

Towards the diagnosis of two intracellular pathogens of grapevine in South Africa

By

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Submitted in fulfilment of the requirements of the degree

MAGISTER SCIENTIAE

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DECLARATION

I declare that the dissertation/thesis, which I hereby submit for the degree M.Sc (Microbiology) at the University of Pretoria, is my own work and has not previously been submitted by me for a degree at this or any other tertiary institution.

Signature: _____

Date:



"What the hell wine is THAT?"

The other night, while eating Asian Take-away, I had occasion To try a cheeky little red -"Pinot noir" I think it said. This of course then got me thinking Just what was it that I was drinking? "Pinot noir", whilst sounding haughty, Sounds maybe just a little naughty -In parts of Asia, be construed As maybe something rather rude. The names of types and kinds of wine Then rattled round my tiny mind. And actually, I'm rather keen To find out what they really mean. I did some drinking, called 'research' -I nearly even went to church. I looked up books - to no avail. The CD's are another tale ... My senses steeled, my mind was set I surfed and trawled the Internet. The list is not exhaustive, true, But what I've found I'll share with you. It certainly, most have agreed, Makes for an interesting read. Burgundy is named in honour Of the thirteenth century's famous scholar. Malbec, it seems was wont to dance With the son of the cousin of the King of France. Merlot too, he loved to sing -A special favourite of the King. In the Louvre he had his guarters, He bonked the Queen and all her daughters.

3



Shiraz, a middle-English word, Its meaning now is seldom heard. Amidst the laughter, hale and hearty, Put very simply, means "Let's Party!" The Duke of Cabernet, it's true, Knew how to drink a thing or two. His parties always had pizzazz -Nicknamed the 'Cabernet Shiraz'. It's said that **riesling** really means What Germans do without their jeans. Those suffering from **Durif** will know The ins and outs of feeling low. The wine was named, among the wattles By one who suffered several bottles. The Spanish writer, El Tarrango Was fascinated by the Tango. His fondness for the grape was famed, So after him a wine was named. Chardonnay, I've heard them say, Will make it really big some day. If only everybody knew That 'Chardonnay' means 'wombat poo'. Moselle was named, so I believe, On a catwalk last year's New years Eve. The Body moseyed down the plank, The judges checked the wine they drank. While all were charged with hormones fearsome, They named it after Elle Macpherson. The Grenache soldiers, it is said, Really liked a drop of red. So President, young Charles de Gaulle Bought them wine - they had a ball! A house of ill-repute in Spain, Hatched a plan, though quite insane,



To knock their noisy patrons out With several wines, while lights were out. The wine they chose, it wasn't yellow, but A vivid green they called **Verdelho**. (I'd like to note I'm well-intentioned, 'Bordello' wasn't even mentioned.

...D'OH!)

Hubble, rubble, toil and trouble, **Champagne** always likes to bubble. Hangover cure is always tricky -Most attempt the 'sham pain' sickie. Well there they are. They may astound, Though these I swear I really found. But As Bill Gates said to the pleb "Who believes the World Wide Web?"

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SUMMARY

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A survey was conducted, from 2001 to 2004, of viruses spreading within certified grapevine material in South Africa. As far as possible, viruses were identified and detection methods established. However, unknown spherical virus-like particles were observed in samples that also contained Grapevine Leafroll Associated Virus-Type 3. The unknown spherical particles were thought to most likely be Grapevine Fleck Virus, which was previously found in South Africa.

A PCR method to be used locally for the routine detection of Grapevine Fleck Virus was established and first used to determine whether any of the greenhouse and field samples with the unknown spherical viruses were infected with Grapevine Fleck Virus.

During the 2001 to 2004 survey, plants with leafroll and reddening symptoms unlike classical grapevine leafroll disease were also observed. No grapevine



leafroll-associated viruses could be detected in these, but the symptoms observed resembled symptoms induced by phytoplasmas in Europe.

A PCR method for the routine universal detection of phytoplasmas was established and this method was used to determine if phytoplasmas were associated with the symptomatic plants found. Sequence information from PCR amplicons suggest the presence of *Candidatus* phytoplasma solani, found for the first time in South Africa. This important finding however requires conformation by a second laboratory.



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ABBREVIATIONS

°C	Degrees Celsius
bp	Basepairs
cDNA	Complementary DNA
CTAB	Cethyl-trimethyl-ammonium bromide
DEPC	Diethylpyrocarbonate
DNA	Deoxyribonucleic acid
dNTP	Deoxyribonucleotide triphosphate
ds	Double stranded
ELISA	Enzyme Linked Immunosorbent Assay
FD	Flavescence doree
g	Gram
GFkV	Grapevine Fleck Virus
GFLV	Grapevine Fanleaf Virus
GLRaV-3	Grapevine Leafroll Associated Virus Type 3
IPTG	Isopropyl β-D-thiogalactosidase
ISEM	Immunosorbent Electron Microscopy
kb	Kilobase pairs
kDa	KiloDalton
LB	Luria-Bertani
М	Molar
min	Minutes
mm	Millimetre
mМ	Millimolar
M-MLV	Moloney-Murine Leukaemia Virus
MTR	Methyltransferase
μg	Microgram
μl	Microliter
μm	Micrometer
nm	Nanometer
nt	Nucleotides
ORF	Open Reading Frame



PCR	Polymerase Chain Reaction
pmol	Picomol
pNPP	para-Nitrophenylphospate
PPRI	Plant Protection Research Institute
PVP	Polyvinylpyrrolidone
RdRp	RNA dependent RNA polymerase
RNA	Ribonucleic acid
rpm	Revolutions per minute
sec	Seconds
Spp	Species
STOL	Stolbur
TNA	Total nucleic acid
U/µl	Units per microliter
UV	Ultraviolet
V	Volt
W/v	Weight per volume
xg	Gravitation force
X-gal	5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside



Chapter 1

Review of Literature



PART I: CERTIFICATION, DIAGNOSTICS AND VIRUS ELIMINATION OF GRAPEVINE

1.1 GENERAL INTRODUCTION

The art of wine making is one of the oldest industries known to civilization. Vineyards existed for the use of Egypt's rulers and nobles in the pre-dynastic and early dynastic periods (~3200 BC).

Reviewed in Kruger (2000) this industry was established in 1652 in South Africa, shortly after the arrival of the Dutch at the Cape of Storms. After 300 years of wine making, the average yield of South African wines in the 1960's was amongst the lowest in the world, and the low yield was accompanied with low quality wines. It is likely that virus and virus combinations were responsible for the low production and quality of wine in South Africa during the 1960's (Kriel, 2000).

According to The American Phytopathological Society (1998), most plant viral infections are latent but cause huge economic losses worldwide. Virus infections cause the plants to grow slower, influence the fruit production and in due course the production time of a crop. As viral infections do not always induce visible symptoms, this dramatic effect could only be noticed once an infected crop was compared with a healthy crop (Martelli and Walter, 1998). The "Koöperatieve Wijnbouwers Verening van Zuid-Afrika Bpkt. (KWV)" realized if they want to improve their wine – they first have to improve the condition of their vineyards (Kriel, 2000).

In 1986 KWV initiated the formation of the Vine Improvement Association (VIA) to improve the quality of South African vineyards, and it is still the official propagation organization in the Government certification scheme for wine grapes (Kriel, 2000).



According to the South African Wine Industry Statistics (SAWIS) nr.29 (2005), South Africa comprises of 124 749-hectare area under vines, has 4406 primary wine producers and 561 wine cellars. South Africa is also ranked 9th in the world regarding wine production and is responsible for 2.7% of the total world wine production. Figure 1.1 is a schematic representation of the South African wine regions.

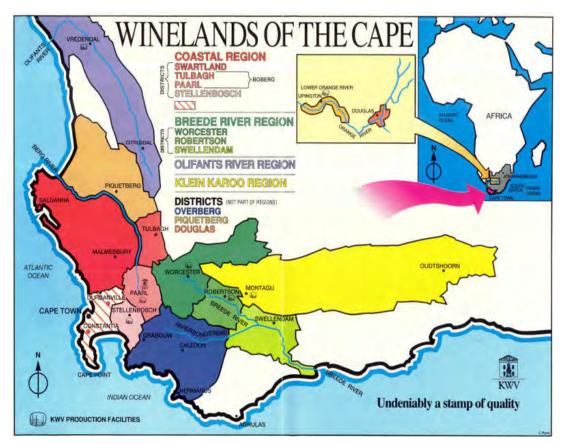


Figure 1.1: Map of South African wine regions (Image: KWV)



1.2 CERTIFICATION SCHEME OF GRAPEVINES WORLDWIDE

1.2.1 Introduction

Certification is the procedure where candidate mother plants, that are going to be used as a source of propagation material, are subjected to treatments to protect trueness-to-type and absence from any number of pathogens, as specified by certain regulations, which differs from country to country (Martelli and Walter, 1998). However, little has been done to promote internationally recognized certification schemes that would allow free trading of high-quality nursery materials among participating countries (Rowhani *et al.*, 2005).

Within specific countries within the modern era there has been a substantial increase in demand for voluntary certification. For this reason, voluntary certification has become widespread. This kind of certification is closely controlled by regulations issued by a certifying authority and is not imposed forcefully (Martelli and Walter, 1998).

Compulsory certification is imposed whenever it becomes essential to prevent the distribution of destructive diseases. There are no restrictions to the kind and number of pathogens that may be considered for elimination in a certification program (Martelli and Walter, 1998).

Certification is a long-lasting effort to attain the desired health level of a crop and to maintain this level through time. Availability of technology for the reliable detection of diseases and their agents and the effective elimination of disease and pathogens are required to implement a certification program (Martelli and Walter, 1998).

Clonal selection is done in selected vineyards with desirable characteristics. Selection is done based on varietal conformity, vegetative vigor, bud fertility, quality and quantity of the field, timing and uniformity of ripening. Vines are



kept under observation for a few years and the best performing and least infected ones are chosen as candidate clones (Martelli and Walter, 1998).

Various virus elimination procedures are currently available for selected clones. Dormant canes are treated with hot water, 50 °C, for 45 minutes to eliminate prokaryotes (Hot water treatment). Vegetating vines are grown at a constant temperature of 36-37 °C for 100 days (Figure 1.2), where after excision and rooting of shoot tips take place to eliminate virus and virus-like diseases (Hot air treatment) (Martelli and Walter, 1998).



Figure 1.2: Example of plants in the heat treatment chamber (Photo: L. Nel)

In vitro culture is often used in conjunction with hot air treatment (Martelli and Walter, 1998). *In vitro* culture involves the excision of the upper most part of the meristem (0.24mm). The meristem is placed on sterile agar and left to develop a root system. The principle behind the combined methods is that virus replication is suppressed at 36-38 °C while the plant grows optimally and theoretically the upper part of the meristem is virus-free. Micrografting of meristem tips are also done onto *in vitro*-grown seedlings (Martelli and Walter, 1998). Once the *in vitro* cultures are large enough, the plants are transferred to greenhouses (Figure 1.3). From there the plants are transferred to containers and placed in nuclear blocks (Figure 1.4).





Figure 1.3: Greenhouse with small grapevine plants (Photo: L. Nel)

From the nuclear block the grapevines are planted into small foundation blocks, which are strictly controlled open blocks. Because of masspropagation, the grapevines are planted from the foundation blocks to bigger, less controlled mother blocks.



Figure 1.4: Nuclear blocks at KWV, Paarl (Photo: L. Nel)



1.2.2 South Africa

The South African Plant Certification scheme for wine grapes (Schedule 1, Article 10) demands specific requirements for the three different units of propagation (Nuclear, Foundation and Mother).

Nuclear units

Nuclear units must be covered in an insect proof greenhouse. The plants in nuclear units must be established in containers, where the soil is free from Grapevine Fanleaf Virus (GFLV) vectors. The floor surface of the greenhouse containing nuclear plants must be covered in such a way that the roots of the plants in the containers cannot penetrate the soil on which the greenhouse was build. The greenhouse must be isolated through means of an isolation area at least two meters wide of other vineyards and virgin soil. No plants, of any kind, may be planted in such an isolation area, unless the authority gives written consent. Irrigation water being used in nuclear units must be free of GFLV vectors and may not be contaminated with drainage- or runoff water from other vineyards.

Foundation units

Foundation units must be isolated through means of an isolation area. If the foundation unit is situated in a greenhouse, the isolation area must be at least one meter wide, otherwise if the foundation unit is situated in the field the isolation area must be twenty-five meters wide. No plants, of any kind, may be planted within five meters of the foundation unit, unless the authority gives written consent.

Mother units

Mother units must be isolated through means of an isolation area. If the mother unit is situated in a greenhouse, the isolation area must be at least one meter wide, otherwise if the mother unit is situated in the field the isolation area must be three meters wide. If the mother unit is not in a greenhouse, it must be at least three hectares in size, unless the authority stipulates otherwise.



Plant material from the nuclear blocks are tested on a yearly basis, with virus specific tests, for pathogens that might be present in the grapevines. Plant material from the foundation blocks are also tested on a regular basis for pathogens. Plant material from the bigger mother blocks are not tested with virus specific tests, but inspectors monitor the blocks for any symptoms of known pathogens.

In addition, certain phytosanitary requirements are also prescribed by the South African Plant Certification scheme for wine grapes (Schedule 2, Article 11(1) (b) (i), 3(a), 12(b)).

Establishment and certification requirements

Plant material that has been established in a unit must comply with certain requirements during the registration term and the presentation of the plants for certification. Plant material and plants of rootstock varieties must be free from Grapevine Fanleaf, Grapevine Fleck, Grapevine Leafroll, Grapevine Corky Bark, Grapevine Stem grooving and Shiraz-disease. The plant material and plants of rootstock varieties must also be visually free from *Agrobacterium radiobacter* pv *tumefaciens, Pythium spp, Phytophthora spp* and *Xylophilus ampelinus.* For the presentation of the plants for certification, the plant material and plants of rootstock varieties must also be visually free from *Margarodes spp, Meloidogyne spp, Pseudococcus spp* and *Viteus vitifoliae.* Plant material and plants of the scions must comply with the requirements as stipulated by the authorities, as far as the diseases and pathogens mentioned for the establishment and certification requirements for rootstocks are concerned.

1.2.3 Europe

In European Union (EU) countries with active viticulture, the incidence of virus and virus-like diseases is high and their spread has been rapid due to the uncontrolled distribution and use of infected cultivar and rootstocks, that took place in the post-war period (Martelli and Walter, 1998).



The alarming sanitary deterioration of grapevines encouraged the EU Council to issue directives for the improvement of the Union's grapevine industry in 1968 and 1971 (Martelli and Walter, 1998). The grapevine is the only woody crop that, since 1968, is the objective of a compulsory certification by the EU (Directive 68/93 EEC) (Rowhani et al., 2005). This regulation prescribes only the absence of harmful virus diseases, notably fanleaf and leafroll from nursery material (Martelli and Walter, 1998). Although some EU member states (France, Germany, Italy, Portugal and Spain) have implemented certification schemes with sanitary requirements that are more restrictive than those of the existing Directive, and use the same virus detection, national protocols are still far apart. It is unlikely that the production with such a low sanitary status would be acceptable to any viticultural country aware of and concerned with the serious virological problems associated with this crop. A recently issued Directive (2002/11 EU) is supposed to harmonize the system (Rowhani et al., 2005). The technical annex to the 2005 Directive complied that the lowest possible level of harmful organisms required the absence of Grapevine fanleaf virus, Arabis mosaic virus, Grapevine leafroll-associated virus 1, Grapevine leafroll-associated virus 3 and for rootstocks only Grapevine fleck virus (Martelli, 2006). The European certification schemes are required to operate under European and Mediterranean Plant Protection Organization (EPPO) guidelines. These include the Italian schemes at the University of Bari, International Council for the Study of Viruses and Virus Diseases of the Grapevine (ICVG), Mediterranean Agronomic Institute and the French certification scheme, Institut National de la Recherche Agronomique (INRA) (Constable and Drew, 2004).

1.2.4 America and Canada

The Canadian certification scheme is required to operate under the Canadian Food Inspection Agency (CFIA), while the American certification scheme (FSP) is supported by the US Department of Agriculture (USDA), the California Department of Food and Agriculture (CDFA) and the University of California, Davis. Canada and America comply with the North American Plant Protection Organization (NAPPO) guidelines for regional risk management



regarding entry, establishment and spread of regulated pathogens (Constable and Drew, 2004). In addition, NAPPO participates with other regional plant protection groups within the western hemisphere and globally to develop international standards (Rowhani *et al.*, 2005). The document "Guidelines for the Importation of Grapevines into a NAPPO Member Country RSPM #15 Part 1: Viruses and Virus-like Pests, Viroids, Phytoplasmas and Bacteria" is the initial regional guideline for the development of harmonized North American Standards for grapevine nursery stock (Rowhani *et al.*, 2005). Canada has a formal national certification program, which is voluntary. The United States operates under voluntary state certification, which combined with strict quarantine regulations have resulted in high-quality nursery stock with a minimum of regulatory infrastructure (Rowhani *et al.*, 2005).

1.3 DIAGNOSTIC TESTS USED FOR PLANT PATHOGENS

A common objective shared by certification schemes worldwide is to identify healthy sources for propagation through the application of time-tested indexing procedures as well as more recently developed molecular assays (Rowhani, *et al.*, 2005). Detection methods in the laboratory are a valuable tool for investigating grapevine pathogens, since diagnosis of grapevine diseases in the field can be inaccurate. Symptoms displayed in the field are seldom exclusive to a particular disease and some infected vines may not show any symptoms at all. This can either be due to low concentration of the disease-causing agent or the infection may be in cultivars that are tolerant to the specific disease-causing agent (Weber *et al.*, 2002).

In addition, some of the infected grapevines only display seasonal symptoms and it is therefore necessary to have detection methods to test vines even if they appear to be healthy. This is very important where material for



propagation is collected and prepared during the dormant season (Weber *et al.*, 2002).

Various detection methods are available, each with its own advantages and disadvantages.

1.3.1 Biological methods

Biological methods are time consuming and require large greenhouse and field space, but are very useful if the vines tested are valuable and a high level of confidence is needed in the diagnosis (Weber *et al.*, 2002).

Biological indexing

Two different groups of indicator plants are used during biological indexing.

The first group of plants are herbaceous, maintained in greenhouses and used to detect mechanically transmissible viruses. These tests can be completed in few weeks time. If the virus transmission is successful, the indicator plants may develop primary symptoms, including localized lesions, after a few days of incubation. Thereafter systemic symptoms appear, including vein clearing and leaf deformation (Rowhani *et al.*, 2005; Martelli, 1993).

The second group of plants are woody and requires a lengthier incubation period, up to three years. Inoculation is either done by cleft grafting, chip-bud grafting, bench grafting or green grafting (Martelli and Walter, 1998). These woody incubator plants usually belong to the same genera as the plant under evaluation and are selected based on the specific diagnostic symptoms it elicits. The indicator plants are inspected annually for two to three seasons for any visible symptoms (Rowhani *et al.*, 2005). This technique has been used for detection and identification of various plant pathogens (Rowhani *et al.*, 1997; Credi, 1997; Habili *et al.*, 1992).



1.3.2 Serological methods

Serological methods are rapid, inexpensive, very specific and a costeffective way for detecting viruses in woody plants (Weber *et al.*, 2002). These methods cannot however be applied to unknown particles and lacks sensitivity to detect viruses present in low concentrations. (Weber *et al.*, 2002).

Enzyme Linked Immunosorbent Assay (ELISA)

ELISA can be used to simultaneously detect various pathogens on using a single plate with different antibodies coated to each well, in triplicate for reproducibility. The major limitation of ELISA is the necessity for polyclonal or monoclonal antibody sera specific for each pathogen (Webster et al., 2004). ELISA utilizes antibody reactions with disease agents, like viruses and bacteria (Weber et al., 2002). In the final step of the test an enzyme and substrate are used to produce a colour reaction, which indicates the presence or absence of the virus in the sample (Weber et al., 2002). A modification of ELISA named voltametric enzyme immunoassay, detects the change in electrical conductivity of the substrate, rather than a color change, when acted upon by an enzyme attached to a secondary antibody. This method is claimed to be an order of magnitude more sensitive than ELISA (Webster et al., 2004). This technique has been used for detection and identification of various plant pathogens (Moris and Bertwick, 1996; Ling et al., 2000; Forsline et al., 1996).

Immunosorbent electron microscopy (ISEM)

ISEM is the trapping of virus particles onto grids, which have been coated with specific virus antibodies, and their subsequent observation under the electron microscope. This technique is costly due to the need for an electron microscope, the labor-intensive sample preparation and the visual identification required. The electron microscope plays a critical role in virus diagnostics because of its sensitivity and its ability to detect viruses in plants, when no antisera or other detection systems are available (Van der Merwe, 2001).



Tissue blot immunoassay (TIBA)

Tissue blotting utilizes antibodies raised against pathogens. Sap from the plant tissue is expressed onto blotting paper, nitrocellulose or nylon membranes and the pathogen is detected by labeled probes (Webster *et al.*, 2004). The procedure is less labor intensive than ELISA, rapid, sensitive, simple because no virus extraction is required, inexpensive, suitable for surveys of 1000-2000 samples per day and the samples can be taken in the field and processed some time later (D'Onghia *et al.*, 2001).

Quartz crystal microbalance (QCM) immunosensors

During this technique a quartz crystal disk is coated with virus specific antibodies. Voltage is applied across the disk, making the disk warp slightly via a piezoelectric effect. Adsorption of virus particles to the crystal surface changes its resonance oscillation frequency in a concentration-dependent manner (Eun *et al.*, 2002). This method is therefore qualitative and quantitative. It is apparently as sensitive but more rapid than ELISA and economical (Webster *et al.*, 2004).

1.3.3 Nucleic acid analysis

Nucleic acid analysis has higher sensitivity and specificity than the other methods. It can be applied to non-immunogenic pathogens and a disease with unknown etiology can be investigated. It can detect multiple viruses and detect plants with mild or even no symptoms. These methods are however quite expensive and specialized facilities are necessary. One of the methods most commonly used to explore molecular genetic identification of pathogens, is the PCR and modifications thereof.

Polymerase Chain Reaction (PCR)

PCR involves the selective amplification of a small part of a pathogen's genome (Weber *et al.*, 2002). Some disadvantages of this technique are the insufficient viral genome sequences available to design primers (although the situation is improving as more information is submitted to



public domains like Genbank), the fact that some plant extracts contain inhibiting substances to PCR and the need for a thermocycler, which can be expensive (Webster et al., 2004). This technique is extremely sensitive, fairly inexpensive and requires minimal skill to perform (Weber *et al.*, 2002). Both RNA and DNA can be detected and identified using this technique. For RNA viruses, a cDNA strand complementary to the virus is made with reverse transcriptase. Oligonucleotide primers, flaking part of the genome of the virus, are extended by a thermostable DNA polymerase in a series of denaturing and extension steps that exponentially increase the target DNA. For DNA viruses, no reverse transcription step is required. There are a number of variations on the basic technique, designed to increase sensitivity, alter specificity or allow automation of detection (Webster et al., 2004). Some of these are listed below:

Multiplex PCR

Multiple strains can be detected in a single reaction by combining oligonucleotide primers specific for different pathogens. The design of a multiplex procedure requires that the same PCR conditions amplify two different sized DNA fragments with balanced efficiency and no cross-reactivity (Clair *et al.*, 2003). This technique has been used for detection and identification of various plant pathogens (Grieco and Gallitelli, 1999; Clair *et al.*, 2003)

<u>Real-time PCR (Fluorescence PCR using Taqman™</u> <u>technology)</u>

Two primers flank the sequence of interest and a third fluorescently labeled primer anneals between them. As the flanking primers extend, the labeled primer is released and fluorescence occurs. The advantages of this method are that no post-reaction processing is required to detect the reaction product and that it is quantitative (Webster *et al.*, 2004). The disadvantage of using real-time PCR include the inability to



monitor amplicon size without opening the system, the incompatibility of some platforms with some fluorogenic chemistries, and the relative restricted multiplex capabilities of current applications (Mackay *et al.*, 2002). Also, unless large-scale testing is envisioned, the cost of a Taqman[™] ABI Prism 7700 Sequence Detection System and the labeled primers may be too expensive (Webster *et al.*, 2004). This technique has been used for detection and identification of various plant pathogens (Roberts *et al.*, 2000; Eun *et al.*, 2000).

Competitive fluorescence PCR

This is a variation on real-time PCR. Using this method, virus and multiple virus infections can be differentiated simultaneously. A number of primer sets are each labeled with a different fluorescent marker and added to the reaction mixture. Virus strains are differentiated with primers that differ only at the 3' end, complementary to a nucleotide position that is polymorphic between strains. Only where the 3' nucleotide is complementary, extension will take place. Only primers that generate amplicons fluoresce and the wavelength emitted identifies the primers that have been extended (Walsh et al., 2001).

Immunocapture PCR

This technique combines the capture of the pathogen particles by antibodies together with amplification by PCR. The virus is adsorbed by the antibody, which is bound to a surface, then removed by heating with a non-ionic surfactant. The nucleic acids of the pathogen are then amplified (Harper *et al.*, 1999). This method is useful in concentrating virus particles from plant species where virus titer is low or where compounds that inhibit PCR are present (Webster *et al.*, 2004). This technique has been used for detection and identification of various plant pathogens (Chevalier *et al.*, 1995; Nolasco *et al.*, 1993).



Nested PCR

Two consecutive PCRs are carried out with the first reaction increasing the amount of template for the second reaction. The method is particularly useful where the pathogen is present in very low titer or inhibitors of DNA polymerase are present in the plant extract. Low-specificity oligonucleotides, usually degenerate, are used in the first rounds of amplification. An aliquot of the first reaction is then placed in a fresh tube for a second PCR with specific primers that anneal within the first amplicon (Webster *et al.*, 2004). This technique has been used for detection and identification of various plant pathogens (Dovas and Katis, 2003; Bertaccini *et al.*, 1999).

Restriction fragment length polymorphism (RFLP)

RFLP describes the patterns of different sizes of DNA that results from cutting the PCR amplicons with restriction enzymes. RFLP is used to identify differences between viruses based on the presence or absence of restriction enzyme-recognition sites. RFLP is a method for identifying pathogens after PCR. After amplification, the amplicon is digested with restriction enzymes and the fragment sizes analyzed by gel electrophoresis (Webster *et al.*, 2004). RFLP has been used routinely for identification of phytoplasmas (Schneider *et al.*, 1997; Gibb *et al.*, 1995; Martini and Murari, 1999; Angelini *et al.*, 2001).

Nucleic acid hybridization

The advantage of this method if that nucleic acid of the virus can be detected in both forms, single-stranded and double-stranded. cRNA probes are labeled with either isotopes or non-radioactive probes. cRNA probes are preferable to cDNA probes when used to detect RNA viruses, because RNA/RNA hybrids are more stable than DNA/RNA hybrids. A nucleic acid extraction from the infected tissue is blotted onto a membrane and the probe hybridized to it and detected (Webster *et al.*, 2004). This technique has been used for detection and identification of carnation mottle virus (Sanchez-Navarro *et al.*, 1996).



Microarrays and Macroarrays

Both these methods have been used for visualizing relative changes in global expression levels of mRNA, as well as single nucleotide polymorphism typing and host-pathogen interactions (Webster et al., 2004). This technique has the ability to simultaneously display the expression of thousands of genes at a time, making it a powerful tool for the simultaneous detection and identification of many plant pathogens (Hadidi et al., 2004). Single-stranded DNA probes are irreversibly fixed as an array of spots to a surface of glass, membrane or polymer (Webster et al., 2004). Base-paring of complementary sequences by hybridization if the underlying principle of arrays. Microarrays are high-density arrays, with a density of the order 1000-10000 spots per cm² or even higher. Macroarrays are generally membrane-based and low-density arrays, with a density of the order of 100 spots per cm² (Hadidi et al., 2004). Arrays printed with probes corresponding to a large number of pathogen can be utilized to simultaneously detect all those pathogens present within the tissue of an infected host. Viral/pathogen nucleic acids are extracted from the host and amplified, then labeled with a probe, either radioactive or fluorescently tagged nucleotides such as fluorescin, Cy3 or Cy5. The labeled target molecule is denatured and allowed to hybridize with the arrayed probes. Excess target is washed from the surface and spots where labeled target molecules have bound, become fluorescent under appropriate lighting conditions. The position of a visible spot corresponds to the presence of a particular pathogen in the plant sample (Webster et al., 2004).

The advantages of microarrays include the simultaneous detection and quantification of thousands of hybridization events and the great scope for high-throughput applications and the development of automated systems. The disadvantage is that this method is very expensive (Hadidi *et al.*, 2004). This technique has been used for detection and identification of various plant pathogens (Boonham *et al.*, 2003; Lee *et al.*, 2003).



From the overview on the diagnostic methods, described above, one can understand that not all pathogens can be detected. Therefore certain pathogens can enter the certification scheme unnoticed and spread rapidly if this infected material is used as propagation material.

PART II: SELECTED GRAFT-TRANSMISSIBLE INTRACELLULAR PATHOGENS INFECTING GRAPEVINE

1.4 GRAPEVINE FLECK VIRUS

Grapevine Fleck Virus (GFkV) is a member of the genus *Maculavirus*. *Maculavirus* (*Macula* – Latin for fleck) is one of three genera in the family *Tymoviridae*. This genus consists of a small group of phloem-limited isometric viruses that is not sap-transmissible and with no known vectors (Adams and Antoniw, 2005). GFkV has been found in Europe and the United States of America but with no evidence of spread (Brunt *et al.*, 1996). It has been found with evidence of spread in South Africa in 1990 (Engelbrecht and Kasdorf, 1990).

No vector up to date has been associated with the transmission of GFkV (Sabanadzovic *et al.*, 2000; El Beaino *et al.*, 2001). GFkV is latent in *Vitis vinifera*, but in the indicator plant *Vitis rupestris* it induces specific foliar symptoms. The phloem cells of infected plant have highly characteristic cytopathic structures called vesiculated bodies, which are deranged mitochondria that have undergone peripheral vesiculation (Castellano and Martelli, 1984; Sabanadzovic *et al.*, 2000; El Beaino *et al.*, 2001).

The symptoms include localized clearing flecks in the veinlets of young leaves (Figure 1.5) and in older leaves the symptoms diffuse into a mosaic pattern



and the leaves wrinkle and curl upward. Grapevines may remain symptomless, but if symptoms do present, these may vary seasonally and could also disappear in time (Foundation Plant Services, 2002).



Figure 1.5: GFkV symptoms on a leaf placed under a light source

The morphology of this genus includes non-enveloped isometrical particles, ~30nm in diameter, with a rounded contour. The genome of GFkV is a monopartite, linear, single-stranded, positive sense RNA genome with a total size of 7564 nt excluding the poly-A tail. The genome has a high cytosine content (49.8%) and consists of four putative reading frames and untranslated regions of 291 nt and 35 nt at the 5' and 3' region, respectively (Sabanadzovic *et al.*, 2000; El Beaino *et al.*, 2001; Martelli *et al.*, 2002) (Figure 1.6).

Open reading frame (ORF) 1 encodes a 215.4-kDa polypeptide, which plays a role during viral replication. ORF 1 has the conserved motifs of replication-associated proteins of positive stranded RNA viruses and a papain-like protease domain. ORF 1 of GFkV lacks a highly conserved 16 nt long subgenomic RNA promoter, known as the Tymobox, present in other members of the *Tymoviridae* family (Martelli *et al.*, 2002).



ORF 2 encodes a 24.3-kDa polypeptide, which has been identified as the coat protein (Martelli *et al.*, 2002).

ORF 3 and ORF 4 are located at the 3' end of the genome and encode proline-rich proteins of 31.4 kDa and 15.9 kDa with unknown functions (Martelli *et al.*, 2002).

Replication is likely to occur in the cytoplasm, with association of vesicles in the mitochondria. This could be due to autoproteolytic cleavage of the 215-kDa polypeptide encoded by ORF 1 as well as the production of sub-genomic RNA (Martelli *et al.*, 2002).

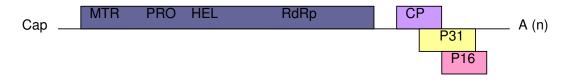


Figure 1.6: Schematic representation of GFkV genome organization, showing the relative position of the ORF's and their products. MTR – Methyltransferase, PRO – Papain-like protease, HEL – Helicase, RdRp – Polymerase, CP – Coat protein, p31 and p16 – Proline rich proteins (Image: Martelli, 2002)

1.5 PHYTOPLASMAS INFECTING GRAPEVINE

Phytoplasmas belonging to the genus *Candidatus* Phytoplasma, class Mollicutes, comprises of 26 species and 15 different phylogenetic groups (Firrao *et al.*, 2004). It is believed that phytoplasmas have diverged from gram-positive eubacteria (Hogenhout, 2004). The reduction in genome size may have resulted from differential loss of genes during evolution. It appears that mollicutes may have lost genes encoding for the synthesis of macromolecule precursors such as cell-wall components, amino acids and long-chain fatty acids (Razin *et al.*, 1998; Lee *et al.*, 2000).



In 1967, Doi *et al.* discovered that particles in ultrathin sections of the phloem of cells affected by yellows diseases, resembled animal and human mycoplasmas. The agents associated with these plant yellows diseases were pleiomorphic in shape, with an average diameter of 200-800 μ m. These agents also lacked rigid cell walls, were surrounded by a single unit membrane and were sensitive to tetracycline antibiotics (Doi *et al.*, 1967; Lee *et al.*, 2000).

From 1967 to 1994, the term mycoplasma-like organisms (MLO) were used to refer to the causal agents of many yellows diseases (Lee and Davis, 1992; McCoy *et al*, 1989). In 1994, the name phytoplasma was adopted by the Phytoplasma Working Team, at the 10th Congress of International Organization of Mycoplasmology (Lee *et al.*, 2000).

Although phytoplasmas appeared as rounded pleiomorphic bodies during single cross sections, other studies revealed a filamentous morphology (Lee and Davis, 1992; Walters and Osborne, 1978; Haggins *et al.*, 1978; Lee and Davis, 1983). Filamentous bodies were especially predominant in infected plant tissue during the early stages of infection (Lee *et al.*, 2000).

Phytoplasmas infecting plants cause disturbances in the normal balance of plant hormones or growth regulators (Chang, 1998; Chang and Lee, 1995). The symptoms include virescence (the development of green flowers and the loss of normal flower pigments), phyllody (the development of floral parts into leafy structures), sterility of flowers, proliferation of auxiliary shoots resulting in a witches'-broom appearance, abnormal elongations of the internodes resulting in slender shoots, generalized stunting (small flowers and leaves and shortened internodes), discoloration of leaves or shoots, leaf curling, bushy appearance of growth at the ends of the stems and generalized decline (stunting, dieback of twigs and unseasonal yellowing or reddening of the leaves). Internally, infections can cause extensive phloem necrosis and excess formation of phloem tissue, resulting in swollen veins (Lee *et al.*, 2000).



Phytoplasmas are phloem-limited plant pathogens that are found primarily in the sieve elements of infected plants (Lee *et al.*, 2000). Phytoplasmal diseases are spread primarily by sap-sucking insect vectors and including vertically between generation of insects (Hogenhout, 2004). These sap-sucking insects belong to the families *Cicadellidea* (Leafhoppers) and *Fulgoridea* (Planthoppers). Insects feed on phloem tissue, where the phytoplasma is acquired and transmitted from plant to plant (Lee *et al.*, 2000). Phytoplasmas cannot be transmitted mechanically and are not seed transmissible, but are graft transmissible (Lee *et al.*, 2000).

In the past few decades, detection and identification of phytoplasmas were never accurate, because of the inability to obtain pure cultures. In the 1980s, the development of molecular probes such as antibodies and cloned phytoplasma-specific DNA advanced the art of phytoplasma diagnostics. PCR-based assays developed in the late 1980s and early 1990s further advanced diagnostics for phytoplasmal diseases (Lee *et al.*, 2000).

The rRNA genes in phytoplasmas are arranged in the same order as in other eubacteria: 5' 16S rRNA – spacer region – 23S rRNA 3'. Sequence analysis of the spacer region revealed that a single tRNA^{ile} (isoleucine transfer RNA) is present in all phytoplasmas (Kirkpatrick *et al.*, 1990; Kuske and Kirkpatrick, 1992; Lee *et al.*, 2000). The 16S rRNA gene is best characterized, and PCR primers designed on the basis of these unique sequences have been used for specific detection of phytoplasmas in infected plant and insect vectors (Lee *et al.*, 2000).

Geographically, phytoplasmas occur worldwide. The different groups of phytoplasma seem to be restricted to one continent or to a specific geographical region (Lee *et al.*, 2000).

1.5.1 Grapevine Flavescence doree

Flavescence doree is associated with a phytoplasma in the genus *Candidatus* Phytoplasma vitis, in the phylogenetic Elm Yellows (16SrV)



group (Firrao *et al.*, 2004). The principle host of Flavescence doree is *Vitis vinifera* as well as *Vitis riparia* (Maixner and Pearson, 1992). During a study done in 1993 by Kuszala *et al.* on grapevines showing yellowing symptoms, from all parts of the world, this phytoplasma was only detected in material from southern France and northern Italy (Kuszala *et al.*, 1993; EPPO/CABI, 1997).

The Flavescence doree phytoplasma is located in the phloem tissue of the infected grapevine and can be obtained by its vector for transmission. No alternative host other than grapevine is known and it is therefore likely that the biological cycle is completed in grapevine and vector (EPPO/CABI, 1997).

The vector of Flavescence doree is a cicadellid, *Scaphoideus titanus*. In 1985, Caudwell and Dalmasso found that this vector was accidentally introduced into Europe from North America (Caudwell and Dalmasso, 1985). *S. titanus* has five larval instars and both the larval stages and adults are capable of acquiring the phytoplasma. The acquisition period is generally 7-8 days, followed by a long latent period, so that transmission takes 38-42 days in total (EPPO/CABI, 1997).

The symptoms of Flavescence doree (adapted from EPPO/CABI, 1997) can be divided into three groups:

Symptoms on the shoots

When early infection occurs, the shoots fail to lignify, are thin, rubbery and hang downward. The shoots later become brittle and there may be necrosis of the apical and lateral buds. During winter the non-lignified branches blacken and die. If the shoots become infected later in the season, the lignification is interrupted (Figure 1.7).



In more resistant cultivars, non-lignification is more pronounced and is limited to certain internodes. Numerous black pustules form along the diseased branches of susceptible cultivars.



Figure 1.7: Photo of limited non-lignification of internodes

Symptoms on the leaves

In white-fruited cultivars there is a yellowing of the portion of the lamina exposed to the sun. Later in the season, distinct creamyyellow spots (of a few mm in diameter) become visible along the main veins. These spots broaden and form continuous yellow bands along the veins.

In red-fruited cultivars similar patterns of colour change develop on the leaves, but the discoloration are reddish. The central portion of the discolored areas becomes necrotic and dries out. The discolored leaves stay on the grapevine longer than the healthy leaves (Figure 1.8).





Figure 1.8: Photo of discolored leaves staying on the grapevine

Symptoms on the fruit

If the grapevine is infected earlier in the season, the fruit setting is reduced and the inflorescence dry out and fall off. In later infection, bunches become brown and shriveled.

1.5.2 Grapevine bois noir

Bois noir (Stolbur) are associated with a phytoplasma in the genus *Candidatus* Phytoplasma solani, in the phylogenetic Stolbur (16SrXII) group (Firroa *et al.*, 2004).

It is thought that grapevine may not be the host of this pathogen and that this pathogen has accidentally been transmitted to grapevine from other hosts (EPPO/CABI, 1997). In 1994 Maixner *et al.* found the bois noir phytoplasma in the plant hopper *Hyalesthus obsoletus*, after years of speculation on whether a vector did exist. *H. obsoletus* feeds on various wild plants and weeds, but rarely on grapevine, and therefore vine-to-vine transmission rarely occurs (Maixner *et al.*, 1994; EPPO/CABI, 1997).

The symptoms of this phytoplasma are more or less the same as described above for Flavescence doree. Bois noir (black wood) refers



to the blackening of the non-lignified shoots in winter (EPPO/CABI, 1997).

1.5.3 Australian Grapevine Yellows

Australian Grapevine Yellows (AGY) phytoplasma is associated with a phytoplasma in the genus *Candidatus* Phytoplasma australiense, in the phylogenetic Stolbur (16SrXII) group (Firroa *et al.*, 2004).

The symptoms include irregular veinal and interveinal yellowing and downward rolling of leaves that overlay one another in a shingled appearance. Shoots display abortion of the flowering bunches early in the season or shriveled berries later in the season. Affected shoots also often display tip death followed by dieback of the shoots, node by node. Leaf blades on affected shoots tend to fall early. The petioles remains attached to the shoots for longer than the leaf blades but would eventually abscise from the shoot. The stem of affected shoots often develops a blue, waxy appearance and remains rubbery later in the season (Constable *et al.*, 2003).

Restricted growth disease (RG) can be expressed in grapevines with AGY. The aetiology of RG is unknown but phytoplasmas may be the possible cause (Constable *et al.*, 2003). To determine the involvement of phytoplasmas, shoots from grapevines with RG have been tested by PCR but no association between phytoplasmas and RG was shown (Bonfiglioli *et al.*, 1995; Padovan *et al.*, 1995; Gibb *et al.*, 1999). Symptoms of RG include retarded growth resulting in shortened shoots and smaller leaves. Affected grapevines have an overall appearance of stunting or lack of vigour throughout the season. Some grapevines with RG may have also display uneven or no bud development, resulting in canes and cordons that are bare in places or entirely bare with little or no bunch development (Constable *et al.*, 2003).

Late season leaf curl disease (LSLC) can also affect grapevines with AGY (Constable *et al.*, 2003). Shoots from grapevines with LSLC were



also tested to determine whether phytoplasmas might be involved (Bonfiglioli *et al.*, 1995; Gibb *et al.*, 1999). Some researchers found a high association with phytoplasmas and LSLC affected shoots (80%) (Bonfiglioli *et al.*, 1995) but others found a low association (10%) (Gibb *et al.*, 1999), thus the association between phytoplasmas and LSLC is still unclear (Constable *et al.*, 2003). Symptoms include leaves on affected shoots, which are rolled tightly downward, remains green and overlays one another in a shingled appearance. The leaves are often tough, leathery and brittle (Constable *et al.*, 2003).

1.6 OTHER DISEASES OF GRAPEVINE

Shiraz decline

Shiraz Decline must not be confused with Shiraz disease. Up to now no correlation has been found between the disease and any fungus, bacteria, phytoplasma, soil type, climate, rootstock, clone or virus disease (Spreeth, 2005).

During a presentation at the meeting of the National Working Group at ENTAV in 2004, studies were related to the possible implication of a phytoplasma in this disease. The first analyses led to detection of phytoplasma belonging to groups 16Srl (Yellow Asters) and 16SrXII (Stolbur) in several samples with or without symptoms (Renault-Spilmont *et al.*, 2005).

In France the symptoms have been observed for the past 10 years and Professor Denis Boubals, editor of the well-known French viticultural magazine "Le Progrès Agricole et Viticole" magazine, contends that all Shiraz vineyards older than 15 years display between 1 and 15% symptoms of the disease, depending on the location and the cultivation conditions of the vineyard (Spreeth, 2005).

The symptoms include thickened graft joints with cracks on the graft joint and red discoloration of the leaves from middle to late summer.



The symptoms are similar to those usually observed in girdled vines or shoots. The bark thickens above the graft joint and deep cracks can be seen on the stem and cordon arms. The vines weaken and usually die back between five to ten years (Spreeth, 2005).

Shiraz disease

Shiraz Disease apparently occurs only in South Africa and causes deterioration in the cultivars Shiraz, Merlot and Malbec (Carstens, 1999). The disease is graft-transmissible although natural transmission has previously been reported (Engelbrecht and Kasdorf, 1990). The disease may be latent in certain cultivars and symptoms will only occur when this latent infected material is grafted onto the above-mentioned indicator cultivars (Carstens, 1999).

Grapevine Virus A (GVA) infection of Shiraz and Merlot cultivars in South Africa has been shown to be associated with Shiraz disease (Goszczynski and Jooste, 2003). According to Habili and Randles (2004), Goszczynski and Jooste (2003) provided evidence that Shiraz disease was associated with GVA infection alone. However Koch's postulates has not yet been proven, and thus there is no evidence that this disease is associated with only one organism.

Symptoms of the disease include reddening of leaves and veins, curling of the leaves, poor lignification of canes, retention of leaves through the winter and restricted growth (Goszczynski and Jooste, 2003). These symptoms are essentially the same as described for Flavescence doree and Stolbur, although no black pustules form on the stem. The question remains if this disease is caused by a complex of viruses and phytoplasmas.

Shiraz Disease is graft transmissible, a typical characteristic of virus and phytoplasma diseases. In 1997 Carstens found with the help of a nucleic acid linked technique that grapevine leafroll associated virus-3 (GLRaV-3) often occurs in material showing symptoms of Shiraz



Disease (Carstens, 1999). In 1993, Burger and Spreeth found Grapevine leafroll associated virus-1 and 2, as well as grapevine virus A (GVA), in different combinations with GLRaV-3 in vines showing symptoms of Shiraz Disease (Carstens, 1999).



PART III: AIMS OF THE STUDY

- 1. Establish a PCR method for the routine detection of Grapevine Fleck Virus in South Africa
- 2. Using this method to determine if the unknown spherical particles in greenhouse and field samples are Grapevine Fleck Virus
- 3. Establish a PCR method for the routine detection of phytoplasmas in South Africa
- 4. Using this method to determine if phytoplasmas are associated with the symptomatic plants found, which lack lignification



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Chapter 2

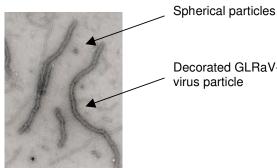
Optimization and implementation of two existing PCR detection systems for GFkV in South Africa



INTRODUCTION 2.1

The elimination of grapevine viruses in nuclear plant material for use in South Africa is effective and for a number of years no example of virus-like infections have occurred in these facilities (Oosthuizen, per comm.). However, because mass production is done in open fields, leafroll re-infection frequently occurs. As reviewed in Alkowni et al., 2004, leafroll disease in grapevine alters fruit coloration and delays fruit maturation. Other symptoms include interveinal reddening in red grape varieties and yellowing in white grape varieties in late summer and fall leaves, as well as downward rolling of leaves and phloem disruption (Alkowni et al., 2004). Winetech, in conjunction with the Agricultural Research Council – Plant Protection Research Institute (ARC-PPRI), drafted a project in 2001 to determine and identify leafroll-associated viruses spreading within certified grapevine material in South Africa and to develop/establish means to detect these viruses.

From 2001 to 2004, motherblocks were surveyed for leafroll symptoms associated with Grapevine Leafroll Associated Virus Type 3 (GLRaV-3), a very serious pathogen of grapevine in South Africa. Motherblocks are open blocks in which the grapevines are being mass propagated and are monitored annually for any symptoms of known pathogens. During Immunosorbent Electron Microscopy (ISEM) analysis of this material, it was found that 15 % of the GLRaV-3 infected plants also contained unknown spherical virus-like particles (Figure 2.1) of about 30nm in diameter (Pietersen, unpublished).



Decorated GLRaV-3 virus particle

Figure 2.1: Electron micrograph of a plant infected with GLRaV-3 and unidentified spherical particles following ISEM with Black Spanish antiserum. (Photo: K. Kasdorf)



Grapevine Fleck Virus (GFkV) is a non-mechanical transmissible spherical virus of 30nm in diameter (Sabanadovic *et al.*, 2000; El Beaino *et al.*, 2001; Martelli *et al.*, 2002) and has been found in South Africa, with evidence of spread (Engelbrecht and Kasdorf, 1990). Therefore, it was hypothesized that the unidentified spherical particles found were most likely GFkV.

Since no molecular detection method is available for GFkV in the current certification scheme for wine grapes in South Africa, GFkV could be present in certified material. Commercial ELISA kits are available for GFkV, but the high import cost makes routine use of these prohibitively expensive. An alternative was to establish a PCR method to detect this virus, which can be used in the South African certification scheme for wine grapes.

Over 40 spherical viruses can potentially infect grapevine. To narrow down the list of possible viruses, mechanical inoculations were done to determine whether these spherical viruses could be mechanically transmitted to various host range plants. ELISA was performed to determine the presence of GFkV, where after different RNA extraction methods were tested. In this study two PCR methods for the routine detection of GFkV within certified grapevine planting material as well as a field survey to determine the spread of GFkV in the field are presented.



2.2 MATERIALS AND METHODS

2.2.1 OPTIMIZATION OF RdRp GENE AND MTR GENE SPECIFIC PCR

2.2.1.1 Virus sources

The positive controls (BU4 and BU21) used during the optimization of the two PCRs, were lyophilized total nucleic acid (TNA) from GFkV-infected vines, obtained from Nina Abou Ghanem-Sabanadzovic, Istituto Agronomico Mediterraneo, Italy.

2.2.1.2 cDNA Synthesis

cDNA synthesis was done in a 20µl reaction following the USB First Strand cDNA Synthesis Protocol (USB Corporation, Ohio, USA) with slight modifications. 2-5µg of TNA were denatured together with 40pmoles of gene specific primer and DEPC-treated water at 65 °C for 5 min and incubated on ice for 2min (i.e. for the RdRp system RD2 primer and for the MTR system MTR1 primer -also see Section 2.2.1.3)

To the denatured RNA mix the following were added as final concentrations in a 20µl reaction: 5x M-MLV Reaction Buffer (USB Corporation, Ohio, USA), 10mM dNTP mix, 25U/µl Ribonuclease Inhibitor and 200 units/µl M-MLV Reverse Transcriptase (USB Corporation, Ohio, USA). The mixture was incubated at 37 ℃ for 30min where after the reaction was inactivated by 70 ℃ for 10min.

2.2.1.3 PCR: RdRp and MTR genes

RdRp gene specific PCR (Sabanadzovic et al., 2000)

In a 50µl reaction the following reagents were used as final concentrations: 10x Promega Reaction Buffer (Promega Corporation, Wisconsin, USA), 2mM MgCl₂, 2,5mM dNTP mix, 30pmol RD1 primer, 30pmol RD2 primer, 5U/µl Taq



DNA polymerase (Promega Corporation, Wisconsin, USA), 3μ l cDNA from positive control and distilled water.

The PCR conditions were as follows:

```
94°C for 120 sec;
94°C for 30 sec;
52°C for 30 sec;
72°C for 60 sec;
72°C for 300 sec.
```

10 μ l of the PCR products were electrophoresed in a 1% (w/v) agarose gel at 100V in 1 x SB buffer (0.004% NaOH, 0.0023% Boric Acid, pH8). The agarose gels were pre-stained with ethidium bromide (0.5 μ g/ml) and the DNA fragments visualized by UV fluorescence.

The RD primer set was modified, as non-specific bands were obtained after PCR. RD1 primer was extended by six nucleotides (RdRp1) and RD2 was extended by six nucleotides (RdRp2). Extension of the primers was done to increase the specificity of the primers during the annealing step. The modifications are shown in red in Table 2.1.

TABLE 2.1: Modification of RdRp gene specific primer set

RD 1	5' CYC ARC AYA ARG TVA	RdRp 1	5' CYC ARC AYA ARG TVA ACG ADV
	ACG A 3'		RCT C 3'
RD2	5' GCG CAT GCA BGT SAG	RdRp 2	5' GCG CAT GCA BGT SAG RGG GCC
	RGG G 3'		RAA Y 3'

The RdRp primer set was optimized using the exact same conditions as during the RD system.

MTR gene specific PCR (Sabanadzovic et al., 2000)

Reactions were done as described above for RdRp using forward primer MTR1 and reverse primer MTR2, final concentration 3mM MgCl₂ and an annealing temperature of 58 ℃.



2.2.1.4 Purification of PCR products

The Promega Wizard® SV Gel and PCR Clean-Up System (Promega Corporation, Wisconsin, USA) was used for purification of PCR products. The Wizard ® SV Gel and PCR Clean-Up System is designed to extract and purify DNA fragments of 100bp to 10kb from standard agarose gels. This system is based on the ability of DNA to bind to silica membranes in the presence of chaotropic salts. Purification was done according to manufacturers instructions (Promega Corporation, Wisconsin, USA, Technical Bulletin No.308).

2.2.2 PREPARATION OF RdRp GENE AND MTR GENE PCR POSITIVE CONTROLS

2.2.2.1 Preparation of competent cells

Competent cells were prepared using the method described by Hanahan *et al.* (1991) with slight modifications.

E. coli (JM109) cells were streaked onto M9 minimal media agar plates (0.05M Na₂HPO₄-2H₂O, 0.02M KH₂PO₄, 8mM NaCl, 0.02M NH₄Cl, 2mM MgSO₄, 0.01M D-glucose, 0.1mM CaCl₂, 1mM thiamine hydrochloride, 1.5 % agar (w/v) pH 7.4) and grown overnight at 37 °C. Single colonies were picked and streaked onto LB-agar plates (1% tryptone, 0.5% yeast extract, 1% NaCl pH7.5, 1.5% (w/v) agar) and grown overnight at 37 °C. Several single colonies were picked and grown overnight in LB-broth (1% tryptone, 0.5% yeast extract, 1% NaCl pH7.5) with agitation at 37 °C. 1:100 dilution of the overnight culture were inoculated in 100ml of pre-warmed LB-Broth and incubated with agitation at 37 °C. The culture was grown until an optical density (OD) of 0.4-0.6 was reached at 550nm. The cells were transferred to a 50ml centrifuge tube and incubated on ice for 10min. The cells were collected by centrifugation at 6000xg for 10min $(4^{\circ}C)$. After the supernatant was aspirated, the cells were resuspended in 25ml of CCMB 80 medium (80mM CaCl₂-2H₂O, 20mM MnCl₂-4H₂O, 10mM MgCl₂-6H₂O, 10mM K-acetate, 10%



(v/v) redistilled glycerol, pH 6.4) and incubated on ice for 30min. The cells were collected by centrifugation at 6000xg for 10min (4°C), and the supernatant aspirated. The cells were resuspended in 1ml of CCMB 80 medium and incubated on ice for 30min. The cells were aliquoted and stored at -70 °C.

2.2.2.2 Ligation reactions

The purified RNA dependent RNA polymerase gene, the amplified product by PCR with the use of the RdRp primer set, and the purified Methyltransferase gene, the amplified product by PCR with the use of the MTR primer set, were ligated and cloned as discussed below.

The vector used for ligation was the pGEM®-T Easy Vector System II (Promega Corporation, Wisconsin, USA). This vector has been prepared by cutting it with EcoRV and adding terminal thymidine residues to both ends. These single T overhangs improve the efficiency of ligation of a PCR product into a plasmid by preventing recircularization of the vector and providing a compatible overhang for PCR products, since Taq polymerase generates 3' adenine overhangs.

The ligation reactions were done according to manufacturers protocol (Promega Corporation, Wisconsin, USA, Technical Manual No.042). Briefly, in a 10 μ l reaction the following reagents were used: 2x Rapid ligation buffer, T4 DNA Ligase, 50ng of pGEM®-T Easy Vector, 30ng of MTR insert or 20ng of RdRp insert (to calculate the appropriate amount of insert to include in the ligation reaction, the following equation was used: [(ng of vector x kb size of insert)/(kb size of vector)] x insert: vector molar ratio (1:1) = ng of insert), 3 Weiss units/µl of T4 DNA Ligase and distilled water to final volume.

The reactions were mixed by pipetting and incubated at room temperature for one hour.



2.2.2.3 Transformation of competent cells

Before transformation of the ligation mixture, the competent cells were first test transformed with a plasmid of known concentration (pUC18, $10ng/\mu$ l) to calculate the transformation efficiency of the cells. The transformation was done using the heat shock method as described by Sambrook *et al.* (Sambrook *et al.*, 1989)

100 µl of the competent cells were placed in 3 pre-chilled Eppendorf tubes. To the first tube 10µl of the ligation reaction was added (RdRp and MTR, respectively), to the second tube a plasmid of known concentration was added (pUC18, 10ng/µl), to serve as a positive control, and to the third tube no DNA was added, to serve as a negative control. The tubes were incubated on ice for 30 min and then placed in a water bath at 42 °C for 90 sec. After the heat shock, the tubes were chilled on ice for 2 min. After addition of 900 µl of pre-warmed LB-broth, the transformation mixture was incubated with agitation at 37 °C for one hour to allow the cells to recuperate and express the ampicillin resistance gene. 100µl of the different mixtures were plated onto LB agar plates supplemented with 50µg/ml ampicillin. Recombinant transformants were selected by blue/white colour selection, based on the inactivation of the lac Z gene. To achieve this, 40µl of 2% X-gal solution and 10µl of 100mM IPTG solution were spread over the surface of the entire plate together with the cells. Recombinant plasmids with a Gal⁻ phenotype were selected for further characterization and grown overnight at 37°C in LB-broth supplemented with ampicillin.

2.2.2.4 Plasmid DNA extractions

Recombinant plasmids were isolated using the alkaline lysis method as described by Sambrook *et al.* (1989) with slight modifications.

Recombinant transformants were streaked out onto LB agar supplemented with ampicillin and grown overnight at 37 °C. Single colonies were picked and grown in LB-broth with ampicillin overnight with agitation at 37 °C. 1.5ml of overnight culture was centrifuged for 1 min at 14000xg. The supernatant was



removed and the bacterial pellets were resuspended in 100µl of ice-cold Solution I (50mM glucose, 25mM Tris-HCl pH8, 10mM EDTA pH8), creating an environment in which the cells are prevented from plasmolysing. The resuspended cells were vortexed and incubated at room temperature for 5min followed by 1min incubation on ice. 200µl of Solution II (0.2M NaOH, 1% SDS) were added to the cells and mixed by inverting and incubated on ice for 5 min. 150µl of ice-cold 7.5M ammonium acetate was added to the cells and vortexed briefly. The cells were then incubated on ice for 15 min and centrifuged for 15 min. The supernatants were transferred to fresh tubes and 2 volumes of 95% ethanol were added. The solution was incubated at -20° C for 30min and centrifuged for 15 min at 14000xg. The DNA pellet was aspirated and washed with 70% ethanol. The pellet was dried and resuspended in 50µl of TE buffer (10mM Tris, 1mM EDTA, pH8). The plasmids were purified using the Promega Wizard® SV Gel and PCR Clean-Up System (Promega Corporation, Wisconsin, USA).

2.2.2.5 PCR: Screening for recombinants

PCR was done on 4 possible MTR recombinants and 3 possible RdRp recombinants using the method described in Section 2.2.1.3.

2.2.2.6 DNA sequencing

The reaction was set up using the BigDye Terminator Version 3.1 (Greiner Labortchnik, Frikenhausen, Germany) according to manufacturers protocol. In a 20µl reaction the following reagents were used: 2.5 x Ready Reaction Premix; 5 x BigDye Sequencing Buffer; 10 pmol primer (RdRp1/MTR1); 100 ng of plasmid DNA and distilled water to volume.

The cycling conditions were as follows:



The sequencing reaction was added to a 1.5ml Eppendorf tube and 100µl of 60% ethanol was added. The tubes were briefly vortexed and incubated at room temperature for 15 min. The reaction was centrifuged for 20min at 14000xg and the supernatant carefully aspirated. The pellet was washed with 250µl of 70% ethanol and briefly vortexed. The tubes were centrifuged for 10 min at 14000xg in the same orientation. The supernatant was aspirated and the pellet was dried for 1 min at 90 °C. Capillary electrophoresis was done (University of Pretoria, South Africa). The nucleotide sequences were analysed using the BLAST (Altschul *et al.*, 1997) and DNAMAN version 4.13 (Lynnon Biosoft, Quebec, Canada) programs.

2.2.3 USE TWO PCRs TO TEST VARIOUS PLANT SAMPLES

2.2.3.1 Virus sources

The virus sources used in this investigation (Appendix 1) were cuttings rooted in sand and grown under greenhouse conditions. These 19 samples all contained unknown spherical particles observed during ISEM studies (Section 2.1). The positive controls used were the constructed recombinant MTR plasmids for the MTR region and for the RdRp region previous amplicons were used as positive controls.

2.2.3.2 Mechanical Inoculations

Mechanical inoculation were done with the 19 original samples to determine whether these particles were mechanically transmissible.

The 19 virus source samples were ground individually in 0.1M PO₄ buffer (0.1M Na₂HPO₄, 0.1M NaH₂PO₄, pH 7.2) containing celite and 2% nicotine. The extract was gently rubbed onto various indicator plants. The indicator plants used in this study included *Nicotiana tabacum* cv. Samsun, *Cucumis sativa* Ashley, *Nicotiana benthamiana*, *Phaseolus vulgaris* Bountiful, *Phaseolus vulgaris* Top Crop, *Lycopersicon esculentum* Red Khaki, *Chenopodium quinoa* and *Chenopodium amaranticolor*. After mechanical



inoculation, local and systemic symptoms were recorded weekly for one month.

2.2.3.3 ELISA

A DAS-ELISA was done on 14 of the 19 original samples along with the following samples 01/5008, 01/5009, 01/5011, 01/3380, 01/3381, 92/1028 and 98/0649 (See Appendix 1 for details).

The SEDIAG diagnosis kit for detection of GFkV (Sediag S.A.S, Dijon, France) was used following the manufacturers instructions with slight modifications during the conjugate step. During the conjugate step the antibodies (GFkV-IgE) was diluted 1/100 in the conjugate buffer (PVP (Mw 10 000 - 40 000), 0.2% BSA, 0.02% NaN₃) instead of 1/1000.

2.2.3.4 RNA extractions

Total RNA extractions were firstly done using the protocol by El Beaino *et al.* (2001) with slight modifications. 300mg of cortical scrapings were finely ground in liquid nitrogen. 3ml of STE buffer (0.1M NaCl, 0.05 M Tris, 0.001M EDTA, pH6.8) containing 1% SDS and 2% mercaptoethanol were added to the finely ground cortical scrapings. The extract was mixed with chloroform (1:1) and centrifuged for 5 min at 10 000xg. 30µl of silica powder and absolute ethanol (to reach a final concentration of 35% ethanol) was added to the supernatant. The mixture was incubated at room temperature with gentle shaking for 45 min. The mixture was washed two times with STE buffer containing 35% ethanol and centrifuged for 5 min at 10 000xg. The supernatant was aspirated and the pellet air-dried. The pellet was eluted in 100µl of nuclease free water.

Alternatively, RNA extractions were done using Promega Wizard® SV Total RNA System (Promega Corporation, Wisconsin, USA). Extractions were done according to manufactures protocol (Promega Corporation, Wisconsin, USA, Technical Manual N0.048). The extraction kit allowed a fast and simple technique for the preparation of purified and intact total RNA. cDNA synthesis



was done as described in Section 2.2.1.2 for the RdRp and MTR genes, respectively, followed by PCR as described in Section 2.2.1.3 for the RdRp and MTR genes, respectively.

2.2.3.5 Double stranded RNA extractions

The method of Valverde (1990) was used with slight modifications. The sample used for ds-RNA extraction was 03/3381, a known GFkV-infected vine.

2 g of plant material was ground in 6ml 1 x STE Buffer (0.1M NaCl, 0.05M Tris, 0.001M EDTA, pH 6.8) and transferred to a 50ml centrifuge tube. 1ml of 10% SDS, 0.5ml of bentonite (25mg/ml) and 9ml of 1x STE-saturated phenol were added and the mixture shaken for 30min at 4°C. The mixture was then centrifuged at 8000xg for 15min at 4°C and 10ml of the upper aqueous phase was placed in a fresh 50ml centrifuge tube. 2.1ml of 95% ethanol was added to the tube and mixed well. Two columns were prepared. Using the barrel of a 20ml plastic syringe plugged with a disk of filter paper, a cellulose suspension consisting of 1g cellulose mixed with 25ml 1 x STE buffer containing 16% v/v ethanol was passed through. The STE buffer was allowed to drain thoroughly. The sample was added to one of the columns and eluted. The column was flushed with 40ml 1 x STE buffer containing 16% v/v ethanol and eluted. 2.5ml of 1 x STE buffer was added to the column and the eluant discarded. 10ml of 1 x STE buffer was added to the column and 10ml was collected in a fresh 50ml tube. 2.1ml of 95% ethanol was added to the 50ml tube and this mixture eluted. The eluant was discarded.

The elution step was repeated but only 6ml was collected in a fresh 50ml tube. 0.5ml of 3M sodium acetate, pH 5.5 as well as 20ml of 95% ethanol was added to the collected 6ml and stored overnight at -20 °C. The samples were centrifuged at 8000xg for 25 min at 4 °C, the supernatant poured off and the pellet air dried for 15 min. The pellet was resuspended in 40µl of TE buffer, labeled and stored at -20 °C.



10μl of the double stranded RNA products were electrophoresed in a 0.8% (w/v) agarose gel at 60V in 1 x SB buffer (0.004% NaOH, 0.0023% Boric Acid, pH8). The agarose gels were pre-stained with ethidium bromide (0.5μg/ml) and the RNA fragments visualized by UV fluorescence. A ND-1000 spectrophotometer (Nanodrop Technologies, USA) was also used to determine the concentration of the ds-RNA. cDNA synthesis was done as described in Section 2.2.1.2 followed by PCR as described in Section 2.2.1.3 for RdRp.

2.2.4 USE OF ELISA TO TEST VARIOUS FIELD SAMPLES

2.2.4.1 Virus sources

The virus sources used in this investigation (Appendix 2 and Figure 2.2) were cane material and petioles collected from Block A and Block B using a judgment sampling method (White, 1998). In this sampling method, selections were made by human choice rather than at random. The advantage of this sampling method was a greater likelihood of getting infected sources, if present at low incidences.

2.2.4.2 ELISA

A DAS-ELISA was done on the 25 field samples.

The SEDIAG diagnosis kit for detection of GFkV (Sediag S.A.S, Dijon, France) was used following manufacturers instructions with slight modifications during the conjugate step.

During the conjugate step the antibodies (GFkV-IgE) were diluted 1/100 in the conjugate buffer (PVP (Mw 10 000 - 40 000), 0.2% BSA, 0.02% NaN₃) instead of 1/1000. During an optimization experiment, the highest absorbance was obtained using the 1/100 dilution.



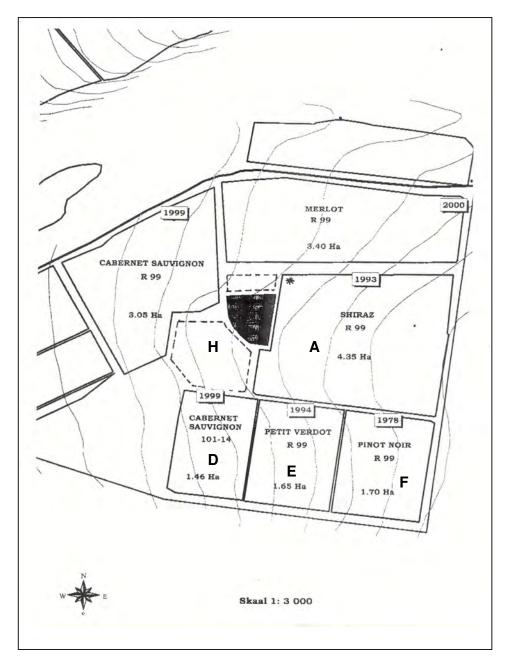


Figure 2.2: Map of Groenhof farm, Stellenbosch (The red star indicates the position of the original GFkV-infected grapevine; subsequently removed)



2.3 RESULTS

2.3.1 OPTIMIZATION OF RdRp GENE AND MTR GENE SPECIFIC PCR

RD system

After amplification with the RD primer set, amplicons of three sizes, ranging from ~200bp to ~400bp, were obtained. One of the bands was the expected size amplicon of 386 nt (Figure 2.3).

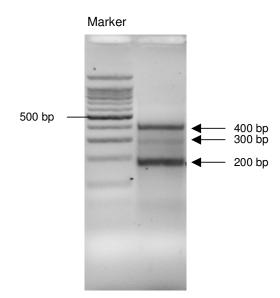


Figure 2.3: Agarose gel electrophoresis of amplicons after PCR optimization with RD primer system

The stringency of the reaction was increased by increasing the annealing temperature and lowering the MgCl₂ concentration, in an attempt to reduce the non-specific bands. The multiple bands were not reduced by increasing the stringency. Therefore, both the RD1 and RD2 primers lengths were increased by six nucleotides to increase the binding specificity of the primers (See Table 2.1 for modifications). Following the modification to primers RdRp1 and RdRp2, the expected size amplicon was obtained with no non-specific bands (Figure 2.4).



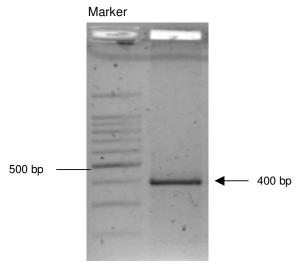


Figure 2.4: Agarose gel electrophoresis of amplicons after PCR optimization with RdRp primer system

MTR primers

After amplification with the MTR primer pair the expected size amplicon, ~600bp, was obtained (Figure 2.5). The MTR system was optimized using various annealing temperatures and MgCl₂ concentrations (Results not shown). The final optimal annealing temperature was 58 °C and the MgCl₂ concentration 3mM.

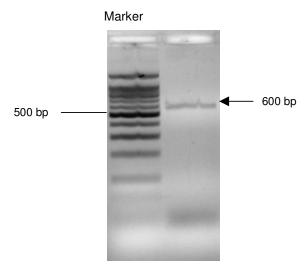


Figure 2.5: Agarose gel electrophoresis of amplicons after PCR optimization with MTR primer system

Both the amplified RdRp and MTR genes were cloned into pGEM®-T Easy Vector System II (Promega Corporation, Wisconsin, USA).



Plasmid extractions were done on recombinant colonies and PCR analysis followed. Two colonies were recombinants containing the MTR gene, while none were obtained for the RdRp gene. Sequencing was done on the positive amplicons obtained from the MTR PCR assay to confirm the presence of the GFkV MTR gene in the vector. These plasmids served as positive controls in subsequent studies.

2.3.2 USE OF TWO PCRs TO TEST VARIOUS PLANT SAMPLES

Mechanical inoculation

Mechanical inoculation was done on all samples to determine if some of the unknown spherical particles were mechanically transmissible. After the host plants were mechanically inoculated, symptoms were recorded for a period of one month. No local or systemic symptoms were observed during this period (Results not shown). Thus, it was concluded that these particles were non-mechanical transmissible viruses, incapable of infecting the selected host range plants.

<u>ELISA</u>

After testing the plants containing the unknown spherical particles with the GFkV-specific ELISA kit, none of the 19 samples was positive for GFkV (Figure 2.6). Four grapevine samples (01/3380, 01/3381, 92/1028 and 98/0649), maintained at the ARC-PPRI (Roodeplaat), tested positive for GFkV.



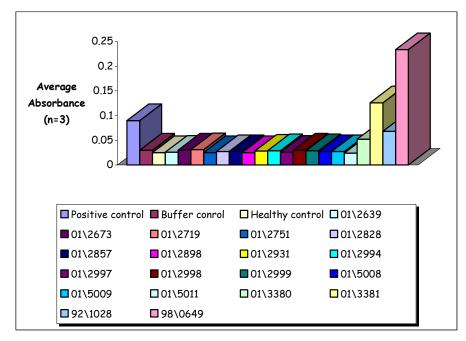


Figure 2.6: Graph of the ELISA results done using a GFkV specific kit

The low absorbance values could possibly be due to the fact that the ELISA was not sensitive enough, if the virus was present in low concentrations. Therefore the samples were tested using both the optimized RdRp and MTR PCR.

RdRp gene specific PCR

Negative results were obtained from the samples using both the extraction method described by Sabanadzovic *et al.* (2001) and the Promega Wizard ® SV Total RNA System. The TNA (BU4 and BU21) used as positive control did however amplify the expected amplicon using the RdRp primer set (Figure 2.7).

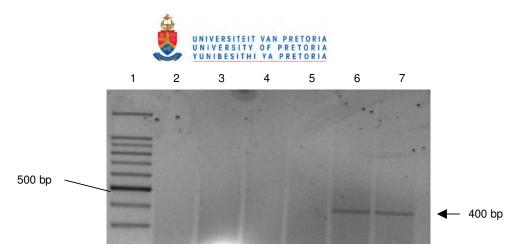


Figure 2.7: Agarose gel electrophoresis of amplicons after PCR on greenhouse samples with RdRp primer system. Lane 1- Molecular marker, Lane 2- 01/2994, Lane 3- 01/2998, Lane 4- 01/2719, Lane 5- 01/5007, Lane 6- BU21, Lane 7- BU4

MTR gene specific PCR

No amplicons could be obtained from the samples using the MTR primer pair, but the positive control did give the expected size band of ~600bp (Figure 2.8). Only one gel is presented.

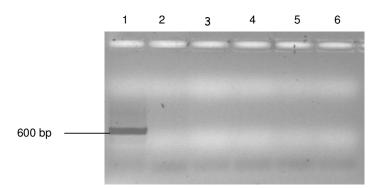


Figure 2.8: Agarose gel electrophoresis of amplicons after PCR with MTR primer system. Lane 1- MTR recombinant plasmid, Lane 2- Buffer control, Lane 3-01/5008, Lane 4-01/5009, Lane 5-01/5011, Lane 6-01/2536

Double stranded RNA extraction

Since the cDNA synthesis and both the PCRs were optimized, another RNA extraction method was tested. Double stranded RNA extraction was carried out on one sample known to be GFkV-infected, 03/3381, and a positive amplicon was obtained after cDNA synthesis and PCR with the MTR primer set (Figure 2.9). The yield of amplicon was not high but this system could be used.



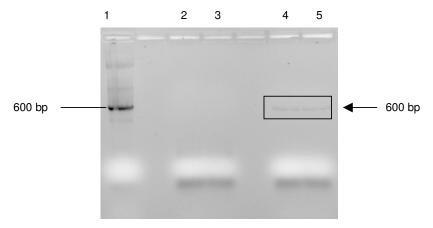


Figure 2.9: Agarose gel electrophoresis of amplicons obtained from ds-RNA after PCR with MTR primer system. Lane 1- MTR recombinant plasmid, Lane 2+3- Buffer control, Lane 4+5-03/3381

2.3.3 USE OF AN ELISA TO TEST VARIOUS FIELD SAMPLES

A GFkV-specific ELISA kit was used to test Block A and Block B on Groenhof, Stellenbosch (Figure 2.2). No positive results were obtained from the field samples tested (Figure 2.10 and Figure 2.11).

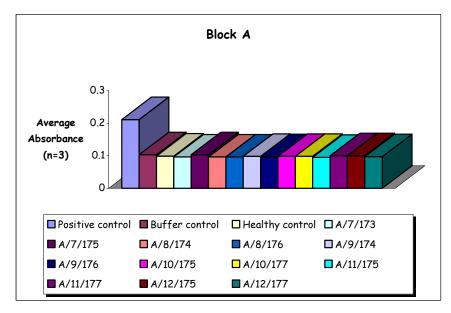


Figure 2.10: Graph of the ELISA results done on block A using a GFkV specific kit



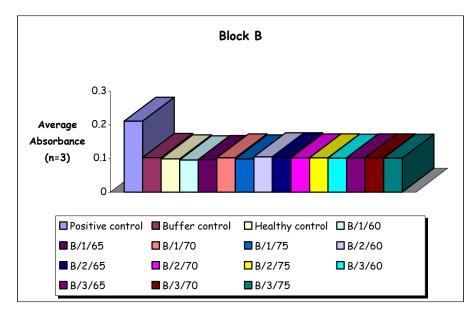


Figure 2.11: Graph of the ELISA results done on Block B using a GFkV specific kit



2.4 DISCUSSION

The re-infection of certified planting material with GLRaV-3 is a big concern for the wine industry in South Africa. During a project in 2001 to determine and identify leafroll-associated viruses spreading within certified grapevine material in South Africa and to develop/establish/implement means to detect these viruses, a number of unknown spherical virus-like particles were observed (Pietersen, unpublished). Since GFkV has been found in South Africa with evidence of spread (Engelbrecht and Kasdorf., 1990) and the morphology of GFkV correlated to that of the unknown spherical particles (Sabanadzovic et al., 2000), it was hypothesized that the unidentified spherical particles could be GFkV. Mechanical inoculation was done with the unidentified spherical particles to determine if they were mechanically transmissible. No local or systemic lesions could be noticed after a period of one month and it was concluded that the unidentified spherical particles were not mechanically transmissible. This finding supports the hypothesis that these agents may be GFkV, a virus well known to not be transmissible by mechanical inoculation (Sabanadzovic et al., 2000).

A commercial GFkV-specific ELISA kit was used to determine if these unknown spherical particles were GFkV. None of the 19 samples tested positive for GFkV, but this did not rule out the fact that GFkV could still be present in the plants. The low absorbance values obtained could be due to the lack of sensitivity to detect viruses present in low concentrations (Van der Merwe, 2001; Weber *et al.*, 2002). Four plants situated at the ARC-PPRI did test positive for GFkV, and it was decided to include these plants as internal positive controls. Since no molecular detection method was available to test certified planting material for GFkV locally, two existing PCR detection methods were implemented in South Africa. The RdRp region of the GFkV genome has been used in previous phylogenetic studies (Sabanadzovic *et al.*, 2000; El Beaino *et al.*, 2001). In this study both the RdRp and the MTR region of the GFkV were included. The advantage of the MTR gene is that it is about



200bp longer than the RdRp gene, which makes it more suitable for phylogenetic studies.

The RdRp gene specific and MTR gene specific PCR methods, with higher sensitivity and specificity, were used to test these samples. No amplification could be obtained from the RdRp gene specific and MTR gene specific PCR, respectively. As samples 01/3380, 01/3381, 92/1028 and 98/0649 were known to be infected with GFkV, the RNA extraction method was suspected of being sub optimal. GFkV is generally present in low concentrations in the plant and the virus titres vary seasonally (Foundation Plant Services, 2002).

Since both the chloroform based RNA extraction method and the commercial RNA extraction kit delivered negative results, double stranded RNA extraction was done on sample 03/3381. Double stranded RNA is present in plants infected with RNA viruses (produced as an intermediate product) and is very resistant to enzymatic degradation (Valverde, 1990). The double stranded RNA template proved the most successful, as a positive amplicon of 600bp was obtained during the MTR gene specific PCR, but this method is labour intensive and too time consuming to use routinely. PCR inhibition could also be the reason for negative results during the previous two RNA extraction The inhibition could be due to the presence of polyphenolic methods. compounds present in grapevines (Koonjul et al., 1998). These compounds are retained in plant vacuoles, but once the cells are broken open they are released and consequently co-purify with nucleic acids. It has been reported that these molecules inactivate certain enzymes, such as DNA polymerases (Koonjul *et al.*, 1998)

During the field survey done on Groenhof farm to determine if GFkV spreads naturally through the field, a commercial GFkV-specific test was used. Even though none of the plants tested positive for GFkV, it cannot be concluded that GFkV is not present on Groenhof farm. Since the collection of the plants was done in November, early summer, the concentration of GFkV in the plants was low. Collection of plants must be done in early spring or late autumn (Weber *et al.*, 2002).



Before the PCR method can be used as a routine diagnostic test, the RNA extraction method need to be optimized. Such optimization includes the dilution of possible inhibitors and using the appropriate parts of the plant, as the virus might be present in different concentrations throughout the plant. Future exploration of these PCR methods remain worthwhile since serological tests, like ELISA, cannot be applied to unknown particles and lacks the sensitivity to detect viruses when present in low concentrations (Weber et al., 2002; Van der Merwe, 2001). During this study two existing PCR methods were optimized and implemented for the detection of Grapevine Fleck Virus in South Africa, but the shortcomings in the preparation of RNA from sample plants have not allowed for a conclusion on the genetic similarities of the unidentified spherical particles with GFkV. Future work may include optimization of a rapid and reliable RNA extraction method. A field survey on Groenhof farm should be done in early spring and the optimized RNA extraction method together with the optimized MTR gene specific PCR system may be used to test the collected plants.



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Chapter 3

Implementation of an existing PCR detection system for phytoplasmas in South Africa



3.1 INTRODUCTION

Winetech, in conjunction the with Agricultural Research Council – Plant Protection Research Institute (ARC-PPRI), drafted a project to determine and identify leafroll-associated viruses spreading within certified grapevine material in South Africa and to develop/establish/implement means to detect these viruses (2001). From 2001 to 2004, motherblocks were surveyed for leafroll symptoms associated with Grapevine Leafroll Associated Virus Type 3 (GLRaV-3), a very serious pathogen of grapevine in South Africa. Motherblocks are open blocks in which the grapevines are being mass propagated and is monitored annually for any symptoms of known pathogens. Because mass production is done in open fields, leafroll re-infection frequently occurs. As reviewed in Alkowni *et al.*, 2004, leafroll disease in grapevine alters fruit coloration and delays fruit maturation. Other symptoms include interveinal reddening in red grape varieties and yellowing in white grape varieties of late summer and fall leaves, downward rolling of leaves and phloem disruption (Alkowni *et al.*, 2004).

A number of plants were observed with leafroll and reddening symptoms unlike classical grapevine leafroll disease. No grapevine Leafroll-associated viruses could be detected in these plants, and the common wisdom from the industry was that these symptoms were due to bark constrictions. In subsequent seasons, monitoring of the vineyards has shown that these plants slowly deteriorate and die. However, on a few occasions new symptomatic plants were found, sometimes in close proximity to the previous infected plants (Pietersen, unpublished), suggestive of an infectious agent. On recent, closer inspection of these symptoms, it appeared that in some instances the symptoms were similar to those induced by some phytoplasmas typically found in Europe (e.g. Flavescence doree and Bois noir) (Lee *et al.*, 2000).

The symptoms included abnormal elongation of internodes, which resulted in slender shoots, generalized stunting and reddening of the leaves with downward curling. The diseases caused by both these phytoplasmas on

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grapevines are destructive in Europe (EPPO/CABI, 1997) and the phytoplasmas are considered quarantine organisms as far as South Africa and some parts of Europe are concerned. It has long been feared that such an organism could enter South Africa. In order to prevent this, all imported material are subjected to heat treatment, however, no diagnostic tests were established to screen imported planting material for phytoplasmas.

In order to assess the possibility that these symptoms were due to phytoplasma infection, it was decided that a universal phytoplasma specific PCR needed to be established in South Africa. Because it is generally known that phytoplasma's occur in low titres in the plant (Schaff *et al.*, 1992) and that polyphenolic compounds in the grapevine can act as inhibitors of the DNA polymerase (Koonjul *et al.*, 1998), it was useful to establish a nested PCR, as this sequentially increases the target molecule and dilutes inhibitors (Webster *et al.*, 2004). During this study, the P1/P7 as well as the 16R758f/m23Sr PCR were implemented in South Africa. Various samples with phytoplasma-like symptoms were collected and tested and it was found that 13 symptomatic plants yielded the expected amplicon during amplification and were sequenced. From these, nine were consistent with *Candidatus* Phytoplasma solani, two with common soil bacteria, one with Flavescence doree and one with Mollicutes from *Vitis vinifera*.



3.2 MATERIALS AND METHODS

3.2.1 Phytoplasma sources

The positive controls (ADN-J7 – Flavescence doree Isolate 92 DNA and ADN-I550 – STOL C DNA) used during the optimization of the PCRs, were total DNA from periwinkle infected with Flavescence doree (FD92) and Stolbur (STOLC), respectively. These samples were kindly supplied by Elizabeth Bourdon-Pardieu, Centre National De La Recherche Scientifique, France. Field samples were collected during winter 2005 (Appendix C) and are from various regions of the Western Cape, South Africa (Figure 3.1).

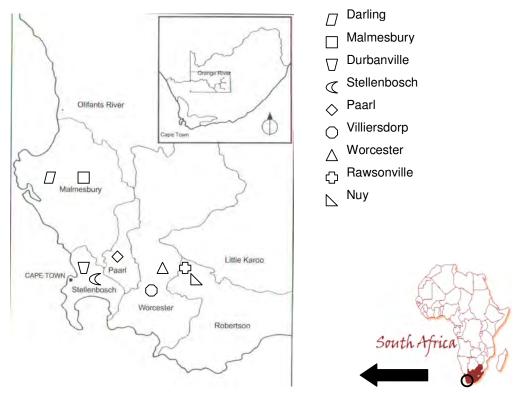


Figure 3.1: Wine regions of South Africa, where field samples where collected (Image: SAWIS nr.29, 2005, with modifications).

3.2.2 DNA extraction

DNA extractions were done based on the method described by Angelini *et al.* (2001). Briefly, 1g of petioles or cortical scrapings were placed into a maceration bag (Bioreba,) together with 5 ml of warm extraction buffer (2% CTAB, 10mM Tris-HCl pH8, 10mM EDTA, 1.4M NaCl, 0.2% 2-



The contents of the bag were finely ground with a mercaptoethanol). macerator (Homex 6, Bioreba) and the suspension (1ml) transferred to a 2ml Eppendorf tube. The suspension was incubated at 65°C for 20min, and thereafter allowed to cool for 3min. Chloroform was added to the tube at a 1:1 ratio and centrifuged at 14000xg for 10 min at room temperature. The chloroform extraction step was repeated. The upper aqueous phase was placed in a new 1ml Eppendorf tube. An equal volume of ice-cold isopropanol was added and gently mixed. The solution was incubated overnight at room temperature and centrifuged at 14000xg for 10min. The supernatant was aspirated and 1ml 70% ethanol was added to the pellet. The pellet and ethanol were incubated for 20min at room temperature where after it was centrifuged at 14000xg for 5 min. After the supernatant was removed, the tubes were air dried at room temperature. The DNA pellet was resuspended in 150µl TE buffer.

<u>3.2.3 PCR</u>

The first primer pair used, P1 (Deng and Hiruki, 1991) and P7 (Smart *et al.*, 1996), amplify 1800bp of the 16S rRNA gene extending through the 16S/23S spacer region and into the beginning of the 23S rRNA gene (Padovan *et al.*, 1995). The second or nested primer pair used, 16R723f and m23Sr (Padovan *et al.*, 1995), amplify 1076 bp, extending from the 16SR rRNA gene through the spacer region and into the start of the 23S rRNA gene (Padovan *et al.*, 1995) (Figure 3.2).

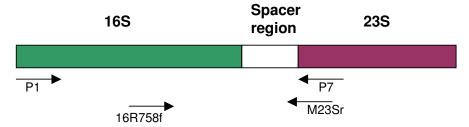


Figure 3.2: Schematic representation of a phytoplasma rRNA operon, including the 16S and 23S rRNA genes and the intergenic spacer region. (Image: Smart et al., 1996, with slight modifications)

The P1/P7 system (Smart *et al.*, 1996) was done in a 25µl reaction using the following reagents as final concentrations: 10x Promega Reaction Buffer



(Promega Corporation, Wisconsin, USA), 3mM MgCl₂, 0.5mM dNTP mix, 0.5pmol P1 primer, 0.5pmol P7 primer, 1.5U/μl Taq DNA polymerase (Promega Corporation, Wisconsin, USA), 1μl DNA and distilled water.

The PCR conditions were as follows:

92 °C for 135 sec; 92 °C for 45 sec; 57 °C for 45 sec; 72 °C for 105 sec; x 35 cycles

10µl of the PCR products were electrophoresed in a 1% (w/v) agarose gel at 100V in 1 x SB buffer (0.004% NaOH, 0.0023% Boric Acid, pH8). The agarose gels were pre-stained with ethidium bromide (0.5µg/ml) and the DNA fragments visualized by UV fluorescence.

The M23Sr/16R758f (nested) PCR was done using the conditions as described for the P1/P7 system. The universal P1/P7 primers were replaced with the forward primer, 16R758f, and reverse primer, M23Sr, and the template used in the nested PCR was 0.5µl PCR product from the first round.

3.2.4 Purification of PCR products

Purification was done as described in Section 2.2.1.4.

3.2.5 DNA sequencing

Sequencing was done as described in Section 2.2.1.10, using primers m23Sr and 16S758f. For each amplicon a forward and reverse sequencing reaction was done to confirm the results obtained.



3.3 RESULTS

PCR Optimization

Before testing could be done on field samples the PCR system had to be optimized, both for 1st and 2nd round of amplification. Different MgCl₂ concentrations were tested and amplicons of 1800bp and 1050bp were successfully amplified in the 1st and 2nd round, respectively. During optimization of the P1/P7 primer system (1st round), the best amplification was obtained using 3mM MgCl₂ in the PCR mixture. Optimal conditions for the m23Sr/16R758f primer system (nested) were the same PCR parameters and conditions as the P1/P7 system.

PCR on field samples

The field samples collected were tested in batches of 17 samples. None of the field samples yielded amplicons during the first round of amplification but the positive control gave the expected size amplicon of 1800bp. While this could mean that the samples did not contain phytoplasmas it could also be due to inhibition of the DNA polymerase, insufficient template DNA or low phytoplasma titers. During the 2nd (nested) round of amplification some of the field samples yielded amplicons of the expected size of 1050bp (Figure 3.3). A representative gel is shown in Figure 3.3.

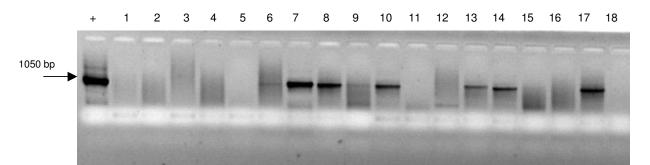


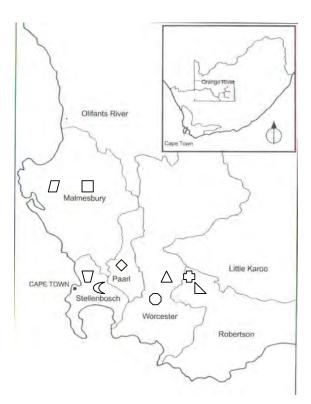
Figure 3.3: Gel photo of 2nd round amplification using m23Sr/16R758f system. Lane +-Positive control (AND-J7), Lane 1- Sample 05/0019, Lane 2- Sample 05/0023, Lane 3-Sample 05/0036, Lane 4- Sample 05/0010, Lane 5- Sample 05/0035, Lane 6- Sample 05/0012, Lane 7- Sample 05/0033, Lane 8- Sample 05/0018, Lane 9- Sample 05/0024, Lane 10- Sample 05/0038, Lane 11- Sample 05/0020, Lane 12- Sample 05/0036, Lane 13- Sample 05/0022, Lane 14- Sample 05/0034, Lane 15- Sample 05/0021, Lane 16- Sample 05/0013, Lane 17- Sample 05/0028 and Lane 18- Buffer control



Sequencing

Amplicons of the expected size from the nested PCR were purified using the Promega Wizard® SV Gel and PCR Clean-Up System (Promega Corporation, Wisconsin, USA). The purified samples were sequenced using the m23Sr and 16R758 primer for each sample, to obtain a double set of sequence information for each sample. The forward and reverse sequences were trimmed and a consensus sequence was obtained. These consensus sequences were compared with known sequence information in the public domain (Genbank) in order to attempt gene-based identification of the sources of the amplicons.

Samples from 25 wine estates, representing 9 different geographical regions of the Western Cape, were tested. Of the 139 samples, 31 samples yielded amplicons of the expected size during the nested PCR. Thirteen of these samples were sequenced (Table A.3). The locations of the samples that yielded the expected size amplicon are shown in Figure 3.4.



- □ Darling (1 positive amplicon)
- Malmesbury (1 positive amplicon)
- \square Durbanville (0 positive amplicons)
- ✓ Stellenbosch (6 positive amplicons)
- Paarl (6 positive amplicons)
- Villiersdorp (1 positive amplicon)
- \triangle Worcester (2 positive amplicons)
- Rawsonville (10 positive amplicons)
- △ Nuy (1 positive amplicons)

Figure 3.4: Location of the positive amplicons obtained during nested PCR, shown on a map of South Africa (Image: SAWIS nr.29, 2005, with modifications).



Pairwise comparisons were all done with a gap penalty of 20 and are shown in Appendix B. Eight samples yielded sequences similar to that of *Candidatus* Phytoplasma solani (Genbank accession no. AJ964960) (Torres *et al.*, unpublished) (Table 3.1). *Candidatus* phytoplasma solani is the genus to which Stolbur is a member.

Sample	Similarity
05-0014	99.23%
05-0018	98.21%
05-0038	99.00%
05-0062	97.92%
05-0102	98.93%
05-0109	99.67%
05-0111	98.82%
05-0122	98.51%
05-0127	99.22%

TABLE	3.1:	Similarity	and	position	of	samples	to	Candidatus
phytopla	asma	solani						

Sample 05-0005 yielded a sequence identical (100%) to that of *Bacillus megaterium*, isolate AC46b1 (Genbank accession no. AJ717381) (Tiago *et al.*, 2004). Sample 05-0077 yielded a sequence that was most similar (95.49%) to that of Mollicutes from *V. vinifera* (Genbank accession no. X76428) (Seemuller *et al.*, 1994). Sample 05-0055 yielded an amplicon with a sequence most similar (97.59%) to that of uncultured bacterium clone 3 (Genbank accession no. DQ011250) (Wei *et al.*, unpublished). However, one of the samples, 05-0033, yielded a sequence identical (100%) to that of Flavescence doree phytoplasma strain 1487 (Genbank accession no. AJ548787) (Torres *et al.*, unpublished).



A multiple alignment (Appendix C) was done in DNAMAN with the sequences of the eighteen samples. From the multiple alignment a phylogenetic tree was constructed in DNAMAN, using 1000 bootstrap replicates (Figure 3.5).

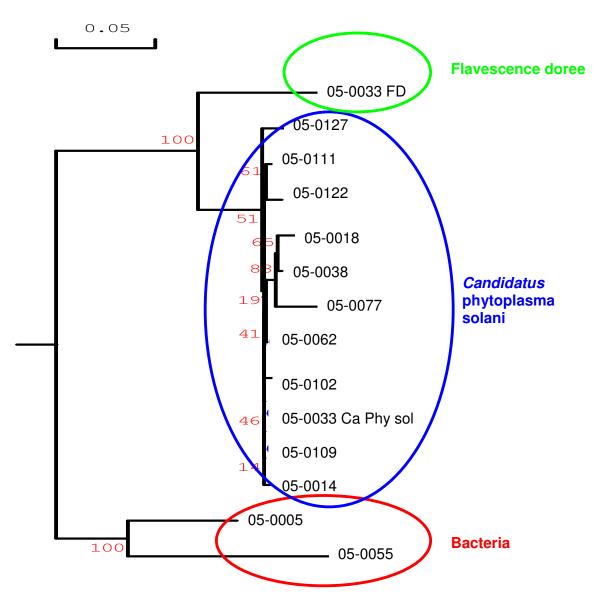


Figure 3.5: Phylogenetic tree of thirteen samples sequenced. Bootstrap=1000.

Sample 05-0033 was re-tested to confirm the results obtained due to the serious nature of this disease and phytosanitary implications of finding the etiological agent in South Africa. A positive amplicon of the expected size was obtained during the nested PCR, but on this occasion the amplicon had a



sequence most similar (99.67%) to that of *Candidatus* phytoplasma solani (Genbank accession no. AJ964960) (Torres *et al.*, unpublished).

During the first DNA extraction procedure on sample 05-0033, that returned a sequence identical to Flavescence doree, petioles were used. During the second DNA extraction procedure however (*vide supra*), cortical scrapings were used. Both the petioles and cortical scrapings were collected during March 2005.

Some of the samples (05-0096, 05-0105, 05-0137, 05-0138 and 05-0139) presented smears after the nested amplification. Therefore, serial dilutions 1:10, 1:50 and 1:100 was done on the 1st round PCR products, serving as templates during the nested PCR, in order to reduce the concentration of the template. With the 1:100 dilution, amplicons of the expected size were obtained during the nested PCR, but the bands were too faint to purify and ultimately sequence.



3.4 DISCUSSION

From 2001 to 2004, a number of plants were observed with reddening symptoms, which appeared to be similar to symptoms induced by some phytoplasmas in Europe (Lee *et al.*, 2000). These phytoplasmas are quarantine organisms in South Africa, but no detection method is available to screen imported planting material.

A universal nested PCR system (Deng and Hiruki, 1991; Smart *et al.*, 1996; Padovan *et al.*, 1995) was optimized and established in South Africa to detect phytoplasma, which can be used in the South African certification scheme for wine grapes. This optimized PCR was used in order to assess the possibility that the reddening symptoms observed were due to phytoplasma infection. During the first round of amplification, no amplification products could be observed when the plant material was used as template. This could be due to inhibitors present in the grapevine (Koonjul *et al.*, 1998). However in spite of this, some of the plant samples gave the expected sized amplicon of 1050bp during the second round of amplification.

From 139 samples, amplicons of the expected size was obtained from 31 samples and 13 of these amplicons were sequenced. Nine of these samples yielded sequences that were most similar to that of *Candidatus* Phytoplasma solani. The phytoplasma belonging to this genus, Stolbur, is present all over the world and it is thought that grapevine may not be the original host of this pathogen and that this pathogen has accidentally been transmitted to grapevine from another host (EPPO/CABI, 1997).

Two samples were found to contain DNA most similar to that of common soil bacteria. Some saprophytic bacteria are present in soil, and the detection of these bacteria could be due to the universal nature of the primer pairs used. Different types of bacteria are present on the bark of the grapevine and since some of the samples did not show any lignification of the cane, the non-



lignified bark was used were normally the bark is removed and only the phloem is used during DNA extractions.

The finding that one of the samples contained DNA with a sequence identical to that of Flavescence doree phytoplasma was of particular concern. Flavescence doree only occurs in France, Italy and Spain (EPPO/CABI, 1997). Therefore, due to the phytosanitary implications of finding the organism in South Africa, the DNA extraction, nested PCR and sequencing was repeated. Surprisingly, the sequenced amplicon obtained from the repeated experiment was in this instance most consistent with *Candidatus* phytoplasma solani. However, different plant material components were used for the DNA extractions although the collection date was the same. Experimentally, a plant can be infected by more than one type of phytoplasma (Lee et al., 2000) and mixed infections in a single plant are evident in nature (Alma et al., 1996; Bianco et al., 1993; Lee et al., 2000). An alternative hypothesis however could be that a false positive was obtained from contaminating positive control. To investigate further, the Flavescence doree positive control for our experiments (ADN-J7) was sequenced and analyzed. It was found that the positive control corresponded with Flavescence doree strain 1487, rather than Flavescence doree isolate FD92 as previously thought, based on NCBI Genbank sequence archives. Therefore, the original amplicons and sequence obtained from the petiole sample 05-0033 may be due to laboratory contamination, since the sequence of the sample was identical to that of the Flavescence doree positive control used during the experiment (Appendix D). Therefore, the occurrence of Flavescence doree in sample 05-0033 is not likely due to a mixed infection, since the results could not be repeated and the sequence was identical to that of the positive control.

Sequence analysis of the amplicon obtained from sample 05-0077 demonstrated a high degree of similarity to that of Mollicutes from *V. vinifera* (Seemuller *et al.*, 1994). This study suggests that the phytoplasma, *Candidatus* Phytoplasma solani, occur at many sites within the industry and may have been present in South Africa for a number years already. This is supported by the fact that sample 05-0127, from a Shiraz block established in



1977, was infected with *Candidatus* Phytoplasma solani. The disease does not seem to be spreading at most of the sites where the phytoplasmas were found, possibly due to the lack of an efficient vector. During the study, a PCR method was established to use for the routine detection of phytoplasmas in South Africa and phytoplasmas were associated with some of the symptomatic plants found. The *Candidatus* phytoplasma solani infected plants will be grafted onto periwinkle to maintain the sources and to prove Koch's postulates.

Even though Boudon-Padieu et al. (2003) highly recommends the current DNA extraction method, this method is too time-consuming for use during routine inspection and only a small portion of plant material can be tested. This poses a problem since phytoplasma infection may be limited to a certain part of the plant or double infection may occur and only the pre-dominant strain will be selected (Constable et al., 2003). The current PCR system is not optimal, since a nested PCR has to be performed to eliminate the inhibitory effect of the polyphenolic compounds (Webster et al., 2004). In addition, even when a positive amplicon is obtained, RFLP or nucleotide sequencing has to be done to confirm phytoplasmal infection, because of the universal nature of the primers. A multiplex nested PCR described by Clair et al. (2003) has been optimized and established in South Africa (Koch, unpublished) using specific primers for Flavescence doree and Stolbur, but the method is limited to these two organisms only and since the PCR has to be used in the certification scheme, the PCR has to detect all possible phytoplasmas.

A full-scale field survey is planned for all the grapevine production areas of South Africa, to determine the extent of this phytoplasma infection as well as spread, if any, of the phytoplasma. Should evidence of spread be observed, vector studies will be conducted. This survey might shed more light on the possibility that Shiraz disease might be caused by the phytoplasma detected in this study, as the two diseases elicit similar symptoms (Goszczynski and Jooste, 2003; EPPO/CABI, 1997). The possibly that the Stolbur phytoplasma can be responsible for Shiraz decline can also be explored since recent



studies has shown the presence of Stolbur phytoplasma in certain plants displaying Shiraz decline symptoms (Renault-Spilmont *et al.*, 2005). This is the first report of *Candidatus* Phytoplasma solani infecting grapevine in South Africa.



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APPENDIX A.1

TABLE A.1: Field samples for testing in PCR

Accession number	Region	Estate	Cultivar clones And Rootstocks	Plant Year	Symptoms April/May 2002
01/2536	Paarl	La Concorde	Merlot	1992	Leafroll
01/2581	Paarl	La Concorde	Merlot x Richter 101-14	1992	Leafroll
01/2639	Paarl	La Concorde	Merlot x Richter 101-14	1992	Healthy
01/2673	Stellenbosch	Rust + Vrede	Cabernet sauvignon x Richter 101-14	1997	Leafroll
01/2751	Paarl	Klompzicht	Cabernet sauvignon x Richter 99	1997	Leafroll
01/2803	Wellington	Soetendal	Pinotage x Richter 110	1995	Leafroll
01/2828	Wellington	Soetendal	Pinotage x Richter 110	1995	Leafroll
01/2852	Paarl	Picardi	Cabernet sauvignon x Richter 99	1998	Leafroll
01/2857	Paarl	Picardi	Cabernet sauvignon x Richter 99	1998	Leafroll
01/2898	Paarl	Plasir de Merle	Cabernet sauvignon	1997	Healthy
01/2906	Worcester	Memel	Shiraz x Richter 99	1993	Leafroll
01/2931	Worcester	Meerlust	Pinotage x Richter 99	1997	Leafroll
01/2997	Worcester	Merwida	Merlot x Richter 99	1994	Healthy
01/2999	Worcester	Merwida	Merlot x Richter 99	1994	Shiraz Disease
01/5014	Worcester	Merwida	Merlot x Richter 99	1994	Leafroll
01/2994	Worcester	Merwida	Merlot x Richter 99	1994	Leafroll
01/2998	Worcester	Merwida	Merlot x Richter 99	1994	Leafroll
01/2719	Stellenbosch	Fransmanskraal	Cabernet sauvignon x Richter 110-14	1996	Leafroll
01/5007	Worcester	Merwida	Merlot x Richter 99	1994	Leafroll
01/5008	Worcester	Merwida	Merlot x Richter 99	1994	Leafroll
01/5009	Worcester	Merwida	Merlot x Richter 99	1994	Shiraz Disease
01/5011	Worcester	Merwida	Merlot x Richter 99	1994	Leafroll
92/1028	Stellenbosch	Groenhof	Cabernet sauvignon	-	-
98/0649	Import number:	12979	Vitis rupestris St. George	-	-



Accession number	Region	Estate	Cultivar clones	And Rootstocks	Plant Year	Symptoms April/May 2002
01/3380	Import number:	12130	Michele Palie	ere	-	-
01/3381	Import number:	12133	Nedeltheff		-	-



APPENDIX A.2

TABLE A.2: Field samples from Groenhof farm

Block, Row, Plant position	Region	Estate	Cultivar	Plant Year
A/7/173	Stellenbosch	Groenhof	Shiraz x Richter 99	1993
A/7/175	Stellenbosch	Groenhof	Shiraz x Richter 99	1993
A/8/174	Stellenbosch	Groenhof	Shiraz x Richter 99	1993
A/8/176	Stellenbosch	Groenhof	Shiraz x Richter 99	1993
A/9/174	Stellenbosch	Groenhof	Shiraz x Richter 99	1993
A/9/176	Stellenbosch	Groenhof	Shiraz x Richter 99	1993
A/10/175	Stellenbosch	Groenhof	Shiraz x Richter 99	1993
A/10/177	Stellenbosch	Groenhof	Shiraz x Richter 99	1993
A/11/175	Stellenbosch	Groenhof	Shiraz x Richter 99	1993
A/11/177	Stellenbosch	Groenhof	Shiraz x Richter 99	1993
A/12/175	Stellenbosch	Groenhof	Shiraz x Richter 99	1993
A/12/177	Stellenbosch	Groenhof	Shiraz x Richter 99	1993
B/1/60	Stellenbosch	Groenhof	Merlot x Richter 99	2000
B/1/65	Stellenbosch	Groenhof	Merlot x Richter 99	2000
B/1/70	Stellenbosch	Groenhof	Merlot x Richter 99	2000
B/1/75	Stellenbosch	Groenhof	Merlot x Richter 99	2000
B/2/60	Stellenbosch	Groenhof	Merlot x Richter 99	2000
B/2/65	Stellenbosch	Groenhof	Merlot x Richter 99	2000
B/2/70	Stellenbosch	Groenhof	Merlot x Richter 99	2000
B/2/75	Stellenbosch	Groenhof	Merlot x Richter 99	2000
B/3/60	Stellenbosch	Groenhof	Merlot x Richter 99	2000
B/3/65	Stellenbosch	Groenhof	Merlot x Richter 99	2000
B/3/70	Stellenbosch	Groenhof	Merlot x Richter 99	2000
B/3/75	Stellenbosch	Groenhof	Merlot x Richter 99	2000



APPENDIX A.3

TABLE a.3: Field samples collected during 2005

Accession number	Date collected	Location	PCR results	Sequencing results	Direct pairwise comparison	BLAST Accession number
Accessio number	Da colle	Loc	PCR r	Seque	Dir pair compa	BLAST Accessic numbei
05-0001	May-05	Merwida, Rawsonville	+	NS		
05-0002	May-05	Merwida, Rawsonville	+	NS		
05-0003	May-05	Merwida, Rawsonville	+	NS		
05-0004	May-05	Merwida, Rawsonville	+	NS		
05-0005	May-05	Merwida, Rawsonville	+	Bacillus megaterium 16S rRNA gene, isolate AC 46 b1	100%	AJ717381
05-0006	May-05	Merwida, Rawsonville	+	NS		
05-0007	May-05	Merwida, Rawsonville	-			
05-0008	May-05	Merwida, Rawsonville	+	NS		
05-0009	May-05	Merwida, Rawsonville	+	NS		
		Merwida, Rawsonville	-			
05-0011	May-05	Merwida, Rawsonville	-			
05-0012	Mar-05	Merwida, Rawsonville	-			
05-0013	Mar-05	Rust en Vrede, Stellenbosch	-			
				<i>Candidatus</i> phytoplasma solani 16rRNA gene, partial 16S-23S IGS and		
		Rust en Vrede, Stellenbosch	+	tRNA ^{ile} gene	99.23%	AJ964960
		Rust en Vrede, Stellenbosch	-			
		Rust en Vrede, Stellenbosch	-			
05-0017	May-05	Rust en Vrede, Stellenbosch	-	<i>Candidatus</i> phytoplasma solani 16rRNA gene, partial 16S-23S IGS and		
05-0018	Mar-05	Rust en Vrede, Stellenbosch	+		98.21%	AJ964960
05-0019	Mar-05	Rust en Vrede, Stellenbosch	-			
05-0020	Mar-05	Rust en Vrede, Stellenbosch	-			
05-0021	Mar-05	Rust en Vrede, Stellenbosch	-			
05-0022	Mar-05	Rust en Vrede, Stellenbosch	+	NS		
05-0023	Mar-05	Rust en Vrede, Stellenbosch	-			
05-0024	Mar-05	Rust en Vrede, Stellenbosch	-			
05-0025	May-05	Rust en Vrede, Stellenbosch	-			
05-0026	May-05	Rust en Vrede, Stellenbosch	-			
05-0027	May-05	Rust en Vrede, Stellenbosch	-			
05-0028	Mar-05	La concordia, Paarl	+	NS		
05-0029	May-05	Freedom Hill, Paarl	+	NS		
05-0030	May-05	Freedom Hill, Paarl	-			
05-0031	May-05	Freedom Hill, Paarl	-			
05-0032	May-05	Freedom Hill, Paarl	-			



Accession number	Date collected	Location	PCR results	Sequencing results	Direct pairwise comparison	BLAST Accession number
				Flavescence doree phytoplasma isolate, 16S rRNA partial, 16S-23S IGS complete and 23 S ribosomal partial,		
05-0033	Mar-05	Freedom Hill, Paarl	+	strain 1487	100%	AF548787
05-0034	Mar-05	Freedom Hill, Paarl	+	NS		
		Freedom Hill, Paarl	-			
		Freedom Hill, Paarl	-			
		Freedom Hill, Paarl Freedom Hill, Paarl	-	Candidatus phytoplasma solani 16rRNA gene, partial 16S-23S IGS and tRNA ^{ile} gene	99%	AJ964960
		Nietvoorbij, Stellenbosch	-		0070	
		Nietvoorbij, Stellenbosch	-			
		Du Toitskloof wine cellar, Rawsonville	-			
		Kanonkop, Stellenbosch	-			
		Location not known	-			
		Location not known	-			
		Location not known	-			
		Location not known	-			
		Location not known	-			
05-0048		Overgaauw, Stellenbosch	-			
		Overgaauw, Stellenbosch	-			
		Overgaauw, Stellenbosch	-			
05-0051		Overgaauw, Stellenbosch	-			
05-0052		Overgaauw, Stellenbosch	-			
05-0053		Overgaauw, Stellenbosch	-			
05-0054	Jun-05	Cloof Wine Estate, Darling	-			
				Uncultured bacteria clone 3 16S rRNA gene and partial 16S-		
		Cloof Wine Estate, Darling	+	23S IGS	97.59%	DQ011250
05-0056		Cloof Wine Estate, Darling	-			
05-0057		Cloof Wine Estate, Darling	-			
05-0058		Cloof Wine Estate, Darling	-			
05-0059		Cloof Wine Estate, Darling	-			
05-0060		Cloof Wine Estate, Darling	-			
05-0061 05-0062		Cloof Wine Estate, Darling La Rhine, Malmesbury	-+	<i>Candidatus</i> phytoplasma solani 16rRNA gene, partial 16S-23S IGS and tRNA ^{ile} gene	97.92%	AJ964960
05-0063	Jun-05	La Rhine, Malmesbury	-			



Accession number	Date collected	Location	PCR results	Sequencing results	Direct pairwise comparison	BLAST Accession number
05-0064	Jun-05	La Rhine, Malmesbury	-			
05-0065	Jun-05	La Rhine, Malmesbury	-			
05-0066	Jun-05	La Rhine, Malmesbury	-			
05-0067	Jun-05	La Rhine, Malmesbury	-			
05-0068	Jun-05	Maastricht, Durbanville	-			
05-0069	Jun-05	Maastricht, Durbanville	-			
05-0070	Jun-05	Maastricht, Durbanville	-			
05-0071	Jun-05	Maastricht, Durbanville	-			
05-0072	Jun-05	Maastricht, Durbanville	-			
05-0073	Jun-05	Maastricht, Durbanville	-			
05-0074	Jun-05	Nitida, Durbanville	-			
05-0075	Jun-05	Nitida, Durbanville	-			
05-0076	Jun-05	Nitida, Durbanville	-			
05-0077	Jun-05	Leipzig, Nuy		Mollicutes (from Vitis vinifera) 16S rRNA gene	95.49%	X76428
05-0078	Jun-05	Leipzig, Nuy	-			
05-0079	Jun-05	Leipzig, Nuy	-			
05-0080	Jun-05	Leipzig, Nuy	-			
05-0081	Jun-05	Leipzig, Nuy	-			
05-0082	Jun-05	Leipzig, Nuy	-			
05-0083	Jun-05	Leipzig, Nuy	-			
05-0084	Jun-05	Leipzig, Nuy	-			
05-0085	Jun-05	Leipzig, Nuy	-			
05-0086	Jun-05	Du Vlei, Nuy	-			
05-0087	Jun-05	Du Vlei, Nuy	-			
05-0088	Jun-05	Du Vlei, Nuy	-			
05-0089	Jun-05	Vrede, Worcester	-			
05-0090	Jun-05	Vrede, Worcester	-			
05-0091	Jun-05	Vrede, Worcester	-			
05-0092	Jun-05	Vrede, Worcester	-			
05-0093	Jun-05	Nooitgedacht, Worcester	NT^{\star}			
05-0094	Jun-05	Nooitgedacht, Worcester	-			
05-0095	Jun-05	Nooitgedacht, Worcester	-			
05-0096	Jun-05	Nooitgedacht, Worcester	+	NS		
05-0097	Jun-05	Statyn, Villiersdorp	NT⁺			
05-0098	Jun-05	Statyn, Villiersdorp	-			
05-0099		Statyn, Villiersdorp	-			
05-0100		Statyn, Villiersdorp	-			
	Jun-05	Statyn, Villiersdorp	-			



Accession number	Date collected	Location	PCR results	Sequencing results	Direct pairwise comparison	BLAST Accession number
			1	Candidatus phytoplasma solani 16rRNA gene, partial 16S-23S IGS and		
		Statyn, Villiersdorp		tRNA ^{ile} gene	98.93%	AJ964960
		Statyn, Villiersdorp	NT			
05-0104		Tawny Acres, Worcester	-	NO.		
		Tawny Acres, Worcester	+	NS		
05-0106		Tawny Acres, Worcester	-			
05-0107 05-0108		Tawny Acres, Worcester	-			
		Bothasguns, Rawsonville Bothasguns, Rawsonville		<i>Candidatus</i> phytoplasma solani 16rRNA gene, partial 16S-23S IGS and tRNA ^{ie} gene	99.67%	AJ964960
05-0110	Jun-05	Bothasguns, Rawsonville	-	Candidatur		
				Candidatus phytoplasma solani 16rRNA gene, partial 16S-23S IGS and		
05-0111		Bothasguns, Rawsonville	+	tRNA ^{ile} gene	98.82%	AJ964960
05-0112		Bothasguns, Rawsonville	-			
05-0113		Hartenberg, Stellenbosch	-			
05-0114		Hartenberg, Stellenbosch	-			
05-0115		Hartenberg, Stellenbosch	-			
05-0116		Hartenberg, Stellenbosch	-			
05-0117	Jun-05	Hartenberg, Stellenbosch	NT			
05-0118		Hartenberg, Stellenbosch	-			
05-0119		Hartenberg, Stellenbosch	-			
05-0120		Hartenberg, Stellenbosch	-			
		Elsenberg, Stellenbosch Elsenberg, Stellenbosch	+	Candidatus phytoplasma solani 16rRNA gene, partial 16S-23S IGS and tRNA ^{iie} gene	98.51%	AJ964960
05-0123	Jun-05	Elsenberg, Stellenbosch	-			
05-0124	Jun-05	Elsenberg, Stellenbosch	+	NS		
05-0125	Jun-05	Elsenberg, Stellenbosch	-			
05-0126		Elsenberg, Stellenbosch	-	Candidatus phytoplasma solani 16rRNA gene, partial 16S-23S IGS and	00.000	
		Lievland, Stellenbosch		tRNA ^{ile} gene	99.22%	AJ964960
05-0128		Lievland, Stellenbosch	-			
05-0129		Plaisir de merle, Paarl	1	NS		
05-0130	Jun-05	Plaisir de merle, Paarl	-			



Accession number	Date collected	Location	PCR results	Sequencing results	Direct pairwise comparison	BLAST Accession number
05-0131	Jun-05	Plaisir de merle, Paarl	-			
05-0132	Jun-05	Plaisir de merle, Paarl	-			
05-0133	Jun-05	Zorgvliet, Stellenbosch	-			
05-0134	Jun-05	Blaauwklippen, Stellenbosch	-			
05-0135	Jun-05	Cloof Wine Estate, Darling	-			
05-0136	May-05	Vredendal	-			
05-0137	Aug-05	Location not known	+	NS		
05-0138	Aug-05	Location not known	+	NS		
05-0139	Aug-05	Location not known	+	NS		

* NT: Not tested, NS: Not sequenced



APPENDIX B

Pairwise comparisons of samples sequenced

Direct pairwise comparison of sample 05-0005 with Bacillus megaterium, isolate AC46b1 (Genbank accession no. AJ717381)

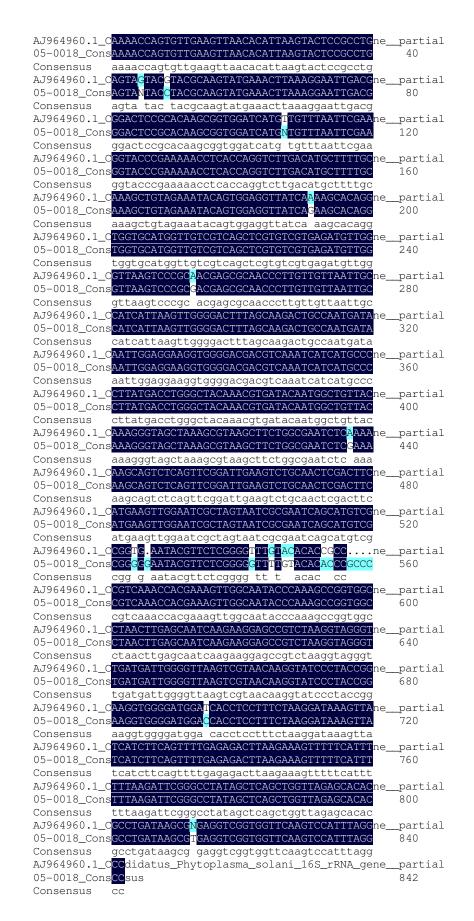
AJ717381.1_BAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGe_AC	46b1
05-0005_ConsAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAG	40
Consensus aacgatgagtgctaagtgttagagggtttccgccctttag	
AJ717381.1_BTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACe_AC	46b1
05-0005_ConsTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTAC	80
Consensus tgctgcagctaacgcattaagcactccgcctggggagtac	
AJ717381.1_BGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGe_AC	46b1
	120
Consensus ggtcgcaagactgaaactcaaaggaattgacgggggcccg	120
AJ717381.1_BCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGe_AC	1661
05-0005_ConsCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCG	160
Consensus cacaagcggtggagcatgtggtttaattcgaagcaacgcg	4 61 1
AJ717381.1_BAAGAACCTTACCAGGTCTTGACATCCTCTGACAACTCTAGe_AC	
	200
Consensus aagaaccttaccaggtcttgacatcctctgacaactctag	
AJ717381.1_BAGATAGAGCGTTCCCCTTCGGGGGACAGAGTGACAGGTGGe_AC	46b1
05-0005_Cons <mark>AGATAGAGCGTTCCCCTTCGGGGGACAGAGTGACAGGTGG</mark>	240
Consensus agatagagcgttccccttcggggggacagagtgacaggtgg	
AJ717381.1_BTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTe_AC	46b1
05-0005_ConsTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT	280
Consensus tgcatggttgtcgtcagctcgtgtcgtgagatgttgggtt	
AJ717381.1_BAAGTCCCGCAACGAGCGCAACCCTTGATCTTAGTTGCCAGe_AC	46b1
	320
Consensus aagtcccgcaacgagcgcaacccttgatcttagttgccag	
AJ717381.1_BCATTTAGTTGGGCACTCTAAGGTGACTGCCGGTGACAAACe_AC	46b1
	360
Consensus catttagttgggcactctaaggtgactgccggtgacaaac	500
AJ717381.1_BCGG.AGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTe_AC	1661
05-0005_ConsCGGGAGGAAGGTGGGGGATGACGTCAAATCATCATGCCCCT	4001
	400
Consensus cgg aggaaggtggggatgacgtcaaatcatcatgcccct	4 6 1- 1
AJ717381.1_BTATGACCTGGGCTACACACGTGCTACAATGGATGGTACAAe_AC	
05-0005_ConsTATGACCTGGGCTACACACGTGCTACAATGGATGGTACAA	440
Consensus tatgacctgggctacacacgtgctacaatggatggtacaa	
AJ717381.1_BAGGGCTGCAAGACCGCGAGGTCAAGCCAATCCCATAAAAACe_AC	
05-0005_ConsAGGGCTGCAAGACCGCGAGGTCAAGCCAATCCCATAAAAC	480
Consensus agggctgcaagaccgcgaggtcaagccaatcccataaaac	
AJ717381.1_BCATTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGe_AC	
05-0005_ConsCATTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATG	520
Consensus cattetcagtteggattgtaggetgeaactegeetacatg	
AJ717381.1_BAAGCTGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGe_AC	46b1
05-0005_ConsAAGCTGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGG	560
Consensus aagctggaatcgctagtaatcgcggatcagcatgccgcgg	
AJ717381.1_BTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACe_AC	46b1
05-0005_ConsTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACAC	600
Consensus tgaatacgttcccgggccttgtacacaccgcccgtcacac	
AJ717381.1_BCACGAGAGTTTGTAACACCCGAAGTCGGTGGAGTAACCGTe_AC	46b1
	640
Consensus cacqaqaqtttqtaacacccqaaqtcqqtqqaqtaaccqt	010
AJ717381.1_BAAGGAGCTAGCCGCCTAAGGTGGGACAGATGATTGGGGTGe_AC	46b1
	680
Consensus aaggagctagccgcctaaggtgggacagatgattggggtg	000
AJ717381.1_BAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGGCTGGAe_AC	16h1
	720
05-0005_consAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGA	120
Consensus aagtegtaacaaggtagcegtateggaaggtgeggetgga	4 6 1 1
AJ717381.1_BTCACCTCCTegaterium_16S_rRNA_geneisolate_AC	
05-0005_Cons <mark>TCACCTCCT</mark>	729
Consensus tcacctcct	



Direct pairwise comparison of sample 05-0014 with Candidatus Phytoplasma solani (Genbank accession no. AJ964960)

AJ964960.1_CCCCTGGTAGTCCACGCCCTAAACGATGAGTACTAAACGTTne 05-0014_ConsCCCTGGTAGTCCACGCCCTAAACGATGAGTACTAAACGTT	partial 40
Consensus ccctggtagtccacgccctaaacgatgagtactaaacgtt AJ964960.1_CGGATAAAACCAGTGTTGAAGTTAACACATTAAGTACTCCGne	partial
05-0014_ConsGGATAAAACCAGTGTTGAAGTTAACACATTAAGTACTCCG Consensus ggataaaaccagtgttgaagttaacacattaagtactccg	80
AJ964960.1_CCTGAGTAGTACGTACGTAGGAACTTAAAGGAATT 05-0014_ConsCCTGAGTAGTACGTACGCAAGTATGAAACTTAAAGGAATT	partial 120
Consensus cctgagtagtacgtacgcaagtatgaaacttaaaggaatt AJ964960.1_CGACGGGACTCCGCACAAGCGGTGGATCATGTTGTTTAATTne	partial
05-0014_ConsGACGGGACTCCGCACAAGCGGTGGATCATGTTGTTTAATT Consensus gacgggactccgcacaagcggtggatcatgttgtttaatt	
AJ964960.1_CCGAAGGTACCCGAAAAACCTCACCAGGTCTTGACATGCTT 05-0014_ConsCGAAGGTACCCGAAAAACCTCACCAGGTCTTGACATGCTT	partial 200
Consensus cgaaggtacccgaaaaacctcaccaggtcttgacatgctt AJ964960.1_CTTCCAAAGCTGTAGAAATACAGTCGAGGTTATCAAAAGCAne	partial
05-0014_Cons <mark>TTGCAAAGCTGTAGAAATACAGTGGAGGTTATCACAAGCA</mark> Consensus ttgcaaagctgtagaaatacagtggaggttatca aagca	240
AJ964960.1_CCAGGTGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTG	partial 280
Consensus caggtggtgcatggttgtcgtcagctcgtgtcgtgagatg AJ964960.1 CITGGGTTAAGTCCCCCAACGAGCGCAACCCTTGTTGTTAAne	partial
05-0014_ConsTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTTGTTAA Consensus ttgggttaagtcccgcaacgagcgcaacccttgttgttaa	320
AJ964960.1_CTTGCCATCATTAAGTTGGGGACTTTAGCAAGACTGCCAAT 05-0014_ConsTTGCCATCATTAAGTTGGGGACTTTAGCAAGACTGCCAAT	partial 360
Consensus ttgccatcattaagttggggactttagcaagactgccaat AJ964960.1_CGATAAATTGGAGG.AAGGTGGGGACGACGTCAAATCATCAhe	partial
05-0014_ConsGATAAATTGGAGGCAAGGTGGGGACGACGTCAAATCATCA Consensus gataaattggagg aaggtggggacgacgtcaaatcatca	400
AJ964960.1_CIGCCCCTTATGACCTGGGCTACAACGTGATACAATGGCTne 05-0014_ConsIGCCCCTTATGACCTGGGCTACAAACGTGATACAATGGCT	partial 440
Consensus tgccccttatgacctgggctacaaacgtgatacaatggct AJ964960.1 CGTTACAAAGGGTACCTAAAGCGTAAGCCTTCTGGCCAATCTne	partial
05-0014_ConsGTTACAAAGGGTAGCTAAAGCGTAAGCCTTCTGGCGAATCT Consensus gttacaaagggtagctaaagcgtaagcttctggcgaatct	480
AJ964960.1_CCAAAAAAGCAGTCTCAGTTCGGATTGAAGTCTGCAACTCGne 05-0014_ConsCAAAAAAGCAGTCTCAGTTCGGATTGAAGTCTGCAACTCG	partial 520
Consensus caaaaaagcagtctcagttcggattgaagtctgcaactcg AJ964960.1_CACTTCATGAAGTTGGAATCGCTAGTAATCGCGAATCAGCAne	partial
05-0014_ConsACTTCATGAAGTTGGAATCGCTAGTAATCGCGAATCAGCA Consensus acttcatgaagttggaatcgctagtaatcgcgaatcagca	560
AJ964960.1_CTGTCGCGGTGAATACGTTCTCGGGGTTTGTACACACCGCCne 05-0014_ConsTGTCGCGGTGAATACGTTCTCGGGGTTTGTACACACCGCC	partial 600
Consensus tgtcgcggtgaatacgttctcggggtttgtacacaccgcc AJ964960.1_CCGTCAAACCACGAAAGTTGGCAATACCCAAAGCCGGT <mark>CGC</mark> ne	partial
05-0014_Cons <mark>CGTCAAACCACGAAAGTTGGCAATACCCAAAGCCGC</mark> GNC Consensus cgtcaaaccacgaaagttggcaatacccaaagccgg g c	640
AJ964960.1_CCTAACTTGAGCAATCAAGAAGGAGCCGTCTAAGGTAGGGTne 05-0014_ConsTAAACTTGAGCAATCAAGAAGGAGCCGTCTAAGGTAGGGT	partial 680
Consensus aacttgagcaatcaagaaggagccgtctaaggtagggt AJ964960.1_C <mark>TGATGATTGGGGTTAAGTCGTAACAAGGTATCCCTACCGG</mark> ne	partial
05-0014_Cons Consensus tgatgattggggttaagtcgtaacaaggtatccctaccgg	720
AJ964960.1_CAAGGTGGGGATGGATCACCTCCTTTCTAAGGATAAAGTTAne 05-0014_ConsAAGGTGGGGATGGATCACCTCCTTTCTAAGGATAAAGTTA	partial 760
Consensus aaggtgggggtggatcacctcctttctaaggataaagtta AJ964960.1_C <mark>TCATCTTCAGTTTTGAGAGAGCTTAAGAAAGTTTTTCATTT</mark> ne	partial
05-0014_Cons TCATCTTCAGTTTTGAGAGAGACTTAAGAAAGTTTTTCATTT Consensus tcatcttcagttttgagagacttaagaaagtttttcattt	800
AJ964960.1_CTTTAAGATTCGGGCCTATAGCTCAGCTGGTTAGAGCACAChe 05-0014_ConsTTTAAGATTCGGGCCTATAGCTCAGCTGGTTAGAGCACAC	partial 840
Consensus tttaagattcgggcctatagctcagctggttagagcacac AJ964960.1_CGCCTGATAAGCCNGAGGTCGGTGGTTCAAGTCCATTTAGGne 05-0014_ConsGCCTGATAAGCGTGAGGTCGGTGGTTCAAGTCCATTTAGG	partial 880
Consensus gcctgataagcg gaggtcggtggttcaagtccatttagg AJ964960.1_CCCCACCAAAATAGGTCACATCTTAAAni_16S_rRNA_gene	
05-0014_ConsCCCACCAAAATAGGTCACATCTAAAA Consensus cccaccaaaataggtcacatct aaa	906





Direct pairwise comparison of sample 05-0018 with Candidatus Phytoplasma solani (Genbank accession no. AJ964960)



Direct pairwise comparison of sample 05-0033 with Flavescence doree phytoplasma strain 1487 (Genbank accession no. AJ548787)

AJ548787.2_FTTAAGTACTCCGCCTGAGTAGTAG	
	CGTACGCAAGTATGAAA_rRNA_gene_a
05-0033FD_TTAAGTACTCCGCCTGAGTAGTAG	CGTACGCAAGTATGAAA 40
Consensus ttaagtactccgcctgagtagtag	cgtacgcaagtatgaaa
AJ548787.2_FCTTAAAGGAATTGACGGGACTCC	GCACAAGCGGTGGATCA_rRNA_gene_a
05-0033FD_CTTAAAGGAATTGACGGGACTCC	GCACAAGCGGTGGATCA 80
Consensus cttaaaggaattgacgggactcco	
AJ548787.2_FTGTTGTTTAATTCGAAGATACACO	
05–0033 FD TGTTGTTTAATTCGAAGATACACO	
Consensus tgttgtttaattcgaagatacaco	
AJ548787.2_FCTTGACATACTCTGCAAAGCTATA	
05-0033FD_CTTGACATACTCTGCAAAGCTATA	
Consensus cttgacatactctgcaaagctata	
AJ548787.2_FTATCAGGGATACAGGTGGTGCAT	
05-0033FD_TATCAGGGATACAGGTGGTGCAT	GGTTGTCGTCAGTTCGT 200
Consensus tatcagggatacaggtggtgcate	ggttgtcgtcagttcgt
AJ548787.2_FGTCGTGAGATGTTAGGTTAAGTCC	CTAAAACGAACGCAACC_rRNA_gene_a
05-0033FD_GTCGTGAGATGTTAGGTTAAGTC	CTAAAACGAACGCAACC 240
Consensus gtcgtgagatgttaggttaagtco	ctaaaacgaacgcaacc
AJ548787.2_FCCTGTCGCTAGTTGCCAGCACGTA	AATGGTGGGGGACTTTAG_rRNA_gene_a
05-0033FD_CCTGTCGCTAGTTGCCAGCACGTA	AATGGTGGGGGACTTTAG 280
Consensus cctgtcgctagttgccagcacgta	
AJ548787.2_FCGAGACTGCCAATTAAACATTGG	
05-0033FD_CGAGACTGCCAATTAAACATTGGA	
Consensus cgagactgccaattaaacattgga	
AJ548787.2_FGTCAAATCATCATGCCCCTTATGA	
05-0033FD_GTCAAATCATCATGCCCCTTATGA	
Consensus gtcaaatcatcatgccccttatga	
AJ548787.2_FGATACAATGGCTATTACAAAGAG	
05-0033FD_GATACAATGGCTATTACAAAGAG	
Consensus gatacaatggctattacaaagagt	
AJ548787.2_FTTTAGCCAATCTCAAAAAGGTAG	ICTCAGTACGGATTGAA_rRNA_gene_a
05-0033FD_TTTAGCCAATCTCAAAAAGGTAG	ICTCAGTACGGATTGAA 440
Consensus tttagccaatctcaaaaaggtagt	ctcagtacggattgaa
AJ548787.2_FGTCTGCAACTCGACTTCATGAAG	CTGG.AATCGCTAGTAA_rRNA_gene_a
05-0033FD_GTCTGCAACTCGACTTCATGAAG	CTGG <mark>G</mark> AATCGCTAGTAA 480
Consensus gtctgcaactcgacttcatgaago	
AJ548787.2_FTCGCGAATCAGCATGTCGCGGTGA	
05-0033 FD TCGCGAATCAGCATGTCGCGGTGA	
	AATACCTICCCCCCCCTIC 520
Consensus tcgcgaatcagcatgtcgcggtga	aatacgttctcggggtt
Consensus tcgcgaatcagcatgtcgcggtga AJ548787.2_F <mark>TGTACACACCGCCCGTCAAACCA</mark>	aatacgttctcgggggtt C <mark>GAAAGTTAGCAATACC</mark> _rRNA_gene_a
Consensus tcgcgaatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCA 05-0033FD_TGTACACACCGCCCGTCAAACCA	aatacgttctcggggtt CGAAAGTTAGCAATACC_rRNA_gene_a CGAAAGTTAGCAATACC 560
Consensus tcgcgatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCA 05-0033FD_TGTACACACCGCCCGTCAAACCA Consensus tgtacacaccgcccgtcaaacca	aatacgttctcggggtt CGAAAGTTAGCAATACC_rRNA_gene_a CGAAAGTTAGCAATACC 560 cgaaagttagcaatacc
Consensus tcgcgaatcagcatgtcgcggtga AJ548787.2_FTGTACACACCCCCGTCAAACCA 05-0033FD_TGTACACACCGCCCGTCAAACCA Consensus tgtacacaccgcccgtcaaacca AJ548787.2_FCGAAAGCAGTGGCTTAACTTCGAA	aatacgttctcggggtt CGAAAGTTAGCAATACC_rRNA_gene_a CGAAAGTTAGCAATACC 560 cgaaagttagcaatacc AAGAAGAGGGAGCTGTC_rRNA_gene_a
Consensus tcgcgaatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCA 05-0033FD_TGTACACACCGCCCGTCAAACCA Consensus tgtacacaccgcccgtcaaacca AJ548787.2_FCGAAAGCAGTGGCTTAACTTCGA 05-0033FD_CGAAAGCAGTGGCTTAACTTCGA	aatacgttctcggggtt CGAAAGTTAGCAATACC_rRNA_gene_a CGAAAGTTAGCAATACC 560 cgaaagttagcaatacc AAGAAGAGGGAGCTGTC_rRNA_gene_a AAGAAGAGGGAGCTGTC 600
Consensus tcgcgatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCAC 05-0033_FD_TGTACACACCGCCCGTCAAACCAC Consensus tgtacacaccgcccgtcaaaccac AJ548787.2_FCGAAAGCAGTGGCTTAACTTCGAA 05-0033_FD_CGAAAGCAGTGGCTTAACTTCGAA Consensus cgaaagcagtggcttaacttcgaa	aatacgttctcggggtt CGAAAGTTAGCAATACC_rRNA_gene_a CGAAAGTTAGCAATACC 560 cgaaagttagcaatacc AAGAAGAGGGAGCTGTC_rRNA_gene_a AAGAAGAGGGAGCTGTC 600 aagaagagggagctgtc
Consensus tcgcgatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCAC 05-0033_FD_TGTACACACCGCCCGTCAAACCAC Consensus tgtacacaccgcccgtcaaaccac AJ548787.2_FCGAAAGCAGTGGCTTAACTTCGAA 05-0033_FD_CGAAAGCAGTGGCTTAACTTCGAA Consensus cgaaagcagtggcttaacttcgaa AJ548787.2_FTAAGGTAGGGTTGATGATGGGGG	aatacgttctcggggtt CGAAAGTTAGCAATACC_rRNA_gene_a CGAAAGTTAGCAATACC 560 Cgaaagttagcaatacc AAGAAGAGGGAGCTGTC_rRNA_gene_a AAGAAGAGGGAGCTGTC 600 aagaagagggagctgtc TTAAGTCGTAACAAGGT_rRNA_gene_a
Consensus tcgcgatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCAC 05-0033_FD_TGTACACACCGCCCGTCAAACCAC Consensus tgtacacaccgcccgtcaaaccac AJ548787.2_FCGAAAGCAGTGGCTTAACTTCGAA 05-0033_FD_CGAAAGCAGTGGCTTAACTTCGAA Consensus cgaaagcagtggcttaacttcgaa AJ548787.2_FTAAGGTAGGGTTGATGATGGGGG 05-0033_FD_TAAGGTAGGGTTGATGATGGGGG	Aatacgttctcggggtt CCAAAGTTAGCAATACC_rRNA_gene_a CCAAAGTTAGCAATACC_560 Cgaaagttagcaatacc AAGAAGAGGGGAGCTGTC_rRNA_gene_a AAGAAGAGGGGAGCTGTC_600 Aagaagaggggggctgtc TTAAGTCGTAACAAGGT_rRNA_gene_a TTAAGTCGTAACAAGGT_640
Consensus tcgcgatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCAC 05-0033_FD_TGTACACACCGCCCGTCAAACCAC Consensus tgtacacaccgcccgtcaaaccac AJ548787.2_FCGAAAGCAGTGGCTTAACTTCGAA 05-0033_FD_CGAAAGCAGTGGCTTAACTTCGAA Consensus cgaaagcagtggcttaacttcgaa AJ548787.2_FTAAGGTAGGGTTGATGATGGGGG 05-0033_FD_TAAGGTAGGGTTGATGATGGGGG Consensus taaggtagggttgatgatggggg	Aatacgttctcggggtt CCAAAGTTAGCAATACC_rRNA_gene_a CCAAAGTTAGCAATACC_560 Cgaaagttagcaatacc AAGAAGAGGGAGCTGTC_rRNA_gene_a AAGAAGAGGGAGCTGTC_600 Aagaagaggggggctgtc TTAAGTCGTAACAAGGT_rRNA_gene_a TTAAGTCGTAACAAGGT_640 ctaagtcgtaacaaggt
Consensus tcgcgatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCAC 05-0033_FD_TGTACACACCGCCCGTCAAACCAC Consensus tgtacacaccgcccgtcaaaccac AJ548787.2_FCGAAAGCAGTGGCTTAACTTCGAA 05-0033_FD_CGAAAGCAGTGGCTTAACTTCGAA Consensus cgaaagcagtggcttaacttcgaa AJ548787.2_FTAAGGTAGGGTTGATGATGGGGG 05-0033_FD_TAAGGTAGGGTTGATGATGGGGG Consensus taaggtagggttgatgatggggg AJ548787.2_FATCCTTACCGGAAGGTGAGGAGGAG	Aatacgttctcggggtt CCAAAGTTAGCAATACC_rRNA_gene_a CCAAAGTTAGCAATACC_560 Cgaaagttagcaatacc AAGAAGAGGGGAGCTGTC_rRNA_gene_a AAGAAGAGGGGAGCTGTC_600 Aagaagaggggggctgtc TTAAGTCGTAACAAGGT_rRNA_gene_a TTAAGTCGTAACAAGGT_640 Ctaagtcgtaacaaggt GATCACCTCCTTTCTAA_rRNA_gene_a
Consensus tcgcgatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCAC 05-0033_FD_TGTACACACCGCCCGTCAAACCAC Consensus tgtacacaccgcccgtcaaaccac AJ548787.2_FCGAAAGCAGTGGCTTAACTTCGAA Consensus cgaagcagtggcttaacttcgaa AJ548787.2_FTAAGGTAGGGTGATGATGGGG 05-0033_FD_TAAGGTAGGGTGATGATGGGG Consensus taaggtaggttgatgattggggt AJ548787.2_FATCCTTACCCGAAGGTGAGGATGC 05-0033_FD_ATCCTTACCGGAAGGTGAGGATGC	aatacgttctcggggtt CGAAAGTTAGCAATACC_rRNA_gene_a CGAAAGTTAGCAATACC_S60 cgaaagttagcaatacc AAGAAGAGGGGAGCTGTC_rRNA_gene_a AAGAAGAGGGGAGCTGTC_600 aagaaggggggctgtc TTAAGTCGTAACAAGGT_rRNA_gene_a TTAAGTCGTAACAAGGT_rRNA_gene_a CAAGCGTCCTTTCTAA_rRNA_gene_a GATCACCTCCTTTCTAA_rRNA_gene_a
Consensus tcgcgatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCAC 05-0033_FD_TGTACACACCGCCCGTCAAACCAC Consensus tgtacacaccgcccgtcaaaccac AJ548787.2_FCGAAAGCAGTGGCTTAACTTCGAA 05-0033_FD_CGAAAGCAGTGGCTTAACTTCGAA Consensus cgaaagcagtggcttaacttcgaa AJ548787.2_FTAAGGTAGGGTTGATGATGGGGG 05-0033_FD_TAAGGTAGGGTTGATGATGGGGG Consensus taaggtagggttgatgatggggg AJ548787.2_FATCCTTACCGGAAGGTGAGGAGGAG	aatacgttctcggggtt CGAAAGTTAGCAATACC_rRNA_gene_a CGAAAGTTAGCAATACC Cgaaagttagcaatacc AAGAAGAGGGGAGCTGTC_rRNA_gene_a AAGAAGAGGGGAGCTGTC TAAGTCGTAACAAGGT_rRNA_gene_a TTAAGTCGTAACAAGGT_rRNA_gene_a CTAAGTCGTAACAAGGT CTAAGTCGTAACAAGGT CTAAGTCGTAACAAGGT CTAAGTCGTAACAAGGT CTAAGTCGTAACAAGGT CACCTCCTTTCTAA_rRNA_gene_a GATCACCTCCTTTCTAA_680
Consensus tcgcgatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCAC 05-0033_FD_TGTACACACCGCCCGTCAAACCAC Consensus tgtacacaccgcccgtcaaaccac AJ548787.2_FCGAAAGCAGTGGCTTAACTTCGAA Consensus cgaagcagtggcttaacttcgaa AJ548787.2_FTAAGGTAGGGTGATGATGGGG 05-0033_FD_TAAGGTAGGGTGATGATGGGG Consensus taaggtaggttgatgattggggt AJ548787.2_FATCCTTACCCGAAGGTGAGGATGC 05-0033_FD_ATCCTTACCGGAAGGTGAGGATGC	aatacgttctcggggtt CGAAAGTTAGCAATACC_rRNA_gene_a CGAAAGTTAGCAATACC Cgaaagttagcaatacc AAGAAGAGGGGAGCTGTC_rRNA_gene_a AAGAAGAGGGGAGCTGTC TTAAGTCGTAACAAGGT_rRNA_gene_a TTAAGTCGTAACAAGGT_rRNA_gene_a CTAAGTCGTAACAAGGT_RNA_gene_a SATCACCTCCTTTCTAA_rRNA_gene_a GATCACCTCCTTTCTAA_680 gatcacctcctttctaa
Consensus tcgcgatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCAC 05-0033_FD_TGTACACACCGCCCGTCAAACCAC Consensus tgtacacaccgcccgtcaaaccac AJ548787.2_FCGAAAGCAGTGGCTTAACTTCGAA 05-0033_FD_CGAAAGCAGTGGCTTAACTTCGAA Consensus cgaaagcagtggcttaacttcgaa AJ548787.2_FTAAGGTAGGGTGATGATGGGGG 05-0033_FD_TAAGGTAGGGTGATGATGGGGG Consensus taaggtaggttgatgatgatgggg AJ548787.2_FATCCTTACCCGAAGGTGAGGATGC 05-0033_FD_ATCCTTACCGGAAGGTGAGGATGG Consensus atccttaccggaaggtgaggatgg	aatacgttctcggggtt CGAAAGTTAGCAATACC_rRNA_gene_a CGAAAGTTAGCAATACC_S60 Cgaaagttagcaatacc AAGAAGAGGGGAGCTGTC_rRNA_gene_a AAGAAGAGGGGAGCTGTC_600 aagaagagggggctgtc TTAAGTCGTAACAAGGT_rRNA_gene_a GATCACCTCCTTTCTAA_rRNA_gene_a GATCACCTCCTTTCTAA_rRNA_gene_a GATCACCTCCTTTCTAA_R80 gatcacctcctttctaa TCTCAGTTTTGAAAGA_rRNA_gene_a
Consensus tcgcgatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCAC 05-0033_FD_TGTACACACCGCCCGTCAAACCAC Consensus tgtacacaccgcccgtcaaaccac AJ548787.2_FCGAAAGCAGTGGCTTAACTTCGAA 05-0033_FD_CGAAAGCAGTGGCTTAACTTCGAA Consensus cgaaagcagtggcttaacttcgaa AJ548787.2_FTAAGGTAGGGTGATGATGGTGG 05-0033_FD_TAAGGTAGGGTGATGATGGGGG Consensus taaggtaggttgatgatggggt AJ548787.2_FATCCTTACCGAAAGGTGAGGATGG 05-0033_FD_ATCCTTACCGAAAGGTGAGGATGC Consensus atccttaccggaaggtgaggatgg AJ548787.2_FGGACATACATATAAAAATCATCA	aatacgttctcggggtt CGAAAGTTAGCAATACC_rRNA_gene_a CGAAAGTTAGCAATACC CGAAAGTTAGCAATACC CGAAAGTTAGCAATACC CGAAAGTTAGCAATACC CGAAAGAGGGGAGCTGTC_rRNA_gene_a AAGAAGAGGGGAGCTGTC TAAGTCGTAACAAGGT_rRNA_gene_a TTAAGTCGTAACAAGGT_rRNA_gene_a GATCACCTCCTTTCTAA_rRNA_gene_a GATCACCTCCTTTCTAA_rRNA_gene_a GATCACCTCCTTTCTAA_rRNA_gene_a CTTCAGGTTTTGAAAGA_rRNA_gene_a TCTTCAGTTTTGAAAGA_rRNA_gene_a
Consensus tcgcgatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCAC 05-0033_FD_TGTACACACCGCCCGTCAAACCAC Consensus tgtacacaccgcccgtcaaaccac AJ548787.2_FCGAAAGCAGTGGCTTAACTTCGAA 05-0033_FD_CGAAAGCAGTGGCTTAACTTCGAA Consensus cgaaagcagtggcttaacttcgaa AJ548787.2_FTAAGGTAGGGTGATGATGGTGGGG Consensus taaggtagggttgatggtgggt AJ548787.2_FATCCTTACCGGAAGGTGAGGATGG 05-0033_FD_ATCCTTACCGGAAGGTGAGGATGG 05-0033_FD_ATCCTTACCGGAAGGTGAGGATGG Consensus atccttaccgaaggtgaggtgg AJ548787.2_FGGACATACATATAAAAATCATCA 05-0033_FD_GGACATACATATAAAAATCATCA 05-0033_FD_GGACATACATATAAAAATCATCA	aatacgttctcggggtt CGAAAGTTAGCAATACC_rRNA_gene_a CGAAAGTTAGCAATACC CGAAAGTTAGCAATACC CGAAAGTTAGCAATACC CGAAAGTTAGCAATACC CGAAAGAGGGGAGCTGTC_rRNA_gene_a AAGAAGAGGGGAGCTGTC CTTAAGTCGTAACAAGGT_rRNA_gene_a GATCACCTCCTTTCTAA_rRNA_gene_a GATCACCTCCTTTCTAA_rRNA_gene_a GATCACCTCCTTTCTAA_rRNA_gene_a CTTCAGTTTTGAAAGA_rRNA_gene_a ICTTCAGTTTTGAAAGA_rRNA_gene_a ICTTCAGTTTTGAAAGA_720 Ccttcagttttgaaaga
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Consensus tcgcgatcagcatgtcgcggtga AJ548787.2_FTGTACACACCGCCCGTCAAACCAC O5-0033_FD_TGTACACACCGCCCGTCAAACCAC Consensus tgtacacaccgccgtcaaaccaa AJ548787.2_FCGAAAGCAGTGGCTTAACTTCGAA O5-0033_FD_CGAAAGCAGTGGCTTAACTTCGAA Consensus cgaaagcagtggcttaacttcgaa AJ548787.2_FTAAGGTAGGGTGATGATGGTGGGG Consensus taaggtagggttgatggtggg AJ548787.2_FATCCTTACCGGAAGGTGAGGAGGAG O5-0033_FD_ATCCTTACCGGAAGGTGAGGAGGAG Consensus atccttaccgaaggtgaggtgg AJ548787.2_FGGACATACATATAAAAATCATCA 05-0033_FD_GGACATACATATAAAAATCATCA Consensus ggacatacatataaaaatcatcaa AJ548787.2_FCTTAGGTTAAATATAAGTTTTT O5-0033_FD_CTTAGGTTAAAATATAAGTTTTT Consensus cttaggttaaaatatagtttttc AJ548787.2_FGTTCTCTTATATAAAAGACCAAA 05-0033_FD_GTTCTCTTATATAAAAGACCAAA Consensus gttctcttatataaagaccaaa AJ548787.2_FTGGTTAGGCCACCGCTGATAAC Consensus tggttagagcacgcctgataaa AJ548787.2_FTGGTTAGGCCACCGCTGATAAC	Aatacgttctcggggtt CGAAAGTTAGCAATACC rRNA_gene_a CGAAAGTTAGCAATACC 560 Cgaaagttagcaatacc AAGAAGAGGGGGGCTGTC rRNA_gene_a AAGAAGAGGGGAGCTGTC 600 aagaagaggggagctgtc TTAAGTCGTAACAAGGT rRNA_gene_a GTTAAGTCGTAACAAGGT rRNA_gene_a SATCACCTCCTTTCTAA rRNA_gene_a CTTTCAGTTTTGAAAGA rRNA_gene_a CTTTCAGTTTTGAAAGA rRNA_gene_a CTTTCTAGTTTTGAAAGA 720 Ccttcagttttgaaaga CTTTTTATAAAAAAAGT rRNA_gene_a CTTTTTATAAAAAAAGT rRNA_gene_a CTTTTTATAAAAAAAGT rRNA_gene_a CTTTTTATAAAAAAAGT rRNA_gene_a CCTTCAGGTTTGGAAGCA rRNA_gene_a CTTTTTATAAAAAAAGT rRNA_gene_a CTTTTTATAAAAAAAGT rRNA_gene_a CGGCGAGGTCGGTGGTT rRNA_gene_a GGGTGAGGTCGGTGGTT rRNA_gene_a GGGTGAGGTCGGTGGTT rRNA_gene_a GGGTGAGGTCGGTGGTT rRNA_gene_a GGGTGAGGTCGGTGGTT rRNA_gene_a TTTATATCAGGAAAATA rRNA_gene_a TTTATATCAGGAAAATA rRNA_gene_a TTTATATCAGGAAAATA 880
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tus Phytoplasma	
r Candida	
with	
Direct pairwise comparison of sample 05-0033 with Candidatus Phytoplasm solani (Genbank accession no. AJ964960)	
pairwise (Genbanl	
Direct solani	

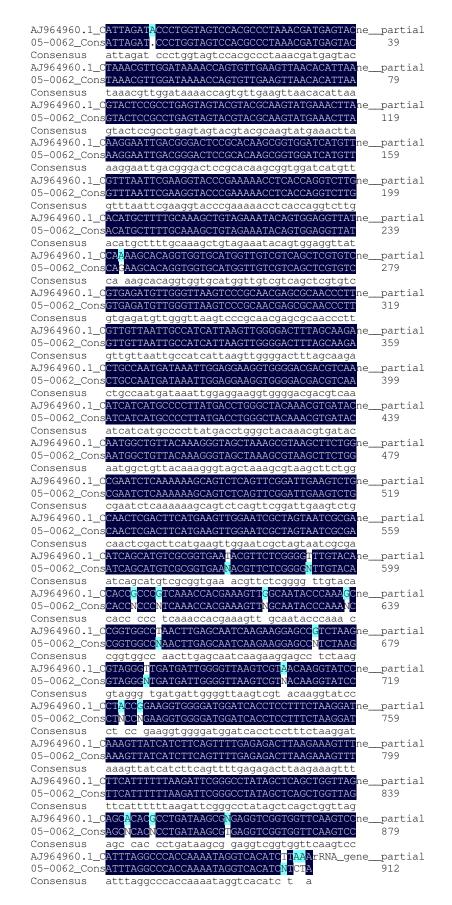
	ACAGGATTAGAT <mark>A</mark> CCCTGGTAGTCCACGCCCTAAACGAThe_ ACAGGATTAGAT.CCCTGGTAGTCCACGCCCTAAACGAT	_partial 39
Consensus aa	acaggattagat ccctggtagtccacgccctaaacgat AGTACTAAACGTTGGATAAAACCAG <mark>TGTTGAAGTTAAC</mark> ne_	_partial
05-0033sto <mark>G</mark>	AGTACTAAACGTTGGATAAAACCAG <mark>G</mark> TGTTGAAGTTAAC agtactaaacgttggataaaaccag tgttgaagttaac	79
AJ964960.1_CAC	CATTAAGTACTCCGCCTGAGTAGTACGTACGCAAGTATGne_ CATTAAGTACTCCGCCTGAGTAGTACGTACGCAAGTATG	_partial 119
Consensus ac	cattaagtactccgcctgagtagtacgtacgcaagtatg AACTTAAAGGAATTGACGGGACTCCCCACAAGCGGTGGAne	partial
05-0033stoA	AACTTAAAGGAATTGACGGGACTCCGCACAAGCGGTGGA aacttaaaqqaattqacqqqactccqcacaaqcqqtqa	parerar 159
AJ964960.1_C <mark>T</mark>	CATGTTGTTTAATTCGAAGGTACCCGAAAAACCTCACCA CATGTTGTTTAATTCGAAGGTACCCGAAAAACCTCACCA	_partial 199
Consensus to	catgttgtttaattcgaaggtacccgaaaaacctcacca GTCTTGACATGCTTTTGCAAAGCTGTAGAAATACAGTGGne	_partial
05-0033stoG	GTCTTGACATGCTTTTGCAAAGCTGTAGAAATACAGTGG gtcttgacatgcttttgcaaagctgtagaaatacagtgg	239
AJ964960.1_CAC	GGTTATCAAAAGCACAGGTGGTGGTGGTGGTCGTCGTCAGCne_ GGTTATCAAAAGCACAGGTGGTGGTGGTGGTGGTCGTCAGC	_partial 279
Consensus ac	Ggttatca aagcacaggtggtgcatggttgtcgtcggc CGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCne	_partial
05-0033sto <mark>T</mark>	CGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGC cgtgtcqtqaqatgttgqqttaagtcccqcaacqaqcqc	parerar 319
AJ964960.1_C <mark>A</mark>	ACCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTne_ ACCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTT	_partial 359
Consensus aa	acccttgttgttaattgccatcattaagttggggacttt GCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGGACGne	partial
05-0033sto <mark>A</mark> 0	GCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGGACG gcaagactgccaatgataaattggaggaaggtggggaag	parerar 399
AJ964960.1_C <mark>AC</mark>	CGTCAAATCATCATCATGCCCCTTATGACCTGGGCTACAAAOne_ CGTCAAATCATCATGCCCCCTTATGACCTGGGCTACAAAC	_partial 439
Consensus ad	cgtcaaatcatcatgccccttatgacctgggctacaaac TGATACAATGGCTGTTACAAAGGGTAGCTAAAGCGTAAGne_	_partial
05-0033sto <mark>G</mark>	TGATACAATGGCTGTTACAAAGGGTAGCTAAAGCGTAAG tgatacaatggctgttacaaagggtagctaaagcgtaag	parerar 479
	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG	_partial 519
05-0033sto <mark>C</mark> Consensus ct	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG ttctggcgaatctcaaaaaagcagtctcagttcggattg	519
05-0033stoC Consensus ct AJ964960.1_CA 05-0033stoA	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG ttctggcgaatctcaaaaaagcagtctcagttcggattg AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA	
05-0033stoC Consensus ct AJ964960.1_CA 05-0033stoA Consensus aa AJ964960.1_CA	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG ttctggcgaatctcaaaaaagcagtctcagttcggattg AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA ne_ AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA agtctgcaactcgacttcatgaagttggaatcgctagta TCGCGAATCAGCATGTCGCGGGTGAATACGTTCTCGGGGTne_	519 _partial 559 _partial
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05-0033sto Consensus ct AJ964960.1_CA 05-0033_sto AJ964960.1_CA 05-0033_sto Consensus at AJ964960.1_CT 05-0033_sto	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG ttctggcgaatctcaaaaaagcagtctcagttcggattg AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA agtctgcaactcgacttcatgaagttggaatcgctagta TCGCGAATCAGCATGTCGCGGGTGAATACGTTCTCGGGGT tcgcgaatcagcatgtcgcggtgaatacgttctcggggt TGTACACACCGCCCGTCAAACCACGAAAGTTGGCAATAC mgTACACACCGCCCGTCAAACCACGAAAGTTGGCAATAC	519 _partial 559 _partial
05-0033sto Consensus ct AJ964960.1_CA 05-0033_sto AJ964960.1_CA 05-0033_sto Consensus at AJ964960.1_CT 05-0033sto Consensus tt AJ964960.1_C	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG ttctggcgaatctcaaaaaagcagtctcagttcggattg AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA agtctgcaactcgacttcatgaagttggaatcgctagta TCGCGAATCAGCATGTCGCGGTGAATACGTTCTCGGGGT ne_ TCGCGAATCAGCATGTCGCGGTGAATACGTTCTCGGGGT tcgcgaatcagcatgtcgcggtgaatacgttctcggggt TGTACACACCGCCCGTCAAACCACGAAGTTGGCAATAC tgtacacaccgcccgtcaaaccacgaaagttggcaatac tgtacacaccgcCGTAACTTGAGCAATCAAGAAGGAGCCne_	519 _partial 559 _partial 599 _partial 639 _partial
05-0033sto Consensus ct AJ964960.1_CA 05-0033_sto AJ964960.1_CA 05-0033_sto Consensus at AJ964960.1_CT 05-0033_sto Consensus tt AJ964960.1_CC 05-0033_sto Consensus ct	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG ttctggcgaatctcaaaaaagcagtctcagttcggattg AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA agtctgcaactcgacttcatgaagttggaatcgctagta TCGCGAATCAGCATGTCGCGGTGAATACGTTCTCGGGGT ne_ TCGCGAATCAGCATGTCGCGGTGAATACGTTCTCGGGGT tcgcgaatcagcatgtcgggggaatacgttctcggggt TGTACACACCGCCCGTCAAACCACGAAAGTTGGCAATAC tgtacaacacgccgtcaaaccacgaagttggcaatac CAAAGCCGGTGGCCTAACTTGAGCAATCAAGAAGGAGCC caaagccggtggcctaacttgggcaatcagaggagcc	519 _partial 559 _partial 639 _partial 639 _partial 679
05-0033sto Consensus ct AJ964960.1_CA 05-0033_sto Consensus aa AJ964960.1_CA Consensus at AJ964960.1_CA Consensus tt AJ964960.1_CC 05-0033_sto Consensus ct AJ964960.1_CC 05-0033_sto Consensus ct AJ964960.1_CC Consensus ct AJ964960.1_CC	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG ttctggcgaatctcaaaaaagcagtctcagttcggattg AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA agtctgcaactcgacttcatgaagttggaatcgctagta TCGCGAATCAGCATGTCGCGGGTGAATACGTTCTCGGGGT ne_ TCGCGAATCAGCATGTCGCGGGTGAATACGTTCTCGGGGT tcgcgaatcagcatgtcgcggtgaatacgttctcggggt TGTACACACCGCCGTCAAACCACGAAAGTTGGCAATAC tgtacacaccgcccgtcaaaccacgaagttggcaatac CAAAGCCGGTGGCCTAACTTGAGCAATCAAGAAGGAGCC caaagccggtggcctaacttgagcaatcaagaaggagcc TCTAAGGTAGGGTTGATGATTGGGGTTAAGTCGTAACAA	519 _partial 559 _partial 599 _partial 639 _partial
05-0033stoC Consensus ct AJ964960.1_CA 05-0033_stoA Consensus az AJ964960.1_CA 05-0033_stoA Consensus at AJ964960.1_CT 05-0033_stoC Consensus cc AJ964960.1_CC Consensus cc AJ964960.1_CC 05-0033_stoC	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG ttctggcgaatctcaaaaaagcagtctcagttcggattg AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA agtctgcaactcgacttcatgaagttggaatcgctagta TCGCGAATCAGCATGTCGCGGGTGAATACGTTCTCGGGGTme_ TCGCGAATCAGCATGTCGCGGGTGAATACGTTCTCGGGGT tcgcgaatcagcatgtcgcggtgaatacgttctcggggt TGTACACACCGCCCGTCAAACCACGAAAGTTGGCAATAC TGTACACACCGCCGTCAAACCACGAAAGTTGGCAATAC tgtacacacgccgtcaaaccacgaaagttggcaatac CAAAGCCGGTGGCCTAACTTGAGCAATCAAGAAGGAGCC caaagccggtggctaactgacagagagcc TCTAAGGTAGGCTGATGATGGGTTAAGTCGTAACAA TCTAAGGTAGGTTGATGATTGGGGTTAAGTCGTAACAA tctaaggtaggttgatgattggggttaagtcgtaacaa GTATCCCTACCGGAAGGTGGGGGGATGGATCACCTCCTTTCne_	519 _partial 559 _partial 639 _partial 679 _partial
05-0033sto Consensus ct AJ964960.1_CA 05-0033_sto AJ964960.1_CA 05-0033_sto Consensus at AJ964960.1_CT 05-0033_sto Consensus ct AJ964960.1_CC 05-0033_sto Consensus cc AJ964960.1_CC Consensus cc AJ964960.1_CC Consensus cc AJ964960.1_CC Consensus cc AJ964960.1_CC Consensus cc Consensus cc AJ964960.1_CC Consensus cc Consensus cc AJ964960.1_CC Consensus cc AJ964960.1_CC CON Consensus cc AJ964960.1_CC CON Consensus cc AJ964960.1_CC CON CON CON CON CON CON CON CON CON C	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG ttctggcgaatctcaaaaaagcagtctcagttcggattg AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA agtctgcaactcgacttcatgaagttggaatcgctagta TCGCGAATCAGCATGTCGCGGGTGAATACGTTCTCGGGGT tcgcgaatcagcatgtcgcggtgaatacgttctcggggt TGTACACACCGCCCGTCAAACCACGAAAGTTGGCAATAC mgTacacaccgccgtcaaaccacgaaagttggcaatac CAAAGCCGGTGGCCTAACTTGAGCAATCAGAGAGGAGCC caaagccggtggcctaacttgagcaatac TCTAAGGTAGGCCTAACTTGAGCAATCAAGAAGGAGCC caaagccggtggcctaacttgagcaatac TCTAAGGTAGGCTTAATGATTGGGGTTAAGTCGTAACAA tctaaggtagggttgatgggttaagtcgtaacaa GTATCCCTACCGGAAGGTGGGGATGGATCACCTCTTTC gtatccctaccggaaggtgggtggatgatcacctcctttc	519 _partial 559 _partial 639 _partial 679 _partial 719 _partial 759
05-0033sto Consensus ct AJ964960.1_CA 05-0033_sto Consensus aa AJ964960.1_CA 05-0033_sto Consensus at AJ964960.1_CT 05-0033_sto Consensus ct AJ964960.1_CC 05-0033_sto Consensus gt AJ964960.1_CG 05-0033_sto Consensus gt AJ964960.1_CG 05-0033_sto Consensus gt AJ964960.1_CG 05-0033_sto Consensus gt AJ964960.1_CG 05-0033_sto Consensus gt AJ964960.1_CT 05-0033_sto Consensus gt	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG ttctggcgaatctcaaaaaagcagtctcagttcggattg AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA agtctgcaactcgacttcatgaagttggaatcgctagta TCGCGAATCAGCATGTCGCGGGTGAATACGTTCTCGGGGTme_ TCGCGAATCAGCATGTCGCGGGTGAATACGTTCTCGGGGT tcgcgaatcagcatgtcgcggtgaatacgttctcggggt TGTACACACCGCCCGTCAAACCACGAAAGTTGGCAATAC TGTACACACCGCCGTCAAACCACGAAAGTTGGCAATAC tgtacacacgccgtcaaaccacgaaagttggcaatac CAAAGCCGGTGGCCTAACTTGAGCAATCAAGAAGGAGCC caaagccggtggctaactagaagaggacc TCTAAGGTAGGCTTAATGGATTAGGTCTAAGAAGGAGCC caaagccggtggctaactgagagagcc TCTAAGGTAGGGTTGATGATTGGGGTTAAGTCGTAACAA tctaaggtaggttgatgattggggttaagtcgtaacaa GTATCCCTACCGGAAGGTGGGATGGATCACCTCCTTTC me_ GTATCCCTACCGGAAGGTGGGGATGGATCACCTCCTTTC	519 _partial 559 _partial 639 _partial 679 _partial 719 _partial
05-0033sto Consensus ct AJ964960.1_CA 05-0033_sto AJ964960.1_CA 05-0033_sto Consensus at AJ964960.1_CT 05-0033_sto Consensus ct AJ964960.1_CC 05-0033_sto Consensus ct AJ964960.1_CG 05-0033_sto Consensus ct AJ964960.1_CG 05-0033_sto Consensus ct AJ964960.1_CG 05-0033_sto Consensus ct AJ964960.1_CG Consensus ct AJ964960.1_CA Consensus ct AJ964960.1_CA	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG ttctggcgaatctcaaaaaagcagtctcagttcggattg AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA agtctgcaactcgacttcatgaagttggaatcgctagta TCGCGAATCAGCATGTCGCGGTGAATACGTTCTCGGGGT ne_ TCGCGAATCAGCATGTCGCGGTGAATACGTTCTCGGGGT tcgcgaatcagcatgtcgcggtgaatacgtctcggggt TGTACACACCGCCCGTCAAACCACGAAAGTTGGCAATAC tgtacacaccgcccgtcaaaccacgaaagttggcaatac CAAAGCCGGTGGCCTAACTTGAGCAATCAGAAGGAGCC caaagccggtggctaactgacaagaaggagcc TCTAAGGTAGGGTTGATGAGTTGGGAATACAA tctaaggtaggttgatgattgggataagagacca GTAAGCCGGCGGAGATTGGGGTTAAGTCGTAACAA tctaaggtaggttgatgattgggtaaaaca GTATCCCTACCGGAAGGTGGGGATAGGACCTCCTTTC gtatccctaccggaaggtgggatggatcacctcctttc AAGGATAAAGTTATCATCTTCAGTTTTGAGAGACTTAAG	519 _partial 559 _partial 639 _partial 679 _partial 719 _partial 759 _partial
05-0033stoC Consensus ct AJ964960.1_CA 05-0033_stoA Consensus aa AJ964960.1_CA Consensus at AJ964960.1_CA 05-0033_stoT Consensus ct AJ964960.1_CC 05-0033_stoC Consensus ct AJ964960.1_CC 05-0033_stoG Consensus gt AJ964960.1_CA Consensus ct AJ964960.1_CA Consensus ta AJ964960.1_CA Consensus ta AJ964960.1_CA Consensus ta AJ964960.1_CA Consensus ta AJ964960.1_CA Consensus ta AJ964960.1_CA Consensus ta AJ964960.1_CA	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG ttctggcgaatctcaaaaaagcagtctcagttcggattg AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA agtctgcaactcgacttcatgaagttggaatcgctagta TCGCGAATCAGCATGTCGCGGGGAATACGTTCTCGGGGT tcgcgaatcagcatgtcgcggtgaatacgttctcggggt TGTACACACCGCCGTCAAACCACGAAGTTGGCAATAC TGTACACCGCCGTCAAACCACGAAGTTGGCAATAC tgtacacaccgcccgtcaaaccacgaaagttggcaatac CAAAGCCGGTGGCCTAACTTGAGCAATCAAGAAGGAGCC caaagccggtggcctaacttgagcaatcagaaggagcc TCTAAGGTAGGGTTGATGATGGGGTTAAGTCGTAACAA tctaaggtagggttgatggtgggttaagtcgtaccaa GTATCCCTACCGGAAGGTGGGCTAAGTCGGAACCACGAAGCCG caaagccggtggcctaacttgagcaatcaagaaggagcc TCTAAGGTAGGGTTGATGATTGGGGTTAAGTCGTAACAA tctaaggtagggttgatggtgggttaagtcgtaccaa GTATCCCTACCGGAAGGTGGGGATGGATCACCTCCTTTC gtatccctaccggaaggtggggatggatcacctctttc AAGGATAAAGTTATCATCTTCAGTTTTGAGAGACTTAAG AAGGATAAAGTTATCATCTTCAGTTTTGAGAGACTTAAG aggataaagttatcatcttcagttttgagagacttaag AAGTTTTCATTTTTAAGATTCGGGCCTATAGCTCAGGne_	519 _partial 559 _partial 639 _partial 679 _partial 719 _partial 759 _partial 759 _partial 799 _partial
05-0033sto Consensus ct AJ964960.1_CA 05-0033_sto AJ964960.1_CA 05-0033_sto Consensus at AJ964960.1_CT 05-0033_sto Consensus ct AJ964960.1_CC 05-0033_sto Consensus ct AJ964960.1_CC 05-0033_sto Consensus gt AJ964960.1_CT 05-0033_sto Consensus ct AJ964960.1_CT 05-0033_sto Consensus ct AJ964960.1_CT 05-0033_sto Consensus ct AJ964960.1_CT Consensus ct AJ964960.1_CT Consensus ct AJ964960.1_CT Consensus ct AJ964960.1_CT Consensus ct AJ964960.1_CT Consensus ct AJ964960.1_CT Consensus ct AJ964960.1_CT Consensus ct AJ964960.1_CT Consensus ct AJ964960.1_CT Consensus ct AJ964960.1_CT	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG ttctggcgaatctcaaaaaagcagtctcagttcggattg AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA agtctgcaactcgacttcatgaagttggaatcgctagta TCGCGAATCAGCATGTCGCGGGTGAATACGTTCTCGGGGT tcgcgaatcagcatgtcgcggtgaatacgttctcggggt TGTACACACCGCCGTCAAACCACGAAGTTGGCAATAC tgtacaaccgcccgtcaaaccacgaagttggcaatac CAAAGCCGGTGGCCTAACTGAGCAATCAGAAGGAGCCC caaagccggtggctaactgaagtaggacc TCTAAGGTAGGGTTGATGATGGGGTTAAGTCGTAACAA tctaaggtagggttgatggttagggtaggaccaaa GTATCCCTACCGGAAGGTGGGGATAAGTCGTAACAA tctaaggtagggttgatggttaggtcaacaa GTATCCCTACCGGAAGGTGGGGATCACCTCCTTTC gtatccctaccggaaggtgggatgatcactcctttc AAGGTAAAGTTACAGTTCAGGGATCACCTCCTTTC gtatcctaccggaaggtgggtgatggatcactcata GTATCCCTACCGGAAGGTGGGGATGGATCACCTCCTTTC gtatcctaccggaaggtggggatggatcactcttc AAGGATAAAGTTATCATCTTCAGTTTTGAGGACTTAAG AAGGTAAAGTTATCATCTTCAGTTTTGAGAGACTTAAG AAGGTAAAGTTATCATCTTCAGTTTTGAGAGACTTAAG AAGGTATAAGTTACACTTCAGTTTTGAGAGACTTAAG AAGGTATAAGTTATCATCTTCAGTTTTGAGAGACTTAAG AAGGTATACATCTTCAGTTTTGAGAGACTTAAG AAGGTATATCATCTTCAGTTTGAGAGACTTAAG AAGGTATATCATCTTCAGTTTTGAGAGACTTAAG AAGGTATACATCTTCAGTTTTGAGAGACTTAAG AAGGTATATCATCTTCAGTTTTGAGAGACTTAAG AAGGTATATCATCTTCAGTTTTGAGAGACTTAAG AAGGTATACATCTTCAGTTTTGAGAGACTTAAG AAGGTATTCCATTTTTTAAGATTCGGCCCTATAGCTCACC AAGTTTTCCATTTTTTTTAAGATTCGGGCCTATAGCTCAGC AAGTTTTCCATTTTTTTTTAAGATTCGGGCCTATAGCTCAGC	519 _partial 559 _partial 639 _partial 679 _partial 719 _partial 759 _partial 799 _partial 799 _partial 839
05-0033sto Consensus ct AJ964960.1_CA 05-0033_sto Consensus as AJ964960.1_CA Consensus at AJ964960.1_CA Consensus ct AJ964960.1_CC Consensus ct AJ964960.1_CC Consensus ct AJ964960.1_CC Consensus ct AJ964960.1_CC Consensus ct AJ964960.1_CC Consensus ct AJ964960.1_CA Consensus ct AJ964960.1_CA Consensus ct AJ964960.1_CA Consensus ct AJ964960.1_CA Consensus ct AJ964960.1_CA Consensus ct AJ964960.1_CC Consensus ct AJ964960.1_CC Consensus ct AJ964960.1_CC Consensus ct AJ964960.1_CC Consensus ct AJ964960.1_CC Consensus ct AJ964960.1_CC	TTCTGGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTG ttctggcgaatctcaaaaaagcagtctcagttcggattg AGTCTGCAACTCGACTTCATGAAGTTGGAATCGCTAGTA agtctgcaactcgacttcatgaagttggaatcgctagta TCGCGAATCAGCATGTCGCGGGTGAATACGTTCTCGGGGT tcgcgaatcagcatgtcgcggtgaatacgttctcggggt TGTACACACCGCCGTCAAACCACGAAGTTGGCAATAC GTACACCGCCGTCAAACCACGAAGTTGGCAATAC tgtacacaccgcccgtcaaaccacgaagttggcaatac CAAAGCCGGTGGCCTAACTTGAGCAATCAAGAAGGAGCC caaagccggtggctaacttgaggagagcc TCTAAGGTAGGGTTGATGATGGGGTTAAGTCGTAACAA tctaaggtagggttgatggttgggttagtcgtacaca GTATCCCTACCGGAAGGTGGGGATCACCTCCTTTC gtatcctaccggaaggtggggatggatcactccttc AAGGTAAGGTTGATCATTGAGGATCACCTCCTTTC gtatcctaccggaaggtggggatggatcactcctcttc AAGGATAAAGTTACATCTCAGTTTTGAGGACTTAAG aggataaagttatcatcttcagttttgaggacttaag AAGGTTATCATTTTTAAGATTCGGCCTATAGCTCACGC aaggtagagatatcatctccagttttgaggacttaag AAGGTTACATCATCTTCAGTTTTGAGAGACTTAAG aggataaagttatcatcttcagttttgaggacttaag AAGTTTTCATTTTTAAGATTCGGCCTATAGCTCACCC aggttatcatttttaagattcgggcctatagctcagc GTTAGAGCACACGCCTGATAAGCC GAGGTCGGTGGCCTAACGTAACCA AGGGTAAAGTATCATCTTCAGTTTGAGAGACTTAAG AAGGTAAAGTATCATCTTCAGTTTGAGAGACTTAAG aggttaaagttatcatcttcagttttgaggacttaag AAGTTTTCATTTTTAAGATTCGGGCCTATAGCTCACCC aggttatcatttttaagattcgggcctatagctcagc GTTAGAGCACACGCCTGATAAGCC GAGGTCGGTGGTGATAAGCC GAGGTCGGTGGTTAAGCCCGGTGGTTNe_	519 _partial 559 _partial 639 _partial 679 _partial 719 _partial 759 _partial 799 _partial 839 _partial



Direct pairwise comparison of sample 05-0055 with uncultured bacterium clone 3 (Genbank accession no. DQ011250)

DQ011250.1_UCCCTGGTAGTCCACGCCGTAAACGATGAGTACTAGGTGTC1_RNA_gene_a	
05-0055_ConsCCCTGGTAGTCCACGCCGTAAACGATGAGTACTAGGTGTC 40 Consensus ccctggtagtccacgccgtaaacgatgagtactaggtgtc	
DQ011250.1_UGGGGGTTACCCCCCTCGGTGCCGCAGCTAACGCATTAAGT1_RNA_gene_a	
05-0055_ConsGGGGGTTACCCCCCTCGGTGCCGCAGCTAACGCATTAAGT 80 Consensus gggggttacccccctcggtgccgcagctaacgcattaagt	
DQ011250.1_UACTCCGCCTGGGAAGTACGCTCGCAAGAGTGAAACTCAAA1_RNA_gene_a	
05-0055_Cons <mark>ACTCCGCCTGGGAAGTACGCTCGCAAGAGTGAAACTCAAA</mark> 120	
Consensus actccgcctgggaagtacgctcgcaagagtgaaactcaaa DQ011250.1_UGGAATTGACGGGGACCCGCACAAGTAGCGGAGCATGTGGT1_RNA_gene_a	
05-0055_ConsGGAATTGACGGGGACCCGCACAAGTAGCGGAGCATGTGGT 160	
Consensus ggaattgacgggggacccgcacaagtagcggagcatgtggt DQ011250.1_UTTAATTCGAAGCAACGCGAAGAACCTTACCTAAGCTTGAC1_RNA_gene_a	
DQ011250.1_UTTAATTCGAAGCAACGCGAAGAACCTTACCTAAGCTTGACl_RNA_gene_a 05-0055_ConsTTAATTCGAAGCAACGCGAAGAACCTTACCTAAGCTTGAC 200	
Consensus ttaattcgaagcaacgcgaagaaccttacctaagcttgac	
DQ011250.1_UATCCCACTGACCTCTCCCTAATCGGAGATTTCCCTTCGGGG1_RNA_gene_a 05-0055 ConsATCCCATTGACCTCTCCCTAATCGGAGATTTCCCCTTNGGG 240	
05-0055_Cons <mark>ATCCCAT</mark> TGACCTCTCCCTAATCGGAGATTTCCCTTNGGG 240 Consensus atccca tgacctctccctaatcggagatttccctt ggg	
DQ011250.1_UGACAGTGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGT1_RNA_gene_a	
05-0055_ConsGACAGTGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGT 280 Consensus gacagtggtgacaggtggtgcatggttgtcgtcagctcgt	
DQ011250.1_UGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC1_RNA_gene_a	
05-0055_ConsGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC 320	
Consensus gtcgtgagatgttgggttaagtcccgcaacgagcgcaacc DQ011250.1_UCTTGCCTTTAGTTGCCAGCATTAAGTTGGGCACTCTAGAG1_RNA_gene_a	
05-0055_ConsCTTGCCTTTAGTTGCCAGCATTAAGTTGGGGCACTCTAGAGI_RNA_GENE_a	
Consensus cttgcctttagttgccagcattaagttgggcactctagag	
DQ011250.1_UGGACTGCCGAGGATAACTCGGAGGAGGAGGGGGGATGACGT1_RNA_gene_a 05-0055_ConsGGACTGCCGAGGATAACTCGGAGGAGGGGGGGGGGGGGG	
Consensus ggactgccgaggataactcggaggaaggtggggatgacgt	
DQ011250.1_UCAAATCATCATGCCCCTTATGCTTAGGGCTACACACGTGC1_RNA_gene_a	
05-0055_ConsCAAATCATCATGCCCCTTATGCTTAGGGCTACACGCGC 440 Consensus caaatcatgccccttatgcttagggctacacacgtgc	
DQ011250.1_UTACAATGGGTGGTACAGAGGGGTTGCCAAGCGCGGAGGTGG1_RNA_gene_a	
05-0055_Cons <mark>TACAATGGGTGGTACAGAGGGTTGCCAA</mark> ACCG <mark>TGAGGTGG</mark> 480	
Consensus tacaatgggtggtacagagggttgccaa ccg gaggtgg DQ011250.1_UAGCTAATCCCTTAAAGCCATTCTCAGTTCGGATTGTAGGC1_RNA_gene_a	
05-0055_ConsAGCTAATCCCTTAAAGCCATTCTCAGTTCGGATTGTAGGC 520	
Consensus agctaatcccttaaagccattctcagttcggattgtaggc	
DQ011250.1_UTGAAACTCGCCTACATGAAGCTGGAGTTACTAGTAATCGCl_RNA_gene_a 05-0055_ConsTGAAACTCGCCTACATGAAGCTGGAGTTACTAGTAATCGC 560	
Consensus tgaaactcgcctacatgaagctggagttactagtaatcgc	
DQ011250.1_UAGATCAGAATGCTGCGGTGAATGCGTTCCCGGGTCTTGTAl_RNA_gene_a	
05-0055_ConsAGATCAGAATGCTGCGGTGAATGCGTTCCCGGGTCTTGTA 600 Consensus agatcagaatgctgcggtgaatgcgttcccggggtcttgta	
DQ011250.1_UCACACCGCCCGTCACACCATGCAAGTTGGGGGGCGCCCGAA1_RNA_gene_a	
05-0055_Cons <mark>CACACCGCCCGTCACACCATGG</mark> CAGTTGGGGGCGCCCAAA 640 Consensus cacaccgcccgtcacaccatgg agttgggggggcgccc aa	
DQ011250.1_UGCCGGTTAGCTAACCTTTTAGGAAGCGGCCGTCGAAGGTG1_RNA_gene_a	
05-0055_Cons <mark>GCCGGTTAGCTAACCTTTTAGGAG</mark> GC <mark>AA</mark> CCGTCGAAGGTG 680	
Consensus gccggttagctaaccttttagga gc ccgtcgaaggtg DQ011250.1_UAAACCAATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAL_RNA_gene_a	
05-0055_ConsAAACCAATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTA 720	
Consensus aaaccaatgactggggtgaagtcgtaacaaggtagccgta	
DQ011250.1_UTCGGAAGGTGCGGCTGGATCACCTCCTTTCTAAGGAGTAAL_RNA_gene_a 05-0055_ConsTCGGAAGGTGCGGCTGGATCACCTCCTTTCTAAGGAGTAA 760	
Consensus tcggaaggtgcggctggatcacctcctttctaaggagtaa	
DQ011250.1_UTTGCCTACTGTTTAATTTTGAGAGCTTATTGTTCTCAAAA1_RNA_gene_a	
05-0055_Cons <mark>TT</mark> ACCTACTGTTTAATTTTGAGGGTTCATTCCTTCAAG 798 Consensus tt cctactgtttaattttgag g t att t a	
DQ011250.1_UTTAGTACTTAATTGTACTTAGTACTTTGAAAACTGCATAA1_RNA_gene_a	
05-0055_Cons	
Consensus ttagtactttgaaaactgcataa DQ011250.1_UCATTTAGTGATGATTAAATAAACCAA.TATAAGAGAAGAAl_RNA_gene_a	
05–0055_Cons <mark>CATTTAGTGATGATTAAATAAACCAA<mark>AC</mark>ATAAGAGAAGAA 861</mark>	
Consensus catttagtgatgattaaataaaccaa ataagagaagaa DQ011250.1_UAACTCTTCAAbacterium_clone_3_16S_ribosomal_RNA_gene_a	
05-0055_ConsAACTCTTAAA 871	
Consensus aactett aa	





Direct pairwise comparison of sample 05-0062 with Candidatus Phytoplasma solani (Genbank accession no. AJ964960)





X76428.1_MolCTCCGCCTGAGT <mark>A</mark> GTACGTACGCAAGTATGAAACTTAAAGRNAsmall_: 05-0077_ConsCTCCGCCTGAGTTGTACGTACGCAAGTATGAAACTTAAAG 40	5
Consensus ctccqcctqaqt qtacqtacqcaaqtatqaaacttaaaq	
X76428.1 MolGAATTGACGGGACTCCCGCACAAGCGGTGGATCATGTTGTTRNAsmall_s	-
05-0077 ConsGAATTGACGGGACTCCGCACAAGCGGTGGATCATGTTGTT 80	5
Consensus gaattgacgggactccgcacaagcggtggatcatgttgtt X76428.1 MolTAATTCGAAGGTACCCGAAAAACCTCACCAGGTCTTGACARNA small s	~
05-0077 ConsTAATTCGAAGGTACCCGAAAAACCTCACCAGGTCTTGACA	5
Consensus taattcgaaggtacccgaaaaacctcaccaggtcttgaca 120	
X76428.1_MolTGCTTTTGCAAAGCTGTAGAAATACAGTGGAGGTTATCAGRNAsmall_s	-
05-0077 ConstGCTTTTGCAAAGCTGTAGAAATACAGTGGAGGTTATCAG	2
Consensus tgcttttgcaaagctgtagaaatacagtggaggttatcag	
X76428.1_MolAAGCACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGRNAsmall_s	~
05-0077_ConsAAGCACAGGTGGTGGCATGGTTGTCGTCAGTCGTGTCGT	2
Consensus aagcacaggtggtgcatggttgtcgtcag tcgtgtcgtg	
X76428.1_MolAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTTRNAsmall_s	-
05-0077_ConsAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 240	ر
Consensus agatgttgggttaagtcccgcaacgagcgcaacccttgtt	
X76428.1_Mol <mark>GTTAATTGCCATCATTAAGTTGGGGACTTTAGCAAGACTG</mark> RNAsmall_s	5
05-0077 ConsGTTAATTGCCATCATTAAGTTGGGGACTTTAGCAAGACTG 280	-
Consensus gttaattgccatcattaagttggggactttagcaagactg	
X76428.1_MolCCAATGATAAATTGGAGGAAGGTGGGGACGACGTCAAATCRNAsmall_s	5
05-0077 ConsCCAATGATAAATTGGAGGAAGGTGGGGACGACGTCAAATC 320	
Consensus ccaatgataaattggaggaaggtggggacgacgtcaaatc	
X76428.1_MolATCATGCCCCTTATGACCTGGGCTACAAACGTGATACAATRNAsmall_s	5
05-0077_ConsATCATGCCCCTTATGACCTGGGCTACAAACGTGATACAAT 360	
Consensus atcatgccccttatgacctgggctacaaacgtgatacaat	
X76428.1_MolGGCTGTTACAAAGGGTAGCT.AAAGCGTAAGCTTCTGGCGRNAsmall_s	3
05-0077_Cons <mark>GGCTGTTACAAAGGGTAGCT</mark> AAAGCGTAAGCTTCTGGCG 400	
Consensus ggctgttacaaagggtagct aaagcgtaagcttctggcg	
X76428.1_MolAATCTCAAAAAAGCAGTCTCAGTTCGGATTGAAGTCTGCARNAsmall_s	3
05-0077_ConsAATCTCAAAAAAGCAGTCTCAGTTCGGATTGAAGTCTGCA 440	
Consensus aatctcaaaaaagcagtctcagttcggattgaagtctgca	
X76428.1_MolACTCGACTTCATGAAGTTGGAATCGCTAGTAATCGCGAATRNAsmall_s	5
05-0077_Cons <mark>ACTCGACTTCATGAAGT<mark>G</mark>GGAATCGCTAGTAATCGCGAAT</mark> 480	
Consensus actcgacttcatgaagt ggaatcgctagtaatcgcgaat	
X76428.1_MolCAGCATGTCGCGGTGAATACGTTCTCGGGGGTTTGTACARNAsmall_s	3
05-0077_Cons <mark>CANCATGTCC</mark> NGGTGAA <mark>ATAC</mark> CTTTCTCGGGGC <mark>GTTTG</mark> TCC 520	
Consensus ca catgtcg ggtgaa c ttctcgggg tt c	
X76428.1_MolCACCGCCCGTCAAACCACGAAAGTTCGCAATACCCAAAGCRNAsmall_s	3
05-0077_cons <mark>cacc</mark> cccccccttca <mark>aac</mark> cgaaagtt <mark>ngcaatacccaaan</mark> c 560	
Consensus cacc ccc a cgaaagtt gcaatacccaaa c	
X76428.1_MolCGGTGGCCTAACTTGAGCAATCAAGAAGGAGCCGTCTAAGRNAsmall_s	5
05-0077_ConsCGGTGGCC <mark>N</mark> AACTTGAGCAATCAAGAAGGAGCCNTCTAAG 600	
Consensus cggtggcc aacttgagcaatcaagaaggagcc tctaag	
X76428.1_MolGTAGGGTTGATGATGGGGTTAAGTCGTAACAAGGTATCCRNAsmall_s	3
05-0077_Cons <mark>GTAGGGNTGATGATTGGGGTTAAGTCGTN</mark> ACAAGGTATCC 640	
Consensus gtaggg tgatgattggggttaagtcgt acaaggtatcc	~
X76428.1_MolCTACCCGAAGGTGGGGATGGATCACCT6S_ribosomal_RNAsmall_: 05-0077 ConscTNCCNGAAGGTGGGGATGGATCACCT 667	5
Consensus ct cc gaaggtgggggatggatcacct	



AJ964960.1_CAACGTTGGATAAAACCAGTGTTGAAGTTAACACATTAAGTne_	_partial
05-0102_consAACGTTGGATAAAACCAGTGTTGAAGTTAACACATTAAGT	40
Consensus aacgttggataaaaccagtgttgaagttaacacattaagt	
AJ964960.1_CACTCCGCCTGAGTAGTACGTACGCAAGTATGAAACTTAAAne_	_partial
05-0102_ConsACTCCGCCTGAGTAGTACGTACGCAAGTATGAAACTTAAA	80
Consensus actccgcctgagtagtacgtacgcaagtatgaaacttaaa AJ964960.1_C <mark>GGAATTGACGGGACTCCGCACAAGCGCTGGATCATGTTGT</mark> ne_	nontiol
05-0102_ConsGGAATTGACGGGACTCCGCGCANGCNNTGGATCATGTTGT	_partial 120
Consensus ggaattgacgggactccgc ca gc tggatc tgttgt	120
AJ964960.1_CTTAATTCGAAGGTACCCGAAAAACCTCACCAGGTCTTGACne_	partial
05-0102_ConsTTAATTCGAAGGTACCCGAAAAACCTCACCAGGTCTTGAC	160
Consensus ttaattcqaaqqtacccqaaaaacctcaccaqqtcttqac	
AJ964960.1_CATGCTTTTGCAAAGCTGTAGAAATACAGTGGAGGTTATCAne_	_partial
05-0102_ConsATGCTTTTGCAAAGCTGTAGAAATACAGTGGAGGTTATCA	200
Consensus atgcttttgcaaagctgtagaaatacagtggaggttatca	
AJ964960.1_CAAAGCACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTne_	_partial
05-0102_ConsGAAGCACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGT	240
Consensus aagcacaggtggtgcatggttgtcgtcagctcgtgtcgt	
AJ964960.1_CGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAACCCTTGne_	_partial 280
05-0102_Cons <mark>GAGATGTTGGGTTAAGTCCCC</mark> GCAACGAGCGCAACCCTTG Consensus gagatgttgggttaagtccc gcaacgagcgcaacccttg	280
Consensus gagatgttgggttaagtccc gcaacgagcgcaacccttg AJ964960.1_CTTGTTAATTGCCATCATTAAGTTGGGGACTTTAGCAAGACne_	partial
05-0102_ConsTTGTTAATTGCCATCATTAAGTTGGGGACTTTAGCAAGAC	320
Consensus ttgttaattgccatcattaagttggggactttagcaagac	020
AJ964960.1_CTGCCAATGATAAATTGGAGGAAGGTGGGGACGACGTCAAAne_	partial
05-0102_ConsTGCCAATGATAAATTGGAGGAAGGTGGGGACGACGTCAAA	360
Consensus tgccaatgataaattggaggaaggtgggggacgacgtcaaa	
AJ964960.1_CTCATCATGCCCCTTATGACCTGGGCTACAAACGTGATACAne_	_partial
05-0102_ConsTCATCATGCCCCTTATGACCTGGGCTACAAACGTGATACA	400
Consensus tcatcatgccccttatgacctgggctacaaacgtgataca	
AJ964960.1_CATGGCTGTTACAAAGGGTAGCTAAAGCGTAAGCTTCTGGCne_	_partial 440
05-0102_Cons <mark>ATGGCTGTTACAAAGGGTAGCTAAAGCGTAAGCTTCTGGC</mark> Consensus atggctgttacaaagggtagctaaagcgtaagcttctggc	440
AJ964960.1_CGAATCTCAAAAAAGCAGTCTCAGTTCGGATTGAAGTCTGCne_	partial
05-0102_consGAATCTCAAAAAAGCAGTCTCAGTTCGGATTGAAGTCTGC	480
Consensus gaatctcaaaaaagcagtctcagttcggattgaagtctgc	
AJ964960.1_CAACTCGACTTCATGAAGTTGGAATCGCTAGTAATCGCGAAne_	_partial
05-0102_ConsaACTCGACTTCATGAAGTTGGAATCGCTAGTAATCGCGAA	520
Consensus aactcgacttcatgaagttggaatcgctagtaatcgcgaa	
AJ964960.1_CTCAGCATGTCGCGG <mark>TG</mark> AATACGTTCTCGGGGTTTGTACne_	_partial
05-0102_Cons <mark>TCAGCATGTCGCGG</mark> GTGAAATACGTTCTCGGGGTTTGTAC	560
Consensus tcagcatgtcgcgg aatacgttctcggggtttgtac	
AJ964960.1_CACACCGCCGTCAAACCACGAAAGTTGGCAATACCCAAAGhe_	_partial 600
05-0102_ConsACACCGCCCGTCAAACCACGAAAGTTGGCAATACCCAAAG Consensus acaccgccgtcaaaccacgaagttggcaatacccaaag	800
AJ964960.1_CCCGGTGGCCTAACTTGAGCAATCAAGAAGGAGCCGTCTAAne_	_partial
05-0102_ConsCCGGTGGCCTAACTTGAGCAATCAAGAAGGAGCCGTCTAA	pa101a1
Consensus ccqqtqqcctaacttqaqcaatcaaqaaqqaqccqtctaa	
AJ964960.1_CGGTAGGGTTGATGATGGGGGTTAAGTCGTAACAAGGTATCne_	_partial
05-0102_Cons <mark>GGTAGGGTTGATGATTGGGGTTAAGTCGTAACAAGGTATC</mark>	680
Consensus ggtagggttgatgattggggttaagtcgtaacaaggtatc	
AJ964960.1_CCCTACCGGAAGGTGGGGATGGATCACCTCCTTTCTAAGGAne_	_partial
05-0102_Cons <mark>CCTACCGGAAGGTGGGGATGGATCACCTCCTTTCTAAGGA</mark>	720
Consensus cctaccggaaggtggggatgggatcacctcctttctaagga AJ964960.1_CTAAAGTTATCATCTTCAGTTTTGAGAGAGACT6S_rRNA_gene_	partial
05-0102_ConsTAAAGTTATCATCTTCAGTTTTGAGAGAGACT	_partial 750
Consensus taaagttatcatcttcagttttgagagact	,

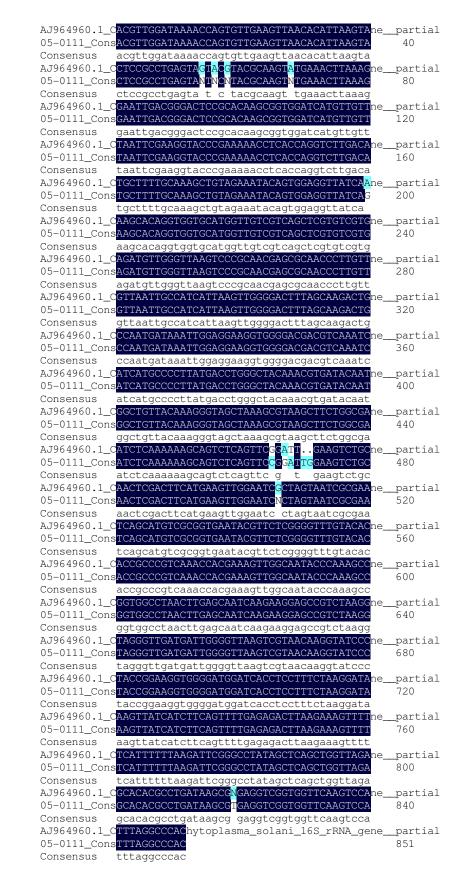
Direct pairwise comparison of sample 05-0102 with Candidatus Phytoplasma solani (Genbank accession no. AJ964960)



Direct pairwise comparison of sample 05-0109 with Candidatus Phytoplasma solani (Genbank accession no. AJ964960)

AJ964960.1_C	GATT <mark>A</mark> GAT <mark>A</mark> CCCTGGTAGTCCACGCCCTAAACGATGAGTA <mark>ne_</mark>	_partial
05-0109_Cons	GATT <mark>C</mark> GAT.CCCTGGTAGTCCACGCCCTAAACGATGAGTA	39
Consensus	gatt gat ccctggtagtccacgccctaaacgatgagta	
AJ964960.1 C	CTAAACGTTGGATAAAACCAGTGTTGAAGTTAACACATTAne	partial
		79
Consensus	ctaaacgttggataaaaccagtgttgaagttaacacatta	15
_	AGTACTCCGCCTGAGTAGTACGTACGCAAGTATGAAACTTne_	_partial
_	AGTACTCCGCCTGAGTAGTACGTACGCAAGTATGAAACTT	119
Consensus	agtactccgcctgagtagtacgtacgcaagtatgaaactt	
AJ964960.1_C	AAAGGAATTGACGGGACTCCGCACAAGCGGTGGATCATGT <mark>ne_</mark>	_partial
05-0109_Cons	AAAGGAATTGACGGGACTCCGCACAAGCGGTGGATCATGT	159
Consensus	aaaggaattgacgggactccgcacaagcggtggatcatgt	
AJ964960.1 C	TGTTTAATTCGAAGGTACCCGAAAAACCTCACCAGGTCTTne_	partial
	TGTTTAATTCGAAGGTACCCGAAAAACCTCACCAGGTCTT	199
Consensus	tgtttaattcgaaggtacccgaaaaacctcaccaggtctt	200
	GACATGCTTTTGCAAAGCTGTAGAAATACAGTGGAGGTTAne_	partial
_	GACATGCTTTTGCAAAGCTGTAGAAATACAGTGGAGGTTA	239
Consensus	gacatgcttttgcaaagctgtagaaatacagtggaggtta	
	TCA <mark>A</mark> AAGCACAGGTGGTGCATGGTTGTCGTCAGCTCGTGT <mark>ne_</mark>	_partial
05-0109_Cons	TCA <mark>G</mark> AAGCACAGGTGGTGCATGGTTGTCGTCAGCTCGTGT	279
Consensus	tca aagcacaggtggtgcatggttgtcgtcagctcgtgt	
AJ964960.1_C	CGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCT <mark>ne_</mark>	partial
05-0109 Cons	CGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCT	319
Consensus	cgtgagatgttgggttaagtcccgcaacgagcgcaaccct	
	TGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTAGCAAne_	partial
	TGTTGTTAATTGCCATCATTAAGTTGGGGGAC <mark>C</mark> TTTAGCAA	
		555
Consensus	tgttgttaattgccatcattaagttggggac tttagcaa	
_	GACTGCCAATGATAAATTGGAGGAAGGTGGGGACGACGTC <mark>ne_</mark>	_partial
05-0109_Cons	GACTGCCAATGATAAATTGGAGGAAGGTGGGGACGACGTC	399
Consensus	gactgccaatgataaattggaggaaggtgggggacgacgtc	
AJ964960.1_C	AAATCATCATGCCCCTTATGACCTGGGCTACAAACGTGAT <mark>ne_</mark>	_partial
	AAATCATCATGCCCCTTATGACCTGGGCTACAAACGTGAT	439
Consensus	aaatcatcatgccccttatgacctgggctacaaacgtgat	
	ACAATGGCTGTTACAAAGGGTAGCTAAAGCGTAAGCTTCTne_	partial
	ACAATGGCTGTTACAAAGGGTAGCTAAAGCGTAAGCTTCT	479
Consensus		115
	GGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTGAAGTCne_	_partial
_	GGCGAATCTCAAAAAAGCAGTCTCAGTTCGGATTGAAGTC	519
Consensus	ggcgaatctcaaaaaagcagtctcagttcggattgaagtc	
AJ964960.1_C	TGCAACTCGACTTCATGAAGTTGGAATCGCTAGTAATCGC	_partial
05-0109_Cons	TGCAACTCGACTTCATGAAGTTGGAATCGCTAGTAATCGC	559
Consensus	tgcaactcgacttcatgaagttggaatcgctagtaatcgc	
AJ964960.1 C	GAATCAGCATGTCGCGGTGAATACGTTCTCGGGGTTTGTAne	partial
_	GAATCAGCATGTCGCGGTGAATACGTTCTCGGGGTTTGTA	599
Consensus	gaatcagcatgtcgcggtgaatacgttctcggggtttgta	555
_	CACACCGCCCGTCAAACCACGAAAGTTGGCAATACCCAAAne_	_partial
_	CACACCGCCCGTCAAACCACGAAAGTTGGCAATACCCAAA	639
Consensus	cacaccgcccgtcaaaccacgaaagttggcaatacccaaa	
	GCCGGTGGCCTAACTTGAGCAATCAAGAAGGAGCCGTCTA <mark>ne_</mark>	_partial
05-0109_Cons	GCCGGTGGCCTAACTTGAGCAATCAAGAAGGAGCCGTCTA	679
Consensus	gccggtggcctaacttgagcaatcaagaaggagccgtcta	
	AGGTAGGGTTGATGATTGGGGGTTAAGTCGTAACAAGGTATne_	partial
	AGGTAGGGTTGATGATTGGGGGTTAAGTCGTAACAAGGTAT	719
Consensus		110
	aggtagggttgatgattgggggttaagtcgtaacaaggtat	partial
	CCCTACCGGAAGGTGGGGATGGATCACCTCCTTTCTAAGGne_	
	CCCTACCGGAAGGTGGGGATGGATCACCTCCTTTCTAAGG	759
Consensus	ccctaccggaaggtggggatggatcacctcctttctaagg	
AJ964960.1_C	ATAAAGTTATCATCTTCAGTTTTGAGAGACTTAAGAAAGT <mark>ne_</mark>	_partial
05-0109_Cons	ATAAAGTTATCATCTTCAGTTTTGAGAGACTTAAGAAAGT	799
Consensus	ataaagttatcatcttcagttttgagagacttaagaaagt	
AJ964960.1_C	TTTTCATTTTTTAAGATTCGGGCCTATAGCTCAGCTGGTTne_	_partial
	TTTTCATTTTTTTAAGATTCGGGCCTATAGCTCAGCTGGTT	839
Consensus	ttttcattttttaagattcgggcctatagctcagctggtt	
	AGAGCACACGCCTGATAAGCC <mark>N</mark> GAGGTCGGTGGTTCAAGTne_	partial
		_partiar 879
	AGAGCACACGCCTGATAAGCG <mark>T</mark> GAGGTCGGTGGTTCAAGT	015
Consensus		
3 TOC 40CO 1	agagcacacgcctgataagcg gaggtcggtggttcaagt	
	CCATTTAGGCCCACCAAAATAGGTCACATCTTAAA <mark>NA_gene_</mark>	_partial
05-0109_Cons	CCATTTAGGCCCACCAAAATAGGTCACATCTTAAANA_gene_ CCATTTAGGCCCACCAAAATAGGTCACATCTTAAA	_partial 914
	CCATTTAGGCCCACCAAAATAGGTCACATCTTAAA <mark>NA_gene_</mark>	





Direct pairwise comparison of sample 05-0111 with Candidatus Phytoplasma solani (Genbank accession no. AJ964960)



AJ964960.1_CAAAACCAGTGTTGAAGTTAACACATTAAGTACTCCGCCTGne	partial
05-0122_ConsAAAACCAGTGTTGAAGTTAACACATTAAGTACTCCGCCTG	40
Consensus aaaaccagtgttgaagttaacacattaagtactccgcctg	
	partial
05-0122_Cons <mark>AGTATNTACCTACGCAAGTATGAAACTTAAAGGAATTGAC</mark> Consensus agta tac tacgcaagtatgaaacttaaaggaattgac	80
	partial
	120
Consensus qq ctccqc caaqcqqtqqatcatqttqtttaattcqa	100
	partial
05-0122_Cons <mark>AGGTACCCGAAAAACCTCACCAGGTCTTGACATGCTTT</mark> G	160
Consensus aggtacccgaaaaacctcaccaggtcttgacatgcttt g	
	partial
05-0122_Cons <mark>CAAAGCTGTAGAAATACAGTGGAGGTTATCAG</mark> AAGC <mark>NCAG</mark> Consensus caaagctgtagaaatacagtggaggttatca aagc cag	200
	partial
	240
Consensus gtggtgcatggttgtcgtcagctcgtgtcgtgagatgttg	
	partial
05-0122_Cons <mark>GGTTAAGTCCC</mark> TTT <mark>ACGAGCGCAACCCTTGTTGTTAATTG</mark>	280
Consensus ggttaagtccc acgagcgcaacccttgttgttaattg	
	partial
—	320
Consensus ccatcattaagttggggactttagcaagactgccaatgat AJ964960.1_CAAATTGGAGGAAGGTGGGGACGACGTCAAATCATCATGCCne	partial
	360
Consensus aaattqqaqqaaqqtqqqqacqacqtcaaatcatcatqcc	500
	partial
	400
Consensus ccttatgacctgggctacaaacgtgatacaatggctgtta	
	partial
	440
Consensus caaagggtagctaaagcgtaagcttctggcgaatctcaaa	nartial
	partial 480
Consensus aaagcagtctcagttcggattgaagtctgcaactcgactt	100
	partial
	520
Consensus catgaagttggaatcgctagtaatcgcgaatcagcatgtc	
	partial
_	560
Consensus gcggtgaatacgttctcggggtttgtacacaccgcccgtc	
	partial 600
Consensus aaaccacqaaaqttqqcaatacccaaaqccqqtqqcctaa	000
	partial
	640
Consensus cttgagcaatcaagaaggagccgtctaaggtagggttgat	
AJ964960.1_CGATTGGGGTTAAGTCGTAACAAGGTATCCCTACCGGAAGGne	partial
	680
Consensus gattggggttaagtcgtaacaaggtatccctaccggaagg	
	partial
	720
	partial
	738
Consensus cttcagttttgagagact	

Direct pairwise comparison of sample 05-0122 with Candidatus Phytoplasma solani (Genbank accession no. AJ964960)

Consensus cttcagttttgagagact



Direct pairwise comparison of sample 05-0127 with Candidatus Phytoplasma solani (Genbank accession no. AJ964960)

AJ964960.1_CCC <mark>TA</mark> AACGATGAGTACTAAACGTTGGATAAAACCAGTGTTne 05-0127_Cons <mark>CCCT</mark> AACGATGAGTACTAAACGTTGGATAAAACCAGTGTT	partial 40
Consensus cc aacgatgagtactaaacgttggataaaaccagtgtt	
AJ964960.1_CGAAGTTAACACATTAAGTACTCCGCCTGAGTAGTACGTAC	partial 80
Consensus gaagttaacacattaagtactccgcctgagtagtacgtac	00
	partial
	120
Consensus gcaagtatgaaacttaaaggaattgacgggactccgc ca AJ964960.1_CAGCGTGGATCATGTTGTTTAATTCGAAGGTACCCGAAAAne	tiol
	partial 160
Consensus agc gtggatcatgttgtttaattcgaaggtacccgaaaa	
	partial
	200
Consensus acctcaccaggtcttgacatgcttttgcaaagctgtagaa AJ964960.1_CATACAGTGGAGGTTATCAAAAGCACAGGTGGTGCATGGTTne	oartial
	240
Consensus atacagtggaggttatca aagcacaggtggtgcatggtt	
	partial
05-0127_Cons GTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGC Consensus gtcgtcagctcgtgtcgtgagatgttgggttaagtccccgc	280
	partial
	320
Consensus aacgagcgcaacccttgttgttaattgccatcattaagtt	
	partial 360
Consensus gggg actttagcaagactgccaatgataaattggaggaa	500
AJ964960.1_CGGTGGGG.ACGACGTCAAATCATCATGCCCCTTATGACCTne	partial
	400
Consensus ggtgggg acgacgtcaaatcatcatgccccttatgacct AJ964960.1_CGGGCTACAAACGTGATACAATGGCTGTTACAAAGGG.TAGne	oartial
	440
Consensus gggctacaaacgtgatacaatggctgttacaaaggg tag	
	partial
05-0127_ConsCTAAAGCGTAAGCTTCTGGCGAATCTCAAAAAAGCAGTCT 4 Consensus ctaaagcgtaagcttctggcgaatctcaaaaaagcagtct	480
	partial
05-0127_ConsCAGTTCGGATTGAAGTCTGCAACTCGACTTCATGAAGTTG	520
Consensus cagttcggattgaagtctgcaactcgacttcatgaagttg	
	partial 560
Consensus gaatcgctagtaatcgcgaatcagcatgtcgcggtgaata	500
	partial
	600
Consensus cgttctcggggtttgtacacaccgcccgtcaaaccacgaa AJ964960.1 CACTTGGCAATACCCAAAGCCGGTGGCCTAACTTGAGCAAThe	oartial
	640
Consensus agttggcaatacccaaagccggtggcctaacttgagcaat	
	partial
05-0127_Cons <mark>CAAGAAGGAGCCGTCTAAGGTAGGGTTGATGATTGGGGG</mark> T (Consensus caagaaqqaqccqtctaaqqtaqqqttqattqqtqqq t	680
	partial
05-0127_Cons <mark>TAAGTCGTAACA</mark> GGTATCCC <mark>C</mark> TACCGGAAGGTGGGGATG	720
Consensus taagtcgtaaca ggtatccc taccggaaggtggggatg	
	partial 760
Consensus gatcacctcctttctaaggataaagttatcatcttcagtt	
AJ964960.1_CTTGAGAGACTPhytoplasma_solani_16S_rRNA_gener	partial
	770
Consensus ttgagagact	



APPENDIX C

Multiple alignment of all the samples sequenced

05-0018 ConsCTCCGCCTGAGTAN. TACCTACGCAAGTATGAAACTTAAAA	39
05-0038_Cons <mark>CTCCGCCTC<mark>AG</mark>TAG.TACGTACGCAAG<mark>TA</mark>TGAAACT<mark>T</mark>AAA</mark>	39
05-0062 Cons <mark>CTCCGCCTG<mark>AC</mark>TAG.T<mark>ACGTA</mark>CGCAAG<mark>TA</mark>TGAAACT<mark>T</mark>AAA</mark>	39
05-0077 ConsCTCCGCCTGAGTTG.TACGTACGCAAGTATGAAACTTAAA	39
05-0033stoctccgcctgagtag.tacgtacgcaagtatgaaacttaaa	39
05-0014_Cons <mark>CTCCGCCTGAGTAG.TACGTACGCAAG</mark> TATGAAACT <mark>T</mark> AAA	39
05-0111_Cons <mark>CTCCGCCTG<mark>AGTAN</mark>.TNC<mark>NTA</mark>CGCAAG<mark>TN</mark>TGAAACT<mark>T</mark>AAA</mark>	39
05-0109 Cons <mark>CTCCGCCTG<mark>AGTAG</mark>.T<mark>ACGTA</mark>CGCAAG<mark>TA</mark>TGAAACT<mark>T</mark>AAA</mark>	39
05-0102 ConsCTCCGCCTG <mark>AGTAG.TACGTA</mark> CGCAAG <mark>TA</mark> TGAAACT <mark>T</mark> AAA	39
05-0127 Cons <mark>CTCCGCCTG<mark>A</mark>GTAG. T<mark>ACGTA</mark>CGCAAG<mark>TA</mark>TGAAACT<mark>T</mark>AAA</mark>	39
05-0122 ConsCTCCGCCTGAGTATNTACCTACGCAAGTATGAAACTTAAA	40
05-0033 FD CTCCGCCTG <mark>AGTAG.TACGTA</mark> CGCAAG <mark>TA</mark> TGAAACT <mark>T</mark> AAA	39
05-0005_ConsCTCCGCCTGGGGAG.TACGGTCGCAAGACTGAAACTCAAA	39
05-0055_Cons <mark>CTCCGCCTG</mark> GA <mark>AG</mark> .T <mark>ACG</mark> CTCGCAAGAGTGAAACTCAAA	39
Consensus ctccgcctg g t c cgcaag tgaaact aaa	
05-0018_Cons <mark>GGAATTGACGG</mark> GACT <mark>CCGCA</mark> CA <mark>AGCGGT</mark> GGA <mark>TCA</mark> TGNTGT	79
05-0038 Cons <mark>GGAATTGACGG<mark>GACT</mark>CCGC<mark>A</mark>CA<mark>AGCGGT</mark>GGA<mark>TCA</mark>TG<mark>TT</mark>GT</mark>	79
05-0062 Cons <mark>GGAATTGACGGGACT</mark> CCGC <mark>A</mark> CA <mark>AGCGGT</mark> GGA <mark>TC</mark> ATG <mark>TT</mark> GT	79
05-0077 ⁻ Cons <mark>GGAATTGACGG<mark>GACT</mark>CCGC<mark>A</mark>CA<mark>AGCGGT</mark>GGA<mark>TC</mark>ATG<mark>TT</mark>GT</mark>	79
05-0033 sto <mark>ggaattgacgg<mark>gact</mark>ccgc<mark>acaa</mark>g<mark>cggt</mark>gga<mark>tca</mark>tg<mark>tt</mark>gt</mark>	79
05-0014 ConsGGAATTGACGGGACTCCGCACAAGCGGTGGATCATGTTGT	79
05-0111 ConsGGAATTGACGGGACTCCGCACAAGCGGTGGATCATGTTGT	79
	79 79
05-0109_ConsGGAATTGACGGGACTCCGCACAAGCGGTGGATCATGTTGT	
05-0102_Consgrattgrcgggrctccgcgcangcnntggatcntgttgt	79
05-0127_Cons <mark>GGAATTGACGGGACT</mark> CCGCNCAA <mark>GCNGTGGATC</mark> ATGTTGT	79
05-0122_Cons <mark>GGAATTGACGGNCCT</mark> CCGC <mark>NCAAGCGGT</mark> GGA <mark>TCATGTT</mark> GT	80
05-0033FD_GGAATTGACGG <mark>GACT</mark> CCGC <mark>ACAA</mark> G <mark>CGGT</mark> GGA <mark>TCA</mark> TG <mark>TT</mark> GT	79
05-0005_Cons <mark>GGAATTGACGG<mark>G</mark>GGC<mark>CCGC<mark>A</mark>CA<mark>AGCGGT</mark>GGA<mark>GCA</mark>TG<mark>TG</mark>GT</mark></mark>	79
05-0055_Cons <mark>GGAATTGACGG</mark> GAC <mark>CCGCA</mark> CAA <mark>G</mark> TAG <mark>CGGAG</mark> CATG <mark>T</mark> GGT	79
Consensus ggaattgacgg ccgc ca g gga c tg gt	
05-0018 ConsTTAATTCGAAGGTACCCGAAAAAACCTCACCAGGTCTTGAC	119
05-0038 Cons <mark>TTAATTCGAAG<mark>GT</mark>AC<mark>C</mark>CGAA<mark>A</mark>AACCT<mark>C</mark>ACC<mark>AGGT</mark>CTTGAC</mark>	119
05-0062_cons <mark>ttaattcgaag</mark> gt <mark>ac</mark> cgaa <mark>a</mark> aacct <mark>c</mark> acc <mark>aggt</mark> cttgac	119
05-0077 ⁻ Cons <mark>tTAATTCGAAG<mark>GT</mark>AC<mark>C</mark>CGAA<mark>A</mark>AACCT<mark>C</mark>ACC<mark>AGGT</mark>CTTGAC</mark>	119
05-0033 stottaattcgaag <mark>gt</mark> ac <mark>c</mark> cgaa <mark>a</mark> aacct <mark>c</mark> acc <mark>aggt</mark> cttgac	119
05-0014 ConstTAATTCGAAG <mark>GT</mark> AC <mark>C</mark> CGAA <mark>A</mark> AACCT <mark>C</mark> ACC <mark>AGGT</mark> CTTGAC	119
05-0111 ConsTTAATTCGAAG <mark>GT</mark> ACCCGAA <mark>A</mark> AACCTCACCAGGTCTTGAC	119
05-0109_ConsTTAATTCGAAGGTACCCGAAAAACCTCACCAGGTCTTGAC	119
05-0102_ConstTAATTCGAAG <mark>GTACC</mark> CGAAAAACCT <mark>C</mark> ACC <mark>AGGT</mark> CTTGAC	119
05-0127_Cons <mark>tTaattcgaag</mark> gtac <mark>ccgaaa</mark> aacct <mark>caccaggt</mark> cttgac	119
05-0122_Cons <mark>TTAATTCGAAG<mark>GT</mark>AC<mark>C</mark>CGAA<mark>A</mark>AACCT<mark>C</mark>ACC<mark>AGGT</mark>CTTGAC</mark>	120
05-0033FD_TTAATTCGAAG <mark>AT</mark> AC <mark>A</mark> CGAA <mark>A</mark> AACCT <mark>T</mark> ACC <mark>AGGT</mark> CTTGAC	119
05-0005_Cons <mark>TTAATTCGAAG</mark> CA <mark>AC</mark> GCGAA <mark>G</mark> AACCT <mark>T</mark> ACC <mark>AGGT</mark> CTTGAC	119
05-0055_Cons <mark>TTAATTCGAAG</mark> CA <mark>ACG</mark> CGAA <mark>G</mark> AACCT <mark>TACC</mark> TAAGCTTGAC	119
Consensus ttaattcgaag ac cgaa aacct acc cttgac	
05-0018 Cons <mark>ATGCTTTTGCAAAGCTGTAGAAATACAGTGGAGGT</mark>	154
05-0038 Cons <mark>ATGCTTT</mark> TGCAAAGCTGTAG <mark>AAAT</mark> ACAGTGGA <mark>GG</mark> T	154
05-0062_Cons <mark>AT</mark> GCTT <mark>T</mark> TGCAAAGCTGTAG <mark>AAA</mark> TACAGTGGA <mark>GG</mark> T	154
05-0077 Cons <mark>ATGC</mark> TTTTGCAAAGCTGTAG <mark>AAAT</mark> ACAGTGGA <mark>GG</mark> T	154
05-0033 sto <mark>atgCttt</mark> tgCaaagCtgtagaaataCagtggaggt	154
	154
05-0014_Cons <mark>AT</mark> GCTTTTGCAAAGCTGTAGAAATACAGTGGAGGT 05-0111_Cons <mark>ATGCTTTTGCAAAGCTGTAGAAATACAGTGGAGG</mark> T	154
05-0100 Construction All Construction	154
05-0109_Cons <mark>ATGCTTTTGCAAAGCTGTAGAAATACAGTGGAGG</mark> T 05-0102_Cons <mark>ATGCTTTTGCAAAGCTGTAGAAATACAGTGGAGG</mark> T	
05-0102_CONSATGOTTTTGCAAAGCTGTAGAAATACAGTGGAGGT	154
05-0127_ConsaTGCTTTTGCAAAGCTGTAGAAATACAGTGGAGGT	154
05-0122_consatgcttttggcaaagctgtagaaatacagtggaggt	155
05-0033FD_ATACTCT.GCAAAGCTATAGAAATATAGTGGAGGT	153
05-0005_ConsATCCTCTGACAACTCTAGAGATAGAGCGTTCCCCTTCGGG	159
05-0055_Cons <mark>AT</mark> CCCAT <mark>TG</mark> ACCTCTCCCTAATCGGAG <mark>AT</mark> TTCCCTTN <mark>GG</mark> G	159
Consensus at c t a t gg	

05-0019_ConsTATCAGAAGCACAGGTGGTGCATGGTTGTCGTCAGTGGT 194 05-003_consTATCAGAAGCACAGGTGGTGCATGGTTGTCGTCAGTGTGT 194 05-003_stoTATCAGAAGCACAGGTGGTGCATGGTTGTCGTCAGTGTGT 194 05-0014_consTATCAGAAGCACAGGTGGTGCATGGTTGTCGTCAGTGCT 194 05-0011_consTATCAGAAGCACAGGTGGTGCATGGTTGTCGTCAGTGCT 194 05-0012_consTATCAGAAGCACAGGTGGTGCATGGTTGTCGTCAGTGCT 194 05-0122_consTATCAGAAGCACAGGTGGTGCATGGTTGTCGTCAGTGCT 194 05-0122_consTATCAGAAGCACAGGTGGTGCATGGTTGTCGTCAGTGCT 194 05-0122_consTATCAGAAGCACAGGTGGTGCATGGTTGTCGTCAGTGCT 195 05-0033_FD_TATCAGAAGCACAGGTGGTGCATGGTTGTCGTCAGTGCT 199 05-0055_consGACAGGGTACAGGTGGTGCATGGTTGTCGTCAGTGCT 199 05-0055_consGACAGGGTACAGGTGGTGCATGGTTGTCGTCAGTGCT 199 05-0055_consGACAGGGTACAGGTGGTGCATGGTTGTCGTCAGTGCT 199 05-0055_consGCCAGTGGTGACAGGTGGTCATGGTTGTCGTCAGTGCT 199 05-0055_consGCCAGTGGTGACAGGTGGTGATGGTGTGTGTGCTCAG 199 05-0055_consGCCAGTGGTGACAGGTGGTGATGGTGTGTGTGCCAG 199 05-0055_consGCGTGAGATGTTGGTTAAGTCCC_GCACGCGCAC 233 05-0033_stCGTGGAGATGTGGGTTAAGTCCC_GCAACGACGCGCAC 233 05-0033_stCGTGGTGAGATGTTGGTTAAGTCCC_GCAACGACGCGCAC 233 05-0033_stCGTGGTGAGATGTTGGTTAAGTCCC_GCAACGACGCGCAC 233 05-0014_consGTCGTGAGATGTGGGTTAAGTCCC_GCAACGACGCGCAC 233 05-0111_consGTCGTGAGATGTTGGTTAAGTCCC_GCAACGACGCGCAC 233 05-0122_consGTCGTGAGATGTTGGTTAAGTCCC_GCAACGACGCGCAC 234 05-0122_consGTCGTGAGATGTTGGTTAAGTCCC_GCAACGACGCGCAC 238 05-00122_consGTCGTGAGATGTTGGTTAAGTCCC_GCAACGACGCGCAC 238 05-00122_consGTCGTGAGATGTTGGTTAAGTCCC_GCAACGACGCGAC 238 05-00122_consGTCGTGAGATGTTGGTTAAGTCCC_GCAACGACGCGAC 238 05-00122_consGTCGTGAGATGTTGGTTAAGTCCC_GCAACGACGCGAC 238 05-00122_consGTCGTGAGATGTTGGTTAAGTCCC_GCAACGACGCGAC 238 05-00122_consGTCGTGAGATGTTGGTTAAGTCCC_GCAACGACGCGAC 238 05-00122_consGTCGTGTGAGATGTTGGTTAAGTCCC_GCAACGACGCGAC 238 05-00122_consGTCGTGTGTGTTAGGTCAACTTAAGTTGCGGCCTTA 271 05-0013_TC_GCGGGGAGTGTGTGTGTAGTCCC_CAACGACGCGCAC 238 05-0013_TD_GCGGGGGTTGGTGTGTGTGTGTAAGTCCC_GCAACGACGCGCAC 238 05-0013_CONSGCGGGGTTGTGTTAGTCGCCCCCAACGGCGCCCTTA 271 05-0013_CONSGCTGGGAGTGCTGCATGTTAGGTGCGCCCTTA 271 05-0013_CONSGCTGGGAGTGTGCATGTTAGGTTAAGTCCC_CAACGGCGCC		
05-0062 ConsTATCAGAAGC AGGTGGTGCATGGTTGTGTGTGAG TGGT 194 05-0077 ConsTATCAGAAGC AGGTGGTGCATGGTTGTGTGTGAG TGGT 194 05-0014 ConsTATCAGAAGC AGGTGGTGCATGGTTGTGTGTGAG TGGT 194 05-0019 ConsTATCAGAAGC AGGTGGTGCATGGTTGTGTGTGCAG TGGT 194 05-0102 ConsTATCAGAAGC AGGTGGTGCATGGTTGTGTGTGCAG TGGT 194 05-0102 ConsTATCAGAAGC AGGTGGTGCATGGTTGTGTGTGCAG TGGT 194 05-0102 ConsTATCAGAAGC AGGTGGTGCATGGTTGTGTGTGCAG TGGT 194 05-0102 ConsTATCAGAAGC AGGTGGTGCATGGTTGTGTGTGCAG TGGT 195 05-0003 _ FD TATCAGAAGC AGGTGGTGCATGGTTGTGTGTGCAG TGGT 195 05-0003 _ ConsGGACAGGTGTACAGTGGTGGTGTGTGTGTGCAG TGGT 199 05-0005 ConsGGACAGGTGTACAGGTGGTGCATGGTTGTGTCAG TGGT 199 05-0005 ConsGGACAGGTGTACAGGTGGTGCATGGTTGTGTGCAG 199 05-0008 ConsGGTGGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 233 05-0003 _ STGTGGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 233 05-0003 _ STGTGGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 233 05-0014 ConsGTGGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 233 05-0014 ConsGTGGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 233 05-0012 ConsGTGGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 233 05-0112 ConsGTGGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 234 05-0127 ConsGTGGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 235 05-0102 ConsGTGGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 236 05-0012 ConsGTGGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 238 05-0012 ConsGTGGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 238 05-0012 ConsGTGGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 238 05-0012 ConsGTGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 238 05-0012 ConsGTGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 238 05-0015 ConsGTGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 238 05-0016 ConsGTGTGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 238 05-0017 ConsGTGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 238 05-0018 ConsGTGTGAGATGTGGGTTAAGTCC . GCAAGGACGGAAC 238 05-0018 ConsGTGTGTGAGATGTGGGTAAGTCC . GCAAGGACGGAAC 238 05-0019 ConsGCGTGTTGTTAATGCCAACTTAGGTGGGGAC . TTTA 271 05-0018 ConsGTGTGTGAGATGTGGGTAAGTCC . GCAAGGACGGAC . TTA 271 05-0018 ConsGCGTGTGTGTATGGTTAAGTCCG . GCAAGGACGGAC . TTA 272 05-0019 ConsGCGTGCAGATGCAATGTAAGTGCG . AGGTGGGGAC . TTA 27	05-0018 Cons <mark>TATCAGAAGCA</mark> CAGGTGGTGCATGGTTGTCGTCAG <mark>C</mark> TCGT	194
05-0077_ConsTATCAGAAGCACAGGTGGTGCATGGTTGTGTGTGAGTTGTGT 05-0013_stoTATCAGAAGCACAGGTGGTGCATGGTTGTGTGTGAG 05-0111_ConsTATCAGAAGCACAGGTGGTGCATGGTTGTGTGTGAG TGT 194 05-0112_ConsTATCAGAAGCACAGGTGGTGCATGGTTGTGTGTGAG 05-0127_ConsTATCAGAAGCACAGGTGGTGCATGGTTGTGTGTGAG 05-0127_ConsTATCAGAAGCACAGGTGGTGCATGGTTGTGTGTGAG 05-0127_ConsTATCAGAAGCACAGGTGGTGCATGGTTGTGTGTGAG 05-0127_ConsTATCAGAAGCACAGGTGGTGCATGGTTGTGTGTGAG 05-0127_ConsTATCAGAAGCACAGGTGGTGCATGGTTGTGTGTGAG 05-0127_ConsTATCAGAAGCACAGGTGGTGCATGGTTGTGTGTGCAG 05-0127_ConsTATCAGAAGCACAGGTGGTGCATGGTTGTGTGTGAG 05-0033_FD_TATCAGAAGCACAGGTGGTGCATGGTTGTGTGTGAG 05-0052_ConsGCACAGGTGACAGGTGGTGCATGGTTGTGTGTGAG 05-0018_ConsGTGGTGAGATGTTGGTTAAGTCCC.GCAACGACGCGCAAC 233 05-0018_ConsGTGGTGAGATGTTGGTTAAGTCCC.GCAACGACGCGCAAC 233 05-0014_ConsGTGGTGAGATGTTGGTTAAGTCCC.GCAACGACGCGCAAC 233 05-0014_ConsGTGGTGAGATGTTGGTTAAGTCCC.GCAACGACGCGCAAC 233 05-0014_ConsGTGGTGAGATGTTGGTTAAGTCCC.GCAACGACGCGCAAC 233 05-0112_ConsGTGGTGAGATGTTGGTTAAGTCCC.GCAACGACGCGCAAC 233 05-0112_ConsGTGGTGAGATGTTGGTTAAGTCCC.GCAACGACGCGCAAC 233 05-0122_ConsGTGGTGAGATGTTGGTTAAGTCCC.GCAACGACGCGCAAC 233 05-0122_ConsGTGGTGAGATGTTGGTTAAGTCCC.GCAACGACGCGAAC 234 05-0033_stoGTGGTGAGATGTTGGTTAAGTCCC.GCAACGACGCGCAC 235 05-0122_ConsGTGGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCGAAC 236 05-0012_ConsGTGGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCGAAC 238 05-0012_ConsGTGTGGAGATGTTGGGTTAAGTCCC.GCAACGACGCGAAC 238 05-0013_CDnGTGTGGAGATGTTGGGTTAAGTCCC.GCAACGACGCGAAC 238 05-0015_ConsGTGTGGAGATGTTGGGTTAAGTCCC.GCAACGACGCGCAAC 238 05-0015_ConsGTGTGTGAGATGTTGGTTAAGTCCC.GCAACGACGCGAAC 238 05-0015_ConsGTGTGTGAGATGTTGGCTAACTCCC.TTTAGCTGCGCC.TTTA 271 05-0016_CONSGTTGTTGTTATTGCCATCATTAGCTTGCGGCAC.TTTA 271 05-0016_CONSGTGTGGAATGTTGGTTAAGTCCC.GCAACGCGCACC 138 05-0015_CONSGTGTGGAAGTGTGGCTACTTAAGTTGCGGCCC.TTTA 272 05-0015_CONSGTTGTTGTTATTGCCATCATTAGCTTGCGGCCC.TTTA 272 05-0015_CONSGTTGTTGTTATTGCCATCATTAGCTTGCGGCCCCCCCCCC	05-0038 Cons <mark>TATCAGAAGCA</mark> CAGGTGGTGCATGGTTGTCGTCAG <mark>C</mark> TCGT	194
05-0032 to TATCAGAAGA CAGETGETGCATGETTEGTCAGETGET 05-0014 Cons TATCAGAAGC ACAGETGETGCATGETTEGTCAGE TGET 194 05-0112 Cons TATCAGAAGC ACAGETGETGCATGETTEGTCAGE TGET 194 05-0122 Cons TATCAGAAGC ACAGETGETGCATGETTEGTCAGE TGET 194 05-0122 Cons TATCAGAAGC ACAGETGETGCATGETTEGTCAGE TGET 194 05-0122 Cons TATCAGAAGC ACAGETGETGCATGETTEGTCAGE TGET 195 05-0035 DT TATCAGAAGC ACAGETGETGCATGETTEGTCAGE TGET 199 05-0055 ConsGGACAGE GTGACAGETGETGCATGETTEGTCAGE TGET 199 05-0055 ConsGGACAGE GTGACAGETGETGCATGETTEGTCAGE TGET 199 05-0055 ConsGGACAGE GTGACAGETGETGCATGETTEGTCAGE TGET 199 05-0055 ConsGCACAGE GTGACAGETGETGCATGETTEGTCAGE TGET 199 05-0056 ConsGTCGTGAGATGTTGGGTTAAGTCC . GCACGAGEGCAC 233 05-0018 ConsGTCGTGAGATGTTGGGTTAAGTCC . GCACGAGEGCAC 233 05-0014 ConsGTCGTGAGATGTTGGGTTAAGTCC . GCACGAGEGCAC 233 05-0014 ConsGTCGTGAGATGTTGGGTTAAGTCC . GCACGAGEGCAC 233 05-0014 ConsGTCGTGAGATGTTGGGTTAAGTCC . GCACGAGEGCAC 233 05-0012 ConsGTCGTGAGATGTTGGGTTAAGTCC . GCACGAGEGCAC 233 05-0012 ConsGTCGTGAGATGTTGGGTTAAGTCC . GCACGAGEGCAC 233 05-0112 ConsGTCGTGAGATGTTGGGTTAAGTCC . GCACGAGEGCAC 233 05-0127 ConsGTCGTGAGATGTTGGGTTAAGTCC . GCACGAGEGCAC 234 05-0127 ConsGTCGTGAGATGTTGGGTTAAGTCC . GCACGAGEGCAC 238 05-0127 ConsGTCGTGAGATGTTGGGTTAAGTCC . GCACGACGCCAC 238 05-0015 ConsGTCGTGAGATGTTGGCTAAGTCC . GCACGACGCCAC 238 05-0015 ConsGTCGTGAGATGTTGGCTAAGTCC . GCACGACGCCAC 238 05-0015 ConsGTCGTGGAGATGTTGGCTAAGTCC . GCACGACGCCAC 239 05-0015 ConsGTCGTGGAGATGTTGGCTAAGTCC . GCACGACGCCAC 236 05-0015 ConsGTCGTGGAGATGTTGGCTAAGTCC . GCACGACGCCCCCCCCCCCCCCCCCCCCCCCCCCC	05-0062 Cons <mark>TATCAGAAGCA</mark> CAGGTGGTGCATGGTTGTCGTCAG <mark>C</mark> TCGT	194
05-0014_ConsTATCAGAAGA_CAGGTGGTGGCATGGTTGGTCAGCTGGT 05-0102_ConsTATCAGAAGCA_CAGGTGGTGGCATGGTTGGTCAGCTGGT 194 05-0122_ConsTATCAGAAGCA_CAGGTGGTGGCATGGTTGGTGCAGCTGGT 194 05-0122_ConsTATCAGAAGCA_CAGGTGGTGGCATGGTTGGTGCAGCTGGT 194 05-0122_ConsTATCAGAAGCA_CAGGTGGTGGCATGGTTGGTGCAGCTGGT 195 05-0033_PD_TATCAGAAGCA_CAGGTGGTGGCATGGTTGGTGCAGCTGGT 199 05-0055_ConsGACAGTGCAGGTGATGGTTGGTGCAGCTGGTGGTG 05-0018_ConsGTCGTGAGATGTTGGGTTAAGTCGC.CGCAGCGCAAC 233 05-0038_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 233 05-0033_stoGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 233 05-0033_stoGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 233 05-0014_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 233 05-0112_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 233 05-0112_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 233 05-0112_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 233 05-0112_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 233 05-0112_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 234 05-0122_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 235 05-0102_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 236 05-0112_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 237 05-0102_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 238 05-0102_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 238 05-0012_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 238 05-0013_ConsCTTGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 238 05-0014_ConsCTTGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 238 05-0015_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 238 05-0012_ConsCTTGTGTGATAATTGCCACATTAGGTGGGGCCTTTA 271 05-0033_stoCCTGGTGGTGAGTTAGTTGGCACATTAGCTGGGGCCTTTA 271 05-0018_CONSCTGTGTGATAATTGCCACATTAGCTGGGGCCTTTA 271 05-0013_consCCTTGTTGTTAATTGCCACATTAGCTGGGGCCCTTTA 272 05-0112_CONSCCTGTTGTTGTTAATTGCCACATTAGCTGGGGCCCTTTA 272 05-0122_CONSCCTGTTGTTAATTGCCACATTAGCTGGGGCCCTTTA 272 05-0013_cONSCCTGTTGTTGTTAATTGCCACATTAGCTGGGGCCCTTTA 272 05-0013_CONSCCTGTTGTTGTTAATTGCCACATTAGCTGGGGCCCTTTA 272 05-0013_CONSCCTGCTGCACATGCTACATTAGCTGCGGCCCTTTA 272 05-010	05-0077 Cons <mark>TATCAGAAGCA</mark> CAGGTGGTGCATGGTTGTCGTCAG <mark>T</mark> TCGT	194
05-0111_Cons TATCAGAAGCAGCAGGTGGTGCATGGTTGTCGTCAGCTGGT 194 05-0102_Cons TATCAGAAGCACAGGTGGTGCATGGTTGTCGTCAGCTGGT 194 05-0122_Cons TATCAGAAGCACAGGTGGTGCATGGTTGTCGTCAGCTGGT 194 05-0122_Cons TATCAGAAGCACAGGTGGTGCCATGGTTGTCGTCAGCTGGT 193 05-0005_Cons GGACAGGTCACAGGTGGTGCATGGTTGTCGTCAGCTGGT 199 05-0055_Cons GGACAGGTCACAGGTGGTGCATGGTTGTCGTCAGCTGGT 199 05-0055_Cons GGCAGAGGTCACAGGTGGTGGCATGGTTGTCGTCAGCTGGT 199 05-0055_Cons GTCGTGAGATGTTGGGTTAAGTCCC. 0CACGAGCGCAAC 233 05-0082_Cons GTCGTGAGATGTTGGGTTAAGTCCC. 0CAACGAGCGCAAC 233 05-0033_cons GTCGTGAGATGTTGGGTTAAGTCCC. 0CAACGAGCGCAAC 233 05-0033_sto GTCGTGAGATGTTGGGTTAAGTCCC. 0CAACGAGCGCAAC 233 05-0014_Cons GTCGTGAGATGTTGGGTTAAGTCCC. 0CAACGAGCGCAAC 233 05-0014_Cons GTCGTGAGATGTTGGGTTAAGTCCC. 0CAACGAGCGCAAC 233 05-0014_Cons GTCGTGAGATGTTGGGTTAAGTCCC. 0CAACGAGCGCAAC 234 05-0114_Cons GTCGTGAGATGTTGGGTTAAGTCCC. 0CAACGAGCGCAAC 235 05-0102_Cons GTCGTGAGATGTTGGGTTAAGTCCC. 0CAACGAGCGCAAC 234 05-0102_Cons GTCGTGAGATGTTGGGTTAAGTCCC. 0CAACGAGCGCAAC 234 05-0102_Cons GTCGTGAGATGTTGGGTTAAGTCCC. 0CAACGAGCGCAAC 234 05-0102_Cons GTCGTGAGATGTTGGGTTAAGTCCC. 0CAACGAGCGCAAC 238 05-0013_DTGTCGTGAGATGTTGGGTTAAGTCCC. 0CAACGAGCGCAAC 238 05-0012_Cons GTCGTGAGATGTTGGGTTAAGTCCC. 0CAACGAGCGCAAC 238 05-0013_Cons GTCGTGAGATGTTGGGTTAAGTCCC. 0CAACGAGCGCAAC 238 05-0014_Cons CCTTGTGTGTAATGCCACATTAGCTGGGGACTTTA 271 05-0016_Cons CCTTGTTGTTAATTGCCATCATTAGCTGGGGACTTTA 271 05-0016_Cons CCTTGTTGTTAATTGCCATCATTAGCTGGGGACTTTA 271 05-0014_Cons CCTTGTTGTTAATTGCCATCATTAGCTGGGGACTTTA 271 05-0014_CONS CCTTGTTGTTAATTGCCATCATTAGCTGGGGACTTTA 271 05-0014_CONS CCTTGTTGTTAATTGCCATCATTAGCTGGGGACTTTA 272 05-0014_CONS CCTTGTTGTTAATTGCCATCATTAGCTGGGGACTTTA 272 05-0014_CONS CCTTGTTGTTAATTGCCATCATTAGCTGGGGACTTTA 272 05-0014_CONS CCTTGTTGTTAATTGCCATCATTAGCTGGGGACTTTA 272 05-0014_CONS CCTTGTTGTTAATTGCCATCATTAGCTGGGGACTTTA 272 05-0014_CONS CCTTGTTGTTAATTGCCATCATTAGCTGGGGACTTTA 272 05-0014_CONS CCTTGTGTGCAATGTTAATTGCAGCAATGTGGGACTTTA	05-0033 sto <mark>tatcagaagca</mark> caggtggtgcatggttgtcgtcag <mark>c</mark> tcgt	194
05-0109_Cons TATCAGAAGA CAGGTGGTGGTAGGTTGGTGGTAG TGGT 05-0102_Cons TATCAGAAGCA CAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 05-0102_Cons TATCAGAAGCA CAGGTGGTGGGTGGTGGTGGTGGGTGGTGGTGGTGGTGGTG	05-0014_Cons <mark>TATCAGAAGCA</mark> CAGGTGGTGCATGGTTGTCGTCAG <mark>C</mark> TCGT	194
05-0102 Cons TATCAGARGA CAGETGETGECATGGTTGETEAG TEGET 05-0127 Cons TATCAGARGA CAGETGETGECATGGTTGETGECAGETGET 194 05-0127 Cons TATCAGARGA CAGETGETGETGETGETTGETEAGETGET 195 05-0035 Cons GGCAGAGTGACAGETGETGECATGGTTGETGETGECTGE 199 05-0055 Cons GGCAGETGECAGETGETGECATGGTTGETGETGECTGE 199 05-0018 Cons GTCGTGAGATGTTGEGTTAGTCCC . GCACCAGEGCACA 05-0018 Cons GTCGTGAGATGTTGEGTTAGTCCC . GCACCAGEGCACA 233 05-0023 Cons GTCGTGAGATGTTGEGTTAGTCCC . GCACCAGEGCACA 233 05-0033 _ sto GTCGTGAGATGTTGEGTTAGTCCC . GCACCAGEGCACA 233 05-0014 Cons GTCGTGAGATGTTGEGTTAGTCCC . GCACCAGEGCACA 233 05-0114 Cons GTCGTGAGATGTTGEGTTAGTCCC . GCACCAGEGCACA 233 05-0112 Cons GTCGTGAGATGTTGEGTTAGTCCC . GCACCAGEGCACA 233 05-0112 Cons GTCGTGAGATGTTGEGTTAGTCCC . GCACCAGEGCACA 233 05-0112 Cons GTCGTGAGATGTTGEGTTAGTCCC . GCACCAGEGCACA 233 05-0112 Cons GTCGTGAGATGTTGEGTTAGTCCC . GCACCAGEGCACA 234 05-0122 Cons GTCGTGAGATGTTGEGTTAGTCCC . GCACCAGEGCACA 235 05-0122 Cons GTCGTGAGATGTTGEGTTAGTCCC . GCACCAGEGCACA 238 05-0122 Cons GTCGTGAGATGTTGEGTTAGTCCC . GCACCAGEGCACA 238 05-0122 Cons GTCGTGAGATGTTGEGTTAGTTAGTCC . GCACCAGEGCACA 238 05-0122 Cons GTCGTGAGATGTTGEGTTAGTTAGTCC . GCACCAGEGCACA 238 05-0013 _ PD GTCGTGAGATGTTGEGTTAGTTAGTCC . GCACCAGEGCACA 238 05-0018 Cons GTCGTGAGATGTTGEGTTAGTTAGTTAGTTA CTCC . GCACCAGEGCACA 238 05-0018 Cons GTTGTGAGATGTTGEGTTAGTTAGTTAGCT . ALACGAGEGCAC 238 05-0018 Cons GTTGTTGTTAATTGCCATCATTAGTTGCGAC . TTTA 271 05-0018 Cons CTTGTTGTTAATTGCCATCATTAGTTGCGAC . TTTA 271 05-0018 Cons CTTGTTGTTAATTGCCATCATTAGTTGCGAC . TTTA 271 05-0018 Cons CTTGTTGTTAATTGCCATCATTAGTTGCGAC . TTTA 271 05-0018 Cons CTTGTTGTTAATTGCCATCATTAGTTGCGAC . TTTA 272 05-0018 Cons CTTGTTGTTAATTGCCATCATTAGTTGCGAC . TTTA 272 05-0012 Cons CTTGTTGTTAATTGCCATCATTAGTTGCGAC . TTTA 272 05-0012 Cons CTTGTTGTTAATTGCCATCATTAGTTGCGAC . TTTA 272 05-0013 _ DD CCTTGTGTGCAATGATTAATTGCGCGCAC . TTTA 272 05-0014 Cons CTTGTTGTTAATTGCCATCATTAGTTGCGGAC . TTTA 272 05-0018 Cons CTTGTGTGTAGTTGCCATCATTAGTTGCGGAC . TTTA 272 05-0018 Cons	05-0111_Cons <mark>TATCAGAAGCA</mark> CAGGTGGTGCATGGTTGTCGTCAG <mark>C</mark> TCGT	194
05-0127_ConsTATCAGAAGCACAGGTGGTGCATGGTTGTCGTCAGCTGGT 194 05-0122_ConsTATCAGAAGCACAGGTGGTGCATGGTTGTCGTCAGCTGGT 195 05-0005_ConsGGACAGAGTGACAGGTGGTGCATGGTTGTCGTCAGCTGGT 199 05-0005_ConsGCACAGAGTGACAGGTGGTGCATGGTTGTCGTCAGCTGGT 199 05-0018_ConsGCGTGAGATGTGGGTTAAGTCGC.GCACGACGCGCAC 233 05-0018_ConsGCGTGAGATGTGGGTTAAGTCGC.GCACGACGCGCAC 233 05-0003_ConsGCGTGAGATGTGGGTTAAGTCGC.GCAAGAGCGCAAC 233 05-0017_ConsGCGTGAGATGTGGGTTAAGTCGC.GCAAGAGCGCAAC 233 05-0011_ConsGCGTGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 233 05-0111_ConsGCGTGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 233 05-0111_ConsGCGTGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 233 05-0111_ConsGCGTGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 233 05-0112_ConsGCGTGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 233 05-0122_ConsGCGTGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 234 05-0122_ConsGCGTGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 238 05-0012_ConsGCGTGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 238 05-0012_ConsGCGTGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 238 05-0012_ConsGCGTGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 238 05-0012_ConsGCGTGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 238 05-0012_ConsGCGTGGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 238 05-0012_ConsGCGTGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 238 05-0013_ConsGCTGGTAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 238 05-0013_ConsGCTGGTGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 238 05-0013_ConsGCTGGTGAGATGTGGGTTAAGTCGC.GCAAGCAGCGCAC 238 05-0013_ConsGCTGGTGAGATGTGGGTAAGTCGC.GCAACGAGCGCAC 238 05-0013_ConsGCTGGTGTAATTGCCATCATTAAGTTGGGGACTTA 271 05-0014_ConsGCTGTGTTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0012_ConsGCTGTGTGTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0012_ConsGCTGTGTGTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0012_ConsGCTGTGTGTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0012_ConsGCTGTGTGTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0012_ConsGCTGTGTGTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0012_ConsGCTGTGTGTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0012_ConsGCTGTGTGTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0012_ConsGCTGTGTGTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0012_ConsGCTGTGTGTAATTGCCATCATTAAGTGGGGACTTA 272 05-	05-0109_Cons <mark>TATCAGAAGCA</mark> CAGGTGGTGCATGGTTGTCGTCAG <mark>C</mark> TCGT	194
05-0122_ConsTATCAGAAGCNCAGGTGGTGCATGGTTGTCGTCAGCTGGT 05-0005_ConsGGACAGTGCAGGTGGCATGGTTGTCGTCAGCTGGT 199 05-0055_ConsGCAGGTGCAGGTGCATGGTGTGTGTGTCGTCAGCTGGT 199 05-0018_ConsGTGGTGACATGTGGGTTAAGTCGC.GCGACGCGACC 233 05-0038_ConsGTGGTGACATGTGGGTTAAGTCGC.GCGACGCGACC 233 05-0038_consGTGGTGACATGTGGGTTAAGTCGC.GCGACGCGACC 233 05-0014_ConsGTGGTGACATGTGGGTTAAGTCGC.GCGACGCGCACC 233 05-0014_ConsGTGGTGACATGTGGGTTAAGTCGC.GCGACGCGCACC 233 05-0014_ConsGTGGTGACATGTGGGTTAAGTCGC.GCGACGCGCACC 233 05-0119_ConsGTGGTGACATGTGGGTTAAGTCGC.GCGACGCGCACC 233 05-0110_ConsGTGGTGACATGTGGGTTAAGTCGC.GCGACGCGCACC 233 05-0110_ConsGTGGTGACATGTGGGTTAAGTCGC.GCGACGCGCACC 233 05-0112_ConsGTGGTGACATGTGGGTTAAGTCGC.GCGACGCGCACC 233 05-0122_ConsGTGGTGACATGTGGGTTAAGTCGC.GCGACGCGCACC 234 05-0122_ConsGTGGTGACATGTGGGTTAAGTCGC.GCGACGCGCACC 234 05-0122_ConsGTGGTGACATGTGGGTTAAGTCGC.GCAACGACGCGACC 238 05-0122_ConsGTGGTGACATGTGGGTTAAGTCGC.GCAACGACGCGACC 238 05-0012_ConsGTGGTGACATGTGGGTTAAGTCGC.GCAACGACGCGCACC 238 05-0012_ConsGTGGTGACATGTGGGTTAAGTCGC.GCAACGACGCGCACC 238 05-0012_ConsGTGGTGACATGTGGGTTAAGTCGC.GCAACGACGCGCACC 238 05-0012_ConsGTGGTGACATGTGGGTTAAGTCGC.GCAACGACGCGCACC 238 05-0012_ConsGTGGTGACATGTGGGTTAAGTCGC.GCAACGACGCGCACC 238 05-0013_CD0GCTGGTGACATGTGGGTTAAGTCGC.GCAACGACGCGCACC 238 05-0014_ConsCCTGGTGGACTGTGGGTTAAGTCGC.GCAACGACGCGCACC 238 05-0013_CD0GCTGGTGGACGTGTGGCTAAGTTGGGTTAAGTGGGGCC.TTTA 271 05-0014_ConsCCTGGTGTGTAATTGCCATCATTAAGTTGGGGCCC.TTA 272 05-0012_ConsCCTGGTGTGTAATTGCCATCATTAAGTTGGGGCCC.TTTA 272 05-0012_ConsCCTGGTGTGTAATTGCCATCATTAAGTTGGGGCCC.TTA 272 05-0012_ConsCCTGGTGTGTAATTGCCATCATTAAGTTGGGGCCC.TTA 272 05-0012_ConsCCTGGTGTGTAATTGCCATCATTAAGTTGGGGCCC.TTA 272 05-0012_ConsCCTGGTGTGTAATTGCCATCATTAAGTTGGGGCCC.TTA 272 05-0012_ConsCCTGGTGTGTAATTGCCATCATTAAGTTGGGGCCCC.TTA 272 05-0012_ConsCCTGGTGTGTAATTGCCATCATTAAGTTGGGGCCCC.TTA 272 05-0012_ConsCCTGGTGTGTAATTGCCATCATTAAGTTGGGGCCCC.TTA 272 05-0012_CONSCCTGGTGCGATGTGCGATCATGCCATCATTAAGTTGGCGCCCC.TTA 272 05-0012_CONSCCTGGCGACTGCCAATG		
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05-0038 Cons GTCGTGAGATGTTGGGTTAAGTCC GCAACGACCGCAAC 233 05-0037 Cons GTCGTGAGATGTTGGGTTAAGTCC GCAACGACCGCAAC 233 05-0033 sto GTCGTGAGATGTTGGGTTAAGTCC GCAACGACCGCAAC 233 05-0014 Cons GTCGTGAGATGTTGGGTTAAGTCC GCAACGACCGCAAC 233 05-0109 Cons GTCGTGAGATGTTGGGTTAAGTCC GCAACGACCGCAAC 233 05-0109 Cons GTCGTGAGATGTTGGGTTAAGTCC GCAACGACCGCAAC 233 05-0102 Cons GTCGTGAGATGTTGGGTTAAGTCC GCAACGACCGCAAC 233 05-0102 Cons GTCGTGAGATGTTGGGTTAAGTCC GCAACGACCGCAAC 233 05-0102 Cons GTCGTGAGATGTTGGGTTAAGTCC GCAACGACCGCAAC 234 05-0127 Cons GTCGTGAGATGTTGGGTTAAGTCC GCAACGACCGCAAC 232 05-0102 Cons GTCGTGAGATGTTGGGTTAAGTCC TAAAACGACCGCAAC 232 05-0005 Cons GTCGTGAGATGTTGGGTTAAGTCC GCAACGACCGCAAC 238 05-0005 Cons GTCGTGAGATGTTGGGTAAGTCC GCAACGACCGCAAC 238 05-0005 Cons GTCGTGAGATGTTGGGTAAGTCC GCAACGACCGCAAC 238 05-0018 Cons CCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC TTTA 271 05-0018 Cons CCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC TTTA 271 05-0019 Cons CCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC TTTA 271 05-00102 Cons CCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC TTTA 271 05-01012 Cons CCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC TTTA 272 05-0102 Cons CCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC TTTA 272 05-0102 Cons CCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC TTA 272 05-0102 Cons CCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC TTA 272 05-0103 _CDn SCCTTGTTGTTATTGCCATCATTAAGTTGGGGAC TTA 272 05-0103 _CDn SCCAGACTGCCAATCGATAAATTGGGGAC TTA 272 05-0103 _CDn SCCAGACTGCCAATCGATAAATTGGGGAC TTA 272 05-0103 _CDn SCCAGACTGCCAATCGATAAATTGGAG .AAGGTGGGGACG 310 05-0033 _FD _CCTTCGCTACTTGCCACACTATAACTGGGGAC TTA 272 05-0033 _FD _CCTGCGTACTATCATAAATTGGAG .AAGGTGGGGACG 310 05-0013 _CDn SCCAGACTGCCAATCGATAAATTGGAG .AAGGTGGGGACG 310 05-0013 _SDCCAGACTGCCAATCGATAAATTGGAG .AAGGTGGGGACG 310 05-0013 _SDCCAGACTGCCAATCGATAAATTGGAG .AAGGTGGGGACG 311 05-0102 CONSCAAGACTG		233
05-0062_Cons GTCGTGAGATGTTGGGTTAAGTCC .GCAACGACCGCAAC 233 05-0033_stoGTCGTGAGATGTTGGGTTAAGTCC .GCAACGACCGCAAC 233 05-0014_Cons GTCGTGAGATGTTGGGTTAAGTCC .GCAACGACCGCAAC 233 05-0111_Cons GTCGTGAGATGTTGGGTTAAGTCC .GCAACGACCGCAAC 233 05-0119_Cons GTCGTGAGATGTTGGGTTAAGTCC .GCAACGACCGCAAC 233 05-0109_Cons GTCGTGAGATGTTGGGTTAAGTCC .GCAACGACCGCAAC 234 05-0127_Cons GTCGTGAGATGTTGGGTTAAGTCC .GCAACGACCGCAAC 234 05-0122_Cons GTCGTGAGATGTTGGGTTAAGTCC .GCAACGACCGCAAC 238 05-0122_Cons GTCGTGAGATGTTGGGTTAAGTCC .GCAACGACCGCAAC 238 05-0033_FD_GTCGTGAGATGTTGGGTTAAGTCC .GCAACGACCGCAAC 238 05-0055_Cons GTCGTGAGATGTTGGGTTAAGTCC .GCAACGACCGCAAC 238 05-0055_Cons GTCGTGAGATGTTGGGTTAAGTCC .GCAACGACCGCAAC 238 05-0055_Cons GTCGTGAGATGTTGGGTTAAGTCC .GCAACGACCGCAAC 238 Consensus gtcgtgagatgtt ggttaagtc macga gcaac 328 05-0055_Cons GTCGTGTGTTGTAATTGCCATCATTAAGTTGGGGAC .TTA 271 05-0018_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC .TTA 271 05-0038_consCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC .TTA 271 05-0039_stoCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC .TTA 271 05-0014_consCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC .TTA 271 05-0011_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC .TTA 271 05-0112_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC .TTA 271 05-0112_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC .TTA 271 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC .TTA 271 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC .TTA 272 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC .TTA 272 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC .TTA 272 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC .TTA 272 05-0013_FD_CCTGTGGCAATCATAATTGGAGA .AGGTGGGGACG 310 05-003_FD_CCTGGTGCTATGTGCCACATTAAGTTGGGGAC .TTA 272 05-0013_COnsCCAAGCTGCCAATCATAAATTGGAG .AGGTGGGGACG 310 05-0018_CONSCAAGCTGCCAATCATAAATTGGAG .AGGTGGGGACG 310 05-0018_CONSCAAGCTGCCAATCATAAATTGGAG .AGGTGGGGACG 310 05-0018_CONSCAAGCTGCCAATCATAAATTGGAG .AGGTGGGGACG 310 05-0014_CONSCAAGCTGCCAATCATAAATTGGAG .AGGTGGGGACG 311 05-0111_CONSCAAGCTGCCAATCATAAATTGGAG .AGGTGGGGACG 311 05-0112_CONSCAAGCTGCCAATCATAAATTGGAG .AGGTGGGGACG 311 05-0127_CONSCAAGCTGCCAATCATAAATTG		
05-003 stoGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCGAAC 233 05-0111 ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 233 05-0109 ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 233 05-0102 ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 234 05-0127 ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 233 05-0122 ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 233 05-0122 ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 232 05-0033 FD GTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 238 05-0055 ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 238 05-0055 ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 238 05-0055 ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 238 05-0015 ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 238 05-0015 ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 238 05-0018 ConsCGTTGTTGTTATTGCCATCATTAGGTGGGGAC.TTTA 271 05-0038 ConsCGTTGTTGTTATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0039 tcoCGTGTTGTTATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0014 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0013 stcoCGTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0014 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0112 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0112 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0127 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0033 FD CCTGGTGTTGTTAATTGCCACATTAAGTTGGGGAC.TTTA 272 05-0032 CONSCCTTGTTGTTAATTGCCACATTAAGTTGGGGAC.TTTA 272 05-0032 CONSCCTTGTTGTTAATTGCCACACTTAAGTTGGGGAC.TTTA 272 05-0032 CONSCCTTGTTGTTAATTGCCACACATTAAGTTGGGGAC.TTTA 272 05-0032 CONSCCTTGTTGTTAATTGCCACACATTAAGTTGGGGAC.TTTA 272 05-0032 CONSCCTTGTTGTTAATTGCCACACATTAAGTTGGGGAC.TTTA 272 05-0033 CONSCCTGCTATAGTTGCCACACATTAAGTTGGGGAC.TTTA 272 05-0032 CONSCCTGCCATGATGATAATTGGAGCAACCTGGGGACG 310 05-0038 CONSCCTGCCATGATGATAATTGGAGCAACGTGGGGACG 310 05-0042 CONSGCAAGACTGCCAATGATAATTGGAGCAACGTGGGGACG 310 05-0014 CONSGCAAGACTGCCAATGATAATTGGAGCAACGTGGGGACG 310 05-0014 CONSGCAAGACTGCCAATGATAATTGGAGCAACGTGGGGACG 311 05-0112 CONSGCAAGACTGCCAATGATAATTGGAGCAACGTGGGGAC	05-0062 Cons <mark>GTCGTGAGATGTT</mark> GGGTTAAGTCC <mark>C.GCA</mark> ACGA <mark>G</mark> CGCAAC	233
05-0014_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGGACCGCAAC 233 05-0119_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGGACGCAAC 233 05-0109_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 233 05-0122_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 234 05-0122_ConsGTCGTGAGATGTTGGGTTAAGTCCC.TTTACGACGGCAAC 235 05-0122_ConsGTCGTGAGATGTTGGGTTAAGTCCC.TTTACGACGCAAC 238 05-0033_FD_GTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 238 05-0055_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 238 05-0055_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 238 05-0055_ConsGTCGTGAGATGTTGGTTAAGTCCC.GCAACGACGCAAC 238 05-0055_ConsGTCGTGAGATGTTGGTTAAGTCCC.GCAACGACGCAAC 238 05-0055_ConsGTCGTGGTGATGTTGGTTAATTGCCATCATTAAGTTGGGGACTTTA 271 05-0018_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 271 05-0018_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 271 05-0014_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 271 05-0014_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 271 05-0102_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0102_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0102_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0102_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0102_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0102_ConsCCTTGTTGTTAATTGCCATCATTAGTTGGCGGACTTTA 272 05-0102_ConsCCTTGTTGTTAATTGCCATCATTAGTTGGCGGACTTTA 272 05-0005_ConsCCTTGTTGTTAATTGCCATCATTAGTTGGCGGACTTTA 272 05-0005_ConsCCTTGTTGTTAATTGCCATCATTAGTTGGCGGACTTTA 272 05-0005_ConsCCTGGTCGTTAGTTGCCACATTAAGTTGGGGGAC.TTA 272 05-0005_ConsCCTGGCTTAGTTGCCACATTAAGTTGGGCGACTTA 276 05-0005_ConsCCTGGAGACTGCCAATGATAATTGGAGC.AAGCTGGGGACG 310 05-0008_CONSCCAGACTGCCAATGATAATTGGAGC.AAGCTGGGGACG 310 05-0008_CONSCCAGACTGCCAATGATAAATTGGAGC.AAGCTGGGGACG 310 05-0018_CONSCCAGACTGCCAATGATAAATTGGAGC.AAGCTGGGGACG 311 05-0018_CONSCAAGACTGCCAATGATAAATTGGAGC.AAGCTGGGGACG 311 05-0014_CONSCAAGACTGCCAATGATAAATTGGAGC.AAGCTGGGGACG 311 05-0014_CONSCAAGACTGCCAATGATAAATTGGAGC.AAGCTGGGGACG 311 05-0112_CONSCAAGACTGCCAATGATAAATTGGAGC.AAGCTGGGGACG 311 05-0122_CONSCAAGACTGCCAATGATAAATTGGAGC.AACCTGGGGACG 311 05-	05-0077_Cons <mark>GTCGTGAGATGTTG</mark> GGTTAAGTCC <mark>C.GCA</mark> ACGA <mark>G</mark> CGCAAC	233
05-0111_ConsGTCGTGAGATGTTCGGTTAAGTCCC.GCAACGACGCGAAC 233 05-0102_ConsGTCGTGAGATGTTCGGTTAAGTCCC.GCAACGACGCGCAAC 234 05-0127_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 234 05-0127_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 232 05-0022_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 238 05-0033_FD_GTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 238 05-0055_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 238 05-0055_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 238 05-0055_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCGCAAC 238 05-0055_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCGCAAC 238 05-0055_ConsGTCGTGGAGATGTTGGGTTAAGTCCC.GCAACGACGCGCAAC 238 05-0055_ConsGTCGTGGAGATGTTGGGTTAAGTCCC.GCAACGACGCGCAAC 238 05-0055_ConsGTCGTGGTGTTAATTGCCATCATTAAGTTGGGCAC.TTTA 2711 05-0036_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 2711 05-0037_stcCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 2711 05-0014_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 2711 05-0013_stcCCTGTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 2721 05-0112_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 2722 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 2722 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 2722 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 2720 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 2720 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 2720 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 2720 05-0122_ConsCCTTGTTCTTAATTGCCATCATTAAGTTGGGGAC.TTTA 2720 05-0033_TD_CCTGTCCTTAGTTGCCACCATTAAGTTGGGGGACC310 05-0033_CONSCAAGACTGCCAATGATAAATTGGAGC_AAGCTGGGGACC310 05-0033_CONSCAAGACTGCCAATGATAAATTGGAGC_AAGCTGGGGACC310 05-0033_stcGCAAGACTGCCAATGATAAATTGGAGC_AAGCTGGGGACC310 05-0033_stcGCAAGACTGCCAATGATAAATTGGAGC_AAGCTGGGGACC310 05-0142_CONSCAAGACTGCCAATGATAAATTGGAGC_AAGCTGGGGACC310 05-0142_CONSCAAGACTGCCAATGATAAATTGGAGC_AAGCTGGGGACC310 05-0142_CONSCAAGACTGCCAATGATAAATTGGAGC_AAGCTGGGGACC310 05-0142_CONSCAAGACTGCCAATGATAAATTGGAGC_AAGCTGGGGACC310 05-0142_CONSCAAGACTGCCAATGATAAATTGGAGC_AAGCTGGGGACC310 05-0122_CONSCAAGACTGCCAATGATAAATTGGAGC_AAGCTGGGGACC3110 05-0122_CONSCAAGACT	05-0033sto <mark>gtcgtgagatgtt<mark>g</mark>ggttaagtcc<mark>c.gca</mark>acga<mark>g</mark>cgcaac</mark>	233
05-0109_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCGAAC 233 05-0122_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCGAAC 233 05-0122_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCGAAC 232 05-0005_ConsGTCGTGAGATGTTGGGTTAAGTCCC.TTTACGACGCGAAC 238 05-0015_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCGAAC 238 05-0018_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCGAAC 238 05-0018_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCGAAC 238 05-0018_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCGAAC 238 05-0018_ConsGTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0018_ConsGTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0023_stoCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0014_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0014_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0014_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0111_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0102_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0102_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0102_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0033_FD_CCCTGTGCCAGCATTAAGTTGGGGAC.TTA 272 05-0035_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTA 272 05-0035_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTA 272 05-0035_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTA 276 05-0035_ConsCCTTGCTTAGTTGCCAGCATTAAGTTGGGGAC.TTA 276 05-0035_ConsCCTTGCCTAGCTAGTAAATTGGAGGAAGCTGGGGACG 310 05-0036_ConsCAAGACTGCCAATCATTAAATTGGAGGAAGCTGGGGACG 310 05-0036_ConsCAAGACTGCCAATCATAAATTGGAGGAAGGTGGGGACG 310 05-0031_stoGCAAGACTGCCAATCATAAATTGGAGGAAAGCTGGGGACG 311 05-0112_ConsCCAAGACTGCCAATCATAAATTGGAGGAAAGGTGGGGACG 311 05-0122_ConsCCAAGACTGCCAATCATAAATTGGAGGAAAGGTGGGGACG 311 05-0122_ConsCCAAGACTGCCAATCATAAATTGGAGGAAAGGTGGGGACG 311 05-0122_ConsCCAAGACTGCCAATCATAAATTGGAGGAAAGGTGGGGACG 311 05-0122_ConsCCAAGACTGCCAATCATAAATTGGAGGAAAGGTGGGGACG 311 05-0122_ConsCCAAGACTGCCAATCATAAATTGGAGGAAGGTGGGGACG 311 05-0122_ConsCCAAGACTGCCAATCATAAATTGGAGGAAGGTGGGGACG 311 05-0035_FD_GCAAGACTGCCAATCATAAATTGGAGGA		
05-0102_ConsGTGTGAGATGTTGGGTTAAGTCCCCGCAACGGCGCAAC 05-0122_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 233 05-0122_ConsGTCGTGAGATGTTGGGTTAAGTCCC.TTAACGAGCGCAAC 234 05-0033_FD_GTCGTGAGATGTTGGGTTAAGTCCC.ACAACGAGCGCAAC 238 05-0055_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 238 05-0055_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 238 Consensusgtcgtgagatgtt_ggttaagtcc_ffaacga_cgcaac 05-0018_ConsCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0038_ConsCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0037_ConsCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0037_consCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0014_ConsCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0014_ConsCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0112_ConsCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0122_ConsCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTA 272 05-0122_ConsCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTA 272 05-0122_ConsCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTA 272 05-0122_ConsCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTA 272 05-0122_ConsCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTA 272 05-0122_ConsCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTA 272 05-0122_ConsCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTA 272 05-0122_ConsCCTTGTTGTAATTGCCATCATTAAGTTGGGGAC.TTA 272 05-0035_FD_CCTTGCGTACTTGCCAGCATTAAGTTGGGGAC.TTA 276 Consensus_CCtg_Tta_ttgTGCCACGCATTAAGTTGGGGAC.TTA 276 Consensus_CCtg_Tta_ttgTGCCAGCATTAAGTTGGGGACC.TTA 276 05-0035_ConsCCTTGCCTTAGTTGCCAGCATTAAGTTGGAGCAC.TTA 276 05-0035_ConsCCTGCCTTAGTTGCCAGCATTAAGTTGGAGCAC.TTA 276 05-0035_ConsCCAAGACTGCCAATGATAAATTGGAGG.AAGCTGGGACG 310 05-0035_ConsCCAAGACTGCCAATGATAAATTGGAGG.AAGCTGGGGACG 310 05-0014_ConsCCAAGACTGCCAATGATAAATTGGAGG.AAGCTGGGGACG 311 05-0112_ConsCCAAGACTGCCAATGATAAATTGGAGG.AAGCTGGGGACG 311 05-0122_ConsCCAAGACTGCCAATGATAAATTGGAGG.AAGCTGGGGACG 311 05-0122_ConsCCAAGACTGCCAATGATAAATTGGAGG.AAGCTGGGGACG 311 05-0122_ConsCCAAGACTGCCAATGATAAATTGGAGG.AAGCTGGGGACG 311 05-0122_ConsCCAAGACTGCCAATGATAAATTGGAGG.AAGCTGGGGACG 311 05-0035_FD_GCAAGACTGCCAATGATAAATTGGAGG.AAGCTGGGGACG		
05-0127_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 233 05-0122_ConsGTCGTGAGATGTTGGGTTAAGTCCC.TTTACGAGCGCAAC 232 05-0003_FD_GTCGTGAGATGTTGGTTAAGTCCC.TAAAACGAACGCGAAC 238 05-0055_ConsGTCGTGAGATGTTGGTTAAGTCCC.GCAACGAGCGCAAC 238 05-0018_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 238 05-0018_ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGAGCGCAAC 238 05-0018_ConsGTTGTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0036_ConsGTTGTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0036_ConsGTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0037_stoCCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0014_ConsGCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0014_ConsGCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0111_ConsGCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0112_ConsGCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 271 05-0112_ConsGCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0122_ConsGCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0122_ConsGCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0122_ConsGCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0122_ConsGCTTGTTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0033_FD_CCTTGTGTTAATTGCCATCATTAAGTTGGGGAC.TTTA 272 05-0032_FD_CCTTGTGTTAATTGCCACGCTTATGTTGGGGAC.TTTA 272 05-0032_FD_CCTTGTGTTAATTGCCACGCATTAAGTTGGGGAC.TTTA 276 05-0018_ConsGCTAGACTGCCAATGATAAATTGGAGGAAGC.TTA 276 05-0018_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0033_stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0033_stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0112_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_COnsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCAAGACTGCCAATGATA		
05-0122 ConsGTCGTGAGATGTTGGGGTTAAGTCCC. TTTACGAGCGCAAC 234 05-0033 FD GTCGTGAGATGTTAGGTTAAGTCCC.GCAACGACGCAAC 232 05-0055 ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCAAC 238 05-0055 ConsGTCGTGAGATGTTGGGTTAAGTCCC.GCAACGACGCCAAC 238 Consensus gtcgtgagatgtt ggttaagtcc the acga cgcaac 100 05-0018 consCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 271 05-0038 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 271 05-0062 consCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 271 05-0077 consCCTTGTTGTTAATTGCCATCATTAACTTGGGGACTTTA 271 05-0014 consCCTTGTTGTTAATTGCCATCATTAACTTGGGGACTTTA 271 05-0111 ConsCCTTGTTGTTAATTGCCATCATTAACTTGGGGACTTTA 271 05-0109 consCCTTGTTGTTAATTGCCATCATTAACTTGGGGACTTTA 271 05-0109 consCCTTGTTGTTAATTGCCATCATTAACTTGGGGACTTTA 271 05-0120 consCCTTGTTGTTAATTGCCATCATTAACTTGGGGACTTTA 272 05-0122 consCCTTGTTGTTAATTGCCATCATTAACTTGGGGACTTTA 272 05-0122 consCCTTGTTGTTAATTGCCATCATTAACTTGGGGACTTTA 272 05-0122 consCCTTGTTGTTAATTGCCATCATTAACTTGGGGACTTTA 272 05-0033 FD CCCTGTCGT TAATTGCCATCATTAACTTGGGGACTTTA 272 05-0055 consCCTTGTTGTTAATTGCCATCATTAACTTGGCGACTTTA 272 05-0055 consCCTTGTCGTTAATTGCCATCATTAACTTGGCGACTTTA 272 05-0055 consCCTTGTCGTTAATTGCCATCATTAACTTGGCGACTTTA 272 05-0055 consCCTTGTCGCTAGTTGCCAGCACGTAATTACTTGGCGACTCTA 276 05-0058 consCCTTGCCTTAGTTGCCAGCACGTAATTACTTGGCGACTCTA 276 05-0038 consCCATGCCTATGATTAACTGGCGCACTCTA 276 05-0038 consCCATGCCAATGATAAATTGGACG.AACGTGGGGACG 310 05-0038 consCCAAGACTGCCAATGATAAATTGGACG.AACGTGGGGACG 310 05-0038 consCCAAGACTGCCAATGATAAATTGGACG.AACGTGGGGACG 310 05-0039 stoGCAAGACTGCCAATGATAAATTGGACG.AACGTGGGGACG 310 05-014 consGCAAGACTGCCAATGATAAATTGGACG.AACGTGGGGACG 310 05-014 consGCAAGACTGCCAATGATAAATTGGACG.AACGTGGGGACG 311 05-0127 consGCAAGACTGCCAATGATAAATTGGACG.AACGTGGGGACG 311 05-0127 consGCAAGACTGCCAATGATAAATTGGACG.AACGTGGGGACG 311 05-0122 consGCAAGACTGCCAATGATAAATTGGACG.AACGTGGGGACG 311 05-0122 consGCAAGACTGCCAATGATAAATTGGACG.AAGCTGGGGACG 311 05-0122 consGCAAGACTGCCAATGATAAATTGGACG.AAGCTGGGGACG 311 05-0122 consGCAAGACTGCCAATGATAAATTGGACG.AAGCTGGGGACG 311 05-003		
05-0033 FD GTCGTGAGATGTTAGGTTAAGTCCT. AAAACGAACGCAAC 232 05-0005 ConsGTCGTGAGATGTTGGGTTAAGTCCC. GCAACGACGCAAC 238 05-0055 ConsGTCGTGAGATGTTGGGTTAAGTCCC. GCAACGACGCAAC 238 Consensus gtcgtgagatgtt ggttaagtct acga cgcacc 05-0018 ConsCCTGTTGTTAATTGCCATCATTAACTTGGCGACTTTA 271 05-0038 ConsCCTGTTGTTAATTGCCATCATTAACTTGGCGACTTTA 271 05-0062 ConsCCTGTTGTTAATTGCCATCATTAACTTGGCGACTTTA 271 05-0077 ConsCCTGTTGTTAATTGCCATCATTAACTTGGGGACTTTA 271 05-0014 ConsCCTGTTGTTAATTGCCATCATTAACTTGGGGACTTTA 271 05-0014 ConsCCTGTTGTTAATTGCCATCATTAACTTGGGGACTTTA 271 05-0111 ConsCCTGTTGTTAATTGCCATCATTAACTTGGGGACTTA 272 05-0102 ConsCCTGTTGTTAATTGCCATCATTAACTTGGGGACTTA 272 05-0122 ConsCCTGTTGTTAATTGCCATCATTAACTTGGGGACTTA 272 05-0122 ConsCCTGTTGTTAATTGCCATCATTAACTTGGGGACTTA 272 05-0122 ConsCCTGTTGTTAATTGCCATCATTAACTTGGGGACTTA 272 05-0122 ConsCCTGTTGTTAATTGCCATCATTAACTTGGGGACTTA 272 05-0122 ConsCCTGTTGTTAATTGCCATCATTAACTTGGGGACTTA 272 05-0005 ConsCCTGTGTCTTAGTTGCCACGATTAACTTGGGGACTTA 272 05-0005 ConsCCTGTGTCTTAGTTGCCACGCATTAACTTGGGGACTTA 272 05-0005 ConsCCTGTGTCTTAGTTGCCACGCATTAACTTGGGCACTTA 272 05-0005 ConsCCTGCCTAGTTGCCACGATTAACTTGGCGACTTA 276 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AACGTGGGGACG 310 05-0032 ConsGCAAGACTGCCAATGATAAATTGGAGG.AACGTGGGGACG 310 05-0032 consGCAAGACTGCCAATGATAAATTGGAGG.AACGTGGGGACG 310 05-0032 stoGCAAGACTGCCAATGATAAATTGGAGG.AACGTGGGGACG 310 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AACGTGGGGACG 310 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AACGTGGGGACG 310 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AACGTGGGGACG 310 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AACGTGGGGACG 310 05-014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AACGTGGGGACG 311 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGG.AACGTGGGGACG 311 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 311 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGCTGGGGACG 311 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGCTGGGGAGG 311 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGCTGGGGAGG 311 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGCTGGGGAGG 311 05-0013 FD GCAGACTGCCCAATGATAAATTGGA		
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05-0018_ConsCCTTGTTGTTATTGCCATCATTAAGTTGCGGACTTTA 271 05-0038_ConsCCTTGTTGTTATTGCCATCATTAAGTTGCGGACTTTA 271 05-0062_ConsCCTTGTTGTTATTGCCATCATTAAGTTGCGGACTTTA 271 05-0033_stoCCTTGTTGTTATTGCCATCATTAAGTTGCGGACTTTA 271 05-0014_ConsCCTTGTTGTTATTGCCATCATTAAGTTGCGGACTTTA 271 05-0014_ConsCCTTGTTGTTATTGCCATCATTAAGTTGCGGACTTTA 271 05-0119_ConsCCTTGTTGTTATTGCCATCATTAAGTTGCGGACTTTA 271 05-0109_ConsCCTTGTTGTTATTGCCATCATTAAGTTGCGGACTTTA 272 05-0102_ConsCCTTGTTGTTATTGCCATCATTAAGTTGCGGACTTTA 272 05-0122_ConsCCTTGTTGTTATTGCCATCATTAAGTTGCGGACTTTA 272 05-0122_ConsCCTTGTTGTTATTGCCATCATTAAGTTGCGGACTTTA 272 05-0122_ConsCCTTGTTGTTATTGCCATCATTAAGTTGCGGACTTTA 272 05-0055_ConsCCTTGTTGTTATTGCCATCATTAAGTTGCGGACTTTA 272 05-0055_ConsCCTTGCTTATTATTGCCACGCATTTAGTTGCGGACTTTA 272 05-0055_ConsCCTTGCTTTACTTGCCAGCACGTAATGGTGGGGACTCTA 276 05-0055_ConsCCTTGCCTTAGTTGTCATTAGTTGCCAGCACTTAAGTTGGGGACTCTA 276 05-0055_ConsCCTTGCCTTAGTTGATAATTGGCAGC.AAGGTGGGGACG 310 05-0038_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0038_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0033_stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0055_ConsAGGTGACTGCCGATGACAATGATAATTGGAGGAGGTGGGGATG 315		238
05-0038_ConsCC TTGTTGTTAATTGCCATCATTAAGTTGCGGACTTTA 271 05-0062_ConsCC TTGTTGTTAATTGCCATCATTAAGTTGCGGACTTTA 271 05-0033_stoCCTTGTTGTTAATTGCCATCATTAAGTTGCGGACTTTA 271 05-0014_ConsCC TTGTTGTTAATTGCCATCATTAAGTTGCGGACTTTA 271 05-0111_ConsCC TTGTTGTTAATTGCCATCATTAAGTTGCGGACTTTA 271 05-0111_ConsCC TTGTTGTTAATTGCCATCATTAAGTTGCGGACTTTA 271 05-0109_ConsCC TTGTTGTTAATTGCCATCATTAAGTTGCGGACTTTA 272 05-0102_ConsCC TTGTTGTTAATTGCCATCATTAAGTTGCGGACTTTA 272 05-0102_ConsCC TTGTTGTTAATTGCCATCATTAAGTTGCGGACTTTA 272 05-0122_ConsCC TTGTTGTTAATTGCCATCATTAAGTTGCGGACTTTA 272 05-0122_ConsCC TTGTTGTTAATTGCCATCATTAAGTTGCGGACTTTA 272 05-0122_ConsCC TTGTTGTTAATTGCCATCATTAAGTTGCGGACTTTA 272 05-0055_ConsCC TTGTTGTTAATTGCCACGCACGTAATGGTGGGGACTTTA 272 05-0055_ConsCC TTGTTGTTAATTGCCACGCACGTAATGGTGGGGACTCTA 276 05-0055_ConsCC TTGCC TTACTTGCCAGCACTTAAGTTGGGGACTCTA 276 05-0058_ConsCC TTGCC TTACTTGCCAGCACTTAAGTTGGGGACTCTA 276 05-0058_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0038_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0077_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0077_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0104_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0104_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0104_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0133_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_CONSGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCGAATGATAAATTGGAGGAAGGTGGGGACG 311	Consensus gtcgtgagatgtt ggttaagtcc acga cgcaac	
05-0062_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0077_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 271 05-0014_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 271 05-0111_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 271 05-0109_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0102_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0102_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0033_FD_CCCTGTCGTCATTATTGCCATCATTAAGTTGGGGACTTTA 272 05-0055_ConsCCTTGATCTTAATTGCCACGCACTTAAGTTGGGGACTCTA 276 05-0055_ConsCCTTGATCTTAGTTGCCAGCACTTAAGTTGGGGACTCTA 276 05-0018_ConsCCTTGATCTTAGTTGCCAGCACTTAAGTTGGGGACTCTA 276 05-0018_ConsCCTTGCCTTAGTTGCCAGCACTTAAGTTGGGGGACG 310 05-0018_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-003_stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-003_stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 312 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-013_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 312 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 313 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 314 05-003_FD_GCGAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 315		271
05-0077_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0033_stoCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 271 05-014_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 271 05-0111_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0102_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 272 05-0035_FD_CCTGTCGTCATTAATTGCCATCATTAGTTGGGGACTTA 272 05-0035_ConsCCTTGATCTTAGTTGCCAGCACGTAATGGTGGGGACTCTA 276 05-0055_ConsCCTTGCTTTAGTTGCCAGCACGTTAGTTGGGCACTCTA 276 05-0018_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0038_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0033_stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0133_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0132_CONSGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0133_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 311 05-0122_CONSGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 312 05-0122_CONSGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 313		
05-0033 stoCC TTG TTGTTAATTGCCATCATTAAGT TGGGGAC. TTTA 271 05-0014 ConsCC TTG TTGTTAATTGCCATCATTAAGT TGGGGAC. TTTA 271 05-0109 ConsCC TTGTTGTTAATTGCCATCATTAAGT TGGGGAC. TTTA 272 05-0109 ConsCC TTGTTGTTAATTGCCATCATTAAGT TGGGGAC. TTTA 272 05-0102 ConsCC TTGTTGTTAATTGCCATCATTAAGT TGGGGAC. TTTA 272 05-0122 ConsCC TTGTTGTTAATTGCCATCATTAAGT TGGGGAC. TTTA 272 05-0122 ConsCC TTGTTGTTAATTGCCATCATTAAGT TGGGGAC. TTTA 272 05-0033 FD CC TGTCGTGGTAGTTGCCAGCACCATCATTAACT TGGGGAC. TTTA 272 05-0005 ConsCC TTGTCGCTAGTTGCCAGCACCATCATTACT TGGGGAC. TTTA 272 05-0005 ConsCC TTGCTTAGTTGCCAGCACTTAACT TGGGGAC. TCTA 276 05-0055 ConsCC TTGCCTTAGTTGCCAGCATTAACT TGGGCAC. TCTA 276 05-0018 CCnsCC TTGCCATCATGATAATTGGAGG. AAGGTGGGGACG 310 05-0018 CCns GCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0038 CCns GCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0038 CCns GCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0033 stoGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0033 stoGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0014 COnsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0111 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0033 FD_GCGAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0052 ConsAGGTGACTGCCGGTGACAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0052 ConsAGGTGACTGCCGGTGACAATGATAAATTGGAGG AAGGTGGGGATG 316 05-0055 ConsAGGTGACTGCCGAGGACGGGACGGACGGAGGGAGGGAGGG		
05-0014_ConsCC TTG TTGTTAATTGCCATCATTAAGT TGGGGACTTA 271 05-0111_ConsCC TTG TTGTTAATTGCCATCATTAAGT TGGGGACTTA 271 05-0109_ConsCC TTG TTGTTAATTGCCATCATTAAGT TGGGGACTTA 272 05-0102_ConsCC TTG TTGTTAATTGCCATCATTAAGT TGGGGACTTA 272 05-0122_ConsCC TTG TTGTTAATTGCCATCATTAAGT TGGGGACTTA 272 05-0122_ConsCC TTG TTGTTAATTGCCATCATTAAGT TGGGGACTTA 272 05-0033_FD_CCC TGTCGCTAGTTGCCAGCACGT AATGGTGGGGACTTA 272 05-0005_ConsCC TTGATCTTAGTTGCCAGCACGT AATGGTGGGGACTCTA 276 05-0005_ConsCC TTGATCTTAGTTGCCAGCACGACGT AATGGTGGGGACTCTA 276 05-0055_ConsCC TTGCCTTAGTTGCCAGCATTAAGTTGGGCACTCTA 276 Consensus_cc tg ta ttgcca ca a t g g g t t ta 05-0018_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0038_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0032_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0033_stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0055_ConsAGGTGACTGCCGGTGACAAACTGGGAGAAGGTGGGAATG 316 05-0055_CONSAGGTGACTGCCGATGACAACCGGGAGAGGAGGGGAGGATG 316	US-UU// CONSIGNINGINGINGINALIGUUMIUMITAMUMIUGUGUAU	
05-0111_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTA 271 05-0109_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0102_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0127_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0122_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0033_FD_CCCTGTCGCTAGTGCCACGACATTAACTTGGGGACTTA 272 05-0005_ConsCCTTGATCTTAGTTGCCAGCACTTAACTTGGGGACTCTA 276 05-0055_ConsCCTTGCCTTAGTTGCCAGCACTTAGTTGGGCACTCTA 276 05-0055_ConsCCTTGCCTTTAGTTGCCAGCATTAACTTGGGCACTCTA 276 Consensus_CC_tg_tta_ttgCca_Ca_Ta_tG_tGGGACGTCTA 276 Consensus_CC_tg_tta_ttgCca_Ca_Ta_tG_tGGGCACTCTA 276 05-0018_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0038_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0038_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0033_stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0102_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0102_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-005_ConsAGGTGACTGCCGGTGACAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-005_ConsAGGTGACTGCCGGTGACAATGCGGGAGGAAGGTGGGGATG 316 05-005_ConsAGGTGACTGCCGGTGACAATGCGGGACGGAAGGTGGGGATG 316		
05-0109 ConsCC TTG TTGTTAATTGCCATCATTAAGTTGGGGACC. TTTA 272 05-0102 ConsCC TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0127 ConsCC TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0122 ConsCC TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTA 272 05-0033 FD CCCTGTCGCTAGTTGCCAGCACGTAATGGTGGGGACTTA 272 05-0005 ConsCC TTGATCTTAGTTGCCAGCACGTAATGGTGGGGACTCTA 276 05-0055 ConsCC TTGATCTTAGTTGCCAGCATTAAGTTGGGCACTCTA 276 05-0055 ConsCC TTGCCTTTAGTTGCCAGCATTAAGTTGGGCACTCTA 276 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0062 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0077 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0111 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0129 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0129 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033 FD GCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0032 FD GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033 FD GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033 FD GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033 FD GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033 FD GCGAGACTGCCAATGATAAATTGGAGG AAGGTGGGGACG 311 05-0035 FD GCGAGACTGCCAATGATAAATTGGAGG AAGGTGGGGACG 311 05-0055 ConsAGGTGACTGCCGGTGACAAACCGGGAGGAGGAGGGGAGG	05-0033 sto <mark>cc</mark> tgttgttaattgccatcattaagttggggacttta	271
05-0102_ConsCC TTG TTGTTAATTGCCATCATTAAGT TGGGGACTTA 272 05-0127_ConsCC TTG TTGTTAATTGCCATCATTAAGT TGGGGACTTA 272 05-0122_ConsCC TTG TTGTTAATTGCCATCATTAAGT TGGGGACTTA 272 05-0033_FD_CCC TGTCGCTAGTTGCCAGCACGT AATGGTGGGGACTTA 272 05-0005_ConsCC TTGATCTTAGTTGCCAGCACGT AATGGTGGGGACTCTA 276 05-0055_ConsCC TTGCCTTTAGTTGCCAGCATTAAGT TGGGCACTCTA 276 05-0018_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0018_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0038_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0062_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0077_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0033_stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0055_ConsAGGTGACTGCCGGTGACAAACCGGGAGGAGGAGGAGGGGAGGATG 316 05-0055_ConsAGGTGACTGCCGGGGACGACGGGGACGGACGGAGGAGGGGAGGGA	05-0033stoCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTA 05-0014_ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTA	271 271
05-0127 ConsCC TTG TTGTTAATTGCCATCATTAAGT TGGGGGGC. TTTA 272 05-0122 ConsCC TTG TTGTTAATTGCCATCATTAAGT TGGGGAC. TTTA 272 05-0033 FD CCC TGTCGCTAGTTGCCAGCACGT AATGGTGGGGAC. TTTA 272 05-0005 ConsCC TTGATCTTAGTTGCCAGCACGT AATGGTGGGGAC. TCTA 276 05-0055 ConsCC TTGCCTTTAGTTGCCAGCATTAAGT TGGGCAC. TCTA 276 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0062 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0077 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0077 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0033 stoGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0111 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0033 FD GCGAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0032 FD GCGAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0033 FD GCGAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0033 FD GCGAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0033 FD GCGAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0033 FD GCGAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311	05-0033 stoccttgttgttaattgccatcattaagttggggacttta 05-0014 Consccttgttgttaattgccatcattaagttggggactt 05-0111 Consccttgttgttaattgccatcattaagttggggactt	271 271 271
05-0033 FD_CCCTGTCGCTAGTTGCCAGCACGTAATGGTGGGGACTTTA 272 05-0005 ConsCCTTGATCTTAGTTGCCAGCATTTAGTTGGGCACTCTA 276 05-0055 ConsCCTTGCCTTTAGTTGCCAGCATTAAGTTGGGCACTCTA 276 Consensus cc tg ta ttgcca ca a t g g g t t ta 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0062 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0077 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0077 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0033 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0111 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0112 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 312 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0123 FD_GCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033 FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033 FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033 FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033 FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311	05-0033 stoCCTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 ConsCCTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 ConsCCTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 ConsCCTTGTTAATTGCCATCATTAAGTTGGGGACTTTA	271 271 271 272
05-0005 ConsCCTTGATCTTAGTTGCCAGCATTTAGTTGGGGCACTCTA 276 05-0055 ConsCCTTGCCTTTAGTTGCCAGCATTAAGTTGGGCACTCTA 276 Consensus cc tg ta ttgcca ca a t g g t t ta 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0062 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0077 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0077 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0033 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0111 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 312 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 312 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033 FD GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033 FD GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311	05-0033 stoCCTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 ConsCCTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 ConsCCTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 ConsCCTTGTTAATTGCCATCATTAAGTTGGGGACC.TTTA 05-0102 ConsCCTTGTTAATTGCCATCATTAAGTTGGGGACTTTA	271 271 271 272 272
05-0055_ConsCCTTTGCCTTTAGTTGCCAGCATTAAGTTGGGGCACTCTA 276 Consensus cc tg ta ttgcca ca a t g g t t ta 05-0018_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0038_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0062_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0077_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0033_stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0102_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 312 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311	05-0033 stoCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACC.TTTA 05-0102 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGGACTTTA	271 271 271 272 272 272 272
Consensus cc tg ta ttgcca ca a t g g t ta 05-0018_ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0038_ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0062_ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0077_ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0033_stoGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 310 05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0102_ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 312 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG. AAGGTGGGGACG 311 05-0055_ConsAGGTGACTGCCGATGACAAACCTGGGAGGAAGGTGGGGATG 316 05-0055_ConsGAGGGACTGCCGAGGATAACTGGGACAAGGTGGGGATG 315	05-0033 stoCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACC.TTTA 05-0102 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA	271 271 272 272 272 272 272 272 272
05-0018_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0038_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0062_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0077_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0033_stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0102_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0127_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 312 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0055_ConsAGGTGACTGCCGGTGACAAACCTGGGAAGGTGGGGATG 316 05-0055_ConsAGGTGACTGCCGAGGATAACTGGGACAAGGTGGGGATG 316	05-0033 stoCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACCTTTA 05-0102 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0127 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0033 FD CCCTGCTGCTAGTTGCCACCATCATTAGTTGGGGACTTA	271 271 272 272 272 272 272 272 272 272
05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0062 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0077 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0033 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0111 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 312 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033 FD GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033 FD GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311	05-0033 stoCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0102 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0127 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0033 FD_CCCTGTCGCTAGTTGCCAGCACGTAATGGTGGGGAC.TTTA 05-0055 ConsCCTTGATCTTAGTTGCCAGCATTTAAGTTGGGCACTCTA	271 271 272 272 272 272 272 272 272 272
05-0062_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0077_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0033_stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTAGGGGACG 311 05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0102_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0102_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 312 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 312 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGATA 311 05-0055_ConsAGGTGACTGCCGAGGATAACTGGGA	05-0033 stoCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0102 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0033 FD CCCTGCTGCTAGTTGCCACCATCATTAGTTGGGGACTTTA 05-0005 ConsCCTTGATCTTAGTTGCCACCATCATTAGTTGGGGACTCTA 05-0055 ConsCCTTGTTAATTGCCACCATTTAGTTGGGCACTCTA	271 271 272 272 272 272 272 272 272 276 276
05-0033_stoGCAAGACTGCCAATGATAAATTGGAGGAAGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGGGAAGGTGGGGACG 311 05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 310 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGAAGGTGGGGACG 311 05-0102_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 311 05-0127_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGGACG 312 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGGACG 312 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGGAAGGTGGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 311 05-0005_ConsAGGTGACTGCCGGTGACAAACCGGGAGGAAGGTGGGGATG 316 05-0055_ConsGAGGGACTGCCGAGGATAACTGCGGAAGGTGGGGATG 315	05-0033 stocc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACCTTTA 05-0102 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0127 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0033 FD CCCTGCTGCTAGTTGCCAGCACGTAATGGTGGGGACTTTA 05-0005 Conscc TTGTTATTGCCAGCACGTAATGGTGGGGACTCTA 05-0055 Conscc TTGTTATTAGTTGCCAGCATTTAAGTTGGGCACTCTA 05-0055 Conscc TTGCTTAGTTGCCAGCATTTAAGTTGGGCACTCTA 05-0055 Conscc TTGCCTTAGTTGCCAGCATTTAAGTTGGGCACTCTA 05-0018 ConsGCAAGACTGCCAATGATAAATTGCAGG.AAAGTGGGGACGC	271 271 272 272 272 272 272 272 276 276 276 310
05-0033_stoGCAAGACTGCCAATGATAAATTGGAGGAAGGGACG 310 05-0014_ConsGCAAGACTGCCAATGATAAATTGGAGGGAAGGTGGGGACG 311 05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 310 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGAAGGTGGGGACG 311 05-0102_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 311 05-0127_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGGACG 312 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGGACG 312 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGGAAGGTGGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 311 05-0005_ConsAGGTGACTGCCGGTGACAAACCGGGAGGAAGGTGGGGATG 316 05-0055_ConsGAGGGACTGCCGAGGATAACTGCGGAAGGTGGGGATG 315	05-0033 stocc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACCTTTA 05-0102 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0127 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGGACTTTA 05-0122 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0033 FD CCCTGTCGC TAGTTGCCAGCACGTAATGGTGGGGACTTTA 05-0055 Conscc TTGTTATTGTTGCCAGCATTTAGTTGGGCACTCTA 05-0055 Conscc TTGCTTAGTTGCCAGCATTTAGTTGGGCACTCTA Consensus cc tg ta ttgcca ca a t g g t t ta 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG	271 271 272 272 272 272 272 272 276 276 276 310 310
05-0111_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 310 05-0109_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0102_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0127_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGGACG 312 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0005_ConsAGGTGACTGCCGATGACAAACCTGGGGAAGGTGGGGATG 316 05-0055_ConsGGGGACTGCCGAGGATAACTCGG.ACGAAGGTGGGGATG 315	05-0033 stocc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACCTTTA 05-0102 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0127 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGGACTTTA 05-0122 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0033 FD CCCTGTCGC TAGTTGCCAGCACGTAATGGTGGGGACTTTA 05-0055 Conscc TTGTTATTGTTGCCAGCATTTAGTTGGGCACTCTA 05-0055 Conscc TTGCTTAGTTGCCAGCATTTAGTTGGGCACTCTA Consensus cc tg ta ttgcca ca a t g g t t ta 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG	271 271 272 272 272 272 272 272 276 276 276 310 310 310
05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 312 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033 FD_GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGATA 311 05-0005 ConsAGGTGACTGCCGATGACAAACCGGGAGGAAGGTGGGGATG 316 05-0055 ConsGAGGGACTGCCGAGGATAACTCGG.ACGAAGGTGGGGATG 315	05-0033 stocc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACCTTTA 05-0102 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0033 FD CCCTGCTGC TAGTTGCCAGCACGTAATGGTGGGGACTTTA 05-0005 Conscc TTGATCTTAGTTGCCAGCATTTAGTTGGGCACTCTA 05-0055 Conscc TTGCTTATTGTTGCCAGCATTTAGTTGGGCACTCTA Consensus cc tg ta ttgcca ca a t g g t t ta 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0062 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0062 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0077 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG	271 271 272 272 272 272 272 276 276 276 310 310 310 310 310
05-0102_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0127_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGGACG 312 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATTAAACATTGGAGG.AAGGTGGGGATA 311 05-0005_ConsAGGTGACTGCCGGTGACAAACCGGGAGGAAGGTGGGGATG 316 05-0055_ConsGAGGGACTGCCGAGGATAACTCGG.AGGAAGGTGGGGATG 315	05-0033 stocc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACCTTTA 05-0102 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACCTTTA 05-0122 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACCTTTA 05-0122 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACCTTTA 05-0122 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACCTTTA 05-0033 FD CCCTGTCGC TAGTTGCCAGCACGTAATGGTGGGGACTTTA 05-0055 Conscc TTGTTATTGTTGCCAGCATTTAGTTGGGCACTCTA 05-0055 Conscc TTGCTTGTTAGTTGCCAGCATTTAGTTGGGCACTCTA Consensus cc tg ta ttgcca ca a t g g t t ta 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0062 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0077 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0033 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0033 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0034 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0035 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0034 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0034 consGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0034 consGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0034 consGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0034 consGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0034 consGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0034 consGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0034 consGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG	271 271 272 272 272 272 272 276 276 276 310 310 310 310 310 310
05-0127_ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGGACG 312 05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033FD_GCGAGACTGCCAATTAAACATTGGAGG.AAGGTGGGGATA 311 05-0005_ConsAGGTGACTGCCGGTGACAAACCGGGAGGAAGGTGGGGATG 316 05-0055_ConsGAGGGACTGCCGAGGATAACTCGG.AGGAAGGTGGGGATG 315	05-0033 stocc TTG TTGT TAATTGCCAT CATTAAGTTGGGGAC TTTA 05-0014 Conscc TTG TTGT TAATTGCCAT CATTAAGTTGGGGAC TTTA 05-0111 Conscc TTG TTGT TAATTGCCAT CATTAAGTTGGGGAC TTTA 05-0109 Conscc TTG TTGT TAATTGCCAT CATTAAGTTGGGGACC TTTA 05-0102 Conscc TTG TTGT TAATTGCCAT CATTAAGTTGGGGACC TTTA 05-0122 Conscc TTG TTGT TAATTGCCAT CATTAAGTTGGGGAC TTTA 05-0122 Conscc TTG TTGT TAATTGCCAT CATTAAGTTGGGGAC TTTA 05-0122 Conscc TTG TTGT TAATTGCCAT CATTAAGTTGGGGAC TTTA 05-0033 FD CC CTG TCG CTAG TTGCCAGC CACGTAATGGTGGGGAC TTTA 05-0005 Conscc TTGATCTTAGTTGCCAGC ATTAAGTTGGGCAC TC TA 05-0055 Conscc TTGCCTTAGTTGCCAGC ATTAAGTTGGGCAC TC TA 05-0055 Conscc TTGCCTTTAGTTGCCAGC ATTAAGTGGGCAC TC TA 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0077 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0033 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG	271 271 272 272 272 272 272 276 276 276 310 310 310 310 310 310 311 310
05-0122_ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 311 05-0033_FD_GCGAGACTGCCAATTAAACATTGGAGG.AAGGTGGGGATA 311 05-0005_ConsAGGTGACTGCCGGTGACAAACCGGGAGGAAGGTGGGGATG 316 05-0055_ConsGAGGGACTGCCGAGGATAACTCGG.AGGAAGGTGGGGATG 315	05-0033 stocc TTG TTGT TAATTGCCAT CATTAAGTTGGGGAC TTTA 05-0014 Conscc TTG TTGT TAATTGCCAT CATTAAGTTGGGGAC TTTA 05-0111 Conscc TTG TTGT TAATTGCCAT CATTAAGTTGGGGAC TTTA 05-0109 Conscc TTG TTGT TAATTGCCAT CATTAAGTTGGGGACC TTTA 05-0102 Conscc TTG TTGT TAATTGCCAT CATTAAGTTGGGGACC TTTA 05-0122 Conscc TTG TTGT TAATTGCCAT CATTAAGTTGGGGACC TTTA 05-0122 Conscc TTG TTGT TAATTGCCAT CATTAAGTTGGGGACC TTTA 05-0122 Conscc TTG TTGT TAATTGCCAT CATTAAGTTGGGGACC TTTA 05-0033 FD CC CTG TCG CTAG TTGCCAGC ACGTAATGGTGGGGACC TTTA 05-0055 Conscc TTGATCTTAGTTGCCAGC ATTAAGTTGGGCAC TC TA 05-0055 Conscc TTGC CTTTAGTTGCCAGC ATTAAGTTGGGCAC TC TA 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0062 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0077 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0033 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0111 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG	271 271 272 272 272 272 272 276 276 276 310 310 310 310 310 311 310 311
05-0033_FD_GCGAGACTGCCAATTAAACATTGCACG.AAGGTGGGGATA 311 05-0005_ConsAGGTGACTGCCGGTGACAAACCGGGAGGAAGGTGGGGATG 316 05-0055_Cons <mark>GAGGGACTGCCGAGGATAACTC</mark> GGAAGGTGGGGATG 315	05-0033 stocc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACCTTTA 05-0102 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACCTTTA 05-0122 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 Conscc TTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0033 FD CCCTGTCGC TAGTTGCCAGCACGTAATGGTGGGGACTTTA 05-0055 Conscc TTGTTATTAGTTGCCAGCATTTAGTTGGGCACTCTA 05-0055 Conscc TTGCTTAGTTGCCAGCATTTAGTTGGGCACTCTA 05-0018 ConscC TTGCCTTAGTTGCCAGCATTAAGTGGGGCACTCTA Consensus cc tg ta ttgcca ca a t g g t t ta 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0038 consGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0039 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0111 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGCACG 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0109 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG	271 271 272 272 272 272 272 272 276 276 276 310 310 310 310 310 311 310 311 311
05-0005_ConsAGGTGACTGCCGGTGACAAACCGGGAGGAAGGTGGGGATG 316 05-0055_Cons <mark>G</mark> AGG <mark>GACTGCCGAGGATAACTCGG.AGGAAGGTGGGGATG 315</mark>	05-0033 stoCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACC.TTTA 05-0102 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACC.TTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0033 FD CCCTGTCGCTAGTTGCCAGCACGTAATGGTGGGGACTTTA 05-0055 ConsCCTTGATCTTAGTTGCCAGCATTTAGTTGGGCACTCTA 05-0055 ConsCCTTGCCTTAGTTGCCAGCATTAAGTTGGGCACTCTA Consensus cc tg ta ttgcca ca a t g g g t t ta 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0039 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0077 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0031 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0101 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTAGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGGAAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 05-0127 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG	271 271 272 272 272 272 272 272 276 276 276 310 310 310 310 310 311 310 311 311 311
05-0055_ConsGAGG <mark>GACTGCC</mark> GAGGATAACTCGG.AGGAAGGTGGGGGATG 315	05-0033 stoCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACC.TTTA 05-0102 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACC.TTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0033 FD CCCTGTCGCTACTTGCCAGCACGTAATGGTGGGGACTTTA 05-0055 ConsCCTTGATCTTACTTGCCAGCATTAAGTTGGGCACTCTA 05-0055 ConsCCTTGCCTTTACTTGCCAGCATTAAGTTGGGCACTCTA Consensus cc tg ta ttgcca ca a t g g g t t ta 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0039 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0039 stoGCAAGACTGCCAATGATAAATTGGACG.AAGGTGGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGACG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGACG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGACG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGACG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGACG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGACG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGACG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGACG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGACG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGACG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGACG.AAGGTGGCGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGACG.AAGGTGGCGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGACG.AAGGTGGCGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGACGAAGGTGGGGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGACGAAGGTGGGGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGACGAAGGTGGGGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGACGAAGGTGGCGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGACGAAGGTGGCGACG	271 271 272 272 272 272 272 272 276 276 276 276
	05-0033 stoCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACC.TTTA 05-0102 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACC.TTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0033 FD CCCTGTCGCTAGTTGCCAGCATCATTAGGTGGGGACTTTA 05-0055 ConsCCTTGATCTTAGTTGCCAGCATTTAGTTGGGCACTCTA 05-0055 ConsCCTTGCCTTTAGTTGCCAGCATTAAGTTGGGCACTCTA Consensus cc tg ta ttgcca ca a t g g g t t ta 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0032 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0033 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGCGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0123 FD GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0133 FD GCGAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG	271 271 272 272 272 272 272 272 276 276 276 310 310 310 310 310 310 311 311 311 311
	05-0033 stoCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0014 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0111 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0109 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACC.TTTA 05-0102 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACC.TTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0122 ConsCCTTGTTGTTAATTGCCATCATTAAGTTGGGGACTTTA 05-0033 FD CCCTGTCGCTAGTTGCCAGCATCATTAGGTGGGGACTTTA 05-0055 ConsCCTTGATCTTAGTTGCCAGCATTAAGTTGGGGCACTCTA 05-0055 ConsCCTTGCCTTTAGTTGCCAGCATTAAGTTGGGCACTCTA Consensus cc tg ta ttgcca ca a t g g g t t ta 05-0018 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0038 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0039 consGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGGACG 05-0032 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0031 stoGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0014 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0111 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGG.AAGGTGGGGACG 05-0102 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 05-0112 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 05-0122 ConsGCAAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 05-0123 FD _GCGAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 05-0033 FD _GCGAGACTGCCAATGATAAATTGGAGGAAGGTGGGGACG 05-0033 FD _GCGAGACTGCCAATGATAAATTGGAGGAAGGTGGGGAATA 05-0005 ConsAGGTGACTGCCGGGGGACGGGGGGGGGGGGGGGGGGGGG	271 271 272 272 272 272 272 276 276 276 276 310 310 310 310 310 310 311 311 311 311





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05-0038_ConsaCGTCAAATCATCATGCCCCTTATGACCTGGGCTACAAAC	350
05-0062_Consacgtcaaatcatcatgccccttatg <mark>acct</mark> gggctaca <mark>a</mark> ac	350
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05-0111_Cons <mark>aCGTCAAATCATCATGCCCCTTATG</mark> ACCTGGGCTACA <mark>A</mark> AC	350
05-0109_Cons ^a CGTCAAATCATCATGCCCCTTATG <mark>ACCT</mark> GGGCTACA <mark>A</mark> AC	351
05-0102_Cons <mark>aCGTCAAATCATCATGCCCCTTATG</mark> ACCTGGGCTACA <mark>A</mark> AC	351
05-0127_Cons ^a CGTCAAATCATCATGCCCCTTATG <mark>ACCT</mark> GGGCTACA <mark>A</mark> AC	352
05-0122_Cons <mark>ACGTCAAATCATCATGCCCCTTATG<mark>ACCT</mark>GGGCTACA<mark>A</mark>AC</mark>	351
05-0033FD_ACGTCAAATCATCATGCCCCTTATG <mark>ATCT</mark> GGGCTACA <mark>A</mark> AC	351
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05-0055_ConsACGTCAAATCATCATGCCCCTTATG <mark>CTTA</mark> GGGCTACA <mark>C</mark> AC	355
Consensus acgtcaaatcatcatgccccttatg gggctaca ac	
05-0018_Cons <mark>GTGATACAATGGCTGTTACAAAG</mark> GGTAGCT.AAAAGCGTAA	389
05-0038_Cons <mark>gtgatacaatggC</mark> tgttacaaagggtagct. aaagcgtaa	389
05-0062_Cons <mark>GTGATACAATGGCTGTTACAAAGGGTAGCT.AAAGC</mark> GTAA	389
05-0077_Cons <mark>GTGATACAATGGCTGTTACAAAGGGTAGCTTAAAAGC</mark> GTAA	390
05-0033 sto <mark>gtgatacaatggc</mark> tgttaca <mark>aagggtagct.aaagc</mark> gtaa	389
05-0014_Cons <mark>GTGATACAATGGCTGTTACAAAGGGTAGCT. AAAGC</mark> GTAA	390
05-0111 Cons <mark>GTGATACAATGGCTGT</mark> TACAAAG <mark>GGTAGCT.AAAGC</mark> GTAA	389
05-0109_Cons <mark>GTGATACAATGGCTGTTACAAAGGGTAGCT. AAAGC</mark> GTAA	390
05-0102_Cons <mark>GTGATACAATGGCTGTTACAAAGGGTAGCT.AAAGC</mark> GTAA	390
05-0127_Cons <mark>GTGATACAATGGCTGT</mark> TACA <mark>AAGG</mark> GTAGCT <mark>AAAG</mark> CGTAA	392
05-0122_Cons <mark>GTGATACAATGGCTGTTACAAAGGCTAGCT.AAAGC</mark> GTAA	390
05-0033 FD GTG <mark>ATACAATGGCTAT</mark> TACA <mark>AAGAG</mark> TAGCT.GAAACGCGA	390
05-0005 Cons <mark>GTGCTACAATGGAT<mark>G</mark>GTACA<mark>AAG</mark>GCT<mark>GC</mark>AAGACCGCG</mark>	394
05-0055_Cons <mark>GTGCTACAATGG</mark> G <mark>TGG</mark> TACA <mark>GAG</mark> GTTGCCAAACCGTG	393
Consensus gtg tacaatgg t taca ag g a a c	
05-0018_Cons <mark>gCT</mark> TCTG <mark>GCGAATCTCGAAAAAGCAG</mark> TCTCAGT <mark>TCG</mark> GATT	429
05-0038_Cons <mark>gCTTCTggcgaatCtCaaaaaaagCag</mark> tCtCagttCggatt	429
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05-0077_Cons <mark>GCTTCTGGCGAATCTCAAAAAAGCAG</mark> TCTCAGTT <mark>C</mark> GGATT	430
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05-0033FD_ <mark>GTT</mark> TTTAGCCAATC <mark>TCAA</mark> AAAG <mark>GTAG</mark> TCTCAGTAC <mark>GGAT</mark> T	430
05-0005_ConsAGGTCAAGCCAATCCCATAAAACCATTCTCAGTTCGGATT	434
05-0055 ConsAGGTGGAGCTAATCCCTTAAAGCCATTCTCAGTTCGGATT	433
concentration of go dates of data a coordige of g o	4.6.6
05-0018_ConsC <mark>AAGTCTGCAACTCGACTTCATGAAG.TTGGAATCG</mark> CT 05-0038_ConsC <mark>AAGT</mark> CTG <mark>C</mark> AACTCG <mark>ACTTCATGAAG.TTGGAATCG</mark> CT	466
05-0062 ConsGAAGTCTGCAACTCGACTTCATGAAG.TTGGAATCGCT	466
05-0077_ConsGAAGTCTGCAACTCGACTTCATGAAG.TGGGAATCGCT	466 467
05-0037 stoGAAGTCTGCAACTCGACTTCATGAAG.TGGGAATCGCT	466
05-0014 ConsGAAGTCTGCAACTCGACTTCATGAAG.TTGGAATCGCT	467
	468
05-0111_ConstG <mark>C</mark> AAG <mark>T</mark> CTG <mark>C</mark> AACTCG <mark>A</mark> CT <mark>T</mark> CATGAAG. <mark>TT</mark> GGA <mark>ATC</mark> NCT 05-0109_ConsC <mark>A</mark> AG <mark>T</mark> CTG <mark>C</mark> AACTCG <mark>A</mark> CT <mark>T</mark> CATGAAG. TT GGA <mark>ATCG</mark> CT	467
	-107
	467
05-0102_consChagTCTGCAACTCGACTTCATGAAG.TTGGAATCGCT	467 469
	469
05-0127 [_] ConsG <mark>A</mark> AG <mark>T</mark> CTG <mark>C</mark> AACTCG <mark>ACTT</mark> CATGAAG. <mark>TT</mark> GGA <mark>ATCG</mark> CT 05-0122 [_] ConsG <mark>A</mark> AG <mark>T</mark> CTG <mark>C</mark> AACTCG <mark>A</mark> CT <mark>T</mark> CATGAAG. TT GGA <mark>ATCG</mark> CT	469 467
05-0127_ConsG <mark>A</mark> AG <mark>T</mark> CTG <mark>C</mark> AACTCG <mark>ACTT</mark> CATGAAG.TTGGAATCGCT 05-0122_ConsGAAGTCTGCAACTCGACTTCATGAAG.TTGGAATCGCT 05-0033_FDG <mark>A</mark> AGTCTGCAACTCG <mark>ACTT</mark> CATGAAGCTGGGA <mark>ATCG</mark> CT	469 467 468
05-0127_ConsGAAGTCTGCAACTCGACTTCATGAAG.TTGGAATCGCT 05-0122_ConsGAAGTCTGCAACTCGACTTCATGAAG.TTGGAATCGCT 05-0033_FDGAAGTCTGCAACTCGACTTCATGAAGCTGGGAATCGCT 05-0005_ConsGTAGGCTGCAACTCGCCTACATGAAG.CTGGAATCGCT	469 467 468 471
05-0127_ConsG <mark>A</mark> AG <mark>T</mark> CTG <mark>C</mark> AACTCG <mark>ACTT</mark> CATGAAG.TTGGAATCGCT 05-0122_ConsGAAGTCTGCAACTCGACTTCATGAAG.TTGGAATCGCT 05-0033_FDG <mark>A</mark> AGTCTGCAACTCG <mark>ACTT</mark> CATGAAGCTGGGA <mark>ATCG</mark> CT	469 467 468



05-0018 ConsAGTAATCGCGAATCAGCATGTCGCGGGGGAATA.CGTTCT	505
05-0038 Consagtaatcgc <mark>ga</mark> atca <mark>gc</mark> atg <mark>tcgc</mark> gg <mark>tg.aata.cg</mark> ttc <mark>t</mark>	504
05-0062 ConsAGTAATCGCGAATCAGCATGTCGCGGTGAANACGTTCT	504
05-0077_ConsAGTAATCGC <mark>GA</mark> ATCANCATG <mark>TCGNGGTGA</mark> AATACC <mark>T</mark> TTCT	507
05-0033	504
05-0014_Cons <mark>AGTAATCGC<mark>GA</mark>ATCA<mark>GC</mark>ATG<mark>TC</mark>GC<mark>GGTGA</mark>A<mark>TA</mark>C<mark>G</mark>TTC</mark> T	505
05-0111 Cons <mark>AGTAATCGC<mark>GA</mark>ATCA<mark>GC</mark>ATG<mark>TC</mark>GCGG<mark>TGAA</mark>TACGTTCT</mark>	506
05-0109 ConsAGTAATCGC <mark>GA</mark> ATCA <mark>GC</mark> ATG <mark>TC</mark> GCGGTGAATACGTTCT	505
05-0102 Cons <mark>agtaatcgc</mark> gaatca <mark>gc</mark> atg <mark>tcgc</mark> ggggg <mark>aaa</mark> tacgttc <mark>t</mark>	507
05-0127 ConsAGTAATCGCGAATCAGCATGTCGCGGTGAATACGTTCT	507
05-0122_ConsAGTAATCGCGAATCAGCATGTCGCGGTGAATACGTTCT	505
05-0033FD_AGTAATCGC <mark>GA</mark> ATCA <mark>GC</mark> ATG <mark>TCGC</mark> GG <mark>TGAATA</mark> C <mark>G</mark> TTC <mark>T</mark>	506
05-0005_Cons <mark>AGTAATCGC<mark>G</mark>GATCA<mark>GC</mark>ATG<mark>CCGC</mark>GG<mark>TGA</mark>A<mark>TA</mark>C<mark>G</mark>TTCC</mark>	509
05-0055 Cons <mark>AGTAATCGC</mark> AG <mark>ATCAG</mark> AATGCTGCGG <mark>TGAAT</mark> GCGTTCC	508
Consensus agtaatcgc atca atg g gg a c ttc	
05-0018 ConsCGGGGGGTTTTGTACACACCCGCCCGTCAAACCACGAAAG	545
05-0038 ConsCGGGG.TTTGGTACACCCGCCCGTCAAACCACGAAAAG	540
05-0062_ConsCGGGGNTTGTACACACCNCCCNTCAAACCACGAAAG	540
05-0077_Cons <mark>CGGGGGTTTGTCCCAC</mark> CCCCCCGTTCAAACCGAAAG	543
05-0033sto <mark>cggggtttgtacacacgccc</mark> gtcaaaccac <mark>gaaag</mark>	540
05-0014_Cons <mark>CGGGG<mark>T</mark>TT<mark>GTACACACCG</mark>CCC<mark>GTCAAA</mark>CCAC<mark>GAA</mark>AG</mark>	541
05-0111 ConsCGGGGTTTGTACACACCGCCCGTCAAACCACGAAAG	542
05-0109 ⁻ Cons <mark>CGGGGTTT</mark> GTACACAC <mark>CGC</mark> CC <mark>GTCAAA</mark> CCAC <mark>GAA</mark> AG	541
05-0102 Cons <mark>CGGGGTTTGTACACACCGCCCGTCAAACCACGAAAG</mark>	543
05-0127 ConsCGGCGTTTGTACACACCCCCCCCGTCAAACCACCAAAG	543
05-0122_ConsCGGGGTTTGTACACACCGCCCGTCAAACCACGAAAG	541
05-0033FD_ <mark>cgggg</mark> tttgtaca <mark>cac</mark> gcccgtcaaaccacgaaag	542
05-0005_Cons <mark>CGGG</mark> CC <mark>TTGTACACACCGC</mark> CCGTCACACCACGAGAG	545
05-0055_Cons <mark>CGGG</mark> TC <mark>TTGTACACACCGCCCGTCA</mark> CACCATGGGAG	544
Consensus cggg tt cac cc a g ag	
05-0018 Cons <mark>TTGGCAATACCCAAAGCCGGTGGCCTAAC</mark> TTGAGCAATCA	585
05-0038 Cons <mark>TTGCCAATACCCAAAAGCCGGTGGCCTAAC</mark> TTGAGCAATCA	580
05-0062 ConstTNGCAATACCCAAAANCCGGTGGCCNAACTTGAGCAATCA	580
05-0077 ConsTTNCCAATACCCAAAANCCGGTGGCCNAACTTGAGCAATCA	583
05-0033 sto <mark>TTGGCAATACCCAAAGCCGGTGGCCTAAC</mark> TTGAGCAATCA	580
05-0014_ConsTTCCAATACCCAAAGCCCCCGCCCCCCCCCCCCCCCCCC	581
05-0111_ConsTTGCCAATACCCAAAGCCGGTGGCCTAACTTGAGCAATCA	582
05-0109_Cons <mark>TTGGCAATACCCAAAGCCGGTGGCCTAAC</mark> TTGAGCAATCA	581
05-0102_Cons <mark>TT<mark>G</mark>GCAATA<mark>CCCAAA</mark>GC<mark>C</mark>G<mark>G</mark>TGGCCTAAC</mark> TTGAGCAATCA	583
05-0127 Cons <mark>TT</mark> GCAATACCCAAAGCCGCTGGCCTAACTTGAGCAATCA	583
05-0122 Cons <mark>TTG</mark> CAATACCCAAAGCCGGTGGCCTAACTTGAGCAATCA	581
05-0033 FD TTAGCAATACCCGAAAAGCAGTGGCTTAACTTCGAAAGA	580
05-0005 ConsTTTGTAACACCCGAAGTCGGTGGAGTAACCGTAA	579
05-0055 ConsTTGGGGGCCCLAAAGCCGGTTAGCTAACCTTTTA	579
	579
Consensus tt g ccc aa c g aac a	
05-0018_ConsAGAAGGAGCCGTCTAAGGTAGGGTTGATGATTGGGG.TTA	624
05-0038_Cons <mark>AGAAGGAGCCGTCTAAGGTAGGGT</mark> TG <mark>ATGATTGGGG</mark> .TTA	619
05-0062_Cons <mark>AGAAGGAGCCNTCTAAGGTAGGGNTGATGATTGGGG.</mark> TTA	619
05-0077 Cons <mark>AGAAGGAGCCNTCTAAGGTAGGGNTGATGATTGGGG.T</mark> TA	622
05-0033 sto <mark>a</mark> ga <mark>aggagccgtctaaggtagggttgatga</mark> ttgggg.tta	619
05-0014_ConsaGaaggagcCCGTCTAAGGTAGGGTTGATGATTGGGGG.TTA	620
05-0111 ConsAGAGGAGCCGTCTAAGGTAGGGTTGATGATTGGGG.TTA	621
05-0109 ConsAGAAGGACCCCGCCTAAGGTAGGGTTGATGATGGGG.TTA 05-0109 ConsAGAAGGACGCCGTCTAAGGTAGGGTTGATGATTGGGG.TTA	
	620
05-0102_ConsAGAAGGAGCCGTCTAAGGTAGGGTTGATGATTGGGG.TTA	622
05-0127_Cons <mark>AGAAGGAGCCGTCTAAGGTAGGGTTGATGAT</mark> TGGGG <mark>G</mark> TTA	623
05-0122_ConslGlagglagglagCCGTCTAAGGTAGGGTTGATGATTGGGG.TTA	620
05-0033 FD AGAGGGAGCTGTCTAAGGTAGGGTTGATGATTGGGGG.TTA	619
05-0005_ConsgCAGCTAGCCGCCTAAGGTGGGACAGATGATTGGGG.TGA	618
05-0055 ConsgGAGGCAACCGTCGAAGGTGAAACCAATGACTGGGG.TGA	
	618
Consensus ga a c c aaggt atga tgggg t a	618



DS-0018_Construction Construction Construction State DS-0018_Construction Construction Construction State State<	05-0018 ConsAGTCGTAACAAGGTATCCC.TACCCGAAGGTGCGGATGGA	امم ا
05-0062 ConsAGTCGTNACAAGGTATCCC. TWCCNGAAGGTGGGATGGA 658 05-0077 ConsAGTCGTNACAAGGTATCCC. TACCGAAGGTGGGATGGA 661 05-0033 stoAGTCGTNACAAGGTATCCC. TACCGAAGGTGGGATGGA 669 05-0111 ConsAGTCGTNACAAGGTATCCC. TACCGAAGGTGGGATGGA 660 05-0109 ConsAGTCGTNACAAGGTATCCC. TACCGAAGGTGGGATGGA 661 05-0127 ConsAGTCGTNACAAGGTATCCC. TACCGAAGGTGGGATGGA 663 05-0122 ConsAGTCGTNACAAGGTATCCC. TACCGGAAGGTGGGATGGA 663 05-0122 ConsAGTCGTNACAAGGTATCCC. TACCGGAAGGTGGGATGGA 663 05-0122 ConsAGTCGTNACAAGGTATCCC. TACCGGAAGGTGGGGATGGA 663 05-0122 ConsAGTCGTNACAAGGTATCCC. TACCGGAAGGTGGGGATGGA 658 05-0033 FD AGTCGTNACAAGGTATCCC. TACCGGAAGGTGGGGATGGA 659 05-0035 ConsAGTCGTNACAAGGTATCCC. TACCGGAAGGTGGGGATGGA 658 05-0055 ConsAGTCGTNACAAGGTACCCG. TATCGGAAGGTGGGGCTGGA 657 05-0055 ConsAGTCGTNACAAGGTACCCG. TATCGGAAGGTGGGGCTGGA 657 05-0058 ConsTCACCTCCTTTCTAAGGATA. AGTTATCATC 669 05-0018 ConsTCACCTCCTTTCTAAGGATA. AGTTATCATC 669 05-0014 ConsTCACCTCCTTTCTAAGGATA. AGTTATCATC 669 05-0014 ConsTCACCTCCTTTCTAAGGATA. AGTTATCATC 669 05-0111 ConsTCACCTCCTTTCTAAGGATA. AGTTATCATC 690 05-0112 ConsTCACCTCCTTTCTAAGGATA. AGTTATCATC 690 05-0112 ConsTCACCTCCTTTCTAAGGATA. AGTTATCATC 690 05-0122 ConsTCACCTCCTTTCTAAGGATA. AGTTATCATC 691 05-0122 ConsTCACCTCCTTTCTAAGGATA. AGTTATCATC 691 05-0122 ConsTCACCTCCTTTCTAAGGATA. AGTTATCATC 691 05-0132 ConsTCACCTCCTTTCTAAGGATA. AGTTATCATC 707 05-014 ConsTCACTCCTTTCTAAGGATA. AGTTATCATC 707 05-0132 ConsTCACTTCTTAGAGACT 706 05-0033 stoTCACTCCTTTCTAAGGATA. ATTACCTCACTGATCATCATC 706 05-0032 stoTCACTCCTTTCTAAGGATA. ATTACCTCCTTC 707 05-0142 ConsTCACTCCTTTCTAAGGATA. ATTACCTCCTTTC 707 05-0112 ConsTCACTTTTGAAGACT 707 05-0112 ConsTCACTTTTGAAGACT 707 05-0112 ConsTCACTTTTGAAGACT 707 05-0122 ConsTCACTTTTGAAGACT 707 05-0122 ConsTCACTTTTGAAGACT 707 05-0122 ConsTCACTTTTGAAGACT 707 05-0033 FD TCACTTTGAAGACT 707 05-00		663
05-0077_ConsAGTCGTNACAAGGTATCCCINCONGAAGGTCGGGATGGA66105-0033_stoAGTCGTAACAAGGTATCCCINCOCGAAGGTGGGGATGGA65805-0111_ConsAGTCGTAACAAGGTATCCCINCCGAAGGTGGGGATGGA66005-0112_ConsAGTCGTAACAAGGTATCCCINCCGAAGGTGGGGATGGA66105-0102_ConsAGTCGTAACAAGGTATCCCINCCGAAGGTGGGGATGGA66305-0122_ConsAGTCGTAACAGGTATCCCINCCGAAGGTGGGGATGGA66305-0122_ConsAGTCGTAACAGGTATCCCINCCGAAGGTGGGGATGGA65905-0122_ConsAGTCGTAACAGGTATCCCINCCGAAGGTGGGGATGGA65805-0033_FD_AGTCGTAACAAGGTACCCCINTCGGAAGGTGGGGATGGA65805-0005_ConsAGTCGTAACAAGGTACCCGINTCGGAAGGTGGGGCTGGA65705-0055_ConsAGTCGTAACAAGGTAGCGCINTCGGAAGGTGGGGCTGGA65705-0018_ConsCACCTCCTTTCTAAGGATAAAGTTATCATC69405-0018_ConsCACCTCCTTTCTAAGGATAAAGTTATCATC69905-0014_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0012_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0012_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0112_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69105-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC692<	05-0058 CONSAGTOGTARCAAGGTATCCC. TACCGGAAGGTGGGGATGGA	
05-0033_stoAGTCGTAACAAGGTATCCCTACCGGAAGGTGGGGATGGA65805-0014_ConsAGTCGTAACAAGGTATCCCTACCGGAAGGTGGGGATGGA65905-0109_ConsAGTCGTAACAAGGTATCCCTACCGGAAGGTGGGGATGGA66005-0102_ConsAGTCGTAACAAGGTATCCCTACCGGAAGGTGGGGATGGA66105-0122_ConsAGTCGTAACAAGGTATCCCTACCGGAAGGTGGGGATGGA66305-0102_ConsAGTCGTAACAAGGTATCCCTACCGGAAGGTGGGGATGGA66305-0122_ConsAGTCGTAACAAGGTATCCCTACCGGAAGGTGGGGATGGA65305-0122_ConsAGTCGTAACAAGGTATCCCTACCGAAGGTGGGGATGGA65705-0005_ConsAGTCGTAACAAGGTACCCTACCGAAGGTGGGCGCTGGA65705-0012_ConsAGTCGTAACAAGGTACCCTACCGAAGGTGGGCGCTGGA65705-0015_ConsAGTCGTAACAAGGTACCCGTATCGGAAGGTGGGCGCTGGA65705-0015_ConsAGTCGTCCTTTCTAAGGATAAAGTTATCATC69405-0016_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC68905-0017_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC68905-0014_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0111_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0112_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69105-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACTCCTTTCTAAGGATAAGTTATCATC69205-0055_ConsTCACTCCTTTCTAAGGATATACATCATC694		
05-0014_ConsAGTCGTAACAAGGTATCCC. TACCGGAAGGTGGGGATGGA 659 05-0111_ConsAGTCGTAACAAGGTATCCC. TACCGGAAGGTGGGGATGGA 660 05-0102_ConsAGTCGTAACAAGGTATCCC. TACCGGAAGGTGGGGATGGA 661 05-0122_ConsAGTCGTAACAAGGTATCCC. TACCGGAAGGTGGGGATGGA 663 05-0122_ConsAGTCGTAACAAGGTATCCC. TACCGGAAGGTGGGGATGGA 659 05-0033_FD_AGTCGTAACAAGGTATCCC. TACCGGAAGGTGGGGATGGA 659 05-0035_ConsAGTCGTAACAAGGTATCCC. TACCGAAGGTGGGGATGGA 657 05-0055_ConsAGTCGTAACAAGGTACCCG. TATCGGAAGGTGGGGCTGGA 657 05-0055_ConsAGTCGTAACAAGGTACCCG. TATCGGAAGGTCGGCTGGA 657 05-0018_ConsCGACTCCTTTCTAAGGATAAGGTATCATC 659 05-0018_ConsTCACTCCTTTCTAAGGATAAGGTATCATC 659 05-0014_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC 659 05-0014_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC 659 05-0014_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC 650 05-0114_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC 650 05-0114_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC 650 05-0112_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC 650 05-0112_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC 650 05-0122_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC 650 05-0122_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC 650 05-0122_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC 650 05-0122_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC 650 05-0122_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC 650 05-0033_FD_TCACCTCCTTTCTAAGGATAAGTTATCATC 650 05-0012_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC 650 05-0035_ConsTCACCTCCTTTCTAAGGATAAGTTATCATC 650 05-0013_FD_TCACCTCCTTTCTAAGGATAAGTTATCATC 650 05-0035_ConsTCACCTCCTTTCTAAGGATATCATTATAAAAATCATC 650 05-0033_FD_TCACCTCCTTTCTAAGGATA 706 05-0035_ConsTCACTTCTTTGAAGGACT 706 05-0014_ConsTCAGTTTGAGAGACT 707 05-0014_ConsTCAGTTTGAGAGACT 706 05-0014_ConsTCAGTTTGAGAGACT 707 05-0014_ConsTCAGTTTGAGAGACT 707 05-0014_ConsTCAGTTTGAGAGACT 707 05-0122_ConsTCAGTTTGAGAGACT 707 05-0122_ConsTCAGTTTGAGAGACT 707 05-0122_ConsTCAGTTTGAGAGACT 707 05-0122_ConsTCAGTTTGAGAGACT 707 05-0122_ConsTCAGTTTGAGAGACT 707 05-0035_ConsTACACTCTTTAGAGAGACT 707 05-0035_CONSTCAGCTTGAGTTGAGAGCT		
05-0111_ConsAGTCGTAACAAGGTATCCCTACCGGAAGGTCGGGATGGA66005-0102_ConsAGTCGTAACAAGGTATCCCTACCGAAGGTCGGGATGGA65905-0102_ConsAGTCGTAACAAGGTATCCCTACCGAAGGTCGGGATGGA66305-0122_ConsAGTCGTAACAAGGTATCCCTACCGAAGGTCGGGATGGA65905-0122_ConsAGTCGTAACAAGGTATCCCTACCGAAGGTCGGGATGGA65805-0003_FDAGTCGTAACAAGGTATCCCTACCGAAGGTCGGGTGGA65705-0015_ConsAGTCGTAACAAGGTAGCCGTATCGAAGGTCGCGCTGGA65705-0015_ConsAGTCGTAACAAGGTAGCCGTATCGAAGGTCGCGCTGGA65705-0018_ConsCCACCTCCTTTCTAAGGATAAAGTTATCATC68905-0018_ConsCCACCTCCTTTCTAAGGATAAAGTTATCATC68905-0016_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC66905-0014_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0112_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0112_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0112_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATCATC69205-0122_ConsTCACCTCCTTTCTAAGGACT70605-0033_FD_TCACCTCCTTTCTAAGGACT70605-0042_ConsTCCACTCCTTTCTAAGGACT70705-0014_ConsTCCACTCCTTTCTAAGGACT70605-0014_ConsTCCACTCCTTTCTAAGGACT70705-0114_Cons		
05-0109_ConslAGTCGTAACAAGGTATCCCTACCGGAAGGTCGGGATGGA65905-0102_ConsAGTCGTAACAAGGTATCCCTACCGAAGGTCGGGATGGA66105-0127_ConsAGTCGTAACAAGGTATCCCTACCGAAGGTCGGGATGGA65905-0033_FD_AGTCGTAACAAGGTATCCCTACCGAAGGTCGGGATGGA65705-0005_ConsAGTCGTAACAAGGTAGCCGTATCGGAAGGTCGGGCTGGA65705-0018_ConsCCACCTCTTTCTAAGGATACGGAAGGTCGGGCTGGA65705-0018_ConsCCACCTCCTTTCTAAGGATAAAGTTATCATC69405-0018_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC68905-0014_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC66905-0014_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC66905-0014_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0111_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0112_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69105-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0033_FD_TCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0033_FD_TCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0033_FD_TCACTCCTTTCTAAGGATAAAGTTATCATC69205-0033_FD_TCACTCCTTTCTAAGGATAAAGTTATCATC69205-0122_ConsTCACTCTTTCTAAGGATAAAGTTATCATC69205-0033_FD_TCACTCCTTTCTAAGGATAATCATATCATC69205-0035_ConsTCACTCCTTTCTAAGGAT		
05-0102_ConsAGTCGTAACAAGGTATCCC.TACCGGAAGGTCGGGATGGA66105-0122_ConsAGTCGTAACAAGGTATCCC.TACCGAAGGTCGGGATGGA66305-0122_ConsAGTCGTAACAAGGTATCCC.TACCGAAGGTCGGGATGGA65905-0033_FD_AGTCGTAACAAGGTATCCC.TACCGAAGGTCGGGCTGGA65705-0055_ConsAGTCGTAACAAGGTAGCCG.TATCGGAAGGTCGGGCTGGA65705-0055_ConsAGTCGTAACAAGGTAGCCG.TATCGGAAGGTCGGGCTGGA65705-0055_ConsAGTCGTAACAAGGTAGCCG.TATCGGAAGGTCGGGCTGGA65705-0018_ConsCACCTCCTTTCTAAGGATAAAGTTATCATC69905-0018_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC68905-0013_stoTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0014_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0102_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0102_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0102_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0102_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0102_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0102_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69005-0102_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69105-0018_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0018_ConsTCACCTCCTTTCTAAGGATAAAGTTATCATC69205-0018_ConsTCACTCCTTTCTAAGGACT70605-0018_ConsTCACTCTTTTGAGAGACT70705-0018_ConsTCAGTTTTGAGAGACT70705-0014_ConsTCAGTTTTGAGAGACT70705-0112_ConsTCAGTTTTGAGAGACT70705-0102_ConsTCAGTTTTGAGAGACT7		
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05-0033FDTCACCTCCTTTCTAAGGACATACATATAAAAATCATCATC69805-0005ConsTCACCTCCTTTCTAAGGATTTTTACATGACGTACGTTT69505-0055ConsTCACCTCCTTTCTAAGGAGTAATTACCTACTGTT691Consensuscacctcctttctaaggaaa05-0018ConsTCAGTTTGAGAGACT71105-0038ConsTCAGTTTGAGAGACT70605-0062ConsTCAGTTTGAGAGACT70605-0077ConsTCAGTTTGAGAGACT70905-0033stoTTCAGTTTGAGAGACT70705-014ConsTCAGTTTGAGAGACT70705-0109ConsTCAGTTTGAGAGACT70705-0102ConsTCAGTTTGAGAGACT70705-0127ConsTCAGTTTGAGAGACT70705-0122ConsTCAGTTTGAGAGACT70705-0123FDTCAGTTTGAGAGACT70705-0124ConsTCAGTTTGAGAGACT70705-0125ConsTCAGTTTGAGAGACT71105-0005ConsTGACACTTTGTCAGTT71205-0005ConsTGACACTTTGTCAGTT71205-0005ConsTAATTTGAGGGTT705		
05-0005ConstCACCTCCTTTCTAAGGATTTTTACATGACGTACGTTT69505-0055ConstCACCTCCTTTCTAAGGAGTAATTACCTACTGTT691Consensuscacctcctttctaaggaat05-0018ConstTCAGTTTGAGAGACT71105-0038ConstTCAGTTTGAGAGACT70605-0062ConstTCAGTTTGAGAGACT70605-0077ConstTCAGTTTGAGAGACT70905-0033stoTTCAGTTTGAGAGACT70705-014ConstTCAGTTTGAGAGACT70705-019ConstTCAGTTTGAGAGACT70705-0102ConstTCAGTTTGAGAGACT70905-0127ConstTCAGTTTGAGAGACT70705-0122ConstTCAGTTTGAGAGACT70705-0133FDTCAGTTTGAGAGACT70705-0120ConstTCAGTTTGAGAGACT70705-0121ConstTCAGTTTGAGAGACT70705-0122ConstTCAGTTTGAGAGACT71105-0033FDTCCAGTTTGAGAGACT71505-0005ConstGACACTTGTCAGTT71205-0055ConstAATTTGAGGGTT705		
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Consensuscacctcctttctaaggaaat05-0018ConstTCAGTTTIGAGAGACT71105-0038ConstTCAGTTTIGAGAGACT70605-0062ConstTCAGTTTIGAGAGACT70905-0033stoTTCAGTTTIGAGAGACT70905-0014ConstTCAGTTTIGAGAGACT70705-019ConstTCAGTTTIGAGAGACT70705-0102ConstTCAGTTTIGAGAGACT70705-0122ConstTCAGTTTIGAGAGACT70905-0123StoTTCAGTTTIGAGAGACT70705-0124ConstTCAGTTTIGAGAGACT70705-0125ConstTCAGTTTIGAGAGACT70705-0033FDTTCAGTTTIGAGAGACT70705-0005ConstGACACTTIGTCAGTT71205-0055ConstAATTITGAGGGTT705		
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05-0062_ConstTCAGTTTTGAGAGACT 706 05-0077_ConsTTCAGTTTTGAGAGACT 709 05-0033_stoTTCAGTTTTGAGAGACT 706 05-0014_ConsTTCAGTTTTGAGAGACT 707 05-0111_ConsTTCAGTTTTGAGAGACT 708 05-0109_ConsTTCAGTTTTGAGAGACT 707 05-0102_ConsTTCAGTTTTGAGAGACT 709 05-0122_ConsTTCAGTTTTGAGAGACT 701 05-0122_ConsTTCAGTTTTGAGAGACT 707 05-0122_ConsTTCAGTTTTGAGAGACT 707 05-0033_FD_TTCAGTTTTGAAAGACT 711 05-0005_ConsTGACACTTTGTTCAGTT 715 05-0005_ConsTAATTTTGAGGGTT 712		
05-0077 ConsTTCAGTTTTGAGAGACT70905-0033 stoTTCAGTTTTGAGAGACT70605-0014 ConsTTCAGTTTTGAGAGACT70705-0111 ConsTTCAGTTTTGAGAGACT70805-0109 ConsTTCAGTTTTGAGAGACT70705-0102 ConsTTCAGTTTTGAGAGACT70905-0127 ConsTTCAGTTTTGAGAGACT71105-0122 ConsTTCAGTTTTGAGAGACT70705-0133 FD TTCAGTTTTGAGAGACT71505-0005 ConsTGACACTTTGTTGAGAGACT71205-0055 ConsTAATTTTGAGGGTT705		
05-0033stoTTCAGTTTTGAGAGACT70605-0014ConsTTCAGTTTTGAGAGACT70705-0111ConsTTCAGTTTTGAGAGACT70805-0109ConsTTCAGTTTTGAGAGACT70705-0102ConsTTCAGTTTTGAGAGACT70905-0127ConsTTCAGTTTTGAGAGACT71105-0122ConsTTCAGTTTTGAGAGACT70705-0033FDTTCAGTTTTGAAGAGACT71505-0005ConsTGACACTTTGTTGAGAGACT71205-0055ConsTAATTTTGAGGGTT705		
05-0014_ConstTCAGTTTTGAGAGACT 707 05-0111_ConstTCAGTTTTGAGAGACT 708 05-0109_ConstTCAGTTTTGAGAGACT 707 05-0102_ConstTCAGTTTTGAGAGACT 709 05-0127_ConstTCAGTTTTGAGAGACT 711 05-0122_ConstTCAGTTTTGAGAGACT 707 05-0123_ConstTCAGTTTTGAGAGACT 707 05-0033_FD_TCAGTTTTGAAGAGACT 715 05-0005_ConstGACACTTTGTCAGTT 712 05-0055_ConstAATTTTGAGGGTT 705		
05-0111_ConstTCAGTTTTGAGAGACT 708 05-0109_ConstTCAGTTTTGAGAGACT 707 05-0102_ConstTCAGTTTTGAGAGACT 709 05-0127_ConstTCAGTTTTGAGAGACT 711 05-0122_ConstTCAGTTTTGAGAGACT 707 05-0133_FD_TCAGTTTTGAAAGACT 715 05-0005_ConstGACACTTTGTTGAGAGACT 712 05-0055_ConstAATTTTGAGGGTT 705		
05-0109_ConstTCAGTTTTGAGAGACT70705-0102_ConstTCAGTTTTGAGAGACT70905-0127_ConstTCAGTTTTGAGAGACT71105-0122_ConstTCAGTTTTGAGAGACT70705-0033_FD_TTCAGTTTTGAAAGACT71505-0005_ConstGACACTTTGTTCAGTT71205-0055_ConstAATTTTGAGGGTT705		708
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05-0122_ConstTCAGTTTTGAGAGACT 707 05-0033_FD_TTCAGTTTTGAAAGACT 715 05-0005_ConstGACACTTTGTTCAGTT 712 05-0055_ConstAATTTTGAGGGTT 705	05-0102 Cons <mark>TCAGTTTTGAGAGAC</mark> T	709
05-0033_FD_TCAGTTTTGAAAGACT 715 05-0005_ConsTGACACTTTGTTCAGTT 712 05-0055_ConsTAATTTTGAGGGTT 705		711
05-0033_FD_TCAGTTTTGAAAGACT 715 05-0005_ConsTGACACTTTGTTCAGTT 712 05-0055_ConsTAATTTTGAGGGTT 705	05-0122_Cons <mark>TTCAGTTTTGAGAGAC</mark> T	707
05-0005_ConsTGACACTTTGTTCAGTT 712 05-0055_ConsTAATTTTGAGGGTT 705	05-0033 FD TTCAGTTTTGAAAGACT	715
		712
Consensus t tt t		705
	Consensus t ttt t	



APPENDIX D

Pairwise comparison of sample 05-0033 and Flavescence doree positive control

05-0033_FD_TAAGTACTCCGCCTGAGTAGTACGTACGCAAGTATGAAAC FDP_CS TAAGTACTCCGCCTGAGTACGTACGTACGCAAGTATGAAAC Consensus taagtactccgcctgagtagtacgtacgcaagtatgaaac	40 40
05-0033_FD_TTAAAGGAATTGACGGGACTCCGCACAAGCGGTGGATCAT FDP_CS TTAAAGGAATTGACGGGACTCCGCACAAGCGGTGGATCAT Consensus ttaaaggaattgacgggactccgcacaagcggtggatcat	80 80
05-0033_FD_GTTGTTTAATTCGAAGATACACGAAAAACCTTACCAGGTC FDP_CS GTTGTTTAATTCGAAGATACACGAAAAACCTTACCAGGTC Consensus gttgtttaattcgaagatacacgaaaaaccttaccaggtc	120 120
05-0033_FD_TTGACATACTCTGCAAAGCTATAGAAATATAGTGGAGGTT FDP_CS TTGACATACTCTGCAAAGCTATAGAAATATAGTGGAGGTT Consensus ttgacatactctgcaaagctatagaaatatagtggaggtt	160 160
05-0033_FD_ATCAGGGATACAGGTGGTGCATGGTTGTCGTCAGTTCGTG FDP_CS ATCAGGGATACAGGTGGTGCATGGTTGTCGTCAGTTCGTG	200 200
Consensus atcagggatacaggtggtgcatggttgtcgtcagttcgtg 05-0033_FD_TCGTGAGATGTTAGGTTAAGTCCTAAAACGAACGCAACCC FDP_CS TCGTGAGATGTTAGGTTAAGTCCTAAAACGAACCGCAACCC	240 240
Consensus tcgtgagatgttaggttaggtcaaacgaacgcaaccc 05-0033_FD_CTGTCGCTAGTTGCCAGCACGTAATGGTGGGGACTTTAGC FDP_CS CTGTCGCTAGTTGCCAGCACGTAATGGTGGGGACTTTAGC	280 280
Consensus ctgctcgctagttgccagcacgtaatggtgggggctttagc 05-0033_FD_GAGACTGCCAATTAAACATTGGAGGAAGGTGGGGATAACG FDP_CS GAGACTGCCAATTAAACATTGGAGGAAGGTGGGGGATAACG Consensus gagactgccaattaaacattggaggagadtaggggataacg Gagactgccaattaaacattggaggagataacg	320 320
05-0033_FD_TCAAATCATCATGCCCCTTATGATCTGGGCTACAAACGTG FDP_CS TCAAATCATGCCCCTTATGATCTGGGCTACAAACGTG	360 360
05-0033_FD_ATACAATGGCTATTACAAAGAGTAGCTGAAACGCGAGTTT FDP_CS ATACAATGGCTATTACAAAGAGTAGCTGAAACGCGAGTTT	400 400
05-0033_FD_TTAGCCAATCTCAAAAAGGTAGTCTCAGTACGGATTGAAG FDP_CS TTAGCCAATCTCAAAAAGGTAGTCTCAGTACGGATTGAAG	440 440
05-0033FD_TCTGCAACTCGACTTCATGAAGCTGCGAATCGCTAGTAAT FDP_CS TCTGCAACTCGACTTCATGAAGCTGG_AATCGCTAGTAAT	480 479
Consensus tctgcaactcgacttcatgaagctgg aatcgctagtaat 05-0033_FD_CGCGAATCAGCATCTCGCGGTGAATACGTTCTCGGGGTTT FDP_CS CGCGAATCAGCATGCCGCGGTGAATACGTTCTCCGGGGTTT	520 519
Consensus cgcgaatcagcatgtcgcggtgaatacgttctcgggggttt 05-0033_FD_GTACACACCGCCGTCAAACCACGAAAGTTAGCAATACCC FDP_CS GTACACCGCCCGTCAAACCACGAAAGTTAGCAATACCC Consensus qtacacaccgcccqtcaaaccacqaaaqttagcaataccc Gtacacaccgccqtcaaaccacqaaaqttagcaataccc	560 559
05-0033_FD_GAAAGCAGTGGCTTAACTTCGAAAGAAGAGGGAGCTGTCT FDP_CS GAAAGCAGTGGCTTAACTTCGAAAGAAGAGGGAGCTGTCT Consensus gaaagcagtggcttaacttcgaaagaagaggagctgtct	600 599
05-0033_FD_AAGGTAGGGTTGATGATGGGGTTAAGTCGTAACAAGGTA FDP_CS AAGGTAGGGTTGATGATGGGGTTAAGTCGTAACAAGGTA Consensus aaggtagggttgatgattgggttaagtcgtaacaaggta	640 639
05-0033_FD_TCCTTACCGGAAGGTGAGGATGATCACCTCCTTTCTAAG FDP_CS TCCTTACCGGAAGGTGAGGATGATCACCTCCTTTCTAAG Consensus tccttaccqqaaqqtqaqqtqaqqtcqaqtacacctcctttctaaq	680 679
05-0033_FD_GACATACATATAAAAATCATCATCTTCAGTTTTGAAAGAC FDP_CS GACATACATATAAAAATCATCATCTTCAGTTTTGAAAGAC Consensus gacatacatataaaaatcatcatcttcagttttgaaagac	720 719
05-0033_FD_TTAGGTTAAAATATAAAGTTTTTCTTTTTATAAAAAAAGTG FDP_CS TTAGGTTAAAATATAAAGTTTTTCTTTTTATAAAAAAAAGTG	760 759
Consensus ttaggttaaaatataagtttttcttttataaaaaaagtg 05-0033_FD_TTTCTTTATATAAAGACCAAAGGGCCTATAGCTCAGTT FDP_CS TTTCCTTATATAAAGACCAAAGGGCCTATAGCTCAGTT	800 799
Consensus tttctcttatataaaagaccaaagggcctatagctcagtt 05-0033_FD_GGTTAGAGCACACCCCTGATAAGCGTGAGGTCGGTGGTTC FDP_CS GGTTAGAGCACACGCCTGATAAGCGTGAGGTCGGTGGTTC	840 839
Consensus ggttagagcacacgcctgataagcgtgaggtcggtggttc 05-0033_FD_AAGTCCACTTAGGCCCACCAATTTTATATCAGGAAAATAT FDP_CS_AAGTCCACTTAGGCCCACCAATTTTATATCAGGAAAATAT	880 879
Consensus aagtccacttaggcccaccaattttatatcaggaaaatat 05-0033_FD_TConsensus FDP_CS I Consensus t	881 880