi et al. 2003; Madani et al. 2003; Abdo-Salem et al. 2006). This was the first known occurrence of a RVF outbreak outside of the African region. The outbreaks lasted until early 2001, and resulted in 245 human deaths and the loss of thousands of sheep and goats. There were approximately 882 infected human cases, with an unusually high mortality rate of 14%, though this was probably due to underreporting of mild and sub-clinical cases. There was speculation that the virus may have been imported from the Horn of Africa with infected animals, possibly during the 1997-98 epidemic in East Africa, as the strain of the virus responsible for that outbreak had a high sequence similarity with the virus isolated from the Saudi Arabian outbreak. Consequently, importation of livestock from the Horn of Africa was banned, which caused substantial economic losses for east African countries, where the main source of income is generated from trading of livestock. (CDC 2000; Bird et al. 2007). Subsequent detection of the immunoglobulin M (IgM) antibody in sentinel sheep suggests that the virus may have become endemic to the Arabian Peninsula (Elfadil et al. 2006). The outbreak highlighted the major socio-economic risks associated with the transmission of RVFV outside its traditional endemic areas and the possibility of a further inter-continental spread (Balkhy and Memish 2003). The prospect of a global threat is further exacerbated by the capability of RVFV to utilise a wide range of mosquito vectors (Hoogstraal et al. 1979; Meegan 1979; Wilson et al. 1994; Turell et al. 2008), and current trends in global climate change which facilitate the spread of vector-borne viruses (Purse et al. 2005).

1.4. The Rift Valley fever virus genome

The L RNA segment is 6404 nucleotides (nt) in length and consists of a single open reading frame which codes for a 243.6 kDa viral polymerase called the L protein (Figure 7). The L protein gene exhibits some sequence homologies to other viral RNA polymerases (Muller *et al.* 1991).

The M segment is 3 885 nt in length and codes for the two envelope glycoproteins G1 and G2 (Figure 7), as well as for two proteins of unknown function, a 14-kDa nonstructural protein (NSm) and a 78-kDa protein (Gentsch and Bishop 1979; Collett 1986). The G1 and G2 glycoproteins are responsible for eliciting and interacting with neutralising antibodies (Rozhon et al. 1981), and are the major determinants of virus virulence (Shope *et al.* 1981). The L and M segments are of negative polarity (Collett 1986; Muller *et al.* 1991).

The S segment of RVFV is 1 690 nt in length and has two open reading frames encoding the non-structural (NSs) and nucleocapsid (N) proteins. In the majority of the members of the *Bunyaviridae*, the genes encoding these two proteins overlap and are translated in different reading frames (Akashi and Bishop 1983). The phleboviruses are unique in that they have an ambisense S RNA segment and translate the N and NSs genes in opposite polarities. The N protein is translated from the 3' half of the negative sense RNA and the NSs protein from the 3' half of the positive sense RNA (Ihara *et al.* 1984; Marriot *et al.* 1989; Billecocq *et al.* 2004; Ikegami *et al.* 2005a). A schematic representation of the coding strategies of the RVFV S RNA segment is shown in Figure 8. Both the N and NSs genes are found in all *Bunyaviridae* S RNA segments, with exception of some Hantaviruses, which lack the NSs gene (Plyusnin 2002; Jaaskelainen *et al.* 2007).



Figure 7. A diagrammatic cross-section representing a virus belonging to the *Bunyaviridae* family. Adapted from Whitehouse 2004.

1.5. Virus replication and transcription

1.5.1. Replication

Viruses belonging to the *Bunyaviridae* family have negative-sense RNA genomes. Each segment of the RVFV genome is closely associated with nucleoproteins and RNA polymerase to form ribonucleoproteins (RNPs) (Figure 7). The viral RNA is not functional unless in the RNP form, which acts as the template for transcription and replication (Emerson and Wagner 1972).

Bunyaviridae viruses tend to replicate within the host cell cytoplasm and mature by budding into smooth-surface vesicles in or near the Golgi region (Murphy *et al.* 1973; Swanepoel and Blackburn 1977; Kuismanen *et al.* 1982; Smith and Pifat 1982). These mature virions are then transported within these vesicles to the plasma membrane where, the membranes fuse and the mature virions are released (Smith and Pifat 1982).





1.5.2. Transcription

The encapsidated negative-sense RNA is transcribed by the RNA polymerase into a positive sense messenger RNA (mRNA), followed by the translation of the primary transcripts, then replication of the genome, and finally the translation of secondary transcripts (Dimmock et al. 2001). As the S RNA segment is ambisense, the NSs gene is translated from the full length, viral complementary RNA (vcRNA) (Figure 8). Translation is primed by a 'cap-snatching' mechanism similar to that used by the influenza virus (Bouloy et al. 1978; Krug 1981). Briefly, the 5' region of the mRNA is capped with non-viral sequences that act as primers (Bishop et al. 1983; Patterson et al. 1984; Jin and Elliott 1993). The "cap-snatching" mechanism appears to be well conserved amongst members of the Bunyaviridae family and the presence of these 5'caps have been identified on the mRNAs of bunyaviruses (Bishop et al. 1983; Patterson et al. 1984; Eshita et al. 1985; Bouloy et al. 1990; Jin and Elliott 1993), phleboviruses (Ihara et al. 1985; Collett 1986; Simons and Pettersson 1991), nairoviruses (Jin and Elliott 1993), and tospoviruses (Kormelink et al. 1992). The 3' end of the mRNA is not polyadenylated and is shorter than the template because the viral RNA polymerase terminates before the 5' end of the template (Elliott 1996; Schmaljohn and Hooper 2001). Within the Bunyaviridae family the only virus which possesses a polyadenylated 3'-end is the hantavirus Sin Nombre, which has a polyadenylated M segment mRNA (Hutchinson et al. 1996).

It has been shown that transcription of the N and NSs mRNAs is terminated in the intergenic region (IGR) between the two genes (Schmaljohn and Hooper 2001). Albarino *et al.* (2007) have recently shown that the exact termini of the N, NSs and M mRNAs of RVFV, Toscana virus (TOSV) and SFSV are found immediately upstream of the conserved sequence 3'C₁₋₃GUCG/A-5'. The same pentanucleotide sequence has also been found within the ten nucleotides of the transcriptional termination sites of the N mRNA of La Crosse virus (LACV), Snowshoe Hare virus (SSHV) and Germiston virus, as well as the M mRNA of Germiston virus (Ikegami *et al.* 2007). However, this pentanucleotide sequence is not found in Punto Toro (PT) and Uukuniemi (UUK) viruses (Giorgi *et al.* 1991).

1.6. The nucleocapsid gene and protein

A mutational analysis has mapped the interacting domain of the N protein to the Nterminal 71 residues. It has been predicted that the N-terminal region contains alphahelices and that the conserved amino acid residues at the N-terminus, tyrosine (Y) 4, phenylalanine (F) 11, aspartic acid (D) 17, and tryptophan (W) 24, are important in the formation of homodimers. Base changes affecting these amino acids could ultimately affect the function of the N protein (Le May *et al.* 2005).

Studies using mini genomes and other systems revealed that the co-expressions of N and L proteins were required for the synthesis of RNA in viruses belonging to the *Bunyaviridae* family (Dunn *et al.* 1995; Lopez *et al.* 1995; Accardi *et al.* 2001; Flick and Pettersson 2001; Blakqori *et al.* 2003; Flick *et al.* 2003).

1.7. The non-structural gene and protein

The NSs gene codes for a nonstructural protein (NSs protein) of 265 amino acids that is abundantly expressed in infected cells. Viral NSs protein is produced shortly after infection (Ikegami *et al.* 2005b) and can be detected in the nucleus as early as 3-5 hours post infection (Le May *et al.* 2004). In RVFV, the NSs protein is found in the nucleus of infected cells, where it forms large filamentous structures composed of thick bundles of fibrils, 50 nm in diameter, that lie parallel to one another (Daubney *et al.* 1931; Swanepoel and Blackburn 1977; Yadani *et al.* 1999; Bouloy *et al.* 2001), whereas in UUKV, the NSs protein has been found to be dispersed throughout the cytoplasm and associated with 40S ribosomal unit (Simons *et al.* 1992).

The NSs protein is the most variable protein among phleboviruses (Giorgi *et al.* 1991), and therefore it has been used as a marker of variability among natural strains of RVFV (Sall *et al.* 1997). The NSs protein is phosphorylated by casein kinase II at two serine residues located in the C-terminus, at positions 252 and 256 (Yadani *et al.* 1999; Billecocq *et al.* 2004). Unlike RVFV, there is no evidence that the NSs of UUKV is phosphorylated. (Simons *et al.* 1992). The acidic amino acids representing the C-terminal domain of the NSs protein are required for self-association and are

essential for filament formation, but not for NSs transport into the nucleus (Yadani *et al.* 1999).

The exact function of the NSs protein is not fully understood. The NSs protein is probably not essential for replication, as clone 13, an isolate of RVFV that lacks the NSs gene, is still capable of infecting cells and replicating (Muller *et al.* 1995). However, it has been shown that co-expression of NSs protein with L and N proteins substantially enhanced minigenome replication and transcription, suggesting that RVFV NSs protein plays some role in RVFV RNA synthesis (Ikegami *et al.* 2005a).

Recent studies have shown that the NSs gene of RVFV is a major virulence factor preventing early induction of interferon- β (IFN- β) during the course of infection (Goodbourn et al. 2000; Bouloy et al. 2001; Billecocq et al. 2004). The IFNs are a large family of multifunctional proteins that function as the first line of innate defence against viral infection (Goodbourn et al. 2000; Billecocq et al. 2004). RVFV has a negative-sense RNA genome and thus it has to produce a double-stranded RNA (dsRNA) during its life cycle in order to replicate. The dsRNA is a strong inducer of IFN- α and IFN- β , which in turn activate an innate immune response (Goodbourn *et al.* 2000; Billecocq et al. 2004). Hence, for RVFV to efficiently infect cells, it needs to prevent activation of an immune response. This is achieved by the shut-down of host protein production through inhibition of host's mRNA synthesis. Inhibition is accomplished by the binding of the NSs protein to the RNA polymerase II transcription factor, TFIIH (Billecocq et al. 2004; Ikegami and Makino 2004). TFIIH is a multisubunit protein complex which is important in the transcription of proteincoding genes, ribosomal RNA synthesis in vivo and in vitro, as well as nucleotide excision repair (NER) (Iben et al. 2002).

The NSs protein interacts with the p44 and XPB subunits of the host TFIIH transcription factor. By sequestering these subunits within the NSs protein filaments, it prevents proper assembly of these subunits into a mature complex. This results in a lowered concentration of cellular TFIIH and consequently decreases the level of phosphorylated RNA polymerase II (RNA Pol II), which in turn lowers the rate of RNA synthesis (Le May *et al.* 2004). This finding has led to the conclusion that the virulence of a given RVFV strain is not dictated by its IFN sensitivity but resides in

its capacity to efficiently block the production of IFN- α and IFN- β (Bouloy *et al.* 2001). Furthermore, by inhibiting host transcription, RVFV increases virus propagation by making free host ribonucleotides available for viral RNA replication (Dasgupta 2004). These studies have shown that NSs inhibits IFN- β expression immediately post infection, though this has been shown to occur without inhibiting IFN- β -specific transcription factors such as IRF3 (interferon regulatory factor 3), NF- κ B (nuclear factor- κ B) and ATF2 (activating transcription factor 2) (Billecocq *et al.* 2004).

The mechanism by which the RVFV NSs protein antagonizes IFN- β gene expression has recently been demonstrated by Le May et al. (2008). These authors demonstrated that SAP30 (Sin3A Associated Protein 30), a subunit of several corepressor complexes associated to NCoR (nuclear receptor corepressor) and/or Sin3A, binds to NSs as well as YY1 (Yin Yang-1), the activator/repressor of interferon transcription. After RVFV infection, a multiprotein complex containing viral NSs protein and host factors YY1/SAP30/NCoR/Sin3A/HDAC-3 (histone deacetylase 3) is recruited on the IFN- β promoter. The binding of NSs stabilizes the multiprotein complex, maintaining the promoter in a silent repressed state. Consequently, IFN- β expression is blocked, allowing the virus to invade the host. The importance of the NSs-SAP30 interaction was confirmed by showing that its disruption negatively affects the interaction of NSs with the IFN- β promoter, and diminishes the ability of NSs to inhibit IFN- β expression, and hence exert its pathogenic effect. The interacting domain in NSs was found to be in the C-terminal region, between 2 proline (P) residues from amino acids 210 to 230. The authors suggest that all genes whose promoters interact with SAP30 and/or YY1 could theoretically be a target for NSs/SAP30-dependant abnormal transcriptional regulation, which could possibly explain some of the pathogenic effects due to virus such as abortion, hemorrhagic fever, hepatitis or encephalitis (Le May et al. 2008).

The function of the RVFV NSs protein is similar in other *Bunyaviridae* viruses. The PTV NSs protein has also been shown to function as a type I IFN antagonist by inhibiting IFN- α and IFN- β *in vivo* and *in vitro* (Perrone *et al.* 2007). The results of a study by Weber *et al.* (2002) suggest that the NSs of Bunyamwera virus (BUNV) is an IFN induction antagonist that blocks the transcriptional activation

of IFN- α and IFN- β , which results in increased virulence of BUNV (Brigden *et al.* 2001; Weber *et al.* 2002). The NSs protein of BUNV shuts down host transcription by inhibiting phosphorylation of serine (S) residues within the C-terminal domain of the cellular RNA pol II (Thomas *et al.* 2004). In contrast to RVFV, the NSs protein of the Tomato spotted wilt virus (TSWV), genus *Tospovirus*, has been found to suppress post-transcriptional gene silencing (Takeda *et al.* 2002), and more recently Soldan *et al.* (2005) have described a similar role for the NSs protein in the LACV virus.

Sall *et al.* (1997) conducted a study of the variability of the RVFV NSs protein and included 18 isolates from different geographic regions in Africa recovered over a period of 38 years from a variety of host species, including arthropods, cattle and humans. Included in this study were the clone 13 isolate, Smithburn neurotropic (SNS) and MP12 strains. The results showed that there were a variety of nucleotide substitutions throughout the entire NSs gene, but no base insertions or deletions were found, except in clone 13. Pairwise comparison among these strains showed percentage divergence ranging from 0% to 9.6% at the nucleotide level which corresponded to 0% to 9.5% at the amino acid level. Phylogenetic analysis based on the NSs gene revealed existence of two major lineages, Egyptian and sub-Saharan. Amino acid sequence alignment showed that the five cysteine (C) residues at positions 39, 40, 150, 179 and 195 are conserved.

1.8. Strains of Rift Valley fever virus

The members of the *Bunyaviridae* family have been found to be genetically stable (Bishop and Shope 1979; Bilsel *et al.* 1988), but point mutations do occur and are most likely due to the high error rate of RNA polymerase (Dimmock *et al.* 2001). In the case of RVFV, point mutations, deletions, and the reassortment between two or more strains have been shown to occur which resulted in the subsequent generation of new strains (Gentsch and Bishop 1976; Turell *et al.* 1990; Sall *et al.* 1999).

A virus isolated in Lunyo, Uganda, was found to be symptomatically similar to RVFV, but produced different histological lesions in mice compared to other virus strains. Attempts to neutralize the virus in infected mice with potent immune sera to RVFV were unsuccessful, suggesting that Lunyo virus might be a variant of RVFV (Weinbren *et al.* 1957).

Zinga virus, first isolated in the Central African Republic (CAR) from *Mansonia africana* in 1969 (Digoutte *et al.* 1974a), has subsequently been classified as a strain of RVFV with a similar pathogenicity for laboratory animals and humans when compared to alternative RVFV strains (Meegan *et al.* 1983). This strain has since been isolated from mosquitoes in the CAR, Senegal, and Madagascar and from naturally infected humans in Senegal and the CAR (Digoutte *et al.* 1974a; Digoutte *et al.* 1974b; Digoutte 1981; Georges *et al.* 1983).

Two isolates were selected from the 1977-78 outbreak in Egypt as prototypes of RVFV, namely the Zagazig 548 (ZH548) strain which was isolated from a 52 year old male patient with an acute febrile illness, and the Zagazig 501 (ZH501) strain which was isolated from a 12 year old Zagazig female who died of a haemorrhagic-like illness. The ZH501 strain has been shown to be significantly more pathogenic for certain laboratory animals than previous isolates of RVFV from Sub-Saharan Africa (Meegan 1979).

The MP12 strain of RVFV was obtained by twelve serial passages in mice of the virulent ZH548 strain in the presence of 5-fluorouracil (Caplen *et al.* 1985). Virulence has been shown to be under polygenic control and, in the case of the MP12 genome, at least one mutation capable of independently attenuating the virus exists on each segment of the genome. Multiple attenuating mutations significantly reduce the possibility of reversion to virulence (Saluzzo and Smith 1990). The MP12 strain is temperature sensitive, attenuated for mice, and compared to its parent ZH548 strain, forms small plaques. When the genome of the MP12 isolate was compared to ZH548, no mutations were noted in the N protein gene or the 3' and 5' non-coding regions (NCRs), however there were three mutations in the NSs gene and one in the IGR of the MP12 strain. Since there is only one amino acid change, occurring at position 513 in the NSs gene, it is possible that this is an important amino acid responsible for
attenuation of RVFV. The MP12 strain has been successfully tested in human volunteers as a potential vaccine (Peters and Linthicum 1994).

The Smithburn neurotropic strain (SNS) of RVFV, isolated from mosquitoes in Uganda during 1944 and passaged intracerebrally in mice, was subjected to further passaging in embryonated chicken eggs and mice in South Africa. The virus was issued in the form of freeze-dried infected mouse brain for use as a partiallyattenuated vaccine for livestock from 1951 onwards. In 1958, reversion was made to the use of a lower mouse passage level of the virus, and since 1971 the virus has been grown in cell cultures for the preparation of freeze-dried vaccine, recommended particularly for use in non-pregnant sheep, as the virus retains some abortogenic and teratogenic properties for a proportion of pregnant ewes (Coetzer and Barnard 1977; Swanepoel and Coetzer 2004). The use of live-attenuated vaccine is restricted to countries where RVFV is endemic and only inactivated virus is recommended for use in RVFV-free regions (Assaad et al. 1983). Immunization of livestock is an important measure of controlling outbreaks of RVF. Annual vaccination of domestic ruminants in endemic countries not only protects these animals against clinical disease, but also prevents the virus from spreading into the human population by lowering the level of virus amplification in animal hosts.

The 74H39 strain of RVF isolated from a human in the CAR was shown to be composed of a heterogeneous population of viruses. When plaque-purified, the clone 13 isolate was shown to be naturally attenuated by having a large deletion in the non-structural (NSs) gene of the S segment (Muller *et al.* 1995; Vialat *et al.* 2000). Clone 13 is a strong IFN inducer and only capable of growing in mice with a compromised type 1 IFN system (Weber and Elliot 2002). It has been shown that the truncated NSs protein of clone 13 is expressed and remains in the cytoplasm, where it is degraded rapidly by the proteasome (Vialat *et al.* 2000). When the S RNA of clone 13 was compared to the ZH548 strain, besides the large deletion in the NSs gene, only one sequence variation in the N protein gene and 6 nucleotide changes in the intergenic region were found. There were no sequence variations within the 5' and 3' NCRs (Muller *et al.* 1995; Vialat *et al.* 1997).

1.9. Aims and objectives

The present study was undertaken to extend the currently available full sequencing data on the S RNA segment of RVFV. Generating full sequencing data on the S segment of RVFV isolates from disparate historic and geographic origins will further contribute to phylogenetic characterization and molecular epidemiology of the virus, including tracking its movement, identification of the sources of RVF outbreaks, and aid investigations of reassortment events.

In addition, a passage series was performed in commonly used *in vitro* and *in vivo* propagation systems to determine the stability of the viral genome during routine laboratory procedures.

A total of 45 isolates of RVFV recovered throughout Africa, Madagascar, and Saudi Arabia over the past 53 years were used. This study undertakes a comprehensive analysis of the NSs gene at the nucleotide and amino acid levels of these isolates. Analysis of the genetic variability within the NSs genes and their products might help in identifying genetic markers that play a role in RVFV virulence.

Specific aims of this project:

- Produce stocks of RVFV isolates available from NICD-SPU by a single passage in Vero cells, for sequencing studies.
- Conduct ten serial passages of two selected RVFV isolates in commonly used *in vitro* and *in vivo* isolation/propagation systems to determine genetic stability and reproducibility of results.
- Design primers for reverse transcriptase polymerase chain reaction (RT-PCR) and sequencing of the RVFV S segment.
- Perform RT-PCR on RNA extracted from stocks of RVFV isolates.
- Perform automated sequencing of the S segment RT-PCR products.
- Analyze and discuss sequencing data.
- Publish the sequencing data in GenBank.

Chapter 2: Methods and Materials

2.1. Culture of Vero cells

An established cell line of green monkey kidney cells (Vero), obtained from the Special Pathogens Unit of the National Institute for Communicable Diseases (SPU-NICD), was maintained in a monolayer at 37° C in 75-cm² tissue culture flasks supplemented with Eagles Minimal Essential Medium (EMEM) (BioWhittakker, MD, USA) containing 10% foetal calf serum (FCS) (Delta Bioproducts, SA) and antibiotics (100 IU penicillin, 100 µg streptomycin, and 0.25 µg Amphotericin B) (BioWhittakker, MD, USA) (Appendix 6.1.1.).

Confluent Vero monolayers were trypsinised and subcultured at a 1:5 ratio weekly. Briefly, the media was removed and cell monolayer rinsed twice with sterile buffered saline phosphate (PBS) (Appendix 6.1.2.). Trypsin-EDTA (ethylenediaminetetracetic acid) solution, at the concentration of 0.25% trypsin and 0.05% EDTA respectively, free of Ca^{++} and Mg^{++} , was then added, and the flask incubated at 37 °C for 10 minutes, allowing the cells to dislodge. Then, 10 ml of EMEM was added to the trypsinised cells and the mixture aspirated with a sterile syringe and needle to ensure complete dislodgment and thorough mixing of the media and cells. A 2 ml aliquot of cell suspension was transferred into a flask containing 18 ml of EMEM, supplemented with 10% FCS and antibiotics. When the cell monolayers reached 100% confluency, the flasks were incubated at 28°C or used immediately for inoculation with RVFV.

2.2. Propagation of Rift Valley fever viral isolates in Vero cells

RVFV isolates (n = 45) recovered throughout Africa, Madagascar, and Saudi Arabia over the past 60 years (Table 1), were obtained from the NICD-SPU. All isolates were originally recovered from specimens, and most of them were then inoculated intracerebrally in 1-2 day old suckling mice. Viral stocks were prepared either by an additional passage in mice or by 1-2 passages in baby hamster kidney (BHK) cells and stored as freeze-dried or wet preparations at -70°C (Paweska, personal communication). Before RNA extractions were carried out, each isolate was propagated once in Vero cells under standard sterile conditions. Briefly, a 1:10 dilution of each banked virus isolate in EMEM was first centrifuged at 3000 x g and then filtered through a 0.22µm filter to remove any possible bacterial or fungal contaminations. Then, 5 ml of the resulting supernatant was inoculated into 75-cm^2 tissue culture flask containing 48-72 hours old monolayers of Vero cells. After one hour incubation at 37°C, inoculated cells were rinsed once with sterile PBS, overlaid with 20 ml EMEM containing standard concentration of antibiotics (Appendix 6.1.1.), and then incubated at 37°C in a 5% CO₂ incubator. Inoculated cells were examined microscopically daily for cytopathic effects (CPE). In the presence of advanced CPE (at least 70%), infective culture medium was centrifuged at 2000 x g, and then 0.5 ml aliquots of the supernatant were prepared in 1.8 ml cryotubes and stored at -70°C until used. A summary of the RVFV isolates used in this study is given in Table 1.

2.2.1. Passaging of Rift Valley fever viral isolates in Vero cells

Two isolates, SPU2223KEN07 and SPU2207KEN07, recovered during the 2006-7 outbreak in Kenya, were passaged through Vero cells. Briefly, 1:10 dilution of each clinical specimen (serum) was first centrifuged at 3000 x g and then filtered through a 0.22 μ m filter to remove any possible bacterial or fungal contaminations. Five ml of the resulting supernatant was inoculated into 75-cm² tissue culture flask containing 48-72 hours old monolayers of Vero cells. After one hour incubation at 37°C, inoculated cells were rinsed once with sterile PBS, overlaid with 20 ml EMEM containing standard concentration of antibiotics, and then incubated at 37°C in a 5% CO₂ incubator. Inoculated cells were examined microscopically daily for cytopathic effects (CPE). In the presence of advanced CPE (at least 70%), infective culture medium was used to make another 1:10 dilution for the next passage. These viruses were passaged through Vero cells 10 times, and RNA extraction was done from the clinical specimen (serum) and from passage 10 in Vero cells (Vero#10) for each isolate.

2.2.2. Passaging of Rift Valley fever viral isolates in mice

The same two Kenyan isolates were also passaged through mice. This was done by a series of 10 serial intracerebral inoculations of 1-2 day old suckling mice. As for the Vero cell passages, RNA was extracted from suckling mouse brain (SMB) passage number 10 (SMB#10) for each isolate. This part of the project was done by SPU staff members under Animal Ethics Code clearance number 107/2006.

Table 1. Identification, origin, year of isolation, source and accession numbers of 45 Rift Valley fever

 virus strains analyzed in this study.

Strain	Location of Origin	Year	Source	Accession Numbers			
56KEN65	Kenya	1965	Bovine	EU312103			
900085MAU88	Mauritania	1988	Human	EU312104			
214445KEN83	Kenya	1983	Aedes mcintoshi	EU312105			
An991MAD91	Madagascar	1991	Bovine	EU312106			
An999MAD91	Madagascar	1991	Bovine	EU312107			
An1000MAD91	Madagascar	1991	Bovine	EU312108			
AnK6087GUI84	Guinea	1984	Bat (Micropteropus pusillus)	EU312109			
AnTAMBULEGY94	Egypt	1994	Animal	EU312110			
Ar74RSA55	South Africa	1955	Aedes circumluteolus	EU312111			
Ar811MAD79	Madagascar	1979	Mosquito	EU312112			
Ar12568RSA71	South Africa	1971	Eratmopodites quinquivittatus	EU312113			
Ar20368RSA81	South Africa	1981	Culex zombaeusis	EU312114			
Ar21229SA00	Saudi Arabia	2000	Mosquito	EU312115			
ArD38661SEN81	Senegal	1983	Aedes dalzieli	EU312117			
B314KEN62	Kenya	1962	Unknown	EU312118			
B1143KEN77	Kenya	1977	Unknown	EU312119			
H1825RSA75	South Africa	1975	Human	EU312120			
LunyoUGA55	Uganda	1955	Mosquito	EU312121			
R1662CAR85	CAR	1985	Human	EU312122			
SPU45ZAMB85	Zambia	1985	Human	EU312123			
SPU77NAMB04	Namibia	2004	Human	EU312124			
SPU204ANGL85	Angola	1985	Human	EU312125			
SPU12002SOM98	Somalia	1998	Caprine	EU312126			
SPU52001RSA99	South Africa	1999	Buffalo	EU312127			
SPU384001KEN97	Kenya	1997	Human	EU312128			
VRL763ZIM70	Zimbabwe	1970	Bovine foetus	EU312130			
VRL825ZIM79	Zimbabwe	1979	Bovine foetus	EU312131			
VRL1032ZIM78	Zimbabwe	1978	Bovine	EU312132			
VRL1290ZIM78	Zimbabwe	1978	Bovine foetus	EU312133			
VRL1516ZIM78	Zimbabwe	1978	Ovine	EU312134			
VRL1887ZIM78	Zimbabwe	1978	Bovine calf	EU312135			
VRL2230ZIM78	Zimbabwe	1978	Bovine foetus	EU312136			
ZH501EGY77	Egypt	1977	Human	EU312137			
ZH548EGY77	Egypt	1977	Human	EU312138			
SPU2207KEN07	Kenya	2006	Human	EU312139			
SPU2223KEN07	Kenya	2006	Human	EU312140			
SPU2214KEN07	Kenya	2006	Human	EU312141			
SPU2215KEN07	Kenya	2006	Human	EU312142			
SPU2220KEN07	Kenya	2006	Human	EU312143			
SPU10301KEN07	Kenya	2007	Human	EU312144			
SPU10302KEN07	Kenya	2007	Human	EU312145			
SPU10307KEN07	Kenya	2007	Human	EU312146			
SPU10315KEN07	Kenya	2007	Human	EU312147			
SPU77RSA08	South Africa	2008	Buffalo	EU709747			
SPU152RSA08	South Africa	2008	Human	EU709748			

2.4. Extraction of RNA from infected tissue culture

The viral RNA was extracted from infected tissue culture supernatants as per the manufacturer's instructions using the QIAamp Viral RNA kit (Qiagen, CA, USA) (Appendix 6.2.1).

2.4. RT-PCR of extracted RNA using primers targeting the S RNA segment

2.4.1. Primer design

Forward and reverse primers (F1 and R4, Table 2) were designed based on the S RNA sequence data of the MM12 strain of RVFV (GenBank accession number X53771). Vector NTI Advance 9 sequence analysis software (Invitrogen) was used to design oligonucleotides of 20 (forward primer F1) and 22 nucleotides (reverse primer R4) in length (Table 2). Primers have a base composition of 50-60% (G + C) and end in C or GC to increase efficiency of priming, with melting temperatures (Tm) between 55-80°C, and with little or no complementarity. The primers were synthesized by the Molecular and Cell Biology Department of the University of Cape Town (Cape Town, South Africa).

Table 2. Primer sequences for the amplification of the Rift Valley fever virus S RNA segment

Primer	Position	Length (nt)	Sequence
F1	1-20	20	5' – ACA CAA AGA CCC CCT AGT GC – 3'
R4	1690-1669	22	5' – ACA CAA AGC TCC CTA GAG ATA C – 3'

2.4.2. Reverse Transcription

The extracted RNA was reverse transcribed using the Expand Reverse Transcriptase (Roche, Germany). The Expand reverse transcriptase is an RNA directed DNA polymerase, which is a genetically engineered version of the Moloney Murine Leukaemia virus reverse transcriptase (M-MuLV-RT) that produces an increased amount of full-length cDNA transcripts.

The RNA was reverse transcribed in a final reaction volume of 10.5 μ l, containing 1 μ g of total RNA, and 20 pmol R4 primer (Table 2) in RNase- and DNase-free 0.2 ml thin-walled PCR tubes. The reaction mixture was incubated in a GeneAmp 2700 thermal cycler (Applied Biosystems, CA, USA) at 60°C for 10 minutes and then chilled on ice. To each reaction, 1x Expand reverse transcriptase buffer, 10 mM DTT, 1 mM dNTP mix, 20 U RNase inhibitor and 50 U Expand Reverse Transcriptase were added to give a final reaction volume of 20 μ l. The reactions were incubated at 43°C for 1 hour. The reverse transcriptase products were stored at 4°C until use.

2.4.3. Polymerase Chain Reaction

The reverse transcriptase products were amplified, according to manufacturer's instructions, using the Expand High Fidelity Kit (Roche, Germany). The Expand High Fidelity PCR system is optimised to efficiently amplify DNA fragments up to 5 kb. It is composed of a unique enzyme mix containing thermostable Taq DNA polymerase and Tgo DNA polymerase, a thermostable DNA polymerase with proofreading activity. This polymerase mixture is designed to generate PCR products of high yield, high fidelity and high specificity from all types of DNA (Barnes 1994). The Expand High Fidelity PCR system shows a 3-fold increase in the fidelity of DNA synthesis compared to Taq DNA polymerase due to the inherent 3' to 5' exonuclease or "proofreading" activity of Tgo DNA polymerase.

Reactions were prepared in sterile RNase- and DNase-free 0.2 ml thin-walled PCR tubes. The PCR master mix consisted of 20 pmol F1 primer, 20 pmol R4 primer (Table 2), 2 x Expand High Fidelity buffer, 10 mM dNTP mix, 2.6 U Expand High Fidelity enzyme mix. Per sample, 5 μ l of cDNA was added with 79.25 μ l nuclease free water to give a final volume of 100 μ l. The PCR was performed using a GeneAmp 2700 thermal cycler (Applied Biosystems, CA, USA), with an initial denaturation step at 94°C for 2 minutes, followed by 35 cycles of denaturation at 94°C for 30 seconds, elongation at 55°C for 30 seconds, and extension at 72°C for 1.5 minute, and then followed by a final elongation step at 72°C for 7 minutes. The amplicons were analyzed with agarose gel electrophoresis using 1.2% agarose gel (Appendix 6.2.2) with a 0.5 x Tris-borate-ethylenediaminetetracetic acid EDTA (TBE) buffer (Appendix 6.1.3.) at 100V for 1 hour. The DNA fragments were stained with 0.5 μ g/ml ethidium bromide (EtBr) and then visualized using a UV transilluminator and the GeneTool software (SynGene, MD, USA).

The PCR products were purified as per manufacturer's instructions using the Wizard® SV Gel and PCR Clean-Up System (Promega, WI, USA) (Appendix 6.1.3), and stored at -20°C until used.

2.5. Automated sequencing of the S segment RT-PCR products

2.5.1. Primer design

The double-stranded DNA of the S segment generated by RT-PCR was sequenced using primers designed during the study (Table 3). Vector NTI Advance 9 sequence analysis software (Invitrogen) was used to design six forward and six reverse primers to meet the following conditions: about 17-22 nucleotides in length, a base composition of 50-60% (G + C), end in C or GC to increase efficiency of priming, melting temperatures (Tm) between 55-80°C, and little or no complementarity to avoid primer dimer formation self complementarity. The primers were synthesized by the Molecular and Cell Biology Department of the University of Cape Town (Cape Town, South Africa).

Table 3. Primer sequences for the sequencing of the Rift Valley fever virus S segment.

Forward Primers									
PrimerPositionLength (nt)Sequence									
F1	1-20	20	5' – ACA CAA AGA CCC CCT AGT GC – 3'						
F2a	461-480	20	5' – TGA GGA GTT GCA AGA TCA CC – 3'						
F2b (2F)	514-536	22	5' – TGG CTT ACA CAG GAT GAT AGC G – 3'						
F3a	909-927	19	5' – AGC CAC TTA GGC TGC TGT C – 3'						
F3b (3F)	1047-1063	17	5' – TGC ATT CAT TGG CTG CG – 3'						
F4	1394-1412	19	5' – TGA GAG CCT CCA CAG TTG C – 3'						

Reverse Primers								
Primer	PrimerPositionLength (nt)Sequence							
R1a	548-531	18	5' – GGA TGG CCT CAG TCG CTA – 3'					
R1b (1R)	394-373	21	5' – AGT GAG GGT TCT CCA AGA GGC – 3'					
R2a	995-977	19	5' – GCC TTT GGA CTT GTG GAT T – 3'					
R2b (2R)	934-910	24	5' TTA CAA GAC AGC AGC CTA AGT GGC 3'					
R3	1458-1440	18	5' – AAC AAG CCC AGG AGG ATG – 3'					
R4	1690-1669	22	5' – ACA CAA AGC TCC CTA GAG ATA C – 3'					

2.5.2. Cycle sequencing

The nucleotide sequences of the amplicons were determined using the BigDye® Terminator v3.1 Cycle Sequencing Ready Reaction kit (Applied Biosystems, Warrington, Great Britain), according to the manufacturer's instructions. The BigDye® Terminator set of dyes are labelled with novel, high-sensitivity dyes by Applied Biosystems using the discoveries of Rosenblum *et al.* (1997).

The cycle sequencing master mix for each primer consisted of: 0.8 pmol primer (Table 3), 5 x BigDye sequencing buffer, 10-40 ng of cDNA, and nuclease free water to give a final volume of 20 μ l. The cycle sequencing reaction was performed using a GeneAmp 2700 thermal cycler (Applied Biosystems, CA, USA), starting with an initial denaturation step at 96°C for 1 minute, followed by 25 cycles as follows: 96°C for 10 seconds, 50°C for 5 seconds, and 60°C for 4 minutes. The sample was then held at 4°C until ready to purify. Products were purified by isopropanol (Appendix 6.2.4).

2.5.3. Sequencing

The cycle sequencing product was analyzed with an ABI Prism 3100 Genetic Analyzer (Applied Biosystems, Warrington, Great Britain) – a fully automated, fluorescence-based capillary electrophoresis platform.

The Applied Biosystems DNA sequencer detects fluorescence from the four different dyes that are used to identify the A, C, G and T extension reactions. Each dye emits light at a different wavelength when excited by an argon ion laser. All four colours, and therefore all four bases, can be detected and distinguished in a single gel lane or capillary injection.

The complete nucleotide sequence data of the RVFV S RNA segments generated in this study were submitted to GenBank and have been assigned GenBank accession numbers given in Table 1.

2.6. Analysis of the sequencing data

The data generated from sequencing was used for nucleotide and amino acid sequence alignment. Sequences were aligned using Sequencher (Gene Codes Corporation). Phylogenetic and molecular evolutionary analysis were conducted using Molecular Evolutionary Genetics Analysis software, version 4 (MEGA4) (Tamura et al. 2007). The Neighbour Joining (NJ) method was used to construct a phylogenetic tree. The NJ method is a simplified version of the Minimum Evolution (ME) method, which uses distance measures to correct for multiple hits at the same sites, and chooses a topology showing the smallest value of the sum of all branches as an estimate of the correct tree. Sequence divergence was done by calculating the average p-distances within and between groups.

The bootstrap test was used to ascertain the reliability of a given branch pattern by examining the frequency of its occurrence in a large number of trees, each based on the re-sampled dataset. MEGA4 used Felsenstein's bootstrap test (Felsenstein 1985), which was evaluated using Efron's bootstrap re-sampling technique.

A total of 75 isolates of RVFV were analyzed, of which 45 were originally sequenced in this study, and the remaining sequencing data for the other 30 isolates was obtained from GenBank. Sequencing data of 72 isolates, representing naturally circulating RVFV from Africa, Madagascar and Saudi Arabia, was used to generate phylogenetic trees to establish the relatedness of isolates based on their S RNA segments, and N and NSs proteins. Artificially generated strains, including the vaccine strains, were not included in the phylogenetic analyses.

Chapter 3: Results

3.1. Sequencing analysis of the Rift Valley fever virus S segment

Of the 45 strains sequenced in this study (Appendix 6.3.), six were recently sequenced by Bird *et al.*, (2007), and are currently available in GenBank. For a more comprehensive analysis of the S RNA segment, the sequencing data from the 45 strains sequenced in this study were analyzed together with the 30 strains available in GenBank, 3 of which are laboratory strains. Only the naturally occurring strains (n = 72) were used for phylogenetic analysis, and aligned to infer a consensus sequence (Figure 9). The three laboratory strains, clone 13, MP12 and SNS, were also included in sequence analysis (n = 75), but not in the phylogenetic analysis.

Phylogenetic analysis indicates that circulating strains are compartmentalized and belong to one of three lineages, namely Egyptian, western African, and central, eastern and southern African. The strains clustered in the Egyptian lineage had an average p-distance of 1.0%, the western African strains 0.9%, and the central, southern and eastern African strains 2.0%.

	1 50
(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATC <mark>ATGGATTACTTTCCTG</mark>
(51)	TGATATCTGTTGATTTGCAGAGTGGTCGTCGTGTTGTGTCAGTGGAGTAC
(101)	ATTAGAGGTGATGGTCCTCCCAGGATACCTTATTCTATGGTTGGGCCCTG
(151)	TTGTGTCTTTCTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGTCGGACTTGGA
(251)	GACTTTGCATCAAACGTTGCACCTCCACCAGCAAAGCCTTTTCAGAGACT
(301)	TATTGATCTAATAGGCCATATGACTCTTAGTGATTTCACAAGGTTCCCCA
(351)	ATCTGAAAGAAGCCATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACATTAGAAGGGA
(451)	TCAGATTGCCACTCTAGCAATGAGGAGCTGCAAGATTACCAATGATCTAG
(501)	AGGACTCCTTTGTTGGCTTACACAGGATGATAGTGACCGAGGCTATCCTC
(551)	AGAGGGATTGACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
(601)	TGCTCACGTACAGTGTGTTCGGCTCCTGCAGGCAGCAAAAGAGGACATTT
(651)	CTAATGCTGTAGTTCCAAACTCAGCCCTCATTGCTCTTATGGAGGAGAGC
(701)	CTGATGCTGCGCTCATCACTTCCTAGCATGATGGGGAGAAACAACTGGAT
(751)	TCCAGTTGTTCCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAAGAGA
(801)	<mark>GTGATGATGATGGATTTGTTGAGGTTGATTAG</mark> AGGTTAA <mark>GGCTGCCC</mark> CA <mark>C</mark>
(851)	CCCCCACCCCCAATCCCGACCGTAACCCCCAACCCCCCTTTTCCCCCCAAC
(901)	CCCC <mark>TGGGCAGCC</mark> ACTTAGGCTGCTGTCTTGTAGCCTGAGCAGCTGCCAT
(951)	GACAGCAGCTGACGGCTTCCCATTAGAATCCACAAGCCCAAAAGCTTTCA
(1001)	AGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCTATTCACTGCTGCA
(1051)	TTCATTGGCTGCGTGAACGTTGCAGCAACCTCCTCCTTTGTTCTACCTCG
(1101)	GAGGTTTGGGTTGATGACCCGGGAGAACTGCAGCAGATACAGAGAGTGAG
(1151)	CATCTAATATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACCATG
(1201)	CCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATGCAGGGGATAGGCC
(1251)	GTCCATGGTAGTCCCAGTGACAGGAAGCCACTCACTCAAGACGACCAAAG
(1301)	CCTGGCATGTCCAGCCAGCCAGGGCGGCAGCAACTCGTGATAGAGTCAAC
(1351)	TCATCCCGGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAGAGC
(1401)	CTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCATCATCCTCCGGG
(1451)	GCTTGTTGCCACGAGTTAGAGCCAGAACAATCATTTTCTTGGCATCCTTC
(1501)	TCCCAGTCAGCCCCACCATACTGCTTTAAGAGTTCGATAACCCTACGGGC
(1551)	ATCAAACCCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCATTGC
(1601)	GGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTCTTGATAGTTGTCC
(1651)	ATTATTGTAATAGTGTTTGTATCTCTAGGGAGCTTTGTGT (1690)

Figure 9. The consensus sequence for the Rift Valley fever virus S segment in the viral sense. The consensus sequence was generated after aligning the 45 strains sequenced in this study and 27 strains available from GenBank. Highlighted yellow region represents the NSs gene and the highlighted green region represents the N gene. The highlighted blue text is the proposed transcription termination motif, and the highlighted red text is the associated C/G-repeats.

To assess the potential for sequence variation to occur in the original material through routine laboratory manipulations, including primary virus isolation and/or subsequent virus propagation to prepare viral stocks, a passage series was done. Two isolates recovered from RVF patients during the 2007 outbreak in Kenya, SPU2223KEN07 and SPU2207KEN07, were passaged in two different amplification systems for RVFV, namely ten times in Vero cells and ten times in mice. Sequencing data generated from the virus RNA present in the original clinical specimens and from RNA extracted from Vero#10 and SMB#10 showed 100% homology for each respective isolate (Appendix 6.6.). These results demonstrate that the RVFV S segment remained stable during ten serial passages in different propagation systems. This finding is important in terms of having confidence regarding originality of the virus genome of the strains selected for this study and their natural genetic relatedness. In addition, obtained results demonstrated the accuracy and reproducibility of the techniques used.

3.1.1. 5' and 3' non -coding regions

The non-coding regions (NCRs) found at the extreme terminal ends of the S RNA segment were found to be highly conserved in the 75 isolates. Only two sequence variations were found in the 5'NCR amongst all of them. The first was a 7A>C transversion in the ArD38388BF83 (Table 5) strain, isolated in Burkina Faso in 1983, and the SPU2214KEN07 strain, isolated in Kenya in 2007 (Table 1). The second sequence variation was a 26A>T transversion which occurred in the SPU52001RSA99 strain isolated in 1999 in South Africa.

Five sequence variations were found in the 3'NCR. The first was a 1658T>C transition in the B314KEN62 strain, isolated in Kenya in 1962, and the SPU77NAMB04 strain, isolated in Namibia in 2004. The second variation was a 1663A>G transition in the SPU2214KEN07 strain, isolated in 2007 in Kenya (Table 1). The third variation was a 1666A>T transversion in the Ar20368RSA81 strain, isolated in 1981 in South Africa (Table 1), and the fourth was a 1671T>A transversion in the ZM657 Egyptian strain, isolated in this country in 1977 (Table 5). The fifth variation was 1697delT in the South African strain SPU77RSA08. This is the only deletion found that is not in the IGR.

3.1.2. The intergenic region

The intergenic region (IGR), a region between the two open reading frames (ORF) encoding the N protein and the NSs protein, was found to be variable. It has a p-distance range of 0 to 9.2%, with an average of 4.8%. This region of the S RNA segment is the only region where insertions and deletions were found.

A feature that makes the IGR very different to the rest of the S RNA segment is the C/G rich repeats. Such repeats, found downstream of the 5'-GGCTGCCC-3' transcription termination motif, are thought to be involved in transcription termination (Hutchinson *et al.* 1996; Ikegami *et al.* 2007). These motifs were found to be highly conserved in all 75 strains of RVFV analyzed in this study. The motif for NSs transcription termination was found at position 840-847, with the C rich repeat from 850-845/5, and for the N gene transcription termination, the motif was found at position 905/6-912/3, with the G rich repeats (when in the complementary sense) from position 899/900-903/4.

The attenuated MP12 strain has four nucleotide variations compared to its parent ZH548 strain, one of which is a transition found within the IGR, 862T>C (Vialat *et al.* 1997). This same transition was found in two of the Kenyan strains, B1143KEN77 and B314KEN62. Another Kenyan strain, SPU10307KEN07, also showed variation at this position, though in the form of a deletion of the nucleotide.

The IGR of clone 13 was found to have six nucleotide variations when compared to the ZH548 strain (Muller *et al.* 1995). When compared to the other strains, besides the section between position 879 and 884, the only other unique difference was a transition, 860C>T.

3.1.3. The NSs gene and protein

The NSs open reading frame (ORF) is 798 nucleotides in length. It begins with an ATG start codon at position 35 and ends with a TAG stop codon at position 832. The ORF encodes a protein of 266 amino acid residues. A total of 167 sequence variations were found in this gene, 65 of which were unique. In the resulting protein a total of 51 amino acid changes were found, 27 of which were unique. Subsequent to the alignment of the amino acid sequences of the strains incorporated into this study, an NSs protein amino acid consensus sequence was defined (Figure 10).

(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMHHRPSH
(51)	EVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLIDLIGHMTLSD
(101)	FTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDDIRRDQIATLAMRSCK
(151)	ITNDLEDSFVGLHRMIVTEAILRGIDLCLLPGFDLMYEVAHVQCVRLLQA
(201)	AKEDISNAVVPNSALIALMEESLMLRSSLPSMMGRNNWIPVVPPIPDVEM
(251)	ESEESDDDGFVEVD

Figure 10. The consensus amino acid sequence for the Rift Valley fever virus NSs protein.

As shown previously by Vialet *et al.* (1997), the MP12 strain varies from its parent strain, ZH548, by three nucleotides within the NSs ORF. These variations were all T>C transitions and were found at positions 208, 403 and 513. The 208T>C transition also occurred in the Ar74RSA55 strain (Table 1), but the remaining two transitions were restricted to the MP12 strain. Of the three variations, only one, 513T>C, resulted in an amino acid change, V160N (Vialat *et al.* 1997).

Amino acid changes that could affect the structure of the protein are of importance. One such change, I23F, occurred in twelve strains, and was due to the 101A>T transversion. A 159T>A transversion unique to the SPU52001RSA99 strain (Table 1), isolated in South Africa in 1999, resulted in the amino acid change I42Y. Another unique variation was found in the Ar20368RSA81 strain (Table 1), isolated in South Africa in 1981, and was due to the 182C>T transition, which resulted in the amino acid change H50Y. There was only one substitution that involved a cysteine, Y67C, which occurred in the SPU45ZAMB85 strain (Table 1), isolated in Zambia in 1985, and the Smithburn strain due to the 234A>G transition.

As defined by Sall *et al.* (2008), the interacting domain of NSs-SAP30 is found between amino acid residues 210 and 230. An analysis of this region found 6 amino acid variations. The first change, V210A, was found in the South African strain Ar20369RSA81 (Table 1). The second change, A214G, occurred in the 2 strains from Guinea, Ank6087GUI84 and ANK3837GUI81, and the Zinga strains from CAR (Table 5). The third variation, A217V, was common to all Egyptian lineage strains. The fourth variation, S222N, was restricted to the SNS vaccine strain. The fifth variation, S227L, occurred in the SPU10301KEN07 and SPU10307KEN07 Kenyan strains (Table 1). The sixth variation, S227T, occurred in the SPU2214KEN07 strain (Table 1). Besides the substitution in the SNS strain, there were no other notable changes.

3.1.4. The N gene and protein

The N gene is read in the complementary sense and starts at position 1652/4 with an ATG start codon. It is 783 nucleotides in length and terminates at position 915/7 with a TAA stop codon. An exception to the stop codon was the LunyoUGA55 strain which contained a TGA stop codon. The N gene encodes a protein made up of 246 amino acid residues. Within the 783 nucleotides there were 134 substitutions, 53 of which were unique. Only 43 of the sequence variations resulted in an amino acid change, 7 of which where unique. The N gene shows almost the same number of nucleotide substitutions as the NSs gene, but fewer of them resulted in unique amino acid changes. The N protein amino acid consensus sequence inferred from the amino acid sequence alignment of the naturally occurring strains included in this study is shown in Figure 11.

(1) MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQYGGADW
 (51) EKDAKKMIVLALTRGNKPRRMMKMSKEGKATVEALINKYKLKEGNPSRD
 (101) ELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDGLSPAYPRHMMHPSFA
 (151) GMVDPSLPEDYLRAILDAHSLYLLQFSRVINPNLRGRTKEEVAATFTQPM
 (201) NAAVNSNFISHEKRREFLKAFGLVDSNGKPSAAVMAAAQAYKTAA

Figure 11. The consensus amino acid sequence for the Rift Valley fever virus N protein.

It has been shown that, besides that large deletion in the NSs gene of clone 13, there was only one other nucleotide substitution which resulted in an amino acid change, an E159G substitution (Muller *et al.* 1995). However, this is not unique to clone 13, since this variation occurred in twelve of the 75 strains analyzed, and is due to the 1180T>C transition.

Of the seven unique sequence variations that resulted in amino acid changes, three where found in the Entebbe strain (Table 5). These three variations were 100T>C, 1036T>C and 1096C>T, which resulted in amino acid changes K219R, S207N and R187K, respectively. The attenuated SNS strain had several unique sequence variations in the N gene, though only one, 1528T>C, resulted in an amino acid change, K43R. Unique sequence variations, 931T>C and 1524C>A, were also found in two Madagascan strains, An999MAD91 and An1000MAD91 (Table 1), and resulted in the amino acid changes K242R and Q44H, respectively. An Egyptian isolate, ZH1776EGY78 (Table 5), had a variation, 1274C>T, that resulted in the amino acid change V128I.

3.2. Phylogeny

3.2.1. The S RNA segment phylogeny

The evolutionary history was inferred using the Neighbour-Joining method (Saitou and Nei 1987). The phylogenetic tree is drawn to scale, with branch lengths in the identical units as those of the evolutionary distances used to infer the tree. In general, isolates from the same geographic locations tend to cluster together (Figure 11), which supports previous phylogenetic analyses that have defined three broad lineages, namely Egyptian, western African, and central, eastern and southern African (Sall *et al.* 1999). These clusters are supported by high bootstrapping values and correlate with the geographic origin of the isolates (Figure 11).

The three main phylogenetic lineages, shown in Figure 11, can be further divided into 16 genotypes (A-P). The chosen parameters of a genotype were groupings that had a bootstrap value of 70-100%, and a p-distance (the proportion of distances, i.e. the number of pairwise nucleotide differences divided by the total number of nucleotides in the sequenced region, calculated with MEGA4) of less than 0.016 to all other members of the phylogenetic cluster, and were based on research by Venter *et al* (2001). These genotypes are shown in Figure 11 and summarized in Table 4.

 Table 4. Average p-distances within the 16 genotypes A-P

А	В	С	D	Е	F	G	Н	Ι	J	Κ	L	М	Ν	0	Р
0.010	-	0.010	-	0.000	0.002	0.010	0.005	-	-	-	-	-	-	-	0.009

(-) Genotypes with non calculable p-distances due to only one representative

The average p-distance for the entire S segment was only 2.5%, with a range from 0 to 4.1%. With such low genetic diversity amongst strains analysed a low average p-distance value must be used for defining a genotype, which is consequently also supported by a low bootstrap value.



Figure 12. Evolutionary relationships of the S RNA segment of 72 strains of Rift Valley fever virus. The evolutionary history was inferred using the Neighbour-Joining method (Saitou and Nei 1987). The bootstrap consensus tree inferred from 1000 replicates (Felsenstein 1985) is taken to represent the evolutionary history of the taxa analyzed (Felsenstein 1985). Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Kimura 2-parameter method (Kimura 1980) and are in the units of the number of base substitutions per site. All positions containing gaps and missing data were eliminated from the dataset (complete deletion option). There were a total of 1682 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 (Tamura *et al.* 2007). The letter designations represent the genotype grouping of the strains. The tree is also divided into the three broad lineages, namely the Egyptian lineage (red), the western African lineage (blue) and the central, eastern and southern African lineages (green). Bold and underlined names represent strains sequenced in this study.

The phylogenetic tree shows the two possible modes of circulation, namely distant spread from one region to another, and local circulation in an enzootic/endemic area. Virus isolates found within the Egyptian lineage are the RVFV strains isolated during the 1977-79 Egyptian outbreak, the Tambul strain, as well as two Zimbabwean strains isolated in 1974 and 1978, and two Madagascar strains isolated in 1979. The strains from the 1977-79 outbreak are all closely related, which is an example of local circulation. Within the Egyptian lineage there is also an example of distance spread, namely the close relatedness of the Zimbabwean and Madagascan strains to the Egyptian strains. The original Madagascan isolate is Ar811MAD79, and the other isolate, MgH824MAD79 was from a laboratory infection whilst handling the Ar811MAD79 strain. The Zimbabwean and Madagascan strains show a close relationship, which suggests that the Ar811MAD79 strain was introduced to the island from the eastern coast of Africa. Furthermore, there is a close relationship to a Namibian strain from 2004, and a South African strain from 1981, which could be due to spread of the Zimbabwean isolates, or due to a reassortment event.

In the West African lineage there are strains from the Mauritanian outbreak in 1987-88, a strain from Burkina Faso in 1983, and a strain from Senegal in 1981. The RVF viruses isolated in Guinea in 1981 and 1984 should, according to geography, be included in this lineage, but have closer homology to members of the central, eastern and southern African lineage. Both strains are closely related to the Zinga strain isolated in CAR in 1969.

The majority of the RVFV strains are part of the central, eastern and southern African lineage. Represented in this lineage are isolates from South Africa, Zimbabwe, Zambia, Angola, CAR, Uganda, Kenya, Somalia, Saudi Arabia, Madagascar, and Guinea, which were collected over a period of 63 years, from 1944-2008. The most recent outbreaks to occur were in Kenya in 2007 and in South Africa in 2008. Viral isolates from these separate outbreaks are genetically very similar. There seems to be a pattern of Kenyan isolates being related to Southern African isolates. A Kenyan isolate from 1965 forms part of the same genotype group (H) as South African isolates from 1970-71 and 1975. Another example is the Kenyan isolates from the 1997-98 outbreak which form part of the same genotype group (G) as a South African isolate from 1999. The majority of the Kenyan isolates are found in the G genotype group and represent strains of RVFV isolated during several different outbreaks, suggesting that these outbreaks could be due to the re-emergence of epizootic viruses.

The South African isolates appear to be distantly related. Isolates from the 1971 and 1975 outbreaks show close homology, whilst isolates from the 1951, 1955 and 1999 outbreaks are genetically more distant. This suggests that more than one strain of RVFV was circulating in the country. This is also notable amongst the Zimbabwean strains. Isolates from the 1978-79 outbreak are more closely related than those from the 1970 and 1974 outbreaks. Isolates from the 1974 outbreak are particularly distinct, with at least two different strains of the virus circulating during the outbreak.

3.2.2. The N gene and protein phylogeny

The N gene was found to have virtually the same degree of sequence variation as the NSs gene. For the N gene, the p-distance ranged from 0 to 4.2%, with an average of 2.2%, and for the N protein, the range was from 0 to 2%, with an average of 0.2%.

When the N gene region is used to generate a phylogenetic tree (Figure 13), the isolates cluster in the same way as is seen for the entire S segment (Figure 12). When the translated proteins of the N gene are inferred in a tree, the tree is dramatically different. The phylogenetic tree inferred for the N gene alignment shows the three distinct geographical divisions (Figure 13), however the phylogenetic tree inferred for N protein alignment only shows two lineages, the Egyptian cluster and central, eastern and southern African cluster, which also contains the western African strains (Figure 14). This is not surprising as 43 of the 134 sequence variations resulted in amino acid changes, and only 7 of those variations were unique to single isolates.



Figure 13. Evolutionary relationships of the N gene of 72 strains of Rift Valley fever virus. The evolutionary history was inferred using the Neighbour-Joining method (Saitou and Nei 1987). The bootstrap consensus tree inferred from 1000 replicates (Felsenstein 1985) is taken to represent the evolutionary history of the strains analyzed (Felsenstein 1985). Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Kimura 2-parameter method (Kimura 1980) and are in the units of the number of base substitutions per site. All positions containing gaps and missing data were eliminated from the dataset (complete deletion option). There were a total of 738 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 (Tamura *et al.* 2007). The tree is also divided into the three broad lineages, namely the Egyptian lineage (red), the western African lineage (blue) and the central, eastern and southern African lineages (green). Bold and underlined names represent strains sequenced in this study.



Figure 14. Evolutionary relationships of the N protein of 72 strains of Rift Valley fever virus. The evolutionary history was inferred using the Neighbour-Joining method (Saitou and Nei 1987). The bootstrap consensus tree inferred from 1000 replicates (Felsenstein 1985) is taken to represent the evolutionary history of the taxa analyzed (Felsenstein 1985). Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. All positions containing gaps and missing data were eliminated from the dataset (complete deletion option). There were a total of 245 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 (Tamura *et al.* 2007). Unlike the other trees, the N protein phylogeny only shows two lineages, the Egyptian lineage (red) and the central, eastern and southern African lineages (green). Bold and underlined names represent strains sequenced in this study.

3.2.3. The NSs gene and protein phylogeny

The NSs gene has almost the same degree sequence variation as the N gene, but more of them result in amino acid changes; 167 variations resulted in 51 amino acid changes of which 27 were unique to single isolates. This is reflected in the phylogenetic trees inferred from the alignment of the NSs gene sequences and the alignment of the NSs protein amino acid sequences. Both phylogenetic trees (Figure 15 and Figure 16) still show many clusters and the division of the isolates into the three broad lineages, showing that the NSs protein has a higher degree of divergence compared to the N protein. The NSs gene has a p-distance range of 0 to 4.6%, with an average of 2.4%, and the NSs protein has a range of 0-3.8%, with an average of 1.7%.



Figure 15. Evolutionary relationships of the NSs gene of 72 strains of Rift Valley fever virus. The evolutionary history was inferred using the Neighbour-Joining method (Saitou and Nei 1987). The bootstrap consensus tree inferred from 1000 replicates (Felsenstein 1985) is taken to represent the evolutionary history of the strains analyzed (Felsenstein 1985). Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Kimura 2-parameter method (Kimura 1980) and are in the units of the number of base substitutions per site. All positions containing gaps and missing data were eliminated from the dataset (complete deletion option). There were a total of 797 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 (Tamura *et al.* 2007). The tree is also divided into the three broad lineages, namely the Egyptian lineage (red), the western African lineage (blue) and the central, eastern and southern African lineages (green). Bold and underlined names represent strains sequenced in this study.



Figure 16. Evolutionary relationships of the NSs protein of 72 strains of Rift Valley fever virus. The evolutionary history was inferred using the Neighbour-Joining method (Saitou and Nei 1987). The bootstrap consensus tree inferred from 1000 replicates (Felsenstein 1985) is taken to represent the evolutionary history of the taxa analyzed (Felsenstein 1985). Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. All positions containing gaps and missing data were eliminated from the dataset (complete deletion option). There were a total of 264 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 (Tamura *et al.* 2007). The tree also shows the three broad lineages, namely the Egyptian lineage (red), the western African lineage (blue) and the central, eastern and southern African lineages (green). Bold and underlined names represent strains sequenced in this study.

Chapter 4: Discussion

In this study, all 45 RVFV S segments were found to be highly conserved. Within the S segment, the N gene was shown to be more genetically stable than the NSs gene. The regions with the most genetic stability were the 5' and 3' terminal NCRs, while the greatest level of genetic variability was found in the IGR. Similar results were obtained by Bird *et al.* (2007), who demonstrated low virus genetic diversity among 33 RVFV S segments representing the virus strains recovered from throughout Africa and Saudi Arabia from 1944 to 2000. Moreover, these authors also showed a higher sequence divergence in the IGR between the N and NSs genes, than in the N and NSs genes. One possible reason for the low genetic diversity is viral maintenance through endemic or enzootic cycles involving little viral activity and hence less possible for mutations to occur (Sall *et al.* 1998).

The segmented genome structure of the members of the *Bunyaviridae* family carries the implication for reassortments to occur in nature, which might result in the appearance of new strains. New strains can also emerge as a result of point mutations, deletions, insertions, and recombination when co-infection of a susceptible host occurs with two or more strains of the virus (Gentsch and Bishop 1976; Turell *et al.* 1990; Sall *et al.* 1999), but recent studies indicate that this does not commonly occur in RVFV (Bird *et al.* 2007).

A part of this study involved serial passaging of two strains of RVFV through two different propagation systems in order to investigate if these routine laboratory procedures would induce any sequence variations within the S segment of the virus. Comparison of sequencing data for each strain analyzed before passaging and after 10 passages in Vero cells and 10 passages in mice did not reveal any mutations. These results are of great importance with regards to having confidence in the originality of virus genomes of the strains analyzed in this study, since all of them were subjected to low passage either in *in vivo* and/or in *in vitro* amplification systems, before RNA was extracted for sequence analysis. The NCRs of RVFV have been shown to be the most conserved. The 5' and 3' NCRs had only two and five mutations, respectively, among the 75 strain sequences. However, these few mutations could still be of importance. The 5' and 3' NCRs of phleboviruses are complementary, which can lead to the formation of circular or panhandle form of RNA (Bouloy *et al.* 1973; Samso *et al.* 1976; Hewlett *et al.* 1977; Pardigon *et al.* 1982), and it has previously been shown that a point mutation in the BUNV S segment at nucleotide 16 resulted in the formation of a loop structure in the panhandle, which caused a decrease in the free energy resulting in a strong increase in N mRNA transcription (Kohl *et al.* 2003). The possible biological significance of mutations in the NCRs found in this study requires further investigation.

The IGR of the S segment was found to be the most variable region, with a maximum pairwise difference of 4.8%. Like the rest of the S segment there were several transitions and transversions. Apart from a deletion found in the 3'NCR of the South African strain SPU77RSA08 (Table 1), the IGR is the only region with insertions and deletions. In several other *Bunyaviridae* the IGR has been found to form stem-loops structures, playing an important role in gene folding (Freier *et al.* 1986; Emery and Bishop 1987), but it is not certain whether the IGR of the RVFV S segment forms loops as the IGR of SFSV, which is most closely related to RVFV, does not form any stem-loop structures (Marriot *et al.* 1989).

The IGR is also the site of transcription termination, thus sequence variations of these termination sites could affect transcriptional termination. The pentanucleotide motifs reported by Albarino *et al.* (2007) were found to be highly conserved in the IGRs of all 75 RVFV strains. These were followed by the predicted C/G homopolymeric repeats, although some strains had longer C/G repeats than others. Ikegami *et al.* (2007) have recently shown that these polymeric C or G sequences found upstream of the CGUCG motif are also involved in efficient transcriptional termination. It has been shown that DNA-dependant RNA polymerases of prokaryotes and eukaryotes undergo slippage during transcription of homopolymeric sequences (Uptain *et al.* 1997) and that RNA-dependant RNA polymerases of negative-strand RNA viruses experience a similar slippage during transcription (Jacques *et al.* 1994; Barr *et al.* 1997). The termination signal motifs were found to function independently of these C/G repeats, and only deletion of the transcription termination motif disrupts

specific mRNA termination. These findings seem to rule out a secondary structure involving this region or some other role for this C/G-rich sequence in mRNA transcription (Albarino *et al.* 2007).

The N gene was found to have nearly the same number of mutations as the NSs gene, but the majority were silent mutations, which is not surprising as the nucleocapsid protein is vital to RVFV replication (Emerson and Wagner 1972) and any amino acid change that would affect its function might be lethal to the virus. It is possible that such mutations have occurred but were so detrimental that the virus was incapable of replication. The N protein has been found to be more conserved within the *Bunyaviridae* than the NSs protein (Giorgi *et al.* 1991). Studies comparing the amino acid sequences of the UUKV N protein with PTV and SFSV showed their homology to be 35 and 32% respectively. When the NSs protein was compared, the relatedness was much lower, with only 15% homology (Simons *et al.* 1990).

In this study, the NSs gene was found to be highly variable in terms of nucleotide substitutions, though these did not all result in amino acid changes. As the NSs protein function depends on its ability to bind the p44 and XPB of the TFIIH transcription factor (Le May et al. 2004), any amino acid changes that would affect its secondary structure could have either a negative or positive effect. Cysteine is a hydrophobic amino acid and is highly reactive, capable of reacting with another cysteine to form a disulphide bond, a covalent bond that functions to stabilize the three-dimensional structure of a protein (Hames and Hooper 2000). Therefore, mutations within the cysteine residues of the NSs protein might influence its ability to sequester the p44 and XPB subunits of the TFIIH transcription factor, and subsequently influence its ability to inhibit the innate immune system and affect the virulence of RVFV strains. In a previous study, an amino acid sequence alignment of the NSs protein of several RVFV strains showed that the five cysteine residues at positions 39, 40, 150, 179 and 195 are conserved (Sall et al. 1997). These cysteine residues were found to be also conserved in all 75 strains analyzed in this study. In addition, it was found that at position 67 there was a missense mutation that resulted in a cysteine in two strains, the SNS strain and the Zambian strain SPU45ZAMB85. The SNS strain is a vaccine virus, and even though this amino acid change alone my not be responsible for its attenuation, as the Zambian strain is not attenuated, it might

be part of multiple variations that contribute to its attenuation. Bird *et al.* (2008) have recently shown that a genetically-engineered RVFV which lacks non-structural protein genes, the NSs gene alone or the NSs/NSm genes in combination, was shown to be highly attenuated, with no detectable viremia and clinical illness observed after lethal challenge of rats (Bird *et al.* 2008).

Results of this study clearly demonstrate that, in general, isolates of RVFV from similar historic and geographic origins tend to cluster together (Figure 12). Similar to previous reports (Sall et al. 1999), the present phylogenetic analysis defined three broad genetic lineages, namely western African, Egyptian and central, eastern and southern African. The Egyptian and western African lineages show the least degree of evolution, whilst the central, eastern and southern African strains show a higher degree of genetic diversity. One possible explanation for the lower genetic diversity within the Egyptian and western African lineages is the relatively recent introduction of RVFV to these regions, and possibly also due to differences in natural mechanisms involved in RVFV maintenance between the various geographic parts of Africa. It is not fully understood how RVFV survives during inter-epidemic periods, but transovarial transmission in mosquitoes and the ability of the virus to persist in transovarial-infected mosquito eggs over long periods of dry seasons is most likely to play an important role (Davies 1975; Linthicum et al. 1985). The dynamics of RVFV transmission within the cryptic cycle, between and within the wildlife-livestockhuman interface, which is likely driven by various competent vectors and genetic susceptibility of host vertebrates, might also greatly influence the evolution and ecology of the virus. Other possible factors preventing high genetic divergence amongst ecologically and biologically diverse strains of RVFV were recently discussed by Bird et al. (2007), and include a "double filter" system. This concept involves maintaining the number of persistently infected mosquitoes above a critical population size, which is achieved by RVFVs ability to infect suitable mammalian amplification hosts easily, which in turn serve as reservoirs for the infection of large numbers of naïve mosquitoes (Bird et al. 2007). Any genetic variations that would limit the host range of RVFV could be detrimental to its survival.
The clustering of RVFV strains within the phylogenetic tree derived from the alignment of the S segment sequences suggests that several different strains of RVFV can co-circulate or be co-dormant within an area, but also that closely related strains are maintained within an area for a long time. For example, among the South African strains, the Ar20368RSA81 strains seemed to be very distantly related to the Ar74RSA55, H1825RSA75 and Ar12568RSA71 strains, and the H1825RSA75 and Ar12568RSA71 strains are very closely related. Another example are the Kenyan isolates B1143KEN77 and 214445KEN83, which were very closely related even though they were isolated years apart.

With a vector such as the mosquito it is easy for RVFV to travel vast distances. Infected mosquitos can transmit the virus to livestock, which in turn act as reservoirs that move to various regions. Infected moquitos can also move great distances by high winds and then infect livestock in the area they end up in. Another possibility it that transovarial-infected mosquito eggs can be carried by animals and even migrating birds to different areas. A good example of how one strain has been spread over vast distances is the 1979 Madagascar strain Ar811MAD79, of the Egyptian lineage, which was found to be closely related to the Zimbabwean strain VRL2250ZIM74, isolated in this country in 1974. Another example is the two West African isolates, ANK3837GUI81 and ANK6087GUI84, which were found to belong to the central, eastern and southern African cluster. These results demonstrate a widespread movement of different RVFV strains throughout Africa, and highlight the possibility of the virus spreading to the rest of the world. Furthermore, the recent and first occurrence of severe outbreaks of RVF in humans and livestock on the Saudi Arabian Peninsula in 2000 (Shoemaker et al. 2002) confirms the virus's ability to unexpectedly extend its distribution outside its traditional geographical confines.

Generated sequencing data contributes to global phylogenetic characterization of RVFV isolates and molecular epidemiology of the virus. In addition, findings of this study will further aid investigation on reassortment events occurring between strains of RVFV and genetically related viruses, the role of NSs protein in the replicative cycle of the virus, the pathogenic effects of NSs within the RVFVinfected host cells, and might help to identify molecular basis of RVFV virulence.

Chapter 5: References

- Abdel-Wahab, K. S., L. M. El Baz, E. M. El-Tayeb, H. Omar, M. A. Ossman and W. Yasin (1978). "Rift Valley Fever virus infections in Egypt: Pathological and virological findings in man." <u>Trans R Soc Trop Med Hyg</u> 72(4): 392-6.
- Abdo-Salem, S., G. Gerbier, P. Bonnet, M. Al-Qadasi, A. Tran, E. Thiry, G. Al-Eryni and F. Roger (2006). "Descriptive and spatial epidemiology of Rift valley fever outbreak in Yemen 2000-2001." <u>Ann N Y Acad Sci</u> 1081: 240-2.
- Accardi, L., C. Prehaud, P. Di Bonito, S. Mochi, M. Bouloy and C. Giorgi (2001). "Activity of Toscana and Rift Valley fever virus transcription complexes on heterologous templates." J Gen Virol 82(Pt 4): 781-5.
- Akashi, H. and D. H. Bishop (1983). "Comparison of the sequences and coding of La Crosse and snowshoe hare bunyavirus S RNA species." <u>J Virol</u> **45**(3): 1155-8.
- Al-Hazmi, M., E. A. Ayoola, M. Abdurahman, S. Banzal, J. Ashraf, A. El-Bushra, A. Hazmi, M. Abdullah, H. Abbo, A. Elamin, T. Al-Sammani el, M. Gadour, C. Menon, M. Hamza, I. Rahim, M. Hafez, M. Jambavalikar, H. Arishi and A. Aqeel (2003). "Epidemic Rift Valley fever in Saudi Arabia: a clinical study of severe illness in humans." <u>Clin Infect Dis</u> 36(3): 245-52.
- Albarino, C. G., B. H. Bird and S. T. Nichol (2007). "A shared transcription termination signal on negative and ambisense RNA genome segments of Rift Valley fever, sandfly fever Sicilian, and Toscana viruses." <u>J Virol</u> 81(10): 5246-56.
- Anderson, G. W., Jr. and C. J. Peters (1988). "Viral determinants of virulence for Rift Valley fever (RVF) in rats." <u>Microb Pathog</u> **5**(4): 241-50.
- Anonymous (2007a). "Outbreaks of Rift Valley fever in Kenya, Somalia and United Republic of Tanzania, December 2006-April 2007." <u>Wkly Epidemiol Rec</u> **82**(20): 169-78.
- Anonymous (2007b). "Outbreak news. Rift Valley fever, Sudan." <u>Wkly Epidemiol</u> <u>Rec</u> 82(46): 401-2.
- Arthur, R. R., M. S. el-Sharkawy, S. E. Cope, B. A. Botros, S. Oun, J. C. Morrill, R. E. Shope, R. G. Hibbs, M. A. Darwish and I. Z. Imam (1993). "Recurrence of Rift Valley fever in Egypt." <u>Lancet</u> 342(8880): 1149-50.
- Assaad, F., F. G. Davies, G. A. Eddy, R. El Karamany, J. M. Meegan, Y. Ozawa, A. Shimshony, R. E. Shope, J. Walker and R. J. Yedloutschnig (1983). "The use of veterinary vaccines for prevention and control of Rift Valley fever: memorandum from WHO/FAO meeting." <u>Bull World Health Organ</u> 61: 261.
- Balkhy, H. H. and Z. A. Memish (2003). "Rift Valley fever: an uninvited zoonosis in the Arabian peninsula." <u>Int J Antimicrob Agents</u> 21(2): 153-7.

- Barnes, W. M. (1994). "PCR amplification of up to 35-kb DNA with high fidelity and high yield from lambda bacteriophage templates." <u>Proc Natl Acad Sci U S A</u> 91(6): 2216-20.
- Barr, J. N., S. P. Whelan and G. W. Wertz (1997). "cis-Acting signals involved in termination of vesicular stomatitis virus mRNA synthesis include the conserved AUAC and the U7 signal for polyadenylation." <u>J Virol</u> 71(11): 8718-25.
- Bi, Z., P. B. H. Formenty and C. E. Roth (2008). "Hantavirus infection: a review and global update." J Infect Dev Countr **2**(1): 3-23.
- Billecocq, A., M. Spiegel, P. Vialat, A. Kohl, F. Weber, M. Bouloy and O. Haller (2004). "NSs protein of Rift Valley fever virus blocks interferon production by inhibiting host gene transcription." <u>J Virol</u> 78(18): 9798-806.
- Bilsel, P. A., R. B. Tesh and S. T. Nichol (1988). "RNA genome stability of Toscana virus during serial transovarial transmission in the sandfly Phlebotomus perniciosus." <u>Virus Res</u> 11(1): 87-94.
- Bird, B. H., C. G. Albarino, A. L. Hartman, B. R. Erickson, T. G. Ksiazek and S. T. Nichol (2008). "Rift valley fever virus lacking the NSs and NSm genes is highly attenuated, confers protective immunity from virulent virus challenge, and allows for differential identification of infected and vaccinated animals." J <u>Virol</u> 82(6): 2681-91.
- Bird, B. H., M. L. Khristova, P. E. Rollin, T. G. Ksiazek and S. T. Nichol (2007). "Complete genome analysis of 33 ecologically and biologically diverse Rift Valley fever virus strains reveals widespread virus movement and low genetic diversity due to recent common ancestry." J Virol 81(6): 2805-16.
- Bishop, D. H., C. H. Calisher, J. Casals, M. P. Chumakov, S. Y. Gaidamovich, C. Hannoun, D. K. Lvov, I. D. Marshall, N. Oker-Blom, R. F. Pettersson, J. S. Porterfield, P. K. Russell, R. E. Shope and E. G. Westaway (1980). "Bunyaviridae." Intervirology 14(3-4): 125-43.
- Bishop, D. H. L., M. E. Gay and Y. Matsuoko (1983). "Nonviral heterogeneous sequences are present at the 5' ends of snowshoe hare bunyavirus S complementary RNA." <u>Nucleic Acids Res</u> 11: 6409-6418.
- Bishop, D. H. L. and R. E. Shope (1979). Bunyaviridae <u>Comprehensive Virology</u>. H. F.-C. R. Wagner. New York, Plenum Press. 14: 1-156.
- Blakqori, G., G. Kochs, O. Haller and F. Weber (2003). "Functional L polymerase of La Crosse virus allows in vivo reconstitution of recombinant nucleocapsids." J <u>Gen Virol</u> 84(Pt 5): 1207-14.
- Bouloy, M., C. Janzen, P. Vialat, H. Khun, J. Pavlovic, M. Huerre and O. Haller (2001). "Genetic evidence for an interferon-antagonistic function of rift valley fever virus nonstructural protein NSs." J Virol 75(3): 1371-7.

- Bouloy, M., S. Krams-Ozden, F. Horodniceanu and C. Hannoun (1973). "Three segment RNA genome of Lumbo virus (bunyavirus)." <u>Intervirology</u> 2(3): 173-180.
- Bouloy, M., N. Pardigon, P. Vialat, S. Gerbaud and M. Girard (1990).
 "Characterization of the 5' and 3' ends of viral messenger RNAs isolated from BHK21 cells infected with Germiston virus (Bunyavirus)." <u>Virology</u> 175(1): 50-8.
- Bouloy, M., S. J. Plotch and R. M. Krug (1978). "Globin mRNAs are primers for the transcription of influenza viral RNA in vitro." <u>Proc Natl Acad Sci U S A</u> **75**(10): 4886-90.
- Brigden, A., F. Weber, J. F. Fazakerley and R. M. Elliott (2001). "Bunyamwera Bunyavirus Nonstructural Protein NSs is a Nonessential Gene Product that Contributes to Viral Pathogenesis." <u>Proc Natl Acad Sci U S A</u> 98(2): 664-669.
- Brown, J. L., J. W. Dominik and R. L. Morrissey (1981). "Respiratory infectivity of a recently isolated Egyptian strain of Rift Valley fever virus." <u>Infect Immun</u> 33(3): 848-53.
- Caplen, H., C. J. Peters and D. H. Bishop (1985). "Mutagen-directed attenuation of Rift Valley fever virus as a method for vaccine development." J Gen Virol 66 (Pt 10): 2271-7.
- CDC (1994). "Rift Valley fever--Egypt, 1993." <u>MMWR Morb Mortal Wkly Rep</u> **43**(38): 693, 699-700.
- CDC (1998). "Rift Valley Fever--East Africa, 1997-1998." <u>MMWR Morb Mortal</u> <u>Wkly Rep</u> **47**(13): 261-4.
- CDC (2000). "Outbreak of Rift Valley fever--Saudi Arabia, August-October, 2000." <u>MMWR Morb Mortal Wkly Rep</u> **49**(40): 905-8.
- CDC (2007). "Rift Valley fever outbreak--Kenya, November 2006-January 2007." <u>MMWR Morb Mortal Wkly Rep</u> **56**(4): 73-6.
- Coetzer, J. A. and B. J. Barnard (1977). "Hydrops amnii in sheep associated with hydranencephaly and arthrogryposis with wesselsbron disease and rift valley fever viruses as aetiological agents." <u>Onderstepoort J Vet Res</u> **44**(2): 119-26.
- Collett, M. S. (1986). "Messenger RNA of the M segment RNA of Rift Valley fever virus." <u>Virology</u> **151**(1): 151-6.
- Dasgupta, A. (2004). "Targeting TFIIH to inhibit host cell transcription by Rift Valley Fever Virus." <u>Mol Cell</u> **13**(4): 456-8.
- Daubney, R., J. R. Hudson and P. C. Garnham (1931). "Enzootic hepatitis or Rift Valley fever: an undescribed virus disease of sheep, catle and man from East Africa." J Pathol Bacteriol 34: 545-579.

- Davies, F. G. (1975). "Observations on the epidemiology of Rift Valley fever in Kenya." J Hyg (Lond) 75(2): 219-30.
- Digoutte, J. P. (1981). "Viruses identified from 1963 to 1981." <u>Rapport sur le</u> fonctionement technique de l'Institut Pasteur de Dakar
- Digoutte, J. P., R. Cordellier, Y. Robin, F. X. Pajot and B. Geoffroy (1974a). "[Zinga virus (Ar B 1976), a new arbovirus isolated in central africa (author's transl)]." <u>Ann Microbiol (Paris)</u> 125B(1): 107-18.
- Digoutte, J. P., J. C. Jacobi, Y. Robin and V. J. Gagnard (1974b). "[Zinga virus infection in man]." <u>Bull Soc Pathol Exot Filiales</u> 67(5): 451-7.
- Digoutte, J. P. and C. J. Peters (1989). "General aspects of the 1987 Rift Valley fever epidemic in Mauritania." <u>Res Virol</u> **140**(1): 27-30.
- Dimmock, N. J., A. J. Easton and K. N. Leppard (2001). <u>Introduction to Modern</u> <u>Virology</u>, Blackwell Science
- Dunn, E. F., D. C. Pritlove, H. Jin and R. M. Elliott (1995). "Transcription of a recombinant bunyavirus RNA template by transiently expressed bunyavirus proteins." <u>Virology</u> 211(1): 133-43.
- Elfadil, A. A., K. A. Hasab-Allah, O. M. Dafa-Allah and A. A. Elmanea (2006). "The persistence of rift valley fever in the Jazan region of Saudi Arabia." <u>Rev Sci</u> <u>Tech</u> **25**(3): 1131-6.
- Elliott, R. M. (1996). The Bunyaviridae. New York, Plenum Press.
- Eloit, M. (2008). Rift Valley fever, Mayotte (Comoros France), WAHID.
- Emerson, S. U. and R. R. Wagner (1972). "Dissociation and reconstitution of the transcriptase and template activities of vesicular stomatitis B and T virions." J <u>Virol</u> 10(2): 297-309.
- Emery, V. C. and D. H. L. Bishop (1987). "Characterization of Punto Toro S mRNA species and identification of an inverted complementary sequence in the intergenic region of Punto Toro phlebovirus ambisense S RNA that is involved in mRNA transcription termination "<u>Virology</u> 156: 1-11.
- Eshita, Y., B. Ericson, V. Romanowski and D. H. Bishop (1985). "Analyses of the mRNA transcription processes of snowshoe hare bunyavirus S and M RNA species." J Virol 55(3): 681-9.
- Evans, A., F. Gakuya, J. T. Paweska, M. Rostal, L. Akoolo, V. A. N. V. PJ, T. Manyibe, J. M. Macharia, T. G. Ksiazek, D. R. Feikin, R. F. Breiman and M. Kariuki Njenga (2007). "Prevalence of antibodies against Rift Valley fever virus in Kenyan wildlife." <u>Epidemiol Infect</u>: 1-9.
- Felsenstein, J. (1985). "Confidence limits on phylogenies: An approach using the bootstrap." <u>Evolution</u> **39**: 783-791.

- Findlay, G. M. (1931). "Rift Valley fever or enzootic hepatitis " <u>Trans R Soc Trop</u> <u>Med Hyg</u> 25(4): 229-262.
- Flick, K., J. W. Hooper, C. S. Schmaljohn, R. F. Pettersson, H. Feldmann and R. Flick (2003). "Rescue of Hantaan virus minigenomes." <u>Virology</u> **306**(2): 219-24.
- Flick, R. and R. F. Pettersson (2001). "Reverse genetics system for Uukuniemi virus (Bunyaviridae): RNA polymerase I-catalyzed expression of chimeric viral RNAs." J Virol 75(4): 1643-55.
- Francis, T. and T. P. Magill (1935). "Rift Valley fever: A report of 3 cases of laboratory infection and the experimental transmission of the disease in ferrets." J Exp Med 62: 433-447.
- Freier, S. M., R. Kierzek, J. A. Jaeger, N. Sugimoto, M. H. Caruthers, T. Neilson and D. H. Turner (1986). "Improved free-energy parameters for predictions of RNA duplex stability." <u>Proc Natl Acad Sci U S A</u> 83(24): 9373-7.
- Gentsch, J. and D. H. Bishop (1976). "Recombination and complementation between temperature-sensitive mutants of a Bunyavirus, snowshoe hare virus." J Virol **20**(1): 351-4.
- Gentsch, J. R. and D. L. Bishop (1979). "M viral RNA segment of bunyaviruses codes for two glycoproteins, G1 and G2." J Virol **30**(3): 767-70.
- Georges, A. J., S. A. Wahid, D. Y. Meunier, M. C. Georges, J. F. Saluzzo, C. J. Peters, J. B. McCormick and J. P. Gonzalez (1983). "Serological evidence of endemic Zinga virus and Rift Valley Fever virus in Central African Republic." <u>Lancet</u> 1(8337): 1338.
- Giorgi, C., L. Accardi, L. Nicoletti, M. C. Gro, K. Takehara, C. Hilditch, S. Morikawa and D. H. Bishop (1991). "Sequences and coding strategies of the S RNAs of Toscana and Rift Valley fever viruses compared to those of Punta Toro, Sicilian Sandfly fever, and Uukuniemi viruses." <u>Virology</u> 180(2): 738-53.
- Goodbourn, S., L. Didcock and R. E. Randall (2000). "Interferons: cell signalling, immune modulation, antiviral response and virus countermeasures." J Gen <u>Virol</u> **81**(Pt 10): 2341-64.
- Hames, B. D. and N. M. Hooper (2000). Amino acids and proteins. <u>Instant notes:</u> <u>Biochemistry</u>. Oxford, BIOS: 19-23.
- Hewlett, M. J., R. F. Pettersson and D. Baltimore (1977). "Circular forms of Uukuniemi virion RNA: an electron microscopic study." <u>J Virol</u> 21(3): 1085-93.
- Hoogstraal, H., J. M. Meegan, G. M. Khalil and F. K. Adham (1979). "The Rift Valley fever epizootic in Egypt 1977-78. 2. Ecological and entomological studies." <u>Trans R Soc Trop Med Hyg</u> **73**(6): 624-9.
- Hutchinson, K. L., C. J. Peters and S. T. Nichol (1996). "Sin Nombre virus mRNA synthesis." <u>Virology</u> 224(1): 139-49.

- Iben, S., H. Tschochner, M. Bier, D. Hoogstraten, P. Hozak, J. M. Egly and I. Grummt (2002). "TFIIH plays an essential role in RNA polymerase I transcription." <u>Cell</u> 109(3): 297-306.
- Ihara, T., H. Akashi and D. H. Bishop (1984). "Novel coding strategy (ambisense genomic RNA) revealed by sequence analyses of Punta Toro Phlebovirus S RNA." <u>Virology</u> 136(2): 293-306.
- Ihara, T., Y. Matsuura and D. H. Bishop (1985). "Analyses of the mRNA transcription processes of Punta Toro phlebovirus (Bunyaviridae)." <u>Virology</u> 147(2): 317-25.
- Ikegami, T. and S. Makino (2004). "[Rift Valley fever virus]." Uirusu 54(2): 229-35.
- Ikegami, T., C. J. Peters and S. Makino (2005a). "Rift valley fever virus nonstructural protein NSs promotes viral RNA replication and transcription in a minigenome system." <u>J Virol</u> 79(9): 5606-15.
- Ikegami, T., S. Won, C. J. Peters and S. Makino (2005b). "Rift Valley fever virus NSs mRNA is transcribed from an incoming anti-viral-sense S RNA segment." J <u>Virol</u> **79**(18): 12106-11.
- Ikegami, T., S. Won, C. J. Peters and S. Makino (2007). "Characterization of Rift Valley fever virus transcriptional terminations." <u>J Virol</u> **81**(16): 8421-38.
- Jaaskelainen, K. M., P. Kaukinen, E. S. Minskaya, A. Plyusnina, O. Vapalahti, R. M. Elliott, F. Weber, A. Vaheri and A. Plyusnin (2007). "Tula and Puumala hantavirus NSs ORFs are functional and the products inhibit activation of the interferon-beta promoter." J Med Virol 79(10): 1527-36.
- Jacques, J. P., S. Hausmann and D. Kolakofsky (1994). "Paramyxovirus mRNA editing leads to G deletions as well as insertions." <u>EMBO J</u> **13**(22): 5496-503.
- Jin, H. and R. M. Elliott (1993). "Non-viral sequences at the 5' ends of Dugbe nairovirus S mRNAs." J Gen Virol 74 (Pt 10): 2293-7.
- Jouan, A., I. Coulibaly, F. Adam, B. Philippe, O. Riou, B. Leguenno, R. Christie, N. Ould Merzoug, T. Ksiazek and J. P. Digoutte (1989). "Analytical study of a Rift Valley fever epidemic." <u>Res Virol</u> 140(2): 175-86.
- Jupp, P. G., A. Kemp, A. Grobbelaar, P. Lema, F. J. Burt, A. M. Alahmed, D. Al Mujalli, M. Al Khamees and R. Swanepoel (2002). "The 2000 epidemic of Rift Valley fever in Saudi Arabia: mosquito vector studies." <u>Med Vet Entomol</u> 16(3): 245-52.
- Karlen, A. (1996). A garden of germs <u>Plague's progress: a social history of man and disease</u>. London, Cassell Group: 149-173.
- Kimura, M. (1980). "A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences " J Mol <u>Evol</u> 16: 111-120.

- Kohl, A., A. Bridgen, E. Dunn, J. N. Barr and R. M. Elliott (2003). "Effects of a point mutation in the 3' end of the S genome segment of naturally occuring and engineered Bunyamwera viruses." J Gen Virol 84: 789-793.
- Kormelink, R., F. van Poelwijk, D. Peters and R. Goldbach (1992). "Non-viral heterogeneous sequences at the 5' ends of tomato spotted wilt virus mRNAs." J Gen Virol 73 (Pt 8): 2125-8.
- Krug, R. M. (1981). "Priming of influenza viral RNA transcription by capped heterologous RNAs." <u>Curr Top Microbiol Immunol</u> **93**: 125-49.
- Kuismanen, E., K. Hedman, J. Saraste and R. F. Pettersson (1982). "Uukuniemi virus maturation: accumulation of virus particles and viral antigens in the Golgi complex." <u>Mol Cell Biol</u> **2**(11): 1444-58.
- Le May, N., S. Dubaele, L. Proietti De Santis, A. Billecocq, M. Bouloy and J. M. Egly (2004). "TFIIH transcription factor, a target for the Rift Valley hemorrhagic fever virus." <u>Cell</u> **116**(4): 541-50.
- Le May, N., N. Gauliard, A. Billecocq and M. Bouloy (2005). "The N terminus of Rift Valley fever virus nucleoprotein is essential for dimerization." J Virol **79**(18): 11974-80.
- Le May, N., Z. Mansuroglu, P. Leger, T. Josse, G. Blot, A. Billecocq, R. Flick, Y. Jacob, E. Bonnefoy and M. Bouloy (2008). "A SAP30 complex inhibits IFNbeta expression in Rift Valley fever virus infected cells." <u>PLoS Pathog</u> 4(1): e13.
- Linthicum, K. J., F. G. Davies, A. Kairo and C. L. Bailey (1985). "Rift Valley fever virus (family Bunyaviridae, genus Phlebovirus). Isolations from Diptera collected during an inter-epizootic period in Kenya." J Hyg (Lond) 95(1): 197-209.
- Lopez, N., R. Muller, C. Prehaud and M. Bouloy (1995). "The L protein of Rift Valley fever virus can rescue viral ribonucleoproteins and transcribe synthetic genome-like RNA molecules." J Virol 69(7): 3972-9.
- Madani, T. A., Y. Y. Al-Mazrou, M. H. Al-Jeffri, A. A. Mishkhas, A. M. Al-Rabeah, A. M. Turkistani, M. O. Al-Sayed, A. A. Abodahish, A. S. Khan, T. G. Ksiazek and O. Shobokshi (2003). "Rift Valley fever epidemic in Saudi Arabia: epidemiological, clinical, and laboratory characteristics." <u>Clin Infect</u> <u>Dis</u> 37(8): 1084-92.
- Marriot, A. C., V. K. Ward and P. A. Nuttal (1989). "The S RNA segment of Sandfly fever Sicilian virus:evidence for an amibisense genome." <u>Virology</u> **169**: 341-345.
- Mathiot, C., J. J. Ribot, Y. Clerc, P. Coulanges and N. Rasolofonirina (1984). "[Rift valley fever and Zinga virus: a pathogenic arbovirus in man and animal new for Madagascar]." <u>Arch Inst Pasteur Madagascar</u> **51**(1): 125-33.

- Meegan, J. M. (1979). "The Rift Valley fever epizootic in Egypt 1977-78. 1. Description of the epizzotic and virological studies." <u>Trans R Soc Trop Med</u> <u>Hyg</u> **73**(6): 618-23.
- Meegan, J. M., J. P. Digoutte, C. J. Peters and R. E. Shope (1983). "Monoclonal antibodies to identify Zinga virus as Rift Valley Fever virus." <u>Lancet</u> 1(8325): 641.
- Meegan, J. M., H. Hoogstraal and M. I. Moussa (1979). "An epizootic of Rift Valley fever in Egypt in 1977." <u>Vet Rec</u> **105**(6): 124-5.
- Mellor, P. S. and C. J. Leake (2000). "Climatic and geographic influences on arboviral infections and vectors." <u>Rev Sci Tech</u> **19**(1): 41-54.
- Miller, W. S., P. Demchak, C. R. Rosenberger, J. W. Dominik and J. L. Bradshaw (1963). "Stability and infectivity of airborne yellow fever and Rift Valley fever viruses "<u>Am J Hyg</u> 77: 114-121.
- Morvan, J., D. Fontenille, J. F. Saluzzo and P. Coulanges (1991). "Possible Rift Valley fever outbreak in man and cattle in Madagascar." <u>Trans R Soc Trop Med Hyg</u> **85**(1): 108.
- Morvan, J., J. L. Lesbordes, P. E. Rollin, J. C. Mouden and J. Roux (1992). "First fatal human case of Rift Valley fever in Madagascar." <u>Trans R Soc Trop Med Hyg</u> **86**(3): 320.
- Muller, R., C. Argentini, M. Bouloy, C. Prehaud and D. H. Bishop (1991). "Completion of the genome sequence of Rift Valley fever phlebovirus indicates that the L RNA is negative sense and codes for a putative transcriptase-replicase [corrected]." <u>Nucleic Acids Res</u> 19(19): 5433.
- Muller, R., J. F. Saluzzo, N. Lopez, T. Dreier, M. Turell, J. Smith and M. Bouloy (1995). "Characterization of clone 13, a naturally attenuated avirulent isolate of Rift Valley fever virus, which is altered in the small segment." <u>Am J Trop Med Hyg</u> 53(4): 405-11.
- Murphy, F. A., C. M. Fauquet, D. H. L. Bishop, S. A. Ghabrial, A. W. Jarvis, G. P. Martelli, M. A. Mayo and M. D. Summers (1995). Family *Bunyaviridae*. <u>Virus</u> <u>Taxonomy: Sixth Report of the International Committee on Taxonomy of</u> <u>Viruses</u>. Vienna and New York, Springer-Verlag: 300-315.
- Murphy, F. A., A. K. Harrison and S. G. Whitfield (1973). <u>Bunyaviridae:</u> <u>morphologic and morphogenetic similarities of Bunyamwera supergroup</u> <u>viruses and several other arthropod-borne viruses</u>.
- Nabeth, P., Y. Kane, M. O. Abdalahi, M. Diallo, K. Ndiaye, K. Ba, F. Schneegans, A. A. Sall and C. Mathiot (2001). "Rift Valley fever outbreak, Mauritania, 1998: seroepidemiologic, virologic, entomologic, and zoologic investigations." <u>Emerg Infect Dis</u> 7(6): 1052-4.

- Nichol, S. T., B. J. Beaty, R. M. Elliott, R. Goldbach, A. Plyusnin, C. S. Schmaljohn and R. B. Tesh (2005). Bunyaviridae. <u>Virus Taxonomy: 8th Report of the</u> <u>International Commitee on Taxonomy of Viruses</u>. C. M. Fauquet, M. A. Mayo, J. Maniloff, U. Desselberger and L. A. Ball. Oxford, Academic Press: 695-716.
- Pardigon, N., P. Vialat, M. Girard and M. Bouloy (1982). "Panhandles and hairpin structures at the termini of germiston virus RNAs (Bunyavirus)." <u>Virology</u> 122(1): 191-7.
- Patterson, J. L., B. Holloway and D. Kolakofsky (1984). "La Crosse virions contain a primer-stimulated RNA polymerase and a methylated cap-dependent endonuclease." J Virol 52(1): 215-22.
- Paweska, J., L. Blumberg, J. Weyer, A. Kemp, P. Leman, B. Archer, D. Nkosi and R. Swanepoel (2008). "Rift Valley fever outbreak in South Africa, 2008." <u>Communicable Diseases Surveillance Bulletin</u> 6(2): 1-2.
- Perrone, L. A., K. Narayanan, M. Worthy and C. J. Peters (2007). "The S segment of Punta Toro virus (Bunyaviridae, Phlebovirus) is a major determinant of lethality in the Syrian hamster and codes for a type I interferon antagonist." J <u>Virol</u> 81(2): 884-92.
- Peters, C. J. and K. J. Linthicum (1994). Rift Valley fever. <u>Handbook of zoonoses.</u> <u>Section B: viral zoonoses, 2nd edition</u>. J. S. GW Beran. Boca Raton, CRC Press: 25-138.
- Peters, C. J. and T. W. Slone (1982). "Inbred rat strains mimic the disparate human response to Rift Valley fever virus infection." J Med Virol **10**(1): 45-54.
- Plyusnin, A. (2002). "Genetics of hantaviruses: implications to taxonomy." <u>Arch</u> <u>Virol</u> **147**(4): 665-82.
- Porter, H. F. (1999). Onward to Africa. <u>Forecast: disaster. The future of El Nino</u>. New York, Dell Publishing: 127-144.
- Purse, B. V., P. S. Mellor, D. J. Rogers, A. R. Samuel, P. P. Mertens and M. Baylis (2005). "Climate change and the recent emergence of bluetongue in Europe." <u>Nat Rev Microbiol</u> 3(2): 171-81.

Rakotosamimanan, J. L. H. (2008). Rift Valley fever, Madagascar, WAHID.

- Rice, R. M., B. J. Erlick, R. R. Rosato, G. A. Eddy and S. B. Mohanty (1980). "Biochemical characterization of Rift Valley fever virus." <u>Virology</u> **105**(1): 256-60.
- Ritter, M., M. Bouloy, P. Vialat, C. Janzen, O. Haller and M. Frese (2000). "Resistance to Rift Valley fever virus in Rattus norvegicus: genetic variability within certain 'inbred' strains." J Gen Virol **81**(Pt 11): 2683-8.

- Rosenblum, B. B., L. G. Lee, S. L. Spurgeon, S. H. Khan, S. M. Menchen, C. R. Heiner and S. M. Chen (1997). "New dye-labeled terminators for improved DNA sequencing patterns." <u>Nucleic Acids Res</u> 25(22): 4500-4.
- Rozhon, E. J., P. Gensemer, R. E. Shope and D. H. Bishop (1981). "Attenuation of virulence of a bunyavirus involving an L RNA defect and isolation of LAC/SSH/LAC and LAC/SSH/SSH reassortants." <u>Virology</u> 111(1): 125-38.
- Saitou, N. and M. Nei (1987). "The neighbor-joining method: a new method for reconstructing phylogenetic trees." <u>Mol Biol Evol</u> **4**(4): 406-25.
- Sall, A. A., A. Z. P. M. de, H. G. Zeller, J. P. Digoutte, Y. Thiongane and M. Bouloy (1997). "Variability of the NS(S) protein among Rift Valley fever virus isolates." J Gen Virol 78 (Pt 11): 2853-8.
- Sall, A. A., P. M. Zanotto, O. K. Sene, H. G. Zeller, J. P. Digoutte, Y. Thiongane and M. Bouloy (1999). "Genetic reassortment of Rift Valley fever virus in nature." <u>J Virol</u> 73(10): 8196-200.
- Sall, A. A., P. M. Zanotto, P. Vialat, O. K. Sene and M. Bouloy (1998). "Molecular epidemiology and emergence of Rift Valley fever." <u>Mem Inst Oswaldo Cruz</u> 93(5): 609-14.
- Saluzzo, J. F., G. W. Anderson, Jr., J. F. Smith, D. Fontenille and P. Coulanges (1989). "Biological and antigenic relationship between Rift Valley fever virus strains isolated in Egypt and Madagascar." <u>Trans R Soc Trop Med Hyg</u> 83(5): 701.
- Saluzzo, J. F. and J. F. Smith (1990). "Use of reassortant viruses to map attenuating and temperature-sensitive mutations of the Rift Valley fever virus MP-12 vaccine." <u>Vaccine</u> **8**(4): 369-75.
- Samso, A., M. Bouloy and C. Hannoun (1976). "[Demonstration of circular ribonucleic acid in the Lumbo virus (Bunyavirus)]." <u>C R Acad Sci Hebd</u> <u>Seances Acad Sci D</u> 282(17): 1653-5.
- Schmaljohn, C. and J. W. Hooper (2001). Bunyaviridae: the viruses and their replication. <u>Fields Virology</u>. D. K. BN Fields. Philadelphia, Lippincott Williams & Williams. 2.2.
- Shoemaker, T., C. Boulianne, M. J. Vincent, L. Pezzanite, M. M. Al-Qahtani, Y. Al-Mazrou, A. S. Khan, P. E. Rollin, R. Swanepoel, T. G. Ksiazek and S. T. Nichol (2002). "Genetic analysis of viruses associated with emergence of Rift Valley fever in Saudi Arabia and Yemen, 2000-01." <u>Emerg Infect Dis</u> 8(12): 1415-20.
- Shope, R. E., G. H. Tignor, E. J. Rozhon and D. H. L. Bishop (1981). The association of the bunyavirus middle-sized RNA segment with mouse pathogenicity <u>Replication of negative strand viruses</u> D. B. R. Compans. New York, Elsevier/North Holland Publishing Co.: 146-152.

- Siam, A. L., J. M. Meegan and K. F. Gharbawi (1980). "Rift Valley fever ocular manifestations: observations during the 1977 epidemic in Egypt." <u>Br J</u> <u>Ophthalmol 64</u>(5): 366-74.
- Simons, J. F., U. Hellman and R. F. Pettersson (1990). "Uukuniemi virus S RNA segment: ambisense coding strategy, packaging of complementary strands into virions, and homology to members of the genus Phlebovirus." J Virol 64(1): 247-55.
- Simons, J. F., R. Persson and R. F. Pettersson (1992). "Association of the nonstructural protein NSs of Uukuniemi virus with the 40S ribosomal subunit." J Virol **66**(7): 4233-41.
- Simons, J. F. and R. F. Pettersson (1991). "Host-derived 5' ends and overlapping complementary 3' ends of the two mRNAs transcribed from the ambisense S segment of Uukuniemi virus." J Virol **65**(9): 4741-8.
- Smith, J. F. and D. Y. Pifat (1982). "Morphogenesis of sandfly viruses (Bunyaviridae family)." <u>Virology</u> 121(1): 61-81.
- Swanepoel, R. and N. K. Blackburn (1977). "Demonstration of nuclear immunofluorescence in Rift Valley fever infected cells." J Gen Virol 34(3): 557-61.
- Swanepoel, R. and J. A. W. Coetzer (2004). Rift Valley Fever. <u>Infectious diseases of</u> <u>livestock with special reference to Southern Africa</u>
- J. A. W. Coetzer and R. C. Tustin, Oxford University Press. 2: 1037-1070.
- Takeda, A., K. Sugiyama, H. Nagano, M. Mori, M. Kaido, K. Mise, S. Tsuda and T. Okuno (2002). "Identification of a novel RNA silencing suppressor, NSs protein of Tomato spotted wilt virus." <u>FEBS Lett</u> 532(1-2): 75-9.
- Tamura, K., J. Dudley, M. Nei and S. Kumar (2007). "MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0." <u>Mol Biol</u> <u>Evol</u> 24(8): 1596-9.
- Thomas, D., G. Blakqori, V. Wagner, M. Banholzer, N. Kessler, R. M. Elliott, O. Haller and F. Weber (2004). "Inhibition of RNA polymerase II phosphorylation by a viral interferon antagonist." J Biol Chem 279(30): 31471-7.
- Turell, M. J., K. J. Linthicum, L. A. Patrican, F. G. Davies, A. Kairo and C. L. Bailey (2008). "Vector competence of selected African mosquito (Diptera: Culicidae) species for Rift Valley fever virus." <u>J Med Entomol</u> 45(1): 102-8.
- Turell, M. J., J. F. Saluzzo, R. F. Tammariello and J. F. Smith (1990). "Generation and transmission of Rift Valley fever viral reassortants by the mosquito Culex pipiens." <u>J Gen Virol</u> 71 (Pt 10): 2307-12.
- Uptain, S. M., C. M. Kane and M. J. Chamberlin (1997). "Basic mechanisms of transcript elongation and its regulation." <u>Annu Rev Biochem</u> **66**: 117-72.

- van Velden, D. J., J. D. Meyer, J. Olivier, J. H. Gear and B. McIntosh (1977). "Rift Valley fever affecting humans in South Africa: a clinicopathological study." <u>S</u> <u>Afr Med J</u> 51(24): 867-71.
- Venter, M., S. A. Madhi, C. T. Tiemessen and B. D. Schoub (2001). "Genetic diversity and molecular epidemiology of respiratory syncytial virus over four consecutive seasons in South Africa: identification of new subgroup A and B genotypes." <u>J Gen Virol</u> 82(Pt 9): 2117-24.
- Vialat, P., A. Billecocq, A. Kohl and M. Bouloy (2000). "The S segment of rift valley fever phlebovirus (Bunyaviridae) carries determinants for attenuation and virulence in mice." J Virol **74**(3): 1538-43.
- Vialat, P., R. Muller, T. H. Vu, C. Prehaud and M. Bouloy (1997). "Mapping of the mutations present in the genome of the Rift Valley fever virus attenuated MP12 strain and their putative role in attenuation." <u>Virus Res</u> 52(1): 43-50.
- Von Bonsdorff, C. H. and R. F. Pettersson (1975). "Surface structure of Uukiniemi virus." <u>J Virol</u> 16(5): 1296-1307.
- Weber, F., A. Bridgen, J. K. Fazakerley, H. Streitenfeld, N. Kessler, R. E. Randall and R. M. Elliott (2002). "Bunyamwera bunyavirus nonstructural protein NSs counteracts the induction of alpha/beta interferon." <u>J Virol</u> 76(16): 7949-55.
- Weber, F. and R. M. Elliot (2002). "Antigenic drift, antigenic shift and interferon antagonists: how bunyaviruses counteract the immune system." <u>Virus Res</u> 88: 129-136.
- Weinbren, M. P., M. C. Williams and A. J. Haddow (1957). "A variant of Rift Valley fever virus." <u>S Afr Med J</u> **31**(38): 951-7.
- Weiss, K. (1957). "Rift Valley fever a review." <u>Bulletin of Epizootic Diseases in</u> <u>Africa 5</u>: 431-458.
- Whitehouse, C. (2004). "Crimean-Congo hemorrhagic fever." <u>Antiviral Research</u> 64: 145-160.
- Wilson, M. L., L. E. Chapman, D. B. Hall, E. A. Dykstra, K. Ba, H. G. Zeller, M. Traore-Lamizana, J. P. Hervy, K. J. Linthicum and C. J. Peters (1994). "Rift Valley fever in rural northern Senegal: human risk factors and potential vectors." <u>Am J Trop Med Hyg</u> 50(6): 663-75.
- Woods, C. W., A. M. Karpati, T. Grein, N. McCarthy, P. Gaturuku, E. Muchiri, L. Dunster, A. Henderson, A. S. Khan, R. Swanepoel, I. Bonmarin, L. Martin, P. Mann, B. L. Smoak, M. Ryan, T. G. Ksiazek, R. R. Arthur, A. Ndikuyeze, N. N. Agata and C. J. Peters (2002). "An outbreak of Rift Valley fever in Northeastern Kenya, 1997-98." <u>Emerg Infect Dis</u> 8(2): 138-44.
- Yadani, F. Z., A. Kohl, C. Prehaud, A. Billecocq and M. Bouloy (1999). "The carboxy-terminal acidic domain of Rift Valley Fever virus NSs protein is essential for the formation of filamentous structures but not for the nuclear localization of the protein." <u>J Virol</u> 73(6): 5018-25.

Zeller, H. G., D. Fontenille, M. Traore-Lamizana, Y. Thiongane and J. P. Digoutte (1997). "Enzootic activity of Rift Valley fever virus in Senegal." <u>Am J Trop Med Hyg</u> **56**(3): 265-72.

Chapter 6: Appendix

6.1. Preparation of reagents

6.1.1. EMEM

To 500ml EMEM add 1% L-Glutamine (5ml), 1% Non-essential amino acids (5ml), 1% Pen/Strep antibiotics (5ml) and 2.5% Amphotericin B (12.5ml). For the preparation of growth media, 10% foetal calf serum was added, and for maintenance medium, 2% foetal calf serum was added.

6.1.2. PBS

To 500ml PBS add 5ml Pen/Strep antibiotics

6.1.3. TBE Buffer

To make a 10X TBE buffer, 108g of Tris base and 55 g of Boric acid were dissolved in one litre of distilled water (dH₂O). To this 40 ml of 0.5 M EDTA (pH 8.0) was added. The buffer was transferred to a 1 litre Schott bottle, autoclaved and stored at room temperature.

6.2. Routine laboratory methodologies

6.2.1. RNA extraction using QIAamp kit

Viral RNA was extracted from infective tissue culture using a QIA amp Viral RNA kit (Qiagen, CA, USA), which combines the selective binding properties of a silicagel-based membrane with the speed of microspin. The infective tissue culture supernatant was added to 560 µl of AVL buffer (provided in kit), containing 5.6 µl carrier RNA (provided in kit), in a 1.5 ml microcentrifuge tube. The mixture was then mixed by pulse vortexing and incubated for 10 minutes at room temperature to allow for lysis to occur. The buffer AVL provides highly denaturing conditions to inactivate RNases and to ensure isolation of intact viral RNA. After ten minutes the mixture is briefly centrifuged to remove any droplets from the sides of the tube. A dilution of 96% ethanol in then added to the sample (560 µl) and then mixed by pulse-vortexing and centrifuged to remove droplets. Half of this mixute, 630 µl, was then applied to the QIA amp spin column in a 2 ml collection tube and centrifuge at 6000 x g for 1 minute. This step was then repeated with the remaining mixture and a clean 2 ml collection tube. After transferring the QIAamp spin column to another new collection tube, 500 µl of Buffer AW1 (provided in kit) was added and the tube centrifuged at 6000 x g for 1 minute. This was followed by adding 500 µl Buffer AW2 (provided in kit) to the QIAamp spin column in a new 2 ml collection tube and centrifugation at 20 000 x g for 3 minutes. The QIAamp spin column was then transferred to a clean 1.5 ml microcentrifuge tube. The the QIAamp spin column, 60 µl Buffer AVE (provided in kit) was added, incubated at room temperature for 1 minute and then centrifuged at 6000 x g for 1 minute. The QIA amp spin column was then discarded and the eluted viral RNA was then stored at -20°C or used immediately.

6.2.2. 1.2% Agarose gel

For a 1.2% agarose gel, 1.2 g of agarose was weighed into a clean 500 ml Schott bottle and constituted with 100 ml 1 x TBE buffer. The mixture was boiled in the microwave to completely dissolve the agarose. After allowing the mixture to cool slightly, 0.5 μ g/ml of ethidium bromide (EtBr) was aliquoted into the mixture. EtBr is an intercalating agent that can insert into the DNA double helix and will fluoresce when exposed to ultraviolet (UV) wavelengths. When mixed, the liquid was poured into a casting tray and allowed to set until firm. The gel was then transferred into an electrophoresis chamber filled with 1 x TBE buffer. The samples to be subjected to electrophoresis were mixed with loading dye at a ratio of 1:5 and loaded into the wells of the gel. In the first lane of the gel, 2 μ l of 1kb molecular weight marker was run to aid in determining the length of the DNA fragments. The DNA fragments were viewed under UV light and the resultant image captured.

6.2.3. PCR product clean-up using the Wizard® SV gel and PCR clean-up system

To each PCR reaction, an equal volume of Membrane Binding solution (provided in kit) is added and mixed. The mixture is then transferred into an SV minicolumn, which is in a collection tube, and incubate at room temperature for 1 minute. The SV minicolumn assembly is then centrifuged at 10 000 x g for 1 minute, after which the flow-through is discarded and the minicolumn re-inserted into the collection tube. To each minicolumn, 700 μ l Membrane Wash solution (provided in kit) is added, and then the minicolumn is centrifuged at 10 000 x g for 1 minute, the flow-through discarded and the minicolumn is re-inserted into the collection tube. This is then repeated using 500 μ l of Membrane Wash solution. The minicolumn is then centrifuged for an extra minute at 10 000 x g to remove any excess solution. The minicolumn is then transferred into a sterile 1.5 ml centrifuge tube. To each minicolumn, 30-50 μ l of nuclease free water is added and allowed to incubate at room temperature for 1 minute, after which it is centrifuged at 10 000 x g for 1 minute. The minicolumn is then discarded and the DNA can be stored at 4°C or - 20°C, or alternatively used immediately.

6.2.4. Isopropanol purification of cycle sequencing product

To each well of the 96-well plate containing cycle sequenced product, 80 µl of 80% isopropanol is added and allowed to stand for 15 minutes. The 96-well plate is then centrifuged for 45 minutes at 2 000 x g. The 96-well plate is then flipped to drain the isopropanol, taking care not to loose the cycle sequencing product. The plate is then centrifuged upside down for 1 minute at 750 x g to drain excess isopropanol. The plate is then allowed to air-dry for 5 minutes to evaporate any remaining isopropanol. To the dried cycle sequencing product, 20 µl of Hi-DiTM Formamide (Applied Biosystems, USA) is added. Hi-Di TM Formamide is a highly deionized formamide that contains a stabilizer and is used as an injection solvent in DNA analysis on the ABI Prism[®] DNA analyzer.

6.3. Full S RNA segment sequencing data

		1 40
214445KEN83	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
56KEN65	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
900085MAU88	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
An1000MAD91	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
An991MAD91	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
An999MAD91	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
AnK6087GUI84	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
AnTAMBULEGY94	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
Ar12568RSA71	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
Ar20368RSA81	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
Ar21229SA00	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
Ar74RSA55	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
Ar811MAD79	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
ArD38661SEN81	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
B1143KEN77	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
B314KEN62	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
H1825RSA75	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
LunyoUGA55	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
R1662CAR85	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU10301KEN07	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU10302KEN07	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU10307KEN07	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU10315KEN07	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU12002SOM98	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU152RSA08	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU204ANGL85	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU2207KEN07	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU2214KEN07	(1)	ACACAA <mark>C</mark> GACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU2215KEN07	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU2220KEN07	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU2223KEN07	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU384001KEN97	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU45ZAMB85	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU52001RSA99	(1)	ACACAAAGACCCCCTAGTGCTTATC <mark>T</mark> AGTATATCATGGAT
SPU77NAMB04	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
SPU77RSA08	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
VRL1032ZIM78	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
VRL1290ZIM78	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
VRL1516ZIM78	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
VRL1887ZIM78	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
VRL2230ZIM78	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
VRL763ZIM70	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
VRL825ZIM79	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
ZH501EGY77	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
ZH548EGY77	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT
Consensus	(1)	ACACAAAGACCCCCTAGTGCTTATCAAGTATATCATGGAT

Figure 17. The complete nucleotide sequence alignment of the S RNA segment of the 45 strains of Rift Valley fever virus sequenced in this study. Areas with black lettering and white background show identical nucleotides. Areas with black lettering and yellow background represent non-similar

nucleotides.

		41 80
214445KEN83	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
56KEN65	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
900085MAU88	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
An1000MAD91	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
An991MAD91	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
An999MAD91	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
AnK6087GUI84	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
AnTAMBULEGY94	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
Ar12568RSA71	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
Ar20368RSA81	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
Ar21229SA00	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
Ar74RSA55	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
Ar811MAD79	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
ArD38661SEN81	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
B1143KEN77	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
B314KEN62	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
H1825RSA75	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
LunyoUGA55	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
R1662CAR85	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
SPU10301KEN07	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
SPU10302KEN07	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
SPU10307KEN07	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
SPUIU3I5KENU/	(41)	
SPUIZUUZSOM98	(4⊥) (41)	
SPUISZRSAU8	(4⊥) (41)	
SPUZU4ANGL85	(41) (41)	
SPUZZU/KENU/	(4⊥) (41)	
SPUZZI4KENU7	(41) (41)	
SPUZZIJKENU/	(41) (41)	
SPUZZZUKENU7	(4⊥) (41)	
SPUZZZJALNU /	(41) (41)	
CDII/577MD05	(41) (41)	
SF04JZAMB0J CDU52001DC300	(41) (41)	
SPUJZUUIKSA99 SPUJZUUIKSA99	(41)	
SPU77RSA08	(41)	
VPL10327TM78	(41)	
VRL12907TM78	(41)	
VRL15167TM78	(41)	
VRL18877.TM78	(41)	ТАСТТТССТСТСТСТСТСТСТСТСТСТСТСТССТССТССТ
VRL22307.TM78	(41)	
VRL7637TM70	(41)	ТАСТТТССТСТСТСТСТСТСТСТСТСТСТСТССТССТССТ
VRL8257TM79	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
ZH501EGY77	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
ZH548EGY77	(41)	TACTTTCCTGTGATATCTGTTGATTTGCAGAGTGGTCGTC
Consensus	(41)	ТАСТТТССТСТСТСТСТСТСТСТСТСТСТССТССТССТС
00110011040	· · - /	

		81 120
214445KEN83	(81)	GTGTTGTGTCAGTGGAGTACATTA <mark>T</mark> AGGTGATGGTCCTCC
56KEN65	(81)	GTGTTGTGTCAGTGGAGTACATTAGAGGTGATGGTCCTCC
900085MAU88	(81)	GTGTTGTGTCAGTGGAGTACATTAGAGGTGATGGTCCTCC
An1000MAD91	(81)	GTGTTGTGTCAGTGGAGTACATTA <mark>A</mark> AGGTGATGGTCCTCC
An991MAD91	(81)	GTGTTGTGTCAGTGGAGTACATTA <mark>A</mark> AGGTGATGGTCCTCC
An999MAD91	(81)	GTGTTGTGTCAGTGGAGTACATTA <mark>A</mark> AGGTGATGGTCCTCC
AnK6087GUI84	(81)	GTGTTGTGTCAGTGGAGTACATTAGAGGTGATGGTCCTCC
AnTAMBULEGY94	(81)	GTGTTGTGTCAGTGGAGTAC <mark>T</mark> TTAGAGG <mark>A</mark> GATGGTCCTCC
Ar12568RSA71	(81)	GTGTTGTGTCAGTGGAGTACATTAGAGGTGATGGTCCTCC
Ar20368RSA81	(81)	GTGTTGTGTCAGTGGAGTACATTAGAGGTGATGGTCCTCC
Ar21229SA00	(81)	GTGTTGTGTCAGTGGAGTACATTA <mark>A</mark> AGGTGATGGTCCTCC
Ar74RSA55	(81)	GTGTTGTGTCAGTGGAGTACATTAGAGGTGATGG <mark>C</mark> CCTCC
Ar811MAD79	(81)	GTGTTGTGTCAGTGGAGTAC <mark>T</mark> TTAGAGG <mark>A</mark> GATGGTCCTCC
ArD38661SEN81	(81)	GTGTTGTGTCAGTGGAGTACATTAGAGGTGATGGTCCTCC
B1143KEN77	(81)	GTGTTGTGTCAGTGGAGTACATTAGAGGTGATGGTCCTCC
B314KEN62	(81)	GTGTTGTGTCAGTGGAGTACATTAGAGGTGATGGTCCTCC
H1825RSA75	(81)	GTGTTGTGTCAGTGGAGTACATTAGAGGTGATGGTCCTCC
LunyoUGA55	(81)	GTGTTGTGTCAGTGGAGTACATTAGAGGTGATGGTCCTCC
R1662CAR85	(81)	GTGTTGTGTCAGTGGAGTACATTAGAGGTGATGGTCCTCC
SPU10301KEN07	(81)	GTGTTGTGTCAGTGGAGTACATTA <mark>A</mark> AGGTGATGGTCCTCC
SPU10302KEN07	(81)	GTGTTGTGTCAGTGGAGTACATTAAAGGTGATGGTCCTCC
SPU10307KEN07	(81)	GTGTTGTGTCAGTGGAGTACATTAAAGGTGATGGTCCTCC
SPU10315KEN07	(81)	GTGTTGTGTCAGTGGAGTACATTAAAGGTGATGGTCCTCC
SPUI2002SOM98	(81)	GTGTTGTGTCAGTGGAGTACATTAAAGGTGATGGTCCTCC
SPUI52RSAU8	(81) (81)	GTGTTGTGTCAGTGGAGTACATTA <mark>A</mark> AGGTGATGGTCCTCC
SPU204ANGL85	(81) (81)	GTGTTGTGTGTGGGGGGGGGGGGGGGGGGGGGGGGGGG
SPUZZU/KENU/	(81) (01)	GTGTTGTGTGTGGGGGGGGGGGGGGGGGGGGGGGGGGG
SPUZZI4KENU7	(81) (01)	GTGTTGTGTGTGGGGGGGGGGGGGGGGGGGGGGGGGGG
SPUZZISKENU/	(81) (01)	GTGTTGTGTGTGGGGGGGGGGGGGGGGGGGGGGGGGGG
SPUZZZUKENU7	(81) (01)	GTGTTGTGTGTGGGGGGGGGGGGGGGGGGGGGGGGGGG
SPUZZZSKENU/	(8⊥) (81)	
SPUSO4UUIREN97	(OI)	
SPU45ZAMB85	(8⊥) (81)	
SPUJZUUIRSA99	(0⊥) (01)	
SPU//NAMDU4 CDII77DCA08	(01) (81)	
5EU77K5AU0	(01) (01)	
VRL103221M78 VDT12007TM78	(01) (81)	
VRL129021M78 VDT15167TM78	(01) (81)	
VRL18877TM78	(01)	
VRL22307TM78	(01)	
VRL7637IM70	(81)	
VRI.8257.TM79	(81)	GTGTTGTCAGTGGAGTAGATGAGGGAGGGAGGGCCCCCCCC
ZH501ECY77	(81)	GTGTTGTCAGTGGAGTACTTTAGAGGGAGAGGTCCTCC
ZH548EGY77	(81)	GTGTTGTCAGTGGAGTACTTTAGAGGAGATGGTCCTCC
Concensus	(81)	
CONSCIISUS	$(0 \pm)$	

 214445KEN83 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT 56KEN65 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT An1000MAD91 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT An991MAD91 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT An991MAD91 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT An7030MAD91 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT An7030K97GU184 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT Ar12568RSA71 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT Ar20368RSA81 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT Ar21229SA00 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT Ar21229SA00 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT Ar38661SEN81 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT B1143KEN77 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT B314KEN62 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT H1825RSA75 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT H1825RSA75 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT SPU1030LKEN67 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT SPU1030LKEN67 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT SPU1030LKEN67 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT SPU1030LKEN67 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT SPU1030LKEN67 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT SPU1030LKEN67 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT SPU2020SM98 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT SPU202NKEN67 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT SPU220KEN67 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT VRL156ZLM78 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT VRL156ZLM78 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT VRL156ZLM78 (121) C			121 160
56KEN65(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT900085MA088(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAn991MAD91(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAn991MAD91(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAn8097GU184(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAn7AMBULEGY94(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr12568R5A81(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr21229SA00(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr21229SA00(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr14RSA55(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB1143KEN77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB143KEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2020SM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2020SM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSP	214445KEN83	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
900085MAU88 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTT An1000MAD91 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTT An999MAD91 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTT An7A901LGGY94 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTT An7A081LGGY94 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTT Ar12568RSA71 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTT Ar20368RSA81 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTT Ar2129SA00 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTT Ar2129SA00 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTT Ar38661SEN81 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTT B1143KEN77 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTT Har38661SEN81 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT B314KEN62 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT H1825RSA75 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S010301KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S010301KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S010301KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S010307KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S010307KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S010307KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S010307KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S010307KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S0102205M98 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S0102205M88 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S012205KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S02207KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S02207KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S012215KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S012205KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S012205KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S012215KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT S01232KFN8 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT VRL1290ZIN78 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT VRL1290ZIN78 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT VRL1290ZIN78 (121) CAGGATACCTTATTCT	56KEN65	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
An1000MD91(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAn991MAD91(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTAnK6087GUI84(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTAnTAMBULEGY94(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr12568RSA71(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr20368RSA81(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr21229SA00(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr2148SA57(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr314MAD79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB114XEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB114XEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB114XEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB114XEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB114XEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU	900085MAU88	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
 An991MAD91 (121) CAGGATACCTTATTCTATGGTTGGGCCTGTTGTGTCTTT AnK60870U184 (121) CAGGATACCTTATTCTATGGTTGGGCCTGTTGTGTCTTT AnTAMBULEGY94 (121) CAGGATACCTTATTCTATGGTTGGGCCTGTTGTGTCTTT An2068RSA81 (121) CAGGATACCTTATTCTATGGTTGGGCCTGTTGTGTCTTT Ar21229SA00 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT Ar21229SA00 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT Ar21229SA00 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT Ar31661SEN81 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT Ar31661SEN81 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT B1143KEN77 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT B1143KEN77 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT B144KEN62 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT B144KEN62 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT SPU10301KEN07 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT SPU204ANGL85 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT SPU204KEN07 (12	An1000MAD91	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
An999MAD91(121)CAGGATACCTTATTCATGGTTGGGCCCTGTTGTGTCTTAnrAMBULEGY94(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTAr12568RSA71(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTAr20368RSA81(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTAr2129SA00(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr2129SA00(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr74RSA55(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB114AD79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB114XEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB14XEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTLuny0UG55(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1030LEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1030LEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1030XEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1030XEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU12002S0M98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2204EN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2204EN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2204EN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2204EN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2204EN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2204EN07 <td>An991MAD91</td> <td>(121)</td> <td>CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT</td>	An991MAD91	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
Ank60876U184(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAnTAMBULEGY94(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr20368RSA81(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr20368RSA81(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr21229SA00(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr74RSA55(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr811MAD79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB1143KEN77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB1143KEN77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTH1825RSA75(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU12002S0M98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU221KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU221KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT	An999MAD91	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
AnTAMEULEGY94(121)CAGGATACCTTATTCTATGGTTGGCCCTGTTGTGTCTTAr12568RSA71(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTAr21229SA00(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTAr21229SA00(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr74RSA55(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr386615EN81(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB1143KEN77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB1143KEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTH1825RSA75(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU12002S0M98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT	AnK6087GUI84	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
Ar125688SA71(121)CAGGATACCTTATTCTATGGTTGGCCCCTGTTGTGTCTTAr20368RSA81(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTAr21229SA00(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTAr74RSA55(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTAr811MAD79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTB1143KEN77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTB1143KEN77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTH1825RSA75(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTLunyoUGA55(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10302KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTSPU	AnTAMBULEGY94	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
Ar203688581(121)CAGGATACCTTATTCTATGGTTGGCCCCTGTTGTGTCTTAr21229SA00(121)CAGGATACCTTATTCTATGGTTGGCCCCTGTTGTGTCTTAr21229SA00(121)CAGGATACCTTATTCTATGGTTGGCCCCTGTTGTGTCTTAr811MAD79(121)CAGGATACCTTATTCTATGGTTGGCCCCGTGTGTGTGTCTTAr811MAD79(121)CAGGATACCTTATTCTATGGTTGGCCCCGTGTGTGTGTCTTB114XEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTB114XEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTH1825RSA75(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTSPU202SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTSPU204AN6L85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTSPU2214KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU320KA	Ar12568RSA71	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
Ar21229SA00(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTAr31MAD79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTArD38661SEN81(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB1143KEN77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB1148KEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTH1825RSA75(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTH1825RSA75(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10302KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1202SM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU452AMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU77NAM64(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT <t< td=""><td>Ar20368RSA81</td><td>(121)</td><td>CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT</td></t<>	Ar20368RSA81	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
Ar74RSA55(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTAr811MAD79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB1143KEN77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTB1143KEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTH1825RSA75(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTLunyoUGA55(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTSPU10302KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2028M98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU77NAMB64(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032Z1M78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290Z1M78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1287Z1M78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT <t< td=""><td>Ar21229SA00</td><td>(121)</td><td>CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT</td></t<>	Ar21229SA00	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
Ar811MAD79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTArD38661SEN81(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB1143KEN77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTH1825RSA75(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTLunyoUGA55(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2214KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2200KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU452AMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU77NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL10322IM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2302IM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT <td>Ar74RSA55</td> <td>(121)</td> <td>CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT</td>	Ar74RSA55	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
ArD38661SEN81(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB1143KEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTH325RSA75(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTLunyoUGA55(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10302KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2020XEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2214KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2203KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU452AMB5(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT <td>Ar811MAD79</td> <td>(121)</td> <td>CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT</td>	Ar811MAD79	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
B1143kEN77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTB314kEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTH1825RSA75(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTR1662CAR85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301kEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307kEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307kEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10315kEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307kEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU12002SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2207kEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215kEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215kEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2223kEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU452AMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT </td <td>ArD38661SEN81</td> <td>(121)</td> <td>CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT</td>	ArD38661SEN81	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
B314kEN62(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTH1825RSA75(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTLunyoUGA55(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1020SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2205KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2205KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2205KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2205KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL10322IM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL10322IM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT	B1143KEN77	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
H1825R375(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTLunyoUGA55(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10202SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2214KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU77NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT <td>B314KEN62</td> <td>(121)</td> <td>CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT</td>	B314KEN62	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
LunyoUGA55(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTR1662CAR85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10202SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU152RSA08(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU77NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1962IM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL187ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT </td <td>H1825RSA75</td> <td>(121)</td> <td>CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT</td>	H1825RSA75	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
R1662CAR85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10302KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU12002SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1202SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1202SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1202SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL10322IM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTC	LunyoUGA55	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
SPU10301KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10302KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU12002S0M98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1202SN088(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2214KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU452AMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL63ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL63ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL85ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT<	R1662CAR85	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
SPU10302KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1202SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1202SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU1202SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU120ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2214KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU452AMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL63ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL63ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL63ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL82SZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT <td>SPU10301KEN07</td> <td>(121)</td> <td>CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT</td>	SPU10301KEN07	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
SPU10307KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU12002SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU152RSA08(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2214KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU452AMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU77NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL763ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCAGGATACCTTATCTATGCTTGGGTCCTGTTGTGTCTTT(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTG	SPU10302KEN07	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
SPU10315KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU12002SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU152RSA08(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2214KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU452AMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU77NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1516ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTG	SPU10307KEN07	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
SPU12002SOM98(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU152RSA08(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU45ZAM85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU77NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1516ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL63ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGT	SPU10315KEN07	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
SP0152RSA08(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSP0204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSP02207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSP02214KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSP02220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSP02223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSP02223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSP0452AMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTATSP0452AMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTATSP077NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL10322IM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL10322IM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1516ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL763ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTCTTTCACGATACCTTATTCTATTGCTTTCCTTTCTTTGGGCCCTGTTGTGTCTTT(121)<	SPU12002SOM98	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
SPU204ANGL85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTSPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTSPU2220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTSPU2223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTSPU2223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU452AMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU77NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1516ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL263ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCACCAPACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGCGTCTTCTCCCCCCTGTTGTGTCTTTCACCAPACCTTATTCTATGTTATCCTTCCCCCCCCTTCTCTCTTCTTTT	SPU152RSAU8	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
SPU2207KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTTSPU2214KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSPU2220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSPU2223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSPU45ZAMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSPU77NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCAPSOPSUS(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT	SPU204ANGL85	(121)	CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT
SPU2214KENU7(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU45ZAMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU77NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1516ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL263ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGASACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGASAC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGCGCCCTG	SPU220/KENU/	(121)	
SP02215KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSPU452AMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTASPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSPU77NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTVRL10322IM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL763ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGASABC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGASABC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGASABC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT	SPUZZI4KENU7	$(\perp \angle \perp)$	
SP02220KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU2223KEN07(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU45ZAMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTASPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTASPU77NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSPU77RSA08(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1516ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTVRL763ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGASABC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGASABC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGASABC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGCCTTCTTCTATGGTTGTGTCTTT	SPUZZISKENU/	$(\perp \angle \perp)$	
SP02223KEN07(121)CAGGATACCTTATICTATGGTTGGGCCCTGTTGTGTCTTTSPU384001KEN97(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU45ZAMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTSPU77NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1516ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL263ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGAPANC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGAPANC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGCGTTCTTCTATGGTTGTGTCTTT	SPUZZZUKENU7	$(\perp \angle \perp)$	
SP0384001REN97(121)CAGGATACCTTATICIATGGTTGGGCCCTGTTGTGTCTTTSP045ZAMB85(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSP05001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTATSP077NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSP077RSA08(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1516ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL763ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGASABC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGASABC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGASABC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGASABC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTTCARGASABC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTGTCTTT	SPUZZZSKENU/	$(\perp \angle \perp)$	
SP0432AMB63(121)CAGGATACCTTATICIATGGTTGGGCCCTGTTGTGTGTTTSPU52001RSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTATSPU77NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU77RSA08(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1516ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL763ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCAGGATACCTTATCTATGGTTGGGCCCTGTTGTGTCTTT(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARSANAC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARSANAC(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT	SPUS04UUIREN97	$(\perp \angle \perp)$	
SP03200TRSA99(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU77NAMB04(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTSPU77RSA08(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1516ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL763ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGATACCTTATCTATGGTTGGGCCCTGTTGTGTCTTT(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT	SPU4JZAMBOJ	$(\perp \angle \perp)$ (121)	
SP077RAMB04(121)CAGGATACCTTATICIATGGTTGGGCCCTGTTGTGTCTTTSP077RSA08(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1516ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL763ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGATACCTTATCTATGGTTGGGCCCTGTTGTGTCTTT(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCARGATACCTTATCTATCGTTAGGTTGGGCCCTGTTGTGTCTTT(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT	SFUJZUUIRSA99 CDU77NAMD04	$(\perp \angle \perp)$ (121)	
SF077K3800(121)CAGGATACCTTATICTATGGTTGGGCCCTGTTGTGTCTTTVRL1032ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1516ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL763ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCODSODSUS(121)CACCATACCTTATTCTATGGTTGGGCCCCTGTTGTGTCTTT	SPU//NAMDU4 CDU77DCA08	(121)	
VRL103221M78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1290ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL1516ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL763ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCODSODSUS(121)CACCATACCTTATTCTATGGTTGGGCCCCTGTTGTGTCTTT	VDI 10327TM78	(121)	
VRL129021M76(121)CAGGATACCTTATICTATGGTTGGGCCCTGTTGTGTCTTTVRL1516ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL763ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCODSODSUS(121)CACCATACCTTATTCTATGCTTCCCCCCCCTCTCTCTCTTCT	VRL103221M70 VDT12007TM78	(121)	
VRL151021M76(121)CAGGATACCTTATICIATGGTTGGGCCCTGTTGTGTCTTTVRL1887ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL763ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCODSODSUS(121)CACCATACCTTATTCTATGCTTCCCCCCCCTCTTCTCTT	VRU129021M70 VDT15167TM78	(121)	
VRL100721M70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL2230ZIM78(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL763ZIM70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTCODSODSUS(121)CACCATACCTTATTCTATGCTTCCCCCCCCTCTTCTCTCTTT	VRL18877.TM78	(121)	
VRL225021M70(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTVRL82521M79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTConsonsus(121)CACGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT	VRL22307TM78	(121)	
VRL825ZIM79(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH501EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTZH548EGY77(121)CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTTConsonsus(121)CACCATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT	VRL7637TM70	(±∠⊥) (121)	
ZH501EGY77 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT ZH548EGY77 (121) CAGGATACCTTATTCTATGGTTGGGCCCTGTTGTGTCTTT Consonsus (121) CACCATACCTTATTCTATGGTTGGGCCCCTGTTGTGTCTTT	VRL8257TM79	(121)	CAGGATACCTTATTCTATGGTTGGGCCCCTGTTGTGTCTTT
ZH548EGY77 (121) CACCATACCTTATCTATGGTTGGGCCCTGTTGTGTCTTT Consonsus (121) CACCATACCTTATCTATGCTTCCCCCCCCTCTTCTCTCTC	ZH501EGY77	(121)	CAGGATACCTTATTCTATGGTTGGGCCCCTGTTGTGTCTTT
	ZH548EGY77	(121)	CAGGATACCTTATTCTATGGTTGGGCCCCTGTTGTGTCTTT
	Consensus	(121)	CAGGATACCTTATTCTATGGTTGGGCCCCTGTTGTGTCTTT

		161 200
214445KEN83	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
56KEN65	(161)	CTCATGC <mark>G</mark> CCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
900085MAU88	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
An1000MAD91	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
An991MAD91	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
An999MAD91	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
AnK6087GUI84	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
AnTAMBULEGY94	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
Ar12568RSA71	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
Ar20368RSA81	(161)	CTCATGCACCATCGTCCTAGT <mark>T</mark> ACGAGGTTCGCTTGCGAT
Ar21229SA00	(161)	CTCATGCACCATCGTCCTAGTCACGAGGT <mark>C</mark> CGCTTGCGAT
Ar74RSA55	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
Ar811MAD79	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
ArD38661SEN81	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
B1143KEN77	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
B314KEN62	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
H1825RSA75	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
LunyoUGA55	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
R1662CAR85	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
SPU10301KEN07	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
SPU10302KEN07	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
SPU1030/KEN07	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
SPUIU3I5KENU/	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
SPUI2002SOM98	(161)	CTCATGCACCATCGTCCTAGTCA <mark>T</mark> GAGGTTCGCTTGCGAT
SPUISZRSAU8	(161) (161)	
SPU204ANGL85	(161) (161)	
SPUZZU/KENU/	(161) (161)	
SPUZZI4KENU/ SDU2215VENO7	(101)	
SPUZZIJKENU/	(101)	
SFUZZZUKENU7	(101)	
CDII38/001KEN07	(101)	
SPUSO4001REN97	(101)	
20115200102AMD03	(101)	
SPU77NAMB04	(101)	
SPU77RSA08	(161)	СТСАТССАССАТССТССТАСТСАССАТСССТТСССАТ
VRI.10327.TM78	(161)	СТСАТССАССАТССТССТАСТСАССАТСССТТСССАТ
VRL12907TM78	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
VRL15167TM78	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
VRL1887ZIM78	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
VRL2230ZIM78	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
VRL763ZIM70	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
VRL825ZIM79	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
ZH501EGY77	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
ZH548EGY77	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT
Consensus	(161)	CTCATGCACCATCGTCCTAGTCACGAGGTTCGCTTGCGAT

		201 240
214445KEN83	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
56KEN65	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
900085MAU88	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCC <mark>C</mark> TACCGAGT
An1000MAD91	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
An991MAD91	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
An999MAD91	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
AnK6087GUI84	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
AnTAMBULEGY94	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
Ar12568RSA71	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
Ar20368RSA81	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
Ar21229SA00	(201)	TCTCTGATTTCTACAATG <mark>C</mark> CGGAGAATTCCCATACCGAGT
Ar74RSA55	(201)	TCTCTGACTTCTATAATGTCGGAGAATTTCCATACCGAGT
Ar811MAD79	(201)	TCTCTGATTTCTACAATGT <mark>T</mark> GGAGAATTCCCATACCGAGT
ArD38661SEN81	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCC <mark>C</mark> TACCGAGT
B1143KEN77	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
B314KEN62	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCG <mark>G</mark> GT
H1825RSA75	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
LunyoUGA55	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
R1662CAR85	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
SPUI0301KEN07	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
SPU10302KEN07	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
SPUI0307KEN07	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCCATACCGAGT
SPUIU3I5KENU/	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCCATACCGAGT
SPUIZUUZSOM98	(201)	
SPUISZRSAU8	(201)	
SPUZU4ANGL85	(201)	
SPUZZU/KENU/	(201)	
SPUZZI4KENU7 SDU2215VEN07	(201)	
SPUZZIJKENU7 SDU2220VENO7	(201)	
SPUZZZUKENU7	(201)	
QDII38/001KEN07	(201)	
SPUIDERANDA SPUIDERANDS	(201)	
SI 0452AMB05	(201)	
SPU77NAMB04	(201)	ΤΟΤΟΙΟΛΙΤΙΟΙΛΟΙΟΙΟΟΟΛΟΛΛΙΤΙΟΟΟΛΙΟΙ ΤΟΤΟΤΟΛΙΤΙΟΙΑΛΙΟΙΟΟΟΛΟΙΑΤΙΟΟΟΛΙΟΙ ΤΟΤΟΤΟΙΟΙΟΙΟΙΟΙΟΙΟΙΟΙΟΙΟΙΟΙΟΙΟΙΟΙΟΙΟ
SPU77RSA08	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCCATACCGAGT
VRL10327TM78	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCCATACCGAGT
VRL12907TM78	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCCATACCGAGT
VRL1516ZIM78	(201)	TCTCTGATTTCTACAATGT <mark>T</mark> GGAGAATTCCCATACCGAGT
VRL1887ZIM78	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
VRL2230ZIM78	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
VRL763ZIM70	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
VRL825ZIM79	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
ZH501EGY77	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
ZH548EGY77	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT
Consensus	(201)	TCTCTGATTTCTACAATGTCGGAGAATTCCCATACCGAGT

		241 280
214445KEN83	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
56KEN65	(241)	CGGACTTGGAGACTTTGCATCAA <mark>G</mark> CGTTGCACCTCCACCA
900085MAU88	(241)	CGG <mark>G</mark> CTTGGAGACTTTGCATCAAA <mark>T</mark> GTTGCACCTCCACCA
An1000MAD91	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
An991MAD91	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
An999MAD91	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
AnK6087GUI84	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
AnTAMBULEGY94	(241)	TGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
Ar12568RSA71	(241)	CGGACTTGGAGACTTTG <mark>T</mark> ATCAAACGTTGCACCTCCACCA
Ar20368RSA81	(241)	CGGACTTGGAGACTTTGCATCAAA <mark>T</mark> GTTGCACCTCCACCA
Ar21229SA00	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
Ar74RSA55	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
Ar811MAD79	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
ArD38661SEN81	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
B1143KEN77	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
B314KEN62	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
H1825RSA75	(241)	CGGACTTGGAGACTTTG <mark>T</mark> ATCAAACGTTGCACCTCCACCA
LunyoUGA55	(241)	TGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
R1662CAR85	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
SPUI0301KEN07	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
SPU10302KEN07	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
SPUI030/KEN0/	(241)	CGGACTITGGAGACTITTGCATCAAACGTTGCACCTCCACCA
SPULU3I5KENU/	(241)	
SPUIZUUZSOM98	(241)	
SPUIJZKSAU8	(241)	
SPUZU4ANGL85	(241)	
SPUZZU/KENU/	(241)	
SFUZZI4KENU7 SDU2215KEN07	(241)	
SFUZZIJKENU7 SDU2220KEN07	(241)	
SPUZZZUKENU7 SDU2223KEN07	(241)	
SP02223REN07	(241)	
SPUIDEREND7	(2 ± 1) (2.11)	
SPU52001RSA99	(241)	
SPU77NAMR04	(241)	
SPU77RSA08	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
VRL10327TM78	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
VRL12907TM78	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
VRL1516ZIM78	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
VRL1887ZIM78	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
VRL2230ZIM78	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
VRL763ZIM70	(241)	CGGACTTGGAGACTTTGCGTCAAACGTTGCACCTCCACCA
VRL825ZIM79	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
ZH501EGY77	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
ZH548EGY77	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA
Consensus	(241)	CGGACTTGGAGACTTTGCATCAAACGTTGCACCTCCACCA

		281 320
214445KEN83	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
56KEN65	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
900085MAU88	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGG <mark>T</mark> CATA
An1000MAD91	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
An991MAD91	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
An999MAD91	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
AnK6087GUI84	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
AnTAMBULEGY94	(281)	GC <mark>G</mark> AAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
Ar12568RSA71	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
Ar20368RSA81	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
Ar21229SA00	(281)	GCAAAGCCTTT <mark>C</mark> CAGAGACTTATTGATCTAATAGGCCATA
Ar74RSA55	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCT <mark>G</mark> ATAGGCCATA
Ar811MAD79	(281)	GC <mark>G</mark> AAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
ArD38661SEN81	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
B1143KEN77	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
B314KEN62	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCT <mark>G</mark> ATAGGCCATA
H1825RSA75	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
LunyoUGA55	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCA <mark>C</mark> A
R1662CAR85	(281)	GCAAAGCCTTTTCAGAGACTTATTGAT <mark>T</mark> TAATAGGCCATA
SPU10301KEN07	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
SPU10302KEN07	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
SPU10307KEN07	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
SPU10315KEN07	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
SPU12002SOM98	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
SPU152RSA08	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
SPU204ANGL85	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
SPU2207KEN07	(281)	GCAAAGCCTTTTCAGAGACTTATTGATCTAATAGGCCATA
SPU2214KEN07	(281)	GCAAAGCCTTTTTCAGAGACTTATTGATCTAATAGGCCATA
SPU2215KENU/	(281)	GCAAAGCCTTTTTCAGAGACTTTATTGATCTAATAGGCCATA
SPU2220KEN07	(281)	GCAAAGCCTTTI'I'CAGAGACTTTAT'I'GATCTAATAGGCCATA
SPU2223KENU/	(281)	GCAAAGCCTTTTTCAGAGACTTTATTGATCTAATAGGCCATA
SPU384001KEN9/	(281)	GCAAAGCCTTTTTCAGAGACTTTATTGATCTAATGGGCCATA
SPU45ZAMB85	(281)	GCAAAGCCTTTTTCAGAGACTTTATTGATCTAAT <mark>T</mark> GGCCATA
SPU52UUIRSA99	(281) (201)	
SPU//NAMBU4	(281) (201)	GCAAAGCCTTTTTCAGAGACTTATTGATCT <mark>G</mark> ATAGGCCATA
SPU//RSAU8	(201)	
VRLIU3ZZIM78	(281)	GCAAAGCCTTTTTCAGAGACTTATTGAT <mark>T</mark> TAATAGGCCATA
VRLIZ9UZIM78	(281)	
VRLIJI6ZIM78	(201) (201)	
VRL188/ZIM/8	(201)	
	(∠ŏ⊥) (201)	
	(∠ŏ⊥) (201)	
VKLOZJZIM/9 7U501ECV77	(∠ŏ⊥) (201)	
ZHOULEGI// 7U5/0ECV77	(∠0⊥) (201)	
ZHJ40EGI//	(∠ŏ⊥) (201)	
consensus	(∠ŏ⊥)	GUAAAGUUTTTTTUAGAGAUTTATTGATUTAATAGGUUATA

		321 360
214445KEN83	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGAAAGA
56KEN65	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGAAAGA
900085MAU88	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGAAAGA
An1000MAD91	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCT <mark>A</mark> AAAGA
An991MAD91	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCT <mark>A</mark> AAAGA
An999MAD91	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCT <mark>A</mark> AAAGA
AnK6087GUI84	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGAAAGA
AnTAMBULEGY94	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGAAAGA
Ar12568RSA71	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGAAAGA
Ar20368RSA81	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGAAAGA
Ar21229SA00	(321)	TGACTCT <mark>A</mark> AGTGATTTCACAAGGTTCCCCAATCT <mark>A</mark> AAAGA
Ar74RSA55	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGAAAGA
Ar811MAD79	(321)	TGACTCTTAGTGA <mark>C</mark> TTCACAAGGTTCCCCAATCTGAAAGA
ArD38661SEN81	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGA <mark>G</mark> AGA
B1143KEN77	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGAAAGA
B314KEN62	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGAAAGA
H1825RSA75	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGAAAGA
LunyoUGA55	(321)	TGACTCTTAGTGATTTCA <mark>T</mark> AAGGTTCCCCAATCTGAAAGA
R1662CAR85	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGAAAGA
SPU10301KEN07	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCT <mark>A</mark> AAAGA
SPU10302KEN07	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCT <mark>A</mark> AAAGA
SPU10307KEN07	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCT <mark>A</mark> AAAGA
SPU10315KEN07	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCT <mark>A</mark> AAAGA
SPU12002SOM98	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGAAAGA
SPU152RSA08	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCT <mark>A</mark> AAAGA
SPU204ANGL85	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCAATCTGAAAGA
SPU220/KENU/	(321)	TGACTCTTAGTGATTTTCACAAGGTTCCCCCAATCTAAAAGA
SPUZZI4KENU/	(321)	TGACTCTCAGTGATTTTCACAAGGTTCCCCCAATCTAAAAGA
SPUZZISKENU/	(321)	
SPUZZZUKENU/	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCCAATCT <mark>A</mark> AAAGA
SPUZZZSKENU/	(3ZI) (221)	
SPUS04UUIREN9/	(321) (321)	
	(3ZI) (221)	
SPUJZUUIRSA99	(321) (321)	
	(321)	
	(321)	
VRL103221M70 VDT12007TM78	(321)	
VRL15167TM78	(321)	
VRL18877TM78	(321)	
VRL22307TM78	(321)	
VRL7637TM70	(321)	ΤΟΛΟΓΟΤΙΤΙΟΙΟΛΙΤΙΙΟΛΟΛΑΘΟΙΙΟΟΟΟΛΑΙΟΙΘΑΑΑΘΑ
VRL8257.TM79	(321)	ΤΟΛΟΓΟΤΙΛΟΙΟΛΙΙΙΙΟΛΟΛΑΟΟΙΙΟΟΟΟΛΑΙΟΙΘΑΑΑΘΑ
7H501ECY77	(321)	ΤΟΛΟΓΟΤΙΛΟΙΟΛΙΙΙΙΟΛΟΛΑΟΟΙΙΟΟΟΟΛΑΙΟΙΘΑΑΑΘΑ
ZH548EGY77	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCCAATCTGAAAGA
Consensus	(321)	TGACTCTTAGTGATTTCACAAGGTTCCCCCAATCTGAAAGA
00110011000	() – –)	00000000000000000000000000000000

		361 400
214445KEN83	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
56KEN65	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCCCTGGCTTTC
900085MAU88	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCCCTGGCTTTC
An1000MAD91	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
An991MAD91	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
An999MAD91	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
AnK6087GUI84	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCA <mark>T</mark> TGGCTTTC
AnTAMBULEGY94	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
Ar12568RSA71	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTC <mark>C</mark> CTGGCTTTC
Ar20368RSA81	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
Ar21229SA00	(361)	AGCCATATCCTGGCCTCTTGGAGAGCCCTCACTGGCTTTC
Ar74RSA55	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACT <mark>A</mark> GCTTTC
Ar811MAD79	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
ArD38661SEN81	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTC <mark>T</mark> CTGGCTTTC
B1143KEN77	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
B314KEN62	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTC <mark>C</mark> CTGGCTTTC
H1825RSA75	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCCCTGGCTTTC
LunyoUGA55	(361)	AGCCATATCCTGGCCTCTTGGAGAGCCCTCCCTAGCTTTC
R1662CAR85	(361)	AGCCATATCCTGGCCTCTTGGCGAACCCTCACTGGCTTTC
SPU10301KEN07	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTAGGCTTTC
SPU10302KEN07	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTAGCTTTC
SPU10307KEN07	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTAGCTTTC
SPU10315KEN07	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTAGGCTTTC
SPU12002SOM98	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
SPU152RSA08	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACT <mark>A</mark> GCTTTC
SPU204ANGL85	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
SPU220/KENU/	(361)	AGCCATATCCTGGCCTCTTGGGGGAACCCTCACTGGCTTTC
SPU2214KENU/	(361)	AGCTATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
SPUZZISKENU/	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCCTCACTAGCTTTC
SPUZZZUKENU/	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTAGCTTTC
SPUZZZSKENU/	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACT <mark>A</mark> GCTTTC
SPU384UUIKEN9/	(301)	
SPU45ZAMB85	(301) (361)	
SPUJZUUIRSA99 CDU77NAMD04	(301)	
SFU//NAMDU4 CDII77DCA08	(361)	
	(301)	
VRL103221M70 VDT12007TM78	(361)	
VRL129021M70 VDT15167TM78	(361)	
VRL18877TM78	(361)	
VRL22307TM78	(361)	
VRL7637IM70	(361)	
VRL8257.TM79	(361)	
ZH501EGY77	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
ZH548EGY77	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
Consensus	(361)	AGCCATATCCTGGCCTCTTGGAGAACCCTCACTGGCTTTC
00110011000	(001)	

 214445KEN83 (401) TTTGACCTAAGCTCTACTAGAGGTGCACAGGATGATGACA 56KEN65 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGATGATGATGACA An1000MD91 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA An991MAD91 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA An991MAD91 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA An991MAD91 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA An4087GU184 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar12568RSA71 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar20368RSA81 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar21229SA00 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar21229SA00 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar31MAD79 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B1143KEN77 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA S9U1301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA S9U1301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA S9U10307KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA S9U203M98 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA S9U201KEN97 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA S9U203M98 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA S9U204NGL85 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA S9U204NGL85 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA S9U204NGL85 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA S9U204NGL85 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA S9U204NGL85 (401) TTT			401 440
 SEKENG5 (401) TTTGACCTAAGCTCTAC AGAGTGCACAGGACTGATGATA 900085MAU88 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGATGACA An1000MAD91 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA An991MAD91 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGATGACA An6087GU184 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGATGACA An7AMBULEGY94 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGATGACA Ar12568RSA81 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGATGACA Ar20368RSA81 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar21229SA00 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar21229SA00 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar2138661SEN81 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar38661SEN81 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B1143KEN77 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B1143KEN77 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B144KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B144KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B144KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10302KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU202SM98 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU20215KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU20215KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2201KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2201KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2201KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2220KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA	214445KEN83	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
900085MAU88 (401) TTTGACCTAGCTCCACTAGAGTGCACAGGAATGATGATGACA An1901MAD91 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGATGACA An999MAD91 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGATGACA AnrABULGGY94 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA AnrABULGGY94 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar12568RSA71 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar20368RSA81 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar21229SA00 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar21329SA00 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar318AB79 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar31861SEN81 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B1143KEN77 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA H1825RSA75 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10307KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU202SMB8 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU202SMB8 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220XKEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2214KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2215KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU3221N78 (401) TTTGAC	56KEN65	(401)	TTTGACCTAAGCTCTAC <mark>C</mark> AGAGTGCACAGG <mark>TC</mark> TGATGA <mark>T</mark> A
An1000MD91(401)TTTGACCTAACCTCTACTAGAGTGCACAGGAATGATGACA An991MAD91An91MAD91(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA AnK6087GUI84AnTAMBULEGY94(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar12568RSA71An120368RSA81(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar20368RSA81Ar20368RSA81(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar2129SA00Ar21229SA00(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar214SA55Ar2138661SEN81(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar811MAD79A101TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B114XEN77B114XEN77(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B114XEN77B144XEN77(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B14XEN62LunyoUGA55(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07G101TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07G401TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10307KEN07G401TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10307KEN07G401TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU12002SOM98G401TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07G401TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07G401TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07G401TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07G401TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07G401TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07	900085MAU88	(401)	TTTGACCT <mark>G</mark> AGCTC <mark>C</mark> ACTAGAGTGCACAGGAATGATGACA
An991MAD91 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA An999MAD91 (401) TTTGACTTAGCTTAAGCTCTACTAGAGTGCACAGGAATGATGACA AnTAMBULEGY94 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA An12568RSA81 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar21229SA0 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar21229SA0 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar21229SA0 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar218561SEN81 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar74RSA55 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar3811MAD79 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B1143KEN77 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10307KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10307KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU204MNGL85 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU207KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU207KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU207KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2207KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU77NAMB04 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU77NAMB04 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU77NAMB04 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL15021M78 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL15021M78 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL15021M78 (401) TTTGACCTAAGC	An1000MAD91	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
An999MAD91 (401) TTTGACTAACTCTACTAGAGTGCACAGGAATGATGACA AnrK6087GUI84 (401) TTTGACCTAACTCTACTAGAGTGCACAGGAATGATGACA Ar12568RSA71 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar20368RSA81 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar21229SA00 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar21229SA00 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar74RSA55 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar38661SEN81 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B1143KEN77 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B314KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10307KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10315KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10202S0M98 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU204ANGL85 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU204ANGL85 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU204ANGL85 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU204ANGL85 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU204KNO7 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL187ZIM78 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL187ZIM78 (401) TTTGACCTAAGCTCTACTA	An991MAD91	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
 AnK6087GUI84 (401) TTTGACCTAGCTCTACTAGAGTGCACAGGAATGATGATA AnTAMBULEGY94 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGATGA Ar20368RSA81 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar20368RSA81 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar21229SA00 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar74RSA55 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar738661SEN81 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B1143KEN77 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B1143KEN77 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA B144KEN62 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA H1825RSA75 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA H1825RSA75 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10301KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10307KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10307KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10307KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10307KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU12002S0M98 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU204NGL85 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2207KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2214KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2207KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2214KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU220KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA 	An999MAD91	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
AnTAMEULECY94(401)TTTGACCTAAGCTCTACTACAGAGTGCATAAGGTGTAGAGA Ar20368R5A81Ar20368R5A81(401)TTTGACCTAAGCTCCACCAGAGATGCACAGGAATGATGACA Ar21229SA00Ar21229SA00(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar74R5A55Ar21229SA00(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA Ar811MAD79Ar03661SEN81(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACA B1143KEN77B1143KEN77(401)TTTGACCTAAGCTCCACCAGGATGCACAGGAATGATGACA B1143KEN77H1825R5A75(401)TTTGACCTAAGCTCCACCAGGAGTGCACAGGAATGATGACA B1145KEN62H1825R5A75(401)TTTGACCTAAGCTCCACCAGGAGTGCCACAGGAATGATGACA R1662CAR85SPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10302KEN07SPU10302KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU10307KEN07SPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU12002S0M98SPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU204ANGL85SPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2215KEN07SPU2215KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2215KEN07SPU2215KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2215KEN07SPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2215KEN07SPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2207KEN97SPU38001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2207KEN97SPU38001KEN97(401)TTTGACCTAAGCTCTACTAGAGT	AnK6087GUI84	(401)	TTTGA <mark>T</mark> CT <mark>T</mark> AGCTCTACTAGAGTGCACAGGAATGATGA <mark>T</mark> A
Ar1256885A71(401)TTTGACCTAAGCTCCACGACAGAGTGCATAGCTCGATGATAAr2036885A81(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGATGATGACAAr212295A00(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAAr74RSA55(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAAr811MAD79(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACAAr1038661SEN81(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACAB1143KEN77(401)TTTGACCTAAGCTCCACTACTAGAGTGCACAGGAATGATGACAB1143KEN77(401)TTTGACCTAAGCTCCACCAGAGTGCACAGGAATGATGACAH1825RSA75(401)TTTGACCTAAGCTCCACCAGAGTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU1002SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2215KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2215KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA<	AnTAMBULEGY94	(401)	TTTGACCTAAGCTCTACTAGAGTGCA <mark>T</mark> AGGAATGATGACA
Ar203688581(401)TTTGACCTAAGCTCTACTACAGAGTGCACAGGAATGATGACAAr212295800(401)TTTGACCTAAGCTCTACTACAGAGTGCACAGGAATGATGACAAr217485455(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAAr811MAD79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAB1143KEN77(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAB114XEN62(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAH1825R5A75(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAR1662CAR85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU1202SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU202SN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2214KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2214KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2214KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2214KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2204ANCL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2204ANCL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA<	Ar12568RSA71	(401)	TTTGACCTAAGCTC <mark>C</mark> AC <mark>AGAGTGCA<mark>T</mark>AGG<mark>TC</mark>TGATGA<mark>T</mark>A</mark>
Ar21229800(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAAr74RSA55(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAArB38661SEN81(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAB1143KEN77(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAB1143KEN62(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAH1825RSA75(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAR1662CAR85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10302KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10315KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10315KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU1202S0M98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2214KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2215KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU220KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU220KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU221M885(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU220KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA<	Ar20368RSA81	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
Ar74RSA55(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAArD38661SEN81(401)TTTGACCTGACTCCACTAGAGTGCACAGGAATGATGACAB1143KEN77(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACAB1143KEN77(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACAH1825RSA75(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAK1662CAR85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10302KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10315KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2028M98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGACASPU2215KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2215KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU384001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU384001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU3220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU384001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU32001RSA99(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA <td>Ar21229SA00</td> <td>(401)</td> <td>TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA</td>	Ar21229SA00	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
Ar811MAD79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAArD38661SEN81(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACAB1143KEN77(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACAH1825RSA75(401)TTTGACCTAAGCTCCACCAGAGTGCACAGGAATGATGACAR1662CAR85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU1022S0M98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU221KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGACASPU221KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU45ZAMB85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU45ZAMB85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA	Ar74RSA55	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
ArD38661SEN81(401)TTTGACCTAGACTCCACTAGACTGCACAGGAATGATGACAB1143KEN77(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAB314KEN62(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAH1825RSA75(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10302KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10315KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10202SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2007KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2215KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2201RSA99(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU52001RSA99(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NSA08(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL187ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA <td>Ar811MAD79</td> <td>(401)</td> <td>TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA</td>	Ar811MAD79	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
B1143kEN77(401)TTTGACCTAAGCTCTACTAGAGTACACAGGAATGATGACAB314kEN62(401)TTTGACCTAAGCTCTACTAGAGTACACAGGAATGATGACAH1825RSA75(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAk1090GA55(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301kEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301kEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307kEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10315kEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307kEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU1002SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207kEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2215kEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2215kEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220kEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2223kEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2223kEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU38401kEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU52001RSA99(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NRS08(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA </td <td>ArD38661SEN81</td> <td>(401)</td> <td>TTTGACCT<mark>G</mark>AGCTC<mark>C</mark>ACTAGAGTGCACAGGAATGATGACA</td>	ArD38661SEN81	(401)	TTTGACCT <mark>G</mark> AGCTC <mark>C</mark> ACTAGAGTGCACAGGAATGATGACA
B314kEN62(401)TTTGACCTAAGCTCTACTAGAGTACACAGGAATGATGACAH1825RSA75(401)TTTGACCTAAGCTCCACCAGAGTGCATAGGTCTGATGATALunyoUGA55(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU102050M98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU1200250M98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU1204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGAC	B1143KEN77	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
H1825R3A75(401)TTTGACCTAAGCTCQACQCAGAGTGCATGATGATGAT LunyoUGA55LunyoUGA55(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAR1662CAR85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU1020SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU1202SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2214KEN07(401)TTTGACCTAAGCTCCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU384001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL187ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1887ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1887ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATG	B314KEN62	(401)	TTTGACCTAAGCTCTACTAGAGT <mark>A</mark> CACAGGAATGATGACA
LunyoUGA55(401)TTTGACCTAAGGTCTACTAGAGTGCACAGGAATGATGACAR1662CAR85(401)TTTGATCTGAGCTCTACTAGAGTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10315KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10202SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU152RSA08(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACGACASPU2215KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACGACASPU2200KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2200KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2200KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU452001RSA99(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU52001RSA99(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1871M7(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1802ZM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL181671M7(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATG	H1825RSA75	(401)	TTTGACCTAAGCTC <mark>C</mark> AC <mark>AGAGTGCA<mark>T</mark>AGG<mark>TC</mark>TGATGA<mark>T</mark>A</mark>
R1662CAR85(401)TTTGATCTGAGCTCTACTAGAGCTGCACAGGAATGATGACASPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10315KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU12002SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU12002SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU12002SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU1202SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGACASPU2215KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU52001RSA99(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATG	LunyoUGA55	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
SPU10301KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10302KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU12002SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU12002SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU1202SNM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2214KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU384001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU452AMB85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1887ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1887ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATG	R1662CAR85	(401)	TTTGA <mark>T</mark> CT <mark>G</mark> AGCTCTACTAGAGTGCACAGGAATGATGACA
SPU10302KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10315KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU1202SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU152RSA08(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGACASPU2215KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU384001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU452AMB85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77RSA08(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1887ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL252ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA <td>SPU10301KEN07</td> <td>(401)</td> <td>TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA</td>	SPU10301KEN07	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
SPU10307KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU10315KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU12002SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU12002SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU1207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2214KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2215KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU384001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU45ZAMB85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NSA08(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1887ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL252ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAAGATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA	SPU10302KEN07	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
 SPU10315KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU12002SOM98 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU152RSA08 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU204ANGL85 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACGACA SPU2207KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGACA SPU2215KEN07 (401) TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACGACA SPU2220KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2220KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU2223KEN07 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU384001KEN97 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU45ZAMB85 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU77NAMB04 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU77NAMB04 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SPU77RSA08 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL1032ZIM78 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL1290ZIM78 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL1887ZIM78 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL230ZIM78 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL230ZIM78 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL63ZIM70 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL825ZIM79 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA <	SPU10307KEN07	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
SPU12002SOM98(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAASPU152RSA08(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAASPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGCACASPU2214KEN07(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGACGCACASPU2215KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU452AMB85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU452AMB85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77RSA08(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL10322IM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1516ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL763ZIM70(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAZH548EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACACADADAUA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACADADAUA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACADADAUA(401)TTTGACCTAAGCTCTACTAGAGTGCAAGAGAATGATGACA	SPU10315KEN07	(401)	TTTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
SP0152RSA08(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAASPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACGACASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGACASPU2215KEN07(401)TTTGACCTAAGCTCCCACTAGAGTGCACAGGAATGATGACGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAASPU2223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAASPU2223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAASPU384001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAASPU452AMB85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAASPU77NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAASPU77RSA08(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAAVRL10322IM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAAVRL1516ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAAZH548EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAACAACAACAACAACAACAACAACAACAACAACAACA	SPUI2002SOM98	(401)	TTTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
SPU204ANGL85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAASPU2207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGACASPU2214KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGACASPU2215KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU384001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU452AMB85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU52001RSA99(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77RSA08(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1516ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL763ZIM70(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACAZH5048EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACH5048EGY77(401)TTTGCACCTAAGCTCTACTAGAGTGCACAGGAATGATGACACH5048EGY77(401)TTTGCACCTAAGCTCTACTAGAGTGCACACGAATGATGACACH5048EGY77(401)TTTGCACCTAAGCTCTACTAGAGTGCACACGAATGATGACA <td>SPUI52RSA08</td> <td>(401)</td> <td>TTTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA</td>	SPUI52RSA08	(401)	TTTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
SP02207KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGACA SP02214KEN07SP02214KEN07(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACA SP02220KEN07SP02220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SP02223KEN07SP02223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SP0384001KEN97SP0384001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SP0452AMB85SP045201RSA99(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SP077NAMB04SP077NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA SP077RSA08VRL10322IM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL1290ZIM78VRL1516ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL230ZIM78VRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL230ZIM78VRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL230ZIM78VRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL230ZIM78VRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL230ZIM78VRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL230ZIM78VRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL230ZIM79VRL230ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA ZH501EGY77VRL230ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA ZH548EGY77VRL230ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACA ZH548EGY77VRL230ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACACCTACACCAGAAT	SPU204ANGL85	(401)	TTTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
SPU2214KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGACASPU2215KEN07(401)TTTGACCTAAGCTCCCACTAGAGTGCACAGGAATGATGACASPU2223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU384001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU45ZAMB85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU52001RSA99(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77RSA08(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1887ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL85ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAZH501EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAZH548EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACADSONSUS(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACADSONSUS(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA	SPUZZU/KENU/	(401)	TTTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGACA
SP02215KEN07(401)TTTGACCTAAGCTCCCACTAGAGTGCACAGGAATGATGACASPU2220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU384001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU452AMB85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU52001RSA99(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL10322IM78(401)TTTGACCTAAGCTCCCACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1516ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAZH501EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACADSADA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACADSADA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACADSADA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACADSADA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACADS	SPUZZI4KENU7	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGACGACA
SP02220KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU2223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU384001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU452AMB85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU52001RSA99(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1516ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL763ZIM70(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAZH501EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)<	SPUZZISKENU/	(401)	
SP02223KEN07(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU384001KEN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU45ZAMB85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU52001RSA99(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77RSA08(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1516ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAZH501EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACADGCD202(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACADGCD202(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA	SPUZZZUKENU/	(401)	
SP038400TREN97(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU45ZAMB85(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU52001RSA99(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACAVRL1516ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1887ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAZH501EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACAZH548EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACARGADAWA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA	SPUZZZSKENU/	(401)	
SP0432AMB83(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU52001RSA99(401)TTTGATCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77NAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77RSA08(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1516ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL763ZIM70(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAZH501EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACADGODAUG(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA	SPUS04UUIREN97	(401)	
SP03200TRSA99(401)TTTGATCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77RSA08(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1516ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1887ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL763ZIM70(401)TTTGACCTAAGCTCCTACTAGAGTGCACAGGAATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAZH548EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA	SPU4JZAMBOJ	(401)	
SF077RAMB04(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACASPU77RSA08(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1516ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1887ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCCACCAGGAGTGCACAGGAATGATGACAVRL763ZIM70(401)TTTGACCTAAGCTCCACCAGGTGCATAGGTCTGATGATAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAZH501EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACARGADAUA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA	SPUJZUUIKSA99 CDU77NAMD04	(401)	
SF077KSA00(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1032ZIM78(401)TTTGACCTAAGCTCTCCACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1516ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1887ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL763ZIM70(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAZH501EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACADGODAUG(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA	20117702708	(401)	
VRL103221M78(401)TTTGACCTAAGCTCCACTAGAGTGCACAGGAATGATGACAVRL1290ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1887ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL763ZIM70(401)TTTGACCTAAGCTCCCCACCAGGAATGATGATGATAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAZH501EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACAZH548EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA	VDT 10327TM78	(401)	
VRL129021M70(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1516ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL763ZIM70(401)TTTGACCTAAGCTCCCCAGGAATGATGATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGATGACAZH501EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACAZH548EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA	VRL12907TM78	(401)	
VRL151021M70(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL1887ZIM78(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAVRL2230ZIM78(401)TTTGACCTAAGCTCCCCACAGGAGTGCACAGGAATGATGACAVRL763ZIM70(401)TTTGACCTAAGCTCCCCCCCCAGGAGTGCACAGGAATGATGACAVRL825ZIM79(401)TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACAZH501EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACAZH548EGY77(401)TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	VRL15167TM78	(401)	
VRL2230ZIM78 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA VRL263ZIM70 (401) TTTGACCTAAGCTCCACCAGGAATGATGATGACA VRL825ZIM79 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA ZH501EGY77 (401) TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA ZH548EGY77 (401) TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA Carcoraux (401) TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA	VRL18877.TM78	(401)	
VRL22021M70 (401) TTTGACCTAAGCTCTAGAGTGCACAGGAATGATGACA VRL763ZIM70 (401) TTTGACCTAAGCTCCCCACCAGGAATGATGATGACA VRL825ZIM79 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA ZH501EGY77 (401) TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA ZH548EGY77 (401) TTTGACCTAAGCTCTACTAGAGTGCATGAGGAATGATGACA Conconsult (401) TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA	VRL22307TM78	(401)	ΤΤΤΟΛΟΟΤΜΑΙΟΟΤΟΤΛΟΤΙΟΛΟΙΟΟΛΟΙΟΟΛΟΙΟΑΙΟΑΙΟΑΟΑ
VRL825ZIM79 (401) TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA ZH501EGY77 (401) TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA ZH548EGY77 (401) TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA	VRI,7637.TM70	(401)	TTTGACCTAAGCTCCACCACCACCACCACCACCACCACCACCACCACCACC
ZH501EGY77 (401) TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA ZH548EGY77 (401) TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA	VRL8257TM79	(401)	TTTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA
ZH548EGY77 (401) TTTGACCTAAGCTCTACTAGAGTGCA <mark>T</mark> AGGAATGATGACA	ZH501EGY77	(401)	TTTGACCTAAGCTCTACTAGAGTGCATAGGAATGATGACA
	ZH548EGY77	(401)	TTTGACCTAAGCTCTACTAGAGTGCA <mark>T</mark> AGGAATGATGACA
	Consensus	(401)	TTTGACCTAAGCTCTACTAGAGTGCACAGGAATGATGACA

		441 480
214445KEN83	(441)	TTAGAAGGGATCAGATTGCTACTCTAGCAATGAGGAGCTG
56KEN65	(441)	TTAGAAGGGA <mark>C</mark> CAGATTGCTACTCTAGCAATGAGGAGCTG
900085MAU88	(441)	TTAG <mark>G</mark> AGGGA <mark>C</mark> CAGATTGC <mark>C</mark> ACTCTAGCAATGAGGAG <mark>T</mark> TG
An1000MAD91	(441)	TTAGAAGGGATCAGATTGCTACTCTAGCAATGAGGAGCTG
An991MAD91	(441)	TTAGAAGGGATCAGATTGCTACTCTAGCAATGAGGAGCTG
An999MAD91	(441)	TTAGAAGGGATCAGATTGCTACTCTAGCAATGAGGAGCTG
AnK6087GUI84	(441)	TTAGAAGGGATCAGATTGC <mark>C</mark> ACTCTAGCAATGAGGAGCTG
AnTAMBULEGY94	(441)	TTAGAAGGGATCAGATTGC <mark>C</mark> ACTCTAGCAATGAGGAG <mark>T</mark> TG
Ar12568RSA71	(441)	TTAGAAGGGA <mark>C</mark> CAGATTGCTACTCTAGCAATGAGGAGCTG
Ar20368RSA81	(441)	TTAGAAGGGATCAGATTGC <mark>C</mark> ACTCTAGCAATGAGGAG <mark>T</mark> TG
Ar21229SA00	(441)	TTAGAAGGGATCAGATTGCTACTCTAGCAATGAGGAGCTG
Ar74RSA55	(441)	TTAGAAG <mark>A</mark> GATCAGATTGC <mark>C</mark> ACTCTAGCAATGAGGAGCTG
Ar811MAD79	(441)	TTAGAAGGGATCAGATTGC <mark>C</mark> ACTCTAGCAATGAGGAG <mark>T</mark> TG
ArD38661SEN81	(441)	TTAGAAGGGA <mark>C</mark> CAGATTGC <mark>C</mark> ACTCTAGCAATGAGGAG <mark>T</mark> TG
B1143KEN77	(441)	TTAGAAGGGATCAGATTGCTACTCTAGCAATGAGGAGCTG
B314KEN62	(441)	TTAGAAGGGATCAGATTGCCACTCTAGCAATGAGGAGCTG
H1825RSA75	(441)	TTAGAAGGGA <mark>C</mark> CAGATTGCTACTCTAGCAATGAGGAGCTG
LunyoUGA55	(441)	TTAGAAGGGATCAGATTGC <mark>C</mark> ACTCTAGCAATGAGGAGCTG
R1662CAR85	(441)	TTAGAAGGGATCAGATTGC <mark>C</mark> ACTCTAGCAATGAGGAGCTG
SPU10301KEN07	(441)	TTAGAAGGGATCAGATTGCTACTCTAGCAATGAGGAGCTG
SPU10302KEN07	(441)	TTAGAAGGGATCAGATTGCTACTCTAGCAATGAGGAGCTG
SPULU30/KENU/	(44⊥) (441)	TTAGAAGGGATCAGATTGCTACTCTAGCAATGAGGAGCTG
SPU10315KEN0/	(44⊥) (441)	TTAGAAGGGATCAGATTGCTACTCTAGCAATGAGGAGCTG
SPUIZUUZSOM98	(44⊥) (441)	
SPUISZRSAU8	(44⊥) (441)	
SPUZU4ANGL85	(44⊥) (441)	
SPUZZU/KENU/	(44⊥) (441)	
SPUZZI4KENU7 SDU2215VEN07	(441) (441)	
SPUZZIJKENU/	(44⊥) (441)	
SPUZZZUKENU7	(441)	
SPUZZZ SKENU / CDU38/001kEN07	(441)	
CDII/577MD85	(441)	
SP0452AMB05	(441)	
SIUSZUUIKSAJJ SDU77NAMBO/	(1 1)	
SI077NAMD04 SPI177RSD08	(441)	
VRL10327TM78	(441)	
VRL12907TM78	(441)	
VRL15167TM78	(441)	
VRL18877.TM78	(441)	TTAGAAGGGATCAGATTGCCAACTCTAGCAATGAGGAGCTG
VRL22307TM78	(441)	TTAGAAGGGATCAGATTGCCACTCTAGCAATGAGGAGCTG
VRL7637TM70	(441)	TTAGAAGGGACCAGATTGCTACTCTAGCAATGAGGAGCTG
VRL825ZIM79	(441)	TTAGAAGGGATCAGATTGCTACTCTAGCAATGAGGAGCTG
ZH501EGY77	(441)	TTAGAAGGGATCAGATTGCCACTCTAGCAATGAGGAGTTG
ZH548EGY77	(441)	TTAGAAGGGATCAGATTGCCACTCTAGCAATGAGGAGTTG
Consensus	(441)	TTAGAAGGGATCAGATTGCTACTCTAGCAATGAGGAGCTG
	. /	

		481 520
214445KEN83	(481)	CAAGATTACCAATGATCTAGAGGACTCCTTTGTTGGCTTA
56KEN65	(481)	CAAGATTACCAATGATCTAGAGGACTCCTTTGTTGGCTTA
900085MAU88	(481)	CAAG <mark>G</mark> T <mark>C</mark> ACCAATGATCT <mark>T</mark> GAGGACTCCTTTGTTGGCTTA
An1000MAD91	(481)	CAAGATT <mark>G</mark> CCAATGATCTAGAGGACTCCTTTGTTGGCTTA
An991MAD91	(481)	CAAGATT <mark>G</mark> CCAATGATCTAGAGGACTCCTTTGTTGGCTTA
An999MAD91	(481)	CAAGATT <mark>G</mark> CCAATGATCTAGAGGACTCCTTTGTTGGCTTA
AnK6087GUI84	(481)	CAAGATTACCAATGATCTAGAGGACTCCTTTGTTGGCTTA
AnTAMBULEGY94	(481)	CAAGAT <mark>C</mark> ACCAATGATCTAGAGGACTCCTTTGTTGGCTTA
Ar12568RSA71	(481)	CAAGATTACCAATGATCT <mark>G</mark> GAGGACTCCTTTGTTGGCTTA
Ar20368RSA81	(481)	CAAGAT <mark>C</mark> ACCAATGATCTAGAGGACTCCTTTGTTGGCTTA
Ar21229SA00	(481)	CAAGATTACCAATGATCTAGAGGACTCCTTTGTTGGCTTA
Ar74RSA55	(481)	CAAGAT <mark>C</mark> ACCAATGATCTAGAGGACTCCTTTGTTGGCTTA
Ar811MAD79	(481)	CAAGAT <mark>C</mark> ACCAATGATCTAGAGGACTCCTTTGTTGGCTTA
ArD38661SEN81	(481)	CAAGAT <mark>C</mark> ACCAATGATCTA <mark>C</mark> AGGACTCCTTTGTTGGCTTA
B1143KEN77	(481)	CAAGATTACCAATGATCTAGAGGACTCCTTTGTTGGCTTA
B314KEN62	(481)	CAAGATTACCAATGATCT <mark>G</mark> GA <mark>A</mark> GACTCCTTTGTTGGCTTA
H1825RSA75	(481)	CAAGATTACCAATGATCT <mark>G</mark> GAGGACTCCTTTGTTGGCTTA
LunyoUGA55	(481)	CAAGATTACCAATGATCTAGA <mark>A</mark> GACTCCTTTGTTGGC <mark>C</mark> T <mark>G</mark>
R1662CAR85	(481)	CAAGATTACCAATGATCTAGAGGACTCCTTTGTTGG <mark>A</mark> TTA
SPU10301KEN07	(481)	CAAGATTACCAATGAT <mark>T</mark> TAGA <mark>A</mark> GACTCCTTTGTTGGCTTA
SPU10302KEN07	(481)	CAAGATTACCAATGAT <mark>T</mark> TAGA <mark>A</mark> GACTCCTTTGTTGGCTTA
SPU10307KEN07	(481)	CAAGATTACCAATGAT <mark>T</mark> TAGA <mark>A</mark> GACTCCTTTGTTGGCTTA
SPU10315KEN07	(481)	CAAGATTACCAATGAT <mark>T</mark> TAGA <mark>A</mark> GACTCCTTTGTTGGCTTA
SPU12002SOM98	(481)	CAAGATTACCAATGATCTAGAGGACTCCTTTGTTGGCTTA
SPU152RSA08	(481)	CAAGATTACCAATGAT <mark>T</mark> TAGA <mark>A</mark> GACTCCTTTGTTGGCTTA
SPU204ANGL85	(481)	CAAGATTACCAATGATCTAGAGGACTCCTTTGTTGGCTTA
SPU2207KEN07	(481)	CAAGATTACCAATGATCTAGAGGACTCCTTTGTTGGCTTA
SPU2214KENU7	(481) (401)	
SPU2215KENU7	(481)	CAAGATTACCAATGATTTAGAAGACTCCTTTGTTGGCTTA
SPUZZZUKENU7	(481) (401)	
SPUZZZSKENU/	(481) (401)	CAAGATTACCAATGAT <mark>T</mark> TAGA <mark>A</mark> GACTCCTTTGTTGGCTTA
SPU384UUIKEN97	(481) (401)	
SPU45ZAMB85	(481) (401)	
SPUSZUUIRSA99	(481) (481)	
SPU//NAMBU4	(401) (401)	
	(401) (401)	
VRL103221M/8	(481) (481)	
VRL129021M/0 VDT15167TM79	(401) (401)	
νκμισιόδιμ/δ νρι1887στμ70	(401) (701)	
	(181)	
VRL7637TM70	(401) (781)	
VRL8257TM70	(<u>101</u>) (<u>1</u> 21)	
ZH501ECV77	(481)	
ZH548EGY77	(481)	
Consensus	(481)	
CONSCISUS	(- 0 -)	01710111 11/00171 0111 0111 0110 00 00 01 00 01 1 0 00 0

		521 560
214445KEN83	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
56KEN65	(521)	CACAGGATGATAGTGAC <mark>T</mark> GAGGCTATCCTCAGAGGGATTG
900085MAU88	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
An1000MAD91	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
An991MAD91	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
An999MAD91	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
AnK6087GUI84	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
AnTAMBULEGY94	(521)	CACAGGATGATAG <mark>C</mark> GAC <mark>T</mark> GAGGC <mark>C</mark> ATCCTCAGAGGGATTG
Ar12568RSA71	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
Ar20368RSA81	(521)	CACAGGA <mark>A</mark> GATAGTGACCGAGGC <mark>C</mark> ATCCTCAGAGGGATTG
Ar21229SA00	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
Ar74RSA55	(521)	CACAGAATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
Ar811MAD79	(521)	CACAGGATGATAG <mark>C</mark> GACCGAGGC <mark>C</mark> ATCCTCAGAGGGATTG
ArD38661SEN81	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
B1143KEN77	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
B314KEN62	(521)	CACAGGATGATAGTGACCGAGGCTAT <mark>T</mark> CTCAGAGGGATTG
H1825RSA75	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
LunyoUGA55	(521)	CACAGGATGATAGTGACCGAGGCTAT <mark>T</mark> CTCAGAGGG <mark>G</mark> TTG
R1662CAR85	(521)	CACAGGATG <mark>G</mark> TAGTGAC <mark>T</mark> GAGGC <mark>C</mark> ATCCTCAGAGGGATTG
SPU10301KEN07	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
SPU10302KEN07	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
SPUI030/KEN0/	(521)	
SPUIU3I5KENU/	(521)	
SPUIZUUZSOM98	(521)	
SPUI52RSAU8	(521)	
SPUZU4ANGL85	(5ZI) (521)	
SPUZZU/KENU/	(⊃∠⊥) (521)	
SPUZZI4KENU7 SDU2215VEN07	(521)	
SPUZZIJKENU7	(JZI)	
SPUZZZUKENU7	(521)	
SPU2223REN07	(521)	
SIUSU400IREN97 SDU/57AMB85	(521)	
SPU52001RS299	(521)	
SPU77NAMR04	(521)	
SPU77RSA08	(521)	
VRL10327.TM78	(521)	CACAGGATAATAGTGACCGAGGCTATCCTCAGAGGGATTG
VRL12907.TM78	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
VRL1516ZIM78	(521)	CACAGGATGATAG <mark>C</mark> GACCGAGGC <mark>C</mark> ATCCTCAGAGGGATTG
VRL1887ZIM78	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
VRL2230ZIM78	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
VRL763ZIM70	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG
VRL825ZIM79	(521)	CACAGGAAGATAGTGACCGAGGCTATCCTCAGAGGGATTG
ZH501EGY77	(521)	CACAGGATGATAGCGACTGAGGGCCATCCTCAGAGGGATTG
ZH548EGY77	(521)	CACAGGATGATAGCGACTGAGGCCATCCTCAGAGGGATTG
Consensus	(521)	CACAGGATGATAGTGACCGAGGCTATCCTCAGAGGGATTG

		561 600
214445KEN83	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
56KEN65	(561)	ACCTGTGCCTGTTGCCAGGCTTTGA <mark>T</mark> CTCATGTATGAGGT
900085MAU88	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
An1000MAD91	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
An991MAD91	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
An999MAD91	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
AnK6087GUI84	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
AnTAMBULEGY94	(561)	ACCTGTGCCTGTTGCCAGGCTTTGA <mark>T</mark> CTCATGTATGAGGT
Ar12568RSA71	(561)	ACTTGTGCCTGTTGCCAGGCTTTGATCTCATGTATGAGGT
Ar20368RSA81	(561)	A <mark>T</mark> CTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
Ar21229SA00	(561)	ACCTGTGCCTG <mark>C</mark> TGCCAGGCTTTGACCTCATGTATGAG <mark>A</mark> T
Ar74RSA55	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
Ar811MAD79	(561)	ACCTGTGCCTGTTGCCAGGCTTTGA <mark>T</mark> CTCATGTATGAGGT
ArD38661SEN81	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
B1143KEN'/'	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
B314KEN62	(561)	A <mark>T</mark> CTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
H1825RSA75	(561)	ACT TGTGCCTGTTGCCAGGCTTTGAT CTCATGTATGAGGT
LunyoUGA55	(561)	ACCTGTGCCTGTTGCCAGGCTTTTGACCTCATGTATGAGGT
RI662CAR85	(561)	
SPULU3ULKENU/	(561) (561)	
SPULU3UZKENU/	(561) (561)	
SPULUSU/KENU/	(301) (561)	
SPULUSISKENU/	(561)	
201200230M90	(561)	
SPU20/ANGL85	(501)	
SPU2207KEN07	(501)	
SPU2214KEN07	(501)	
SPU2215KEN07	(501)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
SPU2220KEN07	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
SPU2223KEN07	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
SPU384001KEN97	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
SPU45ZAMB85	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
SPU52001RSA99	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
SPU77NAMB04	(561)	ACCTGTGCCTGTTGCCAGGCTTTGA <mark>T</mark> CTCATGTATGAGGT
SPU77RSA08	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
VRL1032ZIM78	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
VRL1290ZIM78	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
VRL1516ZIM78	(561)	ACCTGTGCCTGTTGCCAGGCTTTGA <mark>T</mark> CTCATGTATGAGGT
VRL1887ZIM78	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
VRL2230ZIM78	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
VRL763ZIM70	(561)	AC <mark>T</mark> TGTGCCTGTTGCCAGGCTTTGA <mark>T</mark> CTCATGTATGAGGT
VRL825ZIM79	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT
ZH501EGY77	(561)	ACCTGTGCCTGTTGCCAGGCTTTGA <mark>T</mark> CTCATGTATGAGGT
ZH548EGY77	(561)	ACCTGTGCCTGTTGCCAGGCTTTGA <mark>T</mark> CTCATGTATGAGGT
Consensus	(561)	ACCTGTGCCTGTTGCCAGGCTTTGACCTCATGTATGAGGT

		601 640
214445KEN83	(601)	TGCTCACGTACAGTGTGTTCGGCTCCTGCAGGCAGCAAAA
56KEN65	(601)	TGCTCACGT <mark>T</mark> CAGTGTGTTCGGCTCCTGCAGGCAGCAAAA
900085MAU88	(601)	TGCTCA <mark>T</mark> GT <mark>T</mark> CAGTGTGTTCGGCTCCTGCAGGCAGCAAAA
An1000MAD91	(601)	TGCTCACGTACAGTGTGTTCG <mark>A</mark> CTCCTGCAGGCAGCAAAA
An991MAD91	(601)	TGCTCACGTACAGTGTGTTCG <mark>A</mark> CTCCTGCAGGCAGCAAAA
An999MAD91	(601)	TGCTCACGTACAGTGTGTTCG <mark>A</mark> CTCCTGCAGGCAGCAAAA
AnK6087GUI84	(601)	TGCTCACGTACAGTGTGTTCGGCTCCTGCAGGCAGCAAAA
AnTAMBULEGY94	(601)	TGCTCACGTACAGTG <mark>C</mark> GTTCGGCT <mark>T</mark> CTGCA <mark>A</mark> GCAGCAAAA
Ar12568RSA71	(601)	TGCTCACGT <mark>T</mark> CAGTGTGTTCGGCTCCTGCAGGCAGCAA <mark>G</mark> A
Ar20368RSA81	(601)	TGCTCACGTACAGTGTGTTCGGCTCCTGCAGGCAGCAAAA
Ar21229SA00	(601)	TGCTCACGTACAGTGTGTTCGGCTCCTGCAGGCAGCAAAA
Ar74RSA55	(601)	TGCTCATGTTCAGTGTGTTCGGCTCCTGCAGGCAGCAAAA
Ar811MAD79	(601)	TGCTCACGTACAGTG <mark>C</mark> GTTCGGCT <mark>T</mark> CTGCA <mark>A</mark> GCAGCAAAA
ArD38661SEN81	(601)	TGCTCA <mark>T</mark> GT <mark>T</mark> CAGTGTGT <mark>C</mark> CGGCTCCTGCAGGCAGCAAAA
B1143KEN77	(601)	TGCTCACGTACAGTGTGTTCGGCTCCTGCAGGCAGCAAAA
B314KEN62	(601)	TGCTCACGTCCAGTGTGTTCGGCTCCTGCAGGCAGCAAAA
H1825RSA75	(601)	TGCTCACGT <mark>T</mark> CAGTGTGTTCGGCTCCTGCAGGCAGCAA <mark>G</mark> A
LunyoUGA55	(601)	TGCTCACGT <mark>C</mark> CAGTGTGTGTTCGGCTCCTGCAGGCAGCAAAA
RI662CAR85	(601)	TGCTCACGTACAGTGTGTGTTCGGCTCCTGCAGGCAGCAAAA
SPUI0301KEN0/	(601)	TGCTCACGTACAGTGTGTGTTCGGCTCCTGCAGGCAGCAAGA
SPU10302KEN07	(601)	TGCTCACGTACAGTGTGTGTTCGGCTCCTGCAGGCAGCAAGA
SPULU30/KENU/	(601)	TGCTCACGTACAGTGTGTGTTCGGCTCCTGCAGGCAGCAAGA
SPULU315KENU/	(601)	TGCTCACGTACAGTGTGTTCCGGCTCCTGCAGGCAGCAAGA
SPUIZUUZSOM98	(601)	
SPUI5ZRSAU8	(601)	
SPUZU4ANGL85	(601)	
SPUZZU/KENU/	(601)	
SFUZZI4KENU/ SDU2215KEN07	(601)	
QDII2220KEN07	(601)	
SPUZZZORENO7 SDU2223KENO7	(601)	
SPU384001KEN97	(601)	
SPII457AMB85	(601)	
SPU52001RSA99	(601)	TECTCACETACAETETETTCEECTCCTECAECCAECAAAA
SPU77NAMB04	(601)	TGCTCATGTACAGTGTGTGTAGGCTCCTGCAAGCAGCAAAA
SPU77RSA08	(601)	TGCTCACGTACAGTGTGTGTTCGGCTCCTGCAGGCAGCAAGA
VRL10327TM78	(601)	TGCTCACGTACAGTGTGTGTTCGGCTCCTGCAGGCAGCAAAA
VRL12907TM78	(601)	TGCTCACGTACAGTGTGTGTTCGGCTCCTGCAGGCAGCAAAA
VRL1516ZIM78	(601)	TGCTCACGTACAGTGCGTTCGGCTTCGCCAAGCAGCAAAA
VRL1887ZIM78	(601)	TGCTCACGTACAGTGTGTGTACGGCTCCTGCAGGCAGCAAAA
VRL2230ZIM78	(601)	TGCTCACGTACAGTGTGTACGGCTCCTGCAGGCAGCAAAA
VRL763ZIM70	(601)	TGCTCACGTTCAGTGTGTTCGGCTCCTGCAGGCAGCAAGA
VRL825ZIM79	(601)	TGCTCACGTACAGTGTGTTCGGCTCCTGCAGGCAGCAAAA
ZH501EGY77	(601)	TGCTCACGTACAGTG <mark>C</mark> GTTCGGCT <mark>T</mark> CTGCA <mark>A</mark> GCAGCAAAA
ZH548EGY77	(601)	TGCTCACGTACAGTG <mark>C</mark> GTTCGGCT <mark>T</mark> CTGCA <mark>A</mark> GCAGCAAAA
Consensus	(601)	TGCTCACGTACAGTGTGTTCGGCTCCTGCAGGCAGCAAAA

		641 680
214445KEN83	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
56KEN65	(641)	GAGGA <mark>T</mark> ATTTCTAATGCTGTAGTTCCAAACTCAGC <mark>T</mark> CTCA
900085MAU88	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
An1000MAD91	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
An991MAD91	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
An999MAD91	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
AnK6087GUI84	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTC <mark>T</mark> G <mark>G</mark> CCTCA
AnTAMBULEGY94	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
Ar12568RSA71	(641)	GAGGA <mark>T</mark> ATTTCTAATGCTGTAGTTCCAAACTCAGC <mark>T</mark> CTCA
Ar20368RSA81	(641)	GAGGACATTTCTAATGCTGT <mark>G</mark> G <mark>C</mark> TCCAAACTCAGCCCTCA
Ar21229SA00	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
Ar74RSA55	(641)	GAGGACAT <mark>C</mark> TCTAATGCTGTAGT <mark>C</mark> CCAAACTCAGCCCT <mark>T</mark> A
Ar811MAD79	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
ArD38661SEN81	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
B1143KEN77	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
B314KEN62	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
H1825RSA75	(641)	GAGGA <mark>T</mark> ATTTCTAATGCTGTAGTTCCAAACTCAGC <mark>T</mark> CTCA
LunyoUGA55	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
RI662CAR85	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTC <mark>T</mark> GCCCTCA
SPUI0301KEN07	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
SPU10302KEN07	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
SPUIU30/KENU/	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
SPUIU3I5KENU/	(641) (641)	
SPUIZUUZSOM98	(641) (641)	
SPUIJZRSAU8	(641) (641)	
SPUZU4ANGL85	(641) (641)	
SPUZZU/KENU/ SDU221/VEN07	(041) (641)	
SPUZZI4KENU7 SDU2215KEN07	(641)	CACCACATTICIATIGCIGIAGIICCAAAIIICAGCCCICA
SPUZZIJKENU7	(641)	
SPUZZZOKENO7	(6/1)	
SPU384001KEN97	(641)	CACCACATTERATOCIGIAGIICCAACICAGCCCICA CACCACATTECTAATCCTCACACACICAGCCCCTCA
SPU457AMB85	(641)	
SPU52001RSA99	(641)	
SPU77NAMB04	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
SPU77RSA08	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
VRL10327TM78	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTC <mark>T</mark> GCCCTCA
VRL1290ZIM78	(641)	GAGGACATTTCCAAATGCTGTAGTTCCAAACTCAGCCCTCA
VRL1516ZIM78	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
VRL1887ZIM78	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
VRL2230ZIM78	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
VRL763ZIM70	(641)	GAGGA <mark>T</mark> ATTTCTAATGCTGTAGTTCCAAACTCAGC <mark>T</mark> CTCA
VRL825ZIM79	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
ZH501EGY77	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
ZH548EGY77	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA
Consensus	(641)	GAGGACATTTCTAATGCTGTAGTTCCAAACTCAGCCCTCA

		681 720
214445KEN83	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
56KEN65	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCG <mark>T</mark> TCATCACT
900085MAU88	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
An1000MAD91	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
An991MAD91	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
An999MAD91	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
AnK6087GUI84	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
AnTAMBULEGY94	(681)	TTG <mark>T</mark> TCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
Ar12568RSA71	(681)	TTGCTCTTATGGAGGAGAGC <mark>T</mark> TGATGCTGCGCTCATCACT
Ar20368RSA81	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
Ar21229SA00	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
Ar74RSA55	(681)	TTGCTCTTATGGAGGAGAG <mark>T</mark> CTGATGCTGCGCTCATCACT
Ar811MAD79	(681)	TTG <mark>T</mark> TCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
ArD38661SEN81	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
B1143KEN77	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
B314KEN62	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
H1825RSA75	(681)	TTGCTCTTATGGAGGAGAGCCTTGATGCTGCGCTCATCACT
LunyoUGA55	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
R1662CAR85	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
SPU10301KEN07	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCT <mark>T</mark> ATCACT
SPU10302KEN07	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
SPU10307KEN07	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCT <mark>T</mark> ATCACT
SPU10315KEN07	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
SPU12002SOM98	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
SPUI52RSAU8	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
SPU204ANGL85	(681)	TTGCTCTTATGGAGGAGAGCCTGATGCTGCGCTCATCACT
SPU220/KENU/	(681)	
SPUZZI4KENU7	(681)	
SPUZZISKENU7	(681)	
SPUZZZUKENU7	(681) (691)	
SPUZZZSKENU/	(681) (691)	
SPUS04UUIREN97	(001) (601)	
SPU4JZAMBOJ CDU52001DCA00	(001) (601)	
SFUJZUUIKSA99 CDU77NAMD04	(601)	
SPU//NAMBU4	(681)	
VDT 10327TM78	(681)	
VRL103221M70 VDT12007TM78	(681)	
VRL15167TM78	(681)	
VRL18877.TM78	(681)	
VRL22307TM78	(681)	TTGCTCTTTATGCAGCAGCCCTCATCCTCCTCATCACT
VRI,7637.TM70	(681)	TTGCTCTTATGGAGGAGAGCCTTCATCACT
VRL8257.TM79	(681)	TTGCTCTTATGGAGGAGAGCCTTGATGCTGCGCCTCATCACT
7H501ECY77	(681)	TTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
ZH548EGY77	(681)	TTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
Concensiie	(681)	
00110011040	(001)	11001011111001100110110001011001000010A1CAC1
		721 760
----------------------------	----------------	---
214445KEN83	(721)	TCCTAGCATGATGGGGGAGAAACAACTGGATTCCAGTTGTT
56KEN65	(721)	CCTAGCATGATGGGGAGAAACAACTGGGTTCCAGTTGTT
900085MAU88	(721)	CCTAGCATGATGGGGGAGAAACAACTGGATTCCAGTTGTT
An1000MAD91	(721)	TCCTAGCATGATGGGGGAGAAACAACTGGAT <mark>C</mark> CCAGTTGTT
An991MAD91	(721)	TCCTAGCATGATGGGGGGGAGAAACAACTGGAT <mark>C</mark> CCAGTTGTT
An999MAD91	(721)	TCCTAGCATGATGGGGGAGAAACAACTGGATCCCAGTTGTT
AnK6087GUI84	(721)	TCCTAGCATGATGGGGGAGAAACAACTGGATTCCAGTTGTT
AnTAMBULEGY94	(721)	TCC <mark>C</mark> AGCATGATGGGGGAGAAACAACTGGATTCCAGTT <mark>A</mark> TT
Ar12568RSA71	(721)	CCTAGCATGATGGGGAGAAACAACTGGGTTCCAGTTGTT
Ar20368RSA81	(721)	TCCTAGCATGATGGGGGAGAAACAACTGGATTCCAGTTGTT
Ar21229SA00	(721)	TCCTAGCATGATGGGGGAGAAACAACTGG <mark>G</mark> T <mark>C</mark> CCAGTTGTT
Ar74RSA55	(721)	TCCTAGCATGATGGGGGAGAAACAACTGGATTCCAGTTGTT
Ar811MAD79	(721)	TCCTAG <mark>T</mark> ATGATGGGGGAGAAACAACTGGATTCCAGTT <mark>A</mark> TT
ArD38661SEN81	(721)	CCTAGCATGATGGGAAGAAACAACTGGATTCCAGTTA
B1143KEN77	(721)	TCCTAGCATGATGGGGGGGAGAAACAACTGGATTCCAGTTGTT
B314KEN62	(721)	TCCTAGCATGATGGGGGAGAAACAACTGGATTCCAGTTGTT
H1825RSA75	(721)	CCTAGCATGATGGGGGAGAAACAACTGGGTTCCAGTTGTT
LunyoUGA55	(721)	TCCTAGCATGATGGGGGGGAGAAACAACTGGATTCCAGTTGTT
R1662CAR85	(721)	TCCTAGCATGATGGGGGAGAAACAACTGGATTCCAGTTGTT
SPU10301KEN07	(721)	TCCTAGCATGATGGGGGGGAGAAACAACTGGAT <mark>C</mark> CCAGTTGTT
SPU10302KEN07	(721)	TCCTAGCATGATGGGGGAGAAACAACTGGAT <mark>C</mark> CCAGTTGTT
SPU10307KEN07	(721)	TCCTAGCATGATGGGGGGGAGAAACAACTGGAT <mark>C</mark> CCAGTTGTT
SPU10315KEN07	(721)	TCCTAGCATGATGGGGGGGAGAAACAACTGGAT <mark>C</mark> CCAGTTGTT
SPU12002SOM98	(721)	TCCTAGCATGATGGGGGGGAGAAACAACTGGAT <mark>C</mark> CCAGTTGTT
SPU152RSA08	(721)	TCCTAGCATGATGGGGGAGAAACAACTGGAT <mark>C</mark> CCAGTTGTT
SPU204ANGL85	(721)	TCCTAGCATGATGGGGGGGAGAAACAACTGGAT <mark>C</mark> CCAGTTGTT
SPU2207KEN07	(721)	TCCTAGCATGATGGGGGAGAAACAACTGGAT <mark>C</mark> CCAGTTGTT
SPU2214KEN07	(721)	TCCTAGCATGATGGGGGAGAAA <mark>T</mark> AACTGGAT <mark>C</mark> CCAGTTGTT
SPU2215KEN07	(721)	TCCTAGCATGATGGGGGGGAGAAACAACTGGAT <mark>C</mark> CCAGTTGTT
SPU2220KEN07	(721)	TCCTAGCATGATGGGGGAGAAACAACTGGATCCCAGTTGTT
SPU2223KEN07	(721)	TCCTAGCATGATGGGGGGGAGAAACAACTGGATCCCCAGTTGTT
SPU384001KEN9/	(721)	TCCTAGCATGATGGGGGGGAGAAACAACTGGATCCCCAGTTGTT
SPU45ZAMB85	(721)	TCCTAGCATGATGGGGGGAGAAACAACTGGATCCCCAGTTGTT
SPU52001RSA99	(721)	TCCTAGCATGATGGGGGGAGAAACAACTGGAT <mark>C</mark> CCAGTTGTT
SPU//NAMB04	(721)	TCCTAGCATGATGGGGGGGAGAAACAACTGGATTCCAGTTGTC
SPU//RSAU8	(/∠⊥) (⊐01)	TCCTAGCATGATGGGGGGGGAGAAACAACTGGAT <mark>C</mark> CCAGTTGTT
VRLIU3ZZIM/8	(/∠⊥) (フ⊃1)	
VRL129UZIM78	(/∠⊥) (フ⊃1)	
VRLISI6ZIM/8	(/21)	TCCTAGCATGATGGGGGGGAGAAACAACTGGATTCCAGTT <mark>A</mark> TT
VRL100/21M/0	(721)	
	(/∠⊥) (721)	
VEL/USZIM/U VEL8257IM70	(721) (721)	
7H501FCV77	(721)	
ZH5/2FCV77	(721) (721)	
Conconsus	(721) (721)	
CONSENSUS	(/ ム エ)	ICCINGCAIGAIGGGGGGGGAGAAACAACIGGAIICCAGIIGII

		761 800
214445KEN83	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAAGAGA
56KEN65	(761)	TCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAAGAGA
900085MAU88	(761)	CCTCCAATCCCAGATGTTGAGATGGA <mark>T</mark> TCAG <mark>G</mark> GGAAGAGA
An1000MAD91	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAG <mark>G</mark> GGAAGAGA
An991MAD91	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAG <mark>G</mark> GGAAGAGA
An999MAD91	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAG <mark>G</mark> GGAAGAGA
AnK6087GUI84	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAAGAGA
AnTAMBULEGY94	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGA <mark>G</mark> GAGA
Ar12568RSA71	(761)	CCTCCAATCCCAGATGTTGAGAT <mark>A</mark> GAATCAGAGGAAGAGA
Ar20368RSA81	(761)	CCTCCAAT <mark>T</mark> CCAGATGTTGAGATGGAATCAGAGGA <mark>G</mark> GAGA
Ar21229SA00	(761)	CCTCCAATCCCAGATGTTGAGAT <mark>A</mark> GAATCAG <mark>G</mark> GGAAGAGA
Ar74RSA55	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAAGAGA
Ar811MAD79	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGA <mark>G</mark> GAGA
ArD38661SEN81	(761)	CCTCCAATCCCAGATGTTGAGATGGA <mark>T</mark> TCAGAGGA <mark>G</mark> GAGA
B1143KEN77	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAAGAGA
B314KEN62	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAAGAGA
H1825RSA75	(761)	CCTCCAATCCCAGATGTTGAGAT <mark>A</mark> GAATCAGAGGAAGAGA
LunyoUGA55	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAAGAGA
R1662CAR85	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAGGAGA
SPUIU3UIKENU/	(/61)	CCTCCAATCCCAGATGTTGAGATGGAATCAGGGGAAGAGA
SPU10302KEN07	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAG <mark>G</mark> GGAAGAGA
SPUIU30/KENU/	(/61)	CCTCCAATCCCAGATGTTGAGATGGAATCAGGGGAAGAGA
SPULU3ISKENU/	(761)	
SPUIZUUZSOM98	(761)	
SPUIJZKSAUO	(701)	
SPUZU4ANGLOJ SDU2207VEN07	(701)	
SPUZZU/KENU/	(701)	
SPUZZIAKENU7 Spu2215ken07	(761)	
SPU222SKEN07	(761)	
SPU2220REN07	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGGGGAGGGA
SPU384001KEN97	(761)	
SPII45ZAMB85	(761)	
SPU52001RSA99	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAG <mark>G</mark> GGAGA
SPU77NAMB04	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAG
SPU77RSA08	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGGGGAAGAGA
VRL1032ZIM78	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAAGAGA
VRL1290ZIM78	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAAGAGA
VRL1516ZIM78	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAGGAG
VRL1887ZIM78	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAAGAGA
VRL2230ZIM78	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAAGAGA
VRL763ZIM70	(761)	CCTCCAATCCCAGATGTTGAGATAGAATCAGAGGAAGAGA
VRL825ZIM79	(761)	CCTCCAATCCCAGATGTTGAGATGGGATCAGAGGAAGAGA
ZH501EGY77	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGA <mark>G</mark> GAGA
ZH548EGY77	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGA <mark>G</mark> GAGA
Consensus	(761)	CCTCCAATCCCAGATGTTGAGATGGAATCAGAGGAAGAGA

		801 840
214445KEN83	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
56KEN65	(801)	GTGATGA <mark>C</mark> GATGGATTTGTTGAGGTTGATTAGAG <mark>A</mark> TTAAG
900085MAU88	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
An1000MAD91	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGA <mark>A</mark> GTTAAG
An991MAD91	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGA <mark>A</mark> GTTAAG
An999MAD91	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGA <mark>A</mark> GTTAAG
AnK6087GUI84	(801)	GTGATGATGATGGATTTGTTGA <mark>A</mark> GTTGATTAGAGGTTAAG
AnTAMBULEGY94	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
Ar12568RSA71	(801)	GTGATGA <mark>C</mark> GATGGATTTGTTGAGGTTGATTAGAG <mark>A</mark> TTAAG
Ar20368RSA81	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
Ar21229SA00	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
Ar74RSA55	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTA <mark>G</mark> G
Ar811MAD79	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
ArD38661SEN81	(801)	GTGATGATGATGGATTTGTTGAGGTT <mark>A</mark> ATTAGAGGTTAAG
B1143KEN77	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
B314KEN62	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
H1825RSA75	(801)	GTGATGACGATGGATTTGTTGAGGTTGATTAGAGATTAAG
LunyoUGA55	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTT
R1662CAR85	(801)	GTGATGATGATGGATTTGTTGA <mark>A</mark> GTTGATTAGAGGTTA <mark>T</mark> G
SPU10301KEN07	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
SPU10302KEN07	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
SPU10307KEN07	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
SPU10315KEN07	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
SPU12002SOM98	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
SPUI52RSAU8	(801)	GTGATGATGATGGATGGATTTGTTGAGGGTTGATTTAGAGGTTTAAG
SPU204ANGL85	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
SPU220/KENU/	(801)	GTGATGATGATGGATTGTTGAGGGTTGATTAGAGGGTTAAG
SPUZZI4KENU7	(801) (801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTT <mark>G</mark> AG
SPUZZISKENU7	(801) (801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
SPUZZZUKENU7	(801) (801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
SPUZZZSKENU/	(801) (801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
SPUS04UUIREN97	(001) (001)	
SPU4JZAMBOJ CDU52001DCA00	(001) (001)	GIGAIGAIGAIGGAIIIGIIGAAGIIGAIIAGAGGIIAAG
SFUJZUUIKSA99 CDU77NAMD04	(001)	
SPU//NAMBU4	(801)	
VDT 10327TM78	(801)	
VRL103221M70 VDT12007TM78	(801)	
VRL15167TM78	(801)	
VRL18877.TM78	(801)	GTGATGATGATGGATTTGTTGTTGATGATTAGAGGTTAAG
VRL22307IM78	(801)	
VRL7637TM70	(801)	
VRL8257.TM79	(801)	
ZH501EGY77	(801)	GTGATGATGATGGATTTGTTGTGAGGTTGATTAGAGGTTAG
ZH548EGY77	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
Consensus	(801)	GTGATGATGATGGATTTGTTGAGGTTGATTAGAGGTTAAG
	····/	

		841	880
214445KEN83	(841)	GCTGCCCCACCCCC	ACCCCCCAATCCCGACCGTAACCC
56KEN65	(841)	GCTGCCCCACCCCCC-	ACCCCCAATCCCGACCGTAACCC
900085MAU88	(841)	GCTGCCCCACCCCCC	ACCCCCCAATCCCGACCGTAACCC
An1000MAD91	(841)	GCTGCCCCACCCCCC	ACCCCCCAATCCCGACCGTAACCC
An991MAD91	(841)	GCTGCCCCACCCCCC	ACCCCCCAATCCCGACCGTAACCC
An999MAD91	(841)	GCTGCCCCACCCCCC-	ACCCCCCAATCCCGACCGTAACCC
AnK6087GUI84	(841)	GCTGCCCCACCCCCC	ACCCCCCAATCCCGACCGTAACCC
AnTAMBULEGY94	(841)	GCTGCCCCACCCCCC	ACCCCCCAATCCCGACCGTAACCC
Ar12568RSA71	(841)	GCTGCCCCACCCCCC	ACCCCCAATCCCGACCGTAACCC
Ar20368RSA81	(841)	GCTGCCCCACCCCCC-	ACCCCCCAATCCCGACCGTAACCC
Ar21229SA00	(841)	GCTGCCCCACCCCC	ACCCCCCAATCCCGACCGTAACCC
Ar/4RSA55	(841)	GCTGCCCCACCCCCC	ACCCCCCAATCCCGACCGTAACCC
Ar811MAD79	(841)	GCTGCCCCACCCCCC	ACCCCCCAATCCCGACCGTAACCC
ArD38661SEN81	(841)	GCTGCCCCACCCCCC	ACCCCCCAATCCCAACCGTAACCC
BII43KEN//	(841)	GCTGCCCCACCCCCC	ACCCCCTAATCCCGACCGTAACCC
B314KEN62	(841) (841)	GCTGCCCCACCCCCC	ACCCCCTAATCCCGACCGTAACCC
H1825RSA/5	(841) (841)	GCTGCCCCACCCCCC	
LUNYOUGA55	(841) (841)		
RI002CAR03	(841) (841)		
SPUIUSUIKENU7	(841) (841)		
SPULUSUZKENU/	(841) (841)		
SPULUSU/RENU/ SPULUSU/RENU/	(041)	GCIGCCCACCCCC	
SP010515KEN07	(8/1)	GCIGCCCACCCCC	
SPU152RSA08	(841)	GCTGCCCCACCCCC	
SPU204ANGL85	(841)		
SPU2207KEN07	(841)	GCTGCCCTACCCCCC-	
SPU2214KEN07	(841)		ACCCCCCAGTCCCGACCGTAACCC
SPU2215KEN07	(841)	GCTGCCCCACCCCC-	ACCCCCCAATCCCGACCGTAACCC
SPU2220KEN07	(841)	GCTGCCCCACCCCC-	ACCCCCCAATCCCGACCGTAACCC
SPU2223KEN07	(841)	GCTGCCCCACCCCC	ACCCCCCAATCCCGACCGTAACCC
SPU384001KEN97	(841)	GCTGCCCCACCCCC-	ACCCCCCAATCCCGACCGTAACCC
SPU45ZAMB85	(841)	GCTGCCCCACCCCCC	ACCCCCCAATCCCGACTGTAACCC
SPU52001RSA99	(841)	GCTGCCCCACCCCC	ACCCCCCAATCCCGACCGTAACCC
SPU77NAMB04	(841)	GCTGCCCCACCCCC	ACCCCCCAATCCCGACCGTAACCC
SPU77RSA08	(841)	GCTGCCCCACCCCCC-	ACCCCCCAATCCCGACCGTAACCC
VRL1032ZIM78	(841)	GCTGCCCCACCCCCC-	ACCCCCCAATCCCGACCGTAACCC
VRL1290ZIM78	(841)	GCTGCC <mark>T</mark> CACCCCCC <mark>-</mark>	ACCCCCCAATCC <mark>T</mark> GACCGTAACCC
VRL1516ZIM78	(841)	GCTGCCCCACCCCCC	ACCCCCCAATCCCGACCGTAACCC
VRL1887ZIM78	(841)	GCTGCCCCACCCCCC-	ACCCCCCAATCCCGACCGTAACCC
VRL2230ZIM78	(841)	GCTGCCCCACCCCCC-	ACCCCCCAATCCCGACCGTAACCC
VRL763ZIM70	(841)	GCTGCCCCACCCCCC-	
VRL825ZIM79	(841)	GCTGCCCCACCCCCC-	ACCCCCCAATCCCGACCGTAACCC
ZH501EGY77	(841)	GCTGCCCCACCCCCC-	ACCCCCCAATCCCGACCGTAACCC
ZH548EGY77	(841)	GCTGCCCCACCCCCC-	ACCCCCCAATCCCGACCGTAACCC
Consensus	(841)	GCTGCCCCACCCCCC	ACCCCCCAATCCCGACCGTAACCC

 21445KEN83 (880) CAACCCCCAT_TTTCCCCCAACCCCCTGGCAGCCACTTA 56KEN65 (879) CAACCACCCC_TTTTCCCCAACCCCCTGGCAGCCCCTTA An1000MD91 (880) CAACCCCCCT_TTTCCCCAACCCCCCTGGCAGCCCCTTA An991MAD91 (880) CAACCCCCT_TTTCCCCAACCCCCCTGGCAGCCACTTA An991MAD91 (880) CAACCCCCT_TTTCCCCAACCCCCCTGGCAGCCACTTA An7040000000 (880) CAACCCCCT_TTTCCCCAACCCCCCTGGCAGCCACTTA An70400000000000000000000000000000000000			881	920
56KEM65 (879) CAACCACCCT_TTTCCCCAAACCCCCTGGCAGCCACTTA 900085MAU88 (881) CAACCACCCT_TTCCCCAAACCCCCTGGCAGCCACTTA An100MAD91 (880) CAACCCCCT_TTTCCCCAACCCCCTGGCAGCCACTTA An99MAD91 (880) CAACCCCCT_TTTCCCCAACCCCCTGGCAGCCACTTA An709MAD91 (880) CAACCCCCT_TTTCCCCAACCCCCTGGCAGCCACTTA An7080U84 (880) CAACCCCCT_TTCCCCCAACCCCCTGGCAGCCACTTA An712568RSA81 (890) CAACTCCCC_TTTCCCCCAACCCCTGGCAGCCACTTA Ar12568RSA81 (880) CAACTCCCC_TTCCCCCAACCCCTGGCAGCCACTTA Ar21229SA00 (879) CAACCACCCT_TTCCCCCAACCCCTGGCAGCCACTTA Ar38661SEN81 (880) CAACTCCCCT_TTCCCCCAACCCCTGGCAGCCACTTA B1143KEN77 (880) CAACCACCCCT_TTCCCCCAACCCCTGGCAGCCACTTA B1143KEN77 (880) CAACCACCCCT_TTCCCCCAACCCCTGGCAGCCACTTA H1825RSA75 (879) CAACCACCCCT_TTCCCCCAACCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCCT_TCCCCCAACCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCCT_TCCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCCT_TCTCCCCAACCCCCTGGCAGCCACTTA SPU10	214445KEN83	(880)	CAACCCCC <mark>A</mark> T	-TT <mark>C</mark> CCCC <mark>A</mark> ACCCCCTGGGCAGCCACTTA
900085M4088 (881) CAACCACCAT_TTTCCCCAACCCCCTGGCAGCCCTTA An991MAD91 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA An999MAD91 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA An7A0807GU184 (880) CAACCCCCT_TTTCCCCAACCCCCTGGCAGCCACTTA An7A0807GU184 (880) CAACCCCCT_TTTCCCCAACCCCCTGGCAGCCACTTA Ar12568RSA71 (879) CAACCCCCT_TTTCCCCCAACCCCCTGGCAGCCACTTA Ar20368RSA81 (880) CAACCCCCT_TTTCCCCCAACCCCCTGGCAGCCACTTA Ar20368RSA81 (880) CAACCCCCT_TTTCCCCCAACCCCCTGGCAGCCACTTA Ar20368RSA81 (880) CAACCCCCT_TTCCCCCAACCCCCTGGCAGCCACTTA Ar31MAD79 (880) CAACCCCCT_TTCCCCCAACCCCCTGGCAGCCACTTA Ar31MAD79 (880) CAACCCCCT_TTCCCCCAACCCCCTGGCAGCCACTTA B1143KEN77 (880) CAACCCCCT_TTCCCCCAACCCCCTGGCAGCCACTTA B144KEN62 (880) CAACCCCCCT_TTCCCCCAACCCCCTGGCAGCCACTTA H1825RSA75 (879) CAACCACCCCTTTCCCCCAACCCCCTGGCAGCCACTTA H1825RSA75 (879) CAACCACCCCTTTCCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCCTTTCCCCCAACCCCCTGGCAGCCACTTA SPU10302KEN07 (880) CAACCCCCCTTTCCCCCAACCCCCTGGCAGCCACTTA SPU10302KEN07 (880) CAACCCCCCTTTCCCCCAACCCCCTGGCAGCCACTTA SPU10302KEN07 (880) CAACCCCCAT_CTCCCCAACCCCCTGGCAGCCACTTA SPU10302KEN07 (880) CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTA SPU10302KEN07 (880) CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTA SPU10302KEN07 (880) CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTA SPU202S0M8 (879) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU202S0M8 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU202S0M8 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU202S0M8 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU221KEN07 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU221KEN07 (880) CAACCCCCCT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU221KEN07 (880) CAACCCCCCT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU221KEN07 (880) CAACCCCCCT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU221KEN07 (880) CAACCCCCCT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU34001KEN97 (77) CAACCCCCCT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU3201RSA9 (880) CAACCCCCCT_TTTCCCCCAACCCCCTGGCAGCCACTTA VRL1290ZIM78 (880) CAACCCCCCT_TTTCCCCCAACCCCCTGGCAGCCACTTA VRL1290ZIM78 (880) CAACCCCCCT_TTCCCCCAACCCCTGGCAGCCACTTA VRL1232IM78 (880) CAACCCCCCT_TTCCCCCAACCCCCTGGCAGCC	56KEN65	(879)	CAACC <mark>A</mark> CCCT	-TTT <mark>T</mark> CCCCAA <mark>A</mark> CCCCTGGGCAGCCACTTA
An1000MAD91 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA An999MAD91 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA AnK6087GUI84 (880) CAACCCCCT_TTTCCCCAACCCCCTGGCAGCCACTTA AntAMBULEGY94 (880) CAACTCCCC_TTTCCCCAACCCCCTGGCAGCCACTTA Ar1256BRSA11 (879) CAACCCCCC_TTTCCCCAACCCCTGGCAGCCACTTA Ar2036BRSA81 (880) CAACTCCCC_TTTCCCCAACCCCTGGCAGCCACTTA Ar2036BRSA81 (880) CAACTCCCC_TTTCCCCAACCCCTGGCAGCCACTTA Ar21229SA00 (879) CAACCCCCCT_TTCCCCAACCCCTGGCAGCCACTTA Ar214SA55 (880) CAACTCCCCT_TTCCCCAACCCCTGGCAGCCACTTA Ar3811MAD79 (880) CAACTCCCCT_TTCCCCAACCCCTGGCAGCCACTTA B114XEN77 (880) CAACTCCCCT_TTCCCCCAACCCCTGGCAGCCACTTA B114XEN77 (880) CAACCCCCCT_TTCCCCCAACCCCTGGCAGCCACTTA B114KEN62 (880) CAACCACCCCT_TTCCCCCAACCCCTGGCAGCCACTTA H1825RSA75 (879) CAACCACCCCT_TTCCCCCAACCCCTGGCAGCCACTTA LunyoUGA55 (880) TAACCCCCCT_TT_CCCCCAACCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCCT_TT_CCCCCAACCCCTGGCAGCCACTTA SPU10301KEN07 (879) CAACCCCCT_TT_CCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (879) CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTA SPU10307KEN07 (879) CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTA SPU10307KEN07 (879) CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTA SPU10307KEN07 (879) CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTA SPU10307KEN07 (879) CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTA SPU10307KEN07 (880) CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTA SPU204ANGL85 (880) CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTA SPU204ANGL85 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU221KEN07 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU221SKEN07 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU221SKEN07 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU221SKEN07 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU221SKEN07 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU221SKEN07 (880) CAACCCCCAT_TTCCCCAACCCCCTGGCAGCCACTTA SPU77NMB04 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU77NMB04 (880) CAACCCCCAT_TTCCCCAACCCCCTGGCAGCCACTTA VRL132IM78 (880) CAACCCCCAT_TTCCCCCAACCCCCTGGCAGCCACTTA VRL132IM78 (880) CAACCCCCAT_TTCCCCCAACCCCCTGGCAGCCACTTA VRL129ZIM78 (880) CAACCCCCCT_TTCCCCCAACCCCCTGGCAGCCACTTA	900085MAU88	(881)	CAACCACCC	C-TTCCCCCAA <mark>A</mark> CCCCTGGGCAGCC <mark>G</mark> CTTA
An991MAD91 (880) CAACCCCCT TTTCCCCAACCCCCTGGCAGCCACTTA An%087GUI84 (880) CAACCCCCT TTTCCCCAACCCCCTGGCAGCCACTTA AnTAMBULEGY94 (880) CAACTCCCC TTTCCCCAACCCCCTGGCAGCCACTTA Ar12568RSA11 (879) CAACCCCCC TTTCCCCCAACCCCTGGCAGCCACTTA Ar212568RSA1 (880) CAACTCCCC TTTCCCCCAACCCCTGGCAGCCACTTA Ar21229SA00 (879) CAACCCCCT TTTCCCCCAACCCCCTGGCAGCCACTTA Ar21229SA00 (879) CAACCCCCT TTTCCCCCAACCCCCTGGCAGCCACTTA Ar2129SA00 (879) CAACCCCCC TTTCCCCCAACCCCCTGGCAGCCACTTA Ar2128SA07 (880) CAACTCCCC TTTCCCCCAACCCCCTGGCAGCCACTTA Br143KEN77 (880) CAACTCCCC TTTCCCCCAACCCCCTGGCAGCCACTTA B1143KEN77 (880) CAACTCCCC TTTCCCCCAACCCCCTGGCAGCCACTTA B1143KEN77 (880) CAACCACCCC TTTCCCCCAACCCCCTGGCAGCCACTTA B1143KEN77 (880) CAACCACCCC TTTCCCCCAACCCCCTGGCAGCCACTTA LunyoUGA55 (880) CAACCACCCC TTTCCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCT TTCCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCC TTTCCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCT TTCCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCT TTTCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACTTA SPU204MGL85 (880) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACTTA SPU205SM98 (879) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACTTA SPU204KEN07 (880) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACTTA SPU220KEN07 (880) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACTTA SPU220KEN07 (880) CAACCCCCAT CTTCCCCAACCCCCTGGCCAGCCACTTA SPU220KEN07 (880) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACTTA SPU220KEN07 (880) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACTTA SPU220KEN07 (880) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACTTA SPU220KEN07 (880) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACTTA SPU220KEN07 (880) CAACCCCCAT TTCCCCCAACCCCCTGGCAGCCACTTA VRL1290ZIM78 (880) CAACCCCCAT TTCCCCCAACCCCCTGGCAGCCACTTA VRL1290ZIM78 (880) CAACCCCCAT TTCCCCCAACCCCCTGGCAGCCACTTA VRL1290ZIM78 (880) CAACCCCCAT TTCCCCCAACCCCCTGGCAGCCACTTA VRL1291ZIM78 (880) CAACCCCCCT TTCCCCCAACCC	An1000MAD91	(880)	CAACCCCC <mark>A</mark> T	-TTTCCCC <mark>A</mark> ACCCCCTGGGCAGCCACTTA
An999MAD91 (880) CAACCCCCT TTTCCCCAACCCCTGGCAGCCACTTA AntAMBULEGY94 (880) CAACTCCCT TTTCCCCCAACCCCTGGCAGCCACTTA Ar12568RSA71 (879) CAACCACCCT TTTCCCCCAACCCCTGGCAGCCACTTA Ar20368RSA81 (880) CAACTCCCC TTTCCCCCAACCCCTGGCAGCCACTTA Ar21229SA00 (879) CAACCACCCT TTTCCCCAACCCCTGGCAGCCACTTA Ar21229SA00 (879) CAACCACCCT TTTCCCCAACCCCTGGCAGCCACTTA Ar21229SA00 (879) CAACCACCCT TTTCCCCAACCCCTGGCAGCCACTTA Ar74RSA55 (880) CAACCACCCCT TTCCCCCAACCCCTGGCAGCCACTTA Ar138661SEN81 (880) CAACCACCCC TTTCCCCCAACCCCCTGGCAGCCACTTA B1143EN77 (880) CAACCACCCC TTTCCCCCAACCCCCTGGCAGCCACTTA B314KEN62 (880) CAACCACCCC TTTCCCCCAACCCCCTGGCAGCCACTTA B314KEN62 (880) CAACCACCCC TTTCCCCCAACCCCCTGGCAGCCACTTA LunyOGA55 (870) CAACCACCCC TTTCCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCACCCCT TTCCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCT TTCCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (879) CAACCCCCT TTCCCCAACCCCCTGGCAGCCACTTA SPU10307KEN07 (870) CAACCCCCT TTTCCCCAACCCCCTGGCAGCCACTTA SPU10307KEN07 (870) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACCTTA SPU10307KEN07 (880) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACTTA SPU10315KEN07 (880) CAACCCCCAT CTTCCCCAACCCCCTGGCAGCCACTTA SPU10307KEN07 (880) CAACCCCCAT TTTCCCCAACCCCCTGGCAGCCACTTA SPU204ANGL85 (880) CAACCCCCAT TTTCCCCAACCCCCTGGCAGCCACTTA SPU204ANGL85 (880) CAACCCCCAT TTTCCCCAACCCCCTGGCAGCCACTTA SPU204ANGL85 (880) CAACCCCCAT TTTCCCCAACCCCCTGGCAGCCACTTA SPU2207KEN07 (880) CAACCCCCAT TTTCCCCAACCCCCTGGCAGCCACTTA SPU2215KEN07 (880) CAACCCCCAT TTTCCCCAACCCCCTGGCAGCCACTTA SPU2207KEN07 (880) CAACCCCCAT TTTCCCCAACCCCCTGGCAGCCACTTA SPU32001KA99 (880) CAACCCCCAT TTTCCCCAACCCCCTGGCAGCCACTTA VRL1290ZIM78 (880) CAACCCCCAT TTTCCCCCAACCCCCTGGCAGCCACTTA VRL232IM78 (880) CAACCCCCAT T	An991MAD91	(880)	CAACCCCC <mark>A</mark> T	-TTTCCCC <mark>A</mark> A <mark>C</mark> CCCCCTGGGCAGCCACTTA
AnK6087GUI84 (880) CAACCCCCTTTTCCCCAACCCCCTGGCAGCCACTTA AnTAMBULEGY94 (880) CAACTCCCCTTTCCCCCAACCCCTGGCAGCCACTTA Ar20368RSA81 (880) CAACTCCCCTTTTCCCCAACCCCTGGCAGCCACTTA Ar20368RSA81 (880) CAACTCCCCTTTTCCCCAACCCCCTGGCAGCCACTTA Ar2129SA00 (879) CAACCCCCCTTTTCCCCAACCCCCTGGCAGCCACTTA Ar21ASA55 (880) CAACTCCCCTTTCCCCCAACCCCTGGCAGCCACTTA Ar3811MAD79 (880) CAACTCCCCTTTCCCCCAACCCCTGGCAGCCACTTA B1143KEN77 (880) CAACTCCCCTTTCCCCCAACCCCTGGCAGCCACTTA B1143KEN77 (880) CAACCCCCCTTTCCCCCAACCCCTGGCAGCCACTTA B144EN62 (880) CAACCACCCCTTTCCCCCAACCCCTGGCAGCCACTTA B144EN62 (880) CAACCACCCCTTTCCCCAACCCCTGGCAGCCACTTA LunyoUGA55 (879) CAACCACCCCTTTCCCCCAACCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCTTTCCCCCAACCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCTTTCTCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCTTTCTCCCCAACCCCCTGGCAGCCACTTA SPU10307KEN07 (880) CAACCCCCTTTCTCCCCAACCCCCTGGCAGCCACTTA SPU10307KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU10307KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU10307KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU10307KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU12002S0M98 (879) CAACCCCCATCTTCTCCCAACCCCCTGGCAGCCACTTA SPU204ANGL85 (880) CAACCCCCATCTTCTCCCAACCCCCTGGCAGCCACTTA SPU204ANGL85 (880) CAACCCCCATCTTCTCCCAACCCCCTGGCAGCCACTTA SPU204ANGL85 (880) CAACCCCCATCTTCTCCCAACCCCCTGGCAGCCACTTA SPU204KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU220KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU220KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU220KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU220KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU220KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU220KEN07 (880) CAACCCCCATCTTCTCCCAACCCCCTGGCAGCCACTTA SPU220KEN07 (880) CAACCCCCATCTTCTCCCCAACCCCCTGGCAGCCACTTA VRL1932IM78 (880) CAACCCCCTTCTTCCCCAACCCCCTGGCAGCCACTTA VRL1932IM78 (880) CAACCCCCTTTTCCCCCAACCCCCTGGCAGCCACTTA VRL1932IM78 (880) CAACCCCCTTTTCCCCCAACCCCCTGGCAGCCACTTA VRL1932IM78 (880) CAACCCCCCTTTTCCCCCAACCCCCTGGCAGCCACTTA VRL1932IM79 (880)	An999MAD91	(880)	CAACCCCCCT	-TTTCCCC <mark>A</mark> A <mark>C</mark> CCCCCTGGGCAGCCACTTA
AnTAMBULEGY94 (880) CAACTCCCC - TTCCCCCAACCCCTGGGCAGCCACTTA Ar12568RSA1 (870) CAACCACCCC - TTCCCCCAACCCCTGGGCAGCCACTTA Ar21229SA00 (879) CAACCACCCC - TTCCCCCAACCCCTGGGCAGCCACTTA Ar21229SA00 (879) CAACCACCCC - TTCCCCCAACCCCCTGGGCAGCCACTTA Ar21229SA00 (879) CAACCACCCC - TTCCCCCAACCCCCTGGGCAGCCACTTA Ar3036615EN81 (880) CAACCACCCC - TTCCCCCAACCCCCTGGGCAGCCACTTA B1143KEN77 (880) CAACCACCCC - TTCCCCCAACCCCCTGGGCAGCCACTTA B1445EN575 (870) CAACCACCCC - TTCCCCCAACCCCCTGGGCAGCCACTTA LunyoUGA55 (880) CAACCACCCC - TTCCCCCAACCCCTGGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCCT - TTCCCCAACCCCCTGGGCAGCCACTTA SPU10302KEN07 (880) CAACCCCCAT - CTTCCCCAACCCCCTGGGCAGCCACTTA SPU10307KEN07 (880) CAACCCCCAT - CTTCCCCAACCCCCTGGGCAGCCACTTA SPU10307KEN07 (880) CAACCCCCAT - CTTCCCCAACCCCCTGGCAGCCACTTA SPU10307KEN07 (880) CAACCCCCAT - CTTCCCCAACCCCCTGGCAGCCACTTA SPU2025N98 (879) CAACCCCCAT - TTTCCCCAACCCCCTGGCAGCCACTTA SPU214KEN07 (880) CAACCCCCAT - TTTCCCCAACCCCCTGGCAGCCACTTA SPU2204NGL85 (88	AnK6087GUI84	(880)	CAACCCCC <mark>T</mark> T	TT-CCCCCAACCCCTGGGCAGCCACTTA
Ar12568R5A71 (879) CAACCCCCCTTTTCCCCAAACCCCTTGGCAGCACCTATA Ar20368R5A81 (880) CAACTCCCCTTTCCCCAACCCCTTGGCAGCACCTATA Ar74R5A55 (880) CAACCCCCTTTTCCCCCAACCCCTGGCAGCCACTTA Ar811MAD79 (880) CAACTCCCCCTTTCCCCCAACCCCTGGCAGCCACTTA ArB1MAD79 (880) CAACTCCCCCTTCCCCCAACCCCCTGGCAGCCACTTA B1143KEN77 (880) CAACCACCCCTTTCCCCCAACCCCCTGGCAGCCACTTA B114XEN62 (880) CAACCACCCCTTTCCCCCAACCCCCTGGCAGCCACTTA LunyoUGA55 (880) CAACCACCCCCTTTCCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCCTTTCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCTTTCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU10302KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU10315KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU207KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU201KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA SPU207KEN07 (880) CAACCCCCATCTTCCCCAACCCCCTGGCAGCCACTTA <td>AnTAMBULEGY94</td> <td>(880)</td> <td>CAAC<mark>T</mark>CCCC<mark>-</mark></td> <td>TTCCCCCCAACCCCCTGGGCAGCCACTTA</td>	AnTAMBULEGY94	(880)	CAAC <mark>T</mark> CCCC <mark>-</mark>	TTCCCCCCAACCCCCTGGGCAGCCACTTA
Ar2036885A81 (880) CAACTCCCC_TTCCCCAACCCCTTGGCAGCCACTTA Ar212295A00 (879) CAACCCCCT_TTTCCCCAACCCCTGGCAGCCACTTA Ar811MAD79 (880) CAACCCCCCT_TTCCCCCAACCCCCTGGCAGCCACTTA Ar811MAD79 (880) CAACCACCCCT_TTCCCCCAACCCCCTGGCAGCCACTTA B114XEN77 (880) CAACCACCCCT_TTCCCCCAACCCCCTGGGCAGCCACTTA B114XEN62 (880) CAACCACCCCT_TTCCCCCAACCCCCTGGGCAGCCACTTA H1825RSA75 (879) CAACCACCCCTTTTCCCCCAACCCCCTGGGCAGCCACTTA LunyoUGA55 (880) TAACCCCCCT_TT_CCCCCAACCCCCTGGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTA SPU10302KEN07 (880) CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTA SPU10307KEN07 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTA SPU10302SM98 (879) CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTA SPU10302SM98 (879) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU204ANGL85 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU2207KEN07 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTA SPU2214KEN07 (880) CAACCCCCAT_TTTC	Ar12568RSA71	(879)	CAACC <mark>A</mark> CCC <mark>C</mark>	TTTTCCCCAAAACCCCTGGGCAGCCACTTA
Ar21229SA00 (879) CAACCCCCT_TTTCCCCCAACCCCTGGGCAGCCACTTA Ar74RSA55 Ar74RSA55 (880) CAACCACCCCT_TTCCCCCCAACCCCTGGGCAGCCACTTA B1143KEN77 ArD38661SEN81 (880) CAACCACCCCT_TCCCCCCAACCCCTGGGCAGCCACTTA B1143KEN77 B1143KEN77 (880) CAACCACCCCT_TCCCCCCAACCCCTGGGCAGCCACTTA B1143KEN77 B144KEN62 (880) CAACCACCCCT_TCCCCCAACCCCTGGGCAGCCACTTA LUNYOUGA55 H1825RSA75 (879) CAACCACCCCTTTTCCCCCAACCCCTGGGCAGCCACTTA SPU10301KEN07 SPU10302KEN07 (880) CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTA SPU10307KEN07 SPU10307KEN07 (879) CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTA SPU10307KEN07 SPU10305KEN07 (880) CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTA SPU10202S0M98 SPU12002S0M98 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTA SPU204ANGL5 SPU204ANGL5 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTA SPU220KEN07 SPU2214KEN07 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTA SPU220KEN07 SPU2215KEN07 (880) CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTA SPU220KEN07 SPU2220KEN07 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTA SPU220KEN07 SPU220KEN07 (880) CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTA SPU220KEN07 <	Ar20368RSA81	(880)	CAAC <mark>T</mark> CCCC <mark>-</mark>	TTCCCCCCAACCCCTTGGGCAGCCACTTA
Ar74RSA55 (880) CAACCCCCCTTTTCCCCCAAACCCCTGGGCAGCCACTTA Ar038661SEN81 (880) CAACCACCCCTTTCCCCCCAAACCCCTGGGCAGCCACTTA B1143KEN77 (880) CAACCACCCCTTTCCCCCAAACCCCTGGGCAGCCACTTA B1143KEN77 (880) CAACCACCCCTTTCCCCCAAACCCCTGGGCAGCCACTTA LunyoUGA55 (880) CAACCACCCCTTTCCCCCAAACCCCTGGGCAGCCACTTA Ar038661SEN85 (880) CAACCACCCCTTTCCCCCAAACCCCTGGGCAGCCACTTA LunyoUGA55 (880) TAACCACCCCTTTCCCCCAAACCCCTGGGCAGCCACTTA SPU10301KEN07 (880) CAACCACCCCTTCTCCCCCAACCCCCTGGGCAGCCACTTA SPU10301KEN07 (880) CAACCCCCTTCTCCCCAACCCCCTGGGCAGCCACTTA SPU10307KEN07 (879) CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTA SPU10315KEN07 (880) CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTA SPU10315KEN07 (880) CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTA SPU1202SOM98 (879) CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTA SPU1202SOM98 (879) CAACCCCCAT-TTTCCCCAACCCCCCTGGGCAGCCACTTA SPU1202SOM98 (880) CAACCCCCAT-TTTCCCCAACCCCCCTGGGCAGCCACTTA SPU204ANGL85 (880) CAACCCCCAT-TTTCCCCAACCCCCCTGGGCAGCCACTTA SPU2207KEN07 (880) CAACCCCCAT-TTTCCCCAACCCCCCTGGGCAGCCACTTA SPU2214KEN07 (880) CAACCCCCAT-TTTCCCCAACCCCCCTGGGCAGCCACTTA SPU2215KEN07 (880) CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTA SPU2223KEN07 (880) CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTA SPU2223KEN07 (880) CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTA SPU2223KEN07 (880) CAACCCCCAT-TTTCCCCAACCCCCCTGGGCAGCCACTTA SPU45ZAMB5 (880) CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTA SPU45ZAMB5 (880) CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTA SPU52001RSA99 (80) CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTA SPU52001RSA99 (80) CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTA SPU77NAM64 (880) CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTA VRL1032ZIM78 (880) CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTA VRL1032ZIM78 (880) CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTA VRL1872IM78 (880) CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTA VRL1872IM78 (880) CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTA VRL1872IM78 (880) CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTA VRL85ZIM79 (880) CAACCCCCCT-TTCCCCCAACCCCCTGGGCAGCCACTTA VRL85ZIM79 (880) CAACCCCCCT-TTCCCCCAACCCCCTGGGCAGCCACTTA VRL85ZIM79 (880) CAACCCCCCT-TTCCCCCCAACCCCCTG	Ar21229SA00	(879)	CAACCCCC <mark>A</mark> T	-TTT <mark>T</mark> CCC <mark>A</mark> ACCCCCTGGGCAGCCACTTA
Ar811MAD79(880)CAACTCCCC-TTCCCCCAACCCCCTGGCAGCACTTAArD38661SEN81(880)CAACCACCCTTCCCCCAACCCCCTGGCAGCCACTTAB1143EN77(880)CAACCACCCCTTTCCCCCAACCCCCTGGCAGCCACTTAH1825RSA75(879)CAACCACCCCTTTCCCCCAACCCCTGGCAGCCACTTALunyoUGA55(880)CAACCACCCCTTTCCCCCAACCCCTGGCAGCCACTTASPU10301KEN07(880)CAACCCCCTTCTCCCCAACCCCCTGGCAGCCACTTASPU10301KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGCAGCCACTTASPU10307KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGCAGCCACTTASPU10315KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGCAGCCACTTASPU10307KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGCAGCCACTTASPU10307KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU10307KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU202SoM98(877)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU204ANGL85(880)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU2207KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGCAGCCACTTASPU2214KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGCAGCCACTTASPU2220KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU2200KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU452AMB85(880)CAACCCCCAT-TTCCCCAACCCCCTGGCAGCCACTTASPU52001RSA99(880)CAACCCCCT-TTTCCCCAACCCCCTGGCAGCCACTTASPU77NAMB04(880)CAACCCCCT-TTCCCCCAACCCCCTGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCCT-TTCCCCCAACCCCTGGCAGCCACTTAVRL1230ZIM78(880)CAACCCCC	Ar74RSA55	(880)	CAACC <mark>A</mark> CCC <mark>C</mark>	I-TTCCCCCAAAACCCCTGGGCAGCCACTTA
ArD38661SEN81(880)CAACCACCCCT-TCCCCCAACCCCCTGGCAGCACTTAB1143KEN77(880)CAACCACCCC-TTCCCCCAACCCCCTGGCAGCACCTAH1825RSA75(879)CAACCACCCCTTTCCCCCAACCCCTGGCAGCCACTTALunyoUGA55(880)CAACCACCCCTTTCCCCCAACCCCCTGGCAGCCACTCASPU10301KEN07(880)CAACCCCCT-TT-CCCCCAACCCCCTGGCAGCCACTTASPU10302KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGCAGCCACTTASPU10307KEN07(879)CAACCCCCAT-CTTCCCCAACCCCCTGGCAGCCACTTASPU10315KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGCAGCCACTTASPU10315KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU10315KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU10315KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU202ANGL85(880)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU2207KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU2214KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGCAGCCACTTASPU220KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGCAGCCACTTASPU2223KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU52001RSA99(880)CAACCCCCAT-TTTCCCCAACCCCCTGGCCAGCCACTTASPU77NAMB4(880)CAACCCCCAT-TTCCCCCAACCCCCTGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCT-TTCCCCCAACCCCCTGGCAGCCACTTAVRL1887ZIM78(880)CAACCCCCT-TTCCCCCAACCCCCTGGCAGCCACTTAVRL1825ZIM79(880)<	Ar811MAD79	(880)	CAAC <mark>T</mark> CCCC <mark>C</mark>	-TT <mark>C</mark> CCCCCAACCCCTGGGCAGCCACTTA
B1143kEN77(880)CAACCCCCT_TCCCCCAACCCCCTGGCAGCACTTAB314kEN62(880)CAACCACCCC_TTTCCCCCAACCCCCTGGCAGCCACTTAH1825RSA75(870)CAACCACCCCTTTCCCCCAACCCCCTGGCAGCCACTTALunyoUGA55(880)TAACCCCCT_TT_CCCCAACCCCCTGGCAGCCACTTASPU10301kEN07(880)CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTASPU10307kEN07(880)CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTASPU10307kEN07(870)CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTASPU10307kEN07(870)CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTASPU10315kEN07(880)CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTASPU12002SOM98(879)CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTASPU204ANGL85(880)CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTASPU2207kEN07(880)CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTASPU2215kEN07(880)CAACCCCCAT_CTTCCCCAACCCCCTGGCAGCCACTTASPU2215kEN07(880)CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTASPU220kEN07(880)CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTASPU220kEN07(880)CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTASPU352001RSA99(880)CAACCCCCAT_TTTCCCCAACCCCCTGGCAGCCACTTASPU77RSA08(880)CAACCCCCT_TTCCCCAACCCCCTGGCAGCCACTTAVRL1032Z1M78(880)CAACCCCCT_TTCCCCAACCCCCTGGCAGCCACTTAVRL1032Z1M78(880)CAACCCCCT_TTCCCCAACCCCCTGGCAGCCACTTAVRL1032Z1M78(880)CAACCCCCT_TTCCCCCAACCCCTGGCAGCCACTTAVRL1032Z1M78(880)CAACCCCCT_TTCCCCCAACCCCTGGCAGCCACTTAVRL103Z1M78(880)CAACCCCCT_TT	ArD38661SEN81	(880)	CAACC <mark>A</mark> CCC <mark>C</mark>	I-TTCCCCCAAACCCCTGGGCAGCCACTTA
B314kEN62(880)CAACCACCCCTTTCCCCCAAACCCCCTGGGCAGCCACTTAH1825RSA75(879)CAACCACCCCCTTTTCCCCCAAACCCCTGGGCAGCCACTTALunyoUGA55(880)TAACCCCCCTTTTCCCCCAAACCCCTGGGCAGCCACTTASPU10301KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU10307KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU10307KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU10315kEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU10315kEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU10202S0M98(879)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU152RSA08(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU204ANGL85(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU2214kEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU2215kEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU2223kEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU223kEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU384001KEN97(879)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU52001RSA99(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU77NAME04(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1230ZIM78(880)CAACCCCCT-TTCCCCCAACCCCCTGGGCAGCCACTTA <t< td=""><td>B1143KEN77</td><td>(880)</td><td>CAACTCCCCT</td><td>-T<mark>CC</mark>CCCC<mark>A</mark>ACCCCCTGGGCAGCCACTTA</td></t<>	B1143KEN77	(880)	CAACTCCCCT	-T <mark>CC</mark> CCCC <mark>A</mark> ACCCCCTGGGCAGCCACTTA
H1825R375(879)CAACCACCCCCTTTTCCCCAAACCCCCTGGGCAGCCACTTALunyoUGA55(880)CAACCACCCCTTTCCCCCAACCCCCTGGGCAGCCACTCASPU10301KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU10307KEN07(879)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU10307KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU10315KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU10307KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU1202SOM98(879)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU1202SOM98(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU1202SOM98(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU1202SOM98(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU1202SOM98(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU204ANGL85(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU2214KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU220KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU220KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU45ZAME85(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU52001RSA99(880)CAACCCCCAT-TTCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL190ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL187ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCTGGGCAGCCACTTAVRL18230IM78(880)CAACCCCCCT-TTCCCCCAACCCCTGGGCAGCCACTTAVRL2302IM78<	B314KEN62	(880)	CAACC <mark>A</mark> CCC <mark>C</mark>	-TTTCCCCCAA <mark>A</mark> CCCCTGGGCAGCCACTTA
LunyoUGA55(880)CAACCACCCCCTTTCCCCCAACCCCTGGGCAGCCACTCAR1662CAR85(880)TAACCCCCATTCTCCCCAACCCCCTGGGCAGCCACTTASPU10301KEN07(880)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTASPU10307KEN07(879)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTASPU10315KEN07(880)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTASPU10315KEN07(880)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTASPU10202SOM98(879)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTASPU152RSA08(880)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTASPU204ANGL85(880)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTASPU2207KEN07(880)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTASPU2215KEN07(880)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTASPU2220KEN07(880)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTASPU2220KEN07(880)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTASPU452AMB85(880)CAACCCCCATCTTCTCCCAACCCCCTGGGCAGCCACTTASPU52001RSA99(880)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTAVRL187ZIM78(880)CAACCCCCATCTTCCCCAACCCCCTGGGCAGCCACTTAVRL187ZIM78(880)CAACCCCCCTCTTTCCCCAACCCCCTGGGCAGCCACTTAVRL1823UM7(880)CAACCCCCCTCTTTCCCCAACCCCCTGGGCAGCCACTTAVRL1827IM78(880)CAACCCCCCTTTTCCCCCAACCCCTGGGCAGCCACTTAVRL1827IM78(880)CAACCCCCCTTTTCCCCCAACCCCTGGGCAGCCACTTAVRL2230ZIM78(880)	H1825RSA75	(879)	CAACC <mark>A</mark> CCC <mark>C</mark>	CTTT <mark>T</mark> CCCCAA <mark>A</mark> CCCCTGGGCAGCCACTTA
R1662CAR85(880)TAACCCCCCT_TT_CCCCCAACCCCCTGGGCAGCCACTTASPU10301KEN07(880)CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTASPU10307KEN07(879)CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTASPU10315KEN07(880)CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTASPU10315KEN07(880)CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTASPU10202SOM98(879)CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTASPU12002SOM98(879)CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTASPU1202SOM98(880)CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTASPU1202SOM98(880)CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTASPU204ANGL85(880)CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTASPU2217KEN07(880)CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTASPU2215KEN07(880)CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTASPU2220KEN07(880)CAACCCCCAT_TTCCCCAACCCCCTGGGCAGCCACTTASPU2223KEN07(880)CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTASPU2204KN07(879)CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTASPU384001KEN97(879)CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTASPU52001RSA99(880)CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACCCCCAT_TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCCT_TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1290ZIM78(880)CAACCCCCCT_TTCCCCCAACCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCCT_TTCCCCCAACCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCCT_TTCCCCCAACCCCTGGGCAGCCACTTAVRL825	LunyoUGA55	(880)	CAACCACCCC	CTTTCCCCCAA <mark>A</mark> CCCCTGGGCAGCCACT <mark>C</mark> A
SPU10301KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGCAGCCACTTASPU10302KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGCAGCCACTTASPU10315KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGCAGCCACTTASPU12002SOM98(879)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU12002SOM98(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU1202SNM98(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU1202ANGL85(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGTCACTTASPU2207KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCCTGGGCAGTCACTTASPU2215KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU2215KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU2220KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU2223KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU452AMB85(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU52001RSA99(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACCCCCAT-TTCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT-TTCCCCAACCCCCTGGGCAGCCACTTAVRL1290ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1887ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT-TTCCCCCAACCCCTGGGCAGCCACTTAVRL2230ZIM78(880)CAACCCCCT-TTCCCCAACCCCCTGGCAGCCACTTAVRL825ZIM79(880)CAACCCCCT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL825ZIM79 </td <td>R1662CAR85</td> <td>(880)</td> <td>TAACCCCCCT</td> <td>TT-CCCCCAACCCCCTGGGCAGCCACTTA</td>	R1662CAR85	(880)	TAACCCCCCT	TT-CCCCCAACCCCCTGGGCAGCCACTTA
SPU10302KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGCAGCCACTTASPU10307KEN07(879)CAACCCCCAT-CTTCCCCAACCCCCTGGCAGCCACTTASPU10315KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU1202SOM98(879)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU152RSA08(880)CAACCCCCAT-TTTCCCCAACCCCCTGGCAGCCACTTASPU204ANGL85(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU2217KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU2215KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU2220KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU223KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU384001KEN97(879)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU45ZAMB85(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU52001RSA99(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT-TTCCCCAACCCCCTGGGCAGCCACTTAVRL190ZIM78(880)CAACCCCCAT-TTCCCCAACCCCCTGGGCAGCCACTTAVRL1887ZIM78(880)CAACCCCCT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL2230ZIM78(880)CAACCCCCT-TTCCCCAACCCCCTGGCAGCCACTTAVRL2230ZIM78(880)CAACCCCCT-TTCCCCAACCCCCTGGCAGCCACTTAVRL2230ZIM78(880)CAACCCCCT-TTCCCCCAACCCCCTGGCAGCCACTTAVRL225ZIM79(880)CAACCCCCT-TTCCCCCAACCCCCTGGCAGCCACTTAZH501EGY77(880)CAACCCCCT-TTCCCCCAACCCCCTGGCAGCCACTTAConsensus(881) <td>SPU10301KEN07</td> <td>(880)</td> <td>CAACCCCCAT</td> <td>-CTTCCCCAACCCCCTGGGCAGCCACTTA</td>	SPU10301KEN07	(880)	CAACCCCCAT	-CTTCCCCAACCCCCTGGGCAGCCACTTA
SPU10307KEN07(879)CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU10315KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU1202SOM98(879)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU1202SOM98(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU120RANGL85(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU207KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU2214KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU2215KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU2220KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU223KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU384001KEN97(879)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU45ZAMB85(880)CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTASPU45ZAMB85(880)CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1887ZIM78(880)CAACCCCCCT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL2230ZIM78(880)CAACCCCCCT-TTTCCCCCAACCCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACCCCCT-TTTCCCCCAACCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACCCCCT-TTCCCCCAACCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACCCCCT-TTCCCCCAACCCCTGGGCAGCCACTTAZH501EGY77(880)CAACCCCCT-TTCCCCCAACCCCTGGGCAGCCACTTAConsensus <td>SPU10302KEN07</td> <td>(880)</td> <td>CAACCCCCAT</td> <td>-CTTCCCCAACCCCCCTGGGCAGCCACTTA</td>	SPU10302KEN07	(880)	CAACCCCCAT	-CTTCCCCAACCCCCCTGGGCAGCCACTTA
SPU10315KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU12002SOM98(879)CAACCCCCAT-TTTCCCCAACCCCCCTGGGCAGCCACTTASPU152RSA08(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU204ANGL85(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGTCACTTASPU207KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGTCACTTASPU2214KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU2215KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU2220KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU2223KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU384001KEN97(879)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU452AMB85(880)CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACCCCCAT-CTTCCCCCAACCCCCTGGGCAGCCACTTASPU77RSA08(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1990ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL187ZIM78(880)CAACCCCCT-TTCCCCCAACCCCCTGGCAGCCACTTAVRL187ZIM78(880)CAACCCCCT-TTTCCCCCAACCCCCTGGCAGCCACTTAVRL203ZIM78(880)CAACCCCCT-TTCCCCCAACCCCCTGGCAGCCACTTAVRL203ZIM78(880)CAACCCCCT-TTCCCCCAACCCCCTGGCAGCCACTTAVRL1887ZIM79(880)CAACCCCCT-TTTCCCCCAACCCCCTGGCAGCCACTTAVRL203ZIM78(880)CAACCCCCT-TTCCCCCAACCCCCTGGCAGCCACTTAVRL203ZIM79(880)CAACCCCCT-TTCCCCCAACCCCCTGGCAGCCACTTAVRL203ZIM79(8	SPU10307KEN07	(879)	CAACCCCCAT	-CTTCCCCAACCCCCTGGGCAGCCACTTA
SP012002S0M98(879)CAACCCCCAT_TTTCCCCAACCCCCCTGGGCAGCCACTTASPU152RSA08(880)CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTASPU204ANGL85(880)CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTASPU207KEN07(880)CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGTCACTTASPU2214KEN07(880)CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTASPU2215KEN07(880)CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTASPU220KEN07(880)CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTASPU223KEN07(880)CAACCCCCAT_CTTCCCCAACCCCCTGGGCAGCCACTTASPU384001KEN97(879)CAACCCCCAT_TTTCCCCAACCCCCTGGGCAGCCACTTASPU45ZAMB85(880)CAACCCCCAT_TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACCCCCAT_TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77RSA08(880)CAACCCCCAT_TTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT_TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1290ZIM78(880)CAACCCCCT_TTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1887ZIM78(880)CAACCCCCT_TTTCCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT_TTTCCCCCAACCCCCTGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT_TTTCCCCCAACCCCCTGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT_TTTCCCCCAACCCCCTGGCAGCCACTTAVRL25ZIM79(880)CAACCCCCT_TTTCCCCCAACCCCCTGGCAGCCACTTAVRL25ZIM79(880)CAACCCCCT_TTTCCCCCAACCCCCTGGCAGCCACTTAVRL825ZIM79(880)CAACCCCCT_TTTCCCCCAACCCCTGGCAGCCACTTAZH548EGY77(880)CAACTCCC-TTCCCCCCACCCCTGGCCAGCCACTTAConsensus(881) <td>SPULU315KENU/</td> <td>(880)</td> <td>CAACCCCCAT</td> <td></td>	SPULU315KENU/	(880)	CAACCCCCAT	
SP0152RSA08(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU204ANGL85(880)CAACCCCCAT-TTTCCCCAACCCCCCTGGGCAGTCACTTASPU2207KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCCTGGGCAGTCACTTASPU2215KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU2220KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU2223KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU2223KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU384001KEN97(879)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU45ZAMB85(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77RA08(880)CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCTGGGCAGCCACTTAVRL1516ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCTGGGCAGCCACTTAVRL1887ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCTGGGCAGCCACTTAVRL63ZIM70(879)CAACCCCCT-TTTCCCCCAACCCCTGGGCAGCCACTTAVRL63ZIM79(880)CAACCCCCT-TTCCCCCAACCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACCCCCT-TTCCCCCAACCCCTGGGCAGCCACTTAZH548EGY77(880)CAACCCCCT-TTCCCCCAACCCCTGGGCAGCCACTTAConsensus(881)CAACCCCCT <tttcccccaacccctgggcagccactta< td=""></tttcccccaacccctgggcagccactta<>	SPUIZUUZSOM98	(8/9)	CAACCCCCAT	
SP0204ANGL85(880)CAACCCCCAT-TTTCCCCAACCCCCCTGGGCAGCCACTTASP0207KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCCTGGGCAGTCACTTASP02215KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASP02220KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASP02223KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASP02223KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASP02223KEN07(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASP0384001KEN97(879)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASP0452001RSA99(880)CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTASP077NAMB04(880)CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTASP077RSA08(880)CAACCCCCAT-GTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1290ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1887ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT-TTCCCCCAACCCCTGGGCAGCCACTTAVRL325ZIM79(880)CAACCCCC-TTTCCCCCAACCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACCCCC-TTCCCCCAACCCCCTGGGCAGCCACTTAZH501EGY77(880)CAACCCCC-TTCCCCCAACCCCTGGGCAGCCACTTAConsensus(881)CAACCCCCT <tttcccccaaccccctgggcagccactta< td=""></tttcccccaaccccctgggcagccactta<>	SPUI52RSAU8	(880)	CAACCCCCAT	
SPU2207KEN07(880)CAACCCCCAT-TTTCCCC-AACCCCCCTGGGCAGTCACTTASPU2214KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU2215KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU2220KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU2223KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCTGGGCAGCCACTTASPU384001KEN97(879)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU384001KEN97(880)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU452001RSA99(880)CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACCCCCAT-CTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1290ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1887ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT-TTCCCCCAACCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT-TTCCCCCAACCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT-TTCCCCCAACCCCTGGGCAGCCACTTAVRL230ZIM79(880)CAACCCCCT-TTCCCCCAACCCCTGGGCAGCCACTTAVRL252ZIM79(880)CAACCCCCT-TTCCCCCAACCCCTGGGCAGCCACTTAZH501EGY77(880)CAACTCCC-TTCCCCCAACCCCTGGGCAGCCACTTAZH548EGY77(880)CAACTCCC-TTCCCCCAACCCCCTGGGCAGCCACTTAConsensus(881)CAACCCCCT <tttcccccaaccccctgggcagccactta< td=""></tttcccccaaccccctgggcagccactta<>	SPUZU4ANGL85	(880)	CAACCCCCAT	
SPU2214KEN07(880)CAACCCCCAT-TTTCCCCCAACCCCCCTGGGCAGCACTAASPU2215KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU2223KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU384001KEN97(879)CAACCCCCAT-TTTCCCCAACCCCCCTGGGCAGCCACTTASPU384001KEN97(879)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU45ZAMB85(880)CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTASPU52001RSA99(880)CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACCCCCAT-CTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1290ZIM78(880)CAACCCCCCT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1887ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL252IM79(880)CAACCCCCT-TTTCCCCCAACCCCCTGGGCAGCCACTTAZH501EGY77(880)CAACCCCC-TTTCCCCCAACCCCCTGGGCAGCCACTTAZH548EGY77(881)CAACCCCCT-TTCCCCCAACCCCCTGGGCAGCCACTTAConsensus(881)CAACCCCCT <tttcccccaaccccctgggcagccactta< td=""></tttcccccaaccccctgggcagccactta<>	SPUZZU/KENU/	(880)		
SP02215XEN07(880)CAACCCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU2220KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU2223KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU384001KEN97(879)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU45ZAMB85(880)CAACCCCCAT-TTCCCCAACCCCCTGGGCAGCCACTTASPU52001RSA99(880)CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACTCCCC-TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77RSA08(880)CAACCCCCAT-CTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1290ZIM78(880)CAACTCCCC-TTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1516ZIM78(880)CAACCCCCT-AT-CCCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCC-TTTTCCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCC-TTTTCCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCC-TTTTCCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCC-TTTTCCCCCAACCCCCTGGGCAGCCACTTAVRL252IM79(880)CAACCCCCC-TTTTCCCCCAACCCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACTCCCC-TTTCCCCCAACCCCCTGGGCAGCCACTTAZH501EGY77(880)CAACTCCCC-TTTCCCCCCAACCCCCTGGGCAGCCACTTAK81)CAACCCCCCTTTTCCCCCAACCCCCTGGCAGCCACTTA	SPUZZI4KENU/	(000)		
SP02220KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU2223KEN07(880)CAACCCCCAT-CTTCCCCAACCCCCCTGGGCAGCCACTTASPU384001KEN97(879)CAACCCCCAT-TTTCCCCAACCCCCTGGGCAGCCACTTASPU45ZAMB85(880)CAACCCCCAT-TTCCCCCAACCCCCTGGGCAGCCACTTASPU52001RSA99(880)CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACCCCCAT-CTTCCCCCAACCCCCTGGGCAGCCACTTASPU77RSA08(880)CAACCCCCAT-CTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCT-TTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1516ZIM78(880)CAACTCCCC-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1887ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCC-TTTCCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCC-TTTCCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCC-TTTCCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCC-TTTCCCCCAACCCCCTGGGCAGCCACTTAVRL252IM79(880)CAACCCCC-TTTCCCCCAACCCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACTCCCC-TTCCCCCAACCCCCTGGGCAGCCACTTAZH501EGY77(880)CAACTCCCC-TTCCCCCAACCCCCTGGGCAGCCACTTAZH548EGY77(881)CAACCCCCT(881)CAACCCCCTConsensus(881)CAACCCCCTTTTCCCCCAACCCCCTGGGCAGCCACTTA	SPUZZIJKENU/	(000)		
SP02223KEN07(880)CAACCCCCCATCITCCCCAACCCCCTGGGCAGCCACTTASPU384001KEN97(879)CAACCCCCATTTTCCCCAACCCCCTGGGCAGCCACTTASPU45ZAMB85(880)CAACCCCCATTTTCCCCAACCCCCTGGGCAGCCACTTASPU52001RSA99(880)CAACCCCCATTTTCCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACCCCCATTTTCCCCCAACCCCCTGGGCAGCCACTTASPU77RSA08(880)CAACCCCCATTTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCATTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1290ZIM78(880)CAACTCCCCTTCCCCCCAACCCCCTGGGCAGCCACTTAVRL1516ZIM78(880)CAACTCCCCTTCCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCCTATVRL230ZIM78(880)CAACCCCCCTTTCCCCCAACCCCTGGGCAGCCACTTAVRL763ZIM70(879)CAACCACCCCTTTCCCCCAACCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACTCCCCTTCCCCCCAACCCCTGGGCAGCCACTTAZH501EGY77(880)CAACTCCCCTTCCCCCCAACCCCTGGGCAGCCACTTAZH548EGY77(881)CAACTCCCCTTCCCCCAACCCCCTGGGCAGCCACTTA(881)CAACCCCCCTTTTCCCCCAACCCCCTGGGCAGCCACTTA	SPUZZZUKENU/	(000)		
SP0304001KEN97(879)CAACCCCCTT Inteccedad CCCCC16GGCAGCCACTTASPU45ZAMB85(880)CAACCCCCTT-AT-CCCCCAACCCCCTGGGCAGCCACTTASPU52001RSA99(880)CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACCCCCAT-CTTCCCCCAACCCCCTGGGCAGCCACTTASPU77RSA08(880)CAACCCCCAT-CTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCAT-CTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1290ZIM78(880)CAACCCCCAT-TTCCCCCCAACCCCCTGGGCAGCCACTTAVRL1516ZIM78(880)CAACCCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL763ZIM70(879)CAACCCCCC-TTTTCCCCCAACCCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACTCCCC-TTTCCCCCAACCCCCTGGGCAGCCACTTAZH501EGY77(880)CAACTCCCC-TTTCCCCCCAACCCCCTGGGCAGCCACTTAZH548EGY77(881)CAACCCCCT <tttccccccaaccccctgggcagccactta< td="">(881)CAACCCCCTTTTCCCCCAACCCCCTGGGCAGCCACTTA</tttccccccaaccccctgggcagccactta<>	SPUZZZJKENU/ SDU39/001KEN07	(879)		
SP0432AMB03(800)CAACCCCCTT ATCCCCCAACCCCCTGGGCAGCCACTTASPU52001RSA99(880)CAACCCCCAT-TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77NAMB04(880)CAACTCCCC-TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77RSA08(880)CAACCCCCAT-CTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCT-TTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1290ZIM78(880)CAACCCCCAT-TTCCCCCCAACCCCCTGGGCAGCCACTTAVRL1516ZIM78(880)CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTAVRL230ZIM78(880)CAACCCCCCT-AT-CCCCCAACCCCTGGGCAGCCACTTAVRL763ZIM70(879)CAACCACCCC-TTTCCCCCAACCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTAZH501EGY77(880)CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTAZH548EGY77(881)CAACCCCCTTTTCCCCCCAACCCCCTGGGCAGCCACTTA(881)CAACCCCCTTTTCCCCCAACCCCCTGGGCAGCCACTTA	SF0504001REN97 CDII/577MD85	(079)		
SF052001K3A95(880)CAACCCCCA1TITCCCCAACCCCC16GGCAGCCACTTASPU77NAMB04(880)CAACTCCCC-TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77RSA08(880)CAACCCCCAT-CTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCCT-TTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1290ZIM78(880)CAACCCCCC-TTCCCCCAACCCCCTGGGCAGCCACTTAVRL1516ZIM78(880)CAACTCCCC-VRL1887ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL2230ZIM78(880)CTACCCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL763ZIM70(879)CAACCACCCC-VRL825ZIM79(880)CAACTCCCC-ZH501EGY77(880)CAACTCCCC-ZH548EGY77(881)CAACCCCCTConsensus(881)CAACCCCCT	CDU52001DCA00	(880)		
S1077NAMADO4(800)CAACI CCCCT TTTCCCCCAACCCCCTGGGCAGCCACTTASPU77RSA08(880)CAACCCCCAT-CTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1032ZIM78(880)CAACCCCCT-TTTCCCCCCAACCCCCTGGGCAGCCACTTAVRL1290ZIM78(880)CAACCCCCCT-TTCCCCCCAACCCCCTGGGCAGCCACTTAVRL1516ZIM78(880)CAACCCCCCT-AT-CCCCCCAACCCCCTGGGCAGCCACTTAVRL1887ZIM78(880)CAACCCCCCT-AT-CCCCCCAACCCCCTGGGCAGCCACTTAVRL2230ZIM78(880)CTACCCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL763ZIM70(879)CAACCACCCC-TTTTCCCCCAACCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACCCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTAZH501EGY77(880)CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTAConsensus(881)CAACCCCCT <tttccccccaaccccctgggcagccactta< td=""></tttccccccaaccccctgggcagccactta<>	SPUSZUUIKSA99 SPU77NAMBOA	(880)		
VRL1032ZIM78(880)CAAACCCCCTTTCCCCCAACCCCCTGGGCAGCCACTTAVRL1290ZIM78(880)CAACCCCCATTTCCCCCCAACCCCCTGGGCAGCCACTTAVRL1516ZIM78(880)CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTAVRL1887ZIM78(880)CAACCCCCCT-ATCCCCCAACCCCCTGGGCAGCCACTTAVRL2230ZIM78(880)CAACCCCCCT-ATCCCCCAACCCCCTGGGCAGCCACTTAVRL763ZIM70(879)CAACCACCCC-TTTCCCCCAAACCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACCCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTAZH501EGY77(880)CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTAZH548EGY77(880)CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTAConsensus(881)CAACCCCCTTTTCCCCCCAACCCCCTGGGCAGCCACTTA	SPU77RSA08	(880)	CAAC <mark>1</mark> CCCC	
VRL1290ZIM78(880)CAACCCCCAT-TTCCCCCCAACCCCCTGGGCAGCCACTTAVRL1516ZIM78(880)CAACTCCCCTTCCCCCCAACCCCCTGGGCAGCCACTTAVRL1887ZIM78(880)CAACCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL2230ZIM78(880)CAACCCCCC-TTTTCCCCCAACCCCCTGGGCAGCCACTTAVRL763ZIM70(879)CAACCACCCC-TTTTCCCCCAAACCCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACCCCCAT-TTCCCCCCAACCCCCTGGGCAGCCACTTAZH501EGY77(880)CAACTCCCCTTCCCCCCAACCCCCTGGGCAGCCACTTAZH548EGY77(880)CAACTCCCCTTCCCCCCAACCCCCTGGGCAGCCACTTAConsensus(881)CAACCCCCT <tttccccccaaccccctgggcagccactta< td=""></tttccccccaaccccctgggcagccactta<>	VRL10327TM78	(880)		
VRL125021M70(000)CMMCCCCCATTTOCCCCAACCCCTGGGCAGCCACTATVRL1516ZIM78(880)CAACCCCCT ACCCCCCTATCCCCCAACCCCCTGGGCAGCCACTTAVRL2230ZIM78(880)CTACCCCCCT ACCCCCCTTTTCCCCCAACCCCCTGGGCAGCCACTTAVRL763ZIM70(879)CAACCACCCC ACCCCCCTTTTCCCCCAACCCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACCCCCC ACCCCCCTTCCCCCAACCCCCTGGGCAGCCACTTAZH501EGY77(880)CAACTCCCC CCCCCCCCCCCCCCCCCGGCAGCCACTTAZH548EGY77(880)CAACTCCCC CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	VRL12907TM78	(880)		
VRL1887ZIM78(880)CAACCCCCCT-AT-CCCCCCAACCCCTGGGCAGCCACTTAVRL2230ZIM78(880)CTACCCCCCT-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL763ZIM70(879)CAACCACCCC-TTTTCCCCCAAACCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACCCCCAT-TTCCCCCCAACCCCCTGGGCAGCCACTTAZH501EGY77(880)CAACTCCCC-TTTCCCCCCAACCCCCTGGGCAGCCACTTAZH548EGY77(880)CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTAConsensus(881)CAACCCCCT	VRL15167TM78	(880)		
VRL2230ZIM78(880)CTACCCCCCT<-AT-CCCCCAACCCCCTGGGCAGCCACTTAVRL763ZIM70(879)CAACCACCC-TTTTCCCCCAAACCCCTGGGCAGCCACTTAVRL825ZIM79(880)CAACCCCCAT-TTCCCCCCAACCCCCTGGGCAGCCACTTAZH501EGY77(880)CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTAZH548EGY77(880)CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTAConsensus(881)CAACCCCCT	VRL18877.TM78	(880)		
VRL225021M70 (800) CAACCACCCC-TTTTCCCCCAAACCCCTGGGCAGCCACTTA VRL8252IM79 (880) CAACCCCCAT-TTCCCCCCAACCCCCTGGGCAGCCACTTA ZH501EGY77 (880) CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTA ZH548EGY77 (880) CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTA Consensus (881) CAACCCCCT	VRL22307TM78	(880)		
VRL825ZIM79 (880) CAACCCCCAT-TTCCCCCCAACCCCCTGGGCAGCCACTTA ZH501EGY77 (880) CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTA ZH548EGY77 (880) CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTA Consensus (881) CAACCCCCT	VRL7637TM70	(879)	CAACCACCC	-TTTTTCCCCAAACCCCTGGGCAGCCACTTA
ZH501EGY77 (880) CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTA ZH548EGY77 (880) CAACTCCCC-TTCCCCCCAACCCCCTGGGCAGCCACTTA Consensus (881) CAACCCCCCT TTTCCCCCCAACCCCCTGGGCAGCCACTTA	VRL8257TM79	(880)	CAACCCCCAT	-TTCCCCCAACCCCCCTGGGCAGCCACTTA
ZH548EGY77 (880) CAACTCCCCT TTTCCCCCAACCCCCTGGGCAGCCACTTA Consensus (881) CAACCCCCCT TTTCCCCCCAACCCCCTGGGCAGCCACTTA	ZH501EGY77	(880)	CAACTCCCC-	TTCCCCCCAACCCCCTGGGCAGCCACTTA
Consensus (881) CAACCCCCCT TTTCCCCCCAACCCCCTGGGCAGCCACTTA	ZH548EGY77	(880)	CAACTCCCC-	TTCCCCCCAACCCCCTGGGCAGCCACTTA
	Consensus	(881)	CAACCCCCCT	TTTCCCCCAACCCCCTGGGCAGCCACTTA

		921	960
214445KEN83	(919)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
56KEN65	(918)	GGCTGCTGTCTTGTA	AGCCTGAGCAGCTGCCATGACAGC <mark>T</mark>
900085MAU88	(920)	GGCTGCTGTCTTGTA <mark>C</mark>	CGCCTGAGCAGCTGCCATGACAGC <mark>C</mark>
An1000MAD91	(919)	GGCTGCTGTCTTGTA <mark>C</mark>	GCCTGAGCAGCTGCCATGACAGCA
An991MAD91	(919)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
An999MAD91	(919)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
AnK6087GUI84	(918)	GGCTGCTGTCTTGTA <mark>Z</mark>	GCCTGAGCAGCTGCCTTGACAGCA
AnTAMBULEGY94	(918)	GGCTGCTGTCTTGTA	AGCCTGAGC <mark>G</mark> GCTGCCATGACAGCA
Ar12568RSA71	(918)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGC
Ar20368RSA81	(918)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
Ar21229SA00	(918)	GGCTGCTGT <mark>T</mark> TTGTA <mark>C</mark>	GCCTGAGCAGCTGCCATGACAGCA
Ar/4RSA55	(919)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGC
Ar811MAD79	(919)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
ArD38661SEN81	(919)	AGCTGCTGTCTTGTAC	GCCTGAGCAGCTGCCATGACAGC
BII43KEN//	(919)	GGCTGCTGTCTTGTAG	GCCTGAGCAGCTGCCATGACAGCA
B314KEN62	(919)	GGCTGCTGTCTTGTAC	
H1825RSA/5	(919)	GGCTGCTGTCTTGTAC	
LUNYOUGA55	(920)	GGCTGCTGTCTTGTAC	
	(918)	GGCTGCTGTCTTGTA	
SPUIUSUIKENU/	(919)	GGCTGCTGTCTTGTA	GUUTGAGUAGUTGUUATGAUAGUA
SPUIUSUZKENU/	(919)		
SPUIUSU/RENU/ SPUIUSU/RENU/	(910)		
SPUIUSIJKENU/	(919)		
SPU152RSA08	(919)		
SPU204ANGL85	(919)		
SPU2207KEN07	(918)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
SPU2214KEN07	(919)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
SPU2215KEN07	(919)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
SPU2220KEN07	(919)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
SPU2223KEN07	(919)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
SPU384001KEN97	(918)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
SPU45ZAMB85	(918)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
SPU52001RSA99	(919)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
SPU77NAMB04	(918)	GGCTGCTGTCTTGTA	GCCTGGGCAGCTGCCATGACAGCA
SPU77RSA08	(919)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
VRL1032ZIM78	(919)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
VRL1290ZIM78	(919)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA
VRL1516ZIM78	(918)	GGCTGCTGTCTTGTA	AGCCTGAGCAGCTGCCATGACAGCA
VRL1887ZIM78	(918)	GGCTGCTGTCTTGTA <mark></mark>	AGCCTGAGCAGCTGCCATGACAGCA
VRL2230ZIM78	(918)	GGCTGCTGTCTTGTA <mark>Z</mark>	AGCCTGAGCAGCTGCCATGACAGCA
VRL763ZIM70	(918)	GGCTGCTGTCTTGTA <mark>C</mark>	GCCTGAGCAGCTGCCATGACAGC <mark>T</mark>
VRL825ZIM79	(919)	GGCTGCTGTCTTGTA <mark>C</mark>	GCCTGAGCAGCTGCCATGACAGCA
ZH501EGY77	(918)	GGCTGCTGTCTTGTA <mark></mark>	AGCCTGAGC <mark>G</mark> GCTGCCATGACAGCA
ZH548EGY77	(918)	GGCTGCTGTCTTGTA <mark></mark>	AGCCTGAGC <mark>G</mark> GCTGCCATGACAGCA
Consensus	(921)	GGCTGCTGTCTTGTA	GCCTGAGCAGCTGCCATGACAGCA

	961 1000
214445KEN83 (959)	GCTGACGGCTTCCCATTAGAATCCACAAGCCCAAAAGCTT
56KEN65 (958)	GCTGACGGCTTCCCATT <mark>G</mark> GAATCCACAAGCCCAAAAGCTT
900085MAU88 (960)	GCTGACGGCTTCCCATT <mark>G</mark> GAATCCACAAGCCCAAAAGCTT
An1000MAD91 (959)	GCTGACGGCTTCCCATTAGAATCCACAAGCCCAAAAGCTT
An991MAD91 (959)	GCTGACGGCTTCCCATTAGAATCCACAAGCCCAAAAGCTT
An999MAD91 (959)	GCTGACGGCTTCCCATTAGAATCCACAAGCCCAAA <mark>G</mark> GCTT
AnK6087GUI84 (958)	GCTGA <mark>T</mark> GGCTTCCCATTAGAATCCACAAGCCCAAAAGCTT
AnTAMBULEGY94 (958)	GCTGACGGCTTCCCATTAGAATCCACAAG <mark>T</mark> CCAAA <mark>G</mark> GCTT
Ar12568RSA71 (958)	GCTGACGGCTTCCCATT <mark>G</mark> GAATCCACAAGCCCAAAAGCTT
Ar20368RSA81 (958)	GCTGACGGCTTCCCATTAGA <mark>G</mark> TCCACAAGCCCAAAAGCTT
Ar21229SA00 (958)	GCTGACGGCTTCCCATTAGAATCCACAAGCCCAAAAGCTT
Ar74RSA55 (959)	GCTGA <mark>T</mark> GGCTTCCCATT <mark>G</mark> GAATCCACAAGCCCAAAAGCTT
Ar811MAD79 (959)	GCTGACGGCTTCCCATT <mark>G</mark> GAATCCACAAGCCCAAA <mark>G</mark> GCTT
ArD38661SEN81 (959)	GCTGACGGCTTCCCATT <mark>G</mark> GAATCCACAAGCCCAAAAGCTT
B1143KEN77 (959)	GCTGACGGCTTCCCATTAGAATCCACAAGCCCAAAAGCTT
B314KEN62 (959)	GCTGACGGCTTCCCATTAGAATCCACAAGCCCAAAAGCTT
H1825RSA75 (959)	GCTGACGGCTTCCCATTGGAATCCACAAGCCCAAAAGCTT
LunyoUGA55 (960)	GCTGACGGCTTTCCATTAGAATCCACAAGCCCAAAAGCTT
R1662CAR85 (958)	GCTGA <mark>T</mark> GGCTTCCCATTAGAATCCACAAGCCCAAAAGCTT
SPU10301KEN07 (959)	GCTGACGG <mark>T</mark> TTCCCATTAGAATCCACAAGCCCAAAAGCTT
SPU10302KEN07 (959)	GCTGACGGTTTCCCATTAGAATCCACAAGCCCAAAAGCTT
SPU10307KEN07 (958)	GCTGACGGTTTCCCCATTAGAATCCACAAGCCCAAAAGCTT
SPU10315KEN07 (959)	GCTGACGG <mark>T</mark> TTCCCATTAGAATCCACAAGCCCAAAAGCTT
SPU12002SOM98 (958)	GCTGACGGCTTCCCATTAGAATCCACAAGCCCAAAAGCTT
SPU152RSAU8 (959)	GCTGACGG <mark>T</mark> TTCCCATTAGAATCCACAAGCCCAAAAGCTT
SPU204ANGL85 (959)	GCTGACGGCTTCCCATTAGAATCCACAAGCCCAAAAGCTT
SPU220/KENU/ (958)	
SPU2214KENU7 (959)	GUTGAUGGUTTUUUATT <mark>G</mark> GAATUUAUAAGUUUAAAAGUTT
SPU2215KENU7 (959)	
SPU2220KENU7 (959)	
SPUZZZSKENU/ (959)	
CDI1/573MD95 (050)	
SFU4JZAMBOJ (950)	
SPUJZUUIRSA99 (959) SPUJZUUIRSA99 (959)	CCTCACCCCTTCCCATTAGAATCCACAAGCCCCAAAAGCTT
SPUT7RSA08 (950)	
VPI10327TM78 (959)	
VRL12907TM78 (959)	
VRL1516ZIM78 (959)	COTGACGCCTTCCCATTCCACAACCCCCAAAGCCC
VRL18877.TM78 (958)	CCTGACGCCTTCCCATT <mark>C</mark> GAATCCACAAGCCCCAAAAGCTT
VRL2230ZIM78 (958)	
VRI.7637IM70 (958)	GCTGACGGCTTCCCATTGGAATCCACAAGCCCAAAAGCTT
VRI.8257TM79 (959)	GCTGACGGCTTCCCATTAGAATCCACAAGCCCAAAAGCTT
ZH501EGY77 (958)	GCTGACGGCTTCCCATTAGAATCCACAAGTCCAAAG
ZH548EGY77 (958)	GCTGACGGCTTCCCATTGGAATCCACAAGTCCAAAGGCTT
Consensus (961)	GCTGACGGCTTCCCATTAGAATCCACAAGCCCAAAAGCTT

		1001 1040
214445KEN83	(999)	TCAAGAATTC <mark>C</mark> CTCCTCTTCTCATGGCTTATAAAGTTGCT
56KEN65	(998)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
900085MAU88	(1000)	TCAAGAATTCTCTCCTCTTCTCATGGCTTAT <mark>G</mark> AAGTTGCT
An1000MAD91	(999)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
An991MAD91	(999)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
An999MAD91	(999)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
AnK6087GUI84	(998)	T <mark>T</mark> AAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
AnTAMBULEGY94	(998)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
Ar12568RSA71	(998)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
Ar20368RSA81	(998)	TCAAGAATTCTCTCCTCTTCTCATGGCTTAT <mark>G</mark> AAGTTGCT
Ar21229SA00	(998)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
Ar74RSA55	(999)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
Ar811MAD79	(999)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
ArD38661SEN81	(999)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
B1143KEN77	(999)	TCAAGAATTC <mark>C</mark> CTCCTCTTCTCATGGCTTATAAAGTTGCT
B314KEN62	(999)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
H1825RSA75	(999)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
LunyoUGA55	(1000)	TCAAGAAT <mark>C</mark> CTCTCCTCTTCTCATGGCTTAT <mark>G</mark> AA <mark>A</mark> TTGCT
R1662CAR85	(998)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
SPU10301KEN07	(999)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
SPU10302KEN07	(999)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
SPUL0307KEN07	(998)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
SPUIU3I5KENU/	(999)	TCAAGAATTCTCTCTCTTCTCATGGCTTATAAAGTTGCT
SPUI2002SOM98	(998)	TCAAGAATTCTCTCTCTTCTCATGGCTTATAAAGTTGCT
SPUISZRSAU8	(999)	
SPU204ANGL85	(999)	
SPUZZU/KENU/	(998)	TCAAGAATTCTCTCTCTCTCATGGCT <mark>A</mark> ATAAAGTTGCT
SPUZZI4KENU/	(999)	
SPUZZIJKENU7 SDU2220VENO7	(999)	
SPUZZZUKENU/	(999)	
CDII384001KEN07	(999)	
CDII/57AMP85	(990)	
SP0452AMB05	(990)	
SIUSZUUIRSAJJ SPU77NAMB04	(998)	
SPU77RSA08	(999)	
VRI.10327.TM78	(999)	
VRL12907TM78	(999)	
VRL15167.TM78	(998)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
VRL18877.TM78	(998)	TCAAGAATTCTCTCCTCCTCCTCCTCATGGCTTATAAAGTTGCT
VRL22307TM78	(998)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
VRL763ZIM70	(998)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
VRL825ZIM79	(999)	TCAAGAATTCCCTCCTCTCTCATGGCCTTATAAAGTTGCT
ZH501EGY77	(998)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
ZH548EGY77	(998)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT
Consensus	(1001)	TCAAGAATTCTCTCCTCTTCTCATGGCTTATAAAGTTGCT

		1041 1080
214445KEN83	(1039)	ATTTACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
56KEN65	(1038)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
900085MAU88	(1040)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
An1000MAD91	(1039)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGC <mark>G</mark>
An991MAD91	(1039)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGC <mark>G</mark>
An999MAD91	(1039)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGC <mark>G</mark>
AnK6087GUI84	(1038)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
AnTAMBULEGY94	(1038)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
Ar12568RSA71	(1038)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGC <mark>G</mark> GCA
Ar20368RSA81	(1038)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
Ar21229SA00	(1038)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGC <mark>G</mark>
Ar74RSA55	(1039)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGC <mark>G</mark> GCA
Ar811MAD79	(1039)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
ArD38661SEN81	(1039)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
B1143KEN77	(1039)	ATT <mark>T</mark> ACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
B314KEN62	(1039)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
H1825RSA75	(1039)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGC <mark>G</mark> GCA
LunyoUGA55	(1040)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
R1662CAR85	(1038)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
SPU10301KEN07	(1039)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCG
SPU10302KEN07	(1039)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCG
SPUI030/KEN0/	(1038)	ATTCACTGCTGCATTCATTGGCCTGCGTGAACGTTGCAGCG
SPUIU3I5KENU/	(1039)	ATTCACTGCTGCATTCATTGGCCTGCGTGAACGTTGCAGCG
SPUIZUUZSOM98	(1038)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCG
SPUISZRSAU8	(1039)	
SPUZU4ANGL85	(1039)	
SPUZZU/KENU/	(1038)	
SPUZZI4KENU7 SDU2215VEN07	(1039)	
SPUZZIJKENU7	(1039)	
SPUZZZUKENU7	(1039)	
SP02225KEN07	(1039)	
SDU/57AMB85	(1038)	
SPU52001RS299	(1030)	
SIUSZUUIKSAJJ SPU77NAMB04	(1032)	
SPU77RSA08	(1039)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCG
VRL10327TM78	(1039)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
VRL12907TM78	(1039)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
VRL15167TM78	(1038)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
VRL1887ZIM78	(1038)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
VRL2230ZIM78	(1038)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
VRL763ZIM70	(1038)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCGGCA
VRL825ZIM79	(1039)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
ZH501EGY77	(1038)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
ZH548EGY77	(1038)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA
Consensus	(1041)	ATTCACTGCTGCATTCATTGGCTGCGTGAACGTTGCAGCA

 214445KEN83 (1079) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGTGATGA 56KEN65 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA An1000MAD91 (1079) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA An991MAD91 (1079) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA An991MAD91 (1079) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA AnK6087GU184 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA An748087GU184 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA Ar12568RSA71 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA Ar212568RSA71 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA Ar21258RSA71 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA Ar21258RSA71 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA Ar21258RSA71 (1079) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA Ar2185857 (1079) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA B143KEN72 (1079) ACCTCCTCTTGTTCTCCCCGGAGGTTTGGGTGATGA B1445EN77 (1079) ACCTCCTCTTGTTCTCCCCGGAGGTTGGGGTGATGA B145EN77 (1079) ACCTCCTCTTGTTCTCCCCGGAGGTTGGGGTGATGA B145EN77 (1079) ACCTCCTCTTTGTCTCACCTCGGAGGTTGGGGTGATGA B1465CAR85 (1079) ACCTCCTCTTTGTCTCACCTCGGAGGTTGGGGTGATGA SPU10302KEN07 (1079) ACCTCCTCTTTGTCTACCTCGGAGGTTGGGTGATGA SPU10302KEN07 (1079) ACCTCCTCTTTGTCTACCTCGGAGGTTGGGTGATGA SPU1202SOM98 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU220KEN07 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU220KEN07 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU220KEN07 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU220KEN07 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU220KEN07 (1079) ACCTCCTCTTTGTCTACCTCGGAGGTTGGGTGATGA SPU220KEN07 (1079) ACCTCCTCTTTGTCTACCTCGGAGGTTGGGTGATGA SPU220KEN07 (1079) ACCTCCTCTTTGTCTACCTCGGAGGTTGGGTGATGA SPU220KEN07 (1079) ACCTCCCCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU220KEN07 (10			1081 1120
56KEN65 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA 900085MA088 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA An991MAD91 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA An991MAD91 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA An8097GU184 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA An7AMBULEGY94 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA Ar12556RSA71 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA Ar21229SA00 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA Ar21229SA00 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA Ar21229SA00 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA Ar21229SA00 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA Ar14RSA55 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA B1143KEN77 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA H1825RSA75 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU10301KEN07 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU10301KEN07 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGA	214445KEN83	(1079)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
900085MAU88 (1060) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA An1000MAD91 (1079) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA An999MAD91 (1079) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA An7ABULGGY94 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA An7ABULGGY94 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGGTGATGA Ar12568RSA71 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA Ar20368RSA81 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA Ar2129SA00 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA Ar2129SA00 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA Ar38661SEN81 (1079) ACCTCCTCTTTGTCTACCTCGGAGGTTGGGGTGATGA B1143KEN77 (1079) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA B144SEN77 (1079) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA H1825RSA75 (1079) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA B144SEN77 (1079) ACCTCCTCTTGTTCTCCCCCGGAGGTTGGGGTGATGA H1825RSA75 (1079) ACCTCCTCTTGTCTCACCTCGGAGGTTGGGGTGATGA SPU10301KEN07 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA SPU10302KEN07 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA SPU10302KEN07 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA SPU10307KEN07 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA SPU10307KEN07 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA SPU10307KEN07 (1078) ACCTCCTCTTTGTCTACCTCGGAGGTTGGGGTGATGA SPU202SM98 (1079) ACCTCCTCTTTGTCTACCTCGGAGGTTGGGGTGATGA SPU202SM88 (1079) ACCTCCTCTTTGTCTACCTCGGAGGTTGGGGTGATGA SPU202SM88 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU223KEN07 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGTGATGA SPU221KEN07 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGTGATGA SPU221KEN07 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGGTGATGA SPU221KEN07 (1078) ACCTCCTCTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU221KEN07 (1079) ACCTCCTCTTGTCTACCTCGGAGGTTGGGTTGATGA SPU221KEN07 (1078) ACCTCCTCTTGTCTACCTCGGAGGTTGGGTTGATGA SPU221KEN07 (1078) ACCTCCTCTTGTCTACCTCGGAGGTTGGGTGATGA SPU221KEN07 (1078) ACCTCCTCTTGTCTCCCCGGAGGTTGGGTGATGA SPU221KEN07 (1078) ACCTCCTCTTGTCTCCCCGGAGGTTGGGTTGATGA SPU77NAM64 (1078) ACCTCCTCTTGTCTCCCCGGAGGTTGGGTTGATGA SPU77NAM64 (1078) ACCTCCTCTTGTCTCCCCGGAGGTTGGGTTGATGA SPU77NAM64 (1078) ACCTCCTCTTTGTCTCCCCGGAGGTTGGGTTGATGA VRL153ZL	56KEN65	(1078)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
 An1000MAD91 (1079) ACCTCCTCCTTTGTTCTACCTCGAAGGTTTGGGTTGATGA An991MAD91 (1079) ACCTCCTCCTTTGTTCTACCTCGAAGGTTTGGGTTGATGA AnK6087GUI84 (1078) ACCTCCTCCTTTGTTCTACCTCGAAGGTTTGGGTTGATGA An120568RSA1 (1078) ACCTCCTCCTTTGTTCTACCTCGAAGGTTTGGGTTGATGA Ar20368RSA81 (1078) ACCTCCTCCTTTGTTCTACCTCGAAGGTTTGGGTGATGA Ar20368RSA81 (1078) ACCTCCTCCTTTGTTCTACCTCGAAGGTTTGGGTGATGA Ar21229SA00 (1078) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGA Ar4811MAD79 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGA Ar811MAD79 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGA B114XEN62 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGA B114XEN62 (1079) ACCTCCTCCTTTGTTCTACCTCGAAGTTTGGGTGATGA B14XEN62 (1079) ACCTCCTCCTTTGTTCTACCTCGAAGTTTGGGTGATGA B14XEN62 (1079) ACCTCCTCCTTTGTTCTACCTCGAAGTTTGGGTGATGA SPU10301KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGAAGTTTGGGTGATGATGA SPU10301KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGAAGTTTGGGTGATGATGA SPU10301KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGAAGTTTGGGTGATGATGA SPU10301KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGAAGTTGGTGGATGATGA SPU10301KEN07 (1079) ACCTCCTCCTTGTTCTACCTCGAAGTTTGGTTGATGATGA SPU10301KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGAAGTTTGGTTGATGATGA SPU204ANGL85 (1079) ACCTCCTCCTTGTTCTACCTCGGAGGTTGGGTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTG	900085MAU88	(1080)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
 An991MAD91 (1079) ACCTCCTCCTTGTTCTACCTCGAGGTTTGGGTGATGA An999MAD91 (1077) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGA AnTAMBULEGY94 (1078) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGA Ar12568RSA81 (1078) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGA Ar21229SA00 (1078) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGA Ar21229SA00 (1078) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGA Ar21229SA00 (1078) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGATA Ar811MAD79 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGATGA Ar811MAD79 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGATGA B1143EN77 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGATGA B143EN77 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGATGA B143EN77 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGATGA B143EN77 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTGGGTGATGA SPU10301KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU10301KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTGGGTGATGA SPU10307KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGA SPU10307KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGA SPU204KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGATGA SPU204KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTGAT	An1000MAD91	(1079)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
 An999MAD91 (1079) ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTTGATGA AnK6087GU184 (1078) ACCTCCTCTTTGTTCTACCTCGAGGTTTGGGTTGATGA An1XMEULEGY94 (1078) ACCTCCTCTTTTGTTCTACCTCGAGGTTTGGGTTGATGA Ar20368RSA71 (1078) ACCTCCTCTTTGTTCTACCTCGAGGTTTGGGTTGATGA Ar2129SA00 (1078) ACCTCCTCTTTGTTCTACCTCGAGGTTTGGGTTGATGA Ar21229SA00 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA Ar74RSA55 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA Ar74RSA55 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA Ba143KEN72 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA Ba14XEN62 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA Ba14XEN62 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTGATGA Ba14XEN62 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTGATGA Ba14XEN62 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTGATGA Bu10301KEN07 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU10301KEN07 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU10301KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU10307KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU12002S0M98 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU204ANGL85 (1079) ACCTCCCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU204KEN07 (1078) ACCTCCCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU220KEN07 (1079) ACCTCCCCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU220KEN07 (1078) ACCTCCCCTTTGTTCT	An991MAD91	(1079)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
 AnK6087GUI84 (1078) ACCTCCTCTTTGTTCTGCCTCGAGGTTTGGGTTGATGA AnTAMBULGGY94 (1078) ACCTCCTCTTTGTTCTACCTCGAGGTTTGGGTTGATGA Ar20368RSA81 (1078) ACCTCCTCTTTGTTCTACCTCGAGGTTTGGGTTGATGA Ar20368RSA81 (1078) ACCTCCTCTTTGTTCTACCTCGAGGTTTGGGTGATGA Ar21229SA00 (1078) ACCTCCTCTTTGTTCTACCTCGAGGTTTGGGTGATGA Ar74RSA55 (1079) ACCTCCTCTTTGTTCTACCTCGAGGTTTGGGTGATGA B1143KEN77 (1079) ACCTCCTCTTTGTTCTACCTCGAGGTTTGGGTGATGA B1143KEN77 (1079) ACCTCCTCTTTGTTCTACCTCGAGGTTTGGGTGATGA B114XEN62 (1079) ACCTCCTCTTTGTTCTACCTCGAGGTTTGGGTGATGA B114XEN62 (1079) ACCTCCTCTTTGTTCTCCCTCGGAGGTTTGGGTGATGA B144KEN77 (1079) ACCTCCTCTTTGTTCTCCCTCGGAGGTTTGGGTGATGA B144KEN77 (1079) ACCTCCTCTTTGTTCTCCCTCGGAGGTTTGGGTGATGA B140KEN77 (1079) ACCTCCTCTTTGTTCTCCCTCGGAGGTTTGGGTGATGA B1000 ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU10301KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU10301KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10301KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU12002S0M98 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU220KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU221KEN07 (1079) ACCTCCCCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU220KEN07 (1079) ACCTCCCCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU220KEN07 (1079) ACCTCCCCTTGTTCTACCTCGGAGGTTGGGTGATGA SPU220KEN07 (1079) ACCTCCCCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU220KEN07 (1079) ACCTCCCCTTTGTTCTCCCCGGAGGTTGGGTGATGA SPU220KEN07 (1079) ACCTCCCCTTGTTCTCCCCGGAGGTTGGGTGATGA SPU220KEN07 (1079) ACCTCCCCTTGTTCTCCCCGGAGGTTGGGTGATGA	An999MAD91	(1079)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
 AnTAMBULEGY94 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA Ar20368R5A81 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA Ar21229SA00 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA Ar74R5A55 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA Ar74R5A55 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA B1143KEN77 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA B1143KEN77 (1079) ACCTCCTCCTTTGTTCTCCCCGGAGGTTGGGTTGATGA B1143KEN77 (1079) ACCTCCTCCTTTGTTCTCCCGGAGGTTGGGTTGATGA B144KEN62 (1079) ACCTCCTCCTTTGTTCTCCCCGGAGGTTGGGTTGATGA LunyoUGA55 (1080) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGA R1662CAR85 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU10301KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU10307KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU10307KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU12002S0M98 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU1204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU2207KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU2215KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU2214KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU2220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU220KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU220KEN07 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU52001RSA9 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU5201RSA9	AnK6087GUI84	(1078)	ACCTCCTCCTTTGTTCT <mark>G</mark> CCTCGGAGGTTTGGGTTGATGA
Ar12568RSA71(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAAr20368RSA81(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAAr2129SA00(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAAr41MAD79(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAArb1MAD79(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAB1143KEN71(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGAB1143KEN72(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGAB1143KEN72(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGAH1825RSA75(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGASPU10301KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGASPU10301KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGASPU10301KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGASPU10301KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGASPU10301SKEN07(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGASPU10302SKEN07(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGASPU204NGL85(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGASPU2207KEN07(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGASPU2214KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGASPU2215KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGASPU220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGASPU220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGASPU220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGASPU220KE	AnTAMBULEGY94	(1078)	ACCTCCTCTTTTTTTTTTTTTTCTACCTCGGAGGTTTGGGTTGATGA
Ar20368RSA81(1078)ACCTCCTCCTTTGTTCTACCTCGAAGGTTTGGGTTGATGAAr21229SA00(1078)ACCTCCTCCTTTGTTCTACCTCGAAGGTTTGGGTTGATGAAr21229SA00(1079)ACCTCCTCCTTTGTTCTACCTCGAAGGTTTGGGTTGATGAAr811MAD79(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAB1143KEN77(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAB1144KEN62(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAH1825RSA75(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGALunyoUGA55(1080)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10301KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10301KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10307KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10307KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10307KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10307KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU202SOM98(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU202SN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU2214KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU2214KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU2214KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU2214KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA	Ar12568RSA71	(1078)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
 Ar21229SA00 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA Ar74RSA55 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA Ar811MAD79 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA B1143KEN77 (1079) ACCTCCTCCTTGTTCTACCTCGGAGGTTTGGGTTGATGA B1143KEN77 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA B1143KEN77 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA H1825RSA75 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA H1825RSA75 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA R1662CAR85 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10301KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10307KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10315KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10315KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10307KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU204KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2215KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2215KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2215KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2223KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU223KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU223KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTGATGA SPU77NAMB4 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU77NAMB4 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL163ZIM78 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL162ZIM78 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL1230ZIM78 (1079) ACCTCCTCCTTTGTTCTCCCCGGAGGTTGGGTTGATGA	Ar20368RSA81	(1078)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
Ar74RSA55(1079)ACCTCCTCTTTGTTCACCTCGGAGGTTTGGGTTGATGAAr811MAD79(1079)ACCTCCTCTTTTGTTCACCTCGGAGGTTTGGGTTGATGAArD38651SEN81(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAB1143KEN77(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAH1825RSA75(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGALunyoUGA55(1080)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAR1662CAR85(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU1030LEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU1030ZEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU1030ZEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU1031SEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU1202SOM98(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU2207KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU2215KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU2220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU2223KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU384001KEN97(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU77NAMB4(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU77NAMB4(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGAVRL1230ZIM78(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGAVRL1230ZIM78(1078)ACCTCCTCTTTGTTCTCCCCGGAGGTTGGGTTGATGAVRL1230ZIM78(1078)ACCTCCTCTTTGTTCTCCCCGGAGGTTGGGTTGATGA <t< td=""><td>Ar21229SA00</td><td>(1078)</td><td>ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA</td></t<>	Ar21229SA00	(1078)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
Ar811MAD79(1079)ACCTCCTCTTTTTTTTTTTTCTACCTCGGAGGTTTGGGTTGATGAArD38661SEN81(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAB1143KEN77(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAH1825RSA75(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGALunyoUGA55(1080)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10301KEN07(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10302KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10307KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10307KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10307KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10202S0M98(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU204ANGL85(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU221KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU221SKEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU221SKEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU452AMB85(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU52001RSA99(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77NAMB04(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1032ZIM78(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL230ZIM78(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1032ZIM78(1078)ACCTCCTCTTTGTTCTACCTC	Ar74RSA55	(1079)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGAT <mark>A</mark> A
ArD38661SEN81(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAB1143KEN77(1079)ACCTCCTCTTTGTTCTCCCCTGGAGGTTTGGGTTGATGAH325RSA75(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGALunyoUGA55(1080)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10301KEN07(1079)ACCTCCTCCTTTGTTCTCCCCCGGAGGTTTGGGTTGATGASPU10302KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10307KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10315KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10315KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10315KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2020Se0M98(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2207KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2215KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2215KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2205KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2201KSA99(1078)ACCTCCTCCTTTGTTCTACCTCGAGGTTTGGGTTGATGASPU52001RSA99(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1032ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1032ZIM78(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL230ZIM78(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL163ZIM78(1078)ACCTCCTCTTTGTTCTACCTCGGAG	Ar811MAD79	(1079)	ACCTCCTC <mark>T</mark> TTTGTTCTACCTCGGAGGTTTGGGTTGATGA
B1143kEN77(1079)ACCTCCTCCTTTGTTCTACCTCGAGGGTTTGGGTTGATGAB314kEN62(1079)ACCTCCTCTTTGTTCTCCCCGGAGGTTTGGGTTGATGAH1825RSA75(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGALunyoUGA55(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10301kEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10307KEN07(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10315KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10315KEN07(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2020SOM98(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU204ANGL85(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2214kEN07(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2215kEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2215kEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2223kEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU452AMB85(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU52001RSA99(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77NRA08(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1032ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1290ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL187ZIM78(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL190ZIM78(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL190ZIM78(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGA	ArD38661SEN81	(1079)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
 B314KEN62 (1079) ACCTCCTCCTTTGTTCTGCCCCGGAGGTTTGGGTTGATGA H1825RSA75 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA LunyoUGA55 (1080) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10301KEN07 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10307KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10307KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10307KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10307KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU1020SOM98 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU152RSA08 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2207KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2214KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2215KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2223KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU384001KEN97 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU52001RSA99 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU77NAMB04 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU77RSA08 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU77RSA08 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1032ZIM78 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1032ZIM78 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1887ZIM78 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1887ZIM79 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCCCTTTGTTCTACCTCGGAGGTT	B1143KEN77	(1079)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
 H1825RA75 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA LunyoUGA55 (1080) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10301KEN07 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10307KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10307KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10305KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10305KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10202SOM98 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU1204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU207KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2214KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2214KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2223KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU384001KEN97 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU52001RSA99 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU77NAMB04 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU77RSA08 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU77RSA08 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1032ZIM78 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1032ZIM78 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL187ZIM78 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCCTTTTGTTCTACCTCGGAGGTTTG	B314KEN62	(1079)	ACCTCCTCCTTTGTTCT <mark>G</mark> CCTCGGAGGTTTGGGTTGATGA
LunyoUGA55 (1080) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA R1662CAR85 (1078) ACCTCCTCTTTGTTTTGCTCTGCCTCGGAGGTTTGGGTTGATGA SPU10301KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10307KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10315KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU102SOM98 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU152RSA08 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU207KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2215KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2215KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2223KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU223XEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU223KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU52001RSA99 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU52001RSA99 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU77NAMB04 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU77NAMB04 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1032ZIM78 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1290ZIM78 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL187ZIM78 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL187ZIM78 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL1867ZIM78 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL230ZIM78 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL2230ZIM78 (1078) ACCTCCTCTTTGTTCTGCCTCGGAGGTTGGGTTGATGA VRL1867ZIM79 (1078) ACCTCCTCTTTGTTCTGCCTCGGAGGTTGGGTTGATGA VRL2230ZIM78 (1078) ACCTCCTCTTTGTTCTGCCCCGGAGGTTGGGTTGATGA VRL25ZIM79 (1078) ACCTCCTCTTTGTTCTGCCCCGGAGGTTGGGTTGATGA VRL25ZIM79 (1078) ACCTCCTCTTTTTTGTCTCTCCCCGGAGGTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCTTTTTTTGTCTACCTCGGAGGTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCTTTTTTGTCTACCTCGGAGGTTGGGTTGATGA ZH548GY77 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA	H1825RSA75	(1079)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
R1662CAR85 (1078) ACCTCCTCTTTTTTTTTCTCCGCACGAGGTTTGGGTTGATGA SPU10301KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10307KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10315KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU102SOM98 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU12002SOM98 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU1202SOM98 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU2207KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU2215KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU2220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU2220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU2220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU2223KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU2220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU220KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU52001RSA99 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU77NAMB04 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA SPU77NAMB04 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL1032ZIM78 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1290ZIM78 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1887ZIM78 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1887ZIM78 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL2230ZIM78 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL2230ZIM78 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL2230ZIM78 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL2230ZIM78 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL225ZIM79 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGA VRL25ZIM79 (1078) ACCTCCTCTTTTTTTTCTCTCCCCGGAGGTTGGGTTGATGA ZH548EGY77 (1078) ACCTCCTCTTTTTTTTTCTCTCCCCGGAGGTTGGGTTGATGA ZH548EGY77 (1078) ACCTCCTCTTTTTGTTCTACCTCGGAGGTTGGGTTGATGA	LunyoUGA55	(1080)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
SPU10301KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10302KEN07(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU10315KEN07(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU12002S0M98(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU1202S0M98(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU1202S0M98(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU204ANGL85(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2207KEN07(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2215KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2223KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU384001KEN97(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU52001RSA99(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77NAMB04(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1032ZIM78(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1887ZIM78(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1887ZIM78(1078)ACCTCCTCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCCTTTGTTCTACCTC	R1662CAR85	(1078)	ACCTCCTC <mark>T</mark> TTTGTTCT <mark>G</mark> CCTCGGAGGTTTGGGTTGATGA
 SPU10302KEN07 (1079) ACCTCCTCTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10307KEN07 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10315KEN07 (1079) ACCTCCTCTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU1202SOM98 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU152RSA08 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2207KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2214KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2215KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2223KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU384001KEN97 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU52001RSA99 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU77NAMB04 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU77RSA08 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1032ZIM78 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1290ZIM78 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1287ZIM78 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL763ZIM70 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL763ZIM70 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL763ZIM70 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL655ZIM79 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL655ZIM79 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA CATCCTCCTTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL655ZIM79 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL655ZIM79 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA CATCACCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA CATCACCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA CATCACCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATG	SPU10301KEN07	(1079)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
 SPU10307KEN07 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU10315KEN07 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU12002SOM98 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU207KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2214KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU2215KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU2220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU2220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU2223KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU384001KEN97 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU45ZAMB85 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU77NAMB04 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTGATGA SPU77RSA08 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTGATGA VRL1032ZIM78 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1290ZIM78 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1290ZIM78 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1887ZIM78 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL763ZIM70 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCCTTTGTCTACCTCGGAGGTTTGGGTTGATGA <	SPU10302KEN07	(1079)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
 SPU10315KEN07 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU12002SOM98 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU152RSA08 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU204ANGL85 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2207KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2214KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2220KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU2223KEN07 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU223KEN07 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU384001KEN97 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU77NAMB04 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA SPU77RSA08 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1032ZIM78 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1290ZIM78 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL1887ZIM78 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL230ZIM78 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL63ZIM70 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL63ZIM79 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1079) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGA <l< td=""><td>SPU10307KEN07</td><td>(1078)</td><td>ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA</td></l<>	SPU10307KEN07	(1078)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
SPU12002SOM98(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU152RSA08(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU204ANGL85(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2207KEN07(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU2215KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTGGGTTGATGASPU2220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2223KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU223XEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU452AMB5(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77NAMB04(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1032ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1290ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1887ZIM78(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL63ZIM79(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL63ZIM79(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL63ZIM79(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGA<	SPU10315KEN07	(1079)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
SP0152RSA08(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU204ANGL85(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2207KEN07(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2214KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2215KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2223KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU384001KEN97(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU452AMB85(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77NAMB04(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77RSA08(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL10322IM78(1079)ACCTCCTCTTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL15162IM78(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL18872IM78(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL2030ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL2230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1079)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCTTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCTTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCTTTTGTTCTACCTCGGAGGTTTG	SPU12002SOM98	(1078)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
SPU204ANGL85(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2207KEN07(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2214KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2215KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2223KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2223KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU384001KEN97(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU452AMB85(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77NAMB04(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77RSA08(1079)ACCTCCTCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL1032ZIM78(1079)ACCTCCTCCTTTGTTCTCCCGGAGGTTTGGGTTGATGAVRL1516ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL263ZIM79(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL25ZIM79(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAZH501EGY77(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGACDSSEDSUS(1081)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	SPUI52RSA08	(10/9)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGGTTGATGA
SP02207KEN07(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASP02214KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASP02215KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASP02223KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASP0384001KEN97(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASP0452AMB85(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASP052001RSA99(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASP077NAMB04(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASP077RSA08(1079)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL10322IM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1290ZIM78(1079)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL1887ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTGGGTTGATGAVRL230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTGGGTTGATGAZH501EGY77(1078)ACCTCCTCTTTTTTGTCTACCTCGGAGGTTGGGTTGATGAZH548EGY77(1078)ACCTCCTCTTTTTTTCTCCCCGGAGGTTGGGTTGATGACopsepsus(1081)ACCTCCTCTTTGTTCTACCTCGGAGGTTGGGTTGATGA	SPU204ANGL85	(1079)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGGTTGATGA
SPU2214KENU7(1079)ACCTCCTCCTTTGTTCTACCTCGGAGATTTGGGTTGATGASPU2215KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2223KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU384001KEN97(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU452AMB85(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU52001RSA99(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77NAMB04(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL10322IM78(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1290ZIM78(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1887ZIM78(1078)ACCTCCTCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL230ZIM78(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL252IM79(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAZH501EGY77(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAZH548EGY77(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGACORSERSUS(1081)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	SPU220/KEN0/	(1078)	
SP02215KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU384001KEN97(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU452AMB85(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU52001RSA99(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77NAMB04(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77RSA08(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL10322IM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1290ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1887ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL2230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL763ZIM70(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAZH501EGY77(1078)ACCTCCTCTTTTGTTCTACCTCGGAGGTTTGGGTTGATGACONSONUS(1081)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	SPUZZI4KENU/	(1079)	ACCTCCTCCTTTGTTCTACCTCGGAG <mark>A</mark> TTTGGGTTGATGA
SP02220KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU2223KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU384001KEN97(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU45ZAMB85(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU52001RSA99(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77NAMB04(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77RSA08(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1032ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1290ZIM78(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1516ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL2230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL2230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1079)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAZH501EGY77(1078)ACCTCCTCTTTTGTTCTACCTCGGAGGTTTGGGTTGATGAZH548EGY77(1078)ACCTCCTCTTTTGTTCTACCTCGGAGGTTTGGGTTGATGACORSORSUS(1081)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	SPUZZISKENU/	(1079)	
SP02223KEN07(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU384001KEN97(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU45ZAMB85(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU52001RSA99(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77NAMB04(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77RSA08(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1032ZIM78(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1290ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1516ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL2230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL2230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1079)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAZH501EGY77(1078)ACCTCCTCTTTTTTTTTTTTCTCCCGGAGGTTTGGGTTGATGAConsensus(1081)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	SPUZZZUKENU/	(1079)	
SP0384001KEN97(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGASPU45ZAMB85(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGASPU52001RSA99(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77NAMB04(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77RSA08(1079)ACCTCCTCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL1032ZIM78(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1290ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1516ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL2230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL763ZIM70(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1079)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAZH501EGY77(1078)ACCTCCTCTTTTGTTCTACCTCGGAGGTTTGGGTTGATGAConsensus(1081)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	SPUZZZSKENU/	(1079)	
SP0432AMB63(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGASPU52001RSA99(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77NAMB04(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77RSA08(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1032ZIM78(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1290ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1516ZIM78(1078)ACCTCCTCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL763ZIM70(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1079)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAZH501EGY77(1078)ACCTCCTCTTTTTGTTCTACCTCGGAGGTTTGGGTTGATGAConsensus(1081)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	SPUS04UUIREN9/	(1070)	
SP052001RSA99(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77NAMB04(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77RSA08(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1032ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1290ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1516ZIM78(1078)ACCTCCTCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL230ZIM78(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL763ZIM70(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAZH501EGY77(1078)ACCTCCTCTTTTTGTTCTACCTCGGAGGTTTGGGTTGATGAConsensus(1081)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	SPU4JZAMBOJ	(1070)	
SP077NAMB04(1078)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGASPU77RSA08(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1032ZIM78(1079)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL1290ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1516ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL2230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL763ZIM70(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAZH501EGY77(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGACORSORSUS(1081)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	SPUJZUUIRSA99	(1079)	
VRL1032ZIM78(1079)ACCTCCTCTTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL1290ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1516ZIM78(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1887ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL2230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL763ZIM70(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1079)ACCTCCTCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAZH501EGY77(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGACORSORSUS(1081)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	SPU//NAMBU4 CDII77DCA08	(1070)	
VRL103221M78(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1290ZIM78(1079)ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1516ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL2230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL763ZIM70(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1079)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAZH501EGY77(1078)ACCTCCTCTTTTTTTTTTCTACCTCGGAGGTTTGGGTTGATGAZH548EGY77(1078)ACCTCCTCTTTTTTTTTCTACCTCGGAGGTTTGGGTTGATGAConsensus(1081)ACCTCCTCTTTCTACCTCGGAGGTTTGGGTTGATGA	VDI 10327TM78	(1079)	
VRL12902IM76(1079)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAVRL1516ZIM78(1078)ACCTCCTCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL2230ZIM78(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL763ZIM70(1078)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAVRL825ZIM79(1079)ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGAZH501EGY77(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAZH548EGY77(1078)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGAConsensus(1081)ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	VRL103221M70 VDT 12007TM78	(1079)	
VRL131021M78 (1078) ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGA VRL1887ZIM78 (1078) ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGA VRL2230ZIM78 (1078) ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGA VRL763ZIM70 (1078) ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1079) ACCTCCTCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGA ZH501EGY77 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA ZH548EGY77 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	VRL129021M70 VDT15167TM78	(1079)	
VRL2230ZIM78 (1078) ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGA VRL263ZIM70 (1078) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1079) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA ZH501EGY77 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA ZH548EGY77 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	VRI.18877.TM78	(1078)	
VRL225021M70 (1070) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA VRL763ZIM70 (1078) ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGA VRL825ZIM79 (1079) ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGA ZH501EGY77 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA ZH548EGY77 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA Consensus (1081) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	VRL22307TM78	(1078)	
VRL825ZIM79 (1079) ACCTCCTCCTTTGTTCTGCCTCGGAGGTTTGGGTTGATGA ZH501EGY77 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA ZH548EGY77 (1078) ACCTCCTCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA Consensus (1081) ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	VRL7637IM70	(1078)	
ZH501EGY77 (1078) ACCTCCTCTTTTGTTCTACCTCGGAGGTTTGGGTTGATGA ZH548EGY77 (1078) ACCTCCTCTTTTGTTCTACCTCGGAGGTTTGGGTTGATGA	VRL8257.TM79	(1079)	
ZH548EGY77 (1078) ACCTCCTCTTTTTTTTTTTTCTACCTCGGAGGTTTGGGTTGATGA	ZH501EGY77	(1078)	ACCTCCTCTTTTTTTTTTCTTCCCTCCGCAGGTTTGGGTTGATGA
	ZH548EGY77	(1078)	ACCTCCTCTTTTGTTCTACCTCGGAGGTTTGGGTTGATGA
	Consensus	(1081)	ACCTCCTCCTTTGTTCTACCTCGGAGGTTTGGGTTGATGA

		1121 1160
214445KEN83	(1119)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATC <mark>C</mark> AA
56KEN65	(1118)	CCCG <mark>A</mark> GAGAACTGCAGCAGATACAGAGAGTGAGCATC <mark>C</mark> AA
900085MAU88	(1120)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATC <mark>C</mark> AA
An1000MAD91	(1119)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
An991MAD91	(1119)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
An999MAD91	(1119)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
AnK6087GUI84	(1118)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
AnTAMBULEGY94	(1118)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
Ar12568RSA71	(1118)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATC <mark>C</mark> AA
Ar20368RSA81	(1118)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
Ar21229SA00	(1118)	CCCGGGAAAACTGCAGCAGATACAGAGAGTGAGCATCTAA
Ar74RSA55	(1119)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATC <mark>C</mark> AA
Ar811MAD79	(1119)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
ArD38661SEN81	(1119)	CCCGGGAGAACTGCAGCAG <mark>G</mark> TACAGAGAGTGAGCATC <mark>C</mark> AA
B1143KEN77	(1119)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATC <mark>C</mark> AA
B314KEN62	(1119)	CCCG <mark>A</mark> GAGAACTGCAGCAGATACAGAGAGTGAGCATC <mark>C</mark> AA
H1825RSA75	(1119)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATC <mark>C</mark> AA
LunyoUGA55	(1120)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATC <mark>C</mark> AA
R1662CAR85	(1118)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
SPUI0301KEN07	(1119)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
SPU10302KEN07	(1119)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
SPU10307KEN07	(1118)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
SPUIU3I5KENU/	(1119)	
SPUIZUUZSOM98	(1110)	CCCGGGAGAACTG <mark>T</mark> AGCAGATACAGAGAGTGAGCATCTAA
SPUIJZKSAU8	(1119)	
SPUZU4ANGL85	(1119)	
SPUZZU/KENU/	(1110)	
SPUZZI4KENU/ SDU2215KENO/	(1110)	
SPUZZIJKENU/	(1110)	
SPUZZZOKENO7 Spuzzzyken07	(1110)	
QDII38/001KEN07	(1118)	
SPUIDERANDI SPUIDERANDS	(1110)	
SI 0452AMB05	(1110)	CCCCCCCACA ACTICACACACATACA ACACATCACATC
SPU77NAMB04	(1112)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
SPU77RSA08	(1110)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
VRL10327TM78	(1119)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
VRL12907TM78	(1119)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
VRL1516ZIM78	(1118)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
VRL1887ZIM78	(1118)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
VRL2230ZIM78	(1118)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
VRL763ZIM70	(1118)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATC
VRL825ZIM79	(1119)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
ZH501EGY77	(1118)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
ZH548EGY77	(1118)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA
Consensus	(1121)	CCCGGGAGAACTGCAGCAGATACAGAGAGTGAGCATCTAA

		1161 1200
214445KEN83	(1159)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
56KEN65	(1158)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTC <mark>T</mark> ACC
900085MAU88	(1160)	TATTGCCCTTAGGTAGTCTTCTGGTAGAGAAGGGTCCACC
An1000MAD91	(1159)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
An991MAD91	(1159)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
An999MAD91	(1159)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
AnK6087GUI84	(1158)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
AnTAMBULEGY94	(1158)	TATTGCCCTTAGATAGTCT <mark>C</mark> CTGGTAGAGAAGG <mark>A</mark> TCCACC
Ar12568RSA71	(1158)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
Ar20368RSA81	(1158)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
Ar21229SA00	(1158)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
Ar74RSA55	(1159)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
Ar811MAD79	(1159)	TATTGCCCTTAGATAGTCTCCTGGTAGAGAAGGATCCACC
ArD38661SEN81	(1159)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTC <mark>T</mark> ACC
B1143KEN77	(1159)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
B314KEN62	(1159)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
H1825RSA75	(1159)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
LunyoUGA55	(1160)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGG <mark>A</mark> TCCACC
R1662CAR85	(1158)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
SPU10301KEN07	(1159)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
SPU10302KEN07	(1159)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
SPU10307KEN07	(1158)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
SPU10315KEN07	(1159)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
SPU12002SOM98	(1158)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
SPU152RSA08	(1159)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
SPU204ANGL85	(1159)	TATTGCCCT <mark>C</mark> AGATAGTCTTCTGGTAGAGAAGGGTCCACC
SPU220/KEN0/	(1158)	TATTGCCCTTAGATAGTCTTCTGG <mark>C</mark> AGAGAAGGGTCCACC
SPU2214KENU7	(1159)	
SPUZZISKENU/	(1159) (1150)	
SPUZZZUKENU/	(1159) (1150)	
SPUZZZSKENU/	(1159)	
SPU384UUIKEN97	(1150) (1150)	
SPU45ZAMB85	(1150)	
SPUJZUUIRSA99	(1159)	
	(1150)	
VDT 10227TM70	(1150)	
VRL103221M70 VDT12007TM78	(1159)	
VRL129021M70 VDT15167TM78	(1159)	
VRL18877TM78	(1158)	
VRL22307TM78	(1158)	
VRL7637TM70	(1150)	
VRL8257.TM79	(1159)	TATTGCCCTCAGATAGTCTTCAGCTAGAGAGGGGGCCACC
ZH501EGY77	(1158)	TATTGCCCTTAGATAGTCTC
ZH548EGY77	(1158)	TATTGCCCTTAGATAGTCTCCTCCTGGTAGAGAAGGATCCACC
Consensus	(1161)	TATTGCCCTTAGATAGTCTTCTGGTAGAGAAGGGTCCACC
00110011040	()	

		1201 1240
214445KEN83	(1199)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
56KEN65	(1198)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
900085MAU88	(1200)	ATGCCAGCAAAGCTGGGGTGCATCAT <mark>G</mark> TGCCTTGGGTATG
An1000MAD91	(1199)	ATGCCAGCAAAGCTGGG <mark>A</mark> TGCATCATATGCCTTGGGTATG
An991MAD91	(1199)	ATGCCAGCAAAGCTGGG <mark>A</mark> TGCATCATATGCCTTGGGTATG
An999MAD91	(1199)	ATGCCAGCAAAGCTGGG <mark>A</mark> TGCATCATATGCCTTGGGTATG
AnK6087GUI84	(1198)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
AnTAMBULEGY94	(1198)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
Ar12568RSA71	(1198)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
Ar20368RSA81	(1198)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
Ar21229SA00	(1198)	ATGCCAGCAAAGCTGGG <mark>A</mark> TGCATCAT <mark>G</mark> TGCCTTGGGTATG
Ar74RSA55	(1199)	ATGCCAGCAAA <mark>A</mark> CTGGGGTGCATCATATGCCTTGGGTATG
Ar811MAD79	(1199)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
ArD38661SEN81	(1199)	ATGCCAGCAAAGCTGGG <mark>A</mark> TGCATCATATGCCTTGGGTATG
B1143KEN77	(1199)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
B314KEN62	(1199)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
H1825RSA75	(1199)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
LunyoUGA55	(1200)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
R1662CAR85	(1198)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
SPU10301KEN07	(1199)	ATGCCAGCAAAGCTGGG <mark>A</mark> TGCATCATATGCCT <mark>C</mark> GGGTATG
SPU10302KEN07	(1199)	ATGCCAGCAAAGCTGGG <mark>A</mark> TGCATCATATGCCT <mark>C</mark> GGGTATG
SPU10307KEN07	(1198)	ATGCCAGCAAAGCTGGGATGCATCATATGCCTCGGGTATG
SPU10315KEN07	(1199)	ATGCCAGCAAAGCTGGG <mark>A</mark> TGCATCATATGCCT <mark>C</mark> GGGTATG
SPUI2002SOM98	(1198)	ATGCCAGCAAAGCTGGGATGCATCATATGCCTTGGGTATG
SPUI52RSAU8	(1199)	ATGCCAGCAAAGCTGGG <mark>A</mark> TGCATCATATGCCT <mark>C</mark> GGGTATG
SPU204ANGL85	(1199)	ATGCCAGCAAAGCTGGGATGCATCATATGCCTTGGGTATG
SPU220/KENU/	(1198)	ATGCCAGCAAAGCTGGGATGCATCATATGCCTTGGGTATG
SPUZZI4KENU/	(1199)	
SPUZZISKENU/	(1199)	
SPUZZZUKENU/	(1199)	
SPUZZZSKENU/	(1199)	
SPUS04UUIREN9/	(1190)	
SPU4JZAMBOJ	(1190)	
SPUJZUUIKSA99	(1100)	
SPU//NAMDU4 CDII77DCA08	(1100)	
VDI 10327TM78	(1100)	
VRL103221M70 VDI 12007TM78	(1100)	
VRL15167TM78	(1199)	
VRL18877.TM78	(1198)	
VRL22307TM78	(1198)	
VRL7637.TM70	(1198)	ATGCCAGCAAAGCTGGGGGTGCATCATATGCCTTTCCCTTTC
VRL8257TM79	(1199)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
ZH501EGY77	(1198)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
ZH548EGY77	(1198)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTC
Consensus	(1201)	ATGCCAGCAAAGCTGGGGTGCATCATATGCCTTGGGTATG
	(= = = = /	

		1241 1280
214445KEN83	(1239)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG
56KEN65	(1238)	CAGGGGATAGGCC <mark>A</mark> TCCATGGTAGTCCCAGTGACAGGAAG
900085MAU88	(1240)	CAGGGGATA <mark>A</mark> GCC <mark>A</mark> TCCATGGTAGTCCCAGTGACAGGAAG
An1000MAD91	(1239)	CAGGGGATAGGCCGTCCATGGTTGTCCCAGTGACAGGAAG
An991MAD91	(1239)	CAGGGGATAGGCCGTCCATGGT
An999MAD91	(1239)	CAGGGGATAGGCCGTCCATGGT
AnK6087GUI84	(1238)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG
AnTAMBULEGY94	(1238)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG
Ar12568RSA71	(1238)	CAGGGGATAGGCC <mark>A</mark> TCCATGGT <mark>G</mark> GTCCCAGTGACAGGAAG
Ar20368RSA81	(1238)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG
Ar21229SA00	(1238)	CAGGGGATAGGCCGTCCATGGT <mark>T</mark> GTCCCAGTGACAGGAAG
Ar74RSA55	(1239)	CAGGGGATAGGCC <mark>A</mark> TCCATGGTAGTCCCAGTGACAGGAAG
Ar811MAD79	(1239)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG
ArD38661SEN81	(1239)	CAGGGGATAGGCC <mark>A</mark> TCCATGGTAGTCCCAGTGACAGGAAG
B1143KEN77	(1239)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG
B314KEN62	(1239)	CAGGGGATAGGCC <mark>A</mark> TCCATGGTAGTCCCAGTGACAGGAAG
H1825RSA75	(1239)	CAGGGGATAGGCC <mark>A</mark> TCCATGGTAGTCCCAGTGACAGGAAG
LunyoUGA55	(1240)	CAGG <mark>A</mark> GATAGGCC <mark>A</mark> TCCATGGTAGTCCCAGTGACAGGAAG
R1662CAR85	(1238)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG
SPU10301KEN07	(1239)	CAGGGGATAG <mark>A</mark> CCGTCCATGGT <mark>T</mark> GTCCCAGTGACAGGAAG
SPU10302KEN07	(1239)	CAGGGGATAG <mark>A</mark> CCGTCCATGGT <mark>T</mark> GTCCCAGTGACAGGAAG
SPU10307KEN07	(1238)	CAGGGGATAG <mark>A</mark> CCGTCCATGGT <mark>T</mark> GTCCCAGTGACAGGAAG
SPU10315KEN07	(1239)	CAGGGGATAG <mark>A</mark> CCGTCCATGGT <mark>T</mark> GTCCCAGTGACAGGAAG
SPU12002SOM98	(1238)	CAGGGGATAGGCCGTCCATGGT
SPU152RSA08	(1239)	CAGGGGATAG <mark>A</mark> CCGTCCATGGT <mark>T</mark> GTCCCAGTGACAGGAAG
SPU204ANGL85	(1239)	CAGGGGATAGGCCGTCCATGGTTGTCCCAGTGACAGGAAG
SPU2207KEN07	(1238)	CAGGGGATAG <mark>A</mark> CCGTCCATGGT <mark>T</mark> GTCCCAGTGACAGGAAG
SPU2214KEN07	(1239)	CAGGGGA <mark>C</mark> AGGCCGTCCATGGT <mark>T</mark> GTCCCAGTGACAGGAAG
SPU2215KEN07	(1239)	CAGGGGATAG <mark>A</mark> CCGTCCATGGT <mark>T</mark> GTCCCAGTGACAGGAAG
SPU2220KEN07	(1239)	CAGGGGATAG <mark>A</mark> CCGTCCATGGT <mark>T</mark> GTCCCAGTGACAGGAAG
SPU2223KEN07	(1239)	CAGGGGATAG <mark>A</mark> CCGTCCATGGT <mark>T</mark> GTCCCAGTGACAGGAAG
SPU384001KEN97	(1238)	CAGGGGATAGGCCGTCCATGGT
SPU45ZAMB85	(1238)	CAGGGGATAGGCC <mark>A</mark> TCCATGGT <mark>G</mark> GTCCC <mark>G</mark> GTGACAGGAAG
SPU52001RSA99	(1239)	CAGGGGATAGGCCGTCCATGGT <mark>T</mark> GTCCCAGTGACAGGAAG
SPU77NAMB04	(1238)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG
SPU77RSA08	(1239)	CAGGGGATAG <mark>A</mark> CCGTCCATGGT <mark>T</mark> GTCCCAGTGACAGGAAG
VRL1032ZIM78	(1239)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG
VRL1290ZIM78	(1239)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG
VRL1516ZIM78	(1238)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG
VRL1887ZIM78	(1238)	CAGGGGATAGGCC <mark>A</mark> TCCATGGTAGTCCCAGTGACAGGAAG
VRL2230ZIM78	(1238)	CAGGGGATAGGCCATCCATGGTAGTCCCAGTGACAGGAAG
VRL763ZIM70	(1238)	CAGGGGATAGGCC <mark>A</mark> TCCATGGT <mark>G</mark> GTCCCAGTGACAGGAAG
VRL825ZIM79	(1239)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG
ZH501EGY77	(1238)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG
ZH548EGY77	(1238)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG
Consensus	(1241)	CAGGGGATAGGCCGTCCATGGTAGTCCCAGTGACAGGAAG

		1281 1320
214445KEN83	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
56KEN65	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCA <mark>A</mark> GTCCAGCCA
900085MAU88	(1280)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
An1000MAD91	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
An991MAD91	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
An999MAD91	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
AnK6087GUI84	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
AnTAMBULEGY94	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
Ar12568RSA71	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCA <mark>A</mark> GTCCAGCCA
Ar20368RSA81	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
Ar21229SA00	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
Ar74RSA55	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
Ar811MAD79	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
ArD38661SEN81	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
B1143KEN77	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
B314KEN62	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
H1825RSA75	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCA <mark>A</mark> GTCCAGCCA
LunyoUGA55	(1280)	CCACTCACTCAAGACGACCAGAGCCTGGCATGTCCAGCCA
R1662CAR85	(1278)	CCACTCACT ^T AAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU10301KEN07	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU10302KEN07	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU10307KEN07	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU10315KEN07	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU12002SOM98	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU152RSA08	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU204ANGL85	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU2207KEN07	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU2214KEN07	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU2215KEN07	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU2220KEN07	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU2223KEN07	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU384001KEN97	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU45ZAMB85	(1278)	CCACTCACTCAAGACGACCA <mark>G</mark> AGCCTGGCA <mark>A</mark> GTCCAGCCA
SPU52001RSA99	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU77NAMB04	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
SPU77RSA08	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
VRL1032ZIM78	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
VRL1290ZIM78	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
VRL1516ZIM78	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
VRL1887ZIM78	(1278)	CCACTCACTCAAGACGACCA <mark>G</mark> AGCCTGGCATGTCCAGCCA
VRL2230ZIM78	(1278)	CCACTCACTCAAGACGACCA <mark>G</mark> AGCCTGGCATGTCCAGCCA
VRL763ZIM70	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCA <mark>A</mark> GTCCAGCCA
VRL825ZIM79	(1279)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
ZH501EGY77	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
ZH548EGY77	(1278)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA
Consensus	(1281)	CCACTCACTCAAGACGACCAAAGCCTGGCATGTCCAGCCA

		1321 1360
214445KEN83	(1319)	GCCAGGGCGGCAGCAACTCGTGATAGAGTCAACTCATCCC
56KEN65	(1318)	GCCAGGGC <mark>A</mark> GCAGCAACTCGTGATAGAGTCAACTCATCCC
900085MAU88	(1320)	GCCAGGGCGGCAGCAACTCTTGATAGAGTCAACTCATCCC
An1000MAD91	(1319)	GCCAGGGC <mark>A</mark> GCAGCAACTCGTGATAGAGTCAACTCATCCC
An991MAD91	(1319)	GCCAGGGC <mark>A</mark> GCAGCAACTCGTGATAGAGTCAACTCATCCC
An999MAD91	(1319)	GCCAGGGC <mark>A</mark> GCAGCAACTCGTGATAGAGTCAACTCATCCC
AnK6087GUI84	(1318)	GCCAGGGCGGCAGCAACTCGTGATAGAGTCAACTCATCCC
AnTAMBULEGY94	(1318)	GCCAGGGCGGCAGCAACTCGTGATAGAGTCAACTCATCCC
Ar12568RSA71	(1318)	GCCAGGGC <mark>A</mark> GCAGCAACTCGTGATAGAGTCAACTCATCCC
Ar20368RSA81	(1318)	GCCAGGGCGGCAGCAACTCGTGATAGAGT <mark>T</mark> AACTCATCCC
Ar21229SA00	(1318)	GCCAGGGC <mark>A</mark> GCAGCAACTCGTGATAGAGTCAACTCATCCC
Ar74RSA55	(1319)	GCCAGGGC <mark>A</mark> GCAGCAACTCGTGATAGAGTCAACTCATCCC
Ar811MAD79	(1319)	GCCAGGGCGGCAGCAACTCGTGATAGAGTCAACTCATCCC
ArD38661SEN81	(1319)	GCCAGGGCGGCAGCAACTC <mark>T</mark> TGATAGAGTCAACTCATCCC
B1143KEN77	(1319)	GCCAGGGCGGCAGCAACTCGTGATAGAGTCAACTCATCCC
B314KEN62	(1319)	GCCAGGGCGGCAGCAACTCGTGATAGAGT <mark>T</mark> AACTCATCCC
H1825RSA75	(1319)	GCCAGGGC <mark>A</mark> GCAGCAACTCGTGATAGAGTCAACTCATCCC
LunyoUGA55	(1320)	GCCAGGGCGGCAGCAACTCGTGATAGAGTCAACTCATCCC
R1662CAR85	(1318)	GCCAGGGCGGCAGCAACTCGTGATAGAGTCAACTCATC <mark>T</mark> C
SPU10301KEN07	(1319)	GCCAGGGC <mark>A</mark> GCAGCAACTCGTGATAGAGTCA <mark>G</mark> CTCATCCC
SPU10302KEN07	(1319)	GCCAGGGC <mark>A</mark> GCAGCAACTCGTGATAGAGTCA <mark>G</mark> CTCATCCC
SPU10307KEN07	(1318)	GCCAGGGCAGCAACTCGTGATAGAGTCAGCTCATCCC
SPU10315KEN07	(1319)	GCCAGGGC <mark>A</mark> GCAGCAACTCGTGATAGAGTCA <mark>G</mark> CTCATCCC
SPUI2002SOM98	(1318)	GCCAGGGCAGCAACTCGTGATAGAGTCAACTCATCCC
SPU152RSA08	(1319)	GCCAGGGC <mark>A</mark> GCAGCAACTCGTGATAGAGTCA <mark>G</mark> CTCATCCC
SPU204ANGL85	(1319)	
SPU220/KEN0/	(1318)	
SPUZZI4KENU7	(1319)	
SPUZZISKENU/	(1319)	
SPUZZZUKENU/	(1319)	
SPUZZZSKENU/	(1319)	
SPUS04UUIREN97	(1310)	
SPU4JZAMBOJ	(1310)	
SPUJZUUIKSA99 CDU77NIAMD04	(1319)	
20117702308	(1310)	
VDI 10327TM78	(1319)	
VRL12907TM78	(1319)	
VRL15167TM78	(1319)	
VRL18877TM78	(1318)	GCCAGGCGGCAGCAACTCGTGATAGAGTCAACTCATCCC GCCAGGCGGCGGCAGCAACTCGTGATAGAGTCAACTCATCCC
VRL22307TM78	(1318)	GCCAGGCGGCAGCAACTCGTGATAGAGTCAACTCATCCC
VRI.7637.TM70	(1318)	GCCAGGCC <mark>A</mark> CCAGCAACTCGTGATAGAGTCAACTCATCCC
VRL8257.TM79	(1319)	GCCAGGGCGGCAGCAACTCGTGATAGAGTCAACTCATCCC
7H501ECY77	(1318)	GCCAGGGCGGCAGCAACTCGTGATAGAGTCAACTCATCCC
ZH548EGY77	(1318)	GCCAAGGCGGCAGCAACTCGTGATAGAGTCAACTCATCCC
Consensus	(1321)	GCCAGGGCGGCAGCAACTCGTGATAGAGTCAACTCATCCC
00110011000	(+	

		1361 1400
214445KEN83	(1359)	GGGAAGGATTCCC <mark>T</mark> TCCTTTAGCTTATACTTGTTGATGAG
56KEN65	(1358)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
900085MAU88	(1360)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
An1000MAD91	(1359)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
An991MAD91	(1359)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
An999MAD91	(1359)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
AnK6087GUI84	(1358)	G <mark>A</mark> GAAGGATTCCC <mark>T</mark> TCCTTTAGCTTATACTTGTTGATGAG
AnTAMBULEGY94	(1358)	GGGAAGGATTCCCTTTAGCTTATACTTGTTGATGAG
Ar12568RSA71	(1358)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
Ar20368RSA81	(1358)	GGGAAGGATTCCC <mark>T</mark> TCCTTTAGCTT <mark>G</mark> TACTTGTTGATGAG
Ar21229SA00	(1358)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
Ar74RSA55	(1359)	G <mark>A</mark> GAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
Ar811MAD79	(1359)	GGGAAGGATTCCC <mark>T</mark> TCCTTTAGCTTATACTTGTTGATGAG
ArD38661SEN81	(1359)	GGGA <mark>G</mark> GGATT <mark>T</mark> CCCTCCTTTAGCTTATACTTGTTGATGAG
B1143KEN77	(1359)	GGGAAGGATTCCC <mark>T</mark> TCCTTTAGCTTATACTTGTTGATGAG
B314KEN62	(1359)	G <mark>A</mark> GA <mark>G</mark> GGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
H1825RSA75	(1359)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
LunyoUGA55	(1360)	GGGAAGGATTCCCCTCCTTTAGCTT <mark>G</mark> TACTTGTTGATGAG
R1662CAR85	(1358)	GGGAAGGATTCCC <mark>T</mark> TCCTTTAGCTTATA <mark>T</mark> TTGTTGATGAG
SPU10301KEN07	(1359)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
SPU10302KEN07	(1359)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
SPU10307KEN07	(1358)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
SPU10315KEN07	(1359)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
SPU12002SOM98	(1358)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
SPU152RSA08	(1359)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
SPU204ANGL85	(1359)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
SPU2207KEN07	(1358)	GGGAAGGATTCCCCTCCTTTAGCTT <mark>G</mark> TACTTGTTGATGAG
SPU2214KEN07	(1359)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
SPU2215KENU/	(1359)	GGGAAGGATTCCCCCTCCTTTAGCTTATACTTGTTGATGAG
SPU2220KEN07	(1359)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
SPU2223KENU/	(1359)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
SPU38400IKEN97	(1358)	GGGAAGGATTCCCCTCCTTTAGCTTATACTTGTTGATGAG
SPU45ZAMB85	(1358)	
SPU5ZUUIRSA99	(1359)	
SPU//NAMBU4	(1358)	GGGAAGGATTCCCTTTAGCTTATACTTGTTGATGAG
SPU//RSAU8	(1359)	
VRLIU3ZZIM78	(1359)	
VRLIZ9UZIM78	(1359)	
VRLIJI0ZIM70 VDT 10077TM70	(1350)	
	(1350)	
νκμζζουδιμίο νρισέρτμο	(1350) (1350)	
VRL8257TM79	(1350)	
ZH501EGV77	(1358)	
ZH548ECV77	(1358)	
Consensus	(1361)	
00110011000	(+00+)	

214445KEN83(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC56KEN65(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC900085MAU88(1400)AGCCTCCACAGTTGCCTTGCCTTCTTTCGACATTTTCATCAn1000MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAn991MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAn999MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAnK6087GUI84(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAnTAMBULEGY94(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr12568RSA71(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr20368RSA81(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr21229SA00(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr138661SEN81(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTTCATCArD38661SEN81(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCB1143KEN77(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCB144KEN62(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTTCATCB144KEN62(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTTCATC
56KEN65(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC900085MAU88(1400)AGCCTCCACAGTTGCCTTGCCTTCTTTCGACATTTTCATCAn1000MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAn991MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAn999MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTCATCAnK6087GUI84(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTCATCAnTAMBULEGY94(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAr12568RSA71(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAr20368RSA81(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAr74RSA55(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTCATCAr74RSA55(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTCATCArD38661SEN81(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCB1143KEN77(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTCATCB144KEN62(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTCATCB144KEN62(1390)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTCATC
900085MAU88(1400)AGCCTCCACAGTTGCCTTGCCTTCTTTCGACATTTTCATCAn1000MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAn991MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAn999MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAnK6087GUI84(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAnTAMBULEGY94(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAr12568RSA71(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAr20368RSA81(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAr21229SA00(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAr74RSA55(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTCATCAr1038661SEN81(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCB1143KEN77(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCB314KEN62(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTCATC
An1000MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAn991MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAn999MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAnK6087GUI84(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTCATCAnTAMBULEGY94(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAr12568RSA71(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAr20368RSA81(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr21229SA00(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr74RSA55(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTCATCAr811MAD79(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCB1143KEN77(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCB314KEN62(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTCATC
An 991MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAn 999MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAnK6087GUI84(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTTCATCAnTAMBULEGY94(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr12568RSA71(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr20368RSA81(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr21229SA00(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr74RSA55(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr811MAD79(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCB1143KEN77(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCB314KEN62(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTCATC
An999MAD91(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAnK6087GUI84(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTTCATCAnTAMBULEGY94(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr12568RSA71(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr20368RSA81(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr21229SA00(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr74RSA55(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr811MAD79(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTTCATCB1143KEN77(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCB314KEN62(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTCATC
AnK6087GUI84(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTCATCAnTAMBULEGY94(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAr12568RSA71(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAr20368RSA81(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAr21229SA00(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAr74RSA55(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCAr811MAD79(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCArD38661SEN81(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCB1143KEN77(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCB314KEN62(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTCATC
AnTAMBULEGY94(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr12568RSA71(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr20368RSA81(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr21229SA00(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr74RSA55(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr811MAD79(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCArD38661SEN81(1399)AGCCTCCACAGTTGCTTGCCTTCTTTCGACATTTTCATCB1143KEN77(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCB314KEN62(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTCATC
Ar12568RSA71(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr20368RSA81(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr21229SA00(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr74RSA55(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr811MAD79(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTCATCArD38661SEN81(1399)AGCCTCCACAGTTGCCTTGCCTTCTTTCGACATTTCATCB1143KEN77(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTCATCB314KEN62(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTCATC
Ar20368RSA81(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr21229SA00(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr74RSA55(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr811MAD79(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTTCATCArD38661SEN81(1399)AGCCTCCACAGTTGCCTTGCCTTCTTTCGACATTTTCATCB1143KEN77(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCB314KEN62(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTTCATC
Ar21229SA00(1398)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr74RSA55(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr811MAD79(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTTCATCArD38661SEN81(1399)AGCCTCCACAGTTGCCTTGCCTTCTTTCGACATTTTCATCB1143KEN77(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCB314KEN62(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTTCATC
Ar74RSA55(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCAr811MAD79(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTTCATCArD38661SEN81(1399)AGCCTCCACAGTTGCCTTGCCTTCTTTCGACATTTTCATCB1143KEN77(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCB314KEN62(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTCATC
Ar811MAD79(1399)AGCCTCCACAGTTGCTTTGCCTTCTTT TGACATTTTCATCArD38661SEN81(1399)AGCCTCCACAGTTGCCTTGCCTTCTTTCGACATTTTCATCB1143KEN77(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATCB314KEN62(1399)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTTCATC(1200)AGCCTCCACAGTTGCTTTGCCTTCTTTGACATTTTCATC
ArD38661SEN81 (1399) AGCCTCCACAGTTGCCTTGCCTTCTTTCGACATTTTCATC B1143KEN77 (1399) AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC B314KEN62 (1399) AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTTCATC
B1143KEN77 (1399) AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC B314KEN62 (1399) AGCCTCCACAGTTGCTTTGCCTTCTTTTGACATTTTCATC
B314KEN62 (1399) AGCCTCCACAGTTGCTTTGCCTTCTTT U1005D0175 (1200) AGCCTCCACAGTTGCTTTGCCTTCTTTTGGACATTTTCATC
H1825RSA75 (1399) AGCCTCCACAGTTGCTTTGCCTTCTTCGACATTTTCATC
LunyoUGA55 (1400) AGCCTCCACAGTTGCTTTGCCTTC <mark>C</mark> TT <mark>T</mark> GACAT <mark>C</mark> TTCATC
R1662CAR85 (1398) AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC
SPU10301KEN07 (1399) AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC
SPU10302KEN07 (1399) AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC
SPU10307KEN07 (1398) AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC
SPUI0315KEN07 (1399) AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC
SPUI2002SOM98 (1398) AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC
SPUI52RSAU8 (1399) AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC
SPU204ANGL85 (1399) AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC
SPUZZU/KENU/ (1398) AGCCTCTACAGTTGCTTTGCCTTCTTTCGACATTTTCATC
SPU2214KENU7 (1399) AGCCTCTACAGTTGCTTTGCCTTCTTTCGACATTTTCATC
SPU2215KENU7 (1399) AGUUTULALAGTTGUTTTGUUTUTTTUGALATTTTUATU
SPU2220KENU7 (1399) AGUUTULALAGTTGUTTTGUUTUTTTUGALATTTTUATU
SPUZZZSKENU/ (IS99) AGCCICCACAGIIGCIIIGCCIICIIICGACAIIIICAIC
SPUS04UUIREN97 (IS90) AGCCICCACAGIIGCIIIGCCIICIIICGACAIIIICAIC
VRI125021M70 (1393) $ACCCTCCACACTTCCTTTTTCCACACTTCCTTTCCACACTTCCTTCCTTTCCACACTTCCTTTCCTTTCCTTCCTTCCTTCCTTCCTTTCCTTCCTTCCTTTCCTTCCTTTCCTTCCTTTCTTTCTTTCCTTTCCTTTCTTTCCTTTT$
VRL18877.IM78 (1398) AGCCTCCACAGTTGCCTTTGCCTTTTCGACATTTTCATC
VRL7637IM70 (1398) AGCCTCCACAGTTGCCTTTGCCTTTCGACATTTCATC
VRL8257IM79 (1399) AGCCTCCACAGTTGCTTTTACCTTCGACATTTTCATC
ZH501EGY77 (1398) AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC
ZH548EGY77 (1398) AGCCTCCACAGTTGCTTTGCCTTCTTTCGACATTTTCATC
Consensus (1401) AGCCTCCACAGTTGCTTTGCCTTCTTCGACATTTTCATC

		1441 1480
214445KEN83	(1439)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
56KEN65	(1438)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
900085MAU88	(1440)	ATCATCCTCCGGGGCTT <mark>A</mark> TTGCCACGAGT <mark>T</mark> AGAGCCAGAA
An1000MAD91	(1439)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
An991MAD91	(1439)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
An999MAD91	(1439)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
AnK6087GUI84	(1438)	ATCATCCTCCGGGGGCTTGTTGCCACGAGT <mark>T</mark> AGAGCCAGAA
AnTAMBULEGY94	(1438)	ATCATCCTCC <mark>T</mark> GGGCTTGTTGCCACGAGT <mark>T</mark> AGAGCCAGAA
Ar12568RSA71	(1438)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
Ar20368RSA81	(1438)	ATCATCCTCCGGGGGCTTGTTGCCACGAGT <mark>T</mark> AGAGCCAGAA
Ar21229SA00	(1438)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
Ar74RSA55	(1439)	ATCATCCTCCGGGGGCTTGTTGCCACGAGTTAGAGCCAGAA
Ar811MAD79	(1439)	ATCATCCTCC <mark>T</mark> GGGCTTGTTGCCACGAGT <mark>T</mark> AGAGCCAGAA
ArD38661SEN81	(1439)	ATCATCCTCCGGGGCTTGTTGCCACGAGT <mark>T</mark> AGAGCCAGAA
B1143KEN77	(1439)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
B314KEN62	(1439)	ATCATCCTCCGGGGCTTGTTGCCACGAGT <mark>T</mark> AGAGCCAGAA
H1825RSA75	(1439)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
LunyoUGA55	(1440)	ATCATCCTCCGGGGCTTGTTGCCACGAGT <mark>T</mark> AGAGCCAGAA
R1662CAR85	(1438)	ATCATCCTCCGGGGCTTGTTGCCACGAGT <mark>T</mark> AGAGCCAGAA
SPUI0301KEN07	(1439)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
SPU10302KEN07	(1439)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
SPUIU30/KENU/	(1438)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
SPUIU3I5KENU/	(1439)	
SPUIZUUZSOM98	(1438)	
SPUIJZKSAU8	(1439)	
SPUZU4ANGL85	(1439)	
SPUZZU/KENU/	(1430)	
SPUZZI4KENU/ SDU2215KENO/	(1439)	
SPUZZIJAENU/	(1439)	
SPUZZZORENO7 Spuzzzyreno7	(1/39)	
SP02225KEN07	(1439)	
SPUIDSTAMB85	(1/38)	
SI 0452AMB05	(1439)	
SPU77NAMB04	(1438)	ATCATCCTCCGGGGCTTGTTGCCACGAGTTAGAGCCAGAA
SPU77RSA08	(1439)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
VRL10327TM78	(1439)	ATCATCCTCCTGGGCCTTGTTGCCACGAGTTAGAGCCAGAA
VRL12907TM78	(1439)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
VRL1516ZIM78	(1438)	ATCATCCTCCTGGGCCTTGTTGCCACGAGTTAGAGCCAGGA
VRL1887ZIM78	(1438)	ATCATCCTCCGGGGGCTTGTTGCCACGAGTTAGAGCCAGAA
VRL2230ZIM78	(1438)	ATCATCCTCCGGGGCTTGTTGCCACGAGTTAGAGCCAGAA
VRL763ZIM70	(1438)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAGAA
VRL825ZIM79	(1439)	ATCATCCTCCGGGGCTTGTTGCCACGAGTCAGAGCCAG <mark>G</mark> A
ZH501EGY77	(1438)	ATCATCCTCCTGGGGCTTGTTGCCACGAGTTAGAGCCAGAA
ZH548EGY77	(1438)	ATCATCCTCCTGGGGCTTGTTGCCACGAGTTAGAGCCAGAA
Consensus	(1441)	ATCATCCTCCGGGGGCTTGTTGCCACGAGTCAGAGCCAGAA

		1481 1520
214445KEN83	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
56KEN65	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
900085MAU88	(1480)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
An1000MAD91	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
An991MAD91	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
An999MAD91	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
AnK6087GUI84	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
AnTAMBULEGY94	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
Ar12568RSA71	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
Ar20368RSA81	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
Ar21229SA00	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
Ar74RSA55	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTC <mark>T</mark> GCCCCACC
Ar811MAD79	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
ArD38661SEN81	(1479)	C <mark>G</mark> ATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
B1143KEN77	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
B314KEN62	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
H1825RSA75	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
LunyoUGA55	(1480)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
R1662CAR85	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU10301KEN07	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU10302KEN07	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU10307KEN07	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU10315KEN07	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU12002SOM98	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU152RSA08	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU204ANGL85	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU2207KEN07	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU2214KEN07	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU2215KEN07	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU2220KEN07	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU2223KEN07	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU384001KEN97	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU45ZAMB85	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU52001RSA99	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU77NAMB04	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
SPU77RSA08	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
VRL1032ZIM78	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
VRL1290ZIM78	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
VRL1516ZIM78	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
VRL1887ZIM78	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
VRL2230ZIM78	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
VRL763ZIM70	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
VRL825ZIM79	(1479)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
ZH501EGY77	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
ZH548EGY77	(1478)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC
Consensus	(1481)	CAATCATTTTCTTGGCATCCTTCTCCCAGTCAGCCCCACC

 214445KEN83 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC 56KEN65 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC An1000MD91 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC An991MAD91 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC An999MD51 (1519) ATACTGCTTTAAGAGTTCGATAACCCTCGCGGCATCAAAC An748037GU184 (1518) ATACTGCTTTAAGAGTTCGATAACCCTCGCGGCACTCAAAC Ar12568RSA71 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC Ar20368RSA81 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC Ar21229SA00 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC Ar21229SA00 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC Ar21368RS81 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC Ar38661SEN81 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar38661SEN81 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B314KEN62 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B314KEN62 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT H1825RSA75 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B314KEN62 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B314KEN62 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU10302KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU10302KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU10302KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU10302KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU1202SOM98 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU3201KEN97 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU3201KEN97 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC VRL1887ZIM78 (1518			1521 1560
 56KEM65 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAT 900085MAU88 (1520) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC An991MAD91 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC An999MAD91 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC An7099MAD91 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC An7080184 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGCATCAAAC An72568RSA81 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGCATCAAAC Ar212568RSA71 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGCATCAAAC Ar21229SA00 (1518) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC Ar21229SA00 (1518) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC Ar213661SEN81 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC ArD38661SEN81 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAT B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAT B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAT H1825RSA75 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU202SM98 (1518) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU202SM98 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU202SN98 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU202SM98 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU202SM98 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU220KEN07 (1519	214445KEN83	(1519)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC
900085MAU88 (1520) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAT An1000MAD91 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC An999MAD91 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC An7ABULGGY94 (1518) ATACTGCTTTAAGAGTTCGATAACCCTGCGGCACTCAAAC An7ABULGGY94 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC Ar12568RSA71 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC Ar20368RSA81 (1518) ATACTGCTTTAAGAGTTCGATAACCTACGGCATCAAAC Ar21229SA00 (1518) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC Ar21229SA00 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC Ar3866ISEN81 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC Ar3866ISEN81 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC Ar3866ISEN81 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAT H1825RSA75 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC B314KEN62 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAT H1825RSA75 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU10302KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU10302KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU10302KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU10302KEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU10302KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU202SOM98 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU202SOM98 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU202MEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU202SKEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU223KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU224KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU223KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU223KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU223KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU223KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU7NAMB04 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU7NAMB04 (1518) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC VRL133ZLM78 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC VRL133ZLM78 (1	56KEN65	(1518)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAA <mark>T</mark>
 An1000MAD91 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC An999MAD91 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC AnK6087GUI84 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar12568Rs71 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar12568Rs71 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar20368Rs881 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar2129SA00 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar74Rs55 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar74Rs55 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar3811MAD79 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B314KEN62 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B314KEN62 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT H1825Rs75 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10305KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU10305KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU10305KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU205M98 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU214KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU215KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU223KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCG	900085MAU88	(1520)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAA <mark>T</mark>
An991MAD91 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC AnK6087GUI84 (1518) ATACTGCTTTAAGAGTTCGATAACCTTCGGGGCATCAAAC AnTAMBULGGY94 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC Ar12568RSA81 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar21229SA00 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar21229SA00 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar21229SA00 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar74RSA55 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar74RSA55 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT H1825RSA75 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT R1662CAR85 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU204KN0185 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU2001RSA99 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC VRL1290ZIM78 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC VRL12	An1000MAD91	(1519)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC
An999MAD91 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC AntK6087GU184 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar12568RSA71 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar20368RSA81 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar2129SA00 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar2129SA00 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar218SA55 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar38661SEN81 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B144SEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B314KEN62 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT H1825RSA75 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT Luny0UGA55 (1520) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10202S0M98 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204NRGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU220KEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACCGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACCGGCATCAAAC VRL163ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACCGGCATCAAAC VRL163ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACCGGCATCAAAC VRL163ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACCGGCATC	An991MAD91	(1519)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC
 AnK6087GUI84 (1518) ATACTGCTTTAAGAGTTCGATAACCCTGCGGGCATCAAAC Ar12568RSA71 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar20368RSA81 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar20368RSA81 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar21229SA00 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar74RSA55 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar74RSA55 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT H1825RSA75 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT LunyOUGA55 (1520) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10315KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU12002S0M88 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU220KEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU34001KEN97 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC VRL12902IM78 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC VRL12902IM78 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC VRL12902IM78 (1518) ATACTGCTTTAAGAGTTCGATA	An999MAD91	(1519)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC
 AnTAMBULEGY94 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar12568RSAR1 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT Ar20368RSA81 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar21229SA00 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar21229SA00 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC ArB11MAD79 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT B1143KEN62 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT H1825RSA75 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT H1825RSA75 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAT R1662CAR85 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10302KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10202S0M98 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2214KEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2214KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2201RSA9 (1519) ATACTGCTTTAAGAGTTCGATAACCCT	AnK6087GUI84	(1518)	ATACTGCTTTAAGAGTTCGATAACCCT <mark>G</mark> CGGGCATCAAAC
 Ar12568RSA71 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT Ar20368RSA81 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar21229SA00 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar4811MAD79 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT Ar811MAD79 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT H1825RSA75 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT LunyoUGA55 (1520) ATACTGCTTTAAGAGTCGATAACCCTACGGGCATCAAAT R1662CAR85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10302KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10315KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU12002SOM98 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204NGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU2207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU2207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU2215KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2215KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2201KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU384001KEN97 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU384001KEN97 (1518) ATACTGCTTTAAGAGTTCGATA	AnTAMBULEGY94	(1518)	ATACTGCTTTAAGAGTTCGATAAC <mark>T</mark> CTACGGGCATCAAAC
Ar2036885881 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar21229SA00 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar74R5A55 (1519) ATACTGCTTTAGGAGTTCGATAACCCTACGGGCATCAAAC ArD38661SEN81 (1519) ATACTGCTTTAGGAGTTCGATAACCCTACGGGCATCAAAT B114XEN62 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT H1825R5A75 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT LunyoUGA55 (1520) ATACTGCTTTAAGAGTTCGATAACCCTACGGCACCAAAT R1662CAR85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCCATCAAAC SPU202SOM98 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU202NTNN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU220XFEN07	Ar12568RSA71	(1518)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAA <mark>T</mark>
 Ar21229SA00 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC Ar74RSA55 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC ArB38661SEN81 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B1143KEN77 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC B114SCRSA75 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCCATCAAAC G162CAR85 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10302KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10315KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10315KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU1202S0M98 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU2214KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU2214KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU2214KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU77NAMB4 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU77NAMB4 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC	Ar20368RSA81	(1518)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC
Ar74RSA55(1519)ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAATAr811MAD79(1519)ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAATB1143KEN77(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAATB1143KEN62(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAATH1825RSA75(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAATR1662CAR85(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGCCATCAAACSPU10301KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10302KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10307KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10315KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10202S0M98(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2004NGL85(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2207KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2214KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2215KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2223KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU384001KEN97(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAACSPU77NAMB64(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77NAMB64(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL15321M78(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL15421M78(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL1522M78(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCAT	Ar21229SA00	(1518)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC
Ar811MAD79(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAATArD38661sEN81(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAATB1143KEN77(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAATH1825RSA75(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAATLunyoUGA55(1520)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAATR1662CAR85(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10301KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10307KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10307KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10307KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10202S0M98(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU204ANGL85(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAACSPU221KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU221KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU221SKEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU452AMB5(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU52001RSA9(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAACSPU77NAMB04(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1290ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGG	Ar74RSA55	(1519)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAA <mark>T</mark>
ArD38661SEN81(1519)ATACTGCTTTAGGAGTTCGATAACCCTACGGGCATCAAATB1143KEN77(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAATH182SRSA75(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAATLunyoUGA55(1520)ATACTGCTTTAAGAGTCGATAACCCTACGAGCATCAAAATR1662CAR85(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10301KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10302KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10307KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10315KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10315KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2020Se0M98(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2207KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2207KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2215KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU220KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU52001RSA99(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77NSA08(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77NSA08(1519)ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAACVRL1032ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAACVRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCT	Ar811MAD79	(1519)	ATACTGCTTTAAGAGTTCGATAAC <mark>T</mark> CTACGGGCATCAAAC
B1143kEN77(1519)ATACCGCTTTAAGAGTTCGATAACCCTACGGGCATCAAATB314KEN62(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAATH1825RSA75(1519)ATACTGCTTTAAGAGTCGATAACCCTACGAGCATCAAATLunyoUGA55(1520)ATACTGCTTTAAGAGTCGATAACCCTACGAGCATCAAACSPU10301KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10302KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10307KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10315KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10307KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU12002SOM98(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU204ANGL85(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2207KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2215KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2215KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU220KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU220KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU220KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU220KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU220KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU220KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGA	ArD38661SEN81	(1519)	ATACTGCTTTA <mark>G</mark> GAGTTCGATAACCCTACGGGCATCAAA <mark>T</mark>
 B314KEN62 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT H1825RSA75 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT LunyoUGA55 (1520) ATACTGCTTTAAGAGTCGATAACCCTACGGCATCAAAT R1662CAR85 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU1020SOM98 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU1204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2214KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2215KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU2220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU2223KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU2223KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU2200KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU2223KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU384001KEN97 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGCATCAAAC SPU77NAMB04 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGCATCAAAC SPU77NAMB04 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC SPU77RSA08 (1519) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL1032ZIM78 (1519) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL1032ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL1032ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC VRL230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC VRL230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAA	B1143KEN77	(1519)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC
 H1825RSA75 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT LunyoUGA55 (1520) ATACTGCTTTAAGAGCTCGATAACCCTACGAGCATCAAAC R1662CAR85 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10315KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10315KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10315KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10202SOM98 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10202SOM98 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU207KEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2215KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU45ZAMB85 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU45ZAMB85 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU77NAMB04 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU77RSA08 (1519) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL1032ZIM78 (1519) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL1290ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL187ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL187ZIM70 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL825ZIM79 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL825ZIM79 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC<!--</td--><td>B314KEN62</td><td>(1519)</td><td>ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAA<mark>T</mark></td>	B314KEN62	(1519)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAA <mark>T</mark>
LunyoUGA55 (1520) ATACTGCTTTAAGAGCTCGATAACCCTACGAGCATCAAAT R1662CAR85 (1518) ATACTGCTTTAAGAGTTCGATAACCCTGCGAGCATCAAAC SPU10301KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10307KEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10315KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10315KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU12002SOM98 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU152RSA08 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU207KEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2215KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU384001KEN97 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU7NAMB04 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU77NAMB04 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU77NAMB04 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC VRL1032ZIM78 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC VRL1032ZIM78 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC VRL156ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL230ZIM79 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL363ZIM79 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC VRL85ZIM79 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC ZH504EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCACGGGCATCAAAC CANSENSUS (1521) ATACTGCTTTAAGAGTTCGATAACTCACGGGCATCAAAC	H1825RSA75	(1519)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT
R1662CAR85(1518)ATACTGCTTTAAGAGTTCAATAACCCTGCGAGCATCAAACSPU10301KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10307KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10315KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10315KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10202SOM98(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU12002SOM98(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU12002SOM98(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU12002SOM98(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU1202SOM98(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU204ANGL85(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2207KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2215KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2220KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU220KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU384001KEN97(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU52001RSA99(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU7NAMB04(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL10322IM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL150ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL187ZIM78(1518)ATACTGCTTTAAGAGT	LunyoUGA55	(1520)	ATACTGCTTTAAGAG <mark>C</mark> TCGATAACCCTACG <mark>A</mark> GCATCAAA <mark>T</mark>
SPU10301KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10302KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10307KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10315KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU12002S0M98(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU1202S0M98(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU204ANGL85(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU207KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2214KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2223KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU223KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU223KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU223KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU384001KEN97(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU52001RSA99(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU7NAMB04(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1290ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTC	R1662CAR85	(1518)	ATACTGCTTTAAGAGTTC <mark>A</mark> ATAACCCT <mark>G</mark> CG <mark>A</mark> GCATCAAAC
SPU10302KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10307KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU10315KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU1202SOM98(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU152RSA08(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU204ANGL85(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2207KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2214KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2223KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2223KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2223KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU384001KEN97(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU52001RSA99(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77NAMB04(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1290ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1220ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL825ZIM79(1518)ATACTGCTTTAAGAGTT	SPU10301KEN07	(1519)	ATACTGCTTTAAGAGTTCGATAACCCTACG <mark>A</mark> GCATCAAAC
 SPU10307KEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU10315KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU12002SOM98 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU1207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU207KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2214KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU2220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU2223KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU384001KEN97 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU45ZAMB85 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU452ANB85 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU77NAMB04 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU77RSA08 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC VRL1032ZIM78 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC VRL1290ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL763ZIM70 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL825ZIM79 (1519) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL825ZIM79 (1518) ATACTGCTTTAAGAGTTCGATAACTCTAC	SPU10302KEN07	(1519)	ATACTGCTTTAAGAGTTCGATAACCCTACG <mark>A</mark> GCATCAAAC
 SPU10315KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU12002SOM98 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU152RSA08 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU207KEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2214KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGACATCAAAC SPU2220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU2223KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU223KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU384001KEN97 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU452AMB5 (1518) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC SPU77NAMB04 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC SPU77RSA08 (1519) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL1032ZIM78 (1519) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL1516ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL1887ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL8230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL8230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAAC VRL825ZIM79 (1519) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC VRL825ZIM79 (1519) ATACTGCTTTAAGAGTTCGATAACCTACCGGGCATCAAAC VRL825ZIM79 (1518) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC VRL825ZIM79 (1518) ATACTGCTTTAAGAGTTCGATAACCTACGGGCATC	SPU10307KEN07	(1518)	ATACTGCTTTAAGAGTTCGATAACCCTACG <mark>A</mark> GCATCAAAC
SPU12002SOM98(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU152RSA08(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU204ANGL85(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU207KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2214KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2215KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU223KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU384001KEN97(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU45ZAMB5(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77NAMB04(1518)ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAACSPU77RSA08(1519)ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAACVRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAACVRL1516ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAACVRL230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL63ZIM79(1518)ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAACVRL825ZIM79(1518)ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAACVRL825ZIM79(1518)ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAACVRL825ZIM79(1518)ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAACVRL825ZIM79(1518)ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAACVRL825ZIM79(1518)ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAACVRL825ZIM79(1518)ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAAC	SPU10315KEN07	(1519)	ATACTGCTTTAAGAGTTCGATAACCCTACG <mark>A</mark> GCATCAAAC
SPU152RSA08(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU204ANGL85(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2207KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2214KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2215KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2223KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU384001KEN97(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU45ZAMB85(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU452001RSA99(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77NAMB04(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77RSA08(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1516ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1887ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL763ZIM70(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL825ZIM79(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL825ZIM79(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH501EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL825ZIM79(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH5048GY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH5048GY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGG	SPU12002SOM98	(1518)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC
 SPU204ANGL85 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2207KEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU2215KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU220KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU2223KEN07 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAAC SPU2223KEN07 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU384001KEN97 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU452AMB85 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU52001RSA99 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU77NAMB04 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC SPU77RSA08 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC VRL1032ZIM78 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC VRL1290ZIM78 (1519) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL1887ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC VRL825ZIM79 (1518) ATACTGCTTAAGAGTTCGATAACCCTACGGGCATCAAAC VRL825ZIM79 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC ZH501EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCACGGGCATCAAAC ZH548EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC ZH548EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCACGGGCATCAAAC ZH548EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCACGGGCATCAAAC ZH548EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCACGGGCATCAAAC 	SPU152RSA08	(1519)	ATACTGCTTTAAGAGTTCGATAACCCTACG <mark>A</mark> GCATCAAAC
SPU2207KEN07(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2214KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2215KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2223KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU384001KEN97(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU45ZAMB85(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU52001RSA99(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77NAMB04(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1290ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1887ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAACVRL25ZIM79(1518)ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAACVRL825ZIM79(1518)ATACTGCTTTAAGAGTTCGATAACCTACGGGCATCAAACZH501EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH548EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACCODSEDSUS(1521)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCA	SPU204ANGL85	(1519)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC
SPU2214KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU2215KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2223KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU384001KEN97(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU452AMB85(1518)ATACTGCTTTAAGAGTTCGATGACCCTACGGGCATCAAACSPU52001RSA99(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77NAMB04(1518)ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAACSPU77RSA08(1519)ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAACVRL10322IM78(1519)ATACTGCTTTAAGAGTTCGATAACCTCACGGGCATCAAACVRL1290ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1887ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL825ZIM79(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACZH501EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH548EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACCODSEDSUS(1521)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC	SPU2207KEN07	(1518)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC
SPU2215KENU7(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2223KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU384001KEN97(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU452AMB85(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU52001RSA99(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACSPU77NAMB04(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACSPU77RSA08(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1290ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1887ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM79(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL825ZIM79(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH501EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH548EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACCODSEDSUS(1521)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC	SPU2214KEN0/	(1519)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC
SPU2220KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU2223KEN07(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGAGCATCAAACSPU384001KEN97(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU45ZAMB85(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAATSPU52001RSA99(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77NAMB04(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77RSA08(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1290ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1516ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM79(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL825ZIM79(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL825ZIM79(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH501EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH548EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACCODSEDSUS(1521)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC	SPU2215KENU/	(1519)	ATACTGCTTTTAAGAGTTCGATAACCCTACGAGCATCAAAC
SP02223KEN07(1519)ATACTGCTTTAAGAGGTTCGATAACCCTACGAGCATCAAACSPU384001KEN97(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU45ZAMB85(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAATSPU52001RSA99(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77NAMB04(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACSPU77RSA08(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1290ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1516ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL763ZIM70(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL825ZIM79(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH501EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACCODSEDSUS(1521)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC	SPUZZZUKENU/	(1519)	ATACTGCTTTTAAGAGTTCGATAACCCTACGAGCATCAAAC
SP0384001KEN97(1518)ATACTGCTTTAAGAGGTTCGATAACCCTACGGGCATCAAACSPU45ZAMB85(1518)ATACTGCTTTAAGAGTTCGATGACCCTACGGGCATCAAACSPU52001RSA99(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77NAMB04(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77RSA08(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1290ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1516ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL763ZIM70(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL825ZIM79(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH501EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH548EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACConsensus(1521)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC	SPUZZZSKENU/	(1519) (1510)	ATACTGCTTTTAAGAGTTCGATAACCCTACG <mark>A</mark> GCATCAAAC
SP0432AMB85(1518)ATACTGCTTTAAGAGGTTCGATGACCCTACGGGCATCAAALSPU52001RSA99(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77NAMB04(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACSPU77RSA08(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1290ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1516ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL763ZIM70(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL825ZIM79(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACZH501EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH548EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACConsensus(1521)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC	SPU384UUIKEN97	(1518) (1510)	
SP052001RSA99(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACSPU77NAMB04(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACSPU77RSA08(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1290ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1516ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1887ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL763ZIM70(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL825ZIM79(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH501EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH548EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACConsensus(1521)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC	SPU45ZAMB85	(1518) (1510)	ATACTGCTTTAAGAGTTCGAT <mark>G</mark> ACCCTACGGGCATCAAA <mark>1</mark>
SP077NAMB04(1518)ATACTGCTTTAAGAGTTCAATAACTCTACGGGCATCAAACSPU77RSA08(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1290ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1516ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1887ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL763ZIM70(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL825ZIM79(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACZH501EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACCODSEDSUS(1521)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC	SFUJZUUIKSA99 CDU77NAMD04	(1519)	
VRL1032ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1290ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1516ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1887ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL763ZIM70(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL825ZIM79(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACZH501EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH548EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACConsensus(1521)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC	SPU//NAMBU4 CDII77DCA08	(1510)	ATACIGCITTAAGAGITC <mark>A</mark> ATAAC <mark>I</mark> CTACGGGCATCAAAC
VRL103221M78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1290ZIM78(1519)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1516ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL1887ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL763ZIM70(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL825ZIM79(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACZH501EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH548EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACConsensus(1521)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC	VDI 10327TM78	(1519)	
VRL12902IM76(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL1516ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL2230ZIM78(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACVRL763ZIM70(1518)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACVRL825ZIM79(1519)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAACZH501EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACZH548EGY77(1518)ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAACConsensus(1521)ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC	VRL103221M70 VDT12007TM78	(1519)	
VRL15102IM76 (1510) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL1887ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL2230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL763ZIM70 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC VRL825ZIM79 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC ZH501EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC ZH548EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC Consensus (1521) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC	VRL129021M70 VDT15167TM78	(1519)	
VRL100721M70 (1510) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC VRL2230ZIM78 (1518) ATACTGCTTTAAGAGTTCGATAACCTCTACGGGCATCAAAC VRL763ZIM70 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC VRL825ZIM79 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC ZH501EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC ZH548EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC Consensus (1521) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC	VRL18877TM78	(1510)	
VRL225021M70 (1510) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT VRL763ZIM70 (1518) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAT VRL825ZIM79 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC ZH501EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC ZH548EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC Consensus (1521) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC	VRL22307TM78	(1510)	
VRL825ZIM79 (1510) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC VRL825ZIM79 (1519) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC ZH501EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC ZH548EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC Consensus (1521) ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC	VRL7637TM70	(1518)	
ZH501EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC ZH548EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC	VRL8257.TM79	(1519)	
ZH548EGY77 (1518) ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC	ZH501ECY77	(1518)	
	ZH548EGY77	(1518)	ATACTGCTTTAAGAGTTCGATAACTCTACGGGCATCAAAC
	Consensus	(1521)	ATACTGCTTTAAGAGTTCGATAACCCTACGGGCATCAAAC

		1561 1600
214445KEN83	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
56KEN65	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
900085MAU88	(1560)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAAT <mark>T</mark> TCAT
An1000MAD91	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
An991MAD91	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
An999MAD91	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
AnK6087GUI84	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
AnTAMBULEGY94	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
Ar12568RSA71	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
Ar20368RSA81	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
Ar21229SA00	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
Ar74RSA55	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
Ar811MAD79	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
ArD38661SEN81	(1559)	CCTTGATA <mark>G</mark> GCAAACTCTCGGACCCACTGTTCAAT <mark>T</mark> TCAT
B1143KEN77	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
B314KEN62	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
H1825RSA75	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
LunyoUGA55	(1560)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
R1662CAR85	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU10301KEN07	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU10302KEN07	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU10307KEN07	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU10315KEN07	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU12002SOM98	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU152RSA08	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU204ANGL85	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU2207KEN07	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU2214KEN07	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTG <mark>C</mark> TCAATCTCAT
SPU2215KEN07	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU2220KEN07	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU2223KEN07	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU384001KEN97	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU45ZAMB85	(1558)	CCTTGATAAGCAAA <mark>T</mark> TCTCGGACCCACTGTTCAATCTCAT
SPU52001RSA99	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU77NAMB04	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
SPU77RSA08	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
VRL1032ZIM78	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
VRL1290ZIM78	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
VRL1516ZIM78	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
VRL1887ZIM78	(1558)	CC <mark>C</mark> TGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
VRL2230ZIM78	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
VRL763ZIM70	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
VRL825ZIM79	(1559)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
ZH501EGY77	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
ZH548EGY77	(1558)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT
Consensus	(1561)	CCTTGATAAGCAAACTCTCGGACCCACTGTTCAATCTCAT

		1601 1640
214445KEN83	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAG <mark>T</mark> TC
56KEN65	(1598)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
900085MAU88	(1600)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
An1000MAD91	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
An991MAD91	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
An999MAD91	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
AnK6087GUI84	(1598)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
AnTAMBULEGY94	(1598)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
Ar12568RSA71	(1598)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
Ar20368RSA81	(1598)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
Ar21229SA00	(1598)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
Ar74RSA55	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
Ar811MAD79	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
ArD38661SEN81	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
B1143KEN77	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAG <mark>T</mark> TC
B314KEN62	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
H1825RSA75	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
LunyoUGA55	(1600)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
R1662CAR85	(1598)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
SPU10301KEN07	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
SPU10302KEN07	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
SPU10307KEN07	(1598)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
SPU10315KEN07	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
SPU12002SOM98	(1598)	TGCGGTCCACTGCTTGAGCAGC <mark>G</mark> AACTGGATCGCAAGCTC
SPUI52RSA08	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
SPU204ANGL85	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
SPU220/KEN0/	(1598)	
SPUZZI4KENU/	(1599)	
SPUZZISKENU/	(1599)	
SPUZZZUKENU/	(1599)	
SPUZZZSKENU/	(1599)	
SPUS04UUIREN9/	(1590)	
SPU4JZAMBOJ	(1590)	
SFUJZUUIKSA99 CDU77NAMD04	(1500)	
SPU//NAMBU4 CDII77DCA08	(1590)	
VDI 10327TM78	(1599)	
VRL103221M70 VDT12007TM78	(1599)	
VR129021M70 VD115167TM78	(1599)	
VRI.18877.TM78	(1598)	
VRL22307IM78	(1598)	
VRL7637TM70	(1598)	
VRL8257TM79	(1599)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
ZH501EGY77	(1598)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
ZH548EGY77	(1598)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
Consensus	(1601)	TGCGGTCCACTGCTTGAGCAGCAAACTGGATCGCAAGCTC
	(= 2 = 2 = 7	

	1641 1680
214445KEN83 (1639)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
56KEN65 (1638)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
900085MAU88 (1640)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
An1000MAD91 (1639)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
An991MAD91 (1639)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
An999MAD91 (1639)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
AnK6087GUI84 (1638)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
AnTAMBULEGY94 (1638)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
Ar12568RSA71 (1638)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
Ar20368RSA81 (1638)	TTGATAGTTGTCCATTATTGTAAT <mark>T</mark> GTGTTTGTATCTCTA
Ar21229SA00 (1638)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
Ar74RSA55 (1639)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
Ar811MAD79 (1639)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
ArD38661SEN81 (1639)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
B1143KEN77 (1639)	TTGATAGTT <mark>A</mark> TCCATTATTGTAATAGTGTTTGTATCTCTA
B314KEN62 (1639)	TTGATAGTTGTCCATTA <mark>C</mark> TGTAATAGTGTTTGTATCTCTA
H1825RSA75 (1639)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
LunyoUGA55 (1640)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
R1662CAR85 (1638)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
SPU10301KEN07 (1639)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
SPU10302KEN07 (1639)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
SPU10307KEN07 (1638)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
SPU10315KEN07 (1639)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
SPUI2002SOM98 (1638)	
SPUI52RSAU8 (1639)	
SPU204ANGL85 (1639)	
SPU220/KENU/ (1638)	
SPU2214KENU7 (1639)	
SPUZZISKENU7 (1039)	
SPUZZZUKENU/ (1039)	
SPUZZZSKENU/ (1039) SPUZZZSKENU/ (1638)	
CDII/573MD95 (1639)	
SP0452AMB05 (1050) CDU52001DC300 (1630)	
SP052001KSA99 (1039) SP052001KSA99 (1039)	
SPU77RSA08 (1639)	
VRI10327IM78 (1639)	
VRL12907IM78 (1639)	
VRL15167IM78 (1638)	
VRL18877IM78 (1638)	
VRL22307IM78 (1638)	
VRL7637IM70 (1638)	ΤΓΟΛΠΑΘΤΤΟΙΟΟΛΙΤΙΛΙΤΟΙΛΑΙΟΙΟΙΤΙΟΙΑΙΟΙΟΙΑ
VRL825ZIM79 (1639)	TTGATAGTTGTCCATTATTGTATAGTGTTTGTTGTATCTCTA
ZH501EGY77 (1638)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
ZH548EGY77 (1638)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA
Consensus (1641)	TTGATAGTTGTCCATTATTGTAATAGTGTTTGTATCTCTA

		1681 1693
214445KEN83	(1679)	GGGAGCTTTGTGT
56KEN65	(1678)	GGGAGCTTTGTGT
900085MAU88	(1680)	GGGAGCTTTGTGT
An1000MAD91	(1679)	GGGAGCTTTGTGT
An991MAD91	(1679)	GGGAGCTTTGTGT
An999MAD91	(1679)	GGGAGCTTTGTGT
AnK6087GUI84	(1678)	GGGAGCTTTGTGT
AnTAMBULEGY94	(1678)	GGGAGCTTTGTGT
Ar12568RSA71	(1678)	GGGAGCTTTGTGT
Ar20368RSA81	(1678)	GGGAGCTTTGTGT
Ar21229SA00	(1678)	GGGAGCTTTGTGT
Ar74RSA55	(1679)	GGGAGCTTTGTGT
Ar811MAD79	(1679)	GGGAGCTTTGTGT
ArD38661SEN81	(1679)	GGGAGCTTTGTGT
B1143KEN77	(1679)	GGGAGCTTTGTGT
B314KEN62	(1679)	GGGAGCTTTGTGT
H1825RSA75	(1679)	GGGAGCTTTGTGT
LunyoUGA55	(1680)	GGGAGCTTTGTGT
R1662CAR85	(1678)	GGGAGCTTTGTGT
SPU10301KEN07	(1679)	GGGAGCTTTGTGT
SPU10302KEN07	(1679)	GGGAGCTTTGTGT
SPU10307KEN07	(1678)	GGGAGCTTTGTGT
SPU10315KEN07	(1679)	GGGAGCTTTGTGT
SPU12002SOM98	(1678)	GGGAGCTTTGTGT
SPU152RSA08	(1679)	GGGAGCTTTGTGT
SPU204ANGL85	(1679)	GGGAGCTTTGTGT
SPU220/KEN0/	(16/8)	GGGAGCTTTGTGTGT
SPU2214KEN07	(16/9)	GGGAGCTTTGTGTGT
SPU2215KEN0/	(16/9)	GGGAGCTTTGTGTGT
SPU2220KENU7	(16/9)	GGGAGCTTTGTGT
SPUZZZ3KENU/	(1679)	GGGAGCTTTGTGT
SPU384UUIKEN9/	(16/8)	GGGAGCTTTGTGT
SPU45ZAMB85	(16/8)	GGGAGCTTTGTGT
SPUSZUUIRSA99	(1679)	GGGAGCTTTGTGT
SPU//NAMBU4	(1670)	GGGAGCTTTGTGT
	(1070)	GGGAGCIIIGIGI
VRL103221M70 VDT 12007TM79	(1079)	GGGAGCIIIGIGI
VRL129021M70 VDT 15167TM79	(1079)	GGGAGCIIIGIGI
VRL131021M78	(1070)	CCCACCTTTGIGI
VRL100721M70	(1070)	
VRLZZJUZIM70 VDI 7637TM70	(1070)	CCCACCTTTGIGI
VRL/0321M/0 VRL8257TM70	(1679)	
7H501ECV77	(1678)	
ZH548EGY77	(1678)	GGGAGCTTTGIGI
Consensus	(1681)	GGGAGCTTTGTGT
00110011040	(<u> </u>	

6.4. Protein amino acid alignment

6.4.1. N protein amino acid alignment

		1 45
214445KEN83	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
56KEN65	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
900085MAU88	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
An1000MAD91	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
An991MAD91	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
An999MAD91	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
AnK6087GUI84	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
AnTAMBULEGY94	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
Ar12568RSA71	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
Ar20368RSA81	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
Ar21229SA00	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
Ar74RSA55	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
Ar811MAD79	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
ArD38661SEN81	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
B1143KEN77	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
B314KEN62	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
H1825RSA75	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
LunyoUGA55	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
R1662CAR85	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU10301KEN07	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU10302KEN07	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU10307KEN07	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU10315KEN07	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU12002SOM98	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU152RSA08	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU204ANGL85	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU2207KEN07	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU2214KEN07	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU2215KEN07	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU2220KEN07	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU2223KEN07	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU384001KEN97	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU45ZAMB85	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU52001RSA99	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU77NAMB04	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
SPU77RSA08	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
VRL1032ZIM78	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
VRL1290ZIM78	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
VRL1516ZIM78	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
VRL1887ZIM78	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
VRL2230ZIM78	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
VRL763ZIM70	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
VRL825ZIM79	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
ZH501EGY77	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
ZH548EGY77	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY
Consensus	(1)	MDNYQELAIQFAAQAVDRNEIEQWVREFAYQGFDARRVIELLKQY

Figure 18. The deduced N protein amino acid alignment of the 45 strains of Rift Valley fever virus generated in this study. Areas with black lettering and white background show identical nucleotides. Areas with black lettering and green background represent non-similar nucleotides.

		46 90
214445KEN83	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
56KEN65	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
900085MAU88	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
An1000MAD91	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
An991MAD91	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
An999MAD91	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
AnK6087GUI84	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
AnTAMBULEGY94	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
Ar12568RSA71	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
Ar20368RSA81	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
Ar21229SA00	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
Ar74RSA55	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
Ar811MAD79	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
ArD38661SEN81	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
B1143KEN77	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
B314KEN62	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
H1825RSA75	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
LunyoUGA55	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
R1662CAR85	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
SPU10301KEN07	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
SPU10302KEN07	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
SPU10307KEN07	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
SPU10315KEN07	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
SPU12002SOM98	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
SPU152RSA08	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMKMSKEGKATVEALINKY
SPU204ANGL85	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMKMSKEGKATVEALINKY
SPU2207KEN07	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMKMSKEGKATVEALINKY
SPU2214KEN0/	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMKMSKEGKATVEALINKY
SPUZZISKENU/	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMKMSKEGKATVEALINKY
SPU2220KENU/	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMKMSKEGKATVEALINKY
SPUZZZ3KENU/	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMKMSKEGKATVEALINKY
SPU384UUIKEN9/	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
SPU45ZAMB85	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
SPU5ZUUIRSA99	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
SPU//NAMBU4	(46)	GGADWEKDAKKMIVLALTRGNKPRRMMMKMSKEGKATVEALINKY
5PU//R5AU0 10227TM70	(40)	GGADWERDARKMIVIAIRGNRPRRMMMMMSREGRAIVEALINKI
VRLIUJZZIM70	(40)	
VRLIZ9UZIM70	(40)	
νκμισιοσιμισ νρι1807στμσο	(40) (16)	CCJUMEKUJKKUIMI VI AI ADCUKDDDWWWKWGKECKYAMAEYI IMAA GGYDMEKUJKULI A TYTI UGMULKKUMMINGDUGCUTI AFYTINKI
VRI.22207TM79	(40)	CC7DMEKD7KKWIMIY0Y21.46MKLCKKWKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
VRL7637TM70	(46)	CCADWEKDAKKMIVI, ALTRONKERRMMMKMCKECKATVEALINKI
VRL8257TM70	(46)	
ZH501ECV77	(46)	CC7DMEKD7KKWIMIYATA TYATIKGMULUKUKASKECKA WALA TIMKA
ZH548EGY77	(46)	GGADWEKDAKKMIVI,AI,TRGNKPRRMMKMSKEGKATVEALINKI
Consensus	(46)	GGADWEKDAKKMIVI,AI,TRGNKPRRMMKMSKEGKATVEALINKY
0.0110.0110.000	(-0)	

		91 135
214445KEN83	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
56KEN65	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
900085MAU88	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
An1000MAD91	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
An991MAD91	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
An999MAD91	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
AnK6087GUI84	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
AnTAMBULEGY94	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
Ar12568RSA71	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
Ar20368RSA81	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
Ar21229SA00	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
Ar74RSA55	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
Ar811MAD79	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
ArD38661SEN81	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
B1143KEN77	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
B314KEN62	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
H1825RSA75	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
LunyoUGA55	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
R1662CAR85	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU10301KEN07	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU10302KEN07	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU10307KEN07	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU10315KEN07	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU12002SOM98	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU152RSA08	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU204ANGL85	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU2207KEN07	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU2214KEN07	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU2215KEN07	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU2220KEN07	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU2223KEN07	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU384001KEN97	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU45ZAMB85	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU52001RSA99	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU//NAMB04	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
SPU//RSAU8	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
VRL1032ZIM/8	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
VRLIZ90ZIM78	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
VRL1516ZIM/8	(91)	KLKEGNPSRDELTLSRVAAALAGWTCQALVVLSEWLPVTGTTMDG
VKLISS/ZIM/S	(91)	KLKEGNPSKDELTLSKVAAALAGWTCQALVVLSEWLPVTGTTMDG
	(91)	ALALGINESKULLTLSKVAAALAGWTCQALVVLSEWLEVTGTTMDG
	(91)	ALALGINESKULLILSKVAAALAGWICQALVVLSEWLEVIGTIMUG
VKLOZJZIM/9	(91)	
ZHOULEGY / /	(91)	
ZHJ48EGY//	(91)	ALALGINESKULLILSKVAAALAGWICQALVVLSEWLEVIGTIMUG
consensus	(ツエ)	UTURGIAE SKDEPT PSKAWAATAGM.LCAAPA APPLIA.LQLLUDG

		136 180
214445KEN83	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
56KEN65	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
900085MAU88	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
An1000MAD91	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
An991MAD91	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
An999MAD91	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
AnK6087GUI84	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
AnTAMBULEGY94	(136)	LSPAYPRHMMHPSFAGMVDPSLP <mark>G</mark> DYLRAILDAHSLYLLQFSRVI
Ar12568RSA71	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
Ar20368RSA81	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
Ar21229SA00	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
Ar74RSA55	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
Ar811MAD79	(136)	LSPAYPRHMMHPSFAGMVDPSLP <mark>G</mark> DYLRAILDAHSLYLLQFSRVI
ArD38661SEN81	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
B1143KEN77	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
B314KEN62	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
H1825RSA75	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
LunyoUGA55	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
R1662CAR85	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU10301KEN07	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU10302KEN07	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU10307KEN07	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU10315KEN07	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU12002SOM98	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU152RSA08	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU204ANGL85	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU2207KEN07	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU2214KEN07	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU2215KEN07	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU2220KEN07	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU2223KEN07	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU384001KEN97	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU45ZAMB85	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU52001RSA99	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU77NAMB04	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
SPU77RSA08	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
VRL1032ZIM78	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
VRL1290ZIM78	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
VRL1516ZIM78	(136)	LSPAYPRHMMHPSFAGMVDPSLP <mark>G</mark> DYLRAILDAHSLYLLQFSRVI
VRL1887ZIM78	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
VRL2230ZIM78	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
VRL/63ZIM70	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
VRL825ZIM79	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLQFSRVI
ZH501EGY77	(136)	LSPAYPRHMMHPSFAGMVDPSLPGDYLRAILDAHSLYLLQFSRVI
ZH548EGY77	(136)	LSPAYPRHMMHPSFAGMVDPSLP <mark>G</mark> DYLRAILDAHSLYLLQFSRVI
Consensus	(136)	LSPAYPRHMMHPSFAGMVDPSLPEDYLRAILDAHSLYLLOFSRVI

		181 225
214445KEN83	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
56KEN65	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
900085MAU88	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
An1000MAD91	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
An991MAD91	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
An999MAD91	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
AnK6087GUI84	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
AnTAMBULEGY94	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
Ar12568RSA71	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
Ar20368RSA81	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
Ar21229SA00	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
Ar74RSA55	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
Ar811MAD79	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
ArD38661SEN81	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
B1143KEN77	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
B314KEN62	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
H1825RSA75	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
LunyoUGA55	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRR <mark>G</mark> FLKAFGLVD
R1662CAR85	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU10301KEN07	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU10302KEN07	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU10307KEN07	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU10315KEN07	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU12002SOM98	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU152RSA08	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU204ANGL85	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU2207KEN07	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU2214KEN07	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU2215KEN07	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU2220KEN07	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU2223KEN07	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU384001KEN97	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU45ZAMB85	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU52001RSA99	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU77NAMB04	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
SPU77RSA08	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
VRL1032ZIM78	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
VRL1290ZIM78	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
VRL1516ZIM78	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
VRL1887ZIM78	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
VRL2230ZIM78	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
VRL/63ZIM70	(181)	NPNLKGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
VRL825ZIM79	(181)	NPNLRGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
ZH501EGY77	(181)	NPNLKGRTKEEVAATFTQPMNAAVNSNFISHEKRREFLKAFGLVD
ZH548EGY'/'/	(181)	NPNLKGKTKEEVAATETQPMNAAVNSNFISHEKRREFLKAFGLVD
Consensus	(T8T)	NPNLKGRTKEEVAATETQPMNAAVNSNFISHEKRREFLKAFGLVD

		226	246
214445KEN83	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
56KEN65	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
900085MAU88	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
An1000MAD91	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
An991MAD91	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
An999MAD91	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
AnK6087GUI84	(226)	SNGKPSAAV <mark>K</mark> AAAQAYKT	AA <mark>-</mark>
AnTAMBULEGY94	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
Ar12568RSA71	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
Ar20368RSA81	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
Ar21229SA00	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
Ar74RSA55	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
Ar811MAD79	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
ArD38661SEN81	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
B1143KEN77	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
B314KEN62	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
H1825RSA75	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
LunyoUGA55	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
R1662CAR85	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
SPU10301KEN07	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
SPU10302KEN07	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
SPU10307KEN07	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
SPU10315KEN07	(226)	SNGKPSAAVMAAAQAYKT	AA <mark>-</mark>
SPU12002SOM98	(226)	SNGKPSAAVMAAAQAYKT	AA-
SPU152RSA08	(226)	SNGKPSAAVMAAAQAYKT	AA-
SPU204ANGL85	(226)	SNGKPSAAVMAAAQAYKT	AA-
SPU2207KEN07	(226)	SNGKPSAAVMAAAQAYKT	AA-
SPU2214KEN07	(226)	SNGKPSAAVMAAAQAYKT	AA-
SPU2215KEN07	(226)	SNGKPSAAVMAAAQAYKT	AA-
SPU2220KEN07	(226)	SNGKPSAAVMAAAQAYK'I'	AA-
SPU2223KENU/	(226)	SNGKPSAAVMAAAQAYK'I'	AA-
SPU384UUIKEN9/	(226)	SNGKPSAAVMAAAQAYK'I'	
SPU45ZAMB85	(226)	SNGKPSAAVMAAAQAYKT	
SPU5ZUUIRSA99	(226)	SNGKPSAAVMAAAQAYKT	
SPU//NAMBU4	(226)	SNGKPSAAVMAAAQAYKT	
SPU77RSAU8	(226)	SNGKPSAAVMAAAQAYKT	
VRLIU3ZZIM78	(220)	SNGKPSAAVMAAAQAIKT	
VRLIZ9UZIM70	(220)	SNGKPSAAVMAAAQAIKI	
VRLIJI6ZIM78	(220)	SNGKPSAAVMAAAQAIKT	
	(220)	SINGRESAAVMAAAQAYKT	АА - лл
VKLZZJUZIM/8 VDT7627TM70	(226)		АА - Л Л
VRL/0341M/0 VRL8257TM70	(220)	SINGILE SAAVMAAAQAINI	
7H501FCV77	(220)	SUCKDS J J MJ J J U AKA SUGILI DAY MAXAQAT LI	
ZH548ECV77	(220)	SNCKDSDDAMUDDDOAAA	
	(220)	SNCKDSJJANJJJUJAKA SNCKDSJJANJJUJAKA SNCKDSJJANJA	
Consensus	(220)	STOLL STATISTICACY ILL	7777

Figure 18. Continued

6.4.2. NSs protein amino acid alignment

		1 45
214445KEN83	(1)	MDYFPVISVDLQSGRRVVSVEYI <mark>I</mark> GDGPPRIPYSMVGPCCVFLMH
56KEN65	(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMR
900085MAU88	(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
An1000MAD91	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
An991MAD91	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
An999MAD91	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
AnK6087GUI84	(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
AnTAMBULEGY94	(1)	MDYFPVISVDLQSGRRVVSVEYFRGDGPPRIPYSMVGPCCVFLMH
Ar12568RSA71	(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
Ar20368RSA81	(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
Ar21229SA00	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
Ar74RSA55	(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
Ar811MAD79	(1)	MDYFPVISVDLQSGRRVVSVEYFRGDGPPRIPYSMVGPCCVFLMH
ArD38661SEN81	(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
B1143KEN77	(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
B314KEN62	(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
H1825RSA75	(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
LunyoUGA55	(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
R1662CAR85	(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
SPU10301KEN07	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
SPU10302KEN07	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
SPU10307KEN07	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
SPU10315KEN07	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
SPU12002SOM98	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
SPU152RSA08	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
SPU204ANGL85	(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
SPU2207KEN07	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
SPU2214KEN07	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
SPU2215KEN07	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
SPU2220KEN07	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
SPU2223KEN07	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
SPU384001KEN97	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
SPU45ZAMB85	(1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
SPU52001RSA99	(1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVYLMH
SPU//NAMB04	(⊥) (1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
SPU//RSAU8	(⊥) (1)	MDYFPVISVDLQSGRRVVSVEYIKGDGPPRIPYSMVGPCCVFLMH
VRL1032ZIM/8	(⊥) (1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
VRLIZ9UZIM78	(⊥) (1)	MDYFPVISVDLQSGRRVVSVEYIRGDGPPRIPYSMVGPCCVFLMH
VRLISI6ZIM/8	(⊥) (1)	MDYFPVISVDLQSGRRVVSVEYFRGDGPPRIPISMVGPCCVFLMH
VKLIOO/ZIM/O	(⊥) (1)	MDYEDYTCVDLOGCDDWWWEVTDCDCDDDTDV0MUCDCCVFLMH
VKLZZJUZIM/8	(⊥) (1)	
VKL/03ZIM/U	(⊥) (1)	MDVEDVICUDIOCODUVICVEVIDOCODDIDVOMUCDOCVELMI
VKLOZJZIM/9 7u501ecv77	(⊥) (1)	
ADJULEGI//	(⊥) (1)	
ZHJ48EGI//	(⊥) (1)	MDVEDVICUDI OCODUMOVEVID CDCDDDIDVOMUCDCOVELMH
consensus	(⊥)	MUILEATSANTŐPEKKAAPAFIIKENELEKTLIZWAELCCALTWH

Figure 19. The deduced NSs protein amino acid alignment of 45 strains of Rift Valley fever generated in this study. Areas with black lettering and white background show identical nucleotides. Areas with black lettering and green background represent non-similar nucleotides.

		46 90
214445KEN83	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
56KEN65	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASSVAPPPAKPFQRLI
900085MAU88	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
An1000MAD91	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
An991MAD91	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
An999MAD91	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
AnK6087GUI84	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
AnTAMBULEGY94	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
Ar12568RSA71	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFVSNVAPPPAKPFQRLI
Ar20368RSA81	(46)	HRPSYEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
Ar21229SA00	(46)	HRPSHEVRLRFSDFYNAGEFPYRVGLGDFASNVAPPPAKPFQRLI
Ar74RSA55	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
Ar811MAD79	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
ArD38661SEN81	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
B1143KEN77	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
B314KEN62	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
H1825RSA75	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFVSNVAPPPAKPFQRLI
LunyoUGA55	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
R1662CAR85	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU10301KEN07	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU10302KEN07	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU10307KEN07	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU10315KEN07	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU12002SOM98	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU152RSA08	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU204ANGL85	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU2207KEN07	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU2214KEN07	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU2215KEN07	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU2220KEN07	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU2223KEN07	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU384001KEN97	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU45ZAMB85	(46)	HRPSHEVRLRFSDFYNVGEFP <mark>C</mark> RVGLGDFASNVAPPPAKPFQRLI
SPU52001RSA99	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU'/'/NAMB04	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
SPU//RSA08	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
VRL1032ZIM78	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
VRL1290ZIM78	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
VRL1516ZIM78	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
VRL188/ZIM78	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
VRL2230ZIM78	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
VRL/63ZIM/0	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
VKL825ZIM79	(46)	HKPSHEVKLKFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
ZHSUIEGY//	(46)	HKPSHEVKLKFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
ZH548EGY/7	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI
Consensus	(46)	HRPSHEVRLRFSDFYNVGEFPYRVGLGDFASNVAPPPAKPFQRLI

		91 135
214445KEN83	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
56KEN65	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRSDD
900085MAU88	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
An1000MAD91	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
An991MAD91	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
An999MAD91	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
AnK6087GUI84	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
AnTAMBULEGY94	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
Ar12568RSA71	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRSDD
Ar20368RSA81	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
Ar21229SA00	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
Ar74RSA55	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
Ar811MAD79	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
ArD38661SEN81	(91)	DLIGHMTLSDFTRFPNLREAISWPLGEPSLAFFDLSSTRVHRNDD
B1143KEN77	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
B314KEN62	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
H1825RSA75	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRSDD
LunyoUGA55	(91)	DLIGHMTLSDF <mark>I</mark> RFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
R1662CAR85	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU10301KEN07	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU10302KEN07	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU10307KEN07	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU10315KEN07	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU12002SOM98	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU152RSA08	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU204ANGL85	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU2207KEN07	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU2214KEN07	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU2215KEN07	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU2220KEN07	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU2223KEN07	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU384001KEN97	(91)	DLMGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU45ZAMB85	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU52001RSA99	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU77NAMB04	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
SPU77RSA08	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
VRL1032ZIM78	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
VRL1290ZIM78	(91)	DLIGHMTLSDFTRFPNLKEAMSWPLGEPSLAFFDLSSTRVHRNDD
VRL1516ZIM78	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
VRL1887ZIM78	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
VRL2230ZIM78	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
VRL763ZIM70	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRSDD
VRL825ZIM79	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
ZH501EGY77	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
ZH548EGY77	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD
Consensus	(91)	DLIGHMTLSDFTRFPNLKEAISWPLGEPSLAFFDLSSTRVHRNDD

		136 180
214445KEN83	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
56KEN65	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
900085MAU88	(136)	IRRDQIATLAMRSCKVTNDLEDSFVGLHRMIVTEAILRGIDLCLL
An1000MAD91	(136)	IRRDQIATLAMRSCKIANDLEDSFVGLHRMIVTEAILRGIDLCLL
An991MAD91	(136)	IRRDQIATLAMRSCKIANDLEDSFVGLHRMIVTEAILRGIDLCLL
An999MAD91	(136)	IRRDQIATLAMRSCKIANDLEDSFVGLHRMIVTEAILRGIDLCLL
AnK6087GUI84	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
AnTAMBULEGY94	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIATEAILRGIDLCLL
Ar12568RSA71	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
Ar20368RSA81	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHR <mark>K</mark> IVTEAILRGIDLCLL
Ar21229SA00	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
Ar74RSA55	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
Ar811MAD79	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIATEAILRGIDLCLL
ArD38661SEN81	(136)	IRRDQIATLAMRSCKITNDLQDSFVGLHRMIVTEAILRGIDLCLL
B1143KEN77	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
B314KEN62	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
H1825RSA75	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
LunyoUGA55	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGVDLCLL
R1662CAR85	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMVVTEAILRGIDLCLL
SPU10301KEN07	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU10302KEN07	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU10307KEN07	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU10315KEN07	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU12002SOM98	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU152RSA08	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU204ANGL85	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU2207KEN07	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU2214KEN07	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU2215KEN07	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU2220KEN07	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU2223KEN07	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU384001KEN97	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU45ZAMB85	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU52001RSA99	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU77NAMB04	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
SPU77RSA08	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
VRL1032ZIM78	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRIIVTEAILRGIDLCLL
VRL1290ZIM78	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
VRL1516ZIM78	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIATEAILRGIDLCLL
VRL1887ZIM78	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
VRL2230ZIM78	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
VRL763ZIM70	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL
VRL825ZIM79	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHR <mark>K</mark> IVTEAILRGIDLCLL
ZH501EGY77	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIATEAILRGIDLCLL
ZH548EGY77	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIATEAILRGIDLCLL
Consensus	(136)	IRRDQIATLAMRSCKITNDLEDSFVGLHRMIVTEAILRGIDLCLL

Figure 19. Continued

		181 225
214445KEN83	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
56KEN65	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
900085MAU88	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
An1000MAD91	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
An991MAD91	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
An999MAD91	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
AnK6087GUI84	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSGLIALMEESLML
AnTAMBULEGY94	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIVLMEESLML
Ar12568RSA71	(181)	PGFDLMYEVAHVQCVRLLQAAREDISNAVVPNSALIALMEESLML
Ar20368RSA81	(181)	${\tt PGFDLMYEVAHVQCVRLLQAAKEDISNAVAPNSALIALMEESLML}$
Ar21229SA00	(181)	PGFDLMYEIAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
Ar74RSA55	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
Ar811MAD79	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIVLMEESLML
ArD38661SEN81	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
B1143KEN77	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
B314KEN62	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
H1825RSA75	(181)	PGFDLMYEVAHVQCVRLLQAAREDISNAVVPNSALIALMEESLML
LunyoUGA55	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
R1662CAR85	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
SPU10301KEN07	(181)	PGFDLMYEVAHVQCVRLLQAAREDISNAVVPNSALIALMEESLML
SPU10302KEN07	(181)	PGFDLMYEVAHVQCVRLLQAAREDISNAVVPNSALIALMEESLML
SPU10307KEN07	(181)	PGFDLMYEVAHVQCVRLLQAAREDISNAVVPNSALIALMEESLML
SPU10315KEN07	(181)	PGFDLMYEVAHVQCVRLLQAAREDISNAVVPNSALIALMEESLML
SPU12002SOM98	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
SPU152RSA08	(181)	PGFDLMYEVAHVQCVRLLQAAREDISNAVVPNSALIALMEESLML
SPU204ANGL85	(181)	PGFDLMYEVAHVQCVRLLQAAREDISNAVVPNSALIALMEESLML
SPU2207KEN07	(181)	PGFDLVYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
SPU2214KEN07	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
SPU2215KEN07	(181)	PGFDLMYEVAHVQCVRLLQAAREDISNAVVPNSALIALMEESLML
SPU2220KEN07	(181)	PGFDLMYEVAHVQCVRLLQAAREDISNAVVPNSALIALMEESLML
SPU2223KEN07	(181)	PGFDLMYEVAHVQCVRLLQAAREDISNAVVPNSALIALMEESLML
SPU384001KEN97	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
SPU45ZAMB85	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
SPU52001RSA99	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
SPU77NAMB04	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
SPU77RSA08	(181)	PGFDLMYEVAHVQCVRLLQAAREDISNAVVPNSALIALMEESLML
VRL1032ZIM78	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
VRL1290ZIM78	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
VRL1516ZIM78	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIVLMEESLML
VRL1887ZIM78	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
VRL2230ZIM78	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
VRL763ZIM70	(181)	PGFDLMYEVAHVQCVRLLQAAREDISNAVVPNSALIALMEESLML
VRL825ZIM79	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML
ZH501EGY77	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIVLMEESLML
ZH548EGY77	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIVLMEESLML
Consensus	(181)	PGFDLMYEVAHVQCVRLLQAAKEDISNAVVPNSALIALMEESLML

Figure 19. Continued
		226	266
214445KEN83	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
56KEN65	(226)	RSSLPSMMGRNNWVPVVSPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
900085MAU88	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMDS <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
An1000MAD91	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
An991MAD91	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
An999MAD91	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
AnK6087GUI84	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD-	
AnTAMBULEGY94	(226)	RSSLPSMMGRNNWIPVIPPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
Ar12568RSA71	(226)	RSSLPSMMGRNNWVPVVPPIPDVEIESEEESDDDGFVEVD <mark>-</mark>	
Ar20368RSA81	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
Ar21229SA00	(226)	RSSLPSMMGRNNWVPVVPPIPDVEIES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
Ar74RSA55	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD-	
Ar811MAD79	(226)	RSSLPSMMGRNNWIPVIPPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
ArD38661SEN81	(226)	RSSLPSMMGRNNWIPVIPPIPDVEMDSEEESDDDGFVEVN <mark>-</mark>	
B1143KEN77	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
B314KEN62	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD-	
H1825RSA75	(226)	RSSLPSMMGRNNWVPVVPPIPDVEIESEEESDDDGFVEVD-	
LunyoUGA55	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
R1662CAR85	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
SPU10301KEN07	(226)	R <mark>L</mark> SLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
SPU10302KEN07	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
SPU10307KEN07	(226)	R <mark>L</mark> SLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
SPU10315KEN07	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
SPU12002SOM98	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
SPU152RSA08	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
SPU204ANGL85	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD-	
SPU2207KEN07	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
SPU2214KEN07	(226)	RTSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
SPU2215KEN07	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
SPU2220KEN07	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
SPU2223KEN07	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
SPU384001KEN97	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
SPU45ZAMB85	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
SPU52001RSA99	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
SPU77NAMB04	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
SPU77RSA08	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMES <mark>G</mark> EESDDDGFVEVD <mark>-</mark>	
VRL1032ZIM78	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
VRL1290ZIM78	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
VRL1516ZIM78	(226)	RSSLPSMMGRNNWIPVIPPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
VRL1887ZIM78	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
VRL2230ZIM78	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD	
VRL763ZIM70	(226)	RSSLPSMMGRNNWVPVVPPIPDVEIESEEESDDDGFVEVD-	
VRL825ZIM79	(226)	RSSLPSMMGRNNWIPVVPPIPDVEM <mark>G</mark> SEEESDDDGFVEVD <mark>-</mark>	
ZH501EGY77	(226)	RSSLPSMMGRNNWIPVIPPIPDVEMESEEESDDDGFVEVD <mark>-</mark>	
ZH548EGY77	(226)	RSSLPSMMGRNNWIPVIPPIPDVEMESEEESDDDGFVEVD	
Consensus	(226)	RSSLPSMMGRNNWIPVVPPIPDVEMESEEESDDDGFVEVD	

Figure 19. Continued

6.5. Supplementary strain data

Strain	Location of Origin	Year	Source	Accession Number
10911SA00	Saudi Arabia	2000	Human	DQ380170
73HB1449CAR73	CAR	1973	Human	DQ380162
74HB59CAR74	CAR	1974	Human	DQ380163
9800523KEN98	Kenya	1998	Human	DQ380169
AnK3837GUI81	Guinea	1981	Bat	DQ380165
AnK6087GUI84	Guinea	1984	Bat	DQ380166
ArD38388BF83	Burkina Faso	1983	Mosquito	DQ380181
Clone 13	CAR	1974	Plaque pick of 74HB59	DQ380182
EntebbeUGA44	Uganda	1944	Mosquito	DQ380156
HvB375CAR85	CAR	1985	Human	DQ380161
MgH824MAD79	Madagascar	1979	Human	DQ380144
MP12	Egypt	1977	Vaccine strain derived	DQ380154
			from Zh548	
OS1MAU87	Mauritania	1987	Human	DQ380180
OS3MAU87	Mauritania	1987	Human	DQ380178
OS8MAU87	Mauritania	1987	Human	DQ380177
OS9MAU87	Mauritania	1987	Human	DQ380179
R1622CAR85	CAR	1985	Human	DQ380160
SA51RSA51	South Africa	1951	Ovine	DQ380158
SA75RSA75	South Africa	1975	Human	DQ380175
SNS	Uganda	1944		DQ380157
VRL1260ZIM74	Zimbabwe	1978	Bovine	DQ380164
VRL1853ZIM74	Zimbabwe	1978	Bovine	DQ380168
VRL2250ZIM74	Zimbabwe	1974	Bovine	DQ380143
VRL2269ZIM74	Zimbabwe	1974	Bovine	DQ380173
VRL2373ZIM74	Zimbabwe	1974	Bovine	DQ380159
ZC3349EGY78	Egypt	1978	Bovine	DQ380152
ZH1776EGY78	Egypt	1978	Human	DQ380153
ZingaCAR69	CAR	1969	Human	DQ380167
ZM657EGY78	Egypt	1978	Mosquito	DQ380146
ZS6365EGY79	Egypt	1979	Ovine	DQ380145

Table 5. Supplementary strain data, acquired from GenBank.

6.6. Evolutionary relatedness of two passaged strains of Rift Valley fever virus



Figure 20. Evolutionary relationships of 2 passaged strains of Rift Valley fever virus. The evolutionary history was inferred using the Neighbour-Joining method (Saitou and Nei 1987). The bootstrap consensus tree inferred from 1000 replicates (Felsenstein 1985) is taken to represent the evolutionary history of the taxa analyzed (Felsenstein 1985). Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Kimura 2-parameter method (Kimura 1980) and are in the units of the number of base substitutions per site. All positions containing gaps and missing data were eliminated from the dataset (complete deletion option). There were a total of 1691 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 (Tamura *et al.* 2007).

6.7. Ethics clearance certificate

Human Research Ethics Committee (Medical) University of the Witwatersrand, Johannesburg (formerly Committee for Research on Human Subjects (Medical) Secretariat: Research Office, Room SH10005, 10th floor, Senate House • Telephone: +27 11 717-1234 • Fax: +27 11 339-5708 Private Bag 3, Wits 2050, South Africa Ref: W-CJ-0701234					
	TO WHOM IT MAY CONCERN:				
Waiver:	This certifies that the following research does not require clearance from the Human Research Ethics Committee (Medical).				
Investigator:	Susan Aitken				
Project title:	Variations in the S segment of Rift Valley fever virus with special reference to the nonstructural NSs coding				
Reason:	Reference strains in a laboratory will be used. There are no human participants.				
copy: Anisa Keshav, Research Office, Senate House, Wits					