ABSTRACT

PARADA ROJAS, CAMILO HUMBERTO. Novel Microsatellite Markers for the Analysis of *Phytophthora capsici* Populations and Host Resistance for Management of Phytophthora Blight of Pepper. (Under the direction of Dr. Lina Quesada).

Phytophthora blight (caused by *Phytophthora capsici*) is an important disease with a broad host range including Solanaceous, Cucurbitaceous, and Fabaceous crops. Despite its impact in vegetable production, *P. capsici* population structure in North Carolina (NC) is unknown. The release of the *P. capsici* genome allows for design of robust markers for genetic studies. We identified and characterized simple sequence repeats (SSRs) in the *P. capsici* transcriptome. A subset of 50 SSR were assayed in a diverse set of *P. capsici* isolates and evaluated for polymorphism. Polymorphic SSRs were confirmed by fragment analysis and 11 were used for population characterization of 30 *P. capsici* isolates from different states, hosts, mating types, and fungicide sensitivities. Analysis of genetic relationship among isolates revealed significant geographic structure by state and even by field. Our findings highlight the usefulness of the 11 SSRs to characterize the population structure of *P. capsici* and potential transferability to closely-related *Phytophthora* spp. since markers are located in coding regions. This study is a step towards understanding the genetic structure of *P. capsici* populations, which may assist in deployment of disease management strategies.

In that context, we also improved management of Phytophthora blight in peppers by evaluating resistance of commercial and experimental lines of peppers in the greenhouse and the field to *P. capsici*. Field trials were conducted over the summers of 2015 and 2016 to evaluate 32 commercial and experimental pepper cultivars against a mixed isolate inoculum in NC. Cultivars Martha-R, Meeting, and Paladin were classified as highly resistant and resistant to *P. capsici*. Tolerance to *P. capsici* in the field was observed in Fabuloso, Revolution, and

Vanguard among other cultivars. Greenhouse experiments were conducted to determine the response of 48 pepper cultivars when inoculated with two isolates from NC and an isolate from Michigan individually. Isolates exhibited different levels of virulence to the pepper cultivars screened for *P. capsici* resistance. Land races CM334, Fidel, and cultivars Martha-R, Meeting, and Intruder were highly resistant and resistant to all isolates tested. Overall, highly resistant cultivars tended to respond similarly to field inoculations with an isolate mix and greenhouse single isolate inoculations. Our results highlight the importance of screening for resistance with diverse isolates and understanding regional *P. capsici* populations for better deployment of durable pepper resistance.

Novel microsatellite markers for the analysis of *Phytophthora capsici* populations and Host Resistance for Management of Phytophthora Blight of Pepper

by
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DEDICATION

To my incredible girlfriend, Lindsey and her parents Don and Polly. To my mother, father, and brothers. To my mentor, Dr. Lina Quesada.

BIOGRAPHY

Camilo Humberto Parada Rojas was born on April 30th, 1992 in Duitama, Boyaca, Colombia. He received his bachelor of science (B.S.) in biotechnological engineering from Francisco de Paula Santander University in Cucuta, Colombia. While pursuing his B.S. degree, Mr. Parada-Rojas worked on understanding the benefits of mycorrhizal fungi for cilantro and lettuce crops on Colombian farms. He completed his internship and senior thesis at NC State University under the mentorship of Dr. Lina Quesada in the Department of Entomology and Plant Pathology. During his internship, he focused on the development of molecular markers from the transcriptome of *Phytophthora capsici*. In 2014, the results were presented at the annual meeting of the American Phytopathological Society (APS) in Minneapolis, MN.

Mr. Parada-Rojas' successful experience as an intern at NC State University motivated him to pursue a master of science degree in plant pathology. His research focusses on understanding the population structure of the causal agent of Phytophthora blight of peppers in North Carolina. He has received several awards during his career as a graduate student. In 2014, he received a travel award to attend the summer bioinformatics training workshop in Blacksburg, VA. He was awarded by the APS Foundation with a travel award to present his research at the APS annual meeting in Tampa, Florida. Most recently, he was awarded by the Oomycete Molecular Genetics Network with a travel award to present his research at the annual meeting in Asilomar, California. In addition, Mr. Parada-Rojas is a member of the Latin American Student Association, an active member of the SOUL garden at NC State, and an alternate representative for the Graduate Student Association at NC State University.

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This thesis is not only the results of my scientific work from the past two years but the outcome of a long effort and I am glad to acknowledge everyone who contributed to form my scientific personality and therefore the accomplishments on this thesis.

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Finally, I would like to thank my parents Nohora Rojas and Humberto Parada for your constant encouragement and for believing in my dreams. My last words go to my amazing girlfriend Lindsey Becker for all your immense support and love during these years, I thank you for reminding me that everything in life is possible.

TABLE OF CONTENTS

LIST OF TABLES

Chapter I: Literature Review

Chapter II: Analysis of microsatellites from transcriptome sequences of *Phytophthora capsici* and applications for population studies

Chapter III: Characterizing sources of resistance to Phytophthora blight of pepper caused by *Phytophthora capsici* in North Carolina

LIST OF FIGURES

Chapter I: Literature Review

Chapter II: Analysis of microsatellites from transcriptome sequences of *Phytophthora capsici* and applications for population studies

Chapter III: Characterizing sources of resistance to Phytophthora blight of pepper caused by *Phytophthora capsici* in North Carolina

CHAPTER I

Literature Review

Phytophthora blight of peppers

Pepper (*Capsicum*) is an economically important vegetable cultivated worldwide. The genus *Capsicum* belongs to the Solanaceae family, which include other important vegetables such as tomatoes and potatoes. Chile and bell peppers are key elements of many cuisines. Because of their distinctive flavor profile and nutritional attributes, hot peppers are used to add spice to food and bell peppers are commonly found in salads (Bosland and Votava 2012). The genus comprises more than 30 species native to the New World (Moscone et al. 2007). Archeological evidence suggests that *C. annuum* L. and other *Capsicum* species were domesticated 6,000 years Before Present by Native Americans (Perry et al. 2007). Unlike most crops, peppers spread around the world after European contact with the Americas (Bosland and Votava 2012). Central and South America represent the center of diversity of landraces and wild forms of peppers and have high potential for disease resistance.

Global annual production of peppers for 2013 was over 31 million metric tons (FAOSTAT 2015). The United States (US) ranks as a top producer of pepper with 1.15 million tons produced in 2015 (USDA-NASS 2015), from which North Carolina (NC) contributed with 28,952 tons of bell peppers (USDA-NASS 2015). Both Chile and bell peppers are grown on many farms across NC. Besides meeting market demands for quality and food safety, vegetable growers often deal with plant pathogens. Since 1954, the NC vegetable industry is threatened every year by the plant pathogen *Phytophthora capsici* (Crossan et al. 1954).

The oomycete *Phytophthora capsici* was described first in 1922 as the causal agent of a blight of *Capsicum annuum* L. at the New Mexico Agricultural Research Station, US. (Leonian 1922). *P. capsici* infects a wide number of plant species, including solanaceous, fabaceous, cucurbitaceous, and other plant families (Granke et al. 2012b) In pepper, under favorable conditions the infection takes place early in the growing season. The disease appears as small water soaked areas visible at the soil line. During rainfall, the disease progresses to affect the roots, crown, foliage, and fruit (Lamour et al. 2012b). In fruit, expanding lesions produce fresh sporangia over 5 days and develop into a distinctive white "powdered sugar" layer of sporangia on the surface of the fruit visible to the naked eye (Lamour and Hausbeck 2003).

P. capsici impacts pepper production in many areas of the world. In the US, disease has been reported in New Mexico, California, Colorado, Florida, Arizona, New York, New Jersey, South Carolina, Michigan, Illinois, Arkansas, Delaware, Georgia, Hawaii, Kentucky, Louisiana, Massachusetts, Ohio, Oklahoma, Tennessee, Texas, and North Carolina (Granke et al. 2012b). Sanogo and Carpenter (2006) conducted statewide surveys of commercial chile pepper fields in New Mexico from 2002 to 2004. They reported 59 of fields surveyed (80%) suffering Phytophthora blight with disease incidence ranging from 40% to 90%. In Mexico, hydroponic grown cucumbers experienced loss of 50% (Fernández-Pavía et al. 2006). An outbreak of Phytophthora blight of pepper in northern Nigeria caused severe losses in yield estimated to be $1,700 to $3,200 USD per hectare (Alegbejo et al. 2006). The annual damage estimate of *P. capsici* in the US exceeded $100 million in 2008 (Bosland 2008). Since the first report of *P. capsici* in NC (Crossan et al. 1954), infected pepper samples and other vegetables are received and confirmed every year in the Plant Disease and Insect Clinic at NC State University from across the state.

Taxonomy and phylogeny

Phytophthora capsici Leonian is classified in the Kingdom Chromista; Phylum Oomycota; Class Oomycetes; Order Peronosporales; Family Peronosporaceae; Genus Phytophthora; Species capsici (Lamour et al. 2012b).

Leonian (1922) described and morphologically compared for the first time the species *P. capsici* with other *Phytophthora* species. The gnarled mycelium was very distinctive, its large zoosporangia, and basal antheridia allowed to discriminate from *P. syringae.* Additionally, *P. parasitica, P. phaseoli,* and *P. infestans* were discarded because of their smooth hypha, much smaller zoosporangia and because of the lack of ready oospore formation in case of *P. infestans*. The morphology as shown in the first report of *P. capsici* is shown in the Figure. 1.1.

The genus Phytophthora was originally identified and classified under the key of Waterhouse (1963), but when molecular techniques became more powerful in dissecting differences among species a variety of DNA-based identification methods arose. Erwin and Ribeiro (1996a) and Cooke et al. (2000) examined the phylogenetic relationships of Phytophthora species and other oomycetes on the basis of morphology and Internal Transcribed Spacer (ITS) sequences of genomic rDNA respectively. Erwin and Ribeiro (1996a) descriptions grouped *P. capsici* with *P. citricola, P. botryosa, P. citrophthora, P. meadii, P. inflata,* and *P. colocasia* in the clade 2. Likewise, Cooke et al. (2000) clustered *P.*

capsici into clade 2 together with *P. multivesiculata, P. inflate, P. citricola, P. colocasiae, P. botryose,* and *P. citrophthora.* More recently, the use of multi-locus markers derived from complete genome sequences provided evidence to classify Phytophthora species into 10 clades, and *P. capsici* falls into clade 2 clustered with its related sister species *P. mexicana* and *P. tropicalis* (Blair et al. 2008). Blair et al. (2008) multi-gene phylogeny was based on seven loci: 28S Ribosomal DNA, 60S Ribosomal protein, beta-tubulin, elongation factor 1 alpha, enolase, heat shock protein 90, and *tigA* gene fusion protein.

Previously, *P. capsici* and *P. tropicalis* were considered to be the same species based on morphology and isozyme data (McHau and Coffey 1995, Oudemans et al. 1994). Combined with the phylogeny presented by Blair et al. (2008), a study separated both species into two taxa based on morphology and pathogenicity; *P. capsici* isolates recovered from solanaceous and cucurbitaceous plants were virulent to pepper plants, whereas *P. tropicalis* isolates recovered from tropical perennial crops, such as cacao, were avirulent to pepper plants (Aragaki and Uchida 2001).

Disease cycle and epidemiology

The life cycle of *Phytophthora capsici* is polycyclic and mainly depends on the type of reproduction that occurs. *P. capsici* is a heterothallic organism capable of reproducing both asexually and sexually (Erwin and Ribeiro 1996a). When isolates of mating type A1 and A2 come into contact their gametes, antheridia and oogonia, fuse and experience karyogamy resulting in the production of oospores (Lamour et al. 2012b). Oospores are overwintering sexual propagules with the ability to synthesize thick cell walls made of cellulose and β-glucan

(Wang and Bartnicki-Garcia 1980). Oospores persist in the soil for several years and germinate lemon-shaped sporangia with long pedicels under wet conditions (Pavón et al. 2008, Granke et al. 2012b). Sporangia may germinate by producing germ tubes or zoospores (Lamour et al. 2012b). Under suitable environmental conditions, the cytoplasm in the sporangium cleaves around each nucleus and subsequently 20 – 40 zoospores are discharged in water (Erwin and Ribeiro 1996a, Granke et al. 2012b). Because of their ability to move toward the surface water in flooded soil, their attraction to plant roots, and their capability to stick to plant surfaces during the encystment process and produce germ tubes, zoospores represent effective and infectious dispersal inoculum of *P. capsici* (Bernhardt and Grogan 1982, Erwin and Ribeiro 1996a). Both zoospores and sporangia serve as secondary inoculum throughout the growing season and can infect susceptible hosts (Kness 2015). As *P. capsici* colonizes the host tissue, it sporulates, generating copious amounts of sporangia, which are able to infect new plants or new parts of the same plant leading to a field epidemic (Quesada 2010).

Rainfall and soil moisture on a regional scale play an important role in *P. capsici* epidemics. Agricultural water sources, such as precipitation, groundwater, and surface water, influence the survival, production of mycelia and spores, and disease development of *P. capsici* (Sanogo and Ji 2013). In a review article, Sanogo and Ji (2013) elucidated the pathway to crop losses caused by *P. capsici*. Direct (fruit rot) or indirect (root and crown root) crop losses caused by *P. capsici* are driven by several forces including high moisture in soil and air, dispersal of propagules through moving water, and water splash through overhead irrigation or rainfall. Variation on soil moisture from saturation to field capacity affects sporangia formation (Bernhardt and Grogan 1982). Oospore formation and zoospore release highly depended on the presence of free water (Kim et al. 1989, Ploetz et al. 2002). The influence of water on dispersal of *P. capsici* has been well documented in commercial pepper fields of NC. Ristaino et al. (1994) demonstrated that movement of surface water along rows is key in spreading the pathogen. *P. capsici* sporangia are infrequently dispersed among fields by wind, however, water seems to be a carrier of sporangia in short distance dispersal. Granke et al. (2009c) directly observed sporangial dispersal occurring in water with capillary force, and demonstrated that dispersal of sporangia via wind currents is infrequent.

Temperature is another factor influencing disease development of *P. capsici.* Granke and Hausbeck (2010) revealed the effects of different temperatures (10, 15, 20, 25, 30, and 35°C) on development of *P. capsici* in pickling cucumber in controlled growth chamber. Lesions developed on cucumbers incubated at all temperatures tested except 10 and 35°C. Disease severity was greatest on cucumbers incubated at 25°C at 4 days post-inoculation (dpi). The survival of *P. capsici* is influenced by temperature as well as soil moisture. Bowers et al. (1990), reported the first study on the survival of *P. capsici* in natural soil. They demonstrated that oospores despite having low survival rates at -5 and -35 C were still able to cause disease. Little work has been reported on forecasting disease development. Liu et al. (2008) evaluated the mortality of pepper seedlings caused by *P. capsici* under controlled conditions in a growth chamber. They concluded that the optimum condition for infection was a soil temperature of 22 - 28C and soil water content of 40% and proposed a model to predict disease development by *P. capsici.* Jeger and Pautasso (2008) proposed that future forecasting models for plant pathogens like *P. capsici* must include zoospore activity as an explanatory variable. An integrated approach with population genetics input as well as epidemiology data may allow for more accurate predictions of disease development and effective deployment of management strategies such as fungicides and host resistance.

Management

Managing *P. capsici* relies on a combination of control strategies such as avoidance, cultural practices, chemical control, and host resistance (Granke et al. 2012b). Chemical control is extensively used as a management strategy to combat Phytophthora blight and fruit rot in peppers (Sanogo and Ji 2012). Management strategies that keep pathogen population sizes small assists control by limiting the genetic diversity in the pathogen population (McDonald and Linde 2002b).

Chemical management

A list of fungicides to manage *P. capsici* in peppers is published every year in the vegetable crop handbook for southeastern United States (Kemble et al. 2016), and plant disease management reports are generated to evaluate fungicides for control of Phytophthora blight of Peppers (Adams and Quesada-Ocampo 2015, Adams and Quesada-Ocampo 2016). Fungicides with control activity against *P. capsici* include mefenoxam, cyazofamid, dimethomorph, fluopicolide, and more recently oxathiapiprolin.

Mefenoxam is one of the most commonly used fungicides to control *P. capsici* and other oomycete pathogens. As a phenylamide fungicide, mefenoxam inhibits ribosomal RNA synthesis, specifically RNA polymerization (Davidse 1995). While in the past mefenoxam has been successfully used to control *P. capsici*, many populations of *P. capsici* are now insensitive to this fungicide (Granke et al. 2012b). *P. capsici* insensitive isolates to mefenoxam at 100 mg/L have been reported in North Carolina (Parra and Ristaino 2001, Café-Filho and Ristaino 2008), South Carolina (Keinath 2007), Georgia (Mathis et al. 1999), Florida (French-Monar et al. 2006b), New York (Dunn et al. 2010b), Connecticut (Hausbeck and Lamour 2004), and Michigan (Lamour and Hausbeck 2000).

Cyazofamid belongs to the chemical group of cyanoimidazole Fungicide Resistance Action Committee (FRAC) code 21. Cyazofamid affects respiratory pathways at complex III in the mitochondria (Mitani et al. 2001). High concentrations of cyozafamid (1000 ug/ml) inhibit mycelial growth, sporangial production and zoospore germination in *P. capsici* sensitive isolates (Jackson et al. 2012). In 2006, cyozafamid showed activity in controlling *P. capsici* in pepper on crown rot tolerant and susceptible cultivars (McGrath and Davey 2006). In 2008, Kousik and Keinath (2008) first reported insensitivity to cyazofamid among isolates of *P. capsici* from the southeastern US. Jackson et al. (2012) evaluated the effect of cyazofamid on various asexual stages of 40 *P. capsici* isolates from vegetable crops in Georgia. At 500 µg/ml all isolates showed inhibition of mycelial growth and sporangial production.

Dimethomorph is a carboxylic acid amide fungicide from the FRAC group 40. Dimethomorph affects phospholipid biosynthesis (Griffiths et al. 2003) and cell wall deposition (Cohen and Gisi 2007). Low concentrations of dimethomorph in *P. capsici* sensitive isolates reduce mycelial growth, sporangium formation, and zoospore cyst germination (Keinath 2007). Sensitivity of populations of *P. capsici* from South Carolina and Georgia to dimethomorph have been investigated (Keinath 2007, Jackson et al. 2012). All isolates of *P. capsici* tested by Jackson et al. (2012) and Keinath (2007) were reported as sensitive to dimethomorph.

Fluopicolide is a benzamide and pyridine fungicide recently registered to control oomycete pathogens (Jackson et al. 2010). Fluopicolide seems to act by delocalizing a spectrin-like protein that is cytoskeleton-associated (Toquin et al. 2008). Jackson et al. (2010) evaluated fungicidal activity of fluopicolide for controlling *P. capsici* on squash fields in Georgia. Their results indicated that fluopicolide applied through drip irrigation or as a foliar spray at 86.6 or 115.4 g/ha significantly reduce disease and increased squash yield. Additionally, Jackson et al. (2010) found that fluopicolide affects all growth stages of *P. capsici* including release and motility of zoospores, cyst germination, mycelial growth, and sporangial production. Keinath and Kousik (2011) reported the baseline sensitivity of mycelia growth (0.22 mg/L), zoospore germination (2.05 mg/L), and sporangia production (0.048 mg/L) of *P. capsici* isolates from South Carolina, Georgia, Florida, Michigan, and North Carolina to fluopicolide. Additionally, Keinath and Kousik (2011) recommended a concentration of 0.3 or 1 mg/L of fluopicolide to discriminate insensitivity by mycelia growth.

Oxithiapiprolin is the newest fungicide available to control *P. capsici*. It belongs to the new class of piperidinyl thiazole isoxazoline fungicides targeting the oxysterol binding protein. (Bittner and Mila 2016). Ji and Csinos (2015) determined baseline sensitivity of *P. capsici* isolates from vegetable crops in Georgia to oxathiapiprolin and the efficacy of oxathiapiprolin to reduce Phytophthora blight on bell pepper under field conditions. The median EC50 values of oxathiapiprolin concentration was 0.001, 0.0003, and 0.54 mg/L in the mycelial growth, sporangium formation and zoospore germination assays, respectively. The field study concluded that oxathiapiprolin applied at different rates through drip irrigation, or by soil drench plus foliar sprays, reduced Phytophthora blight and increased pepper yield significantly.

Cultural management

The most effective method to control *P. capsici* is by using appropriate cultural practices. Proper cultural management must emphasize water management because of the ability of *P. capsici* to disperse through water in fields (Sanogo and Ji 2013). Initial infection and spread of *P. capsici* highly depends on rainfall and excess soil moisture. Planting in plastic covered raised beds and well-drained fields can prevent bed wash-out during intense rain events, soil moisture accumulation, and reduce weed pressure (Hwang and Kim 1995, Granke et al. 2012b). Moreover, irrigation systems are important to limit the development of Phytophthora blight, crown, root, and fruit rot (Ristaino 1991, Biles et al. 1992, Café-Filho and Duniway 1996). Xie et al. (1999) studied the effects of irrigation method on pepper yields and Phytophthora root rot incidence. They evaluated three irrigation methods, daily drip, 3-day drip and alternate row furrow irrigation. Their results suggested that drip irrigation reduces incidence of Phytophthora root rot and increases pepper yield.

Irrigation water assists in the movement of *P. capsici* from field to field. Many studies have been published indicating the role of irrigation water sources in *P. capsici* epidemics (Roberts et al. 2005, Gevens et al. 2007b, Wang et al. 2009a, Quesada-Ocampo et al. 2011a). Therefore, irrigation from surface water should be monitored to avoid the introduction of *P. capsici* (Granke et al. 2012b). *P. capsici* can also be introduced via infested soil on equipment, disposal of infected cull fruits onto fields, and infected transplants (Granke et al. 2012b). Due to the capability of *P. capsici* to produce oospores, crop rotation and destruction of infected plants are still ineffective as a stand alone practice (Granke et al. 2012b). Babadoost and Pavon (2013) demonstrated that oospores of *P. capsici* can survive and remain virulent in Illinois soils for more than 3 years and Lamour and Hausbeck (2001b) observed oospores after 5 years or more in Michigan soils. Therefore, effective rotations require knowledge of the host range and duration of survival structures in various soils (Tian and Babadoost 2004).

Host resistance

Due to its low environmental impact and its simple implementation, host resistance is a key element in integrated disease management strategies (Granke et al. 2012b). High disease resistance was observed in the land race pepper "Criollo de Morelos 334" (Kimble and Grogan 1960, Barksdale et al. 1984). Land races of peppers and cultivated individuals are often crossed to breed for fruit quality, disease resistance, and other agronomically important traits (Naegele et al. 2015). Despite the availability of resistant peppers cultivars, the genetics behind resistance to *P. capsici* is not well understood. Sy et al. (2005) investigated the inheritance of Phytophthora stem blight, root rot and foliar blight resistance. Their findings suggested that resistance to stem blight and root rot is governed by a different set of genes than resistance to fruit rot and foliar blight. Because *P. capsici* exhibits large variation in virulence on various pepper genotypes (Foster and Hausbeck 2010), breeding for resistant cultivars is challenging and depends on the local *P. capsici* population diversity, as well as environmental factors (Granke and Hausbeck 2010). Although, no commercially available pepper cultivars are completely resistant to *P. capsici*, many pepper cultivars are evaluated every year for resistance to *P. capsici* (Dunn et al. 2013). In field trials conducted over 5 years, Dunn et al. (2014b) reported bell pepper cultivars Archimedes, Aristotle, Intruder, and Paladin as the most resistant to a single isolate of *P. capsici* from NY. Host resistance evaluations are an important effort that must combine the knowledge of local population structure of *P. capsici*, in order to effectively deploy durable resistance (Granke et al. 2012b).

Population diversity

Disease management is clearly linked to the understanding of the pathogen biology and its population dynamics. According to McDonald and Linde (2002b) the genetic structure of plant pathogens is a consequence of interactions among the five forces that affect the evolution of populations. Estimating the variation in DNA sequences can help to elucidate the contribution of each of the forces (mutation, recombination, natural selection, gene flow, random genetic drift, and migration) to the generation and maintenance of diversity in populations. Pathogenicity and fungicide insensitivity traits are under constant pressure to change among pathogen populations. Conducting surveys of local pathogen populations and examining their variations in phenotypic and/or genotypic diversity can ultimately help to direct and implement control management strategies (Cooke and Lees 2004). Given the fact that *P. capsici* stratifies geographically, understanding the genotypic variation can explain the extent and rate at which local populations adapt to environmental conditions, tolerant cultivars, fungicide applications, and other management strategies in that region.

Phenotypic diversity

Understanding the phenotypic variation in *P. capsici* is important towards developing and applying durable management strategies. The more information that we gather about a local population the more effective the control. For example, phenotypic information such as virulence contributes with plant breeding programs to generate genotypes with high disease resistance. If on the contrary, we ignore the variation of the pathogen, deployed resistant cultivars may be overcome when highly virulent local populations of the pathogen are present. Variation in *P. capsici* isolates such as sporangial shape, pedicel length, optimum temperature, and sporangial production has been well documented on several studies (Crossan et al. 1954, Parra and Ristaino 2001, Granke et al. 2011d, Hurtado-Gonzáles et al. 2008). Differences in virulence among *P. capsici* isolates on cucumber, zucchini, tomato and pepper fruits were investigated in a worldwide collection (Granke et al. 2012b). Granke et al. (2012b) observed significant differences in virulence with some isolates being highly virulent on certain hosts and less virulent on others. In addition, a global collection of *P. capsici* isolates was phenotypically characterized on the basis of mating type and sensitivity to mefenoxam (Quesada-Ocampo et al. 2011b). Foster and Hausbeck (2010) evaluated four isolates of *P. capsici* from Michigan on 31 bell and hot pepper cultivars and breeding lines. Differential responses on crown and root rot of pepper cultivars were observed for the four isolates, considered to be four different physiological races. A detailed phenotypic characterization and potential relationships among the phenotypic traits have not been studied in *P. capsici* isolates from NC.

Current understanding of the genetic diversity of Phytophthora capsici

Several studies have been published that report the genetic diversity and population structure of *P. capsici*. Studies employed a wide range of molecular markers such as random amplified polymorphic DNA (RAPD) (Islam et al. 2005a, Silvar et al. 2006, Sun et al. 2008b), amplified fragment length polymorphism (AFLP) (Lamour and Hausbeck 2001b, Bowers et al. 2007b), microsatellites (SSRs) (Wang et al. 2009a, Dunn et al. 2010b, Li et al. 2012, Dunn et al. 2014a), and single nucleotide polymorphism (SNP) (Hurtado-Gonzáles et al. 2008, Hulvey et al. 2011, Gobena et al. 2012).

Quesada-Ocampo et al. (2011b) explored the genetic diversity of 255 *P. capsici* isolates using four mitochondrial and six nuclear loci; isolates were collected from six continents and 21 countries. Bayesian clustering revealed population structure by host, geography, and mefenoxam sensitivity. They presented an initial map of global population structure of *P. capsici*. The genetic diversity in US populations is the result of sexual reproduction and the production of oospores which reflect high levels of genotypic diversity (Granke et al. 2012b, Lamour et al. 2012b). A study by Lamour and Hausbeck (2001b) investigated the dynamics of a field population from MI during 2 years. Nine populations from four vegetable production areas of MI were analyzed using AFLP markers. They observed highly subdivided populations with both mating types, high genotypic diversity, and high levels of genetic differentiation between populations.

Microsatellites

Simple single repeats (SSRs), also known as microsatellites, are tandem repeat nucleotide units that occur scattered throughout the genomes (Ellegren 2004). SSRs are composed of 1-6 base pairs in length with types of repeats known as mono-, di-, tri-, tetra-, penta-, and hexanucleotide repeats (Tóth et al. 2000). SSRs can be found in either non-coding or coding regions and are highly polymorphic making them desirable for population genetic analyses (Vukosavljev et al. 2014a). SSRs have been widely used in recent studies as a marker for diagnostics, population structure assessments, and epidemiological studies in plant pathogens (Lees et al. 2006, Perumal et al. 2008, Wang et al. 2010, Haňáčková et al. 2015, Gagnon et al. 2016a). Many of these publications aim to understand fine scale population genetic structure and diversity of plant pathogens. Other studies aim to test the utility of the SSRs markers in dissecting closely related species. More recently, Wang and Chilvers (2016) demonstrated that a set of 10 SSRs identified in *Fusarium virguliforme* are transferable and useful for species within clade 2 of *F. solani* species complex.

In the past, SSRs discovery pipelines involved enrichment of genomic DNA libraries for a few targeted SSRs motifs, followed by the screening and sequencing of clones through Sanger sequencing. The entire process was labor intensive, resource consuming, and usually yielded a small number of polymorphic markers (Dobrowolski et al. 2002, Prospero et al. 2004). The notion that microsatellites are still developed according to such methodologies is outdated. The advent of next generation sequencing (NGS) technologies has revolutionized genome and transcriptome surveys for microsatellites (Ellegren 2004). At the beginning NGS was not conceived to generate genome-wide polymorphism data, but with the introduction of bioinformatics methods this is now possible. This approach has been implemented to identify SSRs in several species, including Phytophthora species such as *P. nicotianae* (Biasi et al. 2015), *P. ramorum* (Garnica et al. 2006b, Schena et al. 2008), *P sojae* (Garnica et al. 2006b, Schena et al. 2008), *P. infestans* (Schoebel et al. 2013), *P. pulmivora* (Schoebel et al. 2013), and plant pathogens such as *Alternaria brassicicola* (Singh et al. 2014) , *Gaeumannomyces graminis* (Li et al. 2014), *Erisiphe necator* (Frenkel et al. 2012b), *Fusarium verticilliodes*

(Leyva-Madrigal et al. 2014a), and *Fusarium oxysporum* (Mahfooz et al. 2012a). More recently, Gagnon et al. (2016a) exemplifies such methods using the draft genome assembly of an isolate of *Synchytrium endobioticum* to develop polymorphic microsatellite loci.

Despite the availability of genome and predicted transcriptome sequences for *P. capsici*, population genetic studies often rely on a set of SSRs designed from a database of expressed sequence tags (EST) (Wang et al. 2009a, Meitz et al. 2010a). In a recent study, Dunn et al. (2010b) collected 257 *P. capsici* isolates from vegetables in four regions of New York. Population genetic structure was analyzed based on five SSRs loci published by Wang et al. (2009a) and Meitz et al. (2010a). Their microsatellite analysis successfully revealed highly diverse populations, but required additional SSR markers to increase resolution and detect greater diversity. In 1990, a survey of pepper and squash fields in NC provided evidence of diversity based on morphological characteristics and virulence on pepper (Ristaino 1990). However, there are no studies on the genetic diversity of *P. capsici* in NC.

Research project

Taking into consideration the availability of transcript sequences from *P. capsici*, the need to understand the population structure of *P. capsici* in NC, and the importance of evaluating resistance to *P. capsici* in pepper cultivars we aim to: (i) develop a set of informative microsatellite markers from the transcriptome of *P. capsici* that can be employed to understand regional pathogen population structure in NC, and (ii) improve management of Phytophthora blight in peppers by evaluating resistance to *P. capsici* of commercial and experimental lines of peppers in the greenhouse and the field.

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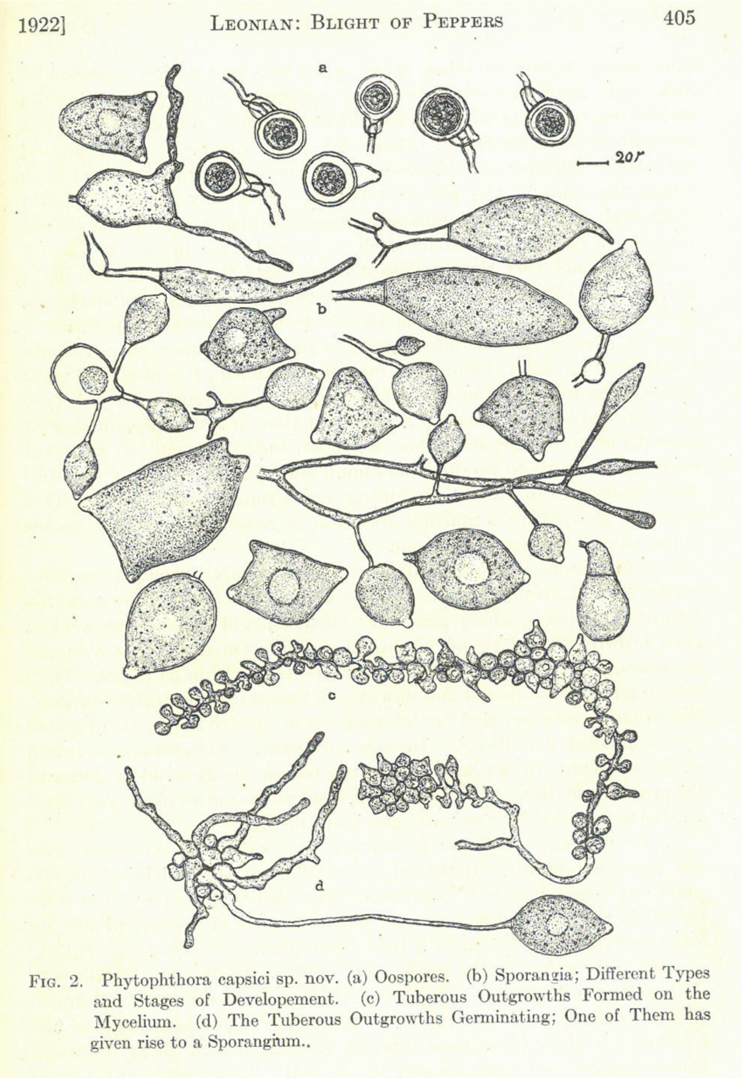

1922] LEONIAN: BLIGHT OF PEPPERS 405

FIG. 2. Phytophthora capsici sp. nov. (a) Oospores. (b) Sporangia; Different Types and Stages of Developement. (c) Tuberous Outgrowths Formed on the Mycelium. (d) The Tuberous Outgrowths Germinating; One of Them has given rise to a Sporangium.

Figure 1.1 Leon Leonian's morphological description of *P. capsici.* Taken from Volume 12 Journal Phytopathology.

CHAPTER II

Analysis of microsatellites from transcriptome sequences of *Phytophthora capsici* and applications for population studies

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ABSTRACT

Phytophthora capsici is a devastating oomycete that affects solanaceous, cucurbitaceous, fabaceous, and other crops in the United States (US) and worldwide. The release of the *P. capsici* genome allows for design of simple sequence repeats (SSRs) markers for genetic studies. We identified and characterized SSRs in the *P. capsici* transcriptome. A subset of 50 SSR were assayed in a diverse set of *P. capsici* isolates and evaluated for polymorphism. Polymorphic SSRs were confirmed by fragment analysis and 11 were used for population characterization of 30 *P. capsici* isolates from different states, hosts, mating types, and fungicide sensitivities. Analysis of genetic relationship among isolates revealed significant geographic structure by state and even by field. Our findings highlight the usefulness of the 11 SSRs to characterize the population structure of *P. capsici* and will complement phenotypic studies of *P. capsici* populations, which may assist in deployment of disease management strategies.

INTRODUCTION

The oomycete *Phytophthora capsici* Leonian is a devastating hemibiotrophic pathogen that causes severe epidemics over a broad host range of crops, including peppers, cucurbits, tomatoes, snap beans, eggplants, and many other plant species in the United States (US) and worldwide (Foster and Hausbeck 2010, Quesada-Ocampo and Hausbeck 2010, Granke et al. 2012a, Lamour et al. 2012c, Foster et al. 2013, Naegele et al. 2013). *P. capsici* can produce numerous symptoms depending on the host, including foliar blighting, damping-off, wilting, and rots of the roots, stem, and fruit (Granke et al. 2012a, Lamour et al. 2012c). In the field, disease management relies primarily on the application of fungicides, in combination with cultural practices that are unfavorable for disease development such as raised beds, plastic mulch, and drip irrigation (Granke et al. 2012a). However, the broad host range of *P. capsici* and its capability to undergo sexual recombination and produce thick-walled oospores as persistent survival structures (Erwin and Ribeiro 1996b) has limited the efficacy of control strategies such as crop rotation (McDonald and Linde 2002a, Gobena et al. 2012). Sexual recombination between the A1 and A2 mating types of this heterothallic oomycete can result in novel genotypes with increased virulence, pathogenicity, and the ability to overcome host resistance and fungicides (Granke et al. 2012a). *P. capsici* sporangia are infrequently dispersed among fields by wind (Lamour and Hausbeck 2001a). Instead, surface water sources for irrigation and movement of infected plant material or infested soil are known to be a key factor in local spread of *P. capsici* and in the development of epidemics (Granke et al. 2009b). Because of the limited dispersal of *P. capsici* and its ability to quickly overcome resistant varieties and fungicides due to frequent sexual reproduction, a better understanding of the regional pathogen population structure would allow for more effective deployment of resistant varieties and breeding for durable host resistance (Quesada-Ocampo et al. 2011b).

The amount and distribution of genetic diversity in *P. capsici* populations have been studied at a global scale within countries (Silvar et al. 2006, Meitz et al. 2010b, Hulvey et al. 2011, Quesada-Ocampo et al. 2011b, Gobena et al. 2012) and at a local scale within states in the US (Lamour and Hausbeck 2001a, Islam et al. 2005b, French-Monar et al. 2006a, Wang et al. 2009b, Dunn et al. 2010a). Studies employed a wide range of molecular markers such as random amplified polymorphic DNA (RAPD) (Islam et al. 2005b, Silvar et al. 2006, Sun et al. 2008a), amplified fragment length polymorphism (AFLP) (Lamour and Hausbeck 2001a, Bowers et al. 2007a, Gevens et al. 2007a), and single nucleotide polymorphism (SNP) (Hulvey et al. 2011, Gobena et al. 2012). Nonetheless, despite the benefits offered by microsatellite markers for population analyses (Cooke and Lees 2004), only a few useful microsatellite loci have been developed to assess genetic diversity on *P. capsici* population studies (Wang et al. 2009b, Meitz et al. 2010b). Microsatellites, also known as simple sequence repeats (SSRs), are short DNA sequences consisting of tandemly repeated units, generally 1 – 6 base pairs in length (Ellegren 2004, Selkoe and Toonen 2006). Microsatellites can be found in either non-coding or coding regions and are highly polymorphic, making them desirable for population genetic analyses (Vukosavljev et al. 2014b, Zhou et al. 2014). Microsatellites have been widely used in recent studies as a marker for diagnostics, population structure assessments, and epidemiological studies in oomycetes (Perumal et al. 2007, Matasci et al. 2010, Li et al. 2013, Schoebel et al. 2013, Yin et al. 2014, Biasi et al. 2015). Genetic diversity in *P. capsici* has also been determined by microsatellites (Wang et al. 2009b, Dunn et al. 2010a, Meitz et al. 2010b, Hu et al. 2013, Dunn et al. 2014a), however, most of these studies relied on a set of microsatellites designed from a database of expressed sequence tags (EST) (Wang et al. 2009b, Meitz et al. 2010b). To date no microsatellites have been identified in the current *P. capsici* genome assembly, which could offer a set of standardized markers to be used by the scientific community (Dunn et al. 2014a).

Traditionally, the methodology for microsatellite identification involved enrichment of genomic DNA libraries for a few targeted microsatellite motifs, followed by the screening and sequencing of clones through Sanger sequencing. The entire process is labor intensive, resource consuming, and usually yields a small number of polymorphic markers (Dobrowolski et al. 2002, Prospero et al. 2004). The publication of the *P. capsici* genome and the predicted transcriptome (Lamour et al. 2012a) and the availability of microsatellite search tools, such as MISA (MIcroSAtellite identification tool) (Thiel et al. 2003), allow identification of microsatellites from whole genomes or transcriptomes. Identifying microsatellites in transcript sequences implies the identification of polymorphisms within coding regions, which represent annotated markers located in genes that may play important roles in pathogen virulence and survival (Li et al. 2002). This approach has been successfully applied to identify microsatellites in an increasing number of species, including *Phytophthora* species such as *P. nicotianae* (Biasi et al. 2015), *P. ramorum* (Garnica et al. 2006a, Schena et al. 2007), *P. sojae* (Garnica et al. 2006a, Schena et al. 2007), *P. infestans* (Schena et al. 2007), *P. plurivora* (Schoebel et al. 2013), *P. multivora* (Schoebel et al. 2013), *P. pini* (Schoebel et al. 2013), and plant pathogens such as *Alternaria brassicicola* (Ruchi et al. 2014), *Gaeumannomyces graminis* (Li et al. 2014), *Erysiphe necator* (Frenkel et al. 2012a), *Fusarium verticillioides* (Leyva-Madrigal et al. 2014b), *F. oxysporum* (Mahfooz et al. 2012b), *Anisogramma anomala* (Cai et al. 2013), and more recently *Synchytrium endobioticum* (Gagnon et al. 2016b). In light of the economic importance of *P. capsici* and the potential insight offered through the use of microsatellites for population analysis we aimed to: (i) Analyze and compare the microsatellite repertoire in transcriptomes of *P. capsici, Phytophthora ramorum,* and *Phytophthora sojae*; (ii) evaluate microsatellites for use on *P. capsici* population analyses; and (iii) characterize the population structure of 30 *P. capsici* isolates from several geographic regions using microsatellite fragment analysis. Our findings indicate that the characterized microsatellites are informative for studies aiming to understand regional pathogen population structure, which will result in improved disease management strategies.

MATERIALS AND METHODS

Identification and analysis of microsatellites in the transcriptomes of *P. capsici*, *P. sojae*, and *P. ramorum*: Transcriptomes from genome sequences of isolate LT1534 of *P. capsici* (Lamour et al. 2012a), *P. ramorum* (Tyler et al. 2006), and *P. sojae* (Tyler et al. 2006) were downloaded as FASTA files from publically available databases at http://genome.jgi.doe.gov/Phyca11/Phyca11.home.html, http://genome.jgi.doe.gov/ramorum1/ramorum1.home.html, and http://genome.jgi.doe.gov/Physo3/Physo3.home.html. The transcriptome data were searched for microsatellite motifs of one to six nucleotides in length using the program MISA (MIcroSAtellite identification tool) (Thiel et al. 2003). Search criteria were set for identification of at least 10 repeat units for mono-nucleotides, six for di-nucleotides and five for tri-, tetra-, penta-, or hexa-nucleotides. Results were compared among species for abundance, frequency, distribution, and relative density of each repeat unit in the transcriptomes as described previously (Leyva-Madrigal et al. 2014b).

Isolates, culture conditions, and DNA extraction: A panel of seven single-spore *P. capsici* isolates were selected for primer evaluation via gel electrophoresis (Table 2.S1). This panel included one isolate from North Carolina (NC19385); one from New Jersey (R328); two from South Carolina (RCZ-11, WLB-8); two from Michigan (12889, SP98); and the isolate used in the *P. capsici* genome sequencing project (LT1534). All isolates were transferred from long term storage cultures to V8 juice broth as described previously (Quesada-Ocampo et al. 2009, Quesada-Ocampo et al. 2011b). Mycelia were harvested through filtration, immediately lyophilized, and stored at -80°C.

Genomic DNA was isolated using the following phenol-chloroform protocol: for each isolate, 200 mg of lyophilized mycelium were ground on an OMNI Bead Ruptor 24 (Omni International, Kennesaw, GA) at a speed of 5 m/s for 60 s, adding 2 mm glass beads. Subsequently, 600 µl of extraction buffer (0.5M Tris pH 8.0, 5M NaCl, 0.5M EDTA, 10% SDS) was added to the powdered tissue and homogenized by vortex. Samples were treated with 4 µl of RNAase A (Invitrogen Life Technologies, Grand Island, NY) and incubated for 10 min at room temperature with occasional gentle mixing. 500 µl of phenol was added and the mixture was centrifuged for 10 min at 21,130 g. The supernatant was transferred to a fresh tube and an equal volume of Phenol:Chloroform was added and mixed by gentle inversion; the mixture was centrifuged for 10 min at 21,130 *g*. The aqueous supernatant was transferred to a new tube and 0.8 volume of Isopropanol was added. Tubes were incubated at -20°C overnight. After incubation, all samples were centrifuged down for 15 min at 21,130 g, the supernatant was discarded and the pellet was precipitated with 80% Ethanol. The pellet was dissolved in 200 µl of sterile water. Quality and integrity of genomic DNA were estimated by measuring the 260/280 nm ratio in a NanoDrop ND-1000 spectrophotometer (Thermo Scientific, Wilmington, DE) and by electrophoresis in a 1% agarose gel in 0.5× Tris-borate-EDTA buffer stained with ethidium bromide (5 µg/ml) for visualization.

Microsatellite evaluation: The MISA output files and Perl programming were used to extract the coordinates of identified microsatellites in the *P. capsici* transcriptome and generate input files for designing primers with the Primer3 program (Rozen and Skaletsky 1999). Primer3 identified primer pairs flanking each microsatellite loci with a melting temperature between 57

°C and 63 °C with an optimum at 60 °C, GC content between 20 and 80% with an optimum of 50%, and PCR products with expected length between 100 and 300 bp. The M13 sequence (5’-GACGGCCAGT-3’) was added at the 5’ end of each forward primer in order to allow for later fluorescent product labeling and fragment analysis as previously described (Schuelke 2000). Ten microsatellite primer pairs each from di-, tri-, tetra-, penta-, and hexa-nucleotide motif length were randomly selected from the Primer3 output to detect polymorphism among 7 *P. capsici* isolates (Table 2.S2). Microsatellite primers selected were synthesized by Integrated DNA Technologies (Coralville, IA, USA). Polymerase chain reactions (PCR) were executed in a T100 thermocycler (Bio-Rad, Hercules, California, USA). A 20 µl of reaction volume contained 1 µl of genomic DNA at 50 ng/µl, 10 µl of GoTaq® Green Master Mix (2X GoTaq Green Master consisting of GoTaq Green Reaction Buffer, 400 µM of each dNTP, and 3 mM MgCl2; Promega, Madison, WI), 1 µl of each 10 µM primer, and 7 µl of sterile water. PCR cycling conditions included an initial denaturation at 94 °C for 3 min; followed by 35 cycles of denaturation 94 °C for 30 s, annealing at 53 °C for 30 s and extension at 72 °C for 30 s; with a final extension at 72 °C for 5 min. PCR products were analyzed for polymorphism by electrophoresis in 4% agarose gels and visualized by ethidium bromide staining. A 100 bp DNA ladder (Invitrogen Life Technologies, Grand Island, NY) was used to estimate allele size.

Population analyses using microsatellites: To determine the effectiveness of the microsatellites developed in this study in understanding population genetic structure and diversity, a subset of 12 microsatellite primers were selected on the basis of polymorphisms in agarose gels. These microsatellites were further analyzed across 30 *P. capsici* isolates from different states, hosts, mefenoxam sensitivities, and mating types via fragment analysis (Table 2.1). PCR products of polymorphic microsatellites were subjected to a second round of PCR. In these PCRs the forward primer of each microsatellite was 5' labelled with four fluorescent dyes (6-FAM, VIC, NED, and PET from Applied Biosystems, Foster City, CA, USA). Prior to fragment analysis, 1 µl of PCR product from 4 microsatellite loci labeled with different fluorescent dyes were pooled and diluted in ratio 1:100 with sterile dH_2O. In order to accurately detect variability in repeat length among isolates, a genotyping reaction was performed suspending 1 µl of diluted PCR product in 8.5 µl HiDi Formamide and 0.5 µl of Gene Scan 600LIZ dye Size Standard (Applied Biosystems, Foster City, CA, USA). Genotyping reactions were subsequently performed by the NCSU Genomic Science Laboratory (GSL, Raleigh, NC) on an ABI 3730xl DNA Analyzer (Applied Biosystems, Foster City, CA, USA).

Allele sizes were called using the Microsatellite Plugin in Geneious version R9.0.5 (Biomatters, New Zealand). In order to reduce the risk of genotyping stutter peaks, we manually removed from the analysis peaks lower than 5% of the signal of the tallest peak at any given locus. We assumed two alleles to be present at each loci because *P. capsici* is a diploid organism belonging to the class Oomycota. Polymorphism indexes such as the number of alleles (Na) and expected heterozygosity (He) were estimated using RStudio (version 0.99.903 and R version 3.2.4; R Core Team, Vienna) and the package Poppr (Kamvar et al. 2014). The polymorphism information content (PIC) was computed using PowerMarker version 3.25 (Liu and Muse 2005).

We used the R package poppr (Kamvar et al. 2014) to estimate the number of multilocus genotypes, the standardized index of association ($\bar{r}_d$) for all isolates and the index of association (I_A) for isolates coming from North Carolina with 1000 permutations (Brown et al. 1980), and the Shannon-Weiner index of genetic diversity. We built a genetic distance tree to assess genetic relatedness between isolates using Bruvo's distance with the R package poppr (Bruvo et al. 2004). Because the set of microsatellites identified in this study are intended to elucidate population structure of *P. capsici*; we assessed whether the 30 *P. capsici* isolates clustered by state, mefenoxam sensitivity, host, or mating type. This was examined using the Bayesian Markov Chain Monte Carlo (MCMC) clustering model using the software STRUCTURE v2.3.4 (Pritchard et al. 2000). The values for length of burnin, chain replication, and lambda were set at 300,000, 500,000, and 1 respectively. Population structure figure defining the state of origin was obtained using Microsoft Excel (version 15.20).

RESULTS

Microsatellite identification and analysis: Identification of microsatellites using MISA examined 20.36 Mb, 22.49 Mb, and 31.41 Mb of the transcriptomes of *P. capsici, P. ramorum,* and *P. sojae* respectively. In *P. capsici*, *P. ramorum*, and *P. sojae* 8.17%, 16.64%, and 16.96% of the sequences contained microsatellites respectively (Supplementary Table 2.S3). A total of 1,855 SSRs, 3,278 SSRs, and 6,157 SSRs were identified in the *P. capsici*, *P. ramorum*, and *P. sojae* transcriptome. Trinucleotide repeats represented the most prevalent motif length in transcript sequences across the three species (Fig. 2.1). In *P. capsici*, trinucleotide motifs (71.00%) were followed by tetranucleotides (13.98%), dinucleotides (9.33%), hexanucleotides (4.53%), and pentanucleotides (1.62%). In *P. ramorum*, dinucleotide motifs were the second most frequently occurring, followed by hexa-, tetra-, and pentanucleotide motifs. In *P. sojae*, dinucleotides were followed by tetra-, hexa-, and pentanucleotide motifs. *P. capsici* transcriptome (20.36 Mb) is smaller than the *P. ramorum* (22.49 Mb), and *P. sojae* (31.31 Mb), and it contains less microsatellites. The number of microsatellites among these *Phytophthora* species seems to be highly correlated with their genome size (Pearson, $r = 0.989$, $P > 0.05$ true correlation is not equal to 0). When accounting for the differences in length of examined sequences between species, the *P. capsici* transcriptome exhibited the lowest microsatellite relative abundance (microsatellite/Mb) and relative density (bp/Mb) 91.09 microsatellite/Mb and 1280.05 bp/Mb respectively, compared to *P. ramorum* (145.75 microsatellite/Mb, 2181.37 bp/Mb, $P < 0.05$) and *P. sojae* (196.04 microsatellite/Mb, 3190.98 bp/Mb, $P < 0.05$) (Table 2.S3). Overall, the *P. capsici* transcriptome contains significantly fewer microsatellites compared to the other *Phytophthora* species.

The frequency, relative abundance, and relative density of each repeat unit in the *P. capsici, P. ramorum*, and *P. sojae* transcriptome is presented in Table 2.2. Results indicated high similarity among the frequencies, relative abundances, and densities of the same repeat unit across the three species. For all three transcriptomes, the trinucleotide microsatellites were the most common motif length corresponding to around 70.00% of microsatellites. *P. capsici* had higher frequency, relative abundance and density of tetranucleotide microsatellites when compared to *P. ramorum*. *P. sojae* had the highest relative abundance and density of all microsatellite motifs when compared to *P. capsici* and *P. ramorum*. The frequency of the most abundant microsatellite motifs in the three *Phytophthora* species is shown in supplementary figure 2.S1, each species harbored a predominant set of microsatellite motifs. The primary dinucleotide motif in *P. capsici* was AC/GT whereas CG/CG was more common for *P. ramorum* and *P. sojae*. The main trinucleotide motif included AAG/CTT for *P. capsici* and AGC/CTG for *P. ramorum* as well as for *P. sojae*. In concordance with dinucleotide and tetranucleotide motifs frequencies, *P. capsici* presented a different primary tetranucleotide motif (ACGG/CCGT) when compared with *P. ramorum* and *P. sojae* (AGCG/CGCT). Pentanucleotide motifs and hexanucleotides motifs showed the lowest frequencies (<1%) across the three species. In all species, regardless the motif, the microsatellite tended to repeat 3, 4, and 5 times more frequently, and very few microsatellites had more than 10 repeats (Fig. 2.2).

Primer3 successfully identified 1,491 primers pairs (80.37 %) flanking microsatellites in the *P. capsici* transcriptome (Appendix A). Of the primers designed, 147, 1,015, 201, 21, and 59 belong to each of the motif lengths di-, tri-, tetra-, penta-, and hexa-nucleotide respectively. We randomly selected and synthesized 50 SSR primer pairs from 5 different motif lengths for agarose gel evaluation (Table 2.S2). Forty-eight primers pairs (96.00%) successfully amplified and produced clear bands on 4% agarose gels. Thirty-four (75.00%) out of 48 primer pairs yielded amplicons at the expected size. In total, 17 SSR primers exhibited polymorphism among the seven *P. capsici* isolates tested. Trinucleotide repeats yielded the greatest number of polymorphic amplicons. Di-, tetra-, penta-, and hexanucleotide primer pairs exhibited the least number of polymorphic bands (Fig. 2.3). Figure 2.4 exemplifies allelic variation for Phyca_SSR14, Phyca_SSR20, and Phyca_SSR40 across 7 *P. capsici* isolates in 4% agarose gels. The fragment analysis profile for Phyca_SSR14 is presented for all tested isolates.

Population analysis with microsatellites: Among the 17 microsatellites considered polymorphic in the agarose gels, we selected the 12-top performing based on consistent amplification and clear polymorphism in their agarose profile for further examination via fragment analysis in a broader panel of isolates. The microsatellites selected were used to assess the genetic relationship of 30 *P. capsici* isolates from different states in the US, exhibiting varying mefenoxam sensitivities, mating types, and from different hosts (Table 2.1).

The number of alleles per locus in the screened panel of isolates were, on average, 3.67 and ranged from 2 to 11 alleles. Most of the markers ranged from 2 to 5 alleles per locus (Table 2.3). The expected heterozygosity varied from 0.28 to 0.83, with an average of 0.59 (Table 2.3). The PIC values fluctuated between 0.24 and 0.80, with an average of 0.51, suggesting high variability of the microsatellites (Table 2.3). Locus Phyca_SSR11 was eliminated from the subsequent analysis since the locus contained missing values larger than 7%. The 30 *P. capsici* isolates were distributed across 27 multilocus genotypes (Table 2.1). The genotype accumulation curve established 11 microsatellites as the minimum number of loci necessary to discriminate between the 30 *P. capsici* isolates (Fig. 2.S2). After clone correction, the standardized index of association ($\bar{r}_d$) for all isolates (N = 27) was 0.045 ($P = 0.001$) which indicates that the isolates were not recombining. When analyzing only NC isolates (N = 15), the index of association (I_A) was 0.18 ($P = 0.119$), indicating random mating, which is supported by the fact that both mating types (A1 and A2) are present in NC isolates. Shannon-Wiener's index was 3.25 indicating high genetic diversity in the panel of *P. capsici* isolates (N=30). NC isolates (N = 15) showed the highest genetic diversity with Shannon-Weiner's index of 2.70.

Analysis of genetic relationship among isolates using Bruvo's distance exhibited significant bootstrap support (>70%) for clustering of isolates from South Carolina, which were collected from the same field (Fig. 2.5). New Jersey isolates R322, R317, and R320 clustered with 81% bootstrap support. The genetic distance tree grouped some NC isolates in the same clade, however, bootstrap support was not significant (< 70%). Isolates LT1534 and LT263 from TN grouped with a 51% bootstrap support, highlighting the known relationship between these two isolates. Overall, the genetic distance tree tended to cluster the isolates by state rather than by host, mating type or mefenoxam sensitivity (Fig. 2.5). The structure analysis based on the Bayesian clustering method established the presence of two population clusters, Group 1 and Group 2 (Fig. 2.6). The delta K plot indicated a clear peak at K = 2 (Supplementary Fig. 2.S3). The six *P. capsici* isolates collected from a SC field were assigned to Group 1 with membership probabilities greater than 0.95 (Fig 2.6). Isolates from NC, TN, NJ, and MI were allocated in Group 2 and unable to resolve by geography. The separation of SC isolates from NC, TN, NJ, and MI in the structure analysis (Fig. 2.6) support the clade identified in the genetic distance tree (Fig. 2.5). None of the population structure analyses (Bruvo's distance tree or Structure) clustered the 30 *P. capsici* isolates by host, mating type, or mefenoxam sensitivity.

DISCUSSION

We successfully identified 1,855 microsatellites in the *P. capsici* transcriptome, which represents a larger number than those discovered in *P. plurivora*, *P. multivora*, *P. pini*, *P. citricola*, or *P. alni* using 454-pyrosequencing-based methods (Abdelkrim et al. 2009, Aguayo et al. 2013, Schoebel et al. 2013). Greater numbers of microsatellites were found in our *P. ramorum* and *P. sojae* transcriptome analysis and a *P. nicotiana* whole genome analysis compared to *P. capsici* (Biasi et al. 2015). The relative abundance and relative density of microsatellites in *P. capsici* differs from *P. ramorum* and *P. sojae*, which may be due to differences among genome sequencing and assembly approaches taken for these three species (Tyler et al. 2006, Lamour et al. 2012a). *P. capsici* genome (64 Mb) was sequenced using 454 and Sanger based sequencing approaches and assembled using a modified version of Arachne (Lamour et al. 2012a). In contrast, the 95 Mb *P. sojae* genome and the 65 Mb *P. ramorum* genome were produced using a whole-genome shotgun approach and assembled with the JGI assembler, Jazz (Tyler et al. 2006). Despite these differences, our results suggest high similarity among the frequencies, relative abundances, and densities of the same repeat unit across the three species. In the different transcriptome sequences analyzed here, trinucleotide microsatellites constituted the most common motif length, consistent with studies in other *Phytophthora spp*. (Garnica et al. 2006a, Biasi et al. 2015), fungal plant pathogens (Mahfooz et al. 2012a, Ruchi et al. 2014, Wang and Chilvers 2016), and plants (Lawson and Zhang 2006). The same studies also report lower abundance of di-, tetra-, and pentanucleotides. Purifying selection for motifs that preserve reading frames explains the predominance of trinucleotide microsatellites in coding regions (Metzgar et al. 2000).

We designed primer pairs for more than 80% of the identified microsatellites. Our results provide information about the reliability and quality of the genome assembly. Garnica et al. (2006a) used transcriptome sequences of *P. ramorum* and *P. sojae* and had similar primer design success rate, greater than 80%, which is comparable with our findings. The insufficient flanking sequence adjacent to the microsatellite, such as microsatellites close to the end of a contig, may be a reason for the 20% primer design failure (Cai et al. 2013). The gel electrophoresis screening of a set of 50 microsatellites in seven *P. capsici* isolates identified 17 highly polymorphic microsatellites. We observed greater amplification efficiency (96.00%) than reported by Wang and Chilvers (2016) (85.00%) and Gagnon et al. (2016b) (79.03%) who examined whole genome sequences of *F. virguliforme* and *S. endobioticum* respectively. Amplification efficiency in our microsatellite screening might be attributed to the stability of coding regions due to functional constrains (Parida et al. 2008). We observed a greater number of alleles in trinucleotide microsatellites, compared to di-, tetra-, penta- and hexa-nucleotide microsatellites. We further narrowed the list of microsatellites for use in population studies from 17 to 12 based on consistent amplification and polymorphism observed via gel electrophoresis, and confirmed the polymorphism via fragment length analysis. Polymorphism indexes such as PIC (0.51) and He (0.59) indicated high potential for these markers to describe diversity in the panel of 30 *P. capsici* isolates. Our PIC values are similar to the ones reported by Li et al. (2013) and Lee and Moorman (2007) when they characterized microsatellites for 96 *P. infestans* isolates and 40 *Pythium spp.* isolates respectively. In this study, the MLG curve reached a plateau with 11 SSR markers out of 12, implying that these markers are sufficient to depict all 27 multilocus genotypes. Filtering for missing data removed loci Phyca_SSR11 from the analysis, however, we still retained enough loci to characterize genetic diversity (data not shown). The $\bar{r}_d$ calculated for all isolates after clone correction suggested non-recombination, which is probably due to the fact that our sampling contained isolates from different states and fields in the US. *P. capsici* populations are known to stratify by geography since long distance movement is unlikely (Quesada-Ocampo et al. 2011b). In contrast, NC isolates seem to undergo random mating based on the index of association, which is supported by the fact that the NC samples contained both A1 and A2 isolates, and recombination via sexual reproduction is more likely to occur. The Shannon-Wiener's index confirmed the presence of high genetic diversity in our sample of 30 *P. capsici* isolates. NC isolates displayed more genetic diversity than any of the *P. capsici* populations reported from 11 different sites in four regions of New York State (Dunn et al. 2010a). This could be a result of our sampling since the 15 NC isolates included in this study come from different location throught the state. Further research is need to determine if such diversity in NC is an effect of more overwintering thus accumulated diversity, or if the large diversity of host in NC is diversifying the population.

The 11 microsatellite markers developed here detected population structure based on geographic regions in a subset of 30 *P. capsici* isolates. In the current study, the Bruvo's genetic distance analysis enabled us to differentiate some isolates by state of origin, and in the case of SC isolates by field from which the isolates were collected. Such genetic differentiation is explained by the fact that *P. capsici* exists in geographically isolated subpopulations in the US (Dunn et al. 2010a, Quesada-Ocampo et al. 2011b). The *P. capsici* genome was generated by sequencing the isolate LT1534, included in this study, that was obtained by crossing isolates LT263 from TN and OP97 from MI (Lamour et al. 2012a). Our genetic distance tree related isolates LT263 and LT1534 with a 51% bootstrap value. In addition, the clustering of isolates based on the STRUCTURE analysis supported the hypothesis of the genetic distance tree. The STRUCTURE analysis clustered all SC isolates collected from the same field together in group 1. We attribute the unresolved group 2 in the structure analysis to the low number of isolates per field from NC, NJ, TN, and MI. Nonetheless, the 11 microsatellite identified here represent an additional set of genetic markers for describing the population structure of *P. capsici* at a geographic scale, which can inform management of *P. capsici* (Granke et al. 2012a).

P. capsici is considered a pathogen with high evolutionary potential, because sexual reproduction increases the probability of developing highly resistant genotypes that overcome management strategies (McDonald and Linde 2002a). These new genotypes could be leading to new and more isolated epidemics (Granke et al. 2012a), and therefore understanding the phenotypic variation and genotypic structure in a particular region becomes highly desirable. Microsatellites as described by Cooke and Lees (2004) represent a powerful molecular maker for genetic analysis, affordable, and reproducible among research groups. Even though genomic approaches are available now, such as genotyping by sequencing, the *P. infestans* community stills relies on microsatellite markers to understand the pathogen biology and its population dynamics (Cooke et al. 2012, Tian et al. 2015, Stroud et al. 2016). In fact, Dunn et al. (2010a) emphasized the need for additional polymorphic markers to increase resolution and detect greater diversity in populations of *P. capsici*. Our study delivers a set of highly polymorphic microsatellites to the *P. capsici* community: these 11 microsatellites represent additional tools to understand the structure and diversity of *P. capsici* populations, allowing for comparisons of datasets generated by different research groups. We foresee an additional application for our microsatellites as transferable markers across species complexes. Quesada-Ocampo et al. (2011b) used SNPs from several genomic regions to separate *P. capsici* and *P. tropicalis* using Bayesian clustering analysis, however, their SNP markers were unable to resolve an intermediate cluster containing both species. Microsatellites developed from coding regions are highly transferable to closely related species, and since *P. capsici* is part of a species complex, our microsatellites may be able to distinguish among closely related species such as *P. capsici, P. tropicalis*, and *P. glovera*. (Ruchi et al. 2014, Liu et al. 2016, Wallace 2016). However, further experiments should be completed to validate this hypothesis.

Taken together, our findings demonstrate that the 11 microsatellites developed from the transcriptome of *P. capsici* amplify reliably, are polymorphic in a diverse panel of isolates, and can describe the diversity of local populations. Future studies may also confirm transferability to closely related species of *P. capsici*. These microsatellites can be used to analyze the genetic structure of populations located in particular geographic regions and fields. The information generated by population studies using these markers may allow for better deployment of fungicides and resistant cultivars.

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Table 2.1. 30 *Phytophthora capsici* isolates used for microsatellite evaluation via fragment analysis.

Isolate	Source	Country	State	Host	Mefenoxam sensitivity	Mating type	MLG[†]
12889	Hausbeck M.	US	MI	Pepper	IS	A1	27
SP98	Hausbeck M.	US	MI	Pepper	S	A2	18
NC17257	PDIC	US	NC	Cucumber	S	A2	5
NC18800	PDIC	US	NC	Pepper	IS	A2	11
NC19385	PDIC	US	NC	Muskmelon	IS	A1	24
NC21064	PDIC	US	NC	Pepper	S	A1	13
NC21810	PDIC	US	NC	Zucchini	IS	A2	6
NC22256	PDIC	US	NC	Pepper	S	A2	14
NCCP18	Wilson Co	US	NC	Creek	I	A2	9
NCCP19	Wilson Co	US	NC	Creek	I	A2	26
NCCP20	Wilson Co	US	NC	Creek	I	A2	19
NCCP3	Guilford Co	US	NC	Squash	S	A2	1
NCCP33	Wilson Co	US	NC	Watermelon	S	A2	20
NCCP48	Wilson Co	US	NC	Cucumber	S	A2	25
NCCP50	Wilson Co	US	NC	Cucumber	S	A2	23
R377	Ristaino J.	US	NC	Pepper	S	A2	8
R388	Ristaino J.	US	NC	Pepper	S	A1	21
R317	Ristaino J.	US	NJ	Pepper	I	A2	4
R320	Ristaino J.	US	NJ	Pepper	IS	A1	3
R322	Ristaino J.	US	NJ	Pepper	I	A2	2
R328	Ristaino J.	US	NJ	Pepper	S	A1	7
LC4	Kousik C.	US	SC	Sponge Gourd	S	A2	16
LC5	Kousik C.	US	SC	Sponge Gourd	S	A2	16
LC6	Kousik C.	US	SC	Sponge Gourd	S	A2	16
MC1	Kousik C.	US	SC	Bitter Gourd	S	A2	15

Table 2.1 Continued

MC2	Kousik C.	US	SC	Bitter Gourd	S	A2	17
RCZ-11	Keinath A.	US	SC	Zucchini	S	A2	17
WLB-8	Kousik C.	US	SC	Watermelon	S	A1	10
LT1534	Lamour K.	US	TN	CFI	S	A2	22
LT263	Lamour K.	US	TN	Pumpkin	S	A2	12

[†] MLG: Multilocus genotype

Table 2.2. Frequency, relative abundance, and relative density of each motif length in *P. capsici*, *P. ramorum*, and *P. sojae* transcriptomes.

	Pathogen	Frequency (%) [a]	Relative abundance [b]	Relative density [c]
Di-	*P. capsici*	9.33	8.50	85.54
	P. ramorum	12.20	17.79	167.27
	P. sojae	13.38	26.24	246.12
Tri-	*P. capsici*	71.00	64.67	754.71
	P. ramorum	73.64	107.34	1218.81
	P. sojae	69.55	136.34	1508.64
Tetra-	*P. capsici*	13.48	12.28	144.57
	P. ramorum	6.41	9.34	108.49
	P. sojae	8.85	17.35	194.61
Penta-	*P. capsici*	1.62	1.47	21.36
	P. ramorum	0.76	1.11	16.01
	P. sojae	1.71	3.34	44.58
Hexa-	*P. capsici*	4.53	4.12	62.76
	P. ramorum	6.96	10.14	178.75
	P. sojae	6.50	12.74	201.93

[a] Frequency was calculated for each organism by dividing the total number of each motif length by the total number of microsatellite count.

[b] Relative abundance is defined as number of microsatellites of each motif length per Mb of analyzed sequence.

[c] Relative density is defined as the total length of microsatellites (bp) per Mb of analyzed sequence.

Table 2.3. Genetic diversity statistics for a population analysis of 30 *P. capsici* isolates using 12 microsatellites.

SSR id	Gene id	SSR motif	Primer sequence	Na	He	PIC
Phyca_SSR07	527040	(GA)6	F: CTCTGGCATTGAAAGAGCGC R: CCCAAAGTTGCGCCATTTGA	2	0.51	0.46
Phyca_SSR11[z]	101366	(CAG)4	F:CAGCAACAGCAACAGTCGTC R:TCCAAGTCGCTCGTCTGAAC	3	0.66	0.69
Phyca_SSR13	13824	(CAG)5	F:GAACACATCCGATTCGCAGC R:TTGCTGCTCAGATCCACTGG	11	0.83	0.80
Phyca_SSR14	7601	(AAG)6	F:CAGAAACACACGTCTCCGGA R:GTTCGAACTGCTCCTGCTCT	4	0.61	0.52
Phyca_SSR15	129784	(AGC)4	F:TCGTCGTTTTCCTCTGTGCA R:TTGAACTTCATCGCAGCCCT	2	0.28	0.24
Phyca_SSR17	15345	(AAG)6	F:TATCGGACGTTCTCGCCATG R:TGAGCGGTTTCTGCTCGAAT	2	0.51	0.37
Phyca_SSR18	121654	(AGC)6	F:GGACGATATCATGCAGCCGA R:CCGAGTCTGAACCCGAAGAG	3	0.59	0.51
Phyca_SSR20	103897	(AAG)7	F:CACGGAAGCTCAACGCAAAA R:GAGGTTGTCAGTGCTGTCGA	4	0.64	0.61
Phyca_SSR30	528924	(CCAG)6	F:CACAGCCTCTCGACCGGA R:CGTTTTCCAGCACACCCTTG	5	0.76	0.71
Phyca_SSR40	572218	(TCCTC)3	F:CAAGTCCCTGTCGTCGTTCT R:CATGGCAGTCACCGTCTCTT	2	0.51	0.37
Phyca_SSR41	570597	(CACGAC)5	F:GACTACGACGTCTACCGCTG R:GACGTCGTGGTGGTCGTAG	3	0.56	0.48
Phyca_SSR50	97293	(ACTTCA)4	F:GGGGCAGAAACGTCTCTGAA R:GGTCGTCGTCTGAGTCTGAC	3	0.63	0.36

Na: Number of alleles
He: Expected heterozygosity
PIC: Polymorphism information content
[z] eliminated locus since contained 7% missing data.

Table 2.S1. *Phytophthora capsici* isolates used for microsatellite evaluation.

Isolate	Host	Origen	Mating type	Source
NC19385	Watermelon	North Carolina	A1	Quesada
R328	Pepper	New Jersey	A2	Ristaino
RCZ-11	Zucchini	South Carolina	A2	Kousik
WLB-8	Watermelon	South Carolina	A1	Kousik
12889	Pepper	Michigan	A1	Hausbeck
SP98	Pumpkin	Michigan	A2	Hausbeck
LT1534	-	Inbred isolate	A2	Lamour

Table 2.S2. Details of 50 *P. capsici* microsatellites validated in 7 *P. capsici* isolates.

Gene ID	Locus screened	Motif	Ta (°C)	Expected size (bp)	Amplification
22063	Phyca_SSR01	(CG)6	53	225	Monomorphism
502925	Phyca_SSR02	(CA)6	53	148	Monomorphism
504309	Phyca_SSR03	(CA)6	53	276	Monomorphism
510484	Phyca_SSR05	(TG)6	53	111	Monomorphism
511652	Phyca_SSR06	(GA)6	53	240	Monomorphism
534614	Phyca_SSR08	(AG)6	53	292	Monomorphism
99537	Phyca_SSR10	(AG)15	53	269	Monomorphism
537480	Phyca_SSR16	(AGC)5	53	269	Monomorphism
10458	Phyca_SSR21	(TCGC)3	53	198	Monomorphism
11692	Phyca_SSR22	(GTGC)3	53	255	Monomorphism
14828	Phyca_SSR23	(GCGG)3	53	207	Monomorphism
21701	Phyca_SSR24	(ACCC)3	53	240	Monomorphism
43145	Phyca_SSR25	(CCAA)3	53	173	Monomorphism
53461	Phyca_SSR26	(GTGC)3	53	126	Monomorphism
7941	Phyca_SSR27	(TCTG)3	53	156	Monomorphism
9314	Phyca_SSR28	(AGTG)3	53	267	Monomorphism
20337	Phyca_SSR29	(GCTG)4	53	130	Monomorphism
107191	Phyca_SSR31	(CCACG)3	53	226	Monomorphism
109106	Phyca_SSR32	(GCACG)3	53	272	Monomorphism
109188	Phyca_SSR33	(TTTTG)3	53	138	Monomorphism
127764	Phyca_SSR35	(CGTGG)3	53	149	Monomorphism
560628	Phyca_SSR38	(CGCCA)3	53	283	Monomorphism
569117	Phyca_SSR39	(ACAGC)3	53	181	Monomorphism
4219	Phyca_SSR42	(CGGCTT)3	53	292	Monomorphism
4390	Phyca_SSR43	(GTTTGA)3	53	265	Monomorphism
534052	Phyca_SSR44	(GAGTAC)3	53	101	Monomorphism
569332	Phyca_SSR45	(CAAGGA)3	53	300	Monomorphism
96582	Phyca_SSR46	(CGGCTT)3	53	300	Monomorphism
112116	Phyca_SSR47	(CTCAGA)4	53	134	Monomorphism

Table 2.S2 Continued

20047	Phyca_SSR48	(CGCTGT)4	53	241	Monomorphism
564747	Phyca_SSR49	(ATGAAC)4	53	299	Monomorphism
564509	Phyca_SSR09	(GT)6	53	248	Non-amplification
12070	Phyca_SSR34	(TCGCA)3	53	130	Non-amplification
504465	Phyca_SSR04	(TG)6	53	273	Polymorphism
527040	Phyca_SSR07	(GA)6	53	216	Polymorphism
101366	Phyca_SSR11	(CAG)4	53	131	Polymorphism
13823	Phyca_SSR12	(CAG)4	53	162	Polymorphism
13824	Phyca_SSR13	(CAG)5	53	109	Polymorphism
7601	Phyca_SSR14	(AAG)6	53	202	Polymorphism
129784	Phyca_SSR15	(AGC)4	53	163	Polymorphism
15345	Phyca_SSR17	(AAG)6	53	116	Polymorphism
121654	Phyca_SSR18	(AGC)6	53	260	Polymorphism
103721	Phyca_SSR19	(AAG)6	53	231	Polymorphism
103897	Phyca_SSR20	(AAG)7	53	235	Polymorphism
528924	Phyca_SSR30	(CCAG)6	53	219	Polymorphism
34485	Phyca_SSR36	(GCGAG)3	53	252	Polymorphism
549994	Phyca_SSR37	(CAAGC)3	53	295	Polymorphism
572218	Phyca_SSR40	(TCCTC)3	53	110	Polymorphism
570597	Phyca_SSR41	(CACGAC)5	53	108	Polymorphism
97293	Phyca_SSR50	(ACTTCA)4	53	234	Polymorphism

Table 2.S3. Number and distribution of microsatellites in the *P. capsici*, *P. ramorum*, and *P. sojae* transcriptome.

Description	***P. capsici***	***P. ramorum***	***P. sojae***
Total number of sequences examined	19,805	15,743	26,584
Total size of examined sequences (Mb)	20.36	22.49	31.41
Total number of identified SSRs	1,855	3,278	6,157
Number of SSRs containing sequences	1,620 (8.17%)	2,620 (16.64%)	4,509 (16.96%)
Number of sequences containing > 1 SSR	180 (0.91%)	472 (2.99%)	1,118 (4.21%)
Number of compound SSRs	75 (4.04%)	180 (5.49%)	502 (8.15%)
Total relative abundance (SSRs/Mb)	91.09	145.75	196.04
Total relative density (bp/Mb)	1280.05	2181.37	3190.98

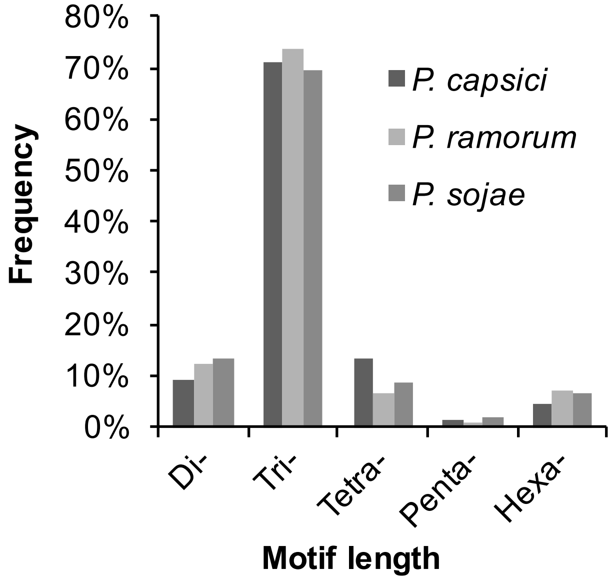

Figure 2.1. Frequency distribution of microsatellites in *P. capsici*, *P. ramorum*, and *P. sojae* by motif length.

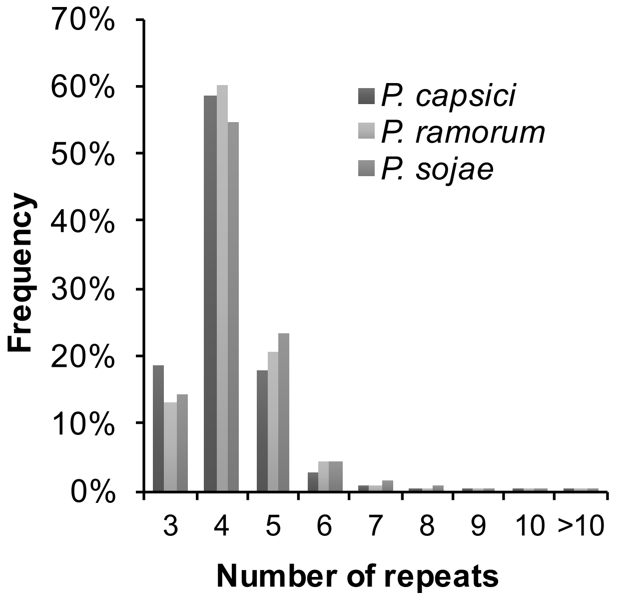

Figure 2.2. Distribution of microsatellites in *P. capsici, P. ramorum* and *P. sojae* by number of repeats.

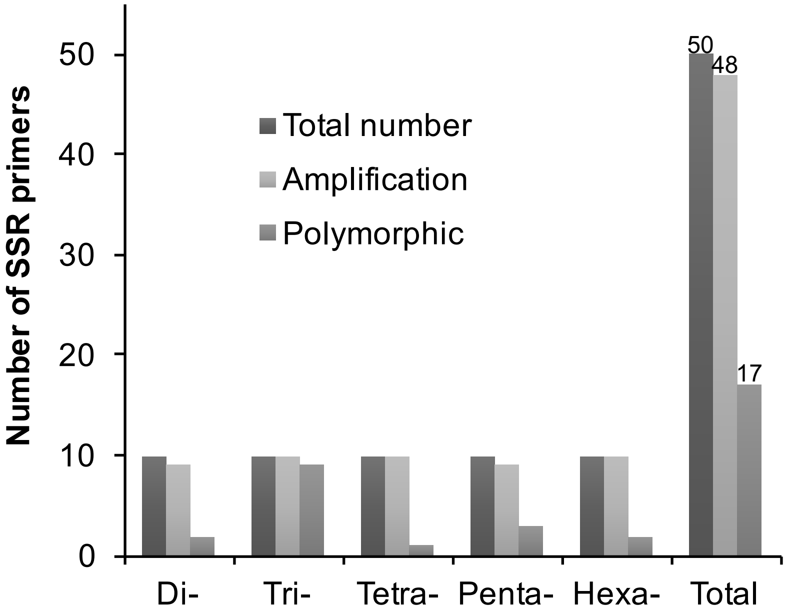

Figure 2.3. Number of microsatellites identified as polymorphic and amplification efficiency among the different types of motif lengths on agarose gel electrophoresis.

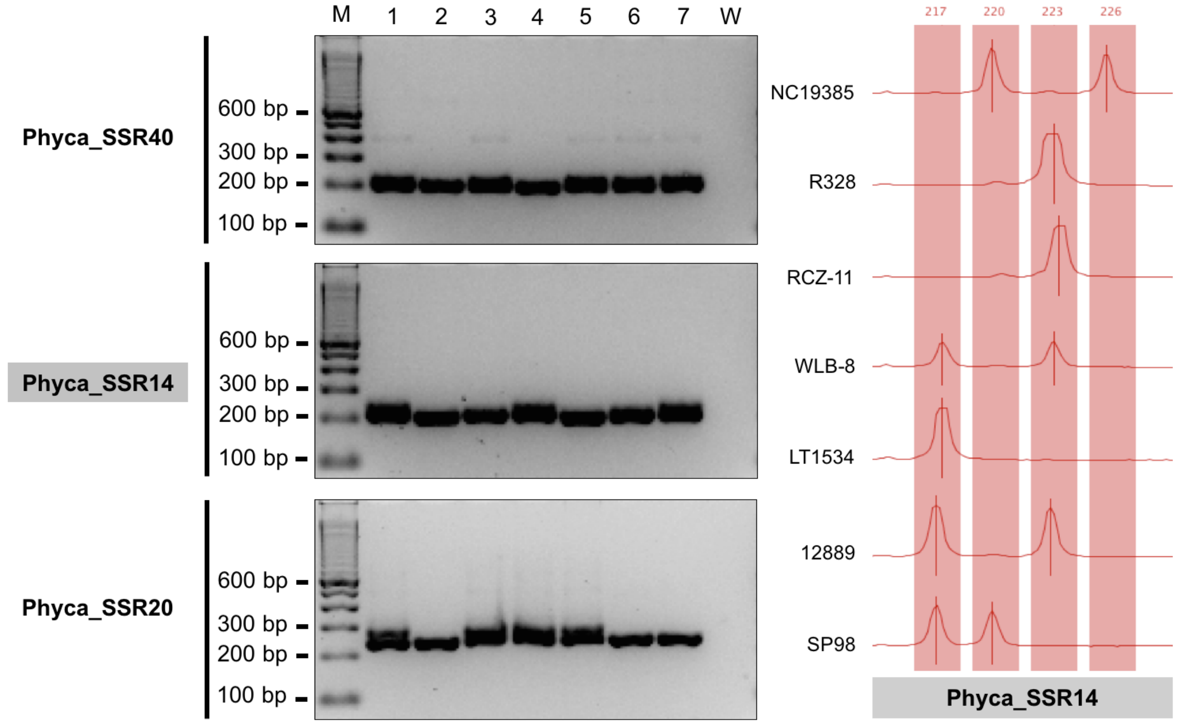

Figure 2.4. Amplification profile from 7 *P. capsici* isolates using the Phyca_SSR40, Phyca_SSR14, and Phyca_SSR20 primers. M: 100bp marker, 1: NC19385, 2: R328, 3: RCZ-11, 4: WLB-8, 5: LT1534, 6: 12889, 7: SP98, and 8: water. PCR products were resolved in 4% agarose gel. Fragment analysis profile for Phyca_SSR14 across the 7 *P. capsici* isolates, ordered as in the gel.

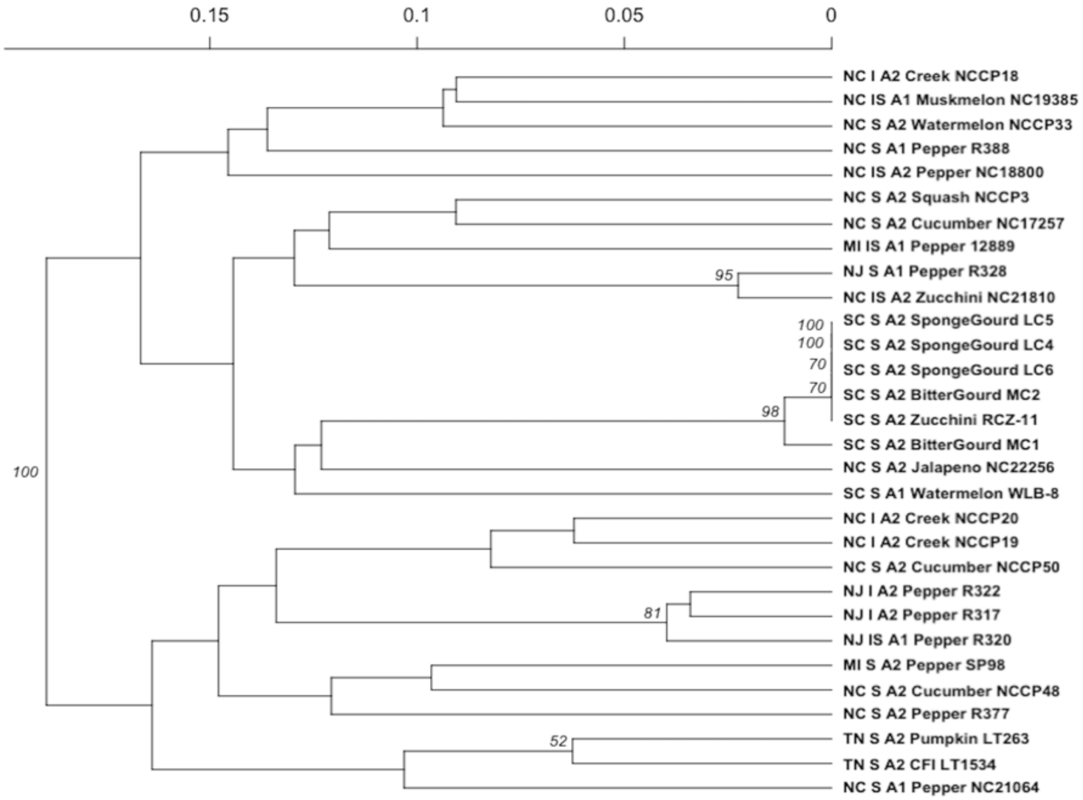

Figure 2.5. UPGMA tree with 1,000 bootstrap replicates based on Bruvo's distance for 30 *P. capsici* isolates. Tip labels define the isolate information by state (NC: North Carolina, SC: South Carolina, NJ: New Jersey, TN: Tennessee, and MI: Michigan), mefenoxam sensitivity (I: insensitive, IS: intermediate sensitivity, and S: sensitive), host, and isolate ID. Branches with bootstrap values greater than 50% are displayed.

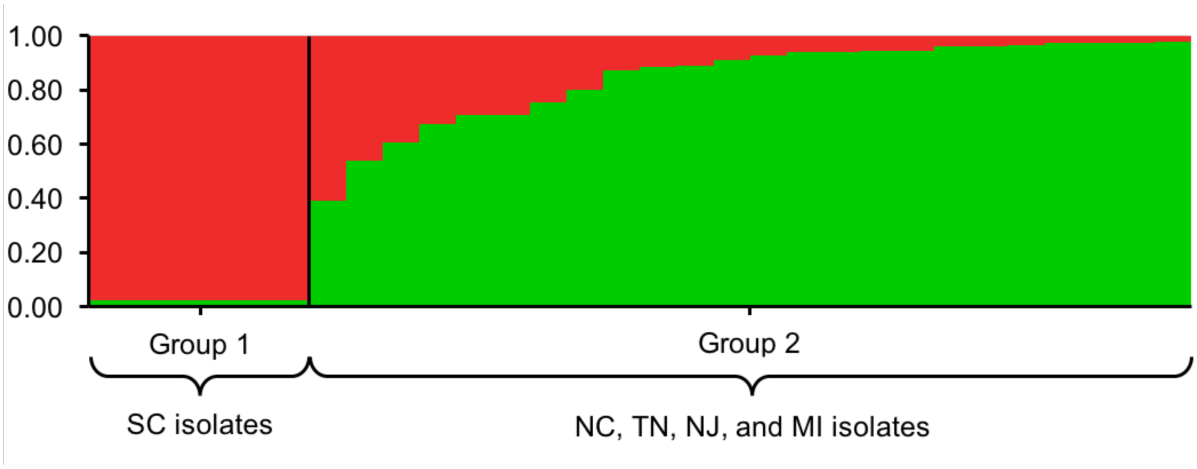

Figure 2.6. Population structure histogram for 30 *P. capsici* isolates when analyzed with 11 microsatellites using STRUCTURE. Color on each bar indicates membership probability of belonging to a corresponding group.

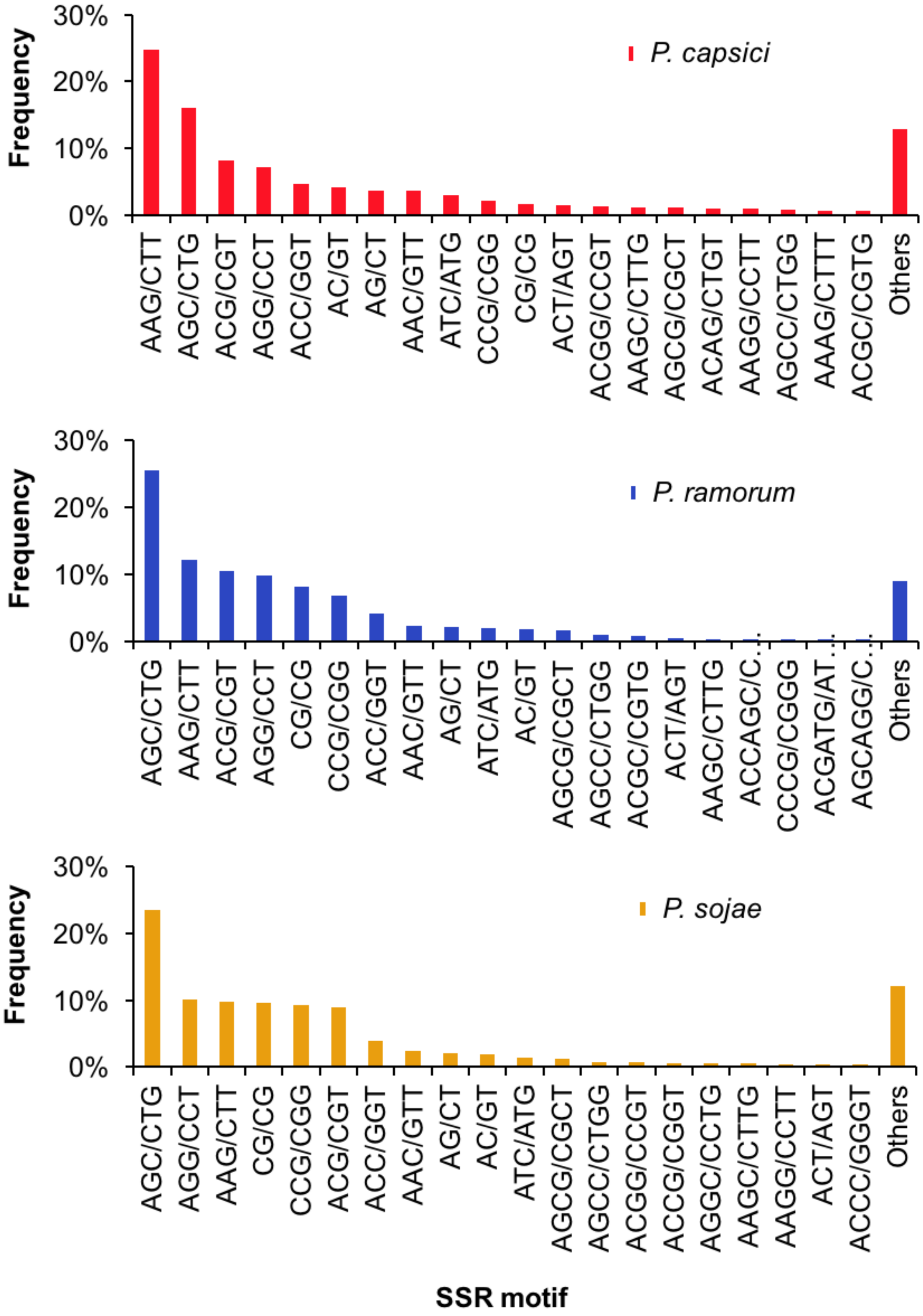

Figure 2.S1. Frequency of the most abundant microsatellite repeat motif in the three *Phytophthora* species. **(red)** *P. capsici*. **(blue)** *P. ramorum*. **(yellow)** *P. sojae*.

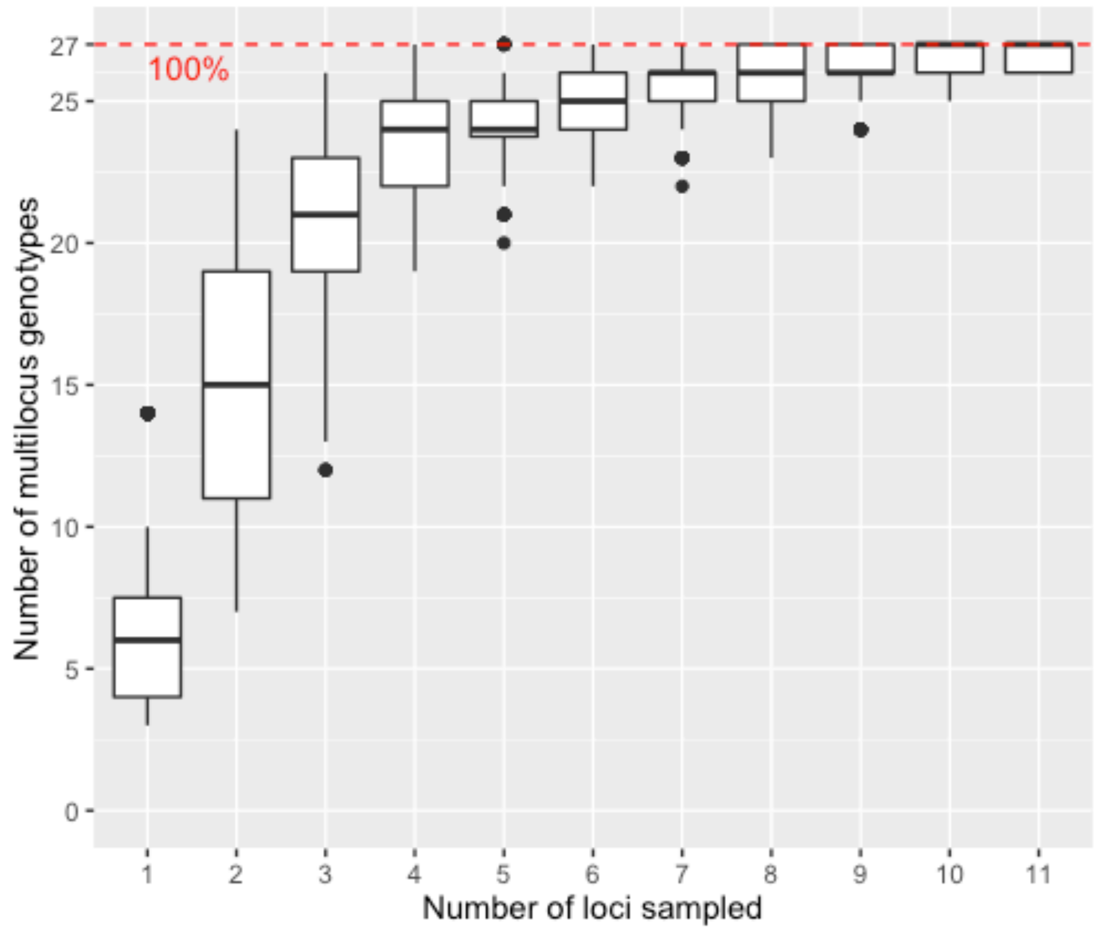

Figure 2.S2. Genotype accumulation curve. 27 multilocus genotypes of *P. capsici* (100%) are detected using 11 microsatellites.

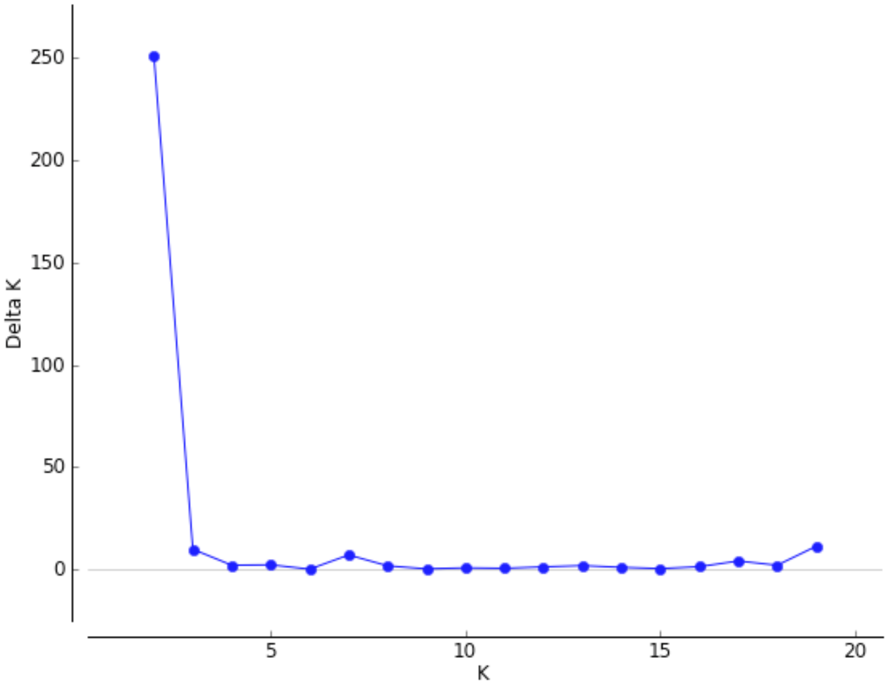

Figure 2.S3. Most optimal number of clusters for 30 *P. capsici* isolates calculated by Structure Harvester. Delta K values plotted against the number of probable clusters (K).

CHAPTER III.

Characterizing sources of resistance to Phytophthora blight of pepper caused by *Phytophthora capsici* in North Carolina

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ABSTRACT

Phytophthora blight (caused by *Phytophthora capsici*) is an important disease that impacts pepper production in the United States and worldwide. *P. capsici* causes crown, root, and fruit rot as well as foliar lesions in peppers. As abnormal weather patterns continue to put pressure on control strategies and influence disease incidence, it becomes essential to screen for resistance to *P. capsici* among pepper cultivars. Field trials were conducted over the summers of 2015 and 2016 to evaluate 32 commercial and experimental pepper cultivars against a mixed isolate inoculum in North Carolina (NC). Cultivars Martha-R, Meeting, and Paladin were classified as highly resistant and resistant to *P. capsici*. Tolerance to *P. capsici* in the field was observed in Fabuloso, Revolution, Vanguard among other cultivars. Greenhouse experiments were conducted to determine the response of 48 pepper cultivars when inoculated with two isolates from NC and an isolate from Michigan individually. Isolates exhibited different levels of virulence to the pepper cultivars screened for *P. capsici* resistance. Land races CM334, Fidel, and cultivars Martha-R, Meeting, and Intruder were highly resistant and resistant to all isolates tested. Overall, highly resistant cultivars tended to respond similarly

to field mix inoculations and greenhouse single isolate inoculations. Our results highlight the importance of screening for resistance with several local isolates and understanding regional *P. capsici* populations to achieve better deployment of durable pepper resistance.

INTRODUCTION

Pepper (*Capsicum annuum*) is an economically important vegetable cultivated worldwide. Many cuisines throughout the world incorporate peppers as key elements in dishes, they are found in salads and are commonly added as spice to food (Bosland and Votava 2012). In 2015, the United States (US) planted 64,200 acres of bell and hot pepper with a total production value of more than $941 million (USDA-NASS 2015). North Carolina (NC) contributed to national production by planting 2,300 acres of bell peppers and producing a total value of more than $21 million in 2015 (USDA-NASS 2015). Besides meeting market demands for quality and food safety, vegetable growers often deal with plant pathogens. Since 1948, the NC vegetable industry is threatened every year by the soilborne oomycete pathogen *Phytophthora capsici* (Crossan et al. 1954). *P. capsici* is a destructive hemibiotrophic pathogen capable of causing disease on a broad range of plant families including solanaceous, cucurbitaceous, and fabaceous crops among others (Quesada-Ocampo et al. 2009, Granke et al. 2012a, Kousik et al. 2015). In pepper, under favorable conditions *P. capsici* infects early in the growing season. The disease, known as Phytophthora blight, root, crown, or fruit rot, appears as small water soaked areas visible at the soil line. During rainfall, the disease progresses to affect the roots, crown, foliage, and fruit (Lamour et al. 2012). In fruit, expanding lesions produce fresh sporangia over 5 days and appears as a distinctive white "powdered sugar" layer on the surface of the fruit, visible to the naked eye (Lamour and Hausbeck 2003).

Managing *P. capsici* relies on an integrated approach that combines control strategies such as water management, crop rotation, fungicide applications, and host resistance (Granke et al. 2012a). Weather patterns impose pressure on management strategies for *P. capsici*.

Increasing rain events and flooding of fields seem to augment disease incidence in NC, South Carolina (SC), and New York (NY) (Quesada-Ocampo et al. 2011a, Bornt et al. 2012). Identifying sources of resistance in pepper becomes highly important when combating Phytophthora blight. Currently, land race peppers such as "Criollo de Morelos 334" are used to breed for disease resistance to *P. capsici* (Xu et al. 2016). However, the genetics behind the resistance is complex, involving multiple genes that confer resistance to different disease symptoms (Naegele et al. 2014, Quesada-Ocampo et al. 2016). Because *P. capsici* exhibits high genetic and phenotypic diversity in the US (Granke et al. 2011, Quesada-Ocampo et al. 2011b, Granka et al. 2012, Granke et al. 2012b), breeding for resistance becomes challenging and relies on the knowledge of local pathogen populations, as well as environmental factors (Granke et al. 2012a). Every year, many pepper cultivars are evaluated for resistance to *P. capsici* (Kimble and Grogan 1960, Foster and Hausbeck 2010a, Dunn et al. 2013, Wyatt et al. 2013). In fields trials conducted over 5 years, Dunn et al. (2014) reported bell pepper cultivars Archimedes, Aristotle, Intruder, and Paladin as the most resistant to a single isolate of *P. capsici* from NY. Greenhouse and field evaluations reported high levels of resistance in Aristotle, Intruder, Paladin, and Revolution (Foster and Hausbeck 2010a, Foster and Hausbeck 2010b, Wyatt et al. 2013). Variation in virulence among isolates of *P. capsici* has also been reported in peppers (Foster and Hausbeck 2010b), highlighting the importance of evaluating pepper cultivars across a panel of *P. capsici* isolates. Effective host resistance evaluations integrate the knowledge of local population structure of *P. capsici* in order to deploy durable resistance (Granke et al. 2012a).

In this context, we aimed to improve management of Phytophthora blight in pepper by characterizing resistance to *P. capsici* of bell and hot pepper cultivars. Specifically, we sought (i) to evaluate commercial and experimental lines of peppers for resistance to *P. capsici* under field and greenhouse conditions, and (ii) to compare the level of resistance among different pepper cultivars against two current *P. capsici* isolates from NC and an isolate from Michigan (MI).

MATERIALS AND METHODS

Isolate selection and inoculum preparation: A panel of 8 single-spore *P. capsici* isolates were selected from the long-term culture collection of Dr. Lina Quesada, NC State University (NCSU), Dr. Jean Ristaino, NCSU, and Dr. Mary Hausbeck, Michigan State University (MSU) for field and greenhouse inoculations. Table 3.1 details isolate information including their source, mating type, mefenoxam sensitivity, and host of origin. *P. capsici* isolates were transferred from long-term storage to unclarified V8 agar (UCV8, 16 g of agar, 3 g of CaCO3, 160 ml of V8 juice, and 840 ml of distilled water), and maintained under constant fluorescent light at room temperature (21 ± 2°C) for 7 days. Before inoculum preparation, the isolates were inoculated on pepper fruits and then re-isolated from the symptomatic tissue to ensure virulence (Quesada-Ocampo and Hausbeck 2010). For field and greenhouse inoculations, millet seed was used as a substrate to grow and deploy *P. capsici* in the soil or potting media. One liter flasks were filled with 100g of millet seed, 72 ml of distilled water, and 0.08 mg of L-asparagine. Flasks were then autoclaved twice for 30 min on consecutive days. Ten 7-mm agar plugs from actively growing cultures of *P. capsici* were added and incubated for 3 to 4 weeks under constant fluorescent light at room temperature with daily mixing (Quesada-Ocampo and Hausbeck 2010).

Field experiment: Twenty-two commercially available pepper cultivars and ten experimental lines were planted to evaluate their resistance to a mix of *P. capsici* isolates (R377, R388, R328, R297, NC21064, and NC21810) in the summers of 2015 and 2016 (Table 3.2). It is worth highlighting that a highly resistant land race pepper known as “Fidel” and a highly susceptible cultivar “Red Knight” were among the cultivars included in this study. Field experiments were located at the Sandhills Research Station, Jackson Springs, NC (35°11'44.2"N latitude and 79°40'59.2"W longitude). The field soil type is Fuquay sand. Pepper seedlings were grown in the greenhouse under natural light for 4 weeks in 72-cell flats filled with peat moss-vermiculite potting media (Conrad Fafard Inc.). Seedlings were left outside in a protected area to harden for 3 days. Pepper seedlings were transplanted in raised beds on 11 June and 26 May for the 2015 and 2016 trial respectively. Treatment plots consisted of 10 plants from each pepper cultivar, that were spaced 0.3 m apart in a row by a mechanical transplanter that also applied a starter fertilizer (17-17-17). Plots were 3 m long and spaced 0.6 m apart. In order to promote disease, plants were transplanted in bare ground soil and irrigated using overhead sprinklers. During the field season, weeds within plots were controlled by hand weeding, while weeds between rows were cultivated. Plots were arranged in a completely randomized block design with four replications. Inoculation was achieved two weeks after transplanting by inserting 1 g of *P. capsici* infested millet seed directly into the soil adjacent to each plant crown, avoiding root or crown injury.

Plants were assessed for wilting and crown rot about a week after inoculation and consecutively every 3 days. Disease severity estimation was based on a 0 to 5 scale, in which 0 = no disease symptom observed, 1 = 1-30% wilting in the older leaves, 2 = 31-50% minor wilting in the older and younger leaves or crown rot observed, 3 = 51-70% advanced wilting of the entire plant but green foliage color still observed, 4 = 71-90% advanced wilting and discoloration observed, 5 = >90% necrotic leaves, defoliation, or plant dead (Fig. 3.1S). The area under the disease progress curve (AUDPC) was calculated for each plant per plot and averaged to each cultivar in each year according to Shaner and Finney (1977). Weather data was downloaded from the NC Climate Retrieval and Observations Network of the Southeast Database (CRONOS) during the two-year growing season. The weather station was located in the Sandhills Research Station at 1-km of distance from the field. Maximum air temperature (°C), daily air temperature (°C), and daily soil temperature (°C) were averaged for each growing season in 2015 and 2016. Total soil moisture (m^3/m^3) and total rainfall (cm) was summed over the growing season. Upon completion of each field trial, 10 % of symptomatic plants were randomly selected for pathogen re-isolation according to the methods of Quesada-Ocampo and Hausbeck (2010).

Greenhouse experiment: Thirty commercial pepper cultivars and 18 experimental lines were screened for resistance to three *P. capsici* isolates (NC21810, 12889, and NCCP3) in controlled conditions (Table 3.4). Among the cultivars tested, we included two land race peppers, CM334 and Fidel, known for their high level of resistance to *P. capsici*. Four-week-old seedlings were grown in 72 cell flats filled with peat moss-vermiculite potting media (Conrad Fafard Inc.) in a greenhouse under natural light. Seedlings were transplanted into 6-in pots filled with same potting media as described above. Plants were carefully watered daily avoiding splash, and fertilized with Osmocote (14N–6.2P–11.6K) at transplanting. The experiment was designed as a split-plot arranged in a complete randomized block design with main plots referring to each of the cultivars and subplots as each of the isolates and control treatments. Each pepper cultivar comprised five seedlings for every isolate or control treatment. The experiment was repeated twice in 2015 and 2016.

One week after transplanting, seedlings were inoculated with each isolate by inserting 1 g of infested millet seed directly into the potting media and close to the root mass. Uninfested milled seed containing sterile V8 agar plugs was added to control plants. Plants were scored for Phytophthora blight symptoms every other day according to a 0 to 5 scale, in which 0 = no disease symptom, 1 = 1-30% wilting in the bottom leaves, 2 = 31-50% wilting of the top and bottom leaves, 3 = 51-70% advanced wilting and discoloration, 4 = 71-90% advance leaves discoloration and necrosis of bottom leaves, 5 = >90% necrosis of top and bottom leaves, or plant dead. (Fig. 3.2S). AUDPC values were calculated for each plant according to Shaner and Finney (1977). Approximately, 10% of the symptomatic plants were randomly selected for re-isolation of the pathogen according to Quesada-Ocampo and Hausbeck (2010).

Statistical analysis: Mean AUDPC values from field and greenhouse experiments were subject to analysis of variance (ANOVA) using the PROC GLIMMIX procedure of SAS v. 9.4 (SAS Institute Inc., Cary, NC). We selected the generalized linear mixed model and assumed gamma distribution because our data violated the normality assumption and AUDPC values are a continuous-skewed response variable type (Stroup 2015). We used the post hoc Tukey-Kramer's honestly significant difference test to examine significant differences (alpha = 0.05) among the means. Pepper cultivars screened in both field and greenhouse experiments were classified into different categories of resistance based on the AUDPC means of each cultivar using the rank-sum method as described by Afolabi et al. (2008). Positive deviations from the grand mean were rated susceptible while negative deviations from the grand mean were rated resistant. Cultivars with deviations between 0 to 2, 2 to 3, and larger than 3 were classified as moderately susceptible, susceptible, and highly susceptible respectively, while cultivars with deviations smaller than 0 to -2, -2 to -3, and smaller than -3 were considered tolerant, resistant, and highly resistant, respectively. In order to determine correlation between the deviations from the grand mean of the ranks and the AUDPC means, we used the Spearman rank correlation test as described by (Ariyo et al. 2010).

RESULTS

Field experiment: One week after inoculations with *P. capsici* infested millet, susceptible pepper plants displayed wilting and crown rot symptoms that progressively developed into advanced wilting or death (Fig. 3.1). Significant differences were detected for AUDPC means calculated among cultivars for both years (ANOVA, $P < 0.0001$). We observed significant differences between years (ANOVA, $P = 0.001$) with the 2015 field experiment yielding higher AUDPC means than 2016. The two-year field trials revealed commercial and experimental pepper cultivars resistant to current NC isolates of *P. capsici* (Table 3.2). Cultivars Martha-R and Meeting, as well as the land race Fidel consistently exhibited the lowest AUDPC means during the two field seasons. The rank-sum analysis categorized Fidel, Martha-R, and Meeting as highly resistant to the NC isolates of *P. capsici* inoculated in the field during both seasons. Paladin and EXP. 9 exhibited higher AUDPC means when compared to Fidel during 2015 and 2016, they were consequently classified as resistant by the rank-sum analysis. In 2015, EXP.9 presented lower AUDPC means than in 2016, whereas Paladin presented higher AUDPC means in 2015 compared to 2016. During 2015 and 2016 field seasons, Bastille presented the highest AUDPC mean among all cultivars, therefore it was categorized as a highly susceptible cultivar by the rank-sum analysis. AUDPC means for Keystone, Camelot, Red Knight, Plato, EXP.10, Karisma, EXP. 2, Quattro, SV3782PP, EXP. 5, EXP. 6, and PS09941819 were not significantly different from Bastille (highly susceptible) for both years.

The rank-sum analysis, considering 2015 and 2016 AUDPC mean ranks, separated these cultivars into two categories, susceptible and moderately susceptible (Table 3.2). The

AUDPC means for most of the susceptible cultivars was higher for the 2015 than the 2016 growing season. Cultivars Fabuloso, Revolution, EXP.3, EXP.8, Vanguard, Archimedes, EXP.4, Aristotle, Ebano-R, Declaration, and EXP.1 displayed intermediate values of AUDPC means and were classified as tolerant by the rank-sum analysis. Among the cultivars classified as tolerant, Revolution, EXP.3, Vanguard, Declaration, and EXP.1 consistently presented intermediate AUDPC means during 2015 and 2016. AUDPC means for cultivars Fabuloso, Archimedes, EXP.4, Aristotle, and EXP.8 exhibited higher AUDPC means in 2015 than in 2016, and were also classified as tolerant by the rank-sum analysis. In contrast, Ebano-R exhibited lower AUDPC means in 2015 than in 2016. Both the 2015 and 2016 field trials were subjected to variation in temperature, soil moisture, and rainfall (Table 3.3). The 2015 growing season was warm and wet based on mean air temperatures, mean daily soil temperature, total soil moisture, and total rainfall. On the contrary, the 2016 growing season was relatively cooler and dryer.

Greenhouse experiment: Disease symptoms observed for inoculated pepper plants included wilting, crown rot, leaf necrosis, and plant death (Fig. 3.2). Initial symptoms of wilting and crown rot were evident 5 days after inoculation with isolate NC21810 in susceptible plants. Symptoms progressed and dead plants were first observed at 12 days after inoculation. We observed significant differences ($P < 0.0001$) among AUDPC means calculated for pepper cultivars, isolates and their interaction. The significant interaction indicates that the cultivar response depends significantly on the isolate inoculated, and the isolate virulence is constrained by the cultivar it is exposed to. AUDPC means calculated for pepper cultivars inoculated with isolate 12889 were not significantly different between the experiments conducted in 2015 and 2016 ($P = 0.2277$). Cultivars inoculated with isolates NC21810 and NCCP3 exhibited higher AUDPC means in 2015 than in 2016 ($P < 0.0001$). Among the cultivars inoculated with isolate NC21810, Paladin, Revolution, Aristotle, and Plato exhibited higher AUDPC means during the 2015 experiment than in 2016. On the contrary Ebano-R presented a lower AUDPC mean in 2015 than in 2016 (Table 3.4). In both experiments, isolate NC21810 caused significantly more disease (highest AUDPC means) than isolate 12889, and both caused significantly more disease than isolate NCCP3 (*data not shown*). Non-inoculated control plants remained asymptomatic during both experiments.

Cultivars Martha-R, Meeting, Intruder, and land race peppers CM334 and Fidel exhibited the lowest AUDPC means when challenged with the three *P. capsici* isolates during both experiments. EXP.8, Paladin, EXP.4, Archimedes, EXP.11, and Ebano-R exhibited significantly higher AUDPC means than CM334 when inoculated with NC21810 and 12889. Touchdown, Bastille, Pepper #1, Keystone, and Plato showed high AUDPC means during both experiments when challenged with NC isolates (NC21810 and NCCP3). When challenged with 12889, Bastille showed the highest AUDPC mean among all cultivars in 2015 and the second highest in 2016. Based on the rank-sum analysis, which ranks the AUDPC mean from each cultivar during both experiments, we determined the disease response of all 48 cultivars when challenged with 2 NC isolates and one isolate from Michigan (Table 3.4). In all cultivars evaluated, 10 cultivars were found to be highly resistant or resistant to isolate NC21810, 9 cultivars were highly resistant or resistant to isolate 12889, and 15 cultivars were resistant to isolate NCCP3. Pepper cultivars CM334, Fidel, Martha-R, Meeting, and Intruder were highly resistant to the isolate NC21810. Intruder was classified as resistant to 12889 and NCCP3. None of the cultivars were categorized as highly resistant to NCCP3. About half of the cultivars tested against the 3 *P. capsici* isolates were classified as moderately susceptible, susceptible, or highly susceptible. The rank-sum analysis classified about 31%, 29%, and 25% of the cultivars as tolerant when inoculated with NC21810, 12889, and NCCP3 respectively. Cultivars Paladin, EXP.4, and Archimedes were resistant to the two NC isolates but tolerant to 12889. Interestingly, Cultivars SV3198HJ and EXP.12 were categorized as tolerant to NC21810 and 12889, but susceptible and moderately susceptible to NCCP3. Cultivars Revolution^{hm}, EXP.14, and EXP.18 were tolerant to isolates 12889 and NCCP3 but moderately susceptible to NC21810. AUDPC means significantly correlated with the deviations from the grand mean of the ranks as revealed by Spearman rank correlation with R = 0.93 for NC21810 in 2015 and R = 0.94 for NC21810 in 2016, R= 0.96 for 12889 both years, and R= 0.89 for NCCP3 in 2015 and R=0.74 for NCCP3 in 2016 ($P = 0$).

DISCUSSION

Deployment of resistant cultivars is one of the most sustainable and effective management strategies to control Phytophthora blight of peppers (Granke et al. 2012a). In the present study, we evaluated a set of commercially available cultivars and experimental lines to identify resistance to *P. capsici* under field and greenhouse conditions. In the field, some pepper cultivars exhibited variation of disease response during two growing seasons in 2015 and 2016. Dunn et al. (2014) reported similar variation when evaluating pepper cultivars for resistance to *P. capsici* over a 5-year field trial in NY. Our field evaluations identified a set of commercially available cultivars that consistently out-performed when challenged with a mix of current *P. capsici* isolates from NC and, thus, are more likely to perform consistently across the state.

Martha-R and Meeting are sweet pepper hybrids commercially advertised as intermediately resistant and resistant to *P. capsici* (Sakata-seed 2017), however, our results suggest that Martha-R and Meeting perform consistently as highly resistant cultivars under high disease pressure. Paladin, Archimedes, and Aristotle were regarded as resistant cultivars to an isolate from NY in the field (Dunn et al. 2014). Our field results confirmed resistance of Paladin to NC isolates of *P. capsici*, and differed with respect to Archimedes and Aristotle which exhibited higher AUDPC means and were classified by the rank-sum analysis as tolerant. Dunn et al. (2013) reported high susceptibility for cultivars Revolution, Declaration, and Vanguard, however in our field experiments, these cultivars exhibited intermediate values of AUDPC means and were classified as tolerant to a mix of current isolates from NC. We observed a high number of cultivars that performed as moderately susceptible, susceptible, and highly susceptible based on the rank-sum analysis. Dunn et al. (2013) classified Karisma, Keystone, and Red Knight as highly susceptible cultivars to an isolate from NY under field conditions. Our field evaluations categorized Keystone and Red Knight as susceptible, and Karisma as a moderate susceptible to the mix of NC isolates used in this study. Our field evaluations suggest that breeding for resistance to *P. capsici* remains a high priority and warrants further evaluation. The 2015 field season presented higher AUDPC means than the 2016 field season; we attributed the variation observed between years to environmental conditions. Dunn et al. (2014) experienced similar variation among field seasons and suggested that higher AUDPC means could be a result of the ability of *P. capsici* to grow, sporulate, and disperse under warm and wet conditions. The 2016 field season had cooler temperatures and low rainfall impeding disease development and resulting in lower disease pressure.

In addition to field evaluations, disease screening methods rely on greenhouse testing to identify resistance to plant pathogens among pepper cultivars. Our greenhouse study revealed different levels of virulence among two representative isolates from NC farms and one isolate from MI. Similarly, Quesada-Ocampo and Hausbeck (2010) reported variation in virulence among *P. capsici* isolates from Michigan used during tomato resistance screenings. When comparing the response of pepper cultivars to inoculations with isolate 12889 in our study and Foster and Hausbeck (2010b); CM334, Karisma, Aristotle, Camelot, Plato, Revelation, and Red Knight exhibited the same disease response agreeing with our results. However, Paladin, Revolution, and Declaration classified as tolerant to 12889 in our study differed when compared with Foster and Hausbeck (2010b) who classified them as susceptible to the same isolate. According to the rank-sum analysis, Paladin and Archimedes exhibited resistance to NC21810 and NCCP3 but were tolerant to 12889 from MI. Dunn et al. (2014) also reported resistance of Paladin and Archimedes using a single isolate from NY under field conditions. Intriguingly, NCCP3 isolated from squash displayed the lowest virulence among the isolates tested, however, cultivars SV3198HJ and EXP.12 were susceptible and moderately susceptible to NCCP3. Our results highlight the importance of uncovering the effector repertoire underlying variation on virulence phenotypes as well as understanding the diversity of current local *P. capsici* populations.

Despite attempts to classify *P. capsici* isolates into races based on virulence to differential pepper genotypes (Oelke et al. 2003, Glosier et al. 2008), there is no formal race classification used by the *P. capsici* research community (Dunn et al. 2014). In fact, the genetic basis of virulence of *P. capsici* remains under investigation as specific effectors associated to isolates with a particular virulence phenotype have not been defined (Schornack et al. 2010, Dunn and Smart 2015). As a soilborne oomycete, *P. capsici* structures by geography due to its inability to disperse by air (Quesada-Ocampo et al. 2011b), and reproduces sexually generating new isolates with a broad range of virulence (Granke et al. 2012b). Our results indicate substantial differences in virulence between *P. capsici* isolates from NC (NC21810 and NCCP3) and MI (12889), and between NC isolates NC21810 and NCCP3.

In the past, several studies have suggested that *P. capsici* isolates display higher virulence on their host of origin than on an alternative host. Ristaino (1990) concluded that cucurbit isolates of *P. capsici* were less virulent on pepper than on cucurbits. Similarly, Lee et al. (2001) suggested that an underlying effector present in pumpkin isolates but absent on pepper isolates favors aggressiveness to pumpkin cultivars. In our experiment, isolate

NC21810 obtained from zucchini produced significantly higher AUDPC means than isolate 12889 (MI) obtained from peppers. Our results contradict Lee et al. (2001) and Ristaino (1990), suggesting that virulence is an isolate trait, and underlying effectors resulting in such virulence may not necessarily be predicted by host of origin. Our findings highlight the importance of including isolates representative of the diversity of *P. capsici* in a geographic region when screening pepper cultivars for resistance to *P. capsici.*

Our study identified a group of commercially available pepper cultivars with high levels of resistance to Phytophthora blight in NC. Cultivars Martha-R, Meeting, Intruder, Paladin, and Archimedes were classified as highly resistant and resistant when challenged with the three *P. capsici* isolates tested in the greenhouse. Foster and Hausbeck (2010b) reported complete susceptibility for commercial cultivars of peppers with only the land race CM334 and breeding lines exhibiting high resistance or resistance to 12889. Our results also report a list of highly susceptible cultivars to *P. capsici*. Touchdown, Bastille, Pepper #1, Keystone, Plato, and Red Knight were consistently susceptible or highly susceptible to all isolates tested under greenhouse conditions. Our findings imply that the disease response of susceptible cultivars remains the same regardless of the variation in virulence among the three *P. capsici* isolates. Despite observing higher AUDPC means in the field than in the greenhouse, highly resistant cultivars tend to respond similarly to high and low single virulent *P. capsici* isolates and mix isolate inoculations. Cultivars classified as highly resistant in the field such as Fidel, Martha-R, and Meeting were also highly resistant in the greenhouse supporting our findings. Interestingly, our data indicates that cultivars Archimedes, Ebano-R and experimental lines EXP.9 and EXP.4 classified as resistant in the greenhouse, to all or two of the isolates, performed as tolerant cultivars under field conditions and mix inoculation pressures. This reiterates the importance of screening under local environmental conditions with a diverse isolate mix that resembles a sexually reproducing population with several isolate genotypes.

Classification of pepper cultivars into different categories of resistance to *P. capsici* rely on several methods and input variables. Foster and Hausbeck (2010b) used a method that utilizes a disease rating scale to classify cultivars between resistant and susceptible. Sy et al. (2008) employed the chi-square method to compare against a resistant control cultivar (CM334) to define disease response among pepper cultivars. In this study, we used the rank-sum method which eliminates the need for previous knowledge of the genetic structure of the pepper cultivars, and utilizes continuous variables such as AUDPC means (Onyeka et al. 2005). We observed strong Spearman rank correlation between deviations from the grand mean of the ranks and the AUDPC means, indicating that the disease response categories obtained by the rank-sum method are consistent with the disease severity data.

In summary, our field evaluations expand the set of commercially available cultivars that can improve disease management of Phytophthora blight of peppers in NC. A group of cultivars consistently performed as highly resistant or resistant when challenged with a mix of current *P. capsici* isolates from NC. The pepper cultivars identified here as highly resistant, resistant, and tolerant are likely to exhibit similar disease response across the state. We observed high variation in the levels of virulence among *P. capsici* isolates. This virulence differential highlights the importance of including diverse *P. capsici* isolates when screening for resistance. Overall, cultivars identified here as highly resistant tend to respond similarly to field mix inoculations and greenhouse single isolate inoculations with a virulent isolate. Host resistance remains a promising management strategy to control *P. capsici* in pepper. Every year abnormal weather patterns put pressure on host resistance and other control strategies by favoring *P. capsici* growth and dispersal. This upholds the need for developing resistant pepper cultivars. Our study emphasizes the importance of accounting for pathogen population structure and screening for resistance using diverse isolates from the region.

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Table 3.1. Eight *Phytophthora capsici* isolates used for field and greenhouse evaluations of resistance in pepper.

Isolate	Source	State	Host	Mefenoxam sensitivity	Mating type
R377[f]	Ristaino J.	NC	Pepper	S	A1
R388[f]	Ristaino J.	NC	Pepper	S	A1
R328[f]	Ristaino J.	NC	Pepper	S	A2
R297[f]	Ristaino J.	NC	Pepper	S	A2
NC21064[f]	Quesada L.	NC	Pepper	IS	A1
NC21810[fg]	Quesada L.	NC	Zucchini	S	A2
NCCP3[g]	Quesada L.	NC	Squash	S	A2
12889[g]	Hausbeck M.	MI	Pepper	I	A1

[f] field experiment

[g] greenhouse experiment

Table 3.2. Commercial and experimental pepper cultivars screened for resistance to *P. capsici* during 2015 and 2016 field experiments. Disease response identified by rank-sum classification method.

Cultivar	**AUDPC[§] 2015**	**AUDPC 2016**	**Cultivar ranking**				**Disease response[†]**
			***a* (2015)**	***b* (2016)**	***c***	***d***	
Fidel	10.99 f	7.51 de	1	2	3	-3.40	HR
Martha-R	14.63 ef	3.46 e	2	1	3	-3.40	HR
Meeting	20.31 def	9.73 cde	3	3	6	-3.06	HR
Paladin	42.77 a-e	10.14 b-e	7	4	11	-2.50	R
EXP.9[Ø]	29.52 c-f	42.88 a	4	10	14	-2.16	R
Fabuloso	56.17 a-d	28.88 abc	10	6	16	-1.93	T
Revolution	41.10 a-e	56.39 a	6	12	18	-1.70	T
EXP.3	45.68 a-e	39.26 a	9	9	18	-1.70	T
EXP.8	59.60 a-d	33.25 abc	11	7	18	-1.70	T
Vanguard	43.41 a-e	58.39 a	8	14	22	-1.25	T
Archimedes	73.59 abc	26.21 a-e	17	5	22	-1.25	T
EXP.4	67.36 abc	45.21 a	15	11	26	-0.79	T
Aristotle	81.63 abc	36.35 ab	18	8	26	-0.79	T
Ebano-R	34.99 b-f	63.34 a	5	22	27	-0.68	T
Declaration	59.98 a-d	62.00 a	12	19	31	-0.23	T
EXP.1	62.96 a-d	61.93 a	14	18	32	-0.11	T
PS_09941819	83.12 abc	59.39 a	19	16	35	0.23	MS
EXP.6	85.48 abc	58.70 a	20	15	35	0.23	MS
SV3198HJ	71.25 abc	62.89 a	16	20	36	0.34	MS
EXP.7	62.20 a-d	71.44 a	13	25	38	0.57	MS
EXP.5	88.36 abc	59.98 a	21	17	38	0.57	MS
Karisma	98.14 ab	57.83 a	26	13	39	0.68	MS
Revelation	89.47 abc	66.79 a	22	23	45	1.36	MS
EXP.2	98.09 ab	71.24 a	25	24	49	1.81	MS
SV3782PP	94.76 abc	74.65 a	23	27	50	1.93	MS
Quattro	97.04 ab	71.84 a	24	26	50	1.93	MS
Camelot	112.85 a	63.33 a	30	21	51	2.04	S

Table 3.2 Continued

Plato	109.46 ab	77.96 a	28	29	57	2.72	S
EXP.10	100.79 ab	82.64 a	27	31	58	2.84	S
Red Knight	111.71 ab	78.64 a	29	30	59	2.95	S
Keystone	121.66 a	76.29 a	31	28	59	2.95	S
Bastille	123.79 a	83.49 a	32	32	64	3.52	HS
					33[††]		

[§] AUDPC means within a column for each cultivar followed by the same letter are not significantly different ($P = 0.05$).

[††] Grand mean of the rank-sums (G); *a:* cultivar ranking based on AUDPC means from 2015; *b:* cultivar ranking based on AUDPC means from 2016; c = Rank-sum ($a + b$) for each cultivar; *d:* deviation from the grand mean (G) of the rank-sums [($d = (c - G)$/standard deviation) x 2].

[†] HR: highly resistance; R: resistant; T: tolerant; MS: moderately susceptible; S: susceptible; and HS: highly susceptible.

[Ø] EXP.# refers to experimental lines tested in this study.

Table 3.3. Temperature, soil moisture, and rainfall for the 2015 and 2016 growing season.

Weather parameter	**2015**	**2016**
Mean max air temperature (°C)	32.94	31.24
Mean daily air temperature (°C)	27.16	25.53
Mean daily soil temperature (°C)	29.84	28.29
Total soil moisture (m^3/m^3)	17.94	14.65
Total rainfall (mm)	221.80	193.30

Table 3.4. Commercial and experimental pepper cultivars screened for resistance to 3 *P. capsici* isolates obtained from NC (NC21810 and NCCP3) and MI (12889).

Cultivar	AUDPC[§] 2015			AUDPC 2016			Disease response[†]		
	NC21810	12889	NCCP3	NC21810	12889	NCCP3	NC21810	12889	NCCP3
CM334 [CI]	0.10 d	0.10 g	0.10 d	0.10 h	0.10 j	0.10 e	HR	HR	R
Fidel [D.R]	0.10 d	0.10 g	0.10 d	0.10 h	0.10 j	0.10 e	HR	HR	R
Martha-R [Sk]	0.10 d	0.10 g	0.10 d	0.10 h	0.10 j	0.10 e	HR	HR	R
Meeting [Sk]	0.10 d	0.10 g	0.10 d	0.10 h	0.10 j	0.10 e	HR	HR	R
Intruder [C]	0.10 d	1.62 c-f	0.10 d	0.10 h	1.59 hi	0.10 e	HR	R	R
EXP.8	18.22 bc	0.39 fg	0.10 d	9.58 f	1.08 hi	0.10 e	R	R	R
Paladin [sy]	33.38 abc	17.56 abc	0.10 d	0.81 g	3.53 gh	0.10 e	R	T	R
EXP.4	27.11 abc	1.01 d-g	0.10 d	18.51 b-f	10.04 c-g	0.10 e	R	T	R
Archimedes [sm]	35.75 abc	11.25 a-d	0.10 d	17.22 c-f	26.54 a-d	0.10 e	R	T	R
EXP.11	40.21 abc	10.99 a-d	0.10 d	16.45 def	0.65 i	0.10 e	R	R	R
Ebano-R [hm]	16.06 c	0.10 g	0.10 d	31.21 a-f	17.65 a-g	0.10 e	T	R	R
SV3198HJ [sm]	48.10 abc	40.31 ab	7.43 abc	27.87 a-f	18.09 a-f	5.91 ab	T	T	S
EXP.12	54.42 abc	13.71 abc	0.10 d	37.10 a-e	16.06 a-g	0.27 de	T	T	MS
Vanguard [hm]	60.55 abc	0.10 g	3.33 abc	34.56 a-f	3.69 fgh	0.10 e	T	R	T
EXP.1	61.91 abc	24.45 ab	5.23 abc	34.23 a-f	17.66 a-g	0.10 e	T	T	T
EXP.5	68.24 abc	43.53 ab	0.10 d	24.92 a-f	21.96 a-d	0.10 e	T	MS	R
Compadre [C]	56.99 abc	37.54 ab	0.10 d	38.07 a-e	17.46 a-g	0.10 e	T	T	R
Revolution [C]	71.74 abc	37.10 ab	2.74 abc	19.78 a-f	5.52 d-g	0.10 e	T	T	T
EXP.13	62.41 abc	45.63 ab	27.13 ab	37.98 a-e	40.12 abc	0.61 cde	T	MS	S
EXP.3	28.35 abc	0.63 efg	0.10 d	47.30 a-e	17.96 a-f	0.10 e	T	T	R

Table 3.4 Continued

EXP.6	53.19 abc	51.54 ab	1.30 bcd	42.17 a-e	19.30 a-e	0.10 e	T	MS	T
Fabuloso ^{sk}	72.65 abc	36.63 ab	28.15 ab	31.00 a-f	14.31 a-g	0.10 e	T	T	MS
Aristotle ^{sm}	82.97 abc	64.05 ab	15.92 ab	12.72 ef	16.05 a-g	0.10 e	T	MS	T
Declaration ^{C}	63.49 abc	11.21 a-d	0.10 d	40.24 a-e	13.27 b-g	0.10 e	T	T	R
EXP.15	67.09 abc	49.78 ab	13.34 ab	40.53 a-e	36.66 abc	0.10 e	T	MS	T
EXP.14	66.26 abc	6.73 b-e	0.40 cd	43.38 a-e	18.52 a-f	0.10 e	MS	T	T
Revolution ^{hm}	68.32 abc	17.56 abc	0.43 cd	43.87 a-e	27.03 a-d	0.10 e	MS	T	T
EXP.2	81.31 abc	47.44 ab	53.27 a	36.22 a-f	23.59 a-d	0.10 e	MS	MS	MS
Karisma ^{hm}	77.18 abc	38.88 ab	3.55 abc	40.77 a-e	35.03 abc	1.94 a-d	MS	MS	S
EXP.7	79.00 abc	54.33 ab	3.40 abc	39.84 a-e	17.81 a-g	0.10 e	MS	MS	T
EXP.16	68.73 abc	61.21 ab	43.26 a	51.80 a-d	53.49 ab	0.10 e	MS	S	MS
PS09941819^{sm}	76.99 abc	56.05 ab	8.76 abc	52.94 a-d	41.03 abc	6.33 ab	MS	MS	S
EXP.18	80.83 abc	24.34 ab	9.74 abc	47.16 a-e	4.22 e-h	0.10 e	MS	T	T
Plato ^{sm}	100.15 a	87.93 a	54.33 a	39.48 a-e	51.86 ab	1.28 bcd	MS	S	HS
Lafayette ^{C}	86.33 abc	52.72 ab	11.86 ab	49.23 a-d	53.49 ab	0.10 e	MS	MS	T
EXP.17	77.61 abc	66.25 ab	13.25 ab	66.68 ab	62.07 ab	0.10 e	MS	S	T
SV3782PP ^{sm}	87.22 abc	81.75 a	46.29 a	50.49 a-d	38.94 abc	0.10 e	MS	S	MS
Gridiron ^{C}	78.33 abc	75.10 ab	54.10 a	66.91 ab	65.34 ab	0.10 e	S	S	MS
Red Knight ^{sm}	83.27 abc	64.92 ab	18.91 ab	57.26 a-d	38.25 abc	0.61 cde	S	MS	S
Keystone ^{wq}	78.78 abc	71.62 ab	44.42 a	68.89 ab	67.68 a	1.91 a-d	S	S	HS
Pepper#1 ^{C}	85.92 abc	66.45 ab	57.40 a	58.03 a-d	51.46 ab	2.42 abc	S	S	HS
Camelot ^{C}	92.49 ab	58.42 ab	37.09 a	56.06 a-d	37.86 abc	0.10 e	S	MS	MS

Table 3.4 Continued

California W [wq]	93.45 ab	83.17 a	36.01 a	54.46 a-d	53.20 ab	0.10 e	S	S	MS
Revelation [sm]	87.35 abc	76.80 ab	28.51 ab	63.13 abc	43.49 abc	0.10 e	S	S	MS
Quattro [hm]	90.49 ab	68.99 ab	37.87 a	59.18 a-d	47.30 abc	0.10 e	S	MS	MS
EXP.10	90.84 ab	79.56 a	35.14 a	58.70 a-d	50.86 abc	1.14 bcd	S	S	S
Bastile [C]	92.74 ab	91.51 a	59.24 a	71.71 a	62.36 ab	17.25 a	HS	HS	HS
Touchdown [C]	94.73 ab	87.58 a	38.44 a	70.09 a	60.72 ab	2.05 a-d	HS	S	HS

[§] AUDPC means within a column for each cultivar followed by the same letter are not significantly different (*P* = 0.05).

[†] Disease response to each *P. capsici* isolate was determined according to the rank-sum method. Cultivar rankings were assigned from the AUDPC means for each cultivar inoculated with each isolate during 2015 and 2016 greenhouse trials. HR: highly resistance; R: resistant; T: tolerant; MS: moderately susceptible; S: susceptible; and HS: highly susceptible.

[sm] Seminis

[hm] Harris Moran

[sk] Sakata

[sy] Syngenta

[wq] Wyatt-Quarles

[C] Clifton seeds

[CI] Chile Pepper Institute

[D.R.] Dr. David Ritchie

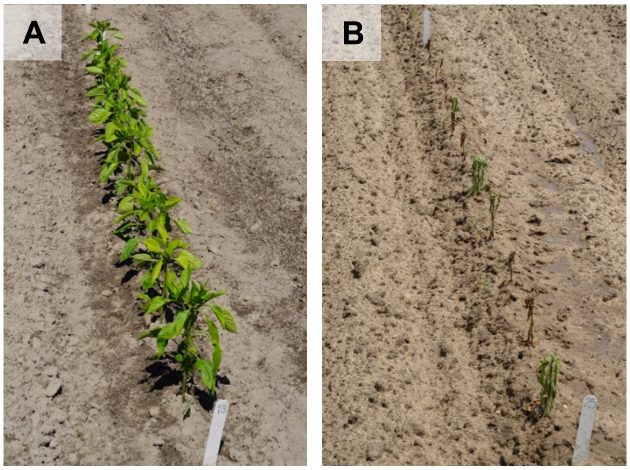

Figure 3.1. A. Cultivar Martha-R and **B.** Red Knight at 3 weeks post inoculation in 2015 field trial.

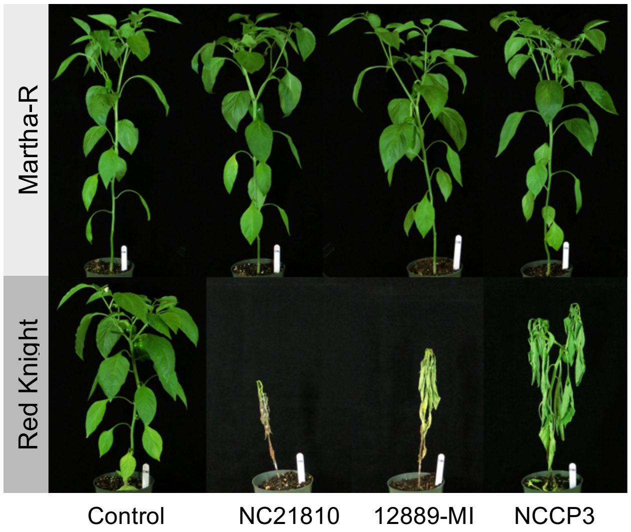

Figure 3.2. Response of cultivar Martha-R and Red Knight to the inoculation of 3 *P. capsici* isolates (NC21810, 12889, and NCCP3) and uninfested millet seed control under greenhouse conditions.

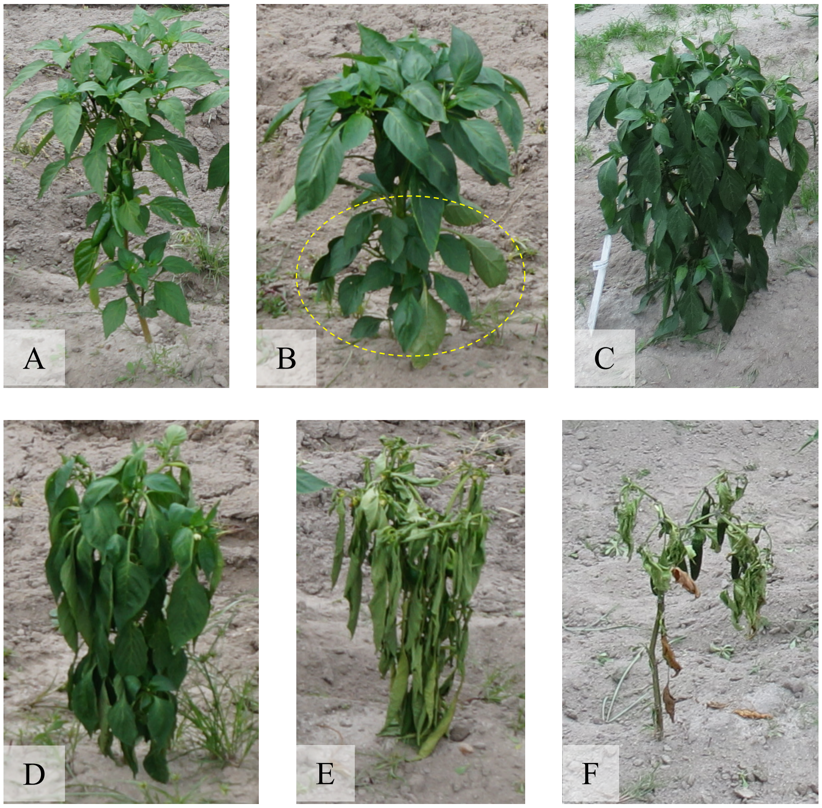

Figure 3.S1. Disease severity rating scale used to evaluate pepper resistance to Phytophthora blight caused by *Phytophthora capsici*. A. 0 = no disease symptom observed; B. 1 = 1-30% wilting in the older leaves; C. 2 = 31-50% minor wilting in the older and younger leaves or crown rot observed; D. 3 = 51-70% advanced wilting at the entire plant but foliage color green still observed; E. 4 = 71-90% advanced wilting and discoloration observed; F. 5 = >90% necrotic leaves, defoliation, or plant dead.

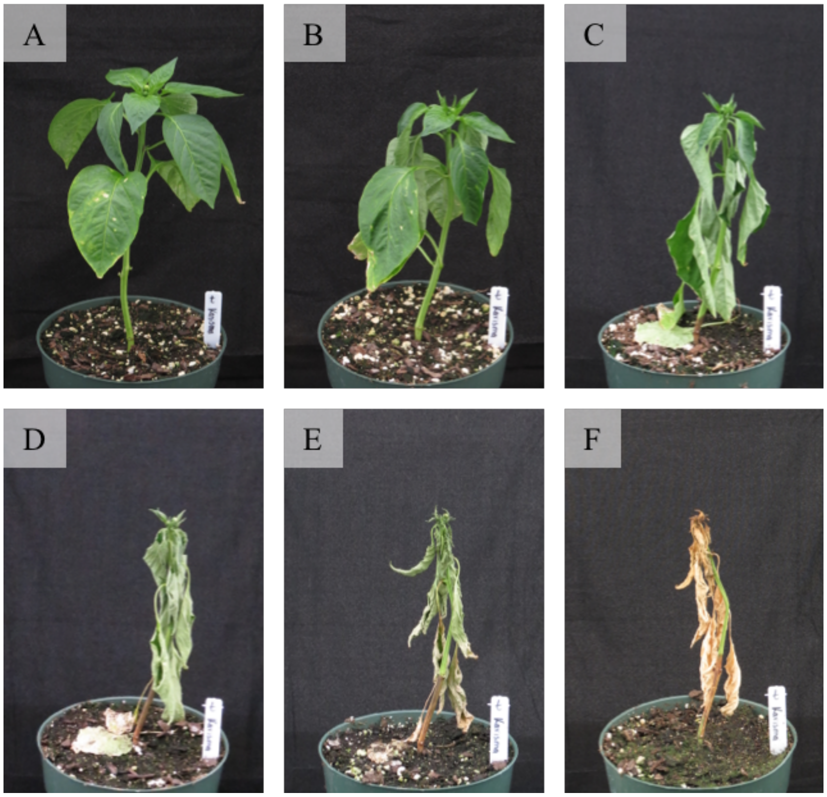

Figure 3.S2. Disease severity rating scale used to evaluate pepper resistance to Phytophthora blight caused by *Phytophthora capsici* in greenhouse conditions. A. 0 = no disease symptom; B. 1 = 1-30% wilting in the bottom leaves; C. 2 = 31-50% wilting of the top and bottom leaves; D. 3 = 51-70% advanced wilting and discoloration; E. 4 = 71-90% advance leaves discoloration and necrosis of bottom leaves; F. 5 = >90% necrosis of top and bottom leaves or plant dead.

APPENDIX

Appendix: CHAPTER II Primer pairs designed for the amplification of microsatellites in *P. capsici*.

Gene id	SSR id	SSR motif	Forward primer	Reverse primer	Expected product size	Gene annotation
>jgi|Phyca11|22063|fgenesh1_pg.PHYCAscaffold_569_#_1	Phyca_SSR01	(CG)6	TGCTCATCGAGTCGCAGTAG	TGGTCATCGTGGTCTTGGTG	225	_Calcium-binding EF-hand
>jgi|Phyca11|502925|fgenesh2_kg.PHYCAscaffold_2_#_41_#_Contig2	Phyca_SSR02	(CA)6	CCGATCTCTGCCGTCATCTC	CTGGTCCATGTTGCGGTAGT	148	_No FA Found
>jgi|Phyca11|504309|fgenesh2_kg.PHYCAscaffold_7_#_61_#_Contig5	Phyca_SSR03	(CA)6	AAGCCCAACAGACACCACAA	TCGTCGTGTAGGTTGTGTGG	276	_No FA Found
>jgi|Phyca11|504465|fgenesh2_kg.PHYCAscaffold_8_#_34_#_4097844	Phyca_SSR04	(TG)6	GGAGGGTTGGAACGCGATAA	AAGCGGTTCTTGTGTCACCA	273	_No FA Found
>jgi|Phyca11|510484|fgenesh2_kg.PHYCAscaffold_61_#_17_#_Contig	Phyca_SSR05	(TG)6	GTAACTATGCCGCTCTCCCC	TTGGTGCTCTCCCTTTCGAC	111	_No FA Found
>jgi|Phyca11|511652|fgenesh2_kg.PHYCAscaffold_94_#_3_#_4100822	Phyca_SSR06	(GA)6	ACATGGAGAAGGGCAAGGTG	TGTGGGTTTTCATTTGTCACT	240	_No FA Found
>jgi|Phyca11|527040|estExt2_fgenesh1_pm.C_PHYCAscaffold_150087	Phyca_SSR07	(GA)6	CTCTGGCATTGAAAGAGCGC	CCCAAAGTTGCGCCATTTGA	216	_No FA Found
>jgi|Phyca11|534614|estExt2_fgenesh1_pg.C_PHYCAscaffold_260039	Phyca_SSR08	(AG)6	CCACCACCAGGATGATGACC	CTCAGCACTTCGGCAGCT	292	_No FA Found
>jgi|Phyca11|564509|estExt2_Genewise1.C_PHYCAscaffold_150132	Phyca_SSR09	(GT)6	CCCAATGGAACGGGACAAGA	ACGTTCCCCATTGTCGTGTT	248	_No FA Found
>jgi|Phyca11|99537|e_gw1.4.1151.1	Phyca_SSR10	(AG)15	CAGATTGTGGAGGCCCAGTT	CGCCTTCCTCGATTGATCCA	269	_Peptidase aspartic, catalytic
>jgi|Phyca11|101366|e_gw1.5.310.1	Phyca_SSR11	(CAG)4	CAGCAACAGCAACAGTCGTC	TCCAAGTCGCTCGTCTGAAC	131	_Pectin lyase fold/virulence factor(pectate lyase)
>jgi|Phyca11|13823|fgenesh1_pg.PHYCAscaffold_5_#_37	Phyca_SSR12	(CAG)4	AACGGATCTCAGCAGCAACA	AGCCAACTTCCTCGATTGGG	162	_Pectin lyase fold/virulence factor
>jgi|Phyca11|13824|fgenesh1_pg.PHYCAscaffold_5_#_38	Phyca_SSR13	(CAG)5	GAACACATCCGATTCGCAGC	TTGCTGCTCAGATCCACTGG	109	_Pectin lyase fold/virulence factor
>jgi|Phyca11|7601|fgenesh1_pm.PHYCAscaffold_20_#_116	Phyca_SSR14	(AAG)6	CAGAAACACACGTCTCCGGA	GTTCGAACTGCTCCTGCTCT	202	_Tubulin-tyrosine ligase
>jgi|Phyca11|129784|e_gw1.87.105.1	Phyca_SSR15	(AGC)4	TCGTCGTTTTCCTCTGTGCA	TTGAACTTCATCGCAGCCCT	163	_No FA Found (necrosis inducing protein NPP5)
>jgi|Phyca11|537480|estExt2_fgenesh1_pg.C_PHYCAscaffold_930015	Phyca_SSR16	(AGC)5	CATGGAGGCTGAAGGCAAGA	GACCTTCCCATTTGGCCGTA	269	_No FA Found (polygalacturonase (ipg13) gene)

>jgi|Phyca11|15345|fgenesh1_pg.PHYCAscaffold_13_#_33	Phyca_SSR17	(AAG)6	TATCGGACGTTCTCGCCATG	TGAGCGGTTTCTGCTCGAAT	116	_WW/Rsp5/WWP
>jgi|Phyca11|121654|e_gw1.44.4.1	Phyca_SSR18	(AGC)6	GGACGATATCATGCAGCCGA	CCGAGTCTGAACCCGAAGAG	260	_No FA Found
>jgi|Phyca11|103721|e_gw1.8.706.1	Phyca_SSR19	(AAG)6	CAAGAGTTGGGGTTTTCGCG	TTCGCGAGCTGTTGTACTGT	231	_Helix-hairpin-helix motif, class 2
>jgi|Phyca11|103897|e_gw1.8.481.1	Phyca_SSR20	(AAG)7	CACGGAAGCTCAACGCAAAA	GAGGTTGTCAGTGCTGTCGA	235	_No FA Found
>jgi|Phyca11|10458|fgenesh1_pm.PHYCAscaffold_49_#_90	Phyca_SSR21	(TCGC)3	CGTTTCCAACCAGCGAACAG	CCGTGGTTGGGATCACATCA	198	_Elicitin
>jgi|Phyca11|11692|fgenesh1_pm.PHYCAscaffold_78_#_16	Phyca_SSR22	(GTGC)3	CTTCCTCATCATGCTGGGCA	TTGTCGAATGCTGAGTCGCT	255	_ABC transporter-like
>jgi|Phyca11|14828|fgenesh1_pg.PHYCAscaffold_9_#_204	Phyca_SSR23	(GCGG)3	GGCTGGGTGGATGTCTTCC	GGTGAGGAACTGGTACGTGG	207	_Peptidase M, neutral zinc metallopeptidases, zinc-bin
>jgi|Phyca11|21701|fgenesh1_pg.PHYCAscaffold_108_#_7	Phyca_SSR24	(ACCC)3	GCACTGTCGTCGTCAACCTA	CGCCTCGCTCTCGTAGAATT	240	_Zinc finger, FYVE/PHD-type
>jgi|Phyca11|43145|gw1.14.128.1	Phyca_SSR25	(CCAA)3	GGCGACATCCTGGACGTTTA	TTACGGGACTGTTTGGCGAA	173	_RNA recognition motif, RNP-1
>jgi|Phyca11|53461|gw1.954.2.1	Phyca_SSR26	(GTGC)3	TGGCGGCTTCATCATTACGA	TTGTCGAATGCTGAGTCGCT	126	_ABC-2 type transporter
>jgi|Phyca11|7941|fgenesh1_pm.PHYCAscaffold_23_#_89	Phyca_SSR27	(TCTG)3	GAGCACCGACAAAGACTGGA	ACCTGTTGCTCGGAAAGAGG	156	_Peptidase, cysteine peptidase active site
>jgi|Phyca11|9314|fgenesh1_pm.PHYCAscaffold_36_#_29	Phyca_SSR28	(AGTG)3	AGGGAGCTGATGTCCCTGAT	TGGTACAAACGATGGTGCGA	267	_ABC transporter-like
>jgi|Phyca11|20337|fgenesh1_pg.PHYCAscaffold_62_#_8	Phyca_SSR29	(GCTG)4	AGAATGCCAGGAACTACGCC	CGACGTAGACGGGAAGATGG	130	_MFS general substrate transporter
>jgi|Phyca11|528924|estExt2_fgenesh1_pm.C_PHYCAscaffold_350081	Phyca_SSR30	(CCAG)6	CACAGCCTCTCGACCGGA	CGTTTTCCAGCACACCCTTG	219	_No FA Found
>jgi|Phyca11|107191|e_gw1.13.390.1	Phyca_SSR31	(CCACG)3	CGGTGTCGTCTGGAACATCA	TCACGCCTCAAGCACTACTG	226	_No FA Found
>jgi|Phyca11|109106|e_gw1.16.250.1	Phyca_SSR32	(GCACG)3	GAGTGGAGTTCTAGCGGCTC	ACGAATGGTCAGTGCTCCAG	272	_No FA Found
>jgi|Phyca11|109188|e_gw1.16.726.1	Phyca_SSR33	(TTTTG)3	CTGGTCAGTGTGGAAGGCC	CCTCTTTGGCGACAGTAGCA	138	_No FA Found
>jgi|Phyca11|12070|fgenesh1_pm.PHYCAscaffold_94_#_27	Phyca_SSR34	(TCGCA)3	TAACAGCGAGATCGTGACGG	CGCGCTGATTCCTTCCTTCT	130	_Pleckstrin-like
>jgi|Phyca11|127764|e_gw1.71.88.1	Phyca_SSR35	(CGTGG)3	TCATCGCTACGACACCACAG	GGGCATCCACAGACTGCATA	149	_No FA Found
>jgi|Phyca11|34485|gw1.34.7.1	Phyca_SSR36	(GCGAG)3	TGTTGGACGAACTGGACGAG	GTCCGTTGGGTCTCGTTTCT	252	_RNA helicase, ATP-dependent, DEAD-box, conserve

>jgi|Phyca11|549994|estExt2_Genewise1Plus.C_PHYCAscaffold_3500	Phyca_SSR37	(CAAGC)3	AGCTCCAGAATGCGGTCAAA	CGTCTGCTGGAGATCAAGCA	295	_No FA Found
>jgi|Phyca11|560628|estExt2_Genewise1.C_PHYCAscaffold_50390	Phyca_SSR38	(CGCCA)3	CAGGCGCAACAAAGACAGAA	GGGGGAGAAACTACAGTGCC	283	_No FA Found
>jgi|Phyca11|569117|estExt2_Genewise1.C_PHYCAscaffold_310248	Phyca_SSR39	(ACAGC)3	TCTGGCCAGCTCTGAAACAG	AAGTATCGAGGCTGTAGCGC	181	_No FA Found
>jgi|Phyca11|572218|estExt2_Genewise1.C_PHYCAscaffold_470074	Phyca_SSR40	(TCCTC)3	CAAGTCCCTGTCGTCGTTCT	CATGGCAGTCACCGTCTCTT	110	_No FA Found
>jgi|Phyca11|101519|e_gw1.5.1248.1	Phyca_SSR41	(TCAGAA)3	CGCTCAACGCTTCGAAGATG	GTCGAATTTGCTCCAGACGC	132	_Zinc finger, CCHC-type
>jgi|Phyca11|4219|fgenesh1_pm.PHYCAscaffold_1_#_132	Phyca_SSR42	(CGGCTT)3	ACGGACAAGTACGGTGGTTC	CAATGCCCTTGAATGCCGTC	292	_NADH:flavin oxidoreductase/NADH oxidase, N-termina
>jgi|Phyca11|4390|fgenesh1_pm.PHYCAscaffold_1_#_303	Phyca_SSR43	(GTTTGA)3	CGAGGTGGATGCTGCAATTG	GTCGTGCAACAAACGCTTCT	265	_EGF-like region, conserved site
>jgi|Phyca11|534052|estExt2_fgenesh1_pg.C_PHYCAscaffold_200013	Phyca_SSR44	(GAGTAC)3	CGACGTCGGCAATCAAAGTG	GGCGCTGGTCTTCTCAAAGA	101	_No FA Found
>jgi|Phyca11|569332|estExt2_Genewise1.C_PHYCAscaffold_320161	Phyca_SSR45	(CAAGGA)3	GGTCTTCTCGGCAAGGACAA	ACCGAGTGCATCACCAACAT	300	_No FA Found
>jgi|Phyca11|96582|e_gw1.1.399.1	Phyca_SSR46	(CGGCTT)3	ACGGACAAGTACGGTGGTTC	AGCCATGACAATGCCCTTGA	300	_NADH:flavin oxidoreductase/NADH oxidase, N-termina
>jgi|Phyca11|112116|e_gw1.21.285.1	Phyca_SSR47	(CTCAGA)4	AAGTTGCTCTTCACGGAGGG	CGAGGTACGCCCTTGATCTC	134	_No FA Found
>jgi|Phyca11|20047|fgenesh1_pg.PHYCAscaffold_55_#_77	Phyca_SSR48	(CGCTGT)4	TGTAGACCCTTCCTTCCGGT	CCGTGTTGTAGGTAGCAGCA	241	_No FA Found
>jgi|Phyca11|564747|estExt2_Genewise1.C_PHYCAscaffold_150570	Phyca_SSR49	(ATGAAC)4	TTTCTCAGCCTGCTCCTTCG	CATCTGTGCCATTTGCTGGG	299	_No FA Found
>jgi|Phyca11|97293|e_gw1.1.1178.1	Phyca_SSR50	(ACTTCA)4	GGGGCAGAAACGTCTCTGAA	GGTCGTCGTCTGAGTCTGAC	234	_Glycoside hydrolase, catalytic core
>jgi|Phyca11|7798|fgenesh1_pm.PHYCAscaffold_22_#_53	Phyca_SSR51	(GAC)4	ATCCAAATGCTGCAGCTCCT	GCCAACATCCGAGAGATCGT	282	_Actin-binding FH2
>jgi|Phyca11|530396|estExt2_fgenesh1_pm.C_PHYCAscaffold_630021	Phyca_SSR52	(AGA)5	ATCGTCCTGACCCTGAAGGA	TTCTGCGAGTTCAGGTGGTC	284	_No FA Found (heat shock protein 90)
>jgi|Phyca11|532013|estExt2_fgenesh1_pg.C_PHYCAscaffold_30186	Phyca_SSR53	(AGC)6	CGACATTTCCGGCTCAAAGC	AACTGCAAACGCTGAAGCTG	268	_No FA Found
>jgi|Phyca11|116988|e_gw1.32.238.1	Phyca_SSR54	(AAG)7	AAAGAGACCAAGCAGTCGGG	GTACAGGTCTCGGTCTGCAC	276	_No FA Found
>jgi|Phyca11|511567|fgenesh2_kg.PHYCAscaffold_90_#_1_#_Contig4	Phyca_SSR55	(AGC)7	GTGCAACCGAGATTGCCAAG	CACACCCACTGACGTAACCA	206	_No FA Found
>jgi|Phyca11|22103|fgenesh1_pg.PHYCAscaffold_699_#_1	Phyca_SSR56	(TGC)8	TGCAGAAGGCTATCGTTCCC	AACGAGTCTTCCAGCCTTGG	268	_NAD(P)-binding

>jgi|Phyca11|551783|estExt2_Genewise1Plus.C_PHYCAscaffold_4302	Phyca_SSR57	(CAG)8	AACACGGGCATGCAGAGTTA	AACTCTGCTGGTGCACGTTA	259	_No FA Found
>jgi|Phyca11|576894|estExt2_Genewise1.C_PHYCAscaffold_980011	Phyca_SSR58	(TCT)10	GGAGTTCGTTCCAGCTCACA	CGAGCTGATCGTTGAGAGCT	233	_No FA Found
>jgi|Phyca11|537271|estExt2_fgenesh1_pg.C_PHYCAscaffold_810014	Phyca_SSR59	(CCT)7	AGAGCAGCTTCAATGGGTCC	GCCTGATTGGAGCTCATCGA	257	_No FA Found
>jgi|Phyca11|101635|e_gw1.5.330.1	Phyca_SSR60	(CAG)4	ATGATGAGTGCAGCAGCCTT	TCTGCTCCCAGACACTCTCA	228	_Pectin lyase fold/virulence factor
>jgi|Phyca11|107078|e_gw1.13.190.1	Phyca_SSR61	(TAC)4	CTGGTTGCTTCGGGTGAGAT	GACCCACTCACCGCCAATAA	102	_No FA Found
>jgi|Phyca11|16626|fgenesh1_pg.PHYCAscaffold_21_#_43	Phyca_SSR62	(TCG)4	CAGTCGATCCGGACATCGTC	CGAGAGCAGCGGTTGAAATG	213	_No FA Found
>jgi|Phyca11|18224|fgenesh1_pg.PHYCAscaffold_34_#_53	Phyca_SSR63	(AGA)4	CCACAGCGAGAGTCACTTGT	ATGTCGATTTCCTCCGCCTC	206	_Peptidase, trypsin-like serine and cysteine
>jgi|Phyca11|21386|fgenesh1_pg.PHYCAscaffold_93_#_20	Phyca_SSR64	(CAG)4	ACTGCCGAGGGAAAGAAAGG	CGTGGTAGTGCCGAGAAACT	270	_Pectin lyase fold/virulence factor
>jgi|Phyca11|508761|fgenesh2_kg.PHYCAscaffold_38_#_13_#_40998	Phyca_SSR65	(GCC)4	AGCCAACTTCCCTCCAACAG	GAGCTCAGGTTCAGCACACT	153	_No FA Found
>jgi|Phyca11|533401|estExt2_fgenesh1_pg.C_PHYCAscaffold_130108	Phyca_SSR66	(TAC)4	TTTGAGACGTACACGGACGG	TCACAAGCCACGGACTTCTC	257	_No FA Found
>jgi|Phyca11|536383|estExt2_fgenesh1_pg.C_PHYCAscaffold_520031	Phyca_SSR67	(GAA)4	CTGTTCGTGGCTGCAGTTTC	TGCGAGATAGCGTCGAAGTC	296	_No FA Found
>jgi|Phyca11|544016|estExt2_Genewise1Plus.C_PHYCAscaffold_1304	Phyca_SSR68	(TAC)4	CTACGGACTGCGGAAGTACC	CTCTCCGCCGATGATCTCAC	196	_No FA Found
>jgi|Phyca11|7208|fgenesh1_pm.PHYCAscaffold_17_#_158	Phyca_SSR69	(ATG)4	GTCCGTCGACTACATTCGCT	AGAGCCAACGACATGTACGG	273	_Peptidase, trypsin-like serine and cysteine
>jgi|Phyca11|82482|gw1.5.1282.1	Phyca_SSR70	(GAA)4	CACCACATCGACTGGTCCAA	CTCGTCGTGGGCATTCTCC	102	_Ubiquinol-cytochrome C reductase, UQCRX/QCR9-lik
>jgi|Phyca11|98628|e_gw1.3.664.1	Phyca_SSR71	(GAC)4	GCTTTAATCGCTGTGCTGGG	TCCGTGCCATCAGACAAGTC	137	_Phospholipase D/Transphosphatidylase
>jgi|Phyca11|12526|fgenesh1_pm.PHYCAscaffold_498_#_1	Phyca_SSR72	(AGTG)3	CCTTCAGTGCTTTCCTCCGT	TGGTACAAACGATGGTGCGA	288	_ABC transporter-like
>jgi|Phyca11|504851|fgenesh2_kg.PHYCAscaffold_10_#_11_#_40987	Phyca_SSR73	(GCAT)3	AGGACGTACGACCGAGAGAA	ACTGCACAAGTTAAGGCGAA	271	_No FA Found
>jgi|Phyca11|548556|estExt2_Genewise1Plus.C_PHYCAscaffold_2901	Phyca_SSR74	(GAAA)3	GATGTTTGCCACCAAGCTGG	TCCTATCAGCATCTCGGGGA	133	_No FA Found
>jgi|Phyca11|570597|estExt2_Genewise1.C_PHYCAscaffold_380054	Phyca_SSR75	(CACGAC)5	GACTACGACGTCTACCGCTG	GACGTCGTGGTGGTCGTAG	108	_No FA Foun (Elicitin)
>jgi|Phyca11|556654|estExt2_Genewise1Plus.C_PHYCAscaffold_9300	Phyca_SSR76	(AGC)5	CATGGAGGCTGAAGGCAAGA	GACCTTCCCATTTGGCCGTA	269	_No FA Found (polygalacturonase (ipg13) gene)

>jgi|Phyca11|507227|fgenesh2_kg.PHYCAscaffold_26_#_30_#_Contig	Phyca_SSR77	(CT)6	GCAGCTCCCTCCTCCTCT	CCACCACCAGGATGATGACC	280	_No FA Found
>jgi|Phyca11|504071|fgenesh2_kg.PHYCAscaffold_5_#_235_#_Contig	Phyca_SSR78	(CT)10	ATTGAACGCAACGAGGCAAC	ACGGCAAGGAACAGAGAGTG	172	_No FA Found
>jgi|Phyca11|100398|e_gw1.4.36.1	Phyca_SSR79	(CA)5	TGCCAGAGCTTTCCTCATGG	GCATCAATGGCCTTGACGAC	285	_Neutral/alkaline nonlysosomal ceramidase
>jgi|Phyca11|100718|e_gw1.5.284.1	Phyca_SSR80	(AG)5	CGTTCCCACCTCAACATCCA	GTCTCCATCACCAGCAGCTT	227	_DNA polymerase alpha/epsilon, subunit B
>jgi|Phyca11|100917|e_gw1.5.353.1	Phyca_SSR81	(GC)5	AGAAGTCGACGGGTTTGGAC	CCCACAGCGTCCACTACTTT	163	_No FA Found
>jgi|Phyca11|100933|e_gw1.5.152.1	Phyca_SSR82	(GT)5	CGGGACTCCAATATTCCGGG	GTTGGGGCAATTCAAAGCGT	186	_SET
>jgi|Phyca11|10181|fgenesh1_pm.PHYCAscaffold_47_#_10	Phyca_SSR83	(TC)5	ACGACTGGAGACGCTGAATG	TCACCAACTTCTTCGGGTCG	296	_WD40 repeat-like
>jgi|Phyca11|101834|e_gw1.6.915.1	Phyca_SSR84	(CT)5	AAGCTTTGAAGGCAATGGCG	ACACGCCACCCTTCTAGTTG	223	_No FA Found
>jgi|Phyca11|102075|e_gw1.6.253.1	Phyca_SSR85	(GT)5	TGTGTACTGGGGCTCTGGTA	TGCCACCTTGTTCTTTGGGT	238	_Thioredoxin-like fold
>jgi|Phyca11|102967|e_gw1.7.568.1	Phyca_SSR86	(TG)5	GCGTTACGAACATCCCGAGA	CGTGGAATGCCGTGTGAAAG	114	_No FA Found
>jgi|Phyca11|103954|e_gw1.8.151.1	Phyca_SSR87	(AG)5	AGCTACAAACGGCGGTACAA	AGGCATCTTTGAGCTGGACC	297	_Ankyrin
>jgi|Phyca11|10414|fgenesh1_pm.PHYCAscaffold_49_#_46	Phyca_SSR88	(GT)5	TGGCCGTTAGTCAGTATCGC	GTCCAAACCCACGCTTTGTC	142	_ABC transporter-like
>jgi|Phyca11|104165|e_gw1.9.548.1	Phyca_SSR89	(GA)5	AGTCATCGGGCGAGCTTATG	TCCCGCTTACCCATTGCAAT	259	_No FA Found
>jgi|Phyca11|10611|fgenesh1_pm.PHYCAscaffold_52_#_32	Phyca_SSR90	(TC)5	CGGTTGACAACTCTGGTCGA	TCCGCATACTGTTGCCACTT	272	_No FA Found
>jgi|Phyca11|106456|e_gw1.12.130.1	Phyca_SSR91	(CA)5	TGCCGGAGCTTGACGTAAAT	GGTTGAAACATGTGTGGCCC	300	_No FA Found
>jgi|Phyca11|108224|e_gw1.15.640.1	Phyca_SSR92	(GT)5	TGGAGCGACACATGGAAGAC	GCCATCGAAATCGGCATTGT	158	_No FA Found
>jgi|Phyca11|108981|e_gw1.16.154.1	Phyca_SSR93	(GA)5	TACTTGCTGTGGAGCTGCTC	CACGTCAACAGAAAGCGCAA	155	_No FA Found
>jgi|Phyca11|109030|e_gw1.16.2.1	Phyca_SSR94	(TG)5	TACAGTGCTGCGGTACAAGG	CGAAAGCCTCCCCATTGCTA	208	_No FA Found
>jgi|Phyca11|111096|e_gw1.19.18.1	Phyca_SSR95	(CT)5	CTGGAGTGGTGCTGTGGAAA	AGCCCCAACAACAACTTGGA	172	_No FA Found
>jgi|Phyca11|112192|e_gw1.21.161.1	Phyca_SSR96	(GT)5	TTGGATTGGAGGTGAGTCGC	GACGTATGGGGCATCGTCAT	277	_No FA Found

>jgi|Phyca11|11227|fgenesh1_pm.PHYCAscaffold_64_#_36	Phyca_SSR97	(TC)5	GGACTTGGCCAAGCGAAAAG	TGTTTGTATCCCGCGACGAA	183	_WD40 repeat-like
>jgi|Phyca11|113969|e_gw1.25.157.1	Phyca_SSR98	(CA)5	GAGGGAGAACGGTTCCCTTG	TGCTGCTGCGATATGGAGAG	183	_No FA Found
>jgi|Phyca11|114778|e_gw1.27.365.1	Phyca_SSR99	(TG)5	TTCTCTCCAGCATCGATCGC	TTGGGCCTGATGACTTGTCC	148	_No FA Found
>jgi|Phyca11|115796|e_gw1.29.486.1	Phyca_SSR100	(GA)5	CCAAGCGAAGTTTTTGCCGA	GATGCCTTCTGTCGAACCCA	249	_No FA Found
>jgi|Phyca11|11714|fgenesh1_pm.PHYCAscaffold_79_#_16	Phyca_SSR101	(GC)5	ACGATGACGAACGTGGTCAA	AGCCGCTTCTGCTTACTGTT	137	_Small-subunit processome, Utp11
>jgi|Phyca11|117462|e_gw1.33.175.1	Phyca_SSR102	(GA)5	CTCTTCGTCCCACAGTGGAC	GTCGATTGCGGCCATCTCTA	182	_No FA Found
>jgi|Phyca11|118320|e_gw1.36.173.1	Phyca_SSR103	(TG)5	ACCGGCAAGAAGTAGCAGTC	CGATCGTCGCTTTCTGCTTG	264	_No FA Found
>jgi|Phyca11|119175|e_gw1.38.22.1	Phyca_SSR104	(TC)5	CACAACGTCACAGCAACTGG	GGGTCATTTTGTTGCGGCTT	260	_No FA Found
>jgi|Phyca11|120483|e_gw1.41.102.1	Phyca_SSR105	(CT)5	GAGTGTCTGTGGTGGTGGAG	CTTCATCCTCGTCCTGCAGG	233	_No FA Found
>jgi|Phyca11|120853|e_gw1.42.387.1	Phyca_SSR106	(CA)5	GGCAGCAGCTCAAAGAACAC	GGTTCTGGTACTCGGTGTGG	238	_No FA Found
>jgi|Phyca11|123909|e_gw1.52.403.1	Phyca_SSR107	(TG)5	CGGGTACTTCGCTATGGGTC	CAATGTTGAGCACCACCAGC	266	_No FA Found
>jgi|Phyca11|124729|e_gw1.54.293.1	Phyca_SSR108	(GC)5	ACTGCACCCAGGAGCTAAAC	ATCTGTTGGGCTCCAAGACG	286	_No FA Found
>jgi|Phyca11|124874|e_gw1.55.76.1	Phyca_SSR109	(GA)5	AACCAGTGTCCGAGTGCTTC	TCACGTGCTGCAGAGTGAAT	264	_No FA Found
>jgi|Phyca11|124917|e_gw1.55.157.1	Phyca_SSR110	(CT)5	CGCGATGTTTGTTTCCGTGT	TAAGGAAGCCACGCCGAATT	244	_No FA Found
>jgi|Phyca11|126109|e_gw1.61.35.1	Phyca_SSR111	(GA)5	GAACACTACCCCAAGCGACA	GTGGCGTACAATCGAATGGC	252	_No FA Found
>jgi|Phyca11|127381|e_gw1.68.73.1	Phyca_SSR112	(TG)5	ATTCTGGCGATACGTGCGAT	TCCTCCAATTGTCACGAGCC	248	_No FA Found
>jgi|Phyca11|128580|e_gw1.77.45.1	Phyca_SSR113	(AC)5	TACGCTGAGTGGGAACAACC	CCTTGAACCAGATCGGCAGT	211	_No FA Found
>jgi|Phyca11|129057|e_gw1.81.42.1	Phyca_SSR114	(CA)5	TCGCACAAGAACTGCAAACG	AAAGTGGCAGCATCGACGTA	148	_No FA Found
>jgi|Phyca11|131592|e_gw1.108.22.1	Phyca_SSR115	(CT)5	AGGAAGTTCCCTCTGTCCCG	CGCACTTATCCCGTTGCATG	142	_No FA Found
>jgi|Phyca11|13215|fgenesh1_pg.PHYCAscaffold_3_#_28	Phyca_SSR116	(AG)5	GGCTGCGGTTTTTGAGGAAG	TCTGCAGCTTGCTCCTTCTC	175	_WW/Rsp5/WWP

>jgi|Phyca11|15342|fgenesh1_pg.PHYCAscaffold_13_#_30	Phyca_SSR117	(CG)5	CCGAAGCGCAAATGGATCAG	GTAGGTGAGCAGTCCGTTCC	226	_SET
>jgi|Phyca11|17070|fgenesh1_pg.PHYCAscaffold_24_#_95	Phyca_SSR118	(GA)5	AAAGACAACGCGTTGCCTTC	TGTTGGTGGTGGAAGTGCTT	177	_No FA Found
>jgi|Phyca11|17833|fgenesh1_pg.PHYCAscaffold_31_#_11	Phyca_SSR119	(TG)5	CGGCTGGACAGATCGTACTC	GATCCAGACTGAGTAGCCGC	151	_Mg2+ transporter protein, CorA-like
>jgi|Phyca11|20087|fgenesh1_pg.PHYCAscaffold_57_#_38	Phyca_SSR120	(GC)5	GTGGACAACGTAGCTGAGCT	GGTCGCCTTGAAGGTCTGAA	300	_No FA Found
>jgi|Phyca11|20259|fgenesh1_pg.PHYCAscaffold_60_#_45	Phyca_SSR121	(TG)5	ATCCAGCACACGGAACACAT	GGCAGTACAGTTCGTCACCA	229	_Ribosomal RNA adenine methylase transferase
>jgi|Phyca11|21719|fgenesh1_pg.PHYCAscaffold_109_#_11	Phyca_SSR122	(CG)5	TAGAAACTGCCACGGAGCAG	TCTTCTTCTGCAGCTGACCG	291	_No FA Found
>jgi|Phyca11|21850|fgenesh1_pg.PHYCAscaffold_158_#_1	Phyca_SSR123	(GC)5	GTGGACAACGTAGCTGAGCT	TGATTGTAAGCGGCGTCTGT	244	_No FA Found
>jgi|Phyca11|22069|fgenesh1_pg.PHYCAscaffold_580_#_1	Phyca_SSR124	(CG)5	CCGCTTCAAGACCAAGACCT	CGGCTTGGTCATCATGGTCT	145	_Polynucleotidyl transferase, Ribonuclease H fold
>jgi|Phyca11|38886|gw1.35.39.1	Phyca_SSR125	(TG)5	ACTCGCGTGTTGGAAGGAAT	TCTGGAACATTTGGTCATCGG	127	_Trehalose-phosphatase
>jgi|Phyca11|4143|fgenesh1_pm.PHYCAscaffold_1_#_56	Phyca_SSR126	(CA)5	AGATCACCAGGCAGTTCGTG	TCCAGCCACACCAATAGCTG	142	_MFS general substrate transporter
>jgi|Phyca11|45010|gw1.52.130.1	Phyca_SSR127	(TG)5	GCCAGTGAGGATTTCCGGAA	TCACTCTTGGCTCCGTTGAC	215	_No FA Found
>jgi|Phyca11|502622|fgenesh2_kg.PHYCAscaffold_1_#_82_#_gi|18908	Phyca_SSR128	(AC)5	TTGACCACTGTCGGCACTTT	AGTGGCGAAAAGACCTCGAG	191	_No FA Found
>jgi|Phyca11|502679|fgenesh2_kg.PHYCAscaffold_1_#_139_#_409729	Phyca_SSR129	(GC)5	CCTCCTCTTCTAGCAGCAGC	AAACTCAGCGGGGATGACTG	212	_No FA Found
>jgi|Phyca11|502783|fgenesh2_kg.PHYCAscaffold_1_#_243_#_Contig	Phyca_SSR130	(GT)5	AGTACTCGGCACAGCTCAAC	AACGAAGCAGTAACTCGGCA	300	_No FA Found
>jgi|Phyca11|503263|fgenesh2_kg.PHYCAscaffold_3_#_128_#_Contig	Phyca_SSR131	(GC)5	CCCAACAAGGTGGACCAGTT	ACTTCTTAGTGCCGGGCTTC	247	_No FA Found
>jgi|Phyca11|503635|fgenesh2_kg.PHYCAscaffold_4_#_174_#_Contig	Phyca_SSR132	(CA)5	AGCAAAGCAATCCCTCCTCC	GAACTCAATGGGCTCCTGCT	291	_No FA Found
>jgi|Phyca11|503949|fgenesh2_kg.PHYCAscaffold_5_#_113_#_409905	Phyca_SSR133	(GA)5	CCCAAGAAGACACTCACGCT	AAGACGCTGCAGATGACGAA	248	_No FA Found
>jgi|Phyca11|503984|fgenesh2_kg.PHYCAscaffold_5_#_148_#_Contig2	Phyca_SSR134	(GA)5	CCCTGGTGCCAAGGACTAAG	ACTCCACTAGTTGAAGCCGC	240	_No FA Found
>jgi|Phyca11|504574|fgenesh2_kg.PHYCAscaffold_8_#_143_#_409934	Phyca_SSR135	(GC)5	GCCTTCCCTGAAGCTGTGAT	CATCTCCTTGGCCAGCTGAA	174	_No FA Found
>jgi|Phyca11|505843|fgenesh2_kg.PHYCAscaffold_16_#_2_#_Contig3	Phyca_SSR136	(AG)5	GCATTGCACTTTGACCAGCA	TTTGGTCCGTTCTAGTGGCC	288	_No FA Found

>jgi|Phyca11|506019|fgenesh2_kg.PHYCAscaffold_17_#_104_#_40970	Phyca_SSR137	(GA)5	ACACACTGTCGGCCTTGTAG	AAGCACTCGTCGGTGTTGAT	300	_No FA Found
>jgi|Phyca11|506234|fgenesh2_kg.PHYCAscaffold_18_#_107_#_Conti	Phyca_SSR138	(AT)5	TCCAAGGCACAGTACTGCAG	GATTGTGGGGGCTCAAATGC	162	_No FA Found
>jgi|Phyca11|506400|fgenesh2_kg.PHYCAscaffold_19_#_106_#_40998	Phyca_SSR139	(AC)5	CCTCAAACCCGATGTCCTCC	GTCTTCTAGTGCGGGACTCG	251	_No FA Found
>jgi|Phyca11|506409|fgenesh2_kg.PHYCAscaffold_19_#_115_#_40983	Phyca_SSR140	(AG)5	CATCGTCGGAGTCGGAAGAG	GATACTCTGGCCGCCCATAC	173	_No FA Found
>jgi|Phyca11|507023|fgenesh2_kg.PHYCAscaffold_24_#_15_#_gi|1890	Phyca_SSR141	(CT)5	AATTGCCACTCTTCAGCCGA	AGCCACTATCGGTCAATGGG	198	_No FA Found
>jgi|Phyca11|507135|fgenesh2_kg.PHYCAscaffold_25_#_19_#_410025	Phyca_SSR142	(TG)5	CCTTCATCAGGCCCCATTGT	GATCACGACCACCTGCTTCA	229	_No FA Found
>jgi|Phyca11|507508|fgenesh2_kg.PHYCAscaffold_28_#_15_#_410194	Phyca_SSR143	(TC)5	CACCCTTCCCCAGTCCAATC	CCGTGGACGAGATAAGCTCC	261	_No FA Found
>jgi|Phyca11|507888|fgenesh2_kg.PHYCAscaffold_30_#_157_#_Conti	Phyca_SSR144	(AG)5	TCGAAACGAGAGAAGTGCGA	CTCGTGACTCTATTGGCCGG	103	_No FA Found
>jgi|Phyca11|508895|fgenesh2_kg.PHYCAscaffold_39_#_62_#_409792	Phyca_SSR145	(GT)5	CCTCAGAAACCAACTCCCCC	CTTGAAAGCCTGGGGAGGTT	133	_No FA Found
>jgi|Phyca11|510024|fgenesh2_kg.PHYCAscaffold_53_#_9_#_Contig2	Phyca_SSR146	(GA)5	CAGTGCAGACTCCAGTCCTG	GTGCTTCGACACCAACACAC	209	_No FA Found
>jgi|Phyca11|510059|fgenesh2_kg.PHYCAscaffold_53_#_44_#_410032	Phyca_SSR147	(GA)5	CACGACAATTGGTGCAACGT	CGGAGCCAAAGGAAGTGGAA	149	_No FA Found
>jgi|Phyca11|510418|fgenesh2_kg.PHYCAscaffold_60_#_6_#_jgi|JGI_	Phyca_SSR148	(CT)5	CTGCAAATGAAACGCAGCCT	TAGCCATTCCAGTGCCAAGG	289	_No FA Found
>jgi|Phyca11|510985|fgenesh2_kg.PHYCAscaffold_72_#_30_#_gi|1890	Phyca_SSR149	(TG)5	CAGTCCAAGCAGCCTAGTCA	GGAGACGCTGAGGATCATGG	188	_No FA Found
>jgi|Phyca11|511240|fgenesh2_kg.PHYCAscaffold_79_#_45_#_Contig	Phyca_SSR150	(CT)5	ACCGCGGGAAGAAGAAAGAG	ACGATTAACTTCATCCTAGCGT	164	_No FA Found
>jgi|Phyca11|511668|fgenesh2_kg.PHYCAscaffold_94_#_19_#_410194	Phyca_SSR151	(CG)5	ACCCCTATCGTGCCTAAGGT	ACCGATAGCCAGAATGCAGG	207	_No FA Found
>jgi|Phyca11|511800|fgenesh2_kg.PHYCAscaffold_100_#_3_#_409813	Phyca_SSR152	(GA)5	CACTCGTGCGCTGTAACAAC	GCACAATGTTGCACTGCTCA	204	_No FA Found
>jgi|Phyca11|525051|estExt2_fgenesh1_pm.C_PHYCAscaffold_10286	Phyca_SSR153	(GA)5	ACTGTGGCGTTGCATTTGTC	TCGCCGTCCAGTATTGCAAT	271	_No FA Found
>jgi|Phyca11|525935|estExt2_fgenesh1_pm.C_PHYCAscaffold_50277	Phyca_SSR154	(CA)5	GTGGTGATCTTCCTGCACCA	AGTGCCCACATGTTACGGAG	281	_No FA Found
>jgi|Phyca11|527201|estExt2_fgenesh1_pm.C_PHYCAscaffold_170079	Phyca_SSR155	(TG)5	CGGCTTCCTCTGTTGATGGT	GCGTCTTTTGTGACCACGAC	270	_No FA Found
>jgi|Phyca11|527907|estExt2_fgenesh1_pm.C_PHYCAscaffold_240026	Phyca_SSR156	(AG)5	TGGACTACCGTCGATCCCTT	TCCGATTTCACCAGGAACCG	240	_No FA Found

>jgi|Phyca11|529241|estExt2_fgenesh1_pm.C_PHYCAscaffold_400075	Phyca_SSR157	(GA)5	TTCCTGCTGCTAACCGGAAG	GCTGACGAATCTGCTCCTGT	216	_No FA Found
>jgi|Phyca11|529676|estExt2_fgenesh1_pm.C_PHYCAscaffold_470058	Phyca_SSR158	(TG)5	CTCGCATGCACAAGCTTCAG	CGCAAGGTGAGAAACTCCCT	272	_No FA Found
>jgi|Phyca11|530755|estExt2_fgenesh1_pm.C_PHYCAscaffold_760038	Phyca_SSR159	(CA)5	AATGTCCCGTATGGCACCAG	AAGCTCATGAACTCCCGGTG	267	_No FA Found
>jgi|Phyca11|533657|estExt2_fgenesh1_pg.C_PHYCAscaffold_160013	Phyca_SSR160	(GC)5	ATGCCATGGCTCAAGTGGAA	CGGTCCACAGGGTTCAATGA	247	_No FA Found
>jgi|Phyca11|534434|estExt2_fgenesh1_pg.C_PHYCAscaffold_230104	Phyca_SSR161	(AG)5	GCAAATGCACGCAAAAGACG	GCGCTGTTCTTCCTCCTTCT	175	_No FA Found
>jgi|Phyca11|535284|estExt2_fgenesh1_pg.C_PHYCAscaffold_330117	Phyca_SSR162	(TG)5	AAATCAGCGACAAGATGCGC	CCCATCGACTTGAGGTGCTT	160	_No FA Found
>jgi|Phyca11|535285|estExt2_fgenesh1_pg.C_PHYCAscaffold_330119	Phyca_SSR163	(TG)5	CCCAACAGAAGTGCACGTTG	CCCATCGACTTGAGGTGCTT	291	_No FA Found
>jgi|Phyca11|536048|estExt2_fgenesh1_pg.C_PHYCAscaffold_460090	Phyca_SSR164	(AC)5	GGCAAGGCTATCGAGAGCAT	GTGAACAACACGACGTCACG	191	_No FA Found
>jgi|Phyca11|536691|estExt2_fgenesh1_pg.C_PHYCAscaffold_600032	Phyca_SSR165	(TG)5	TGGTTTTGCTCAATGGCACG	GTACCTCAGGTGCCCCTTTC	285	_No FA Found
>jgi|Phyca11|53706|gw1.22.98.1	Phyca_SSR166	(TG)5	TTTTGGGGCTGCACAAATCG	CGTACGAACTGCCAGTGACT	223	_WD40 repeat-like
>jgi|Phyca11|537817|estExt2_fgenesh1_pg.C_PHYCAscaffold_208000	Phyca_SSR167	(CG)5	ACGCACAAGTTTGACAAGCC	TGAGCTTGCTTACTTCGGCA	271	_No FA Found
>jgi|Phyca11|540766|estExt2_Genewise1Plus.C_PHYCAscaffold_5055	Phyca_SSR168	(AC)5	TTGAACGTCCGGTTGCGATA	GGCTTAGCTTCGTTGCAACT	123	_No FA Found
>jgi|Phyca11|542172|estExt2_Genewise1Plus.C_PHYCAscaffold_8060	Phyca_SSR169	(CA)5	AATCCTCGACCTCATCCCCA	ACTCTGACCTGGAACATGGA	214	_No FA Found
>jgi|Phyca11|542669|estExt2_Genewise1Plus.C_PHYCAscaffold_9069	Phyca_SSR170	(CA)5	GACAGCCGAGTACGTAGCTC	CACACAGCAGTAGCAGGTGA	245	_No FA Found
>jgi|Phyca11|543720|estExt2_Genewise1Plus.C_PHYCAscaffold_1207	Phyca_SSR171	(GA)5	ACATGGGCACAAATGGGACT	AGGGGAACAGATAGTCGCCT	254	_No FA Found
>jgi|Phyca11|54383|gw1.8.170.1	Phyca_SSR172	(TC)5	AAAATTGAGTGGTGGCGTGC	CAGCGTTCACATCCGTGTTG	283	_Fibronectin, type III-like fold
>jgi|Phyca11|544937|estExt2_Genewise1Plus.C_PHYCAscaffold_1604	Phyca_SSR173	(TG)5	TATCGAGCGCTTCCTTCGTC	TATGAGCAGCGTAACGGGTC	272	_No FA Found
>jgi|Phyca11|547226|estExt2_Genewise1Plus.C_PHYCAscaffold_2400	Phyca_SSR174	(AG)5	TCGCTCTCTACGGAGTGACA	AATTGCCACTCTTCAGCCGA	240	_No FA Found
>jgi|Phyca11|547509|estExt2_Genewise1Plus.C_PHYCAscaffold_2501	Phyca_SSR175	(AC)5	TAGTGAGCCTCAGCCTTTGC	CGAACTCGTACACCGTCACA	271	_No FA Found
>jgi|Phyca11|547672|estExt2_Genewise1Plus.C_PHYCAscaffold_2600	Phyca_SSR176	(GA)5	CGAGCACGTGATCATCGAGA	GCAGTTTGATGTGCGTGTCA	230	_No FA Found

>jgi|Phyca11|548881|estExt2_Genewise1Plus.C_PHYCAscaffold_3003	Phyca_SSR177	(AG)5	GTGCCTAGAGGAGAAGGGGA	GGTGACACACGACGGTACTT	260	_No FA Found
>jgi|Phyca11|549902|estExt2_Genewise1Plus.C_PHYCAscaffold_3402	Phyca_SSR178	(AG)5	GCAGGACTGGAAGAACTCCC	TGCCGCCACCTTCATTCG	206	_No FA Found
>jgi|Phyca11|552608|estExt2_Genewise1Plus.C_PHYCAscaffold_4803	Phyca_SSR179	(GA)5	TGACGGGAGATAAGCCTGGA	ACGCGTCTCTGTTTTGTTGC	207	_No FA Found
>jgi|Phyca11|552634|estExt2_Genewise1Plus.C_PHYCAscaffold_4803	Phyca_SSR180	(GA)5	GTCGTTGCAATTCCTTGGGG	TTCTTTGTCCTTCGGGAGCC	262	_No FA Found
>jgi|Phyca11|552955|estExt2_Genewise1Plus.C_PHYCAscaffold_5002	Phyca_SSR181	(AG)5	TGACAGTGAACCAGGCCATC	ACAATCATCTTCTATTCCTTGT	288	_No FA Found
>jgi|Phyca11|555344|estExt2_Genewise1Plus.C_PHYCAscaffold_7200	Phyca_SSR182	(CA)5	GGAGACGCTGAGGATCATGG	CAGTCCAAGCAGCCTAGTCA	188	_No FA Found
>jgi|Phyca11|555353|estExt2_Genewise1Plus.C_PHYCAscaffold_7200	Phyca_SSR183	(GC)5	AAGATGGACAACACTGGCGG	ACCATCACGTAGCCCAACAG	116	_No FA Found
>jgi|Phyca11|556188|estExt2_Genewise1Plus.C_PHYCAscaffold_8401	Phyca_SSR184	(AG)5	GCTATTGCGAGTGTGCTGTG	AGCGGGAGACACTTGAACAG	159	_No FA Found
>jgi|Phyca11|556483|estExt2_Genewise1Plus.C_PHYCAscaffold_8900	Phyca_SSR185	(CG)5	CCTGCTCGAGATCTTAGGCG	CAACTTGCTCGTCGTCTCCT	281	_No FA Found
>jgi|Phyca11|562095|estExt2_Genewise1.C_PHYCAscaffold_80628	Phyca_SSR186	(GT)5	GTCAAGTTTGGCACCACGAC	AGGTGGCTCTTCATCTTGGC	236	_No FA Found
>jgi|Phyca11|565161|estExt2_Genewise1.C_PHYCAscaffold_170272	Phyca_SSR187	(TC)5	AAGCACTCGTCGGTGTTGAT	ACACACTGTCGGCCTTGTAG	300	_No FA Found
>jgi|Phyca11|566838|estExt2_Genewise1.C_PHYCAscaffold_220535	Phyca_SSR188	(CG)5	CACAACTTCTCGACCCGTGA	TGAGCTTGCTTACTTCGGCA	299	_No FA Found
>jgi|Phyca11|568901|estExt2_Genewise1.C_PHYCAscaffold_300383	Phyca_SSR189	(CG)5	GACCAGAGAAGCAGCTCGAG	AGGTCCACGCCATACTGTTG	178	_No FA Found
>jgi|Phyca11|569580|estExt2_Genewise1.C_PHYCAscaffold_330165	Phyca_SSR190	(AG)5	CTGAAAGTGCAGCAACCGTC	TCCTTCCCCACTGAGGACTC	222	_No FA Found
>jgi|Phyca11|570447|estExt2_Genewise1.C_PHYCAscaffold_370222	Phyca_SSR191	(AC)5	TTAAAGCGGGCGTACGACTT	CCTCACAGTCGATGCCTGTT	283	_No FA Found
>jgi|Phyca11|572192|estExt2_Genewise1.C_PHYCAscaffold_470018	Phyca_SSR192	(GC)5	CCCACGAGTACAAACCACGA	CACTAGCAGGGTCCTCTCCT	231	_No FA Found
>jgi|Phyca11|572497|estExt2_Genewise1.C_PHYCAscaffold_480229	Phyca_SSR193	(CG)5	GACACGGATGAGCTAGTGCA	CTCAGCCTGCAGGACATCAA	258	_No FA Found
>jgi|Phyca11|574185|estExt2_Genewise1.C_PHYCAscaffold_600055	Phyca_SSR194	(GA)5	TGCTGCATCCGATCAACAGT	GTCCACGTAACTCAGCCACA	219	_No FA Found
>jgi|Phyca11|575025|estExt2_Genewise1.C_PHYCAscaffold_680075	Phyca_SSR195	(TG)5	CGATCACTGTGGAGGCAAGT	CAAGCCATTTCCACACTGGC	258	_No FA Found
>jgi|Phyca11|576136|estExt2_Genewise1.C_PHYCAscaffold_840079	Phyca_SSR196	(CA)5	GCGATCGAATCCGTGAGTCT	GGCTACACGATGGCAAGGAT	213	_No FA Found

>jgi|Phyca11|5928|fgenesh1_pm.PHYCAscaffold_8_#_152	Phyca_SSR197	(GT)5	TTTCGCTGTTCACCCGAAGA	CGTGCAACTGACCCAAAGTG	104	_DNA primase, small subunit, eukaryotic and archaeal
>jgi|Phyca11|6021|fgenesh1_pm.PHYCAscaffold_9_#_81	Phyca_SSR198	(TG)5	GCAGTGTGTACCGGAGTTGA	GAACAACGCGAACAACGGAA	249	_Zinc finger, FYVE/PHD-type
>jgi|Phyca11|6121|fgenesh1_pm.PHYCAscaffold_9_#_181	Phyca_SSR199	(GA)5	GGTCCAAGGGTGAGATGCAA	TTCGATCCACTTCTGCTCCG	144	_Fumble
>jgi|Phyca11|64326|gw1.24.235.1	Phyca_SSR200	(TG)5	AAGGAGATCAAGAACGCGCA	TTGACCACGCGAGATACGAG	210	_No FA Found
>jgi|Phyca11|7245|fgenesh1_pm.PHYCAscaffold_18_#_8	Phyca_SSR201	(AG)5	GGCTGAACGAAAAACTGCGT	GCGATGCTGAGCGTTTCTTT	271	_RecF/RecN/SMC protein, N-terminal
>jgi|Phyca11|7638|fgenesh1_pm.PHYCAscaffold_21_#_11	Phyca_SSR202	(CG)5	CTGCTATCAGGCGTGGAGAC	TCTGTTGCGCTCCTTTTTGC	139	_Translation elongation and initiation factors/Ribosoma
>jgi|Phyca11|80503|gw1.6.980.1	Phyca_SSR203	(CG)5	GCTTATAACTCGGGGCGACA	AGGCCTGAACACCCAAACAT	285	_Polynucleotidyl transferase, Ribonuclease H fold
>jgi|Phyca11|8339|fgenesh1_pm.PHYCAscaffold_27_#_85	Phyca_SSR204	(TG)5	GTGAAAGTGGGCGTTGTGAC	GGAAATTAGCTGCAGCACGG	226	_ROK
>jgi|Phyca11|83929|gw1.169.16.1	Phyca_SSR205	(TG)5	TCCCTCTTCCTGGCTGGATC	CGCAAGGTGAGAAACTCCCT	156	_Nucleotidyltransferase, class I, C-terminal-like
>jgi|Phyca11|8846|fgenesh1_pm.PHYCAscaffold_31_#_66	Phyca_SSR206	(CA)5	CTCAGTGTCTCCTTGTCGCC	TCACACGTCGCAGGAAATCA	268	_Cyclin-like
>jgi|Phyca11|9516|fgenesh1_pm.PHYCAscaffold_38_#_65	Phyca_SSR207	(GC)5	CAGCTTTATCACGCCGAAGC	ACGCCATAAAAACGATCGCG	201	_Phospholipid/glycerol acyltransferase
>jgi|Phyca11|9586|fgenesh1_pm.PHYCAscaffold_39_#_52	Phyca_SSR208	(TG)5	GTTACAACATCTGCCGTCGC	GAACCGCGGATAGACGGATT	220	_Regulator of G protein signalling superfamily
>jgi|Phyca11|9646|fgenesh1_pm.PHYCAscaffold_40_#_34	Phyca_SSR209	(TG)5	CGCAATGTCATCCGTCGTTC	TGAGAGACGCGAACGATAGC	250	_ATP-dependent DNA ligase, conserved site
>jgi|Phyca11|9805|fgenesh1_pm.PHYCAscaffold_42_#_13	Phyca_SSR210	(TG)5	CAGGAGAAGCCAAAGGGAGG	CTGCTTGGCGAACATGATGG	299	_No FA Found
>jgi|Phyca11|99952|e_gw1.4.1039.1	Phyca_SSR211	(GC)5	ACACTCGAAGCTGAGGTGAC	AGAGCCATCGGTGCATTTCA	294	_No FA Found
>jgi|Phyca11|100444|e_gw1.4.1012.1	Phyca_SSR212	(GCA)4	ACACGATTGAGGATGCGGTT	CGGAAGCAGAACCTGTCAGT	260	_No FA Found
>jgi|Phyca11|10092|fgenesh1_pm.PHYCAscaffold_46_#_22	Phyca_SSR213	(CGA)4	CCAGTGTTGGTGAGGAGACC	TCGTCAGAGTCTTCCTCCGA	127	_Trimeric LpxA-like
>jgi|Phyca11|101647|e_gw1.5.312.1	Phyca_SSR214	(GAA)4	CATCATGGCATCGACGGAGA	CTCTCGCGCAATTCTCAACG	169	_HSP20-like chaperone
>jgi|Phyca11|101767|e_gw1.6.462.1	Phyca_SSR215	(CAC)4	GGGACCTGTTGACCGAAGAG	CTTGTCTCCGGTCTCAGTCG	167	_Multi antimicrobial extrusion protein MatE
>jgi|Phyca11|10202|fgenesh1_pm.PHYCAscaffold_47_#_31	Phyca_SSR216	(AAG)4	GGATGTGACGGGAAGTGGTT	TGTGGCTCTTCTTGTGCTGT	221	_No FA Found

>jgi|Phyca11|102210|e_gw1.6.213.1	Phyca_SSR217	(AAG)4	CGCAAGAGACAGCTGGATCT	TGCTTCTGCTGAGGAAGAGC	230	_Homeodomain-like
>jgi|Phyca11|102312|e_gw1.6.208.1	Phyca_SSR218	(TGC)4	TTGGCTTTGAGCTCTGGAGG	ACCAGCGGTAATTTCCAGCA	278	_No FA Found
>jgi|Phyca11|102331|e_gw1.6.516.1	Phyca_SSR219	(TGA)4	GTACCCCTATGGCAAGGACG	GCCACTACAACTCCACTGCT	148	_No FA Found
>jgi|Phyca11|102823|e_gw1.7.636.1	Phyca_SSR220	(GAC)4	CATCGACCTCCAAGCAGTCC	GAAGAATGTGCTGCGCGTAG	265	_No FA Found
>jgi|Phyca11|102906|e_gw1.7.573.1	Phyca_SSR221	(GAA)4	GCACGCTACTGAGGTGTCTT	AAGCTGGAAGGTCCTCAAGC	155	_No FA Found
>jgi|Phyca11|103107|e_gw1.7.493.1	Phyca_SSR222	(CGA)4	CGACACGTAGCAGACACTGT	AGGTTTTGCTAGCGCTGGAT	257	_No FA Found
>jgi|Phyca11|103114|e_gw1.7.28.1	Phyca_SSR223	(ACT)4	GGTTTCGCCATTGGAAACCC	CGTCTTGGCAGTGCTCAGTA	181	_Peptidase S10, serine carboxypeptidase
>jgi|Phyca11|103177|e_gw1.7.844.1	Phyca_SSR224	(CGA)4	TGCTGGAGACTTCCCGGATA	TCCGCTTGAGTGAGACGTTC	236	_No FA Found
>jgi|Phyca11|103253|e_gw1.7.241.1	Phyca_SSR225	(CAG)4	CAAAATCGTGGCAGTGGTGG	GCCACGGCTACTCCTGTATC	293	_Zinc finger, CCHC-type
>jgi|Phyca11|103384|e_gw1.8.833.1	Phyca_SSR226	(AAG)4	ATGGGCGATGGAGATAGTCT	TGGGAGATTTCTGCTGGCAG	165	_No FA Found
>jgi|Phyca11|103841|e_gw1.8.608.1	Phyca_SSR227	(CAG)4	TCACTGGTGGCGAGAATGTC	GACGGCTTTGGTGTTGTCAC	144	_Zinc finger, CCHC-type
>jgi|Phyca11|10392|fgenesh1_pm.PHYCAscaffold_49_#_24	Phyca_SSR228	(GAC)4	ATATCGGGGAATCGCTGCAG	CCCTGTACGTCCTGTTGGTC	214	_Concanavalin A-like lectin/glucanase
>jgi|Phyca11|104199|e_gw1.9.417.1	Phyca_SSR229	(GTG)4	GAACCCCTTGCTGTGGATCA	AATCCTGTTTGTGCGTGTGC	105	_No FA Found
>jgi|Phyca11|104316|e_gw1.9.383.1	Phyca_SSR230	(GAA)4	GAACCTCCTAGCACAGACGG	AACACTCGAACGTCTGCTGT	289	_No FA Found
>jgi|Phyca11|104509|e_gw1.9.176.1	Phyca_SSR231	(TGC)4	GCTTCAAGTGTCCGACCTCA	GCCTCAACTAAGTCCTGCGT	141	_No FA Found
>jgi|Phyca11|104585|e_gw1.9.446.1	Phyca_SSR232	(AGG)4	CCAAGAAGGAGCTCATGGCA	TGCATTCAATTCCAACGCGG	296	_No FA Found
>jgi|Phyca11|105104|e_gw1.10.453.1	Phyca_SSR233	(AAG)4	AGGACTTGGAGGTGGAAGAGA	CCCAGAGTTTCCTGAGCCAG	232	_No FA Found
>jgi|Phyca11|105303|e_gw1.10.287.1	Phyca_SSR234	(AGA)4	AGCGCCAGTTTCTACGACAA	CGTTTCCTCAGCTCCACCTT	280	_No FA Found
>jgi|Phyca11|105584|e_gw1.11.647.1	Phyca_SSR235	(GTG)4	CAGCTACTATCCACGCAGGG	TCCCTCTTCAATCATGCGCT	272	_No FA Found
>jgi|Phyca11|105866|e_gw1.11.826.1	Phyca_SSR236	(CAA)4	GGAGATCGTCCGTCTTCCAC	CCAGACCGAGAGAAGGATGC	293	_No FA Found

>jgi|Phyca11|105871|e_gw1.11.114.1	Phyca_SSR237	(TGA)4	TCCGCCTCTCTCCTTTCTCA	ATTCGGGTTGATGGTTGGCT	260	_No FA Found
>jgi|Phyca11|105975|e_gw1.11.562.1	Phyca_SSR238	(AGC)4	GCCGAACGTCGAGTGTATGA	TGTCGGGGAGAGCTAACGTA	184	_No FA Found
>jgi|Phyca11|106045|e_gw1.11.157.1	Phyca_SSR239	(AAC)4	TCGTCATTGCTTGTCTGGCT	ACACTTCTCCGTAGCCTCCT	300	_No FA Found
>jgi|Phyca11|106156|e_gw1.12.144.1	Phyca_SSR240	(TGC)4	ACCGAGGTGGCTTCTCCTAT	TCTGCGTTTGCTGGATCACT	211	_No FA Found
>jgi|Phyca11|106545|e_gw1.12.811.1	Phyca_SSR241	(AGC)4	ACGACTACGATGACCTTCGC	CTACCATCTCGGCAATGGCT	246	_No FA Found
>jgi|Phyca11|106668|e_gw1.12.123.1	Phyca_SSR242	(AAG)4	TCAACTGGCGTTTGCTTTGG	AAGCCGTACGTCCACAACTT	234	_No FA Found
>jgi|Phyca11|106683|e_gw1.12.190.1	Phyca_SSR243	(CAA)4	GTCGGAACAGCCTACACTCC	CTCTATGGACGCTGGAGCTG	286	_No FA Found
>jgi|Phyca11|106736|e_gw1.12.192.1	Phyca_SSR244	(GAA)4	ATCAGAACCGGATGAGCGTC	ATGACACCCTTCACCACGTC	112	_No FA Found
>jgi|Phyca11|106763|e_gw1.12.662.1	Phyca_SSR245	(ATG)4	GGGCCCGTCAATATCCACAA	ACGTCGATGCCGAGAAACTT	104	_No FA Found
>jgi|Phyca11|107267|e_gw1.13.632.1	Phyca_SSR246	(AGC)4	TCCAGTCGCACTACACCAAC	GGGCCCATCAGGTTGGTAAA	293	_No FA Found
>jgi|Phyca11|107321|e_gw1.13.621.1	Phyca_SSR247	(AGC)4	AAGTCGGATGCAGTGCTGAA	GCTTGGTCTTCTTGCAAGCC	271	_No FA Found
>jgi|Phyca11|107696|e_gw1.14.134.1	Phyca_SSR248	(GAA)4	ACGCGTTAAGAAGAAGCCGA	CGATTTCCGGAGCTCCTCAA	289	_No FA Found
>jgi|Phyca11|107843|e_gw1.14.9.1	Phyca_SSR249	(AGA)4	ATCTGAAGGTGGCAAGTCGG	ACCAAAACGATTGCCGCAAG	186	_No FA Found
>jgi|Phyca11|108146|e_gw1.14.615.1	Phyca_SSR250	(GAA)4	CGAGACTGTTGCAGCTGAGA	TCAAGTACTTGCTGCACGGT	286	_No FA Found
>jgi|Phyca11|108274|e_gw1.15.438.1	Phyca_SSR251	(GCT)4	TTTGGCTGCTTGTGACCAGA	TTCTTGGTGCTGATGCTCGT	270	_No FA Found
>jgi|Phyca11|108899|e_gw1.16.205.1	Phyca_SSR252	(AGT)4	GGATCAACTTCACGGCCTGA	GAAACCACGCTGACTCTGGA	174	_No FA Found
>jgi|Phyca11|108966|e_gw1.16.194.1	Phyca_SSR253	(AAG)4	GACACGGAGCTTGAAGTGGA	GCGTTTGCTTCTGCTTCCTC	282	_No FA Found
>jgi|Phyca11|108996|e_gw1.16.577.1	Phyca_SSR254	(AGA)4	AGATCACAGCTCTCCATGCG	GGTCTTCTCCTCTGTCCCCT	283	_No FA Found
>jgi|Phyca11|109068|e_gw1.16.245.1	Phyca_SSR255	(CGA)4	TTGCGGTTCTTGATCCAGCT	CCAGGTCTCTCCCCATACGA	161	_No FA Found
>jgi|Phyca11|109215|e_gw1.16.455.1	Phyca_SSR256	(CGA)4	TCCGCGAAACTACGGTTGAA	CGTCGAACCACACTCTCACA	268	_No FA Found

>jgi|Phyca11|109704|e_gw1.17.425.1	Phyca_SSR257	(GGA)4	ACGGAAGTTTCAGTGCGTCT	ACCTTGCGAGTCGAAATGGT	150	_No FA Found
>jgi|Phyca11|110116|e_gw1.18.613.1	Phyca_SSR258	(AAG)4	TGTAAAGTATGCGCGCTCCT	TAGAAGGGATCGACTGGCCA	196	_No FA Found
>jgi|Phyca11|110159|e_gw1.18.535.1	Phyca_SSR259	(CGA)4	CACGAGCTGAGTTGGATGGT	AGGTTTTGCTAGCGCTGGAT	149	_No FA Found
>jgi|Phyca11|110421|e_gw1.18.329.1	Phyca_SSR260	(GAA)4	GCGACAAGGACAAGGGTACA	GCAATGCCGTCCTTGAGTTC	292	_No FA Found
>jgi|Phyca11|110455|e_gw1.18.167.1	Phyca_SSR261	(CGA)4	TGTCACAGACGCTCTTCGAC	GAAGCCGTTTGCATCAGGTG	241	_No FA Found
>jgi|Phyca11|110762|e_gw1.19.198.1	Phyca_SSR262	(GAC)4	GCTTCACGTTCGTGTCCAAC	GGTCGATTGAGAAGCCCACA	288	_No FA Found
>jgi|Phyca11|110864|e_gw1.19.128.1	Phyca_SSR263	(GAA)4	GGAACGTTCGCGAATGGAAG	CTTAACGCGTGCTTTGCCTT	223	_No FA Found
>jgi|Phyca11|111222|e_gw1.19.315.1	Phyca_SSR264	(CCT)4	GCGGCTTACTCAACCCGATA	CGACGGTCGCATTGGAGATA	111	_No FA Found
>jgi|Phyca11|111479|e_gw1.20.545.1	Phyca_SSR265	(GTG)4	CACTGGAGAGGTATCGACGC	CAGTGCTGCAATCTCCAGGA	183	_No FA Found
>jgi|Phyca11|11175|fgenesh1_pm.PHYCAscaffold_63_#_16	Phyca_SSR266	(GCA)4	AAACGCCTGAAGGAGACGAG	AGTCTGAGCAACCGGTTCTG	269	_Zinc finger, FYVE/PHD-type
>jgi|Phyca11|111948|e_gw1.21.384.1	Phyca_SSR267	(AAG)4	TTCCGTTGTCCTGGTCCATG	GCTGTACAAGAGCGTGGTCT	297	_No FA Found
>jgi|Phyca11|112080|e_gw1.21.182.1	Phyca_SSR268	(GAC)4	TCCGAATGATGATCGCTGGG	GGCGTCGTACATGTCGGTAT	238	_No FA Found
>jgi|Phyca11|112134|e_gw1.21.215.1	Phyca_SSR269	(AAG)4	GGACATGGACACTCTCACGG	ACGTGGATGCTGTCACGAAT	257	_No FA Found
>jgi|Phyca11|11246|fgenesh1_pm.PHYCAscaffold_65_#_13	Phyca_SSR270	(GAA)4	GGTGCAGTGGAGTGGAAGAA	TCCGTCTTCACCTCTTTGGC	188	_tRNA pseudouridine synthase
>jgi|Phyca11|112787|e_gw1.23.30.1	Phyca_SSR271	(AGG)4	AGGGCCGTGAGATGATTGTG	TCACGTTGAGCCTCTGTGTC	256	_No FA Found
>jgi|Phyca11|11299|fgenesh1_pm.PHYCAscaffold_66_#_9	Phyca_SSR272	(AAG)4	CTTCCTAACGCGCCAAATGG	CCTTGTCTGATTCGGCAGGT	223	_No FA Found
>jgi|Phyca11|113170|e_gw1.23.463.1	Phyca_SSR273	(GAA)4	CGGAAGAACAACGTGGCATG	CGTAGTCCCGCATAGACACC	174	_No FA Found
>jgi|Phyca11|113547|e_gw1.24.407.1	Phyca_SSR274	(AAG)4	ACATACGCAGAAGCCCGAAA	AAAGACGTTGACAGCGTTGC	258	_No FA Found
>jgi|Phyca11|113633|e_gw1.24.406.1	Phyca_SSR275	(CGA)4	CTGGTCATCGACGTTCACGA	CGATGGGAAGATCTGGACGG	108	_No FA Found
>jgi|Phyca11|113709|e_gw1.24.605.1	Phyca_SSR276	(AAC)4	TGCTGAATGTGGCAAAGTGC	TTGGAAGACACCACGAGAGC	262	_No FA Found

>jgi|Phyca11|113733|e_gw1.24.463.1	Phyca_SSR277	(ACG)4	GCTCTACCAGGCCGATAACC	TGAGCCAACATGAGGTCGTC	255	_No FA Found
>jgi|Phyca11|113815|e_gw1.25.331.1	Phyca_SSR278	(GAA)4	CGTCCCAAGAACAACCTCGA	TGGTGCCTTCTCCGATCAAC	175	_No FA Found
>jgi|Phyca11|113894|e_gw1.25.292.1	Phyca_SSR279	(AAC)4	ACGCGAATACCGACAACGTA	CCGACACGTTAAGGACCACA	267	_No FA Found
>jgi|Phyca11|114386|e_gw1.26.189.1	Phyca_SSR280	(AAG)4	GTGGGTTTAGTGACGGCTGA	CGGTCCCATCTTCTTGGCTT	144	_No FA Found
>jgi|Phyca11|114488|e_gw1.26.525.1	Phyca_SSR281	(AGA)4	GATATCGCGCCGCCTGTAG	GCAAAACCTCCCTTGCCAAG	158	_No FA Found
>jgi|Phyca11|114557|e_gw1.26.181.1	Phyca_SSR282	(CAT)4	AGCGGATCAACCAACTCCAG	TAAATGAGTGGGTGGCACCG	253	_No FA Found
>jgi|Phyca11|114621|e_gw1.26.336.1	Phyca_SSR283	(GAT)4	GTACCCCTATGGCAAGGACG	CAGGTGGGTTCATCTGTGCT	246	_No FA Found
>jgi|Phyca11|114630|e_gw1.26.250.1	Phyca_SSR284	(ACG)4	ATTCGTTGGCCTCACTGGAG	AGTGTCTCTTTCGTCGCCTG	184	_No FA Found
>jgi|Phyca11|115003|e_gw1.27.387.1	Phyca_SSR285	(AGC)4	CAACTGGACGTGGAACGAGA	CCATATTGCGTCGACGAGGA	238	_No FA Found
>jgi|Phyca11|115111|e_gw1.27.116.1	Phyca_SSR286	(TGC)4	TTACAACCTCCGGATCAGCG	CGAGAGCGTCTTCAGGATCC	250	_No FA Found
>jgi|Phyca11|115323|e_gw1.28.493.1	Phyca_SSR287	(CCT)4	CTCCGCGTATGACGAGAACA	TTCGTCCGTGAGTTGGGAAG	263	_No FA Found
>jgi|Phyca11|115570|e_gw1.28.479.1	Phyca_SSR288	(GAA)4	CGAATTTGCGGCATCTCCAG	CCAGAGAAGTCGTCGATGGG	176	_No FA Found
>jgi|Phyca11|115678|e_gw1.29.529.1	Phyca_SSR289	(GAT)4	TGTGACGGACAAGTCGAAGG	TTACCACTGGAAGCGAGCTG	241	_No FA Found
>jgi|Phyca11|115737|e_gw1.29.335.1	Phyca_SSR290	(TGC)4	GTGCTGCTGTTTTGGAAGCA	GTCGTTGGTGTTAGCCGGTA	212	_No FA Found
>jgi|Phyca11|116254|e_gw1.30.440.1	Phyca_SSR291	(GCT)4	TAGTGAATTGGCCTCGCTGG	TGCCATCTTCGTTCAGCAGT	257	_No FA Found
>jgi|Phyca11|116425|e_gw1.30.417.1	Phyca_SSR292	(GCA)4	CGGTGTATTCGCTCGCAAAG	ATCTTCTTGGTGGCCTCTGC	198	_No FA Found
>jgi|Phyca11|116548|e_gw1.31.369.1	Phyca_SSR293	(CGA)4	CACCTCTTCGACCGGTGATT	AGAGCTTTGGCGACTGACTC	199	_No FA Found
>jgi|Phyca11|116914|e_gw1.32.324.1	Phyca_SSR294	(GAG)4	TGAACGGAGAGCACAAGGTC	CACCCTCAAGCTGAGTGGAG	252	_No FA Found
>jgi|Phyca11|117269|e_gw1.32.210.1	Phyca_SSR295	(GAA)4	CAAGAGGAGGCCAAGAAGCA	TAAAGGCGGATGGAGCGATC	296	_No FA Found
>jgi|Phyca11|117287|e_gw1.33.309.1	Phyca_SSR296	(GAA)4	GTGCGCAACAACAACCTCAT	GGAGTGCGTTGATTTGCTGG	220	_No FA Found

>jgi|Phyca11|117317|e_gw1.33.269.1	Phyca_SSR297	(CGA)4	CTGCAGTCCACTTGCAACAC	TGTGTCGTTCCTTCGGAGTG	298	_No FA Found
>jgi|Phyca11|117748|e_gw1.34.286.1	Phyca_SSR298	(AAC)4	CCACGCTAATTTGGATGCCG	GCTCACTAAGTACGGCTGCA	206	_No FA Found
>jgi|Phyca11|117813|e_gw1.34.278.1	Phyca_SSR299	(GCT)4	GCGCCAAAAGGCTTTCAAGA	GCGGTTGGCAAACTTGGTAG	183	_No FA Found
>jgi|Phyca11|117914|e_gw1.34.64.1	Phyca_SSR300	(AAG)4	ACCACTGCATATTGCCTGCT	TCTTTGGTGAAGAAAGTCCTT	248	_No FA Found
>jgi|Phyca11|117993|e_gw1.35.232.1	Phyca_SSR301	(CTT)4	CTTGCTCCGTTTGAAGACGC	AGCTCTTGTCAGCGTCAGTC	235	_No FA Found
>jgi|Phyca11|118040|e_gw1.35.268.1	Phyca_SSR302	(ACA)4	GAGTGAAGCACTGGGTACCC	GGGCAGTTGAGCTCTTGTCT	140	_No FA Found
>jgi|Phyca11|118218|e_gw1.35.225.1	Phyca_SSR303	(CTG)4	TTCTGGCATCTATAGCGCCG	ACCAACGGCCCAAATGATCT	256	_No FA Found
>jgi|Phyca11|118476|e_gw1.36.218.1	Phyca_SSR304	(CCA)4	GCTTCAGCGTCGCTAGTACT	AACAGCAACCATCAGCCTGA	270	_No FA Found
>jgi|Phyca11|11883|fgenesh1_pm.PHYCAscaffold_85_#_25	Phyca_SSR305	(AGA)4	CGGCAAAGAGTGACTTCCCT	TAACCGAAGTGCATGGCCAT	202	_Zinc finger, C2H2-type
>jgi|Phyca11|118987|e_gw1.37.245.1	Phyca_SSR306	(AGA)4	TGCTTACCTGTTGAGTCACCC	CGAGAGGATCCCGAATGGTG	218	_No FA Found
>jgi|Phyca11|119368|e_gw1.38.437.1	Phyca_SSR307	(CGA)4	CCAAGCTGGAGACTGTGGAG	CTACATGAACGCGTCCTCGT	233	_No FA Found
>jgi|Phyca11|119884|e_gw1.40.259.1	Phyca_SSR308	(AAG)4	ACAGTTGACACAGCAGCACA	TGCGTTCCATGACTCCTTCC	164	_No FA Found
>jgi|Phyca11|119888|e_gw1.40.418.1	Phyca_SSR309	(CAC)4	ACCCGAAGAATCTCCCTGGA	TAGAAGCACAAGAGCGCTCC	207	_No FA Found
>jgi|Phyca11|120570|e_gw1.41.111.1	Phyca_SSR310	(GAA)4	CGCGAAGAGACCATCCAAGA	GCCATCCATCTTGAGGCGTA	252	_No FA Found
>jgi|Phyca11|120700|e_gw1.42.303.1	Phyca_SSR311	(CTC)4	GGAACACTCTCGTCTTGCCA	GTTGAGCTGTACAGGCTGGT	194	_No FA Found
>jgi|Phyca11|120756|e_gw1.42.385.1	Phyca_SSR312	(CGA)4	TCCGCGAAACTACGGTTGAA	CGTCGAACCACACTCTCACA	268	_No FA Found
>jgi|Phyca11|120904|e_gw1.42.274.1	Phyca_SSR313	(AAG)4	TTGCCCACGAAGTAGAGCAG	GGATTGACTGACCACAGCCA	261	_No FA Found
>jgi|Phyca11|12117|fgenesh1_pm.PHYCAscaffold_96_#_14	Phyca_SSR314	(GGA)4	TGGTAAAGGAGTTGGCGGAC	GTCTTGAGCTGGTCTCGCTT	250	_Ureohydrolase
>jgi|Phyca11|121305|e_gw1.43.253.1	Phyca_SSR315	(CGA)4	CCACCAGCCTCTCCACAATT	CATCATCCCGAGCTGAGTCC	291	_No FA Found
>jgi|Phyca11|12143|fgenesh1_pm.PHYCAscaffold_97_#_18	Phyca_SSR316	(CCA)4	CGGATGGAGACGATGAGTGG	ACGAAACAAGCTCGTCCAGT	285	_DNA photolyase, N-terminal

>jgi|Phyca11|121549|e_gw1.44.184.1	Phyca_SSR317	(TGG)4	ACGTGGTTATGGCGACGATT	CGTTGCGCTTTTCCTTTCCA	168	_No FA Found
>jgi|Phyca11|121858|e_gw1.46.281.1	Phyca_SSR318	(AAG)4	GAAGCTCAACTCCCTGTTCG	ACTGGAAAGCCGCTTTCTCA	236	_No FA Found
>jgi|Phyca11|121937|e_gw1.46.430.1	Phyca_SSR319	(AGA)4	CGAAGAGGAGGACGAAGACG	AGAAGTCACGCAGGTTCTCG	203	_No FA Found
>jgi|Phyca11|122332|e_gw1.47.105.1	Phyca_SSR320	(AGA)4	AAGAAGGCATGGGCATCCTC	TCGCGTCTACTTCTTGTTGGT	213	_No FA Found
>jgi|Phyca11|12238|fgenesh1_pm.PHYCAscaffold_102_#_16	Phyca_SSR321	(CGA)4	GAAGCCCAAGAACAGTCCGA	CAGACGAGGGTGGCTTCTTT	253	_No FA Found
>jgi|Phyca11|122796|e_gw1.49.85.1	Phyca_SSR322	(AAG)4	GGCGAAGGACGATTCAGCTA	CGGTCCTTCTCCTGAGCAAG	237	_No FA Found
>jgi|Phyca11|122866|e_gw1.49.226.1	Phyca_SSR323	(TGT)4	ACTGGTAGCAGGATGGCTTG	TCTAACACGCACCTGGTCAC	228	_No FA Found
>jgi|Phyca11|123091|e_gw1.49.76.1	Phyca_SSR324	(ATG)4	AACGGCATTTTTCGCTTGCT	TGTCCCCCTTACCAAAACGG	261	_No FA Found
>jgi|Phyca11|123251|e_gw1.50.117.1	Phyca_SSR325	(ACG)4	CTAGCCCTAGTGCGAGTTCG	GCGTTCTGATGCCGAATGTC	278	_No FA Found
>jgi|Phyca11|123288|e_gw1.50.225.1	Phyca_SSR326	(TGA)4	CGACCTCGGGTTCTATCTGC	CGTCGAGGTCGTTGTCAAGA	243	_No FA Found
>jgi|Phyca11|123391|e_gw1.50.220.1	Phyca_SSR327	(GAA)4	CCCGGTCAACTACGTCGATT	GACATGCCGTTTCTCCTCCA	233	_No FA Found
>jgi|Phyca11|123752|e_gw1.51.336.1	Phyca_SSR328	(AAG)4	TGAGTATTGGCACTGGCAGG	TTGACCATTGACTCCGGGTG	146	_No FA Found
>jgi|Phyca11|123808|e_gw1.52.246.1	Phyca_SSR329	(GAA)4	GATGATTCTGGGCTACGGCA	AGCACAGTGAGTTCTCGCTC	201	_No FA Found
>jgi|Phyca11|124415|e_gw1.53.172.1	Phyca_SSR330	(GCT)4	TACGGCCAGAAACTGACACC	TCGACAAAATCTGCATGGGC	183	_No FA Found
>jgi|Phyca11|124498|e_gw1.54.130.1	Phyca_SSR331	(AAG)4	GGGAAAGGAGCGAGAACCAA	CAACCTTTCCCGAGACCTCC	280	_No FA Found
>jgi|Phyca11|124662|e_gw1.54.160.1	Phyca_SSR332	(CAG)4	CAAAGCTCGACTGCTCTGGA	ATTGAGACGACTGCACCTGG	231	_No FA Found
>jgi|Phyca11|124880|e_gw1.55.195.1	Phyca_SSR333	(GGA)4	CGACCGCTTCAAGGAGTTCT	CTACAGGTTCTTCTTGCGGAG	274	_No FA Found
>jgi|Phyca11|125539|e_gw1.59.136.1	Phyca_SSR334	(CCT)4	CATCGGCGAATTCGAGGGTA	GAATGGCATAGCTTTGCGGG	259	_No FA Found
>jgi|Phyca11|125840|e_gw1.60.6.1	Phyca_SSR335	(GAC)4	GGAGCTCTTCGGCATCTCTC	CTGCGGCATGAAATCCATCG	203	_No FA Found
>jgi|Phyca11|125936|e_gw1.60.195.1	Phyca_SSR336	(GAC)4	GAGCTCAAGGTGTCGGTTGA	GCAGCATCTCGAGACGAACT	247	_No FA Found

>jgi|Phyca11|126132|e_gw1.61.222.1	Phyca_SSR337	(AGA)4	GACTACCAGAGCACAGGCAG	TTGATGACACGAGCTCCAGC	197	_No FA Found
>jgi|Phyca11|126936|e_gw1.65.48.1	Phyca_SSR338	(GAA)4	CCCGCCAGAGAACTTTGCTA	TCCTTATTGCCCGGAACACC	204	_No FA Found
>jgi|Phyca11|127451|e_gw1.68.120.1	Phyca_SSR339	(TAC)4	TCCAGGTGCAGAACTCCAAC	TCGGCTCCAAAACTCTCCAC	277	_No FA Found
>jgi|Phyca11|127741|e_gw1.71.109.1	Phyca_SSR340	(AAG)4	CATGTTGAAGCGTACGCCAG	TTCCTTCACCTCGATTGCCC	263	_No FA Found
>jgi|Phyca11|128092|e_gw1.73.141.1	Phyca_SSR341	(GAA)4	GACGTTGGCCAGTGACGATA	TCAAACTTTGCACAGCTCGC	296	_No FA Found
>jgi|Phyca11|128447|e_gw1.76.153.1	Phyca_SSR342	(CGT)4	CTGGTGGACGAGAAGGTGAC	AGCAGTAGTGTAGCGTGTCC	131	_No FA Found
>jgi|Phyca11|128481|e_gw1.76.45.1	Phyca_SSR343	(GGT)4	ACCGACTAGGCAGCTTCAAC	TCGCATCCGGGATATCAACG	177	_No FA Found
>jgi|Phyca11|128603|e_gw1.77.203.1	Phyca_SSR344	(GAA)4	TCGTAGTTCTGCTGTTGCGT	TATCCGCGTGGTGGTATTCG	260	_No FA Found
>jgi|Phyca11|128924|e_gw1.79.51.1	Phyca_SSR345	(GGA)4	AGTCTCGTGGGGTTATGGGA	ATGAGCTTCACTTCGGCCAA	212	_No FA Found
>jgi|Phyca11|129031|e_gw1.80.51.1	Phyca_SSR346	(GTT)4	GAACTCATCCGCGACTACGT	GCCAGCGTGTTCAGAATGTC	275	_No FA Found
>jgi|Phyca11|12958|fgenesh1_pg.PHYCAscaffold_2_#_54	Phyca_SSR347	(TGC)4	CTGTTATCCTGACCCCGACG	TGAGAGTGCTCACGCTGAAG	238	_Amino acid transporter, transmembrane
>jgi|Phyca11|12991|fgenesh1_pg.PHYCAscaffold_2_#_87	Phyca_SSR348	(CTT)4	TTCGCGACTCGTTCAAGTGA	CCTGCTGAGAAGAGCGTCAA	267	_No FA Found
>jgi|Phyca11|129924|e_gw1.89.53.1	Phyca_SSR349	(AGG)4	TACGCTCGTCTTGCCAGTTT	TCACGGAAGGCCTTCTTGAC	275	_No FA Found
>jgi|Phyca11|130818|e_gw1.98.66.1	Phyca_SSR350	(CGA)4	TCCGCGAAACTACGGTTGAA	GACGTCACTGCCCTGTAACA	237	_No FA Found
>jgi|Phyca11|130982|e_gw1.100.97.1	Phyca_SSR351	(GAA)4	GCTTCCTACGTGAAGCTGGT	CTTGTCCTTGTGGGCGTAGT	273	_No FA Found
>jgi|Phyca11|13188|fgenesh1_pg.PHYCAscaffold_3_#_1	Phyca_SSR352	(AAG)4	AAGGACAAGGAAGCTCGAGC	CCAGCTCACCGATATCCGTC	283	_No FA Found
>jgi|Phyca11|13222|fgenesh1_pg.PHYCAscaffold_3_#_35	Phyca_SSR353	(GAA)4	CCTACCGTCACACTATCCGC	CGCTGTCAGCAGTACCATCT	259	_Zinc finger, C2H2-type
>jgi|Phyca11|132571|e_gw1.182.6.1	Phyca_SSR354	(CAA)4	CGCAACGACTTCACGCTTTT	CCGGACAATCCCTCAACCAA	223	_No FA Found
>jgi|Phyca11|132979|e_gw1.284.6.1	Phyca_SSR355	(TGG)4	TCCGGCTAAACAGGTGACAC	GAGGGCATATTGGGAGCGAA	288	_No FA Found
>jgi|Phyca11|133187|e_gw1.353.3.1	Phyca_SSR356	(GAA)4	GACGAGCTCGAGGATGAAGG	TCCATCGTCAACACCAGCTC	297	_No FA Found

>jgi|Phyca11|133354|e_gw1.422.1.1	Phyca_SSR357	(ACA)4	ATGCTACTGGACAGTGGTGC	TGGGATCGCATAGACAACGG	216	_No FA Found
>jgi|Phyca11|133628|e_gw1.596.4.1	Phyca_SSR358	(CGA)4	ATCCGCCACTTCGTGAACTT	TTTCAGCTCGTCCAACTGCT	251	_No FA Found
>jgi|Phyca11|13470|fgenesh1_pg.PHYCAscaffold_3_#_283	Phyca_SSR359	(GAC)4	AGCTCAACATGGTGTCGAGG	TCGTCTTCTTCTGGCTGCTG	181	_AAA ATPase, conserved site
>jgi|Phyca11|13667|fgenesh1_pg.PHYCAscaffold_4_#_190	Phyca_SSR360	(AGA)4	CATCTTCGGGAGGATCTGGC	GGCCCTTAAGCTGGAACCAT	219	_No FA Found
>jgi|Phyca11|13698|fgenesh1_pg.PHYCAscaffold_4_#_221	Phyca_SSR361	(GAG)4	CGCTCGCCCCTAGTCTTAAG	GGGCACGTTGATGACTCTGA	192	_Phox-like
>jgi|Phyca11|13754|fgenesh1_pg.PHYCAscaffold_4_#_277	Phyca_SSR362	(AAC)4	GTGGATTACCGTCAAACGCG	GAGTAGATCGACGCCTGGTG	260	_WD40 repeat-like
>jgi|Phyca11|13903|fgenesh1_pg.PHYCAscaffold_5_#_117	Phyca_SSR363	(GAA)4	CGAAGCACAGTTCGCTAAGC	TTTTCCTCCTCGTCTGCGTC	252	_SART-1 protein
>jgi|Phyca11|14020|fgenesh1_pg.PHYCAscaffold_5_#_234	Phyca_SSR364	(TCG)4	ACACCTCAGAAACGCGTGAT	GCCAGCTCACGTTCCAGATA	197	_TonB box, conserved site
>jgi|Phyca11|14052|fgenesh1_pg.PHYCAscaffold_5_#_266	Phyca_SSR365	(GAA)4	AGCGCTCAATTTGCACGAAG	GGGACGAAGCGTTGTCTACA	297	_Homeodomain-like
>jgi|Phyca11|14339|fgenesh1_pg.PHYCAscaffold_7_#_78	Phyca_SSR366	(AAG)4	AGAACCCGCTCCAAGATTCG	CACGTCGATCTTCTGGCTCA	295	_No FA Found
>jgi|Phyca11|14853|fgenesh1_pg.PHYCAscaffold_9_#_229	Phyca_SSR367	(ACG)4	GTTACTACGACGCCGAGGAG	CTTTCCCTGCTCGACCCATT	149	_No FA Found
>jgi|Phyca11|14936|fgenesh1_pg.PHYCAscaffold_10_#_82	Phyca_SSR368	(GAA)4	CCAGTTGATGAGGCGAAGGA	TCCTCTGCTGACTCTTCCGA	218	_No FA Found
>jgi|Phyca11|15239|fgenesh1_pg.PHYCAscaffold_12_#_64	Phyca_SSR369	(GAA)4	TGATCGGCTTCAAGAACGAGA	TCGCATTTGGTCAGACGTGA	278	_No FA Found
>jgi|Phyca11|15428|fgenesh1_pg.PHYCAscaffold_13_#_116	Phyca_SSR370	(CTT)4	ACCACGCTCAGAGAAGTGTG	GGCGGTCCCAAATAGAACCA	144	_No FA Found
>jgi|Phyca11|15441|fgenesh1_pg.PHYCAscaffold_13_#_129	Phyca_SSR371	(GGC)4	CCGCGGACGACACAAATAGA	CACCGTGTTCGTCTCTTCGA	267	_No FA Found
>jgi|Phyca11|15709|fgenesh1_pg.PHYCAscaffold_15_#_47	Phyca_SSR372	(GAT)4	AGTCGTGGCTGTTACGGAAG	TACTCGTGCACGTTCTTCCC	258	_No FA Found
>jgi|Phyca11|15727|fgenesh1_pg.PHYCAscaffold_15_#_65	Phyca_SSR373	(GCT)4	CTGGAGCGATCACGTATGCT	GACCTCCGCAGTGGTGATAG	278	_Di-copper centre-containing
>jgi|Phyca11|16136|fgenesh1_pg.PHYCAscaffold_18_#_24	Phyca_SSR374	(GAT)4	GTCGCCCAACAAGACAGAGA	TGTGACTCCAAGCCGTTTCA	160	_No FA Found
>jgi|Phyca11|16158|fgenesh1_pg.PHYCAscaffold_18_#_46	Phyca_SSR375	(ATG)4	ATATGCTGTACCTGGCGTCG	ATACTTTCGCCCGTAGCTGG	144	_No FA Found
>jgi|Phyca11|16290|fgenesh1_pg.PHYCAscaffold_19_#_37	Phyca_SSR376	(ATC)4	CGTCAGATGATCCTCGGTCG	GTGGATGAAGGTTCCCAGCA	288	_Permease for cytosine/purines, uracil, thiamine, allant

>jgi|Phyca11|16362|fgenesh1_pg.PHYCAscaffold_19_#_109	Phyca_SSR377	(AAG)4	TAAGGGAAACAACGCCAGCA	ACTGGAGGAGGAGCTACAGG	126	_Ataxin-2, N-terminal
>jgi|Phyca11|16541|fgenesh1_pg.PHYCAscaffold_20_#_129	Phyca_SSR378	(GGA)4	CGATACACGAAGCAGCAACG	TCTACTTGCACCGCCGAAAT	207	_ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transpo
>jgi|Phyca11|16551|fgenesh1_pg.PHYCAscaffold_20_#_139	Phyca_SSR379	(CCA)4	ACGGAACTTCCAACGATCCC	ATTGTCGGCTCCAGAGTTGG	281	_No FA Found
>jgi|Phyca11|16615|fgenesh1_pg.PHYCAscaffold_21_#_32	Phyca_SSR380	(GCA)4	GGAAGGCCAACAGCTACGTA	CCCTCTTCTTGGGCGCTTAA	217	_No FA Found
>jgi|Phyca11|16661|fgenesh1_pg.PHYCAscaffold_21_#_78	Phyca_SSR381	(GGT)4	AAGCCGGCGTTATAAGTGCT	CGTCACTGCTTCCGTCTTCT	251	_No FA Found
>jgi|Phyca11|16763|fgenesh1_pg.PHYCAscaffold_22_#_42	Phyca_SSR382	(AGA)4	GAGGAGATGGGCCAGTATGC	AACGGTCACCATCTGCACTT	279	_No FA Found
>jgi|Phyca11|16777|fgenesh1_pg.PHYCAscaffold_22_#_56	Phyca_SSR383	(GAG)4	GAGATGGTGGCCACTGTGAA	AGTGACTCACAGCCTTCTGC	283	_DNA/RNA helicase, ATP-dependent, DEAH-box type,
>jgi|Phyca11|16932|fgenesh1_pg.PHYCAscaffold_23_#_79	Phyca_SSR384	(CTT)4	ACCTTCGCGACCCAATCAAG	TCACCACCACCCTGAAGAGA	107	_No FA Found
>jgi|Phyca11|17201|fgenesh1_pg.PHYCAscaffold_26_#_4	Phyca_SSR385	(GGC)4	CGTTTTAAGCGCCCGATCTG	CCCTTCTTCAAGCTGTCCGT	176	_No FA Found
>jgi|Phyca11|17462|fgenesh1_pg.PHYCAscaffold_27_#_145	Phyca_SSR386	(ACG)4	CTGACCTCGTGGATCCGAAG	CGATGACCTTGTCCTTGGCT	201	_Bacterial extracellular solute-binding, family 1
>jgi|Phyca11|17528|fgenesh1_pg.PHYCAscaffold_28_#_63	Phyca_SSR387	(AAG)4	GAAGACAAGAGGTGGACGCA	CAGGGTCGTCCGTATCGAAC	245	_Chromo domain-like
>jgi|Phyca11|17536|fgenesh1_pg.PHYCAscaffold_28_#_71	Phyca_SSR388	(CGA)4	CCAGACTTCGCCTTCGACTT	CTTCCTCACTGAACGGACCC	218	_Thaumatin, pathogenesis-related
>jgi|Phyca11|17545|fgenesh1_pg.PHYCAscaffold_28_#_80	Phyca_SSR389	(GAA)4	GGCGATCGACAGACTATCGG	ACCTCGTACAGCGCTGAAAA	264	_MFS general substrate transporter
>jgi|Phyca11|17598|fgenesh1_pg.PHYCAscaffold_29_#_25	Phyca_SSR390	(ACG)4	TCTGTGCGACGTGTCATCAA	CGCATTGGTAGCCGATGTTG	232	_Glycoside hydrolase, family 3, C-terminal
>jgi|Phyca11|17762|fgenesh1_pg.PHYCAscaffold_30_#_73	Phyca_SSR391	(CAA)4	AGATCGCTAAGGTTTCGGCC	TCTATCATGCTGCGTCGGTC	106	_Zinc finger, FYVE/PHD-type
>jgi|Phyca11|17836|fgenesh1_pg.PHYCAscaffold_31_#_14	Phyca_SSR392	(GTG)4	TGCTGGTGGTAGTGACGAAC	GCCACCACCAGTATGGACTC	184	_No FA Found
>jgi|Phyca11|18035|fgenesh1_pg.PHYCAscaffold_32_#_110	Phyca_SSR393	(CAT)4	ACTACACGCCGGAAATCGAG	CGAAGTCTCCGCCATACTCC	270	_MFS general substrate transporter
>jgi|Phyca11|18366|fgenesh1_pg.PHYCAscaffold_36_#_6	Phyca_SSR394	(AAG)4	ATCCCGTCACCGTCAAAGTC	CCTGTAGGATGGAGGGTGGA	277	_No FA Found
>jgi|Phyca11|18396|fgenesh1_pg.PHYCAscaffold_36_#_36	Phyca_SSR395	(TTC)4	CATGGCTACACGCGAGGTAT	TCGCCACGTTGATATTGGGT	266	_ABC transporter-like
>jgi|Phyca11|18434|fgenesh1_pg.PHYCAscaffold_36_#_74	Phyca_SSR396	(GGA)4	CACGACGAGGAAGAAGCTGT	TGGTCCTTCAACTCGTCACG	212	_No FA Found

>jgi|Phyca11|18501|fgenesh1_pg.PHYCAscaffold_37_#_65	Phyca_SSR397	(AAG)4	TACTGGACCAAGCGGCAATT	ACTCAAGAGCTGCCATCCAC	229	_Pleckstrin-like
>jgi|Phyca11|18579|fgenesh1_pg.PHYCAscaffold_38_#_25	Phyca_SSR398	(CTG)4	ATGACGTCGAGGGTGTTGC	TCTGCTGGAAGTTCTGCTGG	214	_SelT/selW/selH selenoprotein
>jgi|Phyca11|18625|fgenesh1_pg.PHYCAscaffold_38_#_71	Phyca_SSR399	(CAA)4	CGATTACTGCCTTGCTTCGC	GGGAACGTAACGGGTTGGAT	217	_No FA Found
>jgi|Phyca11|18835|fgenesh1_pg.PHYCAscaffold_41_#_29	Phyca_SSR400	(GAA)4	CGGAAAAGGGACGGAGACAA	TCTTCGAGCAACCTTCGCTT	141	_Transcription elongation factor, TFIIS/elongin A/CRSP
>jgi|Phyca11|18874|fgenesh1_pg.PHYCAscaffold_41_#_68	Phyca_SSR401	(AAG)4	CCCGTGTTGATATACGCCCA	AGCTCCATTTCCTGCTTGCT	203	_No FA Found
>jgi|Phyca11|19105|fgenesh1_pg.PHYCAscaffold_43_#_99	Phyca_SSR402	(AGA)4	TTGGAACTGGGATTCGACGG	CGGCTTCCTTGGTACCCTTT	245	_Proteinase inhibitor I1, Kazal
>jgi|Phyca11|19338|fgenesh1_pg.PHYCAscaffold_47_#_42	Phyca_SSR403	(TGC)4	GCCACCGTAACCTGAGGAAA	GGGCCTTGGCCTTCTTGTAA	228	_No FA Found
>jgi|Phyca11|19543|fgenesh1_pg.PHYCAscaffold_49_#_56	Phyca_SSR404	(GAG)4	ACTTCGAGCCTGTGGTGAAG	CCTTTTGGTGCTCCTTGTGC	195	_Ran Binding Protein 1
>jgi|Phyca11|19605|fgenesh1_pg.PHYCAscaffold_50_#_27	Phyca_SSR405	(AAG)4	GCCTGTTCGTACTGGACCAA	TCAGTGGCGGCTTCTTTCAT	295	_No FA Found
>jgi|Phyca11|19611|fgenesh1_pg.PHYCAscaffold_50_#_33	Phyca_SSR406	(ACT)4	GGCTGCTACCACTGAAGGTT	CCGAAGCATCAGTGTCCACT	161	_No FA Found
>jgi|Phyca11|19718|fgenesh1_pg.PHYCAscaffold_51_#_39	Phyca_SSR407	(AGG)4	GATAGTGAAGCCGACGGAGG	CCTTTCTCCGCCTGTTGAGT	197	_No FA Found
>jgi|Phyca11|19734|fgenesh1_pg.PHYCAscaffold_51_#_55	Phyca_SSR408	(GAC)4	GGAGACGACGATCGAGGTTC	GAGTAGTGGCCGTGGTCAAA	190	_No FA Found
>jgi|Phyca11|20009|fgenesh1_pg.PHYCAscaffold_55_#_39	Phyca_SSR409	(GCT)4	GAGGCAAGGGCAAGAAGAGT	TCCTTGGCTGAAGCTACTGC	223	_No FA Found
>jgi|Phyca11|20100|fgenesh1_pg.PHYCAscaffold_57_#_51	Phyca_SSR410	(GTG)4	TGATCGCATCGGTCATCCTG	GTACGTCACGTAGCAACCCA	200	_Amino acid transporter, transmembrane
>jgi|Phyca11|20210|fgenesh1_pg.PHYCAscaffold_59_#_38	Phyca_SSR411	(CAC)4	AACTCGGCAGCTCCTACAAC	CTAGACGACGACGGTAGTGC	120	_No FA Found
>jgi|Phyca11|20214|fgenesh1_pg.PHYCAscaffold_59_#_42	Phyca_SSR412	(TCC)4	GCAAGACGAGGATCTCCGAG	CCTTTTGACTCGGCACTCCT	272	_No FA Found
>jgi|Phyca11|20425|fgenesh1_pg.PHYCAscaffold_64_#_11	Phyca_SSR413	(ACA)4	AAGCGATTACACCAGTGGGG	CACTCTTTTTCCCACTGCGC	107	_No FA Found
>jgi|Phyca11|20760|fgenesh1_pg.PHYCAscaffold_72_#_24	Phyca_SSR414	(AAG)4	CCGGATGAGAAGACTCGAGC	ACTCGTGTGGATCCTCTCGA	246	_No FA Found
>jgi|Phyca11|20813|fgenesh1_pg.PHYCAscaffold_73_#_13	Phyca_SSR415	(AAG)4	GCCAAGAAGGAGAAGCGTCT	CATTGTTCCCTTCCGGTCCA	148	_MRG
>jgi|Phyca11|21102|fgenesh1_pg.PHYCAscaffold_82_#_10	Phyca_SSR416	(GCA)4	GCGCAAGTTTCAGAACAGCA	TAGTGCTTCATCGGCCCTTG	143	_Homeodomain-like

>jgi|Phyca11|21130|fgenesh1_pg.PHYCAscaffold_83_#_3	Phyca_SSR417	(GAA)4	ATGCCGAGATCGAGAAGCTG	CGGAGGAGTTGGCACTTTCT	146	_Myosin head, motor region
>jgi|Phyca11|21279|fgenesh1_pg.PHYCAscaffold_87_#_30	Phyca_SSR418	(GAC)4	TTTCAAGACGTCGAGGTGCA	ACTCGCTGATGACACTGGTG	247	_No FA Found
>jgi|Phyca11|21332|fgenesh1_pg.PHYCAscaffold_91_#_1	Phyca_SSR419	(GTG)4	GTCGTGTTGCTGCAGGTACT	CACAAGCGTCATTACCAGCG	162	_No FA Found
>jgi|Phyca11|21500|fgenesh1_pg.PHYCAscaffold_98_#_4	Phyca_SSR420	(CTT)4	TTCGCGACTCGTTCAAGTGA	TTGAGAAGAGCGTCGACGTC	263	_No FA Found
>jgi|Phyca11|21562|fgenesh1_pg.PHYCAscaffold_101_#_1	Phyca_SSR421	(CTT)4	TCACCTCATTCGAGTGACGT	CATCAGCTCACGCATGTGTG	237	_No FA Found
>jgi|Phyca11|21585|fgenesh1_pg.PHYCAscaffold_102_#_17	Phyca_SSR422	(AGA)4	GAGGAGATGGGCCAGTATGC	AACGGTCACCATCTGCACTT	279	_No FA Found
>jgi|Phyca11|21636|fgenesh1_pg.PHYCAscaffold_104_#_20	Phyca_SSR423	(TCT)4	TCTCGAAAAGCAGCGGATGT	TTCGACTTCCAGCTGCAACT	208	_GAF
>jgi|Phyca11|21725|fgenesh1_pg.PHYCAscaffold_111_#_6	Phyca_SSR424	(CTA)4	GGCAATTTTGACCGATCGGG	TGATGCGGTGACTGAACTGG	129	_No FA Found
>jgi|Phyca11|21726|fgenesh1_pg.PHYCAscaffold_111_#_7	Phyca_SSR425	(CTA)4	ACGACATTGGTGGAGGCAAT	GATGATGCGGCGACTGAACT	145	_No FA Found
>jgi|Phyca11|21824|fgenesh1_pg.PHYCAscaffold_134_#_1	Phyca_SSR426	(GAA)4	AGCGACGATGTTCAACCAGT	CACCCGCTGTTTCCAACTTG	248	_No FA Found
>jgi|Phyca11|21825|fgenesh1_pg.PHYCAscaffold_134_#_2	Phyca_SSR427	(GCT)4	ATGCAAGACGACGCGTTCA	CCAGAACAGCAGCAGACGTA	279	_No FA Found
>jgi|Phyca11|21843|fgenesh1_pg.PHYCAscaffold_151_#_2	Phyca_SSR428	(GCC)4	AGCGCGTCTTCAAGACTTCA	ACATCTCGGACTTCAGACGC	234	_No FA Found
>jgi|Phyca11|21926|fgenesh1_pg.PHYCAscaffold_227_#_1	Phyca_SSR429	(GAA)4	GATCAATTGGCTGGGGCTCT	AGCGCCTTACCAAGCTTCTT	278	_No FA Found
>jgi|Phyca11|21930|fgenesh1_pg.PHYCAscaffold_232_#_2	Phyca_SSR430	(GCT)4	ACCATGTTCCTAGCGTTGGG	CCAGTACACGAACGTCCCAA	195	_ABC transporter-like
>jgi|Phyca11|21962|fgenesh1_pg.PHYCAscaffold_278_#_1	Phyca_SSR431	(GCA)4	AAGCTACGGCATCTGTGGAC	GCGTCTCACCTTCTTCCTCC	288	_No FA Found
>jgi|Phyca11|22019|fgenesh1_pg.PHYCAscaffold_408_#_1	Phyca_SSR432	(GAA)4	GCGACGCAGAGTATCGTACA	TCAGTTGACGCTGATGGCTT	185	_No FA Found
>jgi|Phyca11|22048|fgenesh1_pg.PHYCAscaffold_504_#_1	Phyca_SSR433	(ACG)4	CGACACGAACAACGAGATGC	ACCGGAGACTGGATACTGCT	167	_No FA Found
>jgi|Phyca11|22115|fgenesh1_pg.PHYCAscaffold_787_#_1	Phyca_SSR434	(GGC)4	CGTTTTAAGCGCCCGATCTG	CCCTTCTTCAAGCTGTCCGT	176	_No FA Found
>jgi|Phyca11|22116|fgenesh1_pg.PHYCAscaffold_807_#_1	Phyca_SSR435	(CCA)4	GTTCGTCACTACCACCAGCA	TGATGAACAGGTCCGTGGTG	266	_No FA Found
>jgi|Phyca11|36374|gw1.49.21.1	Phyca_SSR436	(GTG)4	TCCTTCCGTGCGATTGACTC	CTCGACCCTCTTCGATCACG	115	_GTP-binding

>jgi|Phyca11|37532|gw1.25.22.1	Phyca_SSR437	(TTC)4	GCCTCTTCGTTGGCTTCTCT	GCGAACCAGGACAAGAAGGA	142	_No FA Found
>jgi|Phyca11|38494|gw1.23.54.1	Phyca_SSR438	(GGT)4	TAAACATCTCGACAGCGCCG	ACCATCACTGCGACCCATAC	160	_Alpha/beta hydrolase fold-1
>jgi|Phyca11|39725|gw1.44.38.1	Phyca_SSR439	(AGA)4	AAACAGTGTCGCGAACGTTG	CATTATCCGTTCGGCCAGGT	157	_Homeodomain-like
>jgi|Phyca11|4125|fgenesh1_pm.PHYCAscaffold_1_#_38	Phyca_SSR440	(GCA)4	GACATTCCTGAGGCGTGTGA	TTGACCGTTCCCAGGTGATG	210	_Zinc finger, CCHC-type
>jgi|Phyca11|41367|gw1.54.58.1	Phyca_SSR441	(GGA)4	AGACGCTACTGGAAAAGGCC	TTCCCACTGCCATCTTCGTC	196	_Calcium-binding EF-hand
>jgi|Phyca11|4215|fgenesh1_pm.PHYCAscaffold_1_#_128	Phyca_SSR442	(ACC)4	TGTCGGTGGATCTGTGAACG	ATGCGGTAGCCCTTCTTCTG	258	_Bacterial transferase hexapeptide repeat
>jgi|Phyca11|4262|fgenesh1_pm.PHYCAscaffold_1_#_175	Phyca_SSR443	(CAG)4	CGACCAGAAACTTCGTCCGA	GCTTGGAGCTCTTCGAGGAT	247	_Kinesin, motor region
>jgi|Phyca11|43056|gw1.415.4.1	Phyca_SSR444	(AGA)4	CTGGCCTATGCATTGGGACA	TGCAAGCGTAAACACGAAGC	184	_No FA Found
>jgi|Phyca11|44536|gw1.53.62.1	Phyca_SSR445	(CAG)4	GAATCGCCGTGGAATTGCTC	CGAGTACATTGGGCAGACGT	284	_ABC transporter-like
>jgi|Phyca11|4484|fgenesh1_pm.PHYCAscaffold_2_#_80	Phyca_SSR446	(AAC)4	GAGGCTGATGTGGTGACGAA	TAGTTGCGGTGGTTCCTGTC	257	_Protein kinase-like
>jgi|Phyca11|4495|fgenesh1_pm.PHYCAscaffold_2_#_91	Phyca_SSR447	(CAG)4	GACAGAGCTTTCACGCCTCT	CCTCGAGAACGCCAGAGATC	254	_No FA Found
>jgi|Phyca11|4516|fgenesh1_pm.PHYCAscaffold_2_#_112	Phyca_SSR448	(GAT)4	CAAGCACTTTCGTTCCGGTG	TCGAAAAAGGATGCCACCCA	265	_Rhodanese-like
>jgi|Phyca11|4629|fgenesh1_pm.PHYCAscaffold_2_#_225	Phyca_SSR449	(AGC)4	TGACCTCGTTCACCGAAGTG	CAGACAAAGCGATGCGGATG	279	_WD40 repeat-like
>jgi|Phyca11|46491|gw1.57.138.1	Phyca_SSR450	(CTG)4	TCCAGTCAACCCAGCAGTTC	CGCTCGATCCTTGTAGCCTT	253	_No FA Found
>jgi|Phyca11|49642|gw1.39.327.1	Phyca_SSR451	(CAG)4	TTCAGTGGGCTTCGACATCC	TCGCCTCCTCTATCTCCAGG	270	_Zinc finger, FYVE/PHD-type
>jgi|Phyca11|5021|fgenesh1_pm.PHYCAscaffold_4_#_109	Phyca_SSR452	(AGC)4	TGACAAGAACTCGCGGGAAA	AGGAGGAGGTACAGCCACAT	292	_No FA Found
>jgi|Phyca11|502544|fgenesh2_kg.PHYCAscaffold_1_#_4_#_Contig29	Phyca_SSR453	(TGC)4	CAGTGAACACGCTCGCAAAA	CGTCAGTGGTGCATCCTTCT	254	_No FA Found
>jgi|Phyca11|502568|fgenesh2_kg.PHYCAscaffold_1_#_28_#_409799	Phyca_SSR454	(CAG)4	CAGCTTCACCTACACCGGAA	GGTTTTGGCTGGCGAGATTC	178	_No FA Found
>jgi|Phyca11|502583|fgenesh2_kg.PHYCAscaffold_1_#_43_#_410086	Phyca_SSR455	(AAG)4	TTAGGGATTTCTCGGCAGCG	ACCCAGTCGGAGCACTCTAT	261	_No FA Found
>jgi|Phyca11|502585|fgenesh2_kg.PHYCAscaffold_1_#_45_#_Contig9	Phyca_SSR456	(GCA)4	GTGTACCAGCTGCTGTCCTT	CCCACAGAGTCTGCACAGTC	286	_No FA Found

>jgi|Phyca11|502624|fgenesh2_kg.PHYCAscaffold_1_#_84_#_Contig2	Phyca_SSR457	(GAA)4	CGGGTATGGTGGAAGGCATT	TCTTCCAGCAACCGACACTC	271	_No FA Found
>jgi|Phyca11|502676|fgenesh2_kg.PHYCAscaffold_1_#_136_#_410084	Phyca_SSR458	(CAC)4	CGGATACATCACGCACCTGA	CAGTCCTAGAGTAACCTGCAC	299	_No FA Found
>jgi|Phyca11|502777|fgenesh2_kg.PHYCAscaffold_1_#_237_#_gi|1890	Phyca_SSR459	(GAC)4	AGAAGGTTCGGTTAGCACGG	CGAAGTCTAGACGGGGCTTC	165	_No FA Found
>jgi|Phyca11|502808|fgenesh2_kg.PHYCAscaffold_1_#_268_#_409872	Phyca_SSR460	(TGC)4	CGTGATGCAGCGGTATGTTG	TCTTGAAGGAAATCGCGGCT	231	_No FA Found
>jgi|Phyca11|502905|fgenesh2_kg.PHYCAscaffold_2_#_21_#_gi|18908	Phyca_SSR461	(AAG)4	GTGACGAAAGCCCACCAGTA	AGTAGTAATCGGCGCTGGTG	254	_No FA Found
>jgi|Phyca11|502928|fgenesh2_kg.PHYCAscaffold_2_#_44_#_gi|18908	Phyca_SSR462	(GCT)4	TCAGCTACTATCTCGGGCGA	TCATCCCCATCCGAGTCCTT	193	_No FA Found
>jgi|Phyca11|503021|fgenesh2_kg.PHYCAscaffold_2_#_137_#_Contig	Phyca_SSR463	(AGG)4	TATCCGCATCGTGAGCAGTC	CTCTCCTTGCACACCTCCAG	222	_No FA Found
>jgi|Phyca11|503108|fgenesh2_kg.PHYCAscaffold_2_#_224_#_Contig	Phyca_SSR464	(AAG)4	AGGAGGATGGTTCCCCAGAA	ACGAGCTCCACCGTTTTGAT	258	_No FA Found
>jgi|Phyca11|503255|fgenesh2_kg.PHYCAscaffold_3_#_120_#_Contig	Phyca_SSR465	(AGA)4	ACTCGAGCAATGACCTGGTG	AGTGCTTCGAGTTACCCGTG	285	_No FA Found
>jgi|Phyca11|503269|fgenesh2_kg.PHYCAscaffold_3_#_134_#_gi|1890	Phyca_SSR466	(GGA)4	TCGAAGATGGTATCTGGCGC	CGTCTACCAGTTCGCAGAGG	264	_No FA Found
>jgi|Phyca11|503336|fgenesh2_kg.PHYCAscaffold_3_#_201_#_Contig	Phyca_SSR467	(GTC)4	AGCAAGTCAAGATGGCCCTC	CGGGCTCAATCGTCGACATA	240	_No FA Found
>jgi|Phyca11|503349|fgenesh2_kg.PHYCAscaffold_3_#_214_#_410126	Phyca_SSR468	(TCT)4	TCAGCAGTGGACCGTGATTT	TCCCGTCGGTTGTTAAGGTG	273	_No FA Found
>jgi|Phyca11|503358|fgenesh2_kg.PHYCAscaffold_3_#_223_#_Contig	Phyca_SSR469	(CGA)4	CAAGAATGGCAAAACCGGCA	TGAACGCGAAGATCCACGAA	142	_No FA Found
>jgi|Phyca11|503385|fgenesh2_kg.PHYCAscaffold_3_#_250_#_Contig	Phyca_SSR470	(AAG)4	CTGCGCACTTTGATACGTCG	GCCTCCTCTGACCTGTTCAC	238	_No FA Found
>jgi|Phyca11|503414|fgenesh2_kg.PHYCAscaffold_3_#_279_#_Contig	Phyca_SSR471	(ACC)4	GCTCGCAGATTACACAGGCT	GGTGGACAGCGAACTCATGA	264	_No FA Found
>jgi|Phyca11|503428|fgenesh2_kg.PHYCAscaffold_3_#_293_#_409758	Phyca_SSR472	(CTG)4	TGCTCAAAAGGCCGATGCTA	CTTCCAGCTCAGCACTGACA	260	_No FA Found
>jgi|Phyca11|503436|fgenesh2_kg.PHYCAscaffold_3_#_301_#_410203	Phyca_SSR473	(GCT)4	GCGTCGAGAACTGGAGGAAA	GGAGAGAGATGCCTGCGTAC	226	_No FA Found
>jgi|Phyca11|503447|fgenesh2_kg.PHYCAscaffold_3_#_312_#_409709	Phyca_SSR474	(AGA)4	ACAAGGTCTCGGCCATTGAG	GCGTGCTCAATTGCCATGAT	160	_No FA Found
>jgi|Phyca11|503479|fgenesh2_kg.PHYCAscaffold_4_#_18_#_gi|18908	Phyca_SSR475	(GTG)4	CTCAACTGGGCGAGTCCAAT	AGCAACATCTTCGAGGGGTG	203	_No FA Found
>jgi|Phyca11|503499|fgenesh2_kg.PHYCAscaffold_4_#_38_#_Contig2	Phyca_SSR476	(GCA)4	CGTGCGTCTTCAGGAGAGTT	GCCATCTCCTTGTTCCTGCT	106	_No FA Found

>jgi|Phyca11|503535|fgenesh2_kg.PHYCAscaffold_4_#_74_#_gi|1890	Phyca_SSR477	(AGG)4	TACGGGTCAGGAGAGCATCA	TTCACGTGCTTCTCGTCCTC	141	_No FA Found
>jgi|Phyca11|503539|fgenesh2_kg.PHYCAscaffold_4_#_78_#_410413	Phyca_SSR478	(AAG)4	CGACGTGGACGATGCAGATA	GGAGCGGGCCTCTATTTCTT	198	_No FA Found
>jgi|Phyca11|503590|fgenesh2_kg.PHYCAscaffold_4_#_129_#_Contig	Phyca_SSR479	(TGC)4	TCATGGTAACTGCGATCCCG	GGCTGTTCTGCTTGTTGTGG	180	_No FA Found
>jgi|Phyca11|503618|fgenesh2_kg.PHYCAscaffold_4_#_157_#_Contig	Phyca_SSR480	(CAG)4	CGTCAACTGTTACGGCCTCT	ATCTATCAGTGGCTTCGGCG	239	_No FA Found
>jgi|Phyca11|503634|fgenesh2_kg.PHYCAscaffold_4_#_173_#_Contig	Phyca_SSR481	(GAC)4	ACACTCCTCAAGACGTGCTG	AGAGAAGTGCGTGAATGGGG	259	_No FA Found
>jgi|Phyca11|503737|fgenesh2_kg.PHYCAscaffold_4_#_276_#_40981	Phyca_SSR482	(CCG)4	GAAGAAGCGCTTGACATGGC	TGATCCTCACGCAAAGCCTT	255	_No FA Found
>jgi|Phyca11|503769|fgenesh2_kg.PHYCAscaffold_4_#_308_#_40971	Phyca_SSR483	(ATG)4	CAGACCCAAGCTCAAGCACT	GAGATCGTCTCGGGCTTCTG	121	_No FA Found
>jgi|Phyca11|503783|fgenesh2_kg.PHYCAscaffold_4_#_322_#_Contig	Phyca_SSR484	(TGA)4	GCCAGTTCTTCTCACGTGGA	ACGGAGCGTTGGTCAAATCT	192	_No FA Found
>jgi|Phyca11|503791|fgenesh2_kg.PHYCAscaffold_4_#_330_#_40991	Phyca_SSR485	(AGA)4	CTTGCGTCAACAGTTGCAGG	TCGTTCCTGTTGTTCCTCCG	286	_No FA Found
>jgi|Phyca11|503808|fgenesh2_kg.PHYCAscaffold_4_#_347_#_40965	Phyca_SSR486	(CGT)4	CGAACTGCCGGGAAACTTTG	TAGAACGTGGGCAACTGGTC	270	_No FA Found
>jgi|Phyca11|503821|fgenesh2_kg.PHYCAscaffold_4_#_360_#_Contig	Phyca_SSR487	(GAA)4	GAGGATCGAGGAGCATCGTG	GAGCTGCTGATACAGTCGCT	192	_No FA Found
>jgi|Phyca11|503853|fgenesh2_kg.PHYCAscaffold_5_#_17_#_Contig1	Phyca_SSR488	(GAG)4	CGCCGATATGACAGTGTCGA	CGGGCATCTATTCCTCGCTT	227	_No FA Found
>jgi|Phyca11|503894|fgenesh2_kg.PHYCAscaffold_5_#_58_#_Contig3	Phyca_SSR489	(AAG)4	TGAACACGCACATCTTCCGA	ATGGACCTCCCCATCCGAAT	116	_No FA Found
>jgi|Phyca11|503942|fgenesh2_kg.PHYCAscaffold_5_#_106_#_41019	Phyca_SSR490	(CCA)4	CAGCAACCGTACTACCAGCA	GCCACCTCCATAACCACCTC	231	_No FA Found
>jgi|Phyca11|503954|fgenesh2_kg.PHYCAscaffold_5_#_118_#_40972	Phyca_SSR491	(GCT)4	TGAAGGCGAAGGACATGGAC	CCAGAGGCTCATCATCGTCC	273	_No FA Found
>jgi|Phyca11|503971|fgenesh2_kg.PHYCAscaffold_5_#_135_#_41019	Phyca_SSR492	(CAG)4	GCACCACCACGGAAAACATC	CACGATATGCACGTCCTCGA	133	_No FA Found
>jgi|Phyca11|504028|fgenesh2_kg.PHYCAscaffold_5_#_192_#_Contig	Phyca_SSR493	(CAA)4	GAAATTGATGCTCCGCCACC	TATCCAGGATTCGCTTGGGC	188	_No FA Found
>jgi|Phyca11|504040|fgenesh2_kg.PHYCAscaffold_5_#_204_#_Contig	Phyca_SSR494	(CAG)4	GAGCAGCAACGCAAACAGAA	ATCGTGGCCGTTGTTTGTTG	170	_No FA Found
>jgi|Phyca11|504052|fgenesh2_kg.PHYCAscaffold_5_#_216_#_Contig	Phyca_SSR495	(AGC)4	CCTTGTTCTGTTGGAAGCGC	GTTCCAGATCCGAGTGCACA	287	_No FA Found
>jgi|Phyca11|504097|fgenesh2_kg.PHYCAscaffold_6_#_14_#_Contig4	Phyca_SSR496	(CGA)4	ACGCTAGCGACCAGTTCTTC	AAATTCCGGCATGTCCTCGT	293	_No FA Found

>jgi|Phyca11|504098|fgenesh2_kg.PHYCAscaffold_6_#_15_#_4102091	Phyca_SSR497	(CGA)4	ATGCGTTCTCGGACATGGAG	CGCCATGTCTGGGTCTTCAT	119	_No FA Found
>jgi|Phyca11|504102|fgenesh2_kg.PHYCAscaffold_6_#_19_#_Contig6	Phyca_SSR498	(TCT)4	TGGACTCCTTGCCTCGTTTC	GCTTCATTAGGCAATGGGCG	256	_No FA Found
>jgi|Phyca11|504124|fgenesh2_kg.PHYCAscaffold_6_#_41_#_Contig4	Phyca_SSR499	(AAG)4	GCTGGCTGAGAACGAGACAT	GTTCTCGGCCTTCTTCAGCT	178	_No FA Found
>jgi|Phyca11|504128|fgenesh2_kg.PHYCAscaffold_6_#_45_#_4099918	Phyca_SSR500	(AAG)4	CATGCGCTTCTGATTGGCTC	CGGAACTCGAACTGGACTCC	292	_No FA Found
>jgi|Phyca11|504222|fgenesh2_kg.PHYCAscaffold_6_#_139_#_gi|1890	Phyca_SSR501	(AAC)4	GCTGCCATCTCGATCGTGTA	TCCGTGAGTGAGAAACCGTG	188	_No FA Found
>jgi|Phyca11|504259|fgenesh2_kg.PHYCAscaffold_7_#_11_#_Contig1	Phyca_SSR502	(TGG)4	GCGTATGAACCCATCGTCCT	GGTGGAACAAGACCTCTCCG	243	_No FA Found
>jgi|Phyca11|504408|fgenesh2_kg.PHYCAscaffold_7_#_160_#_410391	Phyca_SSR503	(CAG)4	TCCAGATGCGGAACAGCAAT	CCAACAGACATGAGCCCCAT	273	_No FA Found
>jgi|Phyca11|504475|fgenesh2_kg.PHYCAscaffold_8_#_44_#_jgi|JGI_	Phyca_SSR504	(AAC)4	TGGAGCGGAACATTGTTATCA	CCTCGAGTTGTGGAGCTGTT	154	_No FA Found
>jgi|Phyca11|504549|fgenesh2_kg.PHYCAscaffold_8_#_118_#_409670	Phyca_SSR505	(GAA)4	AGCGATCACGACGACATTGT	TCCTCCGTCTTGTTGCTCAC	300	_No FA Found
>jgi|Phyca11|504635|fgenesh2_kg.PHYCAscaffold_9_#_26_#_gi|18908	Phyca_SSR506	(TGC)4	CGCGCTTTGTGTGGAAGTAC	AACATCTACCTTGAGCCGGC	290	_No FA Found
>jgi|Phyca11|504801|fgenesh2_kg.PHYCAscaffold_9_#_192_#_409685	Phyca_SSR507	(AGC)4	CTATGCAAGTTGAGCGACGC	CGTTGTGGCATCTCTGGAGT	248	_No FA Found
>jgi|Phyca11|504902|fgenesh2_kg.PHYCAscaffold_10_#_62_#_409691	Phyca_SSR508	(GCT)4	CATCTCGGCCAAGTCCAACT	GTCCTCATCGGGAAGAGGGA	199	_No FA Found
>jgi|Phyca11|504936|fgenesh2_kg.PHYCAscaffold_10_#_96_#_Contig	Phyca_SSR509	(CGA)4	CGCCGATGACGTATGAAGGA	TGGTGGTTCAGCACAACCTT	175	_No FA Found
>jgi|Phyca11|504974|fgenesh2_kg.PHYCAscaffold_10_#_134_#_Contig	Phyca_SSR510	(GAA)4	GGCCGAGAAGTACAACGACA	CTTGCTTGGCCACGAAATCC	152	_No FA Found
>jgi|Phyca11|504994|fgenesh2_kg.PHYCAscaffold_10_#_154_#_Contig	Phyca_SSR511	(GAG)4	TGTAACGACCACTGTGACGG	CGTCACTGCCGTCTTCTTCT	242	_No FA Found
>jgi|Phyca11|505099|fgenesh2_kg.PHYCAscaffold_11_#_45_#_410009	Phyca_SSR512	(GCT)4	ATGTTCTCCCGTGTGTCTCG	CGGCCAATCACCTCACTGAT	296	_No FA Found
>jgi|Phyca11|505236|fgenesh2_kg.PHYCAscaffold_12_#_24_#_410126	Phyca_SSR513	(TCT)4	TCAGCAGTGGACCGTGATTT	TCCCGTCGGTTGTTAAGGTG	273	_No FA Found
>jgi|Phyca11|505240|fgenesh2_kg.PHYCAscaffold_12_#_28_#_409957	Phyca_SSR514	(CCA)4	GCTCTACGTGATCTCCAGCC	GATGCGGTGAGGACGGATAG	253	_No FA Found
>jgi|Phyca11|505246|fgenesh2_kg.PHYCAscaffold_12_#_34_#_Contig	Phyca_SSR515	(GAG)4	ATCGTGCAAGGGAAAGCTGA	ACCTCCTCGAGTTTCTTCTCC	198	_No FA Found
>jgi|Phyca11|505339|fgenesh2_kg.PHYCAscaffold_12_#_127_#_Contig	Phyca_SSR516	(CCA)4	ATACGACGAGGGGAGTGGAA	CCCTCTCTTCTTCTGGCAGC	220	_No FA Found

>jgi|Phyca11|505393|fgenesh2_kg.PHYCAscaffold_13_#_43_#_410003	Phyca_SSR517	(CGT)4	TACACCCGTGTTCGAACCTG	CACAAGGCCTTCGGTCTTCT	279	_No FA Found
>jgi|Phyca11|505405|fgenesh2_kg.PHYCAscaffold_13_#_55_#_410184	Phyca_SSR518	(GCA)4	CGAGCAGGACTTCCTCGATC	CGCGAACGATACCTGTCCTT	172	_No FA Found
>jgi|Phyca11|505409|fgenesh2_kg.PHYCAscaffold_13_#_59_#_Contig	Phyca_SSR519	(CTG)4	GCGCAAGAAGTTGACGTTGT	AACTCGTCCAGAAGCTGTCG	198	_No FA Found
>jgi|Phyca11|505478|fgenesh2_kg.PHYCAscaffold_13_#_128_#_41019	Phyca_SSR520	(GCT)4	GTTAGTATCGGGCACGGAGG	TTGTTGTGCTGGCGGTAGAT	126	_No FA Found
>jgi|Phyca11|505556|fgenesh2_kg.PHYCAscaffold_14_#_37_#_Contig	Phyca_SSR521	(ACG)4	GATGGAGCTCGAGCACATGA	CCCGGGTGATATTGGTTGCT	218	_No FA Found
>jgi|Phyca11|505561|fgenesh2_kg.PHYCAscaffold_14_#_42_#_409673	Phyca_SSR522	(ACG)4	GATGGAGCTCGAGCACATGA	GAAGGCGTAGGACGAGAAGG	295	_No FA Found
>jgi|Phyca11|505565|fgenesh2_kg.PHYCAscaffold_14_#_46_#_409673	Phyca_SSR523	(ACG)4	GATGGAGCTCGAGCACATGA	GTGTGGTATTGGTTGCTGCG	215	_No FA Found
>jgi|Phyca11|505567|fgenesh2_kg.PHYCAscaffold_14_#_48_#_Contig	Phyca_SSR524	(CCG)4	CTCACCGTCTTCAGCCACAT	GACAGGCACGATTGTCACCA	222	_No FA Found
>jgi|Phyca11|505569|fgenesh2_kg.PHYCAscaffold_14_#_50_#_Contig	Phyca_SSR525	(AGC)4	TTCGGTGCAGCACAGAAGAA	CATCTGCTGAACGTGCGATG	158	_No FA Found
>jgi|Phyca11|505713|fgenesh2_kg.PHYCAscaffold_15_#_20_#_Contig	Phyca_SSR526	(GAA)4	CCCACATCACTCCGGGAATT	GACGCTCCTCTTGCTGTCTT	186	_No FA Found
>jgi|Phyca11|505770|fgenesh2_kg.PHYCAscaffold_15_#_77_#_gi|1890	Phyca_SSR527	(GAC)4	GAATGGTGATCGGTGTGGGT	GCTGTGGAAAACGCTTCAGG	220	_No FA Found
>jgi|Phyca11|505828|fgenesh2_kg.PHYCAscaffold_15_#_135_#_40984	Phyca_SSR528	(ACG)4	ACGAGAAGAAGGGTGGCAAG	CTGAAAGTGCTCGCATACGC	222	_No FA Found
>jgi|Phyca11|505861|fgenesh2_kg.PHYCAscaffold_16_#_20_#_409760	Phyca_SSR529	(TGA)4	TGAAAGAGTCGACCAGTGCC	CTTAGTCCCATTCGCCCCAG	210	_No FA Found
>jgi|Phyca11|505901|fgenesh2_kg.PHYCAscaffold_16_#_60_#_409933	Phyca_SSR530	(AGA)4	CGACAGCAATTACCCACCCT	TCACTGCCAATATATGCAGCT	208	_No FA Found
>jgi|Phyca11|505922|fgenesh2_kg.PHYCAscaffold_17_#_7_#_4101655	Phyca_SSR531	(GAC)4	AGCGACATGGGAAAGAAGCG	CGATGGCCTCCTCAATCTCC	181	_No FA Found
>jgi|Phyca11|505935|fgenesh2_kg.PHYCAscaffold_17_#_20_#_409680	Phyca_SSR532	(GCC)4	TCTGTCCGTCGTACCAGAGT	TAGCCTTGGACGACTCGGTA	255	_No FA Found
>jgi|Phyca11|506056|fgenesh2_kg.PHYCAscaffold_17_#_141_#_gi|189	Phyca_SSR533	(GAG)4	TATGGAGCTGGAACCCGAGA	CTACAGGCTCAGCTGGTTCC	140	_No FA Found
>jgi|Phyca11|506219|fgenesh2_kg.PHYCAscaffold_18_#_92_#_Contig	Phyca_SSR534	(GCT)4	TAAGGCCACGAAGGATGCTG	AGGCTTCTTAGATCCCCGGT	298	_No FA Found
>jgi|Phyca11|506323|fgenesh2_kg.PHYCAscaffold_19_#_29_#_410054	Phyca_SSR535	(CTG)4	CGCCTTCACCCACGAAAAAG	CATTCTCCTCCTCCGCCATC	267	_No FA Found
>jgi|Phyca11|506382|fgenesh2_kg.PHYCAscaffold_19_#_88_#_409682	Phyca_SSR536	(ATG)4	CTCATTGCCAACACGTGCAA	CGTCGTCCACGTAGTAGAGC	106	_No FA Found

>jgi|Phyca11|506486|fgenesh2_kg.PHYCAscaffold_20_#_32_#_Contig	Phyca_SSR537	(CTG)4	AATCACTGACTCCATGGGGG	CGAGAACCGGCTAGCCTTAG	262	_No FA Found
>jgi|Phyca11|506621|fgenesh2_kg.PHYCAscaffold_20_#_167_#_4102	Phyca_SSR538	(AAC)4	TTCTTCCACGAGCACTGCAT	ATATATTTCGTTGCGGCGCC	173	_No FA Found
>jgi|Phyca11|506633|fgenesh2_kg.PHYCAscaffold_21_#_5_#_Contig2	Phyca_SSR539	(GCA)4	TACCATTTGCCGCTGGTTCT	CTCGCAGGACACAGTCAACT	230	_No FA Found
>jgi|Phyca11|506635|fgenesh2_kg.PHYCAscaffold_21_#_7_#_Contig2	Phyca_SSR540	(CAG)4	AACAGCAGCAACAGCGAATG	GTTGCTGAGCTTGCTGGTTC	243	_No FA Found
>jgi|Phyca11|506642|fgenesh2_kg.PHYCAscaffold_21_#_14_#_Contig	Phyca_SSR541	(GGA)4	TTCGCTTTTTCGCTTGGAGC	TTGCAGTGGATGTGCGATCT	260	_No FA Found
>jgi|Phyca11|506648|fgenesh2_kg.PHYCAscaffold_21_#_20_#_Contig	Phyca_SSR542	(CAA)4	ATGCAGCAACAGCAAATGCA	ATCTGGTTGGACTGCTGAGC	134	_No FA Found
>jgi|Phyca11|506653|fgenesh2_kg.PHYCAscaffold_21_#_25_#_Contig	Phyca_SSR543	(GAC)4	GTATCCCAGTCATCGAGGCG	CTGCTGTACTTCGGAAGGCA	114	_No FA Found
>jgi|Phyca11|506701|fgenesh2_kg.PHYCAscaffold_21_#_73_#_40975	Phyca_SSR544	(ATC)4	TCGCGATTCTGGTACGGATG	GCAGGAATCCACGACCAGAA	233	_No FA Found
>jgi|Phyca11|506740|fgenesh2_kg.PHYCAscaffold_21_#_112_#_Conti	Phyca_SSR545	(GCA)4	GCCACTCAAGTCGCTACCAT	ACTCTTCCACCTCATCCGGA	180	_No FA Found
>jgi|Phyca11|506759|fgenesh2_kg.PHYCAscaffold_21_#_131_#_4101	Phyca_SSR546	(GAC)4	CGACTGCTGCGAATGTGAAG	GATGTCACCGTGCTAGCGTA	232	_No FA Found
>jgi|Phyca11|506768|fgenesh2_kg.PHYCAscaffold_22_#_7_#_409774	Phyca_SSR547	(AAG)4	TCCTGCGTGCGATCAGAAAT	TTGCTCTTTGTGCTCGTTGC	297	_No FA Found
>jgi|Phyca11|506804|fgenesh2_kg.PHYCAscaffold_22_#_43_#_41011	Phyca_SSR548	(TAC)4	GGAGGCTTGGGCTTCATCTT	ACTTATACCCCTCTCCGCGT	176	_No FA Found
>jgi|Phyca11|506901|fgenesh2_kg.PHYCAscaffold_23_#_32_#_40975	Phyca_SSR549	(AAG)4	AACAGCTACTGGGTCAGCAC	TTCACGGACACATCGAAGCA	270	_No FA Found
>jgi|Phyca11|506932|fgenesh2_kg.PHYCAscaffold_23_#_63_#_40968	Phyca_SSR550	(GCA)4	GGTCTTACTGGAGGTGACGC	GCTGTGAAGTCTGAGGTCCC	232	_No FA Found
>jgi|Phyca11|506956|fgenesh2_kg.PHYCAscaffold_23_#_87_#_40965	Phyca_SSR551	(ACC)4	ACCATCACTGCGACCCATAC	CCTGCTCGAACACATCCACT	262	_No FA Found
>jgi|Phyca11|507000|fgenesh2_kg.PHYCAscaffold_23_#_131_#_Conti	Phyca_SSR552	(ACC)4	TTCGGTCTGTTCACGCATGA	TTACATGGCGCAGTCCTTGT	270	_No FA Found
>jgi|Phyca11|507062|fgenesh2_kg.PHYCAscaffold_24_#_54_#_40971	Phyca_SSR553	(GCT)4	TCGTGGAAGGCACAGAACTC	TCCTTCTTAGGGGCCACGTA	299	_No FA Found
>jgi|Phyca11|507120|fgenesh2_kg.PHYCAscaffold_25_#_4_#_Contig3	Phyca_SSR554	(CAC)4	TATTACCCGCCTCCACCTCA	AGGCAATTTAGTCCAGCGCT	271	_No FA Found
>jgi|Phyca11|507281|fgenesh2_kg.PHYCAscaffold_26_#_84_#_Contig	Phyca_SSR555	(CTG)4	TATCTCTTCGGCCATGCTGC	AGCGCCATGTACTGACACAA	286	_No FA Found
>jgi|Phyca11|507282|fgenesh2_kg.PHYCAscaffold_26_#_85_#_40991	Phyca_SSR556	(CTG)4	TATCTCTTCGGCCATGCTGC	AGCGCCATGTACTGACACAA	286	_No FA Found

>jgi|Phyca11|507314|fgenesh2_kg.PHYCAscaffold_26_#_117_#_gi|189	Phyca_SSR557	(GGA)4	GAGGACCCTGCCACTAGAGA	CGATCTGGATTTGCGGCATG	181	_No FA Found
>jgi|Phyca11|507337|fgenesh2_kg.PHYCAscaffold_27_#_11_#_410193	Phyca_SSR558	(TGA)4	CCCAGTGGGTACATCCAACC	TACCTTCCGAGAGTCTGGGG	274	_No FA Found
>jgi|Phyca11|507387|fgenesh2_kg.PHYCAscaffold_27_#_61_#_409792	Phyca_SSR559	(TAA)4	CGGGCAGAGAAGCTTCCATT	GGAAGGCCTCGTACGTGAAA	105	_No FA Found
>jgi|Phyca11|507476|fgenesh2_kg.PHYCAscaffold_27_#_150_#_Conti	Phyca_SSR560	(ACA)4	GAGGCGACAAGAGCAACAAC	ACCACTAACTAACACGGCCG	211	_No FA Found
>jgi|Phyca11|507525|fgenesh2_kg.PHYCAscaffold_28_#_32_#_Contig	Phyca_SSR561	(CAG)4	GCAACTTGCATGCAACTGGA	GGATGAAAGCGGGTAGAATT	129	_No FA Found
>jgi|Phyca11|507608|fgenesh2_kg.PHYCAscaffold_29_#_4_#_gi|18908	Phyca_SSR562	(TCT)4	CGTCGTCTGGAGAGATGCTC	CGCCAGCAGTCGATCAATTG	231	_No FA Found
>jgi|Phyca11|507624|fgenesh2_kg.PHYCAscaffold_29_#_20_#_Contig	Phyca_SSR563	(CTG)4	CTGGGGGTTGTACTGTTGCT	AGCCTCAACAGCAGCAGAAT	152	_No FA Found
>jgi|Phyca11|507646|fgenesh2_kg.PHYCAscaffold_29_#_42_#_gi|1890	Phyca_SSR564	(GAA)4	AAACGTCATGGCTGGTCAGT	TCGTTCTCTGCTGCTCGTTT	267	_No FA Found
>jgi|Phyca11|507690|fgenesh2_kg.PHYCAscaffold_29_#_86_#_gi|1890	Phyca_SSR565	(GCA)4	CAGCTTCCACCGGTTTTGTG	CTGTAGCTGCTGGTTCTGCT	281	_No FA Found
>jgi|Phyca11|507722|fgenesh2_kg.PHYCAscaffold_29_#_118_#_40973	Phyca_SSR566	(TTG)4	ACCGGCTGAGATGATACCCT	AGTGGGTAACGCGAAAGGAG	108	_No FA Found
>jgi|Phyca11|507791|fgenesh2_kg.PHYCAscaffold_30_#_60_#_409731	Phyca_SSR567	(GCA)4	TCCTCAAGGTCAGCAAGCAG	GCAAGCCAACACGAAAGGAG	158	_No FA Found
>jgi|Phyca11|507795|fgenesh2_kg.PHYCAscaffold_30_#_64_#_409993	Phyca_SSR568	(CCT)4	GTGGTTTCCCCGATCATGGT	AATGGAGGAGAACCGAAGCG	289	_No FA Found
>jgi|Phyca11|507989|fgenesh2_kg.PHYCAscaffold_31_#_70_#_409937	Phyca_SSR569	(TGA)4	AGTCGGATCAATTGCTGCCA	TGTTCCTTCTGGACCAGCAC	297	_No FA Found
>jgi|Phyca11|508065|fgenesh2_kg.PHYCAscaffold_32_#_24_#_Contig	Phyca_SSR570	(GCT)4	GTCTCGACCTCACTTGGCAA	TACAACGCTGCCAACAATGC	242	_No FA Found
>jgi|Phyca11|508140|fgenesh2_kg.PHYCAscaffold_32_#_99_#_409963	Phyca_SSR571	(TGT)4	CGCCAACCAGAAAGTCTCCT	CCGAAAACGCACTGAAGTCG	185	_No FA Found
>jgi|Phyca11|508192|fgenesh2_kg.PHYCAscaffold_33_#_51_#_Contig	Phyca_SSR572	(AGA)4	CTCCCATTGATGTTGCCCCT	GGAACGCCGGATTCTCTAGG	237	_No FA Found
>jgi|Phyca11|508208|fgenesh2_kg.PHYCAscaffold_33_#_67_#_gi|1890	Phyca_SSR573	(CAC)4	CCCCGATGTGCTGTACAAGT	GGCGTTGCTTGCTATACGTG	296	_No FA Found
>jgi|Phyca11|508211|fgenesh2_kg.PHYCAscaffold_33_#_70_#_410040	Phyca_SSR574	(CAC)4	CCCCGATGTGCTGTACAAGT	GGCGTTGCTTGCTATACGTG	296	_No FA Found
>jgi|Phyca11|508230|fgenesh2_kg.PHYCAscaffold_33_#_89_#_gi|1890	Phyca_SSR575	(GTC)4	GTTGCATGACCTGGTGGAGA	TGGCGCTGTATCTCGATGAC	149	_No FA Found
>jgi|Phyca11|508429|fgenesh2_kg.PHYCAscaffold_35_#_12_#_409993	Phyca_SSR576	(GCT)4	GAAGGACAGGCTCAACACGA	ACCTCCGAGCGTGTTATTGT	208	_No FA Found

>jgi|Phyca11|50846|gw1.290.7.1	Phyca_SSR577	(AAC)4	CATCCTAGAGCCTGACGCAG	GTTCTGCGACAGGATGTCCA	106	_Glycoside hydrolase, family 6
>jgi|Phyca11|508507|fgenesh2_kg.PHYCAscaffold_35_#_90_#_gi|1890	Phyca_SSR578	(GAA)4	GAGTGGCTGCACTGTGTACT	CGATGCAGGACTCCTCGTAC	273	_No FA Found
>jgi|Phyca11|508592|fgenesh2_kg.PHYCAscaffold_36_#_45_#_Contig	Phyca_SSR579	(ACG)4	CCGTCCTGGCAGCAGATAAA	AATGACGGATGCGAGTTGGT	245	_No FA Found
>jgi|Phyca11|508749|fgenesh2_kg.PHYCAscaffold_38_#_1_#_Contig2	Phyca_SSR580	(CTG)4	ACCAGACCGAAGAAGCTGTG	CCTCGTCATCTTCCACCAGG	288	_No FA Found
>jgi|Phyca11|508855|fgenesh2_kg.PHYCAscaffold_39_#_22_#_40969	Phyca_SSR581	(TTC)4	CCAAGAAGCGCAAAGTGTCC	CTGTCTGCCTTGCTTCTCCA	204	_No FA Found
>jgi|Phyca11|508893|fgenesh2_kg.PHYCAscaffold_39_#_60_#_Contig	Phyca_SSR582	(AAG)4	AGGAAGAAGCGACTGGTGTG	GAAGGCGTAATTGGGGTGGA	296	_No FA Found
>jgi|Phyca11|508915|fgenesh2_kg.PHYCAscaffold_40_#_4_#_Contig2	Phyca_SSR583	(AAG)4	TCCCCATACGAGGCCAAGTA	TTTGTCCCATTCGATCGCCA	160	_No FA Found
>jgi|Phyca11|508918|fgenesh2_kg.PHYCAscaffold_40_#_7_#_Contig1	Phyca_SSR584	(CGT)4	AGTGACGACGAAGCCAACAT	TGAACCGTCTGCATCTGCTT	257	_No FA Found
>jgi|Phyca11|508920|fgenesh2_kg.PHYCAscaffold_40_#_9_#_409890	Phyca_SSR585	(CGT)4	AGTGACGACGAAGCCAACAT	GATACGGTCGCGCAAGAAAC	135	_No FA Found
>jgi|Phyca11|508955|fgenesh2_kg.PHYCAscaffold_40_#_44_#_Contig	Phyca_SSR586	(CAA)4	TCCCGCAGTTACTACGAGGA	GAGCATCGCCTCCTCTTGTT	243	_No FA Found
>jgi|Phyca11|508974|fgenesh2_kg.PHYCAscaffold_40_#_63_#_40976	Phyca_SSR587	(AGG)4	CTGCTGAGAAGGCTGTGACA	TAACGCCAGACTTCAGTGCC	215	_No FA Found
>jgi|Phyca11|509134|fgenesh2_kg.PHYCAscaffold_42_#_41_#_Contig	Phyca_SSR588	(GAC)4	CGCGTGTCTTCTGGCAAAAA	CCTGTCAGCGACATCGGAAT	255	_No FA Found
>jgi|Phyca11|509200|fgenesh2_kg.PHYCAscaffold_42_#_107_#_4096	Phyca_SSR589	(CTG)4	AGTATGTGGAAGTGCCGTCG	ACACGATCACAGCCGAGTTT	271	_No FA Found
>jgi|Phyca11|509239|fgenesh2_kg.PHYCAscaffold_43_#_37_#_41019	Phyca_SSR590	(CAG)4	CTTCCCCACCTCACTCGATG	GAGTCTGTTGGGTCTGAGCC	135	_No FA Found
>jgi|Phyca11|509295|fgenesh2_kg.PHYCAscaffold_43_#_93_#_gi|1890	Phyca_SSR591	(CAG)4	ATTGCCAGCTCCCTTCCTTC	GCCTCGCTAGAGTCCATGTC	179	_No FA Found
>jgi|Phyca11|509300|fgenesh2_kg.PHYCAscaffold_43_#_98_#_Contig	Phyca_SSR592	(GCT)4	GCCGTTGTTATTGCTAGCGG	CGGAATAGAATGTTGGCGCG	203	_No FA Found
>jgi|Phyca11|509314|fgenesh2_kg.PHYCAscaffold_43_#_112_#_Conti	Phyca_SSR593	(TGT)4	AACACCTCAGCGATCACAGG	TACAATCCGGCAGTGCACAA	281	_No FA Found
>jgi|Phyca11|509331|fgenesh2_kg.PHYCAscaffold_43_#_129_#_4099	Phyca_SSR594	(CGA)4	CCATTCTGGTCAAGGGTGCT	TGCCGATCGTGTTGGAAGAA	174	_No FA Found
>jgi|Phyca11|509335|fgenesh2_kg.PHYCAscaffold_43_#_133_#_Conti	Phyca_SSR595	(CTG)4	GTGCATACCTGGGGCTATCC	CGTCGATGCATCTGAAAGCG	243	_No FA Found
>jgi|Phyca11|509339|fgenesh2_kg.PHYCAscaffold_43_#_137_#_Conti	Phyca_SSR596	(GCA)4	CGTACGCGCATCGAACAAAT	AGCCCACCATTCTTCTCTGC	119	_No FA Found

>jgi|Phyca11|509370|fgenesh2_kg.PHYCAscaffold_44_#_8_#_Contig3	Phyca_SSR597	(ATT)4	CCGGCAAGCGTGTTAAGAAG	TGTATTGATACTCCATGGCTAT	283	_No FA Found
>jgi|Phyca11|509388|fgenesh2_kg.PHYCAscaffold_44_#_26_#_409680	Phyca_SSR598	(GGA)4	GGGCCTCACGTCTAACACAA	TGTCGATGATACGGCGACTG	299	_No FA Found
>jgi|Phyca11|509410|fgenesh2_kg.PHYCAscaffold_44_#_48_#_gi|1890	Phyca_SSR599	(GAG)4	TACGGCGAAAACGACGAAGA	CTCGTCCAGAAATGGCTCGT	192	_No FA Found
>jgi|Phyca11|509423|fgenesh2_kg.PHYCAscaffold_46_#_8_#_Contig4	Phyca_SSR600	(AAC)4	TCGCTGCATGAACTGTGACT	AAGTACTGCGGAGTCTGCAC	159	_No FA Found
>jgi|Phyca11|509453|fgenesh2_kg.PHYCAscaffold_46_#_38_#_410298	Phyca_SSR601	(GAA)4	TCACGGGAAGAAGAAGGTGC	AACCAGTTACCGCTGCTTGT	207	_No FA Found
>jgi|Phyca11|509468|fgenesh2_kg.PHYCAscaffold_46_#_53_#_gi|1890	Phyca_SSR602	(GAA)4	GCGTGGTTTGATATGACGGC	AGCTCTCCACAAGCTTCACC	293	_No FA Found
>jgi|Phyca11|509515|fgenesh2_kg.PHYCAscaffold_47_#_6_#_4098474	Phyca_SSR603	(GTG)4	CGCAAACTGGAAGGCAACAA	CACGGTGTGCTTGATCTTGC	213	_No FA Found
>jgi|Phyca11|509548|fgenesh2_kg.PHYCAscaffold_47_#_39_#_gi|1890	Phyca_SSR604	(TCC)4	CGTCGCTACCATCTGGATCC	CGGCCACTAGGAGATTCGAC	242	_No FA Found
>jgi|Phyca11|509554|fgenesh2_kg.PHYCAscaffold_47_#_45_#_409677	Phyca_SSR605	(TGC)4	CGTCCGCAATGCAATCTCTG	GATTCTACCGAGCGTCCAGG	206	_No FA Found
>jgi|Phyca11|509570|fgenesh2_kg.PHYCAscaffold_47_#_61_#_Contig	Phyca_SSR606	(GAC)4	ACCAGCAGAAGAAGGACACG	TGTCGTTGGTGCTCTCCTTC	264	_No FA Found
>jgi|Phyca11|509608|fgenesh2_kg.PHYCAscaffold_48_#_11_#_410088	Phyca_SSR607	(GGT)4	AGAAGAGCCTCGTCCTGGAT	GCGGCTTACTGACTCAGCTT	297	_No FA Found
>jgi|Phyca11|509616|fgenesh2_kg.PHYCAscaffold_48_#_19_#_Contig	Phyca_SSR608	(AAG)4	CCCCTCCGCACAAGTCTAAA	GTACAGGATCACAGGGACGC	242	_No FA Found
>jgi|Phyca11|509650|fgenesh2_kg.PHYCAscaffold_48_#_53_#_410363	Phyca_SSR609	(GCT)4	AAATACCAATGACGGCCGAC	CATTGGGCTGAGCTCTTGGA	157	_No FA Found
>jgi|Phyca11|509686|fgenesh2_kg.PHYCAscaffold_48_#_89_#_409693	Phyca_SSR610	(AGC)4	TATCCTCCTCCGTGCTCCAA	CATCGAGACGGGAGCTTCTC	279	_No FA Found
>jgi|Phyca11|509825|fgenesh2_kg.PHYCAscaffold_50_#_26_#_409659	Phyca_SSR611	(CAC)4	GCAGTGGTAACGAGCAGACT	CAACCTGAGCGACACAAACG	297	_No FA Found
>jgi|Phyca11|509994|fgenesh2_kg.PHYCAscaffold_52_#_50_#_Contig	Phyca_SSR612	(GCA)4	TGGTCGCGGTATTGATACGG	TCCGTAACAGTCGCAGTTCC	201	_No FA Found
>jgi|Phyca11|510004|fgenesh2_kg.PHYCAscaffold_52_#_60_#_Contig	Phyca_SSR613	(GAA)4	GAGTGCAAGCTCAAACGCAA	ATGAGCAGGATGTCGGCAAA	238	_No FA Found
>jgi|Phyca11|510006|fgenesh2_kg.PHYCAscaffold_52_#_62_#_Contig	Phyca_SSR614	(CGT)4	GCGTGTCTAGACCCAACGAA	GCAAGTCTCTGCGTCTCCTT	125	_No FA Found
>jgi|Phyca11|510034|fgenesh2_kg.PHYCAscaffold_53_#_19_#_gi|1890	Phyca_SSR615	(AGA)4	AGGACGAAGAAACCGAGACG	AATTTCTCCTTCCGCAGCGA	285	_No FA Found
>jgi|Phyca11|510170|fgenesh2_kg.PHYCAscaffold_54_#_64_#_409984	Phyca_SSR616	(GTC)4	GCTCCTATTCGACCACGGAG	TTATGCGGCAGGGAAGGATG	207	_No FA Found

>jgi|Phyca11|510199|fgenesh2_kg.PHYCAscaffold_55_#_16_#_409836	Phyca_SSR617	(AGA)4	AGGTTGAAGAGCCAGTGCAA	CGCAGCCTCGTTTTCAAACA	257	_No FA Found
>jgi|Phyca11|510266|fgenesh2_kg.PHYCAscaffold_57_#_10_#_Contig	Phyca_SSR618	(AAG)4	AAGTGGAGGAGAAAGCACCG	CTTGAGAGGCCAAGCTCTCC	216	_No FA Found
>jgi|Phyca11|510284|fgenesh2_kg.PHYCAscaffold_57_#_28_#_Contig	Phyca_SSR619	(GTG)4	GCGTCGGTTCTTCTGAAGGA	GTACGTCACGTAGCAACCCA	195	_No FA Found
>jgi|Phyca11|510376|fgenesh2_kg.PHYCAscaffold_59_#_14_#_gi|1890	Phyca_SSR620	(GGT)4	AGGTTGTGCCTCGACTATGC	GAGTTGGCGCTGGTAGTTCT	186	_No FA Found
>jgi|Phyca11|510409|fgenesh2_kg.PHYCAscaffold_59_#_47_#_Contig	Phyca_SSR621	(TCC)4	GGGAGATGAAGAAGCCGAGG	AGGACAAGCCATTTCGAGCA	199	_No FA Found
>jgi|Phyca11|510438|fgenesh2_kg.PHYCAscaffold_60_#_26_#_gi|1890	Phyca_SSR622	(GTT)4	TTTGTTGCAACTCGCTGAGC	CTCCCTTGCGTTGGCTTCTA	157	_No FA Found
>jgi|Phyca11|510534|fgenesh2_kg.PHYCAscaffold_62_#_5_#_Contig1	Phyca_SSR623	(CGT)4	GGCTTCCTCTGTCTGTTGCT	GATCGACTACTCGGCCTTGG	231	_No FA Found
>jgi|Phyca11|510602|fgenesh2_kg.PHYCAscaffold_63_#_41_#_gi|1890	Phyca_SSR624	(AAG)4	GCAAGTCCAGATCTCGGAGG	TCTGGGAACGACAGCTTCAC	207	_No FA Found
>jgi|Phyca11|510629|fgenesh2_kg.PHYCAscaffold_64_#_22_#_410162	Phyca_SSR625	(CGC)4	CTGTGCAATTGGGTGCTGTG	TGCTCGAGTGAATTGACGCT	236	_No FA Found
>jgi|Phyca11|510656|fgenesh2_kg.PHYCAscaffold_64_#_49_#_410051	Phyca_SSR626	(TGC)4	GTGTTATCCGTCGTGCTGCA	TAGTCCAAAGCGCACAAGGT	291	_No FA Found
>jgi|Phyca11|510658|fgenesh2_kg.PHYCAscaffold_64_#_51_#_410467	Phyca_SSR627	(TGC)4	GTGCGCAACGAATTCTGGAG	GGATCGACTTGGCGAGTTCT	280	_No FA Found
>jgi|Phyca11|510671|fgenesh2_kg.PHYCAscaffold_65_#_11_#_gi|1890	Phyca_SSR628	(GCA)4	CTTCTACGCTATGCTCGCCA	AGATGGCCAAAGGTGCCTTT	150	_No FA Found
>jgi|Phyca11|510686|fgenesh2_kg.PHYCAscaffold_65_#_26_#_Contig	Phyca_SSR629	(CAA)4	CGCAGAAAAACCGTGTGGAG	CTGCATCCTCGTCTGCAGAT	273	_No FA Found
>jgi|Phyca11|510751|fgenesh2_kg.PHYCAscaffold_66_#_25_#_409997	Phyca_SSR630	(GAA)4	GCCCGAGACAACTACGACAA	GACGTAGCTCCTCCATCGTG	172	_No FA Found
>jgi|Phyca11|510753|fgenesh2_kg.PHYCAscaffold_66_#_27_#_409912	Phyca_SSR631	(GCG)4	GTGCATTGGTGTTTGAGCGT	CTCAACCTCAGCTCTTGCCA	131	_No FA Found
>jgi|Phyca11|510793|fgenesh2_kg.PHYCAscaffold_67_#_4_#_Contig1	Phyca_SSR632	(ACT)4	GCACAGACCAGCAACTCAAC	CGTTGGAGCAGTTGTCGTTG	246	_No FA Found
>jgi|Phyca11|510798|fgenesh2_kg.PHYCAscaffold_67_#_9_#_Contig2	Phyca_SSR633	(AGT)4	GGGGAAACGAACCTAGCCAA	AAGTTTCCTCGGGTGCAACA	220	_No FA Found
>jgi|Phyca11|510836|fgenesh2_kg.PHYCAscaffold_68_#_12_#_Contig	Phyca_SSR634	(CCA)4	CAGTAGAGGTGAATCGCCCC	TCGCTGTCTCCTTTCGCAAT	294	_No FA Found
>jgi|Phyca11|510938|fgenesh2_kg.PHYCAscaffold_71_#_38_#_Contig	Phyca_SSR635	(CAG)4	GGGCTCCTTACGAAGTTGCT	TGTTGTCGCTCTGGTCCATC	297	_No FA Found
>jgi|Phyca11|510959|fgenesh2_kg.PHYCAscaffold_72_#_4_#_Contig3	Phyca_SSR636	(GGC)4	CAACGTAGTGCTCGTGGACT	CGACTCGGTGTAGAAGTCGG	169	_No FA Found

>jgi|Phyca11|511096|fgenesh2_kg.PHYCAscaffold_75_#_6_#_4099660	Phyca_SSR637	(GTG)4	TCTGCCGAGATACCCGTGTA	AGTCTCCGACTTCGATGAAAA	256	_No FA Found
>jgi|Phyca11|511140|fgenesh2_kg.PHYCAscaffold_76_#_41_#_409948	Phyca_SSR638	(GCA)4	TCTCTAAAGTTACTTAACGATG	AGAACTTGAGCGACTGCACA	281	_No FA Found
>jgi|Phyca11|511142|fgenesh2_kg.PHYCAscaffold_76_#_43_#_Contig	Phyca_SSR639	(GGA)4	GAAGCGTTCGTGAAGGAAGC	GCAACCTGCAGCAGTTTCTC	251	_No FA Found
>jgi|Phyca11|511148|fgenesh2_kg.PHYCAscaffold_77_#_3_#_4099640	Phyca_SSR640	(CTG)4	AAGCCCAGCACCATCTGTAC	GGCCCCGAGATGAACTCAAA	168	_No FA Found
>jgi|Phyca11|511168|fgenesh2_kg.PHYCAscaffold_78_#_3_#_4100385	Phyca_SSR641	(TTC)4	CCATTCTTCTCCGAGGCAGG	ATCAGTTATTGCCGTGGCCA	129	_No FA Found
>jgi|Phyca11|511213|fgenesh2_kg.PHYCAscaffold_79_#_18_#_410048	Phyca_SSR642	(CTG)4	AGTCTCAGTGTCGCCACAAG	GAGGTAACCCGCATCGCATA	168	_No FA Found
>jgi|Phyca11|511287|fgenesh2_kg.PHYCAscaffold_80_#_31_#_410166	Phyca_SSR643	(CCT)4	CGTCAACAGCAGCAACAGTC	TCCTGGGTACGTGCAATGAC	251	_No FA Found
>jgi|Phyca11|511390|fgenesh2_kg.PHYCAscaffold_84_#_6_#_4097637	Phyca_SSR644	(AGA)4	CCCACGCAGGTAACCAAGAT	CGTCACTTCCGTCTTGAGCT	225	_No FA Found
>jgi|Phyca11|511498|fgenesh2_kg.PHYCAscaffold_87_#_4_#_Contig2	Phyca_SSR645	(TTC)4	CCTCAGCTCCCTTGGCTTAC	TTCATCGTCCTCAGTGTCGC	280	_No FA Found
>jgi|Phyca11|511527|fgenesh2_kg.PHYCAscaffold_87_#_33_#_Contig	Phyca_SSR646	(GAT)4	ATCCCCGCAACAAACAGCTA	AGACGCAAGCACTTCACGTA	249	_No FA Found
>jgi|Phyca11|511533|fgenesh2_kg.PHYCAscaffold_87_#_39_#_409753	Phyca_SSR647	(GAA)4	TATGCAGGACCGAGTGGAGA	CGTCTCCACTTGTGACTGCT	184	_No FA Found
>jgi|Phyca11|511571|fgenesh2_kg.PHYCAscaffold_90_#_5_#_Contig4	Phyca_SSR648	(TCG)4	GTTGTACTGTGCTGTCGGGA	AATGGCTACTGCGGACGAAA	229	_No FA Found
>jgi|Phyca11|511574|fgenesh2_kg.PHYCAscaffold_90_#_8_#_4097953	Phyca_SSR649	(ACG)4	AATGGCTACTGCGGACGAAA	GTTGTACTGTGCTGTCGGGA	229	_No FA Found
>jgi|Phyca11|511583|fgenesh2_kg.PHYCAscaffold_90_#_17_#_Contig	Phyca_SSR650	(ACG)4	CCGAGGTCGAGACGATTCTG	GCTCCCGGTACTGTTGAGTC	281	_No FA Found
>jgi|Phyca11|511585|fgenesh2_kg.PHYCAscaffold_90_#_19_#_409865	Phyca_SSR651	(ACG)4	CCGAGGTCGAGACGATTCTG	GCTCCCGGTACTGTTGAGTC	281	_No FA Found
>jgi|Phyca11|511597|fgenesh2_kg.PHYCAscaffold_90_#_31_#_409695	Phyca_SSR652	(CGT)4	TGTGACGACGAAGGTTGGAG	CCTCTGTTGCCAGCTACGAA	262	_No FA Found
>jgi|Phyca11|511778|fgenesh2_kg.PHYCAscaffold_97_#_28_#_Contig	Phyca_SSR653	(AAG)4	CAGAGTCGGAGTCGGATTCG	AATCCGCTTCTCCACGTCTG	254	_No FA Found
>jgi|Phyca11|511781|fgenesh2_kg.PHYCAscaffold_97_#_31_#_410029	Phyca_SSR654	(CAG)4	TGGAGTGACGACGACAATGG	GAAAAGCGAGCTGTATGGCG	249	_No FA Found
>jgi|Phyca11|511927|fgenesh2_kg.PHYCAscaffold_105_#_25_#_40988	Phyca_SSR655	(GAG)4	TCGAAGCGACCGAAGCTATC	TTGATGCCTTACCATGCCGT	289	_No FA Found
>jgi|Phyca11|512010|fgenesh2_kg.PHYCAscaffold_112_#_15_#_Conti	Phyca_SSR656	(GAC)4	CCCGCAACAATCTCCTTCCT	ATCGTTGGAGGTGTCGGAAC	291	_No FA Found

>jgi|Phyca11|512023|fgenesh2_kg.PHYCAscaffold_117_#_4_#_Contig	Phyca_SSR657	(CTT)4	GTTGGAGTGACAACGTTGGC	CCTGCACTTCACCAAACTGC	279	_No FA Found
>jgi|Phyca11|512044|fgenesh2_kg.PHYCAscaffold_119_#_13_#_Conti	Phyca_SSR658	(TTC)4	GTACAAGTACCGTGGTGCCA	ACGTGTAGAAAGCCTCCACG	281	_No FA Found
>jgi|Phyca11|512110|fgenesh2_kg.PHYCAscaffold_178_#_1_#_40984	Phyca_SSR659	(GTG)4	TGTTGCAGCGCTTTGAGAAC	AAGCCTTGGACCAGATGACG	108	_No FA Found
>jgi|Phyca11|512120|fgenesh2_kg.PHYCAscaffold_191_#_2_#_Contig	Phyca_SSR660	(GAC)4	GACTTTACCAGCCTTCGCCT	AGTGAATCGCAAGTGGACGT	255	_No FA Found
>jgi|Phyca11|512124|fgenesh2_kg.PHYCAscaffold_216_#_1_#_Contig	Phyca_SSR661	(CAG)4	TCGATCGTCATTGGAGCGAG	TCTCGCAGATCCAAAAGCGT	189	_No FA Found
>jgi|Phyca11|512192|fgenesh2_kg.PHYCAscaffold_539_#_1_#_40966	Phyca_SSR662	(CTG)4	CGCCACGGATATCAACCTGA	ACACGATCACAGCCGAGTTT	282	_No FA Found
>jgi|Phyca11|5152|fgenesh1_pm.PHYCAscaffold_4_#_240	Phyca_SSR663	(GAA)4	CGGCTATTGTCAACTTGGCG	TTGCCCTTGCCATCATCCTT	226	_No FA Found
>jgi|Phyca11|5171|fgenesh1_pm.PHYCAscaffold_4_#_259	Phyca_SSR664	(TTC)4	CGGTGTTAAGCTTGGCCAAC	GCCAGCGAGCAAGACAAAAA	128	_ABC transporter-like
>jgi|Phyca11|52331|gw1.138.29.1	Phyca_SSR665	(AAG)4	CAGTCGGAGGATTGGGTGAC	ACATTTTGCGTTGTCCACCG	150	_No FA Found
>jgi|Phyca11|525124|estExt2_fgenesh1_pm.C_PHYCAscaffold_20058	Phyca_SSR666	(GCA)4	AGGTGGACATTTACGCTCCG	TGCGAAATCCGAGTCAGCTT	140	_No FA Found
>jgi|Phyca11|525182|estExt2_fgenesh1_pm.C_PHYCAscaffold_20132	Phyca_SSR667	(TGG)4	TGCCGGATCTCTCTAACCCA	GCCGCATCATTAGCTTGGTG	165	_No FA Found
>jgi|Phyca11|525206|estExt2_fgenesh1_pm.C_PHYCAscaffold_20167	Phyca_SSR668	(AAG)4	GGCGTTAGAGGACAGAGAGC	GGATCGTCATGTTGCGCTTC	248	_No FA Found
>jgi|Phyca11|525356|estExt2_fgenesh1_pm.C_PHYCAscaffold_30114	Phyca_SSR669	(AGG)4	GTGAAGAAACGCAAGCTGCA	TGAAAGATGCGCCTTCACCT	274	_No FA Found
>jgi|Phyca11|525358|estExt2_fgenesh1_pm.C_PHYCAscaffold_30116	Phyca_SSR670	(CAA)4	ATCAAGTGGCCGGTGAGATG	TGGTTCGTTGGCATCTCGAA	280	_No FA Found
>jgi|Phyca11|525498|estExt2_fgenesh1_pm.C_PHYCAscaffold_40027	Phyca_SSR671	(GAC)4	AAGCAGTACATGGCCACGAA	GATGTGTCTGCTGCCTCCTT	203	_No FA Found
>jgi|Phyca11|525523|estExt2_fgenesh1_pm.C_PHYCAscaffold_40057	Phyca_SSR672	(CGG)4	GCTTCTGTTCGTGCAGGTTG	GTTGAACGTCTCAGAACGCG	298	_No FA Found
>jgi|Phyca11|525556|estExt2_fgenesh1_pm.C_PHYCAscaffold_40093	Phyca_SSR673	(TGA)4	AGAAAAAGCTCGCGGGATGA	TCGGAAGCTACACTGGCAAG	276	_No FA Found
>jgi|Phyca11|525732|estExt2_fgenesh1_pm.C_PHYCAscaffold_50020	Phyca_SSR674	(GAC)4	TGTGGCCAAGCATCTACTGG	CAAAGCGCTGACCGATAAGC	218	_No FA Found
>jgi|Phyca11|525875|estExt2_fgenesh1_pm.C_PHYCAscaffold_50196	Phyca_SSR675	(AGA)4	GAGCCACAACAAACACCGAC	TGTTGCACTGGAAGACCACA	161	_No FA Found
>jgi|Phyca11|525885|estExt2_fgenesh1_pm.C_PHYCAscaffold_50210	Phyca_SSR676	(AGA)4	ATTGGAACCCACACAGTGCA	TCCTCCCAGATAGCAGGCTT	242	_No FA Found

>jgi|Phyca11|525949|estExt2_fgenesh1_pm.C_PHYCAscaffold_60015	Phyca_SSR677	(AAG)4	GCTTCATTAGGCAATGGGCG	TGGACTCCTTGCCTCGTTTC	256	_No FA Found
>jgi|Phyca11|525953|estExt2_fgenesh1_pm.C_PHYCAscaffold_60019	Phyca_SSR678	(AGA)4	GCTCGTGCCGTCGAAGTATA	CATCACCTGCGGGTAGTCTC	210	_No FA Found
>jgi|Phyca11|526032|estExt2_fgenesh1_pm.C_PHYCAscaffold_60116	Phyca_SSR679	(GCT)4	TGTGGTGGATCCTCGAGCTA	CCCAGATCGCATCTCCACTC	263	_No FA Found
>jgi|Phyca11|526358|estExt2_fgenesh1_pm.C_PHYCAscaffold_90087	Phyca_SSR680	(CTT)4	CGTCCCTGTCTCAAGTGCTC	GACCGAGATCACCGTACGTC	274	_No FA Found
>jgi|Phyca11|526496|estExt2_fgenesh1_pm.C_PHYCAscaffold_100043	Phyca_SSR681	(AGA)4	TCGGCCGAGAAGGAGTTCTA	CTGCTACTGGACTTGCTGCT	227	_No FA Found
>jgi|Phyca11|526613|estExt2_fgenesh1_pm.C_PHYCAscaffold_110061	Phyca_SSR682	(GAG)4	AACCCGAGCTCAAGATGACG	ACCTTGGCTTAGAACTCGGC	211	_No FA Found
>jgi|Phyca11|526731|estExt2_fgenesh1_pm.C_PHYCAscaffold_120086	Phyca_SSR683	(AGA)4	GCGGTTGTAGCCAAGAAACG	CGGAGTGACGCCAAAGTTTG	113	_No FA Found
>jgi|Phyca11|526972|estExt2_fgenesh1_pm.C_PHYCAscaffold_140123	Phyca_SSR684	(CGA)4	AACGTTCGTGAAGCCTCCAT	TTGGATAGCAGCACGTGAGG	173	_No FA Found
>jgi|Phyca11|526982|estExt2_fgenesh1_pm.C_PHYCAscaffold_150003	Phyca_SSR685	(GAT)4	GCAAGCGACGATGACATGAC	CTCTCGTCGTCGCTCTCTTC	107	_No FA Found
>jgi|Phyca11|527211|estExt2_fgenesh1_pm.C_PHYCAscaffold_170091	Phyca_SSR686	(ACG)4	CTTCCGGACAGCATGGAACT	ACGTTCGATTCCGTCCTCAC	216	_No FA Found
>jgi|Phyca11|527595|estExt2_fgenesh1_pm.C_PHYCAscaffold_200135	Phyca_SSR687	(TCC)4	TTTCATGCCGTGCGTCATTC	GATTTGGTCGCAGATGCAGC	144	_No FA Found
>jgi|Phyca11|527618|estExt2_fgenesh1_pm.C_PHYCAscaffold_210020	Phyca_SSR688	(CAA)4	ATCAGCAACAAGGACCTCCG	TGCTTAGGTGCTTGAGAGGC	208	_No FA Found
>jgi|Phyca11|527667|estExt2_fgenesh1_pm.C_PHYCAscaffold_210082	Phyca_SSR689	(GGA)4	AGCAACCGACGAGAACTGAG	TTCAGGAAGTTCCCAGCGTC	112	_No FA Found
>jgi|Phyca11|527674|estExt2_fgenesh1_pm.C_PHYCAscaffold_210092	Phyca_SSR690	(CAG)4	CTCGATGATCCCTTCAGGCC	GACGCTCTTGACCTTCTGCT	145	_No FA Found
>jgi|Phyca11|527718|estExt2_fgenesh1_pm.C_PHYCAscaffold_220027	Phyca_SSR691	(GCT)4	AGGAGACGGTACTTCGAGCT	AAGATGCGACACAGACCCAG	283	_No FA Found
>jgi|Phyca11|527819|estExt2_fgenesh1_pm.C_PHYCAscaffold_230038	Phyca_SSR692	(TGG)4	GACCGCCCCGAAATTATTGC	CAGTACTCCGGTTCCACACC	179	_No FA Found
>jgi|Phyca11|527845|estExt2_fgenesh1_pm.C_PHYCAscaffold_230070	Phyca_SSR693	(CTC)4	AGCTCGGACTTTGACGTTGT	CTGAGCGCAAGTCGAACATG	244	_No FA Found
>jgi|Phyca11|527885|estExt2_fgenesh1_pm.C_PHYCAscaffold_230116	Phyca_SSR694	(AAG)4	TTTTACGCGGAAGGAGGACC	CTGCACCTGAAAGAGCTCCA	179	_No FA Found
>jgi|Phyca11|527887|estExt2_fgenesh1_pm.C_PHYCAscaffold_240003	Phyca_SSR695	(AAG)4	CTTCAGTGGACGCTGGTTCT	GCCACCCACTCGTCATGTAA	283	_No FA Found
>jgi|Phyca11|527893|estExt2_fgenesh1_pm.C_PHYCAscaffold_240009	Phyca_SSR696	(AGC)4	CAAACGCTTCAACGACAGCA	TTGCGCTCGTGAAGTTTGTG	229	_No FA Found

>jgi|Phyca11|527901|estExt2_fgenesh1_pm.C_PHYCAscaffold_240017	Phyca_SSR697	(GAC)4	CAACGACAACCACAACGACC	GGCAAATTGGTGCATGAGCT	223	_No FA Found
>jgi|Phyca11|527908|estExt2_fgenesh1_pm.C_PHYCAscaffold_240027	Phyca_SSR698	(TCG)4	AACCCATACGCTCACATGCA	GCCGATGGGATAGTACCAGC	198	_No FA Found
>jgi|Phyca11|528008|estExt2_fgenesh1_pm.C_PHYCAscaffold_250067	Phyca_SSR699	(TGC)4	TGCTGCTGAAGACACTGGAG	AGATCGAAGAGGCTTACGCG	226	_No FA Found
>jgi|Phyca11|528038|estExt2_fgenesh1_pm.C_PHYCAscaffold_260026	Phyca_SSR700	(TCG)4	TGTACAAGGACAAGGGCGAC	CACCTTGTTGTTCAGGTGCG	287	_No FA Found
>jgi|Phyca11|528165|estExt2_fgenesh1_pm.C_PHYCAscaffold_270069	Phyca_SSR701	(GAG)4	TCAGAGCTCTTTCCAGCAGC	GTGCTTGCACACTCAGTTGG	188	_No FA Found
>jgi|Phyca11|528181|estExt2_fgenesh1_pm.C_PHYCAscaffold_270085	Phyca_SSR702	(TGA)4	GTGGCGGAGTCTATGACGAG	GCTGCCACCATTCTTTTCGG	185	_No FA Found
>jgi|Phyca11|528249|estExt2_fgenesh1_pm.C_PHYCAscaffold_270160	Phyca_SSR703	(ACG)4	AGCTGCTCGAGTACAAACCC	CCAGCCGTACTTCTCAACGT	257	_No FA Found
>jgi|Phyca11|528365|estExt2_fgenesh1_pm.C_PHYCAscaffold_290051	Phyca_SSR704	(CAG)4	CTAAGTCTCGACCCGACGTG	CACTGCTCTGCTCACTGTCA	177	_No FA Found
>jgi|Phyca11|528395|estExt2_fgenesh1_pm.C_PHYCAscaffold_290091	Phyca_SSR705	(CAA)4	TGTACGCCTACAACGTGCTT	TTCAGCGAGAAGAGCAGCAA	290	_No FA Found
>jgi|Phyca11|528429|estExt2_fgenesh1_pm.C_PHYCAscaffold_300020	Phyca_SSR706	(GTC)4	GAATGGCAATTCGGTCACGG	GACCACATCACTCAGCGGAA	172	_No FA Found
>jgi|Phyca11|528598|estExt2_fgenesh1_pm.C_PHYCAscaffold_310081	Phyca_SSR707	(GTG)4	ACGATGACAGTGGCGGTATC	TGCGGGCTGGAATACTGTTT	282	_No FA Found
>jgi|Phyca11|528693|estExt2_fgenesh1_pm.C_PHYCAscaffold_320110	Phyca_SSR708	(ACA)4	CCGAAAACGCACTGAAGTCG	CGCCAACCAGAAAGTCTCCT	185	_No FA Found
>jgi|Phyca11|528723|estExt2_fgenesh1_pm.C_PHYCAscaffold_330042	Phyca_SSR709	(AGG)4	CAGGAAGCTTTGGAGACGGT	GTACACGTTCGTTATGCCGC	285	_No FA Found
>jgi|Phyca11|528779|estExt2_fgenesh1_pm.C_PHYCAscaffold_330105	Phyca_SSR710	(AAG)4	AACGTGAAGGAGACGAGCTG	GGGTCTCCAGTTCACGAAGG	276	_No FA Found
>jgi|Phyca11|528877|estExt2_fgenesh1_pm.C_PHYCAscaffold_350023	Phyca_SSR711	(GCT)4	CCTTTGCTTTGGGTGCGATC	TAGTCTTGCGCAGGTTCTGG	184	_No FA Found
>jgi|Phyca11|528890|estExt2_fgenesh1_pm.C_PHYCAscaffold_350037	Phyca_SSR712	(GAC)4	TGGTACAGTCAGTTTGGGGC	GTCATGAGGGGAAGACGGAC	297	_No FA Found
>jgi|Phyca11|528942|estExt2_fgenesh1_pm.C_PHYCAscaffold_350100	Phyca_SSR713	(GCT)4	TTCTAGAGCGCTACGTGCAG	GTCGAGCCCGCGAATAAAAC	227	_No FA Found
>jgi|Phyca11|528957|estExt2_fgenesh1_pm.C_PHYCAscaffold_360022	Phyca_SSR714	(GGA)4	TGAAGCCATGTTGTTGCGTG	CGTTCTCTCCGTTGCTGTCT	164	_No FA Found
>jgi|Phyca11|529156|estExt2_fgenesh1_pm.C_PHYCAscaffold_390040	Phyca_SSR715	(CCA)4	CTCTGTGCCGAAGACTCCAA	ATCATCTCTGCCATGCCGAG	271	_No FA Found
>jgi|Phyca11|529235|estExt2_fgenesh1_pm.C_PHYCAscaffold_400066	Phyca_SSR716	(GGA)4	GGAAGGACGCAGAGAACGAA	CTGTGGTGGGGAGCTTGTAG	269	_No FA Found

>jgi|Phyca11|529249|estExt2_fgenesh1_pm.C_PHYCAscaffold_400087	Phyca_SSR717	(AAG)4	CAGAAGCGACTCCAAGAGGG	GTCTCCACTGCATTCCGGAA	137	_No FA Found
>jgi|Phyca11|529355|estExt2_fgenesh1_pm.C_PHYCAscaffold_420044	Phyca_SSR718	(AGA)4	AGGACACTCATGCCGAACAG	ACGTGTTCCCCGTCATCTTC	274	_No FA Found
>jgi|Phyca11|529418|estExt2_fgenesh1_pm.C_PHYCAscaffold_430023	Phyca_SSR719	(CTT)4	GCAGGATGGGGAAGAGAACC	AAATCACCGCCCCGTACAAA	299	_No FA Found
>jgi|Phyca11|529424|estExt2_fgenesh1_pm.C_PHYCAscaffold_430030	Phyca_SSR720	(CCA)4	GAGCAAAAGAAACGCCAGCA	ATGCTTTCGACCCGGAAGTT	156	_No FA Found
>jgi|Phyca11|529532|estExt2_fgenesh1_pm.C_PHYCAscaffold_440043	Phyca_SSR721	(GAG)4	CGCTTTTTCCGCTGCGTATT	CGTCTTGAGCTCCGAAACCT	226	_No FA Found
>jgi|Phyca11|529559|estExt2_fgenesh1_pm.C_PHYCAscaffold_460012	Phyca_SSR722	(AGA)4	ACCACAGAACAGTTGGTGCA	TCCTCCGAATGTCGAGTCCT	129	_No FA Found
>jgi|Phyca11|529600|estExt2_fgenesh1_pm.C_PHYCAscaffold_460065	Phyca_SSR723	(AAG)4	GACGTGGCTGTTGAGAAGGA	CGCGCAGTAGTAGCATGGTA	297	_No FA Found
>jgi|Phyca11|529620|estExt2_fgenesh1_pm.C_PHYCAscaffold_460092	Phyca_SSR724	(AGG)4	GATGAAAATCGAGCGCCCAC	CACGCTTCCTGATCATTGCG	293	_No FA Found
>jgi|Phyca11|529649|estExt2_fgenesh1_pm.C_PHYCAscaffold_470025	Phyca_SSR725	(GCA)4	TGTGTTCGGTGCACGTATGA	AAGTCCGAGCCGAACTTGTC	132	_No FA Found
>jgi|Phyca11|529791|estExt2_fgenesh1_pm.C_PHYCAscaffold_490008	Phyca_SSR726	(AGA)4	AGAAAGCCGACGCGATAGAG	TGTGGTCATTTGATCTTCACTT	135	_No FA Found
>jgi|Phyca11|529849|estExt2_fgenesh1_pm.C_PHYCAscaffold_490086	Phyca_SSR727	(CAA)4	GAGGCATAGTCCCTGGCATG	CGCCACCATCCATAGCGTAA	291	_No FA Found
>jgi|Phyca11|529932|estExt2_fgenesh1_pm.C_PHYCAscaffold_510040	Phyca_SSR728	(CTT)4	ATGCTGGTGACGTACTGCC	CGTCTCCTTGCAGCTGGTTA	190	_No FA Found
>jgi|Phyca11|530200|estExt2_fgenesh1_pm.C_PHYCAscaffold_580039	Phyca_SSR729	(CAG)4	ATGGAGATGCAACGCCTTGA	GCTGCCACGAATTTTGGTGT	151	_No FA Found
>jgi|Phyca11|530299|estExt2_fgenesh1_pm.C_PHYCAscaffold_610001	Phyca_SSR730	(CTT)4	CATCACCCTGTTCGTGACCA	ACATTCGCCACCTTCTCGTT	162	_No FA Found
>jgi|Phyca11|530583|estExt2_fgenesh1_pm.C_PHYCAscaffold_700023	Phyca_SSR731	(GCT)4	GACGACCAACCTGGAAACCT	TCCCCGTACCAAAAGTCGTG	292	_No FA Found
>jgi|Phyca11|530603|estExt2_fgenesh1_pm.C_PHYCAscaffold_710011	Phyca_SSR732	(AGC)4	CCCAGAAGCAGCAGGATGAA	AGGATCAATGAGCAGTGGTCT	231	_No FA Found
>jgi|Phyca11|530616|estExt2_fgenesh1_pm.C_PHYCAscaffold_710025	Phyca_SSR733	(ACG)4	GTAAAGCTGCCCGCAACAAA	TCGGCTCTCCAAAATGTCCC	236	_No FA Found
>jgi|Phyca11|530940|estExt2_fgenesh1_pm.C_PHYCAscaffold_850011	Phyca_SSR734	(AAG)4	GAACAGCCAGGAAGCCTCAA	TGTCGGCGTCCATATTCGAG	152	_No FA Found
>jgi|Phyca11|531266|estExt2_fgenesh1_pm.C_PHYCAscaffold_104001	Phyca_SSR735	(GCG)4	CGACGACGACGATGGAAACT	CCTCCGACTGGAAATCGTCG	245	_No FA Found
>jgi|Phyca11|531269|estExt2_fgenesh1_pm.C_PHYCAscaffold_104001	Phyca_SSR736	(TCG)4	GACGATCGTCCGAGTCTTCC	ACTGCTGTCACTTGGGCTAC	275	_No FA Found

>jgi|Phyca11|531377|estExt2_fgenesh1_pm.C_PHYCAscaffold_1290000	Phyca_SSR737	(GCT)4	ACTGCAGGTGGATCTCAAGC	CTGCAGGTGGCTTTGGTAGA	296	_No FA Found
>jgi|Phyca11|531500|estExt2_fgenesh1_pg.C_PHYCAscaffold_10078	Phyca_SSR738	(GAA)4	TTTACCCGTTCAGCCTCCAC	CTACCGTTTCTGGTGCTGGT	116	_No FA Found
>jgi|Phyca11|531502|estExt2_fgenesh1_pg.C_PHYCAscaffold_10080	Phyca_SSR739	(GAA)4	GGTGGCACCTCGAAGAAGAA	TGTTCTCCGTTCTCAGTGGC	278	_No FA Found
>jgi|Phyca11|531577|estExt2_fgenesh1_pg.C_PHYCAscaffold_10205	Phyca_SSR740	(GAA)4	AGCAGACGAGCCAGAAGAAC	TTTAGTGCTGCGTCGTCCTT	129	_No FA Found
>jgi|Phyca11|531832|estExt2_fgenesh1_pg.C_PHYCAscaffold_20218	Phyca_SSR741	(GCT)4	ACGGTCGAACGAAGCACTAG	GGCTTCCAGTGCAATGGTTG	247	_No FA Found
>jgi|Phyca11|532007|estExt2_fgenesh1_pg.C_PHYCAscaffold_30180	Phyca_SSR742	(CAG)4	TTCAGGGACATCGTTCCAGC	GTAGAACTGCGGGGCTGATT	300	_No FA Found
>jgi|Phyca11|532069|estExt2_fgenesh1_pg.C_PHYCAscaffold_30261	Phyca_SSR743	(ACA)4	CAGACGGACGCCAACAATTC	GAGACTCGTCTTCCCTGTGC	252	_No FA Found
>jgi|Phyca11|532072|estExt2_fgenesh1_pg.C_PHYCAscaffold_30264	Phyca_SSR744	(GCA)4	GGAGAGAGATGCCTGCGTAC	GCGTCGAGAACTGGAGGAAA	226	_No FA Found
>jgi|Phyca11|532176|estExt2_fgenesh1_pg.C_PHYCAscaffold_40118	Phyca_SSR745	(GAC)4	CTGCCTTAGCCGAGATCCTG	CCTTCGAGCACCACTTCCAT	268	_No FA Found
>jgi|Phyca11|532286|estExt2_fgenesh1_pg.C_PHYCAscaffold_40263	Phyca_SSR746	(AGG)4	CGCACTGGACAAGTTTGACG	GCTTGGAGCTCTTCGTGAGT	203	_No FA Found
>jgi|Phyca11|532303|estExt2_fgenesh1_pg.C_PHYCAscaffold_40284	Phyca_SSR747	(CAA)4	GTCCCTCGATCGAACGGTAC	ATCCGCGTACGAGTCAGTTC	288	_No FA Found
>jgi|Phyca11|532429|estExt2_fgenesh1_pg.C_PHYCAscaffold_50166	Phyca_SSR748	(AGA)4	ATGTGTTCTTAGCCTCGGCC	GGTATCCTCCTGGGGGTGAT	277	_No FA Found
>jgi|Phyca11|532601|estExt2_fgenesh1_pg.C_PHYCAscaffold_60140	Phyca_SSR749	(GAT)4	CCATCGACTGCTACCATCCC	GTAGGACGTCGAGGAGGGAT	299	_No FA Found
>jgi|Phyca11|532615|estExt2_fgenesh1_pg.C_PHYCAscaffold_60161	Phyca_SSR750	(AAG)4	TCGTGGCTAATGGGAGCATC	CAGGCTGTCTGCTCTTCCTC	280	_No FA Found
>jgi|Phyca11|532745|estExt2_fgenesh1_pg.C_PHYCAscaffold_80012	Phyca_SSR751	(GCT)4	GAATCGCTCAAAGACGCGTC	ACTCAAACTCTGGCACTCCG	199	_No FA Found
>jgi|Phyca11|532846|estExt2_fgenesh1_pg.C_PHYCAscaffold_80154	Phyca_SSR752	(GAT)4	GCATCAACGCGTCAGCTAAG	TTTCGGTGCTGGAGCTTCAT	287	_No FA Found
>jgi|Phyca11|533060|estExt2_fgenesh1_pg.C_PHYCAscaffold_100047	Phyca_SSR753	(CTT)4	CTGCTACTGGACTTGCTGCT	TCGGCCGAGAAGGAGTTCTA	227	_No FA Found
>jgi|Phyca11|533117|estExt2_fgenesh1_pg.C_PHYCAscaffold_100126	Phyca_SSR754	(GGA)4	GAATCTACGAGCGCTCCGAA	CTTCTTCAAAGCCGCAGCAG	300	_No FA Found
>jgi|Phyca11|533155|estExt2_fgenesh1_pg.C_PHYCAscaffold_110021	Phyca_SSR755	(CGA)4	TCCACACCCAACGCTGTAC	TGATACTGGTCGCGGATGTG	269	_No FA Found
>jgi|Phyca11|533185|estExt2_fgenesh1_pg.C_PHYCAscaffold_110062	Phyca_SSR756	(GAA)4	AGCGAGCTCCATCATCTTCG	ACGCATTTCATTCTGGCTTCTC	115	_No FA Found

>jgi|Phyca11|533460|estExt2_fgenesh1_pg.C_PHYCAscaffold_140029	Phyca_SSR757	(ACG)4	CGACACGAACAACGAGATGC	ATGGTTGTGCTCCCTTCTCG	128	_No FA Found
>jgi|Phyca11|533584|estExt2_fgenesh1_pg.C_PHYCAscaffold_150062	Phyca_SSR758	(GAA)4	AAGGTGGAGATGGAGACGGA	CTCCGTCAGTGTATCCACCG	228	_No FA Found
>jgi|Phyca11|533633|estExt2_fgenesh1_pg.C_PHYCAscaffold_150127	Phyca_SSR759	(GAA)4	GACGTCATAGCCTCCGACAG	CTGCGTCAGGAGCTTCTGAA	234	_No FA Found
>jgi|Phyca11|533658|estExt2_fgenesh1_pg.C_PHYCAscaffold_160024	Phyca_SSR760	(AAG)4	AACTCTCAAGGAGCTCGTGC	GGCCCGTAGATTGAGTAGCC	225	_No FA Found
>jgi|Phyca11|533673|estExt2_fgenesh1_pg.C_PHYCAscaffold_160046	Phyca_SSR761	(GAC)4	CGTACGAGAGGGAGGTTTCG	TGCGGTGTGAGTTCTTCCTC	204	_No FA Found
>jgi|Phyca11|533823|estExt2_fgenesh1_pg.C_PHYCAscaffold_170159	Phyca_SSR762	(CAG)4	TCTCCGCAATGTTTCGGTCA	AAAGGACGGATCGCCAACTT	260	_No FA Found
>jgi|Phyca11|534078|estExt2_fgenesh1_pg.C_PHYCAscaffold_200046	Phyca_SSR763	(CTG)4	AGGCGTTTAAATGGCCTCGA	ATATCCGCTACCACACGCTG	237	_No FA Found
>jgi|Phyca11|534123|estExt2_fgenesh1_pg.C_PHYCAscaffold_200110	Phyca_SSR764	(CGA)4	CTGTCCAACGCAGAGCTGTA	GAGGGTTCAACAGACTGCGA	253	_No FA Found
>jgi|Phyca11|534149|estExt2_fgenesh1_pg.C_PHYCAscaffold_200140	Phyca_SSR765	(AGG)4	AACTCGAGGGTTTCCGCAAT	GACGGTAGCGCGTTGAGATA	283	_No FA Found
>jgi|Phyca11|534200|estExt2_fgenesh1_pg.C_PHYCAscaffold_210041	Phyca_SSR766	(TTC)4	GTTTGTGGTGACGCTGTTCC	GGAGAAGAGGACGCAAACCA	121	_No FA Found
>jgi|Phyca11|534256|estExt2_fgenesh1_pg.C_PHYCAscaffold_210124	Phyca_SSR767	(GGA)4	GTAGGCAAGCCCATCTTCGT	CCCGAACCGTTGATCACAGA	266	_No FA Found
>jgi|Phyca11|534276|estExt2_fgenesh1_pg.C_PHYCAscaffold_220016	Phyca_SSR768	(GAC)4	TTCTTCGTGCTCTTCGTGCT	GTGTTTCCGGAGACTGGAGG	215	_No FA Found
>jgi|Phyca11|534354|estExt2_fgenesh1_pg.C_PHYCAscaffold_230001	Phyca_SSR769	(AAG)4	TGGGAGCCTATCAGTGACGA	TCAATGAGTCCGTCTCGCAG	269	_No FA Found
>jgi|Phyca11|534363|estExt2_fgenesh1_pg.C_PHYCAscaffold_230011	Phyca_SSR770	(AAG)4	CAACCAGCGCAAAAAGACGA	CGTTCTAGGACGAGGCAGAC	215	_No FA Found
>jgi|Phyca11|534447|estExt2_fgenesh1_pg.C_PHYCAscaffold_230117	Phyca_SSR771	(CGT)4	ATTCTCTGCGCTCGTAGACG	GAATGTTGTTGTACGGGCCG	160	_No FA Found
>jgi|Phyca11|534488|estExt2_fgenesh1_pg.C_PHYCAscaffold_240048	Phyca_SSR772	(GAA)4	ATTGGCAAGACTGAGCACGA	CAGTGACGAGACCAAGCACT	262	_No FA Found
>jgi|Phyca11|534702|estExt2_fgenesh1_pg.C_PHYCAscaffold_270031	Phyca_SSR773	(GAA)4	TGTTGACTCCGATTGCAGCT	CACCTCACCGTTCGATTCCA	299	_No FA Found
>jgi|Phyca11|534813|estExt2_fgenesh1_pg.C_PHYCAscaffold_280056	Phyca_SSR774	(AGA)4	GGACTCAGTGGCGTATCTCG	CTCCTTCTTCTGCCGCTTCA	235	_No FA Found
>jgi|Phyca11|534864|estExt2_fgenesh1_pg.C_PHYCAscaffold_290016	Phyca_SSR775	(CAG)4	TGGTGAGTCAGCAGATGCAG	TAAATGGGTGGCACGCTCTT	224	_No FA Found
>jgi|Phyca11|535057|estExt2_fgenesh1_pg.C_PHYCAscaffold_310044	Phyca_SSR776	(AGG)4	GTGAAGGAGCTGGTGTTCGA	GAGTCCACATGCGTGACTGA	236	_No FA Found

>jgi|Phyca11|535074|estExt2_fgenesh1_pg.C_PHYCAscaffold_310065	Phyca_SSR777	(CAA)4	GTGGAGGATGAGTCTGTGGC	AGAAAGAGTCGGGTTGGCTG	288	_No FA Found
>jgi|Phyca11|535097|estExt2_fgenesh1_pg.C_PHYCAscaffold_310096	Phyca_SSR778	(AAG)4	GGAGAACCTGCGTTTCCGTA	CAGACCAGCAAGCATACGGA	253	_No FA Found
>jgi|Phyca11|535165|estExt2_fgenesh1_pg.C_PHYCAscaffold_320081	Phyca_SSR779	(TGC)4	AACCGCATTTTCGAGGAGGT	GTCGTACGTGTCGTCATGGA	294	_No FA Found
>jgi|Phyca11|535286|estExt2_fgenesh1_pg.C_PHYCAscaffold_330120	Phyca_SSR780	(GCT)4	CACGAACGACCAGAACCTGA	TAAGATTGCCAGCGACACGT	190	_No FA Found
>jgi|Phyca11|535325|estExt2_fgenesh1_pg.C_PHYCAscaffold_340047	Phyca_SSR781	(AGA)4	GCTCGTGCTCGACTTATGGA	GTTGCTCTCGCTTCGTCTCT	268	_No FA Found
>jgi|Phyca11|535379|estExt2_fgenesh1_pg.C_PHYCAscaffold_350032	Phyca_SSR782	(AGA)4	TAATCCGCTGTCTACCGCAC	AAAGCGGTAGTTGGCATGGA	266	_No FA Found
>jgi|Phyca11|535447|estExt2_fgenesh1_pg.C_PHYCAscaffold_360034	Phyca_SSR783	(GCT)4	CATCGGAATCGGGAGGAAGG	TCCTGTTGTCGTGTAGCCAC	181	_No FA Found
>jgi|Phyca11|535506|estExt2_fgenesh1_pg.C_PHYCAscaffold_370049	Phyca_SSR784	(TGA)4	TGGCGAATGTCCGTACAACA	GCCAAAACACAGCCAAGAGG	272	_No FA Found
>jgi|Phyca11|535610|estExt2_fgenesh1_pg.C_PHYCAscaffold_390007	Phyca_SSR785	(GGA)4	TCCGTCGTCAATCCATGGTG	CTGGTCGTCGTTGTACCACA	266	_No FA Found
>jgi|Phyca11|535691|estExt2_fgenesh1_pg.C_PHYCAscaffold_400059	Phyca_SSR786	(GAT)4	TTTCGCGTCCCACTTAACGA	TCGTTCTAGCGGCTGATGAC	257	_No FA Found
>jgi|Phyca11|535709|estExt2_fgenesh1_pg.C_PHYCAscaffold_400083	Phyca_SSR787	(ACA)4	TCGCAAACATTGACAGCAGC	GCATCGAACAGTGCGTCTTC	211	_No FA Found
>jgi|Phyca11|535901|estExt2_fgenesh1_pg.C_PHYCAscaffold_430052	Phyca_SSR788	(AGC)4	ATGCCGTAGATCGTCAGCAG	ACGGGATGACTTATGTGGGC	277	_No FA Found
>jgi|Phyca11|536029|estExt2_fgenesh1_pg.C_PHYCAscaffold_460057	Phyca_SSR789	(TCT)4	ATTCCCGAGAGCTCTTCCCT	CACGAGGTTCTTGGTCGACA	214	_No FA Found
>jgi|Phyca11|536081|estExt2_fgenesh1_pg.C_PHYCAscaffold_470035	Phyca_SSR790	(GCA)4	TGTGTTCGGTGCACGTATGA	AAGTCCGAGCCGAACTTGTC	132	_No FA Found
>jgi|Phyca11|536099|estExt2_fgenesh1_pg.C_PHYCAscaffold_470061	Phyca_SSR791	(CTT)4	TATGAGTGCGTTGGGCTCTG	TCCACGTCGGAGAAGAGACT	264	_No FA Found
>jgi|Phyca11|536234|estExt2_fgenesh1_pg.C_PHYCAscaffold_490049	Phyca_SSR792	(GAG)4	TGGACGTGGCTCAAGAGAAC	GCTGCCGTTCTACATGAGGT	263	_No FA Found
>jgi|Phyca11|536369|estExt2_fgenesh1_pg.C_PHYCAscaffold_520008	Phyca_SSR793	(GCT)4	CGGCGCAAAGGAAAACAAGA	CGTCCTTGGCGTTCGTTTTT	293	_No FA Found
>jgi|Phyca11|536486|estExt2_fgenesh1_pg.C_PHYCAscaffold_540035	Phyca_SSR794	(GAC)4	GCACGACGTGACACTACAGA	TGCTTGTCGCTCGTGAAGAT	283	_No FA Found
>jgi|Phyca11|536708|estExt2_fgenesh1_pg.C_PHYCAscaffold_610002	Phyca_SSR795	(CTT)4	ACTCGCACATCGGTCTCATC	CCCACATACGTACATGCCGA	265	_No FA Found
>jgi|Phyca11|536980|estExt2_fgenesh1_pg.C_PHYCAscaffold_700024	Phyca_SSR796	(GCT)4	CTCGTTGGTGAGCAGAAGGT	TTGCTTTCCATGCACTTGCC	260	_No FA Found

>jgi|Phyca11|537189|estExt2_fgenesh1_pg.C_PHYCAscaffold_770031	Phyca_SSR797	(GAA)4	ACAACAGCGGAAGAAGGAGG	TCGCCGTCCGTAAAGTCAAA	213	_No FA Found
>jgi|Phyca11|537323|estExt2_fgenesh1_pg.C_PHYCAscaffold_840018	Phyca_SSR798	(TCT)4	TGAGGTTCTTACGTGGCAGC	CCAGCATAGCACGCAATGAC	261	_No FA Found
>jgi|Phyca11|537682|estExt2_fgenesh1_pg.C_PHYCAscaffold_105001	Phyca_SSR799	(GCT)4	GCTCCAGCTGATCCAGTTGT	ACGTCACGAATGAACAGGCT	284	_No FA Found
>jgi|Phyca11|537721|estExt2_fgenesh1_pg.C_PHYCAscaffold_109000	Phyca_SSR800	(CCG)4	CTGCTTCGGAGTATGCTCGT	TCACGTCCGTGTCCTCCTTA	294	_No FA Found
>jgi|Phyca11|537876|estExt2_fgenesh1_pg.C_PHYCAscaffold_663000	Phyca_SSR801	(CGA)4	AGAAGGTCGAGGAGGAGGAC	TCTTATGATGCCGCTGGTCC	213	_No FA Found
>jgi|Phyca11|537937|estExt2_Genewise1Plus.C_PHYCAscaffold_1005	Phyca_SSR802	(ACT)4	ACTTGGCCGGCTTTGAAAAC	ACGTCCTTAAGGAGCTGCAC	286	_No FA Found
>jgi|Phyca11|538207|estExt2_Genewise1Plus.C_PHYCAscaffold_1069	Phyca_SSR803	(AGA)4	AAGCTGCAGCAGAATCGAGT	TGACGGTAAGATATGTTCTCG	225	_No FA Found
>jgi|Phyca11|538759|estExt2_Genewise1Plus.C_PHYCAscaffold_2037	Phyca_SSR804	(AGG)4	ACTGGAAAGAGCAGTCTGCC	TTCCAGGACCGAAACCCTTG	156	_No FA Found
>jgi|Phyca11|538968|estExt2_Genewise1Plus.C_PHYCAscaffold_2072	Phyca_SSR805	(CTC)4	CCATCGAGTTCGTCCGAGTC	ACCTCGACTCTGGTACCGAA	296	_No FA Found
>jgi|Phyca11|539340|estExt2_Genewise1Plus.C_PHYCAscaffold_3028	Phyca_SSR806	(GAA)4	CTGCTCAGCAAACACGCTTT	TTGGACGAAGAGGGAATCGC	265	_No FA Found
>jgi|Phyca11|539475|estExt2_Genewise1Plus.C_PHYCAscaffold_3052	Phyca_SSR807	(CAC)4	ATCGCAGGTTGATCAGGCAA	TGATGACGTGTGTGATGCCA	176	_No FA Found
>jgi|Phyca11|539640|estExt2_Genewise1Plus.C_PHYCAscaffold_3086	Phyca_SSR808	(AGG)4	TGTTCGTGACTAAGGACGGC	ACGAAGTATGGTCCAGCACC	264	_No FA Found
>jgi|Phyca11|539721|estExt2_Genewise1Plus.C_PHYCAscaffold_3096	Phyca_SSR809	(GCT)4	GTGGTGGCTTCGAGATTGGA	GGAGAGAGATGCCTGCGTAC	231	_No FA Found
>jgi|Phyca11|53999|gw1.13.151.1	Phyca_SSR810	(AGC)4	GCTTCCTAGACAAGCACCGT	CTCTTGAGTGGGTTCGGCTT	259	_IQ calmodulin-binding region
>jgi|Phyca11|540026|estExt2_Genewise1Plus.C_PHYCAscaffold_4035	Phyca_SSR811	(CGT)4	AGAGAAGTGCGTGAATGGGG	ACACTCCTCAAGACGTGCTG	259	_No FA Found
>jgi|Phyca11|540044|estExt2_Genewise1Plus.C_PHYCAscaffold_4037	Phyca_SSR812	(CAG)4	ATGCCTACTCCTGGTGCCTA	GGTGCATGGTTTCCAGGGTA	245	_No FA Found
>jgi|Phyca11|540210|estExt2_Genewise1Plus.C_PHYCAscaffold_4063	Phyca_SSR813	(GAA)4	TACCGCTGCATTCAACGACT	TTCTCACCCGGCACCTTTTT	147	_No FA Found
>jgi|Phyca11|540342|estExt2_Genewise1Plus.C_PHYCAscaffold_4083	Phyca_SSR814	(CGT)4	CCCCACAGTATGTTCGACCC	GGCAAGAAGACATGGAGGCT	121	_No FA Found
>jgi|Phyca11|540391|estExt2_Genewise1Plus.C_PHYCAscaffold_4089	Phyca_SSR815	(AAC)4	GTGGATTACCGTCAAACGCG	GAGTAGATCGACGCCTGGTG	260	_No FA Found
>jgi|Phyca11|540937|estExt2_Genewise1Plus.C_PHYCAscaffold_5085	Phyca_SSR816	(TCT)4	GGTCTCCGTCCATCACTTCG	CGACTCATCCAGTGGCAAGT	263	_No FA Found

>jgi|Phyca11|540949|estExt2_Genewise1Plus.C_PHYCAscaffold_5089	Phyca_SSR817	(CGT)4	ACCTTAAAGATGTGGGCCCG	AGGAAGTGATTGCGCTTGGA	266	_No FA Found
>jgi|Phyca11|540977|estExt2_Genewise1Plus.C_PHYCAscaffold_5092	Phyca_SSR818	(GAA)4	GTACGCGAAACACGAGCATC	TGAACCAGCTTCGTCTCCAG	152	_No FA Found
>jgi|Phyca11|541261|estExt2_Genewise1Plus.C_PHYCAscaffold_6039	Phyca_SSR819	(CGC)4	AACTTGGCGTCCTGTGTAGG	ATGACGCAGGACAAGCAGAA	290	_No FA Found
>jgi|Phyca11|541412|estExt2_Genewise1Plus.C_PHYCAscaffold_6072	Phyca_SSR820	(CCA)4	TACTCGACGGCGGAGAGTTA	CCGGATCTCGCCACTTAGAC	198	_No FA Found
>jgi|Phyca11|541447|estExt2_Genewise1Plus.C_PHYCAscaffold_6080	Phyca_SSR821	(GCA)4	TGGTTGCTGGAACGGTATCC	AACCGACGTCATACCCACAC	289	_No FA Found
>jgi|Phyca11|541448|estExt2_Genewise1Plus.C_PHYCAscaffold_6081	Phyca_SSR822	(GCA)4	TGGTTGCTGGAACGGTATCC	GCCATACCCACACCTGGAAA	282	_No FA Found
>jgi|Phyca11|541961|estExt2_Genewise1Plus.C_PHYCAscaffold_8018	Phyca_SSR823	(GTT)4	CCTCGAGTTGTGGAGCTGTT	CCTAGCAACACTGGCAGTCA	180	_No FA Found
>jgi|Phyca11|542182|estExt2_Genewise1Plus.C_PHYCAscaffold_8061	Phyca_SSR824	(TGA)4	TCAGAGGAGGAGGTTCCCTG	CCCTGATTCAGCCGAGGTTT	119	_No FA Found
>jgi|Phyca11|542247|estExt2_Genewise1Plus.C_PHYCAscaffold_9001	Phyca_SSR825	(CCA)4	AGCTCCTTCAACAGCAAGCT	TGACCCAGCTCGTACGAGTA	278	_No FA Found
>jgi|Phyca11|542491|estExt2_Genewise1Plus.C_PHYCAscaffold_9041	Phyca_SSR826	(TGA)4	CGAGAAGGGACCTCGTAACG	TACTCGTCGTCATCGTCGTC	135	_No FA Found
>jgi|Phyca11|5425|fgenesh1_pm.PHYCAscaffold_5_#_228	Phyca_SSR827	(AAG)4	GGCAAGAAAAGCAGTGCGAA	TTCTTGGCTGAGGCGTCTTT	209	_Galactose oxidase/kelch, beta-propeller
>jgi|Phyca11|542805|estExt2_Genewise1Plus.C_PHYCAscaffold_1002	Phyca_SSR828	(GAC)4	ACAAGCACCAGAAGGAGAGC	GCGTCTTGTGCTCGTTGTTT	237	_No FA Found
>jgi|Phyca11|542836|estExt2_Genewise1Plus.C_PHYCAscaffold_1002	Phyca_SSR829	(TCT)4	ACACAGTGCACGTTATGGTTG	GTGTAGTCGTGGCTGTTCCA	215	_No FA Found
>jgi|Phyca11|542897|estExt2_Genewise1Plus.C_PHYCAscaffold_1004	Phyca_SSR830	(AAG)4	GAGGCAGACTACGACATCGG	AGCCAATGAGATCCTCGTATT	279	_No FA Found
>jgi|Phyca11|543332|estExt2_Genewise1Plus.C_PHYCAscaffold_1105	Phyca_SSR831	(CTC)4	TAAACTCGACGCGAACCACA	TGATCGCCACATTGAGCTGT	149	_No FA Found
>jgi|Phyca11|543907|estExt2_Genewise1Plus.C_PHYCAscaffold_1302	Phyca_SSR832	(AGA)4	GCAAAGAAGGAAAGGGCTGC	CGTTCTTCGCTGGAGGAAGT	178	_No FA Found
>jgi|Phyca11|544004|estExt2_Genewise1Plus.C_PHYCAscaffold_1304	Phyca_SSR833	(TGG)4	CGGACCAGGTGGACTTCATC	GAGCTGGTCCTTCTTGCTGT	230	_No FA Found
>jgi|Phyca11|544217|estExt2_Genewise1Plus.C_PHYCAscaffold_1401	Phyca_SSR834	(GCG)4	TCACCTGTTAGCACGTCGAC	AAAGATCGTCTGCTGCTGCT	229	_No FA Found
>jgi|Phyca11|544662|estExt2_Genewise1Plus.C_PHYCAscaffold_1503	Phyca_SSR835	(AGG)4	CAAGATGTTGGTCAGTGCGC	GCCGACATGTAGCCGAAGTA	267	_No FA Found
>jgi|Phyca11|545221|estExt2_Genewise1Plus.C_PHYCAscaffold_1703	Phyca_SSR836	(TGC)4	TGCCTCGAATTCTTGGCACT	AGGATAACACTTGCCAGGGC	262	_No FA Found

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<tr><td>>jgi|Phyca11|548194|estExt2_Genewise1Plus.C_PHYCAscaffold_2704</td><td>Phyca_SSR849</td><td>(TGC)4</td><td>AGGACAAAGATGGAGGACGC</td><td>GCTTGCCGCCCATAATCATG</td><td>163</td><td>_No FA Found</td></tr>
<tr><td>>jgi|Phyca11|549603|estExt2_Genewise1Plus.C_PHYCAscaffold_3301</td><td>Phyca_SSR850</td><td>(TGA)4</td><td>CACGACAGAGAGCTCTCCAC</td><td>CCCTTCTCAACCAACACCGA</td><td>263</td><td>_No FA Found</td></tr>
<tr><td>>jgi|Phyca11|549905|estExt2_Genewise1Plus.C_PHYCAscaffold_3402</td><td>Phyca_SSR851</td><td>(CTG)4</td><td>GTGGACGGTCGTGATCAACT</td><td>TCCCGGTGCTATCTTCAGGA</td><td>226</td><td>_No FA Found</td></tr>
<tr><td>>jgi|Phyca11|550156|estExt2_Genewise1Plus.C_PHYCAscaffold_3502</td><td>Phyca_SSR852</td><td>(AGA)4</td><td>GCGCAGTCTATCGGGTACAA</td><td>ACGATCTTGTGGCTGTTCGT</td><td>239</td><td>_No FA Found</td></tr>
<tr><td>>jgi|Phyca11|550196|estExt2_Genewise1Plus.C_PHYCAscaffold_3600</td><td>Phyca_SSR853</td><td>(TCT)4</td><td>TTTTCGACCGAACCCTCAGG</td><td>ATGCACATCCGAGCTTTGGA</td><td>190</td><td>_No FA Found</td></tr>
<tr><td>>jgi|Phyca11|550198|estExt2_Genewise1Plus.C_PHYCAscaffold_3601</td><td>Phyca_SSR854</td><td>(CTT)4</td><td>CCCCTTTTGAGGACCCAGAC</td><td>CGTGCCCAGAAAGCTAGGAA</td><td>194</td><td>_No FA Found</td></tr>
<tr><td>>jgi|Phyca11|550201|estExt2_Genewise1Plus.C_PHYCAscaffold_3601</td><td>Phyca_SSR855</td><td>(GAA)4</td><td>GAAGACGACCTGGACATGGG</td><td>TTCTCGTTGGTTCTGGGCTC</td><td>234</td><td>_No FA Found</td></tr>
<tr><td>>jgi|Phyca11|550269|estExt2_Genewise1Plus.C_PHYCAscaffold_3602</td><td>Phyca_SSR856</td><td>(GCA)4</td><td>CACTTCGGTGTCTTCGGTGA</td><td>GTCTGCTGAGTCGAGTCGTC</td><td>179</td><td>_No FA Found</td></tr>
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>jgi|Phyca11|550392|estExt2_Genewise1Plus.C_PHYCAscaffold_3700	Phyca_SSR857	(TCT)4	CTGTGGTTTGGAAGTGTGCG	CACCAATACGACGTCCACCA	263	_No FA Found
>jgi|Phyca11|550400|estExt2_Genewise1Plus.C_PHYCAscaffold_3701	Phyca_SSR858	(AGC)4	GGCGGATCCTGATGAGTCTG	AGGAGGAGGAAGTAGCTGGG	175	_No FA Found
>jgi|Phyca11|550667|estExt2_Genewise1Plus.C_PHYCAscaffold_3801	Phyca_SSR859	(TGC)4	GCATCCCTATCTGCTTCCCG	AATGGCTTGGGAAGGTGCTT	253	_No FA Found
>jgi|Phyca11|550669|estExt2_Genewise1Plus.C_PHYCAscaffold_3801	Phyca_SSR860	(TGC)4	ATCCCCATTTGCATCCCGTG	TGGTGGTGGTAGTTGTCACG	122	_No FA Found
>jgi|Phyca11|550947|estExt2_Genewise1Plus.C_PHYCAscaffold_3903	Phyca_SSR861	(AGA)4	GCCCACCAGTGTGTATTCCA	TTTTGCCAGCTCTCGCAATG	243	_No FA Found
>jgi|Phyca11|551109|estExt2_Genewise1Plus.C_PHYCAscaffold_4002	Phyca_SSR862	(GAA)4	ACCCTTTGGAGCTTCGGATG	GAGCTTTTGGTTTCGCACGT	202	_No FA Found
>jgi|Phyca11|551304|estExt2_Genewise1Plus.C_PHYCAscaffold_4102	Phyca_SSR863	(GAA)4	GTGGTGAATCCCAGGACAGG	TGATGTCACCTCTGCTGCTG	261	_No FA Found
>jgi|Phyca11|551310|estExt2_Genewise1Plus.C_PHYCAscaffold_4102	Phyca_SSR864	(GCT)4	TATTGCCTGTGTGAGCGACC	TTGGAAAAGCTGGAGCCGAT	249	_No FA Found
>jgi|Phyca11|551390|estExt2_Genewise1Plus.C_PHYCAscaffold_4200	Phyca_SSR865	(AGC)4	GAGATGGTGGCGTTCCTGAA	ACAACGACGACCGAGATGTC	287	_No FA Found
>jgi|Phyca11|551655|estExt2_Genewise1Plus.C_PHYCAscaffold_4301	Phyca_SSR866	(GGA)4	TTCATCTACTCGCCGTTCGG	TACTTGGACGGGTCAATGGC	236	_No FA Found
>jgi|Phyca11|551663|estExt2_Genewise1Plus.C_PHYCAscaffold_4301	Phyca_SSR867	(ACA)4	ACCAGGTGCTATGAACCAGC	TGAGTTCACCGTCAATCGCA	247	_No FA Found
>jgi|Phyca11|551973|estExt2_Genewise1Plus.C_PHYCAscaffold_4403	Phyca_SSR868	(CTG)4	TGCTGGCTATACGGGGTACT	GAGCTCGTACGAGTCTTCCG	217	_No FA Found
>jgi|Phyca11|552194|estExt2_Genewise1Plus.C_PHYCAscaffold_4603	Phyca_SSR869	(CAA)4	TTGCAGTTCCCTTCGGACTC	CGGTTGCTGGAGAGGTTGAT	172	_No FA Found
>jgi|Phyca11|552341|estExt2_Genewise1Plus.C_PHYCAscaffold_4702	Phyca_SSR870	(GCA)4	CCAACACCAAAGCTGAAGCC	AGGAACGTACGAGCTGTTGG	119	_No FA Found
>jgi|Phyca11|552363|estExt2_Genewise1Plus.C_PHYCAscaffold_4702	Phyca_SSR871	(TCC)4	AGAAGCCCCACAAACCCAAA	GAATGGGAGCAGCCTTCTGT	174	_No FA Found
>jgi|Phyca11|552564|estExt2_Genewise1Plus.C_PHYCAscaffold_4802	Phyca_SSR872	(GGT)4	CATGCACAGCGTACCAAAGG	GGCAATTAGGCGATGGCTTG	212	_No FA Found
>jgi|Phyca11|552701|estExt2_Genewise1Plus.C_PHYCAscaffold_4900	Phyca_SSR873	(GCC)4	AACTAGGAATCCTGCGAGCG	CTTAAAGGAGGGGGAAGCCC	296	_No FA Found
>jgi|Phyca11|553155|estExt2_Genewise1Plus.C_PHYCAscaffold_5101	Phyca_SSR874	(GAA)4	TGCCCCTTATTGCTGTGAGG	ACACGGAAGTTTTCGCTTGC	185	_No FA Found
>jgi|Phyca11|553331|estExt2_Genewise1Plus.C_PHYCAscaffold_5202	Phyca_SSR875	(AAG)4	CGCTCAGATCGGACTCCTTC	GTATGCGTTTGGACCATCGC	282	_No FA Found
>jgi|Phyca11|553378|estExt2_Genewise1Plus.C_PHYCAscaffold_5300	Phyca_SSR876	(AGA)4	AATGGACAACCGCCAATTGC	GATCTCCTTCTCGAGTGCCG	289	_No FA Found

>jgi|Phyca11|553411|estExt2_Genewise1Plus.C_PHYCAscaffold_5300	Phyca_SSR877	(TGA)4	CGACGATCCGAGACCTCAAG	TGGTCTCCACTGGGAATTGC	297	_No FA Found
>jgi|Phyca11|553527|estExt2_Genewise1Plus.C_PHYCAscaffold_5302	Phyca_SSR878	(AAG)4	GCGTGGACCCGTACTTTTTG	CGTGTTCAACACCGCCAAAT	290	_No FA Found
>jgi|Phyca11|553643|estExt2_Genewise1Plus.C_PHYCAscaffold_5401	Phyca_SSR879	(AGG)4	CAGCCCAGCACAACAAACTC	CTCTTGCCCTGCCGCATATA	293	_No FA Found
>jgi|Phyca11|553918|estExt2_Genewise1Plus.C_PHYCAscaffold_5701	Phyca_SSR880	(AAG)4	GGCAGTGACGGTGAAGAAGA	TTCATCGCTGCTGTCACTGT	115	_No FA Found
>jgi|Phyca11|553919|estExt2_Genewise1Plus.C_PHYCAscaffold_5701	Phyca_SSR881	(CTT)4	CAGGTTTGACCGGTGCTTTG	AGCAGAAGCAGCAGAGGAAG	165	_No FA Found
>jgi|Phyca11|554070|estExt2_Genewise1Plus.C_PHYCAscaffold_5801	Phyca_SSR882	(TGA)4	GCCGATGAGGACGAAGACAT	CTCCAGAAGCTCGGGTCTTG	153	_No FA Found
>jgi|Phyca11|554408|estExt2_Genewise1Plus.C_PHYCAscaffold_6101	Phyca_SSR883	(AAG)4	TGACCTGTTGTTCGGCCTAC	GCGTCCAGGGATCTTCACAA	175	_No FA Found
>jgi|Phyca11|554424|estExt2_Genewise1Plus.C_PHYCAscaffold_6101	Phyca_SSR884	(GAT)4	AGGATGAAAACGTCCCCGAC	AGTCGTCATCGTCATCGTCG	135	_No FA Found
>jgi|Phyca11|554548|estExt2_Genewise1Plus.C_PHYCAscaffold_6300	Phyca_SSR885	(GAA)4	GCTGCTGCTCCTAAGAAGCT	TGGCGTCAATCTGCTTGAGT	217	_No FA Found
>jgi|Phyca11|554975|estExt2_Genewise1Plus.C_PHYCAscaffold_6601	Phyca_SSR886	(GCT)4	AATTGACCTCAGACGCGGTT	GTTAAGCTCGCCCCAGAACT	278	_No FA Found
>jgi|Phyca11|555183|estExt2_Genewise1Plus.C_PHYCAscaffold_7100	Phyca_SSR887	(AAG)4	GAGAGGCTGTGAGTGCAGTT	CGAAACCCGTAGTAGTCCGG	157	_No FA Found
>jgi|Phyca11|555263|estExt2_Genewise1Plus.C_PHYCAscaffold_7101	Phyca_SSR888	(AGA)4	CTCTATGACGTCCGAGCCAC	GATGATGAGCTTGCTGCACG	242	_No FA Found
>jgi|Phyca11|555655|estExt2_Genewise1Plus.C_PHYCAscaffold_7600	Phyca_SSR889	(GAT)4	GTACACGCACAAGAGTCCCA	GGTTTGTGTGCTCGTCTTCG	137	_No FA Found
>jgi|Phyca11|555715|estExt2_Genewise1Plus.C_PHYCAscaffold_7700	Phyca_SSR890	(CAG)4	CAAGAAATCGGCACAGTGGC	GCAGCACAGTCTGAAGTTGC	203	_No FA Found
>jgi|Phyca11|556263|estExt2_Genewise1Plus.C_PHYCAscaffold_8500	Phyca_SSR891	(AAC)4	CATCCTAGAGCCTGACGCAG	GTTCTGCGACAGGATGTCCA	106	_No FA Found
>jgi|Phyca11|556448|estExt2_Genewise1Plus.C_PHYCAscaffold_8900	Phyca_SSR892	(TCC)4	GCACAATTGGGCGAGTTGTT	GAAGAGACCGAACCCGACTG	197	_No FA Found
>jgi|Phyca11|556678|estExt2_Genewise1Plus.C_PHYCAscaffold_9301	Phyca_SSR893	(ATG)4	TTCAGACGCTACCAACACCC	TGTCGGTTTAAGAACGGGGG	294	_No FA Found
>jgi|Phyca11|557105|estExt2_Genewise1Plus.C_PHYCAscaffold_1020	Phyca_SSR894	(GAA)4	AGCAGTTGCCATCTGACGAA	TCGTTGTTGAACCGAAACGC	121	_No FA Found
>jgi|Phyca11|557159|estExt2_Genewise1Plus.C_PHYCAscaffold_1030	Phyca_SSR895	(AGG)4	GACTTCTTCACTGGTGCCGA	CGTCGTCCAGAATCTCCTCG	226	_No FA Found
>jgi|Phyca11|557220|estExt2_Genewise1Plus.C_PHYCAscaffold_1040	Phyca_SSR896	(TGA)4	ACGAGCACTACGGCTACATG	TCAGTTGAAGGTGAGCGGAC	226	_No FA Found

>jgi|Phyca11|557455|estExt2_Genewise1Plus.C_PHYCAscaffold_1170	Phyca_SSR897	(CTT)4	TGTGACCAACCTCATGACGG	CCGATGTAAGTACACGCCGA	258	_No FA Found
>jgi|Phyca11|557827|estExt2_Genewise1Plus.C_PHYCAscaffold_7170	Phyca_SSR898	(GAA)4	CCCGCCAGAGAACTTTGCTA	TCCTTATTGCCCGGAACACC	204	_No FA Found
>jgi|Phyca11|557901|estExt2_Genewise1.C_PHYCAscaffold_10062	Phyca_SSR899	(ACG)4	TCAGCTTACCAGGGTGCAAG	AGGCATACAACTGGACCAGC	292	_No FA Found
>jgi|Phyca11|558094|estExt2_Genewise1.C_PHYCAscaffold_10479	Phyca_SSR900	(GAC)4	TTCTGGAACAAGATCCCGGC	GTACGGTTCGTCCTGGAAGG	174	_No FA Found
>jgi|Phyca11|558196|estExt2_Genewise1.C_PHYCAscaffold_10770	Phyca_SSR901	(CTG)4	GAATCCTAATGACGCGTGGC	TCTTCCCCATAGCGGTCGTA	286	_No FA Found
>jgi|Phyca11|558324|estExt2_Genewise1.C_PHYCAscaffold_11032	Phyca_SSR902	(AGG)4	CACGCGATCGGCTTTTCAAT	GTGGGACTGAGGAGCTTCAC	291	_No FA Found
>jgi|Phyca11|55845|gw1.38.237.1	Phyca_SSR903	(GTG)4	GGGAGCTTTTCACAGGAGCT	AGCATTCGTTAACCCTGCCA	284	_AMP-dependent synthetase and ligase
>jgi|Phyca11|558527|estExt2_Genewise1.C_PHYCAscaffold_11463	Phyca_SSR904	(GAA)4	AAGGATGCGATCAAGACGCA	GTCTTTCTCCGTCAGCCACA	114	_No FA Found
>jgi|Phyca11|558582|estExt2_Genewise1.C_PHYCAscaffold_20151	Phyca_SSR905	(TTC)4	CCCAGGAGTTCGCTGACTTT	CTCCGATCGCCACAAGAAGT	150	_No FA Found
>jgi|Phyca11|558843|estExt2_Genewise1.C_PHYCAscaffold_20622	Phyca_SSR906	(AGA)4	AGAAGCGGAGGAAAACGGAG	GCTAGTCCCTGCCACATTGT	259	_No FA Found
>jgi|Phyca11|559091|estExt2_Genewise1.C_PHYCAscaffold_21071	Phyca_SSR907	(CGA)4	GCAAGCCTTCAAAAGCACGA	TCCACGCAATCACCAGTACC	290	_No FA Found
>jgi|Phyca11|559135|estExt2_Genewise1.C_PHYCAscaffold_21155	Phyca_SSR908	(GCT)4	CCTCGTGTTCATGTCGTCCA	AGCTCACAATCACGAGGGTG	300	_No FA Found
>jgi|Phyca11|559296|estExt2_Genewise1.C_PHYCAscaffold_30275	Phyca_SSR909	(CTT)4	GCATCCAAGGTCTGTTCCGA	GGATGCCGAACTCCGAGTAG	300	_No FA Found
>jgi|Phyca11|559325|estExt2_Genewise1.C_PHYCAscaffold_30332	Phyca_SSR910	(AAG)4	GGGGTTTCTGTCTGCCAAGA	GAAGTATCCGGTCAGGCTCG	281	_No FA Found
>jgi|Phyca11|559382|estExt2_Genewise1.C_PHYCAscaffold_30422	Phyca_SSR911	(TTG)4	TGGTTCGTTGGCATCTCGAA	ATCAAGTGGCCGGTGAGATG	280	_No FA Found
>jgi|Phyca11|559752|estExt2_Genewise1.C_PHYCAscaffold_40052	Phyca_SSR912	(AAG)4	TCCTCGAGATGAATCTGCGC	GGGTGAACTGTGAGCACGTA	246	_No FA Found
>jgi|Phyca11|559983|estExt2_Genewise1.C_PHYCAscaffold_40364	Phyca_SSR913	(ACC)4	CAAGCTTTTGGGCACGTTCA	CCAGGAACATCTTCGCCAGT	213	_No FA Found
>jgi|Phyca11|560887|estExt2_Genewise1.C_PHYCAscaffold_50883	Phyca_SSR914	(AGA)4	TTACAGTGTCTGGGTGCTGC	AGGTCCTTCCGTCCAGCTAT	220	_No FA Found
>jgi|Phyca11|561125|estExt2_Genewise1.C_PHYCAscaffold_60267	Phyca_SSR915	(GCC)4	CTTACTGCGGGCCATGAGAA	CTGTAGCTGCTAGACGGTCG	187	_No FA Found
>jgi|Phyca11|561240|estExt2_Genewise1.C_PHYCAscaffold_60490	Phyca_SSR916	(AAG)4	TGGAAGAGGAGGAACGCAAC	AAAATGATCACCCGGTCCCC	139	_No FA Found

>jgi|Phyca11|561297|estExt2_Genewise1.C_PHYCAscaffold_60592	Phyca_SSR917	(GAG)4	TTACGTCGCACTGCTGACTT	CCGTACCGAACAGACTTCCC	269	_No FA Found
>jgi|Phyca11|56185|gw1.9.187.1	Phyca_SSR918	(TGC)4	ACACCACGAGCTATGAACGG	AAGCCATTCCAGCATCGGAA	228	_Ankyrin
>jgi|Phyca11|562062|estExt2_Genewise1.C_PHYCAscaffold_80504	Phyca_SSR919	(GTG)4	AGATCCCCGTCGACTTCTCA	TTTCAGTCTGGGTTGTCGGG	171	_No FA Found
>jgi|Phyca11|5622|fgenesh1_pm.PHYCAscaffold_6_#_142	Phyca_SSR920	(GAA)4	TTAAGCCCTTCTTCCAGCGG	CTCGCCCATAAATTGGCGTG	230	_C2 calcium/lipid-binding region, CaLB
>jgi|Phyca11|562243|estExt2_Genewise1.C_PHYCAscaffold_90086	Phyca_SSR921	(AGC)4	TATCCGACAGCAGCACGATC	CTTCTCTTTGGCGCTTGAGC	110	_No FA Found
>jgi|Phyca11|562434|estExt2_Genewise1.C_PHYCAscaffold_90419	Phyca_SSR922	(GAA)4	CAGTGGTGGGTCTACGTGAC	CGTGAGTCTTGCCACCATCT	253	_No FA Found
>jgi|Phyca11|562678|estExt2_Genewise1.C_PHYCAscaffold_100102	Phyca_SSR923	(AAG)4	TGTTGTCTCTCGCTGACCAC	TAGCCAGAGTACCCCTTCCC	295	_No FA Found
>jgi|Phyca11|562935|estExt2_Genewise1.C_PHYCAscaffold_100543	Phyca_SSR924	(CGT)4	AGAAGAGGAACGGAAGCTGC	TTGCGTTCCTCAGCCAATCT	255	_No FA Found
>jgi|Phyca11|563060|estExt2_Genewise1.C_PHYCAscaffold_110115	Phyca_SSR925	(CTG)4	ATGATCCTCAACCTGAGCGC	GTTGCTCTTCTGGATGGCCT	297	_No FA Found
>jgi|Phyca11|563239|estExt2_Genewise1.C_PHYCAscaffold_110460	Phyca_SSR926	(CAG)4	TAGCGGCATTCGGACTGTTT	TGTTGGGTGTGCATTGACCT	173	_No FA Found
>jgi|Phyca11|563293|estExt2_Genewise1.C_PHYCAscaffold_110568	Phyca_SSR927	(GGA)4	TCTCCAGCAGTGGTATCGGA	ACTTGCGTCCAATCTCCGTT	113	_No FA Found
>jgi|Phyca11|563421|estExt2_Genewise1.C_PHYCAscaffold_120148	Phyca_SSR928	(TCG)4	AGCCATGAAGCAGAACTCGA	GTCCATGAAGGCTTCGTCCA	127	_No FA Found
>jgi|Phyca11|563934|estExt2_Genewise1.C_PHYCAscaffold_130387	Phyca_SSR929	(CGT)4	TTTTCCACCGACATGAGCGT	GCTGTCGAGAGATGTCGGAG	148	_No FA Found
>jgi|Phyca11|564193|estExt2_Genewise1.C_PHYCAscaffold_140152	Phyca_SSR930	(GTC)4	GTGGTATTGGTTGCTGCGAC	CCCATGTCGTCACTGGAACA	245	_No FA Found
>jgi|Phyca11|564492|estExt2_Genewise1.C_PHYCAscaffold_150107	Phyca_SSR931	(CAG)4	GCTGCGAATACCCTGAGTGT	CCTACTACACGCTCCTGTGC	221	_No FA Found
>jgi|Phyca11|564883|estExt2_Genewise1.C_PHYCAscaffold_160398	Phyca_SSR932	(CTT)4	GGTCTTCTCCTCTGTCCCCT	AGATCACAGCTCTCCATGCG	283	_No FA Found
>jgi|Phyca11|564884|estExt2_Genewise1.C_PHYCAscaffold_160399	Phyca_SSR933	(CTT)4	GGTCTTCTCCTCTGTCCCCT	AGATCACAGCTCTCCATGCG	283	_No FA Found
>jgi|Phyca11|564993|estExt2_Genewise1.C_PHYCAscaffold_160608	Phyca_SSR934	(GAG)4	GCTCTCCGGACTTGGAACTC	GCCACAGCTCCCTGAATCTT	226	_No FA Found
>jgi|Phyca11|565278|estExt2_Genewise1.C_PHYCAscaffold_170447	Phyca_SSR935	(GAA)4	ACATTCCGACCGACGTTTGA	CGAGGCACCTCTTCCTCTTC	221	_No FA Found
>jgi|Phyca11|565402|estExt2_Genewise1.C_PHYCAscaffold_180036	Phyca_SSR936	(AGG)4	TTTGGCAAGGCAGGAGTAGG	GGTTCACACGATGCATACGC	280	_No FA Found

>jgi|Phyca11|565415|estExt2_Genewise1.C_PHYCAscaffold_180059	Phyca_SSR937	(GAG)4	GCGATGATGAGAGCGAGGAA	CTTCTCCTTCCTCAGCCAGC	189	_No FA Found
>jgi|Phyca11|566695|estExt2_Genewise1.C_PHYCAscaffold_220218	Phyca_SSR938	(CTA)4	GTGTTCACTTTGCGGTGGAC	GTGATGATGCCGGCGTAGTA	269	_No FA Found
>jgi|Phyca11|567184|estExt2_Genewise1.C_PHYCAscaffold_240009	Phyca_SSR939	(CAG)4	GACGCGCCTAGTACTACACC	AATCCACGACAACCCAAGGC	150	_No FA Found
>jgi|Phyca11|567398|estExt2_Genewise1.C_PHYCAscaffold_240463	Phyca_SSR940	(ATG)4	ACCATACGAACATGACCCCG	TTTGCGCAAAGAGCTCACAC	251	_No FA Found
>jgi|Phyca11|568052|estExt2_Genewise1.C_PHYCAscaffold_270283	Phyca_SSR941	(GCA)4	CAGCAGCAACAACAACCTCC	CGACATGTCAAAGGGGTCCA	276	_No FA Found
>jgi|Phyca11|568110|estExt2_Genewise1.C_PHYCAscaffold_270349	Phyca_SSR942	(GAA)4	ACCTATGGAACCTTCACGCG	CGACAGCAGCAGACAAGAGA	269	_No FA Found
>jgi|Phyca11|568256|estExt2_Genewise1.C_PHYCAscaffold_280181	Phyca_SSR943	(AGA)4	GAGGTGCTGAAGAGGACGAC	GTCGGCAGCAAGAAATCGTC	232	_No FA Found
>jgi|Phyca11|568435|estExt2_Genewise1.C_PHYCAscaffold_290015	Phyca_SSR944	(CTG)4	CAGCTCCCTGAAGCCATTGA	ATCAGTCCCCAAAGCACGAG	221	_No FA Found
>jgi|Phyca11|568441|estExt2_Genewise1.C_PHYCAscaffold_290035	Phyca_SSR945	(TGC)4	GCTCGCTCCAGCATTTCAAG	CGCCTTCAAACGTAAAGCCC	164	_No FA Found
>jgi|Phyca11|568644|estExt2_Genewise1.C_PHYCAscaffold_290409	Phyca_SSR946	(GCT)4	CAGTTCTACGGTCGCAAGGT	CCAGACGATGACGATACCCG	299	_No FA Found
>jgi|Phyca11|569047|estExt2_Genewise1.C_PHYCAscaffold_310157	Phyca_SSR947	(CGA)4	TCTCTGGAAAAACCCGACGG	CGCACCTCTAACATCCCTCC	248	_No FA Found
>jgi|Phyca11|569235|estExt2_Genewise1.C_PHYCAscaffold_320020	Phyca_SSR948	(AGA)4	GGAGGAGATGACGCAGACAG	CCCTCGATCTGTTTGCCTGT	201	_No FA Found
>jgi|Phyca11|570034|estExt2_Genewise1.C_PHYCAscaffold_350131	Phyca_SSR949	(CGA)4	GTTTGTGTCACACCGTGCTC	AGGTAGCGCTTGCCTTTCTT	261	_No FA Found
>jgi|Phyca11|570644|estExt2_Genewise1.C_PHYCAscaffold_380147	Phyca_SSR950	(AGA)4	TAAGAAGCGGCAGTCACTGG	CCTTAAGCGGATCGAGACCC	233	_No FA Found
>jgi|Phyca11|570796|estExt2_Genewise1.C_PHYCAscaffold_390048	Phyca_SSR951	(CAG)4	TTCAGTGGGCTTCGACATCC	TCGCCTCCTCTATCTCCAGG	270	_No FA Found
>jgi|Phyca11|571228|estExt2_Genewise1.C_PHYCAscaffold_410155	Phyca_SSR952	(ACA)4	TACCCGCTGAGCAAGATGAC	TCGCCCTTGACAACCTTCTC	284	_No FA Found
>jgi|Phyca11|571405|estExt2_Genewise1.C_PHYCAscaffold_420119	Phyca_SSR953	(TTC)4	ACGTGTTCCCCGTCATCTTC	GAGGACACTCATGCCGAACA	275	_No FA Found
>jgi|Phyca11|571712|estExt2_Genewise1.C_PHYCAscaffold_430233	Phyca_SSR954	(AAG)4	GAACATGGGCCAAGGACAGA	TTTTCTTACGACGCTTGCGC	140	_No FA Found
>jgi|Phyca11|571795|estExt2_Genewise1.C_PHYCAscaffold_430340	Phyca_SSR955	(GAA)4	TCAAAGATTGGCGTCCTGCT	GAAGTTCAACCGCCGGTTTC	132	_No FA Found
>jgi|Phyca11|571830|estExt2_Genewise1.C_PHYCAscaffold_430388	Phyca_SSR956	(GAG)4	ACCCAGAGTACTGCGGCTA	AGAACATGCTCTCACGCACA	115	_No FA Found

>jgi|Phyca11|571966|estExt2_Genewise1.C_PHYCAscaffold_460011	Phyca_SSR957	(AGC)4	ACAAGGACTTCTCCGCACAG	GCCTCAAGGAGACCAACACA	271	_No FA Found
>jgi|Phyca11|572181|estExt2_Genewise1.C_PHYCAscaffold_460371	Phyca_SSR958	(AGC)4	AGAAGAATGCGCTGGCTGTA	GTGTTCTCAAACGTCACGGC	235	_No FA Found
>jgi|Phyca11|572372|estExt2_Genewise1.C_PHYCAscaffold_480019	Phyca_SSR959	(CAG)4	CGCCAGGAAGTCAAGGACAT	GTGGTGTTTGAGGAGCTCGA	205	_No FA Found
>jgi|Phyca11|572387|estExt2_Genewise1.C_PHYCAscaffold_480045	Phyca_SSR960	(CCT)4	GACAGTGACCTGGACTCTGC	TTTTGCGCGGCTTTTTAGCT	180	_No FA Found
>jgi|Phyca11|572653|estExt2_Genewise1.C_PHYCAscaffold_490072	Phyca_SSR961	(GCC)4	AACTAGGAATCCTGCGAGCG	CTTAAAGGAGGGGGAAGCCC	296	_No FA Found
>jgi|Phyca11|573217|estExt2_Genewise1.C_PHYCAscaffold_520109	Phyca_SSR962	(AGA)4	ACTGGAAGAGCAAACGCGTA	TGTCTGTAGGAGGACGTCGA	263	_No FA Found
>jgi|Phyca11|573444|estExt2_Genewise1.C_PHYCAscaffold_530236	Phyca_SSR963	(GTG)4	CTTCCCGTGGCACTGTGTAT	AGACGGACGACAATGTGTCC	262	_No FA Found
>jgi|Phyca11|573584|estExt2_Genewise1.C_PHYCAscaffold_540143	Phyca_SSR964	(TCG)4	TGCTTGTCGCTCGTGAAGAT	GCACGACGTGACACTACAGA	283	_No FA Found
>jgi|Phyca11|573714|estExt2_Genewise1.C_PHYCAscaffold_550085	Phyca_SSR965	(AGG)4	GGATGAGAAGTTCACGGCCA	TCAGCAAGCTTGGCTTCGTA	159	_No FA Found
>jgi|Phyca11|574276|estExt2_Genewise1.C_PHYCAscaffold_610002	Phyca_SSR966	(CTT)4	GACCATCGAGTACTGGCTGG	ACGTTCGCCACCTTCTCATT	147	_No FA Found
>jgi|Phyca11|574571|estExt2_Genewise1.C_PHYCAscaffold_640044	Phyca_SSR967	(GAA)4	GCGTCTAGCTGCCAAGGTTA	ACAAGGCACACGATAACGGT	199	_No FA Found
>jgi|Phyca11|574695|estExt2_Genewise1.C_PHYCAscaffold_650023	Phyca_SSR968	(GCT)4	GCAGTACCCTACGCTCATCC	GTAACCAGGAGTGCCGTTGA	295	_No FA Found
>jgi|Phyca11|5748|fgenesh1_pm.PHYCAscaffold_7_#_114	Phyca_SSR969	(TGC)4	GCACGGAGCAGACTCAAGAT	TCTGTGCGCTTCGTTGTAGT	216	_WW/Rsp5/WWP
>jgi|Phyca11|574927|estExt2_Genewise1.C_PHYCAscaffold_670021	Phyca_SSR970	(GGA)4	TGATCGCCGGTTTGACAGAA	TGCAGCTTCTTCGACGTGAT	277	_No FA Found
>jgi|Phyca11|575227|estExt2_Genewise1.C_PHYCAscaffold_710149	Phyca_SSR971	(GAA)4	TAACAAGGAGGTGACGGTGC	TTAGTGGCTTCCTCTGCTGC	240	_No FA Found
>jgi|Phyca11|575758|estExt2_Genewise1.C_PHYCAscaffold_780091	Phyca_SSR972	(CTG)4	GCTGCTTGGAATGGAGACCT	AAACAAACGCGTTCTCGGTG	155	_No FA Found
>jgi|Phyca11|575772|estExt2_Genewise1.C_PHYCAscaffold_780107	Phyca_SSR973	(GAA)4	CGGGTGCATCCAGAAGAGTT	GTCTCTTCTGGCTTGGCACT	158	_No FA Found
>jgi|Phyca11|576021|estExt2_Genewise1.C_PHYCAscaffold_820035	Phyca_SSR974	(TCG)4	CACTCGCAGTTACTGGAGCA	TACGTCCTTTGCCTGCGAAT	271	_No FA Found
>jgi|Phyca11|57674|gw1.29.142.1	Phyca_SSR975	(GAA)4	AAACGTCATGGCTGGTCAGT	TCGTTCTCTGCTGCTCGTTT	267	_No FA Found
>jgi|Phyca11|577084|estExt2_Genewise1.C_PHYCAscaffold_1020014	Phyca_SSR976	(GAG)4	CGACATTGCTATGCCTGTGC	AATCAGCACGACGTTCAGGT	274	_No FA Found

>jgi|Phyca11|577126|estExt2_Genewise1.C_PHYCAscaffold_1020080	Phyca_SSR977	(GCT)4	GAGTAGTCGAGCGCATTCGA	GGAGTGTTTGGAGCTGACGA	296	_No FA Found
>jgi|Phyca11|577333|estExt2_Genewise1.C_PHYCAscaffold_1080003	Phyca_SSR978	(GCG)4	GCTAGGTCTCTGCTTCGTCC	GGTACTTCTGGAGCGTCTCG	262	_No FA Found
>jgi|Phyca11|577399|estExt2_Genewise1.C_PHYCAscaffold_1120030	Phyca_SSR979	(GCA)4	AGAGAACATGTCGACGACCG	GGAGATGACGTCACTGCACA	217	_No FA Found
>jgi|Phyca11|577618|estExt2_Genewise1.C_PHYCAscaffold_1810018	Phyca_SSR980	(ATG)4	GGTGGTACCCTTCACAGCTC	TAGCGCCAATGTACTTGCCA	298	_No FA Found
>jgi|Phyca11|577650|estExt2_Genewise1.C_PHYCAscaffold_1960011	Phyca_SSR981	(CTG)4	GCTGCTTGGAATGGAGACCT	AAACAAACGCGTTCTCGGTG	155	_No FA Found
>jgi|Phyca11|5942|fgenesh1_pm.PHYCAscaffold_9_#_2	Phyca_SSR982	(AGA)4	AAGCGGACGAGACATTTGGT	GGGAATCCGCAACTGTCTCA	255	_Zinc finger, C2H2-type
>jgi|Phyca11|59630|gw1.67.177.1	Phyca_SSR983	(AAC)4	ACCACATGCAATTCGCCAAC	CTTGATTGGGGCACACCTCT	280	_No FA Found
>jgi|Phyca11|5985|fgenesh1_pm.PHYCAscaffold_9_#_45	Phyca_SSR984	(CGT)4	CAGGTCTTCAGATACCGCCC	CAAGCGCCACAATGACAACA	163	_PDZ/DHR/GLGF
>jgi|Phyca11|61794|gw1.12.403.1	Phyca_SSR985	(AGC)4	GTGTCCGTGCCTCCCAAATA	TTCGTCAAATCAAACGCCCG	142	_No FA Found
>jgi|Phyca11|6218|fgenesh1_pm.PHYCAscaffold_10_#_65	Phyca_SSR986	(CTG)4	GCAACCGAGTGTGTTGTTCC	CGACTCGAAGTACGCGATCA	247	_ABC transporter-like
>jgi|Phyca11|6221|fgenesh1_pm.PHYCAscaffold_10_#_68	Phyca_SSR987	(TCT)4	CGTCAGGGTCCTCTTCAACC	TGAAGGGAAATGGTCGTCGG	155	_Protein kinase-like
>jgi|Phyca11|6236|fgenesh1_pm.PHYCAscaffold_10_#_83	Phyca_SSR988	(AAC)4	TAAAGGAGGCACAAGCGGAG	CGCTTTCAGTCCCCATGTCT	201	_Calcium-binding EF-hand
>jgi|Phyca11|63065|gw1.28.305.1	Phyca_SSR989	(GTC)4	TAGGCCCCTACCTATCGACG	TTCACGAGTGTAGCCCATCG	206	_No FA Found
>jgi|Phyca11|6388|fgenesh1_pm.PHYCAscaffold_11_#_104	Phyca_SSR990	(ACT)4	TCGACTGTTGACACTGGCTC	GCATTAGTGGATGGGCTCGA	104	_No FA Found
>jgi|Phyca11|6432|fgenesh1_pm.PHYCAscaffold_12_#_12	Phyca_SSR991	(AAG)4	CTACGCAGTGGGACGTTCTT	AGGACGGACATTAGGGTGGA	248	_DNA/RNA helicase, C-terminal
>jgi|Phyca11|6476|fgenesh1_pm.PHYCAscaffold_12_#_56	Phyca_SSR992	(AAG)4	TGGAGCCCGTGAATTCAGTC	TCGTGTTCCTTGCCATCCTC	231	_Armadillo-type fold
>jgi|Phyca11|64992|gw1.31.233.1	Phyca_SSR993	(TCA)4	TGTCGGAGTTTTCCCTCACG	TCCCGGATTCAGAGTAGCCA	236	_MFS general substrate transporter
>jgi|Phyca11|6846|fgenesh1_pm.PHYCAscaffold_15_#_7	Phyca_SSR994	(AGG)4	ACGACGACTTGTACGACTCG	CTTCTGGCAGCTCCTCCAAA	246	_No FA Found
>jgi|Phyca11|70884|gw1.7.536.1	Phyca_SSR995	(CTT)4	ACCACGCTCAGAGAAGTGTG	TTCTGCGTGAGTCGAGTTCC	178	_No FA Found
>jgi|Phyca11|71255|gw1.28.529.1	Phyca_SSR996	(AGA)4	ACCGCTTGGGATACTGCAAA	CGCACAACCCGATCCAATTC	187	_No FA Found

>jgi|Phyca11|7315|fgenesh1_pm.PHYCAscaffold_18_#_78	Phyca_SSR997	(TGC)4	ATCTCTGGACCCCGTACGAA	GCTTTCTTCGTGGGAGATCCA	191	_Tetrapyrrole biosynthesis, hydroxymethylbilane syntha
>jgi|Phyca11|73386|gw1.14.468.1	Phyca_SSR998	(ACG)4	CGACACGAACAACGAGATGC	GATGGCTGTGCTCCCTTCTC	129	_No FA Found
>jgi|Phyca11|7371|fgenesh1_pm.PHYCAscaffold_19_#_25	Phyca_SSR999	(AGG)4	GGTCGAAGCTGGAAGTTGGA	CTCCACCTTCCCCATCCAAC	113	_Acyl-CoA N-acyltransferase
>jgi|Phyca11|73986|gw1.29.509.1	Phyca_SSR100	(GAG)4	TTCGTGACAGTACTGGACGC	CTTCCACCTCAACTGCGACT	176	_AARP2CN
>jgi|Phyca11|7659|fgenesh1_pm.PHYCAscaffold_21_#_32	Phyca_SSR100	(CTT)4	CATTGACGCGCGTACGATTT	AGATCAAGAAACGCGGCAGA	255	_ABC transporter-like
>jgi|Phyca11|79622|gw1.5.936.1	Phyca_SSR100	(CCT)4	GCGAATCCGAGGGTACTCAG	GTGGTCCGTGGTCAGCTAAA	236	_No FA Found
>jgi|Phyca11|80082|gw1.15.753.1	Phyca_SSR100	(GAT)4	CACTCCTTGAGCGTTGGGAT	CAATTTCGGCTACACGCTCG	252	_No FA Found
>jgi|Phyca11|80827|gw1.3.1127.1	Phyca_SSR100	(TGC)4	GATCGAGCTGCTGCAATTGG	TCAACTACGTCAAGGTGGCC	122	_Ankyrin
>jgi|Phyca11|81603|gw1.5.1157.1	Phyca_SSR100	(GAA)4	TGGTGAAGCTGTTTTGTGCG	TCTTTCTCCGTCAGCCACAC	202	_No FA Found
>jgi|Phyca11|82056|gw1.24.644.1	Phyca_SSR100	(ACA)4	ACCGTATATTAAAGGGAAGTA	CCAACCTCCACCAGATTCCC	228	_Protein kinase-like
>jgi|Phyca11|82761|gw1.10.825.1	Phyca_SSR100	(AGC)4	CTACCGACTCCGCAGATGAC	TGGCATTTCCAGAGTTGTTCC	180	_No FA Found
>jgi|Phyca11|8443|fgenesh1_pm.PHYCAscaffold_28_#_26	Phyca_SSR100	(AGC)4	GGCGTCCGAGAAAATGATGC	ATCAAGGCTCGTTCGTCGTT	250	_No FA Found
>jgi|Phyca11|8502|fgenesh1_pm.PHYCAscaffold_28_#_85	Phyca_SSR100	(TGC)4	TCTCGGCTCCAAGTGCTTTC	TCCAGTAATGCCACCCAACC	180	_Esterase, SGNH hydrolase-type
>jgi|Phyca11|8556|fgenesh1_pm.PHYCAscaffold_29_#_37	Phyca_SSR101	(AGA)4	AGACAGAGAAAGGCTGGCAC	TTGGTCGTTGCTGAGTCTCC	183	_Zinc finger, C2H2-type
>jgi|Phyca11|8853|fgenesh1_pm.PHYCAscaffold_31_#_73	Phyca_SSR101	(GAA)4	AGGTGAACGCTGATGGTGAG	ACGACGGTTGATACGAGCTC	266	_No FA Found
>jgi|Phyca11|8856|fgenesh1_pm.PHYCAscaffold_31_#_76	Phyca_SSR101	(GAA)4	CGTGTGGATGGACAAAGGGA	TCTGGAAATGGGTCGAGTGC	254	_Cupredoxin
>jgi|Phyca11|8998|fgenesh1_pm.PHYCAscaffold_33_#_22	Phyca_SSR101	(AAG)4	AGACAGCTTCGACTGGCAAA	GACGAAGAAGCACCACCAGA	238	_Programmed cell death protein 2, C-terminal
>jgi|Phyca11|9132|fgenesh1_pm.PHYCAscaffold_34_#_49	Phyca_SSR101	(TGC)4	GGCTCGGACGGATCTAAGTG	TTCTCCTTGAGGAACGCCAC	221	_Carbohydrate/puine kinase, PfkB, conserved site
>jgi|Phyca11|9291|fgenesh1_pm.PHYCAscaffold_36_#_6	Phyca_SSR101	(TGC)4	GATAGCCTTCGTGACCGGAG	TTGCGTGTACGGAAATCCCA	298	_NAD(P)-binding
>jgi|Phyca11|9440|fgenesh1_pm.PHYCAscaffold_37_#_91	Phyca_SSR101	(AAG)4	CAAATTGGTGCGTTGAACCC	GCGTAATTCGAGCGACACAC	198	_Helix-loop-helix DNA-binding

>jgi|Phyca11|9495|fgenesh1_pm.PHYCAscaffold_38_#_44	Phyca_SSR101	(TCG)4	CGAGTGCTGTGCTCTCTGAA	ATGGGGCCCTGTAGACAGAT	245	_Rieske [2Fe-2S] region
>jgi|Phyca11|96584|e_gw1.1.1722.1	Phyca_SSR101	(CCT)4	GACCACCTTAACGGACTGGG	GGTGTTGAAGCGGACAAACC	153	_No FA Found
>jgi|Phyca11|9670|fgenesh1_pm.PHYCAscaffold_40_#_58	Phyca_SSR101	(TCT)4	AGAGGGACGTGCAACACAAA	TAGGGGGAGCCAGCAATAGT	300	_MFS general substrate transporter
>jgi|Phyca11|96762|e_gw1.1.162.1	Phyca_SSR102	(AAG)4	GGCCTCAACGTGAGCTTCA	CATGAAGCGGAAGGTCTGGT	153	_No FA Found
>jgi|Phyca11|96990|e_gw1.1.1729.1	Phyca_SSR102	(AAG)4	TTGCCCACGAAGTAGAGCAG	GGATTGACTGACCACAGCCA	261	_No FA Found
>jgi|Phyca11|97362|e_gw1.1.470.1	Phyca_SSR102	(GCT)4	GCGTCAGATGTACGATCCGT	GATGCTCAAATTCCACCGGC	272	_Taurine catabolism dioxygenase TauD/TfdA
>jgi|Phyca11|97491|e_gw1.2.1214.1	Phyca_SSR102	(CAC)4	ACCCGAAGAATCTCCCTGGA	TAGAAGCACAAGAGCGCTCC	225	_No FA Found
>jgi|Phyca11|9772|fgenesh1_pm.PHYCAscaffold_41_#_66	Phyca_SSR102	(GAA)4	CAGACACAGCAGGCAGTACA	CCTTGGCCTTCTGCTTGGTA	232	_C2 calcium/lipid-binding region, CaLB
>jgi|Phyca11|97809|e_gw1.2.1146.1	Phyca_SSR102	(AGA)4	ACCGCTTGGGATACTGCAAA	CTCCCGTGCTGAGAAAGTGT	159	_No FA Found
>jgi|Phyca11|97969|e_gw1.2.679.1	Phyca_SSR102	(GGA)4	AGGCTGCTGAAGACTGTGAC	TACCAACACCGACCTGCTTC	226	_WD40 repeat-like
>jgi|Phyca11|98452|e_gw1.2.451.1	Phyca_SSR102	(GAC)4	CCGACGACTAAGCCGCTATT	ACGAGCTAGCACTGCATTGT	120	_WW/Rsp5/WWP
>jgi|Phyca11|98753|e_gw1.3.496.1	Phyca_SSR102	(CGA)4	ATGCATGAGTGGTTGCGAGA	ACGCTCTTCGAACCAGTACG	161	_No FA Found
>jgi|Phyca11|98824|e_gw1.3.28.1	Phyca_SSR102	(GTG)4	CTCAGCCATGAACCTGGTGT	GCCAACCTTGCGATTGTTGT	262	_ABC transporter, transmembrane region, type 1
>jgi|Phyca11|99107|e_gw1.3.487.1	Phyca_SSR103	(ACT)4	TGGCTCTTGGCGCTAAATGA	TACGGCAGCTGTATTAGGCG	144	_CENP-B protein
>jgi|Phyca11|99315|e_gw1.3.993.1	Phyca_SSR103	(AGA)4	AGCGCCAGTTTCTACGACAA	CGTTTCCTCAGCTCCACCTT	277	_No FA Found
>jgi|Phyca11|99345|e_gw1.3.595.1	Phyca_SSR103	(AGC)4	TTACGAACTTAAGGCCCCCG	GAGATGAATAGCCCCACCCG	283	_Site-specific DNA-methyltransferase (cytosine-N4-spe
>jgi|Phyca11|9976|fgenesh1_pm.PHYCAscaffold_43_#_90	Phyca_SSR103	(ACA)4	AGTCTGCCAAAGAGCCGTAC	AACACCTCAGCGATCACAGG	298	_Annexin
>jgi|Phyca11|99958|e_gw1.4.612.1	Phyca_SSR103	(GAG)4	GGGCGAGGAGAACAAAGAGT	CAAGCACTCAGGCTTCAGGA	172	_RNA helicase, DEAD-box type, Q motif
>jgi|Phyca11|99996|e_gw1.4.1212.1	Phyca_SSR103	(GAA)4	TGACCAGGCACTCCACTCTA	AACACACAACCAGCCTGGAA	168	_No FA Found
>jgi|Phyca11|100791|e_gw1.5.596.1	Phyca_SSR103	(ACGC)3	ATCCAGCCAAGTTGCCCTAC	AGGTCTCGGTACTCGTGGAA	243	_No FA Found

>jgi|Phyca11|101012|e_gw1.5.1236.1	Phyca_SSR103	(GGAC)3	AGCGGTGGTCTCTCCTTTTG	AGCGGGTGTAGATCTGGTCT	251	_No FA Found
>jgi|Phyca11|103818|e_gw1.8.402.1	Phyca_SSR103	(TGGC)3	GCGATTGGACTGGAATGTGC	GAGGAAGACACACCACCGAG	255	_No FA Found
>jgi|Phyca11|105940|e_gw1.11.567.1	Phyca_SSR103	(CTTC)3	ATGAGCCTGTTACGAGCCTG	AGTATTCGCCTGACGCACAA	238	_No FA Found
>jgi|Phyca11|106647|e_gw1.12.635.1	Phyca_SSR104	(GAAA)3	CTGTCGTGTATGTACTGTTTCG	GCGTCACAGTCCCAACACTA	235	_No FA Found
>jgi|Phyca11|107879|e_gw1.14.455.1	Phyca_SSR104	(GATC)3	GCAAAACGCCCAGACAACAT	TGGTGTATGGTCCAACACGG	236	_No FA Found
>jgi|Phyca11|108142|e_gw1.14.443.1	Phyca_SSR104	(CAGC)3	ATTGCGCTGGAGTTCGAGAA	ACTCTCCAAGGAAACAGCGG	169	_No FA Found
>jgi|Phyca11|108546|e_gw1.15.608.1	Phyca_SSR104	(GATC)3	GACCGCTGATTTCACCCAGA	CATGCGATCATCGGGGAGAT	103	_No FA Found
>jgi|Phyca11|108694|e_gw1.15.125.1	Phyca_SSR104	(GGAA)3	CCACCGGTCTCTACTTACGC	GCGCATTCACGATGAAGTCC	197	_No FA Found
>jgi|Phyca11|10974|fgenesh1_pm.PHYCAscaffold_59_#_14	Phyca_SSR104	(CTCG)3	TCCTCGAGCAAGCAATGGTT	CGCATCCTTGGCAATCTTCG	101	_Armadillo-type fold
>jgi|Phyca11|110909|e_gw1.19.291.1	Phyca_SSR104	(CGAG)3	CAGAAACGACTAGCGGGACA	CCACCACTGTTTCGGTCGTA	223	_No FA Found
>jgi|Phyca11|112507|e_gw1.22.512.1	Phyca_SSR104	(GGAC)3	TGGCGGACTGAAAGCAGAAT	TGCTGCTTGATCGGCTTACT	176	_No FA Found
>jgi|Phyca11|113854|e_gw1.25.214.1	Phyca_SSR104	(CTCG)3	CTTGTTGCCTTGACACTGGC	GAGGCTCGTCATCACTCAGG	166	_No FA Found
>jgi|Phyca11|114308|e_gw1.26.111.1	Phyca_SSR104	(GACG)3	ACCACCACATGAAGCACCAA	CTCATTTCAGCGCGTACAGC	285	_No FA Found
>jgi|Phyca11|115961|e_gw1.29.25.1	Phyca_SSR105	(CGTA)3	TCGATCCACGAGCAACTTCG	CGTGACCAGCTCCAAGGAAT	192	_No FA Found
>jgi|Phyca11|116364|e_gw1.30.564.1	Phyca_SSR105	(CAAC)3	CAAACCCACACAAGAGCTGC	ATCACCGAGCGCCTTATGAG	298	_No FA Found
>jgi|Phyca11|116574|e_gw1.31.204.1	Phyca_SSR105	(GCCA)3	CGTTACCTTCAGCTGGCTCA	GGGTCCAACGAAGCCAAAAC	244	_No FA Found
>jgi|Phyca11|117946|e_gw1.34.416.1	Phyca_SSR105	(AGCG)3	CGAGTCAGGCAAGAACCAGT	TCTTCCCCATTGCTGCAGAG	287	_No FA Found
>jgi|Phyca11|118597|e_gw1.36.259.1	Phyca_SSR105	(ATCG)3	AACCAAGTCCTCGCGACATT	GGATATCTGCAGGTGGGTCG	235	_No FA Found
>jgi|Phyca11|119447|e_gw1.38.138.1	Phyca_SSR105	(ATAC)3	TCAGGCTTCATGTGACCACC	CATTCGACACGTCCAAACCG	215	_No FA Found
>jgi|Phyca11|119783|e_gw1.39.228.1	Phyca_SSR105	(GGAT)3	TGCGACGGTAAACCCTTTGA	AGTTGGCTTTCTTGCTCTCCA	295	_No FA Found

>jgi|Phyca11|119807|e_gw1.39.180.1	Phyca_SSR105	(GGAT)3	CGGTAAGCCCTTTGACGTCT	GCTCTCCAGCACACGACG	280	_No FA Found
>jgi|Phyca11|120438|e_gw1.41.46.1	Phyca_SSR105	(CGAG)3	CGAAGACCAAGAAGCCTCGA	GAGGTCCAACTCGGCTTTCA	287	_No FA Found
>jgi|Phyca11|121297|e_gw1.43.156.1	Phyca_SSR105	(ATTT)3	ACTTGTTCGTGGTGGTGGTT	TTCGAGACCTCTTGCACCAC	204	_No FA Found
>jgi|Phyca11|121416|e_gw1.44.56.1	Phyca_SSR106	(GCTG)3	ACGGTCCTGCTTCAAGAGTG	ACGTTGCTGTAGATTGGCCA	225	_No FA Found
>jgi|Phyca11|121804|e_gw1.46.284.1	Phyca_SSR106	(GGAT)3	AAGGACGATGTTGCTGGTGT	CACTTGTCGCCTGTTGCAAA	108	_No FA Found
>jgi|Phyca11|123134|e_gw1.49.69.1	Phyca_SSR106	(GAGC)3	TCTAGGAAACGCCGTCACAC	CAGCGCCACAATGAGAATCG	234	_No FA Found
>jgi|Phyca11|124947|e_gw1.55.146.1	Phyca_SSR106	(GTCC)3	GCCTCGTGGTGTTCCCTTTA	TGACGTCCAAGGTGTTACCG	129	_No FA Found
>jgi|Phyca11|125463|e_gw1.58.148.1	Phyca_SSR106	(GTGG)3	CACGACAACGAGTTCGCTTC	CTACGGTGAGCCAATCAGGG	196	_No FA Found
>jgi|Phyca11|125983|e_gw1.60.29.1	Phyca_SSR106	(AGCA)3	GTCAGCACTTGGAGACGTCA	CAACTGGACTTGCACATGCC	143	_No FA Found
>jgi|Phyca11|126401|e_gw1.63.189.1	Phyca_SSR106	(GATC)3	TCATGGAAGCTGTTGCCACA	AGCGCTCAACATCCTTCCTC	300	_No FA Found
>jgi|Phyca11|127013|e_gw1.66.187.1	Phyca_SSR106	(GATG)3	CACAGATCAGCAAGGACGGT	CCCGGGGAATCGAAGCAATA	202	_No FA Found
>jgi|Phyca11|128053|e_gw1.73.13.1	Phyca_SSR106	(GACA)3	TATTGGAAAGTGGGGCGGAC	TCCGTCTGTTCGAGATTGGC	128	_No FA Found
>jgi|Phyca11|128065|e_gw1.73.197.1	Phyca_SSR106	(CAAG)3	GTCCTCCTTACAAGCCCACC	GCCTCTTCCGAGAGCTTGTT	156	_No FA Found
>jgi|Phyca11|128339|e_gw1.75.28.1	Phyca_SSR107	(CCAA)3	GAGCTCGTCCAGGCACTATC	ACTTGCCGGTATCCACTGTG	189	_No FA Found
>jgi|Phyca11|128655|e_gw1.77.202.1	Phyca_SSR107	(ACGT)3	GGACAAGGTGGATCCAGTGG	AGAAAGCTTCGACCTTGCCA	278	_No FA Found
>jgi|Phyca11|128908|e_gw1.79.95.1	Phyca_SSR107	(CAGC)3	GTCTCGCGAGATTCTGAGGG	TCAATCACTGGCAGCCAAC	235	_No FA Found
>jgi|Phyca11|129113|e_gw1.81.47.1	Phyca_SSR107	(CAGA)3	GAACTGCTCACCTGGGTCAA	TTTCACCCAAGCGTCGAAGA	297	_No FA Found
>jgi|Phyca11|129462|e_gw1.84.2.1	Phyca_SSR107	(GGAA)3	ATCGTGCTTCGGTATTCCCC	CCGTGTCCAGTTCATCTGCT	279	_No FA Found
>jgi|Phyca11|129549|e_gw1.85.117.1	Phyca_SSR107	(TTCA)3	GCTATTCCAACGTCTTCGGC	CAACCAATGCTTGTGACCGA	158	_No FA Found
>jgi|Phyca11|129896|e_gw1.89.61.1	Phyca_SSR107	(GAGT)3	ATCCGTGACCGTGACTATGC	GCACAACGATGGAGCGAATC	215	_No FA Found

>jgi|Phyca11|130418|e_gw1.93.13.1	Phyca_SSR107	(GGCG)3	CCTATCCCTAATGGCTGCCG	ATAAGGGAACAGCGCCAGTC	152	_No FA Found
>jgi|Phyca11|130486|e_gw1.94.76.1	Phyca_SSR107	(GCGA)3	CGGAGTCGATCGTGTGGAAG	AGTTGTGCAGGTGGAAATCCA	159	_No FA Found
>jgi|Phyca11|130615|e_gw1.96.24.1	Phyca_SSR107	(TGCT)3	GATGCTGCACGATACGGAGA	TTACTTTTCCTCCGTGCAGT	181	_No FA Found
>jgi|Phyca11|130666|e_gw1.96.61.1	Phyca_SSR108	(TGCG)3	CGAACAGCTGTACGGCATTG	AGCGCGAGTTTCTTGTAGCT	249	_No FA Found
>jgi|Phyca11|130906|e_gw1.99.84.1	Phyca_SSR108	(ACTG)3	CGTATTTCTGGAGCGCGTTG	CAAACGTTGTTGGATGCCGA	147	_No FA Found
>jgi|Phyca11|131444|e_gw1.106.41.1	Phyca_SSR108	(GACA)3	ATCGCCAGACACGACAAAGT	GCCGTTCGTATGAAACACCG	268	_No FA Found
>jgi|Phyca11|132113|e_gw1.136.10.1	Phyca_SSR108	(CCAT)3	CTTTCGACGTCGCATGACAC	CCCTCTGTCCCGTGAATGAC	189	_No FA Found
>jgi|Phyca11|132126|e_gw1.136.18.1	Phyca_SSR108	(TTCA)3	ATGGTGTGGGAGTTCGCAAA	CAAGAGACAACCGATTGCGC	118	_No FA Found
>jgi|Phyca11|132376|e_gw1.158.18.1	Phyca_SSR108	(CATT)3	GAAGCAACTATTCCGCTGCG	AGCTGATGTTGGCGATCACA	206	_No FA Found
>jgi|Phyca11|132444|e_gw1.167.22.1	Phyca_SSR108	(ATGC)3	TCGTGCGGTGAACAGAATGA	GAGCACCGCAGTATACAGCA	283	_No FA Found
>jgi|Phyca11|133559|e_gw1.551.1.1	Phyca_SSR108	(TATT)3	CGGAACCAGGTGCGTCATTA	TGACATCTTCGCGATCCTCG	167	_No FA Found
>jgi|Phyca11|14024|fgenesh1_pg.PHYCAscaffold_5_#_238	Phyca_SSR108	(GGAA)3	GTCTCTCTTTGCCGGTTGGA	ACGTCAGGTTGAACAGGTCC	251	_No FA Found
>jgi|Phyca11|14110|fgenesh1_pg.PHYCAscaffold_6_#_32	Phyca_SSR108	(CCGT)3	AGGAAGAGGGTGGCTACGAT	TTCAGCCGATTTCTGAGCGT	227	_No FA Found
>jgi|Phyca11|14271|fgenesh1_pg.PHYCAscaffold_7_#_10	Phyca_SSR109	(GAAA)3	TCGCAAGAGATCGAGCATCC	TGTCTGGGTACGTTGTCAGC	220	_T-complex 10/CenJ, C-terminal
>jgi|Phyca11|18478|fgenesh1_pg.PHYCAscaffold_37_#_42	Phyca_SSR109	(GATG)3	AGTTTGTTCCAGGGCGACAA	CTCTTCGACTGAGGCAGACG	300	_Zinc finger, C2H2, LYAR-type
>jgi|Phyca11|18575|fgenesh1_pg.PHYCAscaffold_38_#_21	Phyca_SSR109	(TTCG)3	GACGAAGCACTGGAGGCTTT	TACGGGACACATCAACGGTG	217	_No FA Found
>jgi|Phyca11|18723|fgenesh1_pg.PHYCAscaffold_40_#_14	Phyca_SSR109	(TGCA)3	ATGGGCGTGTGTAGCATTCA	AACTTCGTCTCGTCAGCCAG	242	_WD40 repeat-like
>jgi|Phyca11|20520|fgenesh1_pg.PHYCAscaffold_65_#_64	Phyca_SSR109	(ACGC)3	CGACCGTATTCATCGCCTCA	CTGTCGCTTTATGCCGCTTC	260	_AWS
>jgi|Phyca11|21266|fgenesh1_pg.PHYCAscaffold_87_#_17	Phyca_SSR109	(CTCC)3	GCATTTCAAGGCGGCTGAAA	TCGACGGTCCATTTTCTCGT	112	_No FA Found
>jgi|Phyca11|21377|fgenesh1_pg.PHYCAscaffold_93_#_11	Phyca_SSR109	(ATCG)3	GTGGCAATGACGAGCAATCC	TCAAGGACCAGCATTGACCC	272	_EGF-like region, conserved site

>jgi|Phyca11|34538|gw1.41.10.1	Phyca_SSR109	(TGTC)3	GTGAAGCTCCACACATCCCA	TATCCTTGCGTCGCAGTTGT	115	_DNA/RNA helicase, ATP-dependent, DEAH-box type,
>jgi|Phyca11|39204|gw1.13.86.1	Phyca_SSR109	(CGTA)3	CGGCGAATCGGAGGGAAATA	ACGTGGCTCTTCACTCCAAG	265	_Phosphoglycerate/bisphosphoglycerate mutase
>jgi|Phyca11|40265|gw1.28.61.1	Phyca_SSR109	(TCTG)3	GAGCACCGACAAAGACTGGA	GATGAAGGTCAACGCATCGC	223	_Peptidase, cysteine peptidase active site
>jgi|Phyca11|4500|fgenesh1_pm.PHYCAscaffold_2_#_96	Phyca_SSR110	(CTCG)3	AAAGAAGGAGGCCGAAGCTC	ACATGAACAGCTGCAGTGGA	213	_No FA Found
>jgi|Phyca11|47653|gw1.206.7.1	Phyca_SSR110	(CAAA)3	TGAAGCAATTTGTGGTGCGG	CTTTCCAACGCTGCTCAACC	258	_HAT dimerisation
>jgi|Phyca11|49781|gw1.687.1.1	Phyca_SSR110	(GTTT)3	CACAGCCTCCGGGAATACTC	CTGTACTGGTAGCGAGCTCG	114	_GroEL-like chaperone, ATPase
>jgi|Phyca11|502542|fgenesh2_kg.PHYCAscaffold_1_#_2_#_Contig26	Phyca_SSR110	(CGAG)3	TGAGTACGAGCTTCGATGGC	CGGCTTGCCTTCTATCGGAT	222	_No FA Found
>jgi|Phyca11|502920|fgenesh2_kg.PHYCAscaffold_2_#_36_#_Contig4	Phyca_SSR110	(ACAG)3	GCGCTGTCTCCTTCGAGTAA	GCGAAAAAGACGTGTCTCGG	252	_No FA Found
>jgi|Phyca11|503038|fgenesh2_kg.PHYCAscaffold_2_#_154_#_gi|1890	Phyca_SSR110	(ACTG)3	CGCCAAGGAGGTGCAAAGTA	CTTCGTCTAAGATCGGCCCC	278	_No FA Found
>jgi|Phyca11|503235|fgenesh2_kg.PHYCAscaffold_3_#_100_#_Contig	Phyca_SSR110	(ACTA)3	AGGATGAGCAGTCGTTGTCG	GTAGTAGTCTCGCTGCTGCC	264	_No FA Found
>jgi|Phyca11|503545|fgenesh2_kg.PHYCAscaffold_4_#_84_#_Contig5	Phyca_SSR110	(CAAC)3	TGCAGTCCAAACTCATTCCTCA	ACCGCGTAGAATTCTTGGCA	260	_No FA Found
>jgi|Phyca11|503678|fgenesh2_kg.PHYCAscaffold_4_#_217_#_Contig	Phyca_SSR110	(AAGC)3	CTGTTGCGTGAAACGATGCA	TTTGTCGCCTCCAGTACACC	197	_No FA Found
>jgi|Phyca11|503876|fgenesh2_kg.PHYCAscaffold_5_#_40_#_409863	Phyca_SSR110	(GAAG)3	AGCCAGACACTGTTCGTCTG	AGGAGTTGCAGTTGGAGCTC	283	_No FA Found
>jgi|Phyca11|503886|fgenesh2_kg.PHYCAscaffold_5_#_50_#_Contig5	Phyca_SSR111	(CGAA)3	GACACCGACCAGTCTTCGTT	TAACGTCAGCCGATCAAGCA	166	_No FA Found
>jgi|Phyca11|504126|fgenesh2_kg.PHYCAscaffold_6_#_43_#_Contig2	Phyca_SSR111	(AAGA)3	CTTTCCAATGTTGTGCGCCA	CACTGCCAGATTCGGACTCA	256	_No FA Found
>jgi|Phyca11|504776|fgenesh2_kg.PHYCAscaffold_9_#_167_#_Contig	Phyca_SSR111	(GCTC)3	ACAGCGTGTGGACAAGAGTC	GAAGAGCAGGTTCAGTGGCT	216	_No FA Found
>jgi|Phyca11|504947|fgenesh2_kg.PHYCAscaffold_10_#_107_#_Conti	Phyca_SSR111	(GTGC)3	TTCATCCTCTTTGGCGGCTT	GAGGAGTCTGCATCAGTCCG	265	_No FA Found
>jgi|Phyca11|505086|fgenesh2_kg.PHYCAscaffold_11_#_32_#_40973	Phyca_SSR111	(AACG)3	GGATTCCCCGTATCCGACAC	ACCCTTCGAAGCACTCCTTG	248	_No FA Found
>jgi|Phyca11|505476|fgenesh2_kg.PHYCAscaffold_13_#_126_#_4101	Phyca_SSR111	(ACCA)3	AGCGACATCCATTGCTTCCA	GTAGTCGTAGTGAGGCGTCG	181	_No FA Found
>jgi|Phyca11|505958|fgenesh2_kg.PHYCAscaffold_17_#_43_#_40966	Phyca_SSR111	(GCTG)3	TCCAGCTACGAGTCTCACGA	CGTCAGCTCCTCCAAAAGGT	183	_No FA Found

>jgi|Phyca11|506274|fgenesh2_kg.PHYCAscaffold_18_#_147_#_4101	Phyca_SSR111	(TCCG)3	CTCGGGTATTCTCGCTCACC	TCGAGCATTTCCTTGTCGCT	240	_No FA Found
>jgi|Phyca11|506513|fgenesh2_kg.PHYCAscaffold_20_#_59_#_41005	Phyca_SSR111	(GCTC)3	CCTACCCCTTGAAGAGTGCG	TTCGAGGGAAAGTGTCGAGC	273	_No FA Found
>jgi|Phyca11|506606|fgenesh2_kg.PHYCAscaffold_20_#_152_#_Conti	Phyca_SSR111	(GACA)3	CAGGGCCACTACAGAAACGT	CTCCAAGGCGTGAAACTTGC	279	_No FA Found
>jgi|Phyca11|506620|fgenesh2_kg.PHYCAscaffold_20_#_166_#_gi|18	Phyca_SSR112	(GCAA)3	TTGACTTGGGAGCTTTGCCA	AGAATTGCGTGTCGGTCAGT	282	_No FA Found
>jgi|Phyca11|507073|fgenesh2_kg.PHYCAscaffold_24_#_65_#_Contig	Phyca_SSR112	(GGCA)3	GAGAACAGCAGCACAGAGGA	ACTCAAGACACACCACAGCC	116	_No FA Found
>jgi|Phyca11|507143|fgenesh2_kg.PHYCAscaffold_25_#_27_#_gi|189	Phyca_SSR112	(GGAC)3	GATCGACTCGAACGCGTACT	GTTGACGGACGTCCTTGTCT	194	_No FA Found
>jgi|Phyca11|507158|fgenesh2_kg.PHYCAscaffold_25_#_42_#_41043	Phyca_SSR112	(CAGC)3	CCGCTAAGTCCTGGTACGTC	CCAAAAGCTCTGGACAACGC	279	_No FA Found
>jgi|Phyca11|507502|fgenesh2_kg.PHYCAscaffold_28_#_9_#_Contig1	Phyca_SSR112	(CTTA)3	GTTTCGTATTCGGGGGTGGT	GCACCGTCCTGTATCTAGCC	184	_No FA Found
>jgi|Phyca11|507861|fgenesh2_kg.PHYCAscaffold_30_#_130_#_Conti	Phyca_SSR112	(GTGA)3	TCACCTTCGCAGCTGGAATT	GCGCTTTTTCCCTCTCCTCT	292	_No FA Found
>jgi|Phyca11|508226|fgenesh2_kg.PHYCAscaffold_33_#_85_#_Contig	Phyca_SSR112	(ACGT)3	AAGCCGAGTCAGACGTGAAG	AAAGCCAGCACCTTGGAGTT	273	_No FA Found
>jgi|Phyca11|508566|fgenesh2_kg.PHYCAscaffold_36_#_19_#_41018	Phyca_SSR112	(CAAC)3	TAAACGACCACAAGCCCTCC	TGTACTGCGACAGGTTGGTC	274	_No FA Found
>jgi|Phyca11|508797|fgenesh2_kg.PHYCAscaffold_38_#_49_#_Contig	Phyca_SSR112	(GGCT)3	ACAGGAGGCAAGCAGAACTC	ACAACCTCTTCGCCCTTCTG	202	_No FA Found
>jgi|Phyca11|508904|fgenesh2_kg.PHYCAscaffold_39_#_71_#_Contig	Phyca_SSR112	(AAGC)3	TGTCTCCGTCCGTTCAAGTG	TCAAAATGCCGTCTCTGCAC	199	_No FA Found
>jgi|Phyca11|509033|fgenesh2_kg.PHYCAscaffold_41_#_29_#_40973	Phyca_SSR113	(CAGA)3	TTCGAGAGCTCCAGGACGTA	TCGTTCGACAGCACGTTGTA	241	_No FA Found
>jgi|Phyca11|509786|fgenesh2_kg.PHYCAscaffold_49_#_78_#_40972	Phyca_SSR113	(GTGC)3	TGTGCTGGTACGAACAGGTC	TGACATCGCCTGCTCGATAC	272	_No FA Found
>jgi|Phyca11|509812|fgenesh2_kg.PHYCAscaffold_50_#_13_#_gi|189	Phyca_SSR113	(GCTC)3	GACGATTCCTCTGCCTCAGG	GAGTAGATCCGCTTCCTGGC	191	_No FA Found
>jgi|Phyca11|509814|fgenesh2_kg.PHYCAscaffold_50_#_15_#_41015	Phyca_SSR113	(GAAG)3	AGATGTTGTACCGGTGGCAG	TCCATTGTGACCGCCATCTC	286	_No FA Found
>jgi|Phyca11|509888|fgenesh2_kg.PHYCAscaffold_51_#_15_#_Contig	Phyca_SSR113	(GAGC)3	ACCGCTTGGTTGTGAGAGAG	CCTGCTACCTTTGGACTGGG	179	_No FA Found
>jgi|Phyca11|510818|fgenesh2_kg.PHYCAscaffold_67_#_29_#_Contig	Phyca_SSR113	(CCGA)3	ATGGTGGATCTGTTGCACGT	GAAGTACCGGCCGATAAGGG	219	_No FA Found
>jgi|Phyca11|510843|fgenesh2_kg.PHYCAscaffold_68_#_19_#_Contig	Phyca_SSR113	(AGCA)3	TGCAACGTGAATGTCGAGGA	CGTTGGTAGGACAGAAGCGT	286	_No FA Found

>jgi|Phyca11|510891|fgenesh2_kg.PHYCAscaffold_70_#_37_#_410188	Phyca_SSR113	(GTAG)3	CACGAGACACTGCAGGACTT	CCATGCAGGTCTATCTCTGCA	122	_No FA Found
>jgi|Phyca11|511030|fgenesh2_kg.PHYCAscaffold_73_#_1_#_4098799	Phyca_SSR113	(CCAC)3	GTTGCCACTACCCGAGAACA	ACGTTATGCAGTCGCTTCCA	172	_No FA Found
>jgi|Phyca11|511179|fgenesh2_kg.PHYCAscaffold_78_#_14_#_gi|1890	Phyca_SSR113	(GTGC)3	GGGCTTCAAGTGTCCTCCTC	TTGTCGAATGCTGAGTCGCT	183	_No FA Found
>jgi|Phyca11|511258|fgenesh2_kg.PHYCAscaffold_80_#_2_#_Contig7	Phyca_SSR114	(GATG)3	CTAATACCCCGTCGCTGCAT	CACGCCTCAATGAACTCCCT	280	_No FA Found
>jgi|Phyca11|511297|fgenesh2_kg.PHYCAscaffold_80_#_41_#_Contig	Phyca_SSR114	(AGTA)3	TGAGAGAGAAATGCAGGGCG	CTTCACTGCTACGACGTGGA	222	_No FA Found
>jgi|Phyca11|511525|fgenesh2_kg.PHYCAscaffold_87_#_31_#_409872	Phyca_SSR114	(TCGC)3	CCTACCAGACCACCAACACC	TCTTCTTCCTCGAAACGGCC	148	_No FA Found
>jgi|Phyca11|511697|fgenesh2_kg.PHYCAscaffold_95_#_26_#_Contig	Phyca_SSR114	(TGTC)3	TCCACTCGTCTTTGGGCATC	GAAACTTTCGCAAGCCTCCG	269	_No FA Found
>jgi|Phyca11|512033|fgenesh2_kg.PHYCAscaffold_119_#_2_#_Contig	Phyca_SSR114	(TGAC)3	AAGCTACAGGAAGTGCGTCC	AGGTAGTAGCCCATGGACGT	213	_No FA Found
>jgi|Phyca11|512133|fgenesh2_kg.PHYCAscaffold_243_#_1_#_jgi|JGI_	Phyca_SSR114	(TCCT)3	GTACAACACGCAGGAGGACA	TGACAAATCCCGATGCAGCT	160	_No FA Found
>jgi|Phyca11|512156|fgenesh2_kg.PHYCAscaffold_341_#_1_#_Contig	Phyca_SSR114	(GTGC)3	CTAACCCGATCTCCAGCGTC	GAGCGAGTAATCTCCGACCG	233	_No FA Found
>jgi|Phyca11|512178|fgenesh2_kg.PHYCAscaffold_447_#_1_#_jgi|JGI_	Phyca_SSR114	(TCCT)3	GTACAACACGCAGGAGGACA	AATCCCGATGTAGCTGGTCG	155	_No FA Found
>jgi|Phyca11|525644|estExt2_fgenesh1_pm.C_PHYCAscaffold_40197	Phyca_SSR114	(ACCG)3	GGTAAAACGGGGCCTACGAA	CGTAGATCCTTCACCTCGGC	269	_No FA Found
>jgi|Phyca11|525779|estExt2_fgenesh1_pm.C_PHYCAscaffold_50073	Phyca_SSR114	(AGTG)3	CATGGGCTACTACGGCTCTG	GGTGGTGGGTTCCTCATCAG	273	_No FA Found
>jgi|Phyca11|526027|estExt2_fgenesh1_pm.C_PHYCAscaffold_60111	Phyca_SSR115	(CAGA)3	TGTGGACCGTGCACAGTATC	GTAAACCTGCCACCACTCGA	257	_No FA Found
>jgi|Phyca11|526037|estExt2_fgenesh1_pm.C_PHYCAscaffold_60122	Phyca_SSR115	(ACGT)3	GCGACGTTGTAAACACCGAG	CGTAGGACAACTGCCATCGA	290	_No FA Found
>jgi|Phyca11|526800|estExt2_fgenesh1_pm.C_PHYCAscaffold_130057	Phyca_SSR115	(TCGT)3	GCCCAGCACACTTGAAACTT	GGTTCCTTCGACACCTCTGG	133	_No FA Found
>jgi|Phyca11|526928|estExt2_fgenesh1_pm.C_PHYCAscaffold_140061	Phyca_SSR115	(GGTA)3	TCAACAACATCAAGTGCGCG	TGTTTTCGATAGTATTGAGGT	263	_No FA Found
>jgi|Phyca11|527198|estExt2_fgenesh1_pm.C_PHYCAscaffold_170075	Phyca_SSR115	(AGAA)3	GCTGGATGGGTAGAGCGTAC	GCTTGCACGTCATGTAGCAG	150	_No FA Found
>jgi|Phyca11|528091|estExt2_fgenesh1_pm.C_PHYCAscaffold_260086	Phyca_SSR115	(TTGC)3	GACAGCATCGGACAAGGGAA	CCTGAACCCTCAGCAGTGAG	192	_No FA Found
>jgi|Phyca11|528148|estExt2_fgenesh1_pm.C_PHYCAscaffold_270048	Phyca_SSR115	(CTGG)3	ACCGGAACCACATAGGCAAG	AACGTATCCCCGACCAACAC	140	_No FA Found

>jgi|Phyca11|528642|estExt2_fgenesh1_pm.C_PHYCAscaffold_320048	Phyca_SSR115	(ACGT)3	GTCCAAGGACTATCTCCGCG	TCACCCGCTCCAATTGTCTC	225	_No FA Found
>jgi|Phyca11|528937|estExt2_fgenesh1_pm.C_PHYCAscaffold_350095	Phyca_SSR115	(AGCG)3	TGAGTGATGGAGCAGGTGTG	AGACGCCAAGAAACGACCAT	228	_No FA Found
>jgi|Phyca11|530562|estExt2_fgenesh1_pm.C_PHYCAscaffold_680026	Phyca_SSR115	(ATGT)3	GCTATTCAGTGCTGCAGTGC	CTCTTCTCGAGCTCACCGTC	107	_No FA Found
>jgi|Phyca11|530950|estExt2_fgenesh1_pm.C_PHYCAscaffold_850021	Phyca_SSR116	(TCAC)3	GTTCACACAGGTCCCGAAGT	ATCGGAGACCAACAAAGCGT	275	_No FA Found
>jgi|Phyca11|531146|estExt2_fgenesh1_pm.C_PHYCAscaffold_970012	Phyca_SSR116	(ACAG)3	TTGGAGGATGCCAAGTGGAC	GACTGAAGCACTGGAGCTGT	286	_No FA Found
>jgi|Phyca11|531311|estExt2_fgenesh1_pm.C_PHYCAscaffold_107001	Phyca_SSR116	(CCCA)3	TGCCATTCAATCAGCCTGGT	GAATCGATAGCTGGCACGGA	190	_No FA Found
>jgi|Phyca11|531464|estExt2_fgenesh1_pg.C_PHYCAscaffold_10026	Phyca_SSR116	(ACGT)3	TATCTCGCGTCTTGGGAAGC	GTGGGCTTTGCAAGTGTGAG	233	_No FA Found
>jgi|Phyca11|533168|estExt2_fgenesh1_pg.C_PHYCAscaffold_110039	Phyca_SSR116	(GATA)3	AGAAGCCTAGTGGACGTCCA	ACGCTCTGGTGGAGTTTGAG	273	_No FA Found
>jgi|Phyca11|533217|estExt2_fgenesh1_pg.C_PHYCAscaffold_110113	Phyca_SSR116	(TTCC)3	ACAGAGTTGAGGAAGCCACG	AAATTCCACGCCACGAGTCT	167	_No FA Found
>jgi|Phyca11|533232|estExt2_fgenesh1_pg.C_PHYCAscaffold_110133	Phyca_SSR116	(TTGC)3	GGAGGATCGGTTGATGGGAC	CCCCAGAGCATGACGACAC	104	_No FA Found
>jgi|Phyca11|534866|estExt2_fgenesh1_pg.C_PHYCAscaffold_290018	Phyca_SSR116	(GCTC)3	AGTTGAACCAATTGCCCCCA	GCCCGTTTCGACCAATAGGA	203	_No FA Found
>jgi|Phyca11|535249|estExt2_fgenesh1_pg.C_PHYCAscaffold_330076	Phyca_SSR116	(CGCT)3	TGCAGGTGAACAAGGCTGAT	CTCGCTCCACAGTGTTGTCT	213	_No FA Found
>jgi|Phyca11|535439|estExt2_fgenesh1_pg.C_PHYCAscaffold_360023	Phyca_SSR116	(CAAC)3	TAAACGACCACAAGCCCTCC	TGTACTGCGACAGGTTGGTC	274	_No FA Found
>jgi|Phyca11|537060|estExt2_fgenesh1_pg.C_PHYCAscaffold_720032	Phyca_SSR117	(GTCC)3	TCAACACGTCCTACTTCCGC	GCACCGATAACAGTGTGCAC	202	_No FA Found
>jgi|Phyca11|537104|estExt2_fgenesh1_pg.C_PHYCAscaffold_740005	Phyca_SSR117	(TGCT)3	CTCCGTTGTACTTGGCCTGT	CCGTCATAGCGTCCACATCA	288	_No FA Found
>jgi|Phyca11|537138|estExt2_fgenesh1_pg.C_PHYCAscaffold_760004	Phyca_SSR117	(ACCC)3	AGACGTCACAGCTCAAGTGG	GCTCTCCACAAGTGCCGTAA	256	_No FA Found
>jgi|Phyca11|538602|estExt2_Genewise1Plus.C_PHYCAscaffold_2005	Phyca_SSR117	(CAGT)3	ACGCCAAGAAGGTCGTTCAT	TCCTTCTGCAACGCTTCGAT	268	_No FA Found
>jgi|Phyca11|541695|estExt2_Genewise1Plus.C_PHYCAscaffold_7054	Phyca_SSR117	(TGTC)3	AGGCGAAAACATTGCTGCAG	GCAAGCGTTCAAACTCAGCA	287	_No FA Found
>jgi|Phyca11|543113|estExt2_Genewise1Plus.C_PHYCAscaffold_1101	Phyca_SSR117	(TATC)3	ACGCTCTGGTGGAGTTTGAG	AGAAGCCTAGTGGACGTCCA	273	_No FA Found
>jgi|Phyca11|546107|estExt2_Genewise1Plus.C_PHYCAscaffold_2001	Phyca_SSR117	(TTCA)3	TTCCATCCACAAGGCCATCC	GTGGCTTCTGGCTTGGATCT	235	_No FA Found

>jgi|Phyca11|546111|estExt2_Genewise1Plus.C_PHYCAscaffold_2001	Phyca_SSR117	(TGAA)3	GTGGCTTCTGGCTTGGATCT	TTCCATCCACAAGGCCATCC	235	_No FA Found
>jgi|Phyca11|546150|estExt2_Genewise1Plus.C_PHYCAscaffold_2001	Phyca_SSR117	(CCAG)3	TCTTGATAGACAGCGCACGC	CCGTTCTTGCGCATATTGGG	114	_No FA Found
>jgi|Phyca11|546202|estExt2_Genewise1Plus.C_PHYCAscaffold_2002	Phyca_SSR117	(CTCA)3	CCACTGCTAGAAACCCATTCG	CGGCAACAGGTTCTTGTGTG	270	_No FA Found
>jgi|Phyca11|547508|estExt2_Genewise1Plus.C_PHYCAscaffold_2501	Phyca_SSR118	(CGGT)3	GTCCTGCGAGTCCAAACAGA	GCCGCTACTGTCGTTATCGA	147	_No FA Found
>jgi|Phyca11|547538|estExt2_Genewise1Plus.C_PHYCAscaffold_2501	Phyca_SSR118	(GCTG)3	CCAAAAGCTCTGGACAACGC	CCGCTAAGTCCTGGTACGTC	279	_No FA Found
>jgi|Phyca11|548420|estExt2_Genewise1Plus.C_PHYCAscaffold_2804	Phyca_SSR118	(AGCA)3	TTGCGTCGCCTCTCTGAAAT	CCGATACCCCATTCACCGAG	211	_No FA Found
>jgi|Phyca11|549506|estExt2_Genewise1Plus.C_PHYCAscaffold_3300	Phyca_SSR118	(TGCC)3	GTGCTCAAGATCACGGGGAA	CCTATCTACGCCGTCGCAAA	214	_No FA Found
>jgi|Phyca11|549509|estExt2_Genewise1Plus.C_PHYCAscaffold_3300	Phyca_SSR118	(GACG)3	CAGCGCAGGATGATTTGAGC	GTTGCCTCACACGGTTGTTC	174	_No FA Found
>jgi|Phyca11|549954|estExt2_Genewise1Plus.C_PHYCAscaffold_3403	Phyca_SSR118	(AGCA)3	CCGCATCGAGCTGTTACTCT	AGATTGCAGAGGCTGTTCGA	215	_No FA Found
>jgi|Phyca11|551325|estExt2_Genewise1Plus.C_PHYCAscaffold_4102	Phyca_SSR118	(TTCG)3	CTGTGAGTACATCTGCCGCA	GTCGTTCTTCTCCGCGTACA	277	_No FA Found
>jgi|Phyca11|552134|estExt2_Genewise1Plus.C_PHYCAscaffold_4602	Phyca_SSR118	(ACGA)3	ATCATCGCCGTGTTCAACCT	TTTGGCCCAAACTTCCACCT	225	_No FA Found
>jgi|Phyca11|555389|estExt2_Genewise1Plus.C_PHYCAscaffold_7201	Phyca_SSR118	(CGGA)3	TGAGCAAGAACGCCAAGACT	CGCTCGCTTCTACACATCCT	295	_No FA Found
>jgi|Phyca11|557914|estExt2_Genewise1.C_PHYCAscaffold_10075	Phyca_SSR118	(ACGT)3	GTGGGCTTTGCAAGTGTGAG	TATCTCGCGTCTTGGGAAGC	233	_No FA Found
>jgi|Phyca11|558545|estExt2_Genewise1.C_PHYCAscaffold_20041	Phyca_SSR119	(GCCT)3	TGCTTTTGGCCATGCAGTTC	AGAACATTCTGCACGGCGTA	232	_No FA Found
>jgi|Phyca11|559648|estExt2_Genewise1.C_PHYCAscaffold_30964	Phyca_SSR119	(ATGG)3	AGGTATTGGATAGCAGCGCC	CCTGGCGTTCTCTATCGCAA	230	_No FA Found
>jgi|Phyca11|562802|estExt2_Genewise1.C_PHYCAscaffold_100269	Phyca_SSR119	(CGTC)3	ACACTCAATCTGCGCTCTGT	TAAGTGCTGGGCATGGACTG	136	_No FA Found
>jgi|Phyca11|562804|estExt2_Genewise1.C_PHYCAscaffold_100271	Phyca_SSR119	(CGTC)3	ACACTCAATCTGCGCTCTGT	TAAGTGCTGGGCATGGACTG	136	_No FA Found
>jgi|Phyca11|563078|estExt2_Genewise1.C_PHYCAscaffold_110148	Phyca_SSR119	(GACG)3	TTTGGTGGACTACTGGCGAC	GGGATTACCACCACACCGTT	248	_No FA Found
>jgi|Phyca11|565136|estExt2_Genewise1.C_PHYCAscaffold_170234	Phyca_SSR119	(TTTC)3	TCTGGAAGCTTGCACGTCAT	GCTGGATGGGTAGAGCGTAC	157	_No FA Found
>jgi|Phyca11|568605|estExt2_Genewise1.C_PHYCAscaffold_290324	Phyca_SSR119	(AGGA)3	GTAATGGGTGGCCAGAAGCT	CGCCTAGAAGAGACTCCAACA	145	_No FA Found

>jgi|Phyca11|571208|estExt2_Genewise1.C_PHYCAscaffold_410098	Phyca_SSR119	(CTGT)3	TCGTTCGACAGCACGTTGTA	AGGACGTACTCACCTCCCTC	229	_No FA Found
>jgi|Phyca11|572182|estExt2_Genewise1.C_PHYCAscaffold_460372	Phyca_SSR119	(GCCA)3	TTAAGGGCGACGTGGACTTC	TTCTTGGTGTAGTCCACGGC	196	_No FA Found
>jgi|Phyca11|572777|estExt2_Genewise1.C_PHYCAscaffold_490288	Phyca_SSR119	(GCAC)3	TGACATCGCCTGCTCGATAC	TGTGCTGGTACGAACAGGTC	272	_No FA Found
>jgi|Phyca11|573965|estExt2_Genewise1.C_PHYCAscaffold_580106	Phyca_SSR120	(TTAT)3	TGCAGCCTTTGTGGTAACGA	TTAGCAGTCGCATGGTTGGT	182	_No FA Found
>jgi|Phyca11|574237|estExt2_Genewise1.C_PHYCAscaffold_600185	Phyca_SSR120	(CGGA)3	GAGGCGCTGCAGAAGTTCTA	GGCTGTGTGCAGTTTCTTGG	141	_No FA Found
>jgi|Phyca11|575325|estExt2_Genewise1.C_PHYCAscaffold_720114	Phyca_SSR120	(TCCG)3	CGCTCGCTTCTACACATCCT	TGAGCAAGAACGCCAAGACT	295	_No FA Found
>jgi|Phyca11|577434|estExt2_Genewise1.C_PHYCAscaffold_1160013	Phyca_SSR120	(CGAA)3	TCGTGGTCAATTCCAGGACG	TTCCACCAGGTCATCCATGC	184	_No FA Found
>jgi|Phyca11|577500|estExt2_Genewise1.C_PHYCAscaffold_1220003	Phyca_SSR120	(GAAA)3	AAGAGCCCCAAGTCCGAATG	AGACACGAGTTCACGAGCTG	172	_No FA Found
>jgi|Phyca11|63203|gw1.26.276.1	Phyca_SSR120	(AGGA)3	GACCAACGCGATGGATTTCG	ACGTCGCTGCATTGTCAATG	113	_Ankyrin
>jgi|Phyca11|64031|gw1.18.327.1	Phyca_SSR120	(GGAA)3	CGGCTCTATTGCGTCAAACG	ACGACAGATTACCCCCTCGA	210	_Ankyrin
>jgi|Phyca11|6489|fgenesh1_pm.PHYCAscaffold_12_#_69	Phyca_SSR120	(AAGA)3	CACAGCGCCTCACACTAGAG	TTGTTTGCGCAGGTTGCTAC	260	_No FA Found
>jgi|Phyca11|6670|fgenesh1_pm.PHYCAscaffold_13_#_137	Phyca_SSR120	(CCTT)3	CTGTAGGGGCTGGCGTTTTA	AAAGCAGCATCGTGGAGGAA	232	_AMP-dependent synthetase and ligase
>jgi|Phyca11|66715|gw1.8.391.1	Phyca_SSR120	(GAGC)3	GGGACGGCTGTTGTAGTCAA	CCCAGGGCTGCTTCATAGAG	263	_Protein kinase-like
>jgi|Phyca11|69578|gw1.28.472.1	Phyca_SSR121	(CAAG)3	GATGACTACCGCATCGTCGT	CCGCATATCACCCTTGGACA	282	_No FA Found
>jgi|Phyca11|80768|gw1.75.191.1	Phyca_SSR121	(GGAC)3	AGGCGGAGTTGGACAAGTTC	AGAAACGAATCCCACCGTCC	261	_RNA-directed DNA polymerase (reverse transcriptase
>jgi|Phyca11|80771|gw1.102.107.1	Phyca_SSR121	(GGAC)3	AGGCGGAGTTGGACAAGTTC	AGAAACGAATCCCACCGTCC	261	_RNA-directed DNA polymerase (reverse transcriptase
>jgi|Phyca11|8418|fgenesh1_pm.PHYCAscaffold_28_#_1	Phyca_SSR121	(TCTG)3	GAGCACCGACAAAGACTGGA	GATGAAGGTCAACGCATCGC	223	_Peptidase, cysteine peptidase active site
>jgi|Phyca11|84666|gw1.2.1473.1	Phyca_SSR121	(GGAC)3	AGGCGGAGTTGGACAAGTTC	CGAGATCGGCTTACTGTCCC	110	_RNA-directed DNA polymerase (reverse transcriptase
>jgi|Phyca11|84962|gw1.478.7.1	Phyca_SSR121	(GGAC)3	TGTCGACTCCTTCAAGCGAC	CCGTGTCCTTAACCGTGACA	275	_No FA Found
>jgi|Phyca11|96029|e_gw1.1.1005.1	Phyca_SSR121	(CACT)3	GCGTCTCTCGATGAACGGAT	GCGTCCTGCCGGTTTATCAT	114	_C2 calcium/lipid-binding region, CaLB

>jgi|Phyca11|98350|e_gw1.2.607.1	Phyca_SSR121	(CGGC)3	CGGTTCTATGTGTTGCCCCT	CGTCTCGGAATCGAACACCA	100	_No FA Found
>jgi|Phyca11|98627|e_gw1.3.1034.1	Phyca_SSR121	(GCAA)3	GACGAAGGAGACTGCCACAA	TTTCTTGAAAACCCGCGCAG	160	_No FA Found
>jgi|Phyca11|10113|fgenesh1_pm.PHYCAscaffold_46_#_43	Phyca_SSR121	(AGA)5	GGAGGATGTCGTCAAGGTGG	TGCGCCGCTTCTTGTTATTG	173	_No FA Found
>jgi|Phyca11|101439|e_gw1.5.655.1	Phyca_SSR122	(AAG)5	CGGAGAAGTAGTTCCCGACG	GAAGCCCTTGACACCTCGAA	136	_Peptidase M24, catalytic core
>jgi|Phyca11|101677|e_gw1.5.389.1	Phyca_SSR122	(GAC)5	GCCTACCGCGTCTACTTCTC	AGCTTGCGTGAAGAAGTCGA	129	_Thioredoxin-like fold
>jgi|Phyca11|109476|e_gw1.16.756.1	Phyca_SSR122	(AGA)5	AATGTTACCGGAACCGCAGT	ACCTCCCATTTGTGGCACTT	224	_No FA Found
>jgi|Phyca11|110429|e_gw1.18.207.1	Phyca_SSR122	(GCA)5	CACCTTCAACCTACGGACCC	TCCCACGTCGTCAGAGTAGT	255	_No FA Found
>jgi|Phyca11|112136|e_gw1.21.542.1	Phyca_SSR122	(GAA)5	AAAACCAAGTGCTGTTCGCC	CGCTTGGTCCTGGTAGTGTT	204	_No FA Found
>jgi|Phyca11|114153|e_gw1.25.273.1	Phyca_SSR122	(GAA)5	TTGCGTATCTCGAGAGCCAC	ATCCGAGAATCAATCCGCCC	234	_No FA Found
>jgi|Phyca11|114899|e_gw1.27.1.1	Phyca_SSR122	(AAG)5	GTCCCGAACATCCAGGATGG	AAGAAAGCGGGCGGATACAA	236	_No FA Found
>jgi|Phyca11|116857|e_gw1.31.159.1	Phyca_SSR122	(GAA)5	TGAAGATGCAGAGGAAGCCG	CGCTTGGTCCTGGTAGTGTT	123	_No FA Found
>jgi|Phyca11|118720|e_gw1.36.578.1	Phyca_SSR122	(GAA)5	TTCCACCCTGCACGTCTTAC	TCCGTTCTGTTTGCCTTCGA	237	_No FA Found
>jgi|Phyca11|120327|e_gw1.41.354.1	Phyca_SSR122	(GCT)5	GAGGAAGCGACGCAAGCC	TGCACATACAGCACCGTCTT	225	_No FA Found
>jgi|Phyca11|124731|e_gw1.54.272.1	Phyca_SSR123	(CTG)5	GTACTGGAGGCTCATCGACG	CTGGCAGTACCACTTCCCTG	281	_No FA Found
>jgi|Phyca11|12927|fgenesh1_pg.PHYCAscaffold_2_#_23	Phyca_SSR123	(TTC)5	TCTGGCAGCTTGGACTTGAG	CAGTCGTAGGTGCAGGTGTT	112	_No FA Found
>jgi|Phyca11|132663|e_gw1.206.13.1	Phyca_SSR123	(GCA)5	GAAGAAGAGCCACAACCGCA	AATAACGGGCCCCCTAGACT	162	_No FA Found
>jgi|Phyca11|13940|fgenesh1_pg.PHYCAscaffold_5_#_154	Phyca_SSR123	(CTC)5	ACGTCAGTCTCAACCGGTTC	CAAGGATCGCGGTAGGAGTC	255	_No FA Found
>jgi|Phyca11|14397|fgenesh1_pg.PHYCAscaffold_7_#_136	Phyca_SSR123	(TGC)5	ATGAGTCAAGGAGGCGGC	TCCGGTTACAACGTCCCAAG	216	_No FA Found
>jgi|Phyca11|14650|fgenesh1_pg.PHYCAscaffold_9_#_26	Phyca_SSR123	(GAA)5	AGGCTCAGGGTCTTCGATCT	AATGGCCTCGTAGTTCCGTG	202	_No FA Found
>jgi|Phyca11|15125|fgenesh1_pg.PHYCAscaffold_11_#_111	Phyca_SSR123	(CGA)5	AGGTGTACACTGACTGCGTG	GCAGTAGTCGTTGGAGCTGT	163	_Glycoside hydrolase, family 11

>jgi|Phyca11|15139|fgenesh1_pg.PHYCAscaffold_11_#_125	Phyca_SSR123	(CAG)5	CAACCAGTCTCAAGGCGGAT	ATTGCGGTTCCATTGGCAAC	240	_RNA recognition motif, RNP-1
>jgi|Phyca11|15170|fgenesh1_pg.PHYCAscaffold_11_#_156	Phyca_SSR123	(AGA)5	CAAGTGGAACGAGAACGGGA	CCTCTACGTCATCCACTGCC	229	_No FA Found
>jgi|Phyca11|15844|fgenesh1_pg.PHYCAscaffold_16_#_22	Phyca_SSR123	(AGA)5	TTGTCGGTGAACCAGAGCTC	GAGCCAAAAGTGCTTCGGTG	289	_No FA Found
>jgi|Phyca11|16580|fgenesh1_pg.PHYCAscaffold_20_#_168	Phyca_SSR124	(CCG)5	CTTACCTACGCCTCCGACTC	GTTGGCGAATGATGGCATCC	292	_No FA Found
>jgi|Phyca11|17368|fgenesh1_pg.PHYCAscaffold_27_#_51	Phyca_SSR124	(GAG)5	GTCGCGCTACCGGAAATAGA	TGAAACCCTTCCGCAATCGA	256	_No FA Found
>jgi|Phyca11|18636|fgenesh1_pg.PHYCAscaffold_38_#_82	Phyca_SSR124	(AGC)5	ACGAGACAACCAGGAAGCAG	ATTCGTCCAGTGCGAACAGT	258	_No FA Found
>jgi|Phyca11|18991|fgenesh1_pg.PHYCAscaffold_42_#_93	Phyca_SSR124	(CAC)5	CACCAGCATGAACACGTTCG	ACTTGTCCGTGGTGCTAGTG	137	_No FA Found
>jgi|Phyca11|19590|fgenesh1_pg.PHYCAscaffold_50_#_12	Phyca_SSR124	(GAC)5	TGCAGGCTGATTATGACGCA	CCTGCTGACGTTCCTTCAGT	282	_UvrB, C-terminal UvrC-binding
>jgi|Phyca11|20089|fgenesh1_pg.PHYCAscaffold_57_#_40	Phyca_SSR124	(CGT)5	CAAAGGAAGGAGCCCGATCA	GGTAACGTGGGTTCAAGCCG	264	_No FA Found
>jgi|Phyca11|20614|fgenesh1_pg.PHYCAscaffold_68_#_5	Phyca_SSR124	(ACG)5	ACGAGTCTCCAGAGCCAGAT	TCCTCCTCACGTGCAGAAAC	283	_No FA Found
>jgi|Phyca11|20873|fgenesh1_pg.PHYCAscaffold_75_#_2	Phyca_SSR124	(TGC)5	ATGAGTCAAGGAGGCGGC	ATAGTTGATCTCGCCAGCCG	290	_No FA Found
>jgi|Phyca11|20877|fgenesh1_pg.PHYCAscaffold_75_#_6	Phyca_SSR124	(CTT)5	TTACGTTCAAGGTCGGTCCG	GTCGGGTTTGTCTCGTCCTT	190	_Acetyl-CoA carboxylase, central region
>jgi|Phyca11|20936|fgenesh1_pg.PHYCAscaffold_77_#_4	Phyca_SSR124	(TTC)5	GTTCGGAGAGTCCAAGTGGG	CAGTTCCGTTGTCCTGAGCT	256	_No FA Found
>jgi|Phyca11|21177|fgenesh1_pg.PHYCAscaffold_84_#_37	Phyca_SSR125	(GAA)5	CGTGGAGTTTGACAGACCGA	CTCCACCTGCACTTGTGTCA	275	_No FA Found
>jgi|Phyca11|21187|fgenesh1_pg.PHYCAscaffold_84_#_47	Phyca_SSR125	(AAG)5	CTGGAGGCTGCAGAACATGA	CCACTCAACGGGGTCAATGA	194	_No FA Found
>jgi|Phyca11|21764|fgenesh1_pg.PHYCAscaffold_118_#_2	Phyca_SSR125	(GGA)5	CAGTGGTTCGGGCAATCAAG	CGCCAGGAGATTTCCAACCT	173	_No FA Found
>jgi|Phyca11|21815|fgenesh1_pg.PHYCAscaffold_129_#_6	Phyca_SSR125	(GAC)5	ATTCGGACGGCGATGACTTT	GTCCAGGTTGTTCACGTTGC	174	_No FA Found
>jgi|Phyca11|21973|fgenesh1_pg.PHYCAscaffold_310_#_1	Phyca_SSR125	(AGA)5	ACTCCGTTCGCCAATATCCC	AAGGGGGAGTGATTGGCTTG	147	_No FA Found
>jgi|Phyca11|4582|fgenesh1_pm.PHYCAscaffold_2_#_178	Phyca_SSR125	(AGA)5	GAGGTGGATGCAGGAAACGA	CCCATTCCTCGAGCGACTAC	291	_GC-rich sequence DNA-binding factor-like
>jgi|Phyca11|502652|fgenesh2_kg.PHYCAscaffold_1_#_112_#_Contig	Phyca_SSR125	(TGA)5	GGAGGCCAATGGTTGAGTCA	CGTTGGAAGCATACGCATGG	275	_No FA Found

>jgi|Phyca11|503116|fgenesh2_kg.PHYCAscaffold_2_#_232_#_409937	Phyca_SSR125	(CGA)5	GGAGCACAGGTCCTGATGAC	CACGACCTCAGTGCAGTCAT	203	_No FA Found
>jgi|Phyca11|503344|fgenesh2_kg.PHYCAscaffold_3_#_209_#_410248	Phyca_SSR125	(ACC)5	AGCGTGCTGAGAACGAGAAA	CAATTTGCTGAGCCACGCTT	229	_No FA Found
>jgi|Phyca11|503455|fgenesh2_kg.PHYCAscaffold_3_#_320_#_Contig	Phyca_SSR125	(TCT)5	ACTCATCGACACTCCCTCCA	CGATCACTCCGATGCTGACA	300	_No FA Found
>jgi|Phyca11|503684|fgenesh2_kg.PHYCAscaffold_4_#_223_#_gi|1890	Phyca_SSR126	(GAA)5	GCACGTCGCCAATTTGGATT	TAGCGTTGATGATCTGGGGC	240	_No FA Found
>jgi|Phyca11|504055|fgenesh2_kg.PHYCAscaffold_5_#_219_#_409831	Phyca_SSR126	(GAA)5	AATCCCGTCAACTCAAGCGT	GCAGGACAAGTGAACGGGTA	267	_No FA Found
>jgi|Phyca11|504180|fgenesh2_kg.PHYCAscaffold_6_#_97_#_4101566	Phyca_SSR126	(AAG)5	ACCAGTGGATTTGGCGACTT	GTCAGGGACGTCACCTTTGT	277	_No FA Found
>jgi|Phyca11|504393|fgenesh2_kg.PHYCAscaffold_7_#_145_#_gi|1890	Phyca_SSR126	(AGC)5	AACAACAAATCGAGCACGCC	TCCGCCAACGTGATCATAGG	233	_No FA Found
>jgi|Phyca11|504403|fgenesh2_kg.PHYCAscaffold_7_#_155_#_gi|1890	Phyca_SSR126	(GAA)5	CAGCCATTGAAATCGCGGAG	TCACAAGCAGTAGAACGCGT	288	_No FA Found
>jgi|Phyca11|504657|fgenesh2_kg.PHYCAscaffold_9_#_48_#_Contig1	Phyca_SSR126	(GGC)5	GGAGTGGATCTCGAGGACCT	TGACTCGCCGCCTTAAACTT	297	_No FA Found
>jgi|Phyca11|504752|fgenesh2_kg.PHYCAscaffold_9_#_143_#_Contig	Phyca_SSR126	(GAA)5	TGCTATGGACTGGGACGAGA	AGCTTCGACCTCCTCCTTCT	202	_No FA Found
>jgi|Phyca11|504908|fgenesh2_kg.PHYCAscaffold_10_#_68_#_gi|1890	Phyca_SSR126	(CTT)5	GACTTTCGCCACCATGGGTA	CGCCAAACACAACAGTCCAG	100	_No FA Found
>jgi|Phyca11|505258|fgenesh2_kg.PHYCAscaffold_12_#_46_#_410165	Phyca_SSR126	(CAC)5	ACCACTCGGTAGACTACGCT	CCTGCACCTTCGATCAGGTT	225	_No FA Found
>jgi|Phyca11|505323|fgenesh2_kg.PHYCAscaffold_12_#_111_#_Conti	Phyca_SSR126	(TTC)5	AGACACCGTGCACTGAGAAG	CGTCGAACTGGTCACCAAGA	147	_No FA Found
>jgi|Phyca11|505419|fgenesh2_kg.PHYCAscaffold_13_#_69_#_409881	Phyca_SSR127	(CGA)5	TGCATGCACACACTTGATGC	GGGACTCCAGCATCAGGTTC	233	_No FA Found
>jgi|Phyca11|506007|fgenesh2_kg.PHYCAscaffold_17_#_92_#_gi|1890	Phyca_SSR127	(ACG)5	AAAGGCTGCTGCTACTCCAG	TTGGACGAACCCTCAGCTTC	147	_No FA Found
>jgi|Phyca11|506992|fgenesh2_kg.PHYCAscaffold_23_#_123_#_gi|189	Phyca_SSR127	(AGC)5	GACAAACCGCAGAAGATCGC	CAGTAGCGCCTCATCCACAT	273	_No FA Found
>jgi|Phyca11|507523|fgenesh2_kg.PHYCAscaffold_28_#_30_#_jgi|JGI_	Phyca_SSR127	(AAG)5	CTGAACAAGGCGACAACACG	CACCATCTCGTCCAGCTCTC	270	_No FA Found
>jgi|Phyca11|508367|fgenesh2_kg.PHYCAscaffold_34_#_63_#_410448	Phyca_SSR127	(CAA)5	CGATGCAGCAACCACAACAA	TTCAAAACCTGGGGTGGCTT	178	_No FA Found
>jgi|Phyca11|50894|gw1.79.118.1	Phyca_SSR127	(GAA)5	GCTGAAGCTGTTTTGTGCGA	GTCTTTCTCCGTCAGCCACA	205	_No FA Found
>jgi|Phyca11|508943|fgenesh2_kg.PHYCAscaffold_40_#_32_#_410453	Phyca_SSR127	(GCA)5	CGCGCAGTGAATTCGAGATG	GTGCTGCTCTTGGTCACTCT	240	_No FA Found

>jgi|Phyca11|509157|fgenesh2_kg.PHYCAscaffold_42_#_64_#_gi|1890	Phyca_SSR127	(CAG)5	CTCGCAGTCCAAGTTCACCA	GTTGGTCTCGCTAGATCCCG	214	_No FA Found
>jgi|Phyca11|509732|fgenesh2_kg.PHYCAscaffold_49_#_24_#_Contig	Phyca_SSR127	(CAG)5	GCTGCACATGGTACTGGACT	ACCGCGTTCTCTTTCTGGTT	153	_No FA Found
>jgi|Phyca11|509841|fgenesh2_kg.PHYCAscaffold_50_#_42_#_409810	Phyca_SSR127	(TCC)5	TCACTTCACCATGGGCAACT	TTTGGCCGAGACGATTTCGA	109	_No FA Found
>jgi|Phyca11|510611|fgenesh2_kg.PHYCAscaffold_64_#_4_#_Contig1	Phyca_SSR128	(CAG)5	TCACCATTCCTTCCATGGCC	TCATCCTCACGTGCCTCAAC	207	_No FA Found
>jgi|Phyca11|510872|fgenesh2_kg.PHYCAscaffold_70_#_18_#_Contig	Phyca_SSR128	(ACA)5	ATGCAGCACCCTGATGTGAA	CCCACGGAAAATTGGTGCTG	240	_No FA Found
>jgi|Phyca11|511063|fgenesh2_kg.PHYCAscaffold_74_#_13_#_Contig	Phyca_SSR128	(GCA)5	CTCCAGCTAGCTATGGCGTC	GTTTGCTGCTCTTGGACACG	124	_No FA Found
>jgi|Phyca11|511132|fgenesh2_kg.PHYCAscaffold_76_#_33_#_410174	Phyca_SSR128	(CTG)5	AAGACGATCTGGCCAACCTG	TGCACGAAGCCAAAAACCAG	281	_No FA Found
>jgi|Phyca11|511433|fgenesh2_kg.PHYCAscaffold_85_#_1_#_gi|18908	Phyca_SSR128	(AGA)5	CGACCAAATGGATGCCAACG	GCACTCGTCAACACCGAAAC	271	_No FA Found
>jgi|Phyca11|511488|fgenesh2_kg.PHYCAscaffold_86_#_25_#_Contig	Phyca_SSR128	(AAG)5	AGGAGTTCGAGGCTGCTCTA	TCCGCCGCTTTCTTCTTCTT	241	_No FA Found
>jgi|Phyca11|511707|fgenesh2_kg.PHYCAscaffold_95_#_36_#_Contig	Phyca_SSR128	(GCT)5	ACCTCATTCTGGTGCCTTCG	GGAAGCCTCAGTCCCAATGG	297	_No FA Found
>jgi|Phyca11|512003|fgenesh2_kg.PHYCAscaffold_112_#_8_#_Contig	Phyca_SSR128	(CTG)5	GCCCACACCTCACGAGTAC	CGTGGTGAGGTTCAGTGTCA	143	_No FA Found
>jgi|Phyca11|512065|fgenesh2_kg.PHYCAscaffold_122_#_1_#_Contig	Phyca_SSR128	(CAG)5	CGTCCCACTCACTTGCCC	GTCATGTTGTTCGGGTGCAC	253	_No FA Found
>jgi|Phyca11|527369|estExt2_fgenesh1_pm.C_PHYCAscaffold_180095	Phyca_SSR128	(AAG)5	GCATTGTCGGAACTGATCGC	CCAACACGCTTGCGATATCG	292	_No FA Found
>jgi|Phyca11|527659|estExt2_fgenesh1_pm.C_PHYCAscaffold_210070	Phyca_SSR129	(GGT)5	CGAAACGGCAAAGGCATCAA	GATTTCAATCACCTGGCCGC	292	_No FA Found
>jgi|Phyca11|528025|estExt2_fgenesh1_pm.C_PHYCAscaffold_260011	Phyca_SSR129	(GGC)5	CGAGATGACTACGGACGTGG	TGTCTAGAAGTCCCCTGCAA	159	_No FA Found
>jgi|Phyca11|529946|estExt2_fgenesh1_pm.C_PHYCAscaffold_520015	Phyca_SSR129	(GAA)5	TGCACGCGTTCTTGAACAAG	TTTTGGCTGGACGGGTAGAC	253	_No FA Found
>jgi|Phyca11|530232|estExt2_fgenesh1_pm.C_PHYCAscaffold_590004	Phyca_SSR129	(GCT)5	CCTCTGCTTGAGAACCTGGG	GCGTCATTGGAGGAGGTAGG	215	_No FA Found
>jgi|Phyca11|530781|estExt2_fgenesh1_pm.C_PHYCAscaffold_770034	Phyca_SSR129	(AGC)5	GGATGCTGGCGCTGTTAATG	TCCCGTTCTGCACAACTCTC	287	_No FA Found
>jgi|Phyca11|530843|estExt2_fgenesh1_pm.C_PHYCAscaffold_800019	Phyca_SSR129	(AGC)5	CGGCGGATCGATCAACAGTA	CCAAGAGCTGTGTCAGTCGT	278	_No FA Found
>jgi|Phyca11|531163|estExt2_fgenesh1_pm.C_PHYCAscaffold_980013	Phyca_SSR129	(ACG)5	TCGATAGTGCGATCGTGTGG	AGACGTAGCGGCTTCGTTAC	137	_No FA Found

>jgi|Phyca11|531664|estExt2_fgenesh1_pg.C_PHYCAscaffold_10329	Phyca_SSR129	(AAG)5	TTTTGGTCTCCCAGTTGCGA	CAGTTCGTCCAGAAGCGTCT	133	_No FA Found
>jgi|Phyca11|531674|estExt2_fgenesh1_pg.C_PHYCAscaffold_10340	Phyca_SSR129	(AAG)5	TCAAGAACGGCGAGGTGTAC	CCTTTACGGCCCTGTGTCTT	265	_No FA Found
>jgi|Phyca11|532048|estExt2_fgenesh1_pg.C_PHYCAscaffold_30237	Phyca_SSR129	(CAA)5	ATCAAAACGCACAGAACCGC	GAGTACACGTTGGGGGTCTG	178	_No FA Found
>jgi|Phyca11|532594|estExt2_fgenesh1_pg.C_PHYCAscaffold_60129	Phyca_SSR130	(CGC)5	GGAGAACCAATCACCGAGCA	CCCTCGCACTTTTTCACGTG	134	_No FA Found
>jgi|Phyca11|533379|estExt2_fgenesh1_pg.C_PHYCAscaffold_130080	Phyca_SSR130	(CTT)5	CACAATCTCGTCTGGGCTGT	GTTTGGTGAATCGCAAGCGT	281	_No FA Found
>jgi|Phyca11|533886|estExt2_fgenesh1_pg.C_PHYCAscaffold_180060	Phyca_SSR130	(AAG)5	ATGACAGCACGCAGGAGAAA	TGACAATCGCGTATCCTCCG	159	_No FA Found
>jgi|Phyca11|534605|estExt2_fgenesh1_pg.C_PHYCAscaffold_260029	Phyca_SSR130	(GCA)5	CAACAGCAGCAACAGGGAAC	ATACTCGCCGCTTGATGAGG	289	_No FA Found
>jgi|Phyca11|536610|estExt2_fgenesh1_pg.C_PHYCAscaffold_580032	Phyca_SSR130	(CCT)5	CAAGGACGCCAAGATCGGAA	CGGGTGCTTGAGTGGTAGTT	260	_No FA Found
>jgi|Phyca11|537026|estExt2_fgenesh1_pg.C_PHYCAscaffold_710040	Phyca_SSR130	(GAA)5	TGCGTGAGTCTCAGCAAGAG	GGCTTCAGTTGCACCTTTCG	286	_No FA Found
>jgi|Phyca11|537210|estExt2_fgenesh1_pg.C_PHYCAscaffold_790005	Phyca_SSR130	(GAA)5	GCTGAAGCTGTTTTGTGCGA	GTCTTTCTCCGTCAGCCACA	205	_No FA Found
>jgi|Phyca11|53838|gw1.47.243.1	Phyca_SSR130	(AAG)5	CACAACGTGGTTGGCTGAAG	TCGCTTCGGGTCCAATGAAA	184	_WW/Rsp5/WWP
>jgi|Phyca11|538799|estExt2_Genewise1Plus.C_PHYCAscaffold_2045	Phyca_SSR130	(CTC)5	TGCCCATTAACACGGGCTAG	TCTCGCTGTTGCTTCTCCTG	215	_No FA Found
>jgi|Phyca11|540450|estExt2_Genewise1Plus.C_PHYCAscaffold_4099	Phyca_SSR130	(AGA)5	TCGAGCCAACAGTGAAGGAC	ACGTCTCCATAGTGTTGCAC	132	_No FA Found
>jgi|Phyca11|5426|fgenesh1_pm.PHYCAscaffold_5_#_229	Phyca_SSR131	(CTG)5	GTACTGGAGGCTCATCGACG	CTGGCAGTACCACTTCCCTG	254	_Zinc finger, FYVE/PHD-type
>jgi|Phyca11|542784|estExt2_Genewise1Plus.C_PHYCAscaffold_1001	Phyca_SSR131	(AGA)5	CGCCAAACACAACAGTCCAG	GACTTTCGCCACCATGGGTA	100	_No FA Found
>jgi|Phyca11|544507|estExt2_Genewise1Plus.C_PHYCAscaffold_1500	Phyca_SSR131	(GAC)5	ATACGGACGATGACGGTGTG	TCCTCCTCCTCTTCGGAAGG	226	_No FA Found
>jgi|Phyca11|545091|estExt2_Genewise1Plus.C_PHYCAscaffold_1700	Phyca_SSR131	(GAA)5	CCGACGGCCTTGAAAAGTTC	TTCTTTGTCATTGCGTGGCG	126	_No FA Found
>jgi|Phyca11|545551|estExt2_Genewise1Plus.C_PHYCAscaffold_1802	Phyca_SSR131	(AAG)5	AGCATGTTCATGACGCCTGA	AGCTGCAACTTGGCGAAAAG	161	_No FA Found
>jgi|Phyca11|546163|estExt2_Genewise1Plus.C_PHYCAscaffold_2002	Phyca_SSR131	(GCT)5	GCGCACTAACGGTGTTGAAG	GTTGTAGCCCGAGTCCGATC	291	_No FA Found
>jgi|Phyca11|546414|estExt2_Genewise1Plus.C_PHYCAscaffold_2100	Phyca_SSR131	(AGA)5	ACTTCATCCGTTCGAAGCGT	TCTTCTTCACCTTGGCCACC	270	_No FA Found

>jgi|Phyca11|546834|estExt2_Genewise1Plus.C_PHYCAscaffold_2204	Phyca_SSR131	(AAG)5	GAGAAGGAGGAGGCCACAAC	GACAGCTCCTGCAACAGTCT	218	_No FA Found
>jgi|Phyca11|548120|estExt2_Genewise1Plus.C_PHYCAscaffold_2703	Phyca_SSR131	(GAA)5	AGCGGAAGAGGTTGCATCAA	AGTGCGTTCGACTGCAGTAA	213	_No FA Found
>jgi|Phyca11|548428|estExt2_Genewise1Plus.C_PHYCAscaffold_2804	Phyca_SSR131	(AGC)5	GATTGCAGCGTCTGAAGCAG	CCTCTTGCTGGCCGATAGAG	273	_No FA Found
>jgi|Phyca11|548602|estExt2_Genewise1Plus.C_PHYCAscaffold_2902	Phyca_SSR132	(GGC)5	TCGGTGCTAGGGATTACCGT	AAAAGACACTAGGGCCGACG	297	_No FA Found
>jgi|Phyca11|549032|estExt2_Genewise1Plus.C_PHYCAscaffold_3100	Phyca_SSR132	(AGC)5	TTCGGTGCAGCACAGAAGAA	GAGCTGGTTGGGGTCTTCTC	101	_No FA Found
>jgi|Phyca11|549042|estExt2_Genewise1Plus.C_PHYCAscaffold_3100	Phyca_SSR132	(GAC)5	TCCTGCTCTTCTGCAACTCG	GCCGCTCATACTCATCGTCA	224	_No FA Found
>jgi|Phyca11|549936|estExt2_Genewise1Plus.C_PHYCAscaffold_3402	Phyca_SSR132	(CAG)5	GTCGTTTCGTCTGCCAATGG	GTGCCTTGACCAGCAACTTG	164	_No FA Found
>jgi|Phyca11|550581|estExt2_Genewise1Plus.C_PHYCAscaffold_3703	Phyca_SSR132	(GAG)5	GGCCAGTCTGTCAGCTCTTT	CGTCCTCGTCTTCTTCTCCA	284	_No FA Found
>jgi|Phyca11|551085|estExt2_Genewise1Plus.C_PHYCAscaffold_4001	Phyca_SSR132	(CAG)5	ACCACCATCTCAATGCAGCA	ACGACGTGCAAGTAAGCAGA	294	_No FA Found
>jgi|Phyca11|557260|estExt2_Genewise1Plus.C_PHYCAscaffold_1050	Phyca_SSR132	(GAA)5	TTTCGAAACCACACGCCATG	CATGCGCTTCAATGGAGACG	123	_No FA Found
>jgi|Phyca11|558317|estExt2_Genewise1.C_PHYCAscaffold_11022	Phyca_SSR132	(AAT)5	TCCGAGTGGCTTTTCTTGCT	ATGCGTAACAAGCCGATTGC	202	_No FA Found
>jgi|Phyca11|563613|estExt2_Genewise1.C_PHYCAscaffold_120626	Phyca_SSR132	(GAA)5	CGTCGAACTGGTCACCAAGA	AGACACCGTGCACTGAGAAG	147	_No FA Found
>jgi|Phyca11|5642|fgenesh1_pm.PHYCAscaffold_7_#_8	Phyca_SSR132	(AGA)5	AGGCAGTTGGAAGCGAAGAA	AGATCACTGCCACTGCCTTC	272	_No FA Found
>jgi|Phyca11|564706|estExt2_Genewise1.C_PHYCAscaffold_150508	Phyca_SSR133	(TCT)5	TTGTATGTGCCTGCACCACT	TGCTCTGTGAATGTCTGCGT	160	_No FA Found
>jgi|Phyca11|565060|estExt2_Genewise1.C_PHYCAscaffold_170098	Phyca_SSR133	(CTT)5	TTCTTTGTCATTGCGTGGCG	CCGACGGCCTTGAAAAGTTC	126	_No FA Found
>jgi|Phyca11|565179|estExt2_Genewise1.C_PHYCAscaffold_170294	Phyca_SSR133	(AAG)5	CGCTACCAAGGCTGACAAGA	GGGAAGAGAAAACCGCAACG	299	_No FA Found
>jgi|Phyca11|566919|estExt2_Genewise1.C_PHYCAscaffold_230094	Phyca_SSR133	(CCT)5	AGAAACCTGCGACTGCTTCA	AGTCAACGCAGATTGAGGCA	293	_No FA Found
>jgi|Phyca11|568096|estExt2_Genewise1.C_PHYCAscaffold_270335	Phyca_SSR133	(AGG)5	TTGGTACACTCACCTTCGCC	CACGCTTGAACACACCAACC	243	_No FA Found
>jgi|Phyca11|570091|estExt2_Genewise1.C_PHYCAscaffold_350227	Phyca_SSR133	(AAG)5	TTTGGCCCCCTTCATCCTTC	TTGCTATCGGCCTTCTCGTC	225	_No FA Found
>jgi|Phyca11|570961|estExt2_Genewise1.C_PHYCAscaffold_400055	Phyca_SSR133	(GAG)5	GCCTACCGCTTCGAAGAGTT	GGGGTTTCTACCACCACGAG	248	_No FA Found

>jgi|Phyca11|574624|estExt2_Genewise1.C_PHYCAscaffold_640111	Phyca_SSR133	(GCT)5	CCTGGTCCTGTTCACCTGTC	CCGGTGATGATCAGACCCAG	153	_No FA Found
>jgi|Phyca11|575261|estExt2_Genewise1.C_PHYCAscaffold_720032	Phyca_SSR133	(GAA)5	AAAGTCGACGACCTCACCAC	TATCGCTTTGGCTTGCTCCA	173	_No FA Found
>jgi|Phyca11|577071|estExt2_Genewise1.C_PHYCAscaffold_1010033	Phyca_SSR133	(GAA)5	TGGAGGCGGTGTATGAACTG	ATGGACAAACAGCGGCAGTA	287	_No FA Found
>jgi|Phyca11|6748|fgenesh1_pm.PHYCAscaffold_14_#_52	Phyca_SSR134	(AGA)5	GGAGATCACGACAGGCCAAA	CGTCTTCCTCGGTGTTGGAA	284	_Nucleic acid-binding, OB-fold-like
>jgi|Phyca11|8366|fgenesh1_pm.PHYCAscaffold_27_#_112	Phyca_SSR134	(AGG)5	TTGGTACACTCACCTTCGCC	CACGCTTGAACACACCAACC	243	_MORN motif
>jgi|Phyca11|9105|fgenesh1_pm.PHYCAscaffold_34_#_22	Phyca_SSR134	(TGA)5	CATGGAGATGCGGAGGAGAC	ACGTGGATCACAGTGTCACC	281	_No FA Found
>jgi|Phyca11|9515|fgenesh1_pm.PHYCAscaffold_38_#_64	Phyca_SSR134	(AAG)5	TGCATTGAACGCATTGCCAA	TGGAACGCAATTGCCACAAG	215	_Bacterial methyltransferase
>jgi|Phyca11|9863|fgenesh1_pm.PHYCAscaffold_42_#_71	Phyca_SSR134	(GAC)5	TCATCGTCATCGGAGGAGGT	CTAGTGCCAGTGCTTTCCGA	211	_No FA Found
>jgi|Phyca11|504388|fgenesh2_kg.PHYCAscaffold_7_#_140_#_410165	Phyca_SSR134	(TTTCG)3	AGGAAGCTGTGCCGTACTTC	GCCACTTCGAGTCCTCCTTC	120	_No FA Found
>jgi|Phyca11|505601|fgenesh2_kg.PHYCAscaffold_14_#_82_#_Contig	Phyca_SSR134	(ACGCT)3	GCTGTGGTGACTGCTGATCT	GCCACCTTGATACCAGCCTT	185	_No FA Found
>jgi|Phyca11|506546|fgenesh2_kg.PHYCAscaffold_20_#_92_#_Contig	Phyca_SSR134	(TCACT)3	CAATTTACCTGCCTCATAGACT	GTCCGGGTTGTTCATCAGGT	205	_No FA Found
>jgi|Phyca11|506791|fgenesh2_kg.PHYCAscaffold_22_#_30_#_gi|1890	Phyca_SSR134	(CCAGT)3	CAGCAACTTTGTGCCGACTC	CGCTAAATTCTGAGCACCGC	261	_No FA Found
>jgi|Phyca11|511157|fgenesh2_kg.PHYCAscaffold_77_#_12_#_410136	Phyca_SSR134	(GCTCC)3	TCTACCACCCGAGCAAACAC	GCCAGTCGATTGGGGGAATA	235	_No FA Found
>jgi|Phyca11|536585|estExt2_fgenesh1_pg.C_PHYCAscaffold_570041	Phyca_SSR135	(CCTCG)3	TCTAGCGGAGAAGTCCAGCA	AGAGGTTGAAGGACGCCTTG	131	_No FA Found
>jgi|Phyca11|541765|estExt2_Genewise1Plus.C_PHYCAscaffold_7066	Phyca_SSR135	(TTTCG)3	AGGAAGCTGTGCCGTACTTC	TTGCCGTTGAACCTCCACTT	133	_No FA Found
>jgi|Phyca11|545630|estExt2_Genewise1Plus.C_PHYCAscaffold_1804	Phyca_SSR135	(GTATG)3	ACTGATCAATTAACGCGCGC	CACAGCCAAAGCAGCGATAC	219	_No FA Found
>jgi|Phyca11|575764|estExt2_Genewise1.C_PHYCAscaffold_780099	Phyca_SSR135	(CAGCT)3	CCATTCCAGACTCACGCCTT	CGAGGTGACCATTGAGTGCA	182	_No FA Found
>jgi|Phyca11|61815|gw1.18.251.1	Phyca_SSR135	(TGGAG)3	TTTTTCTGTGGGCAGCTCCT	TCGTTTTTCTGGTGTGCAAAGT	176	_No FA Found
>jgi|Phyca11|62156|gw1.13.408.1	Phyca_SSR135	(GGATG)3	CTAGTCGACACGGATCTGGC	TCATGAGTTCACTGCACCCC	280	_No FA Found
>jgi|Phyca11|510108|fgenesh2_kg.PHYCAscaffold_54_#_2_#_Contig14	Phyca_SSR135	(AG)8	TCATCTGCTGGGCTCTGTTG	CGTGTATCGAGTCTCCAGCC	129	_No FA Found

>jgi|Phyca11|530039|estExt2_fgenesh1_pm.C_PHYCAscaffold_54000	Phyca_SSR135	(CT)8	CGTGTATCGAGTCTCCAGCC	TCATCTGCTGGGCTCTGTTG	129	_No FA Found
>jgi|Phyca11|502702|fgenesh2_kg.PHYCAscaffold_1_#_162_#_41006	Phyca_SSR135	(CAAC)4	GTGCAGTACACCGTACTTGA	ACAGGTTCATCTGCGAGGTG	228	_No FA Found
>jgi|Phyca11|510020|fgenesh2_kg.PHYCAscaffold_53_#_5_#_Contig4	Phyca_SSR135	(GACA)4	TGTAGTGTCCAAGTGGCGAC	CAATTGGCCCAAGAATCCGC	227	_No FA Found
>jgi|Phyca11|511809|fgenesh2_kg.PHYCAscaffold_100_#_12_#_4098	Phyca_SSR136	(GCAA)4	GCATTCGCACATGACTGGTC	CGTGTTCGGAGCTCAGAAGA	176	_No FA Found
>jgi|Phyca11|563895|estExt2_Genewise1.C_PHYCAscaffold_130326	Phyca_SSR136	(GAAG)4	GCTTAACAACGACAAGCGCT	TGTAGGCAAGTTAGCACGGG	178	_No FA Found
>jgi|Phyca11|576985|estExt2_Genewise1.C_PHYCAscaffold_1000030	Phyca_SSR136	(TTGC)4	GAGCGCTCAATAGACCGACA	GCATTCGCACATGACTGGTC	277	_No FA Found
>jgi|Phyca11|127545|e_gw1.70.129.1	Phyca_SSR136	(CAC)6	TTGTACATGCGCCCGATCTT	GGTCGTACGTGTTAGTGCCA	211	_No FA Found
>jgi|Phyca11|129264|e_gw1.82.46.1	Phyca_SSR136	(GAA)6	CGGTGATGTTTTCGGCAAGG	TCCCCCTGCGAATACCCTTA	275	_No FA Found
>jgi|Phyca11|16581|fgenesh1_pg.PHYCAscaffold_20_#_169	Phyca_SSR136	(CCG)6	CTTACCTACGCCTCCGACTC	GTTGGCGAATGATGGCATCC	295	_No FA Found
>jgi|Phyca11|18529|fgenesh1_pg.PHYCAscaffold_37_#_93	Phyca_SSR136	(TAG)6	ATGATCCAAGTGCCGCACG	CAGGTGTGTGACGAGCTTCT	198	_SMAD/FHA domain
>jgi|Phyca11|18635|fgenesh1_pg.PHYCAscaffold_38_#_81	Phyca_SSR136	(GAG)6	GTTGTCAAGGCTCGCAACAG	CGACACTTGGAAGCCTAGCA	217	_No FA Found
>jgi|Phyca11|19101|fgenesh1_pg.PHYCAscaffold_43_#_95	Phyca_SSR136	(TCT)6	AGGTCCGCAGTTTGGATGAG	ATCAAAGGAGCGCTCGAACA	164	_No FA Found
>jgi|Phyca11|20211|fgenesh1_pg.PHYCAscaffold_59_#_39	Phyca_SSR136	(AGA)6	CGCTTCTCCAACACGCAAAA	GAGTGACTGGTTTGGCCCTT	211	_No FA Found
>jgi|Phyca11|21793|fgenesh1_pg.PHYCAscaffold_122_#_4	Phyca_SSR137	(GAA)6	TTTCCTACTGGTGCTGCCTG	CTCAGTAGCGACGTGGATCC	285	_No FA Found
>jgi|Phyca11|21906|fgenesh1_pg.PHYCAscaffold_208_#_2	Phyca_SSR137	(AGA)6	TCCAACACGCAAGATCTCCC	CGTAGGAGTTGGTGTTGGCT	294	_No FA Found
>jgi|Phyca11|44449|gw1.51.83.1	Phyca_SSR137	(CAG)6	CTTCCCCACCTCCTCTACGA	ATAGCCAGGTTGTCCAGTGC	272	_Polynucleotidyl transferase, Ribonuclease H fold
>jgi|Phyca11|503953|fgenesh2_kg.PHYCAscaffold_5_#_117_#_Contig	Phyca_SSR137	(AGA)6	GAACAACCTGGCGTTCATCG	GCCTTTATCACATCCGCAGC	240	_No FA Found
>jgi|Phyca11|505071|fgenesh2_kg.PHYCAscaffold_11_#_17_#_40984	Phyca_SSR137	(ACG)6	GAAAACGCATCACCCCAACC	TGTCCAACACAGCAACCACT	284	_No FA Found
>jgi|Phyca11|506312|fgenesh2_kg.PHYCAscaffold_19_#_18_#_Contig	Phyca_SSR137	(CAG)6	GGACGATCTGCTACTGGACG	CACTTCAGCGTCTGTGTTGC	253	_No FA Found
>jgi|Phyca11|506574|fgenesh2_kg.PHYCAscaffold_20_#_120_#_Conti	Phyca_SSR137	(TTC)6	CTCGGTCCTACTCACCTCGA	GTTCTTCCGACTTAGGGGCC	247	_No FA Found

>jgi|Phyca11|507331|fgenesh2_kg.PHYCAscaffold_27_#_5_#_gi|18908	Phyca_SSR137	(CAC)6	ACGATCATCATGCCCACCAA	TTGCGGAAGTTCTTAGGCGT	134	_No FA Found
>jgi|Phyca11|510644|fgenesh2_kg.PHYCAscaffold_64_#_37_#_gi|1890	Phyca_SSR137	(AAG)6	CGACAAACAGTGGCAAGTGG	GTCGTCCAGAAAGCTGTGGA	255	_No FA Found
>jgi|Phyca11|511104|fgenesh2_kg.PHYCAscaffold_76_#_5_#_Contig4	Phyca_SSR137	(GCA)6	TACTTCAAGTGCCGATGCGT	CCTAGCTGCGCTAATGTTGC	223	_No FA Found
>jgi|Phyca11|511131|fgenesh2_kg.PHYCAscaffold_76_#_32_#_gi|1890	Phyca_SSR138	(GAC)6	GTTCTTCCTCGCACTCGTCA	ATTGCACTGCCTACACTGCT	289	_No FA Found
>jgi|Phyca11|511850|fgenesh2_kg.PHYCAscaffold_102_#_5_#_40981	Phyca_SSR138	(AAG)6	GTCGTATGAGTGTCCACGCA	TGGAGAGGTTTTCGTCGTCG	194	_No FA Found
>jgi|Phyca11|524955|estExt2_fgenesh1_pm.C_PHYCAscaffold_10175	Phyca_SSR138	(GCT)6	TTTCCTGAACGGATGCAGCT	TTTTGGCAGCAGCAAGTTCC	161	_No FA Found
>jgi|Phyca11|533960|estExt2_fgenesh1_pg.C_PHYCAscaffold_190041	Phyca_SSR138	(GAC)6	CTGAGTCGGTTTGGTGACGA	ACGCATCTTCGTCAACACCT	115	_No FA Found
>jgi|Phyca11|552671|estExt2_Genewise1Plus.C_PHYCAscaffold_4900	Phyca_SSR138	(CAG)6	GACGCCTACAACTTCCCCAA	TCCTGCGTGTGAACCTTACC	290	_No FA Found
>jgi|Phyca11|560550|estExt2_Genewise1.C_PHYCAscaffold_50261	Phyca_SSR138	(CAG)6	CGGATGTTATTGTGCCGTCG	GCTACTGCAAAGGTCGTCCT	221	_No FA Found
>jgi|Phyca11|6573|fgenesh1_pm.PHYCAscaffold_13_#_40	Phyca_SSR138	(AAG)6	TGCTGTCCACTGACGATGAC	GCCTCTCGCTCTTCCTTCTC	193	_Heat shock protein DnaJ, N-terminal
>jgi|Phyca11|105327|e_gw1.10.219.1	Phyca_SSR138	(CAACAG)3	CAACATCATGGCGAGCTTCG	TGGACGTGGAGCCATCATTC	145	_No FA Found
>jgi|Phyca11|108907|e_gw1.16.89.1	Phyca_SSR138	(TGAGAG)3	AGTCTGCGCGGATAACAACA	CGCTGGCTAATACACAGGCT	281	_No FA Found
>jgi|Phyca11|110485|e_gw1.18.592.1	Phyca_SSR138	(TCAGAA)3	GCAGAATTTGCGTGCAGACA	CAAGTGGGCACAAAACCTGG	281	_No FA Found
>jgi|Phyca11|111741|e_gw1.20.379.1	Phyca_SSR139	(GTACTC)3	TGTTGACAAGATCAGCGGCT	GTAGGCGACGTCAGCTACAA	202	_No FA Found
>jgi|Phyca11|114067|e_gw1.25.264.1	Phyca_SSR139	(CCTCCA)3	CGAAGAAGACGAGGGTGTCC	AAGAGCTGTTTGGGGACTGG	193	_No FA Found
>jgi|Phyca11|115245|e_gw1.28.290.1	Phyca_SSR139	(TCAGAA)3	GCAGAATTTGCGTGCAGACA	GGCTGAATTTGCACCAGTCG	208	_No FA Found
>jgi|Phyca11|120666|e_gw1.42.255.1	Phyca_SSR139	(CAACGT)3	AAGCTCGTGCAGTCGATGAA	CTTAGCGTAGTACGTGGCGT	252	_No FA Found
>jgi|Phyca11|122144|e_gw1.47.229.1	Phyca_SSR139	(GTGGTC)3	TGGTCGAGGTGGTTTCCAAG	TACAGCTGACACAGTGCCTG	261	_No FA Found
>jgi|Phyca11|131958|e_gw1.122.12.1	Phyca_SSR139	(GGCGGA)3	GCTGAAACCGGACAGGATGA	AATCCCGATCTCGTTCACGG	157	_No FA Found
>jgi|Phyca11|14555|fgenesh1_pg.PHYCAscaffold_8_#_109	Phyca_SSR139	(GAGGAA)3	GTGGAAGCAACGACTGAGGA	TGGCGTGCTTGTTAACTTGC	223	_No FA Found

>jgi|Phyca11|14821|fgenesh1_pg.PHYCAscaffold_9_#_197	Phyca_SSR139	(CGATGA)3	AGTGTGGCTTCGCTTGATGA	TCGTGACTTCCGTGACCTTG	227	_PDZ/DHR/GLGF
>jgi|Phyca11|16353|fgenesh1_pg.PHYCAscaffold_19_#_100	Phyca_SSR139	(GCGCTG)3	GCGACTGCTGATGAACGTTC	TACATGAGACGGACGCACTG	251	_No FA Found
>jgi|Phyca11|19555|fgenesh1_pg.PHYCAscaffold_49_#_68	Phyca_SSR139	(GGAGCT)3	GATATGGAGCGCACAGTGGA	GCTACATGCGTTCGAAGCTG	263	_No FA Found
>jgi|Phyca11|20202|fgenesh1_pg.PHYCAscaffold_59_#_30	Phyca_SSR140	(GAGGAA)3	GAGCATCTGCCGTGAGTGAT	TGATGAATTGGGGCCCAGTC	144	_No FA Found
>jgi|Phyca11|20208|fgenesh1_pg.PHYCAscaffold_59_#_36	Phyca_SSR140	(CACGAC)3	ACAACGACTACGGACACCAC	CTAGACGACGACGGTAGTGC	111	_No FA Found
>jgi|Phyca11|21129|fgenesh1_pg.PHYCAscaffold_83_#_2	Phyca_SSR140	(GCGCTG)3	GCGACTGCTGATGAACGTTC	TACATGAGACGGACGCACTG	251	_No FA Found
>jgi|Phyca11|21924|fgenesh1_pg.PHYCAscaffold_222_#_1	Phyca_SSR140	(TCGTGA)3	GGGGGACATGGAGTTTCAGG	GACTGTGGGGGACGACCA	257	_No FA Found
>jgi|Phyca11|22046|fgenesh1_pg.PHYCAscaffold_501_#_1	Phyca_SSR140	(CAAGCT)3	GGGAGTGGAGTTCCTCAAGC	TGAGCTTGAGGTCCAGCTTG	157	_No FA Found
>jgi|Phyca11|44035|gw1.42.86.1	Phyca_SSR140	(AGTGAC)3	AGTTGCTGACATCGCCTGAA	TCATGGGTGAGCTCGTTGTC	217	_No FA Found
>jgi|Phyca11|502970|fgenesh2_kg.PHYCAscaffold_2_#_86_#_gi|18908	Phyca_SSR140	(GACGAG)3	CAGCCGATGACAAAAGCGAG	CTGGGTCTTTCCTGGTCGAC	271	_No FA Found
>jgi|Phyca11|503785|fgenesh2_kg.PHYCAscaffold_4_#_324_#_409904	Phyca_SSR140	(GCCGAC)3	CGGAAGATCGTCGGGTGAAG	CAGTCCTTGGGCGTCTTCAT	242	_No FA Found
>jgi|Phyca11|506540|fgenesh2_kg.PHYCAscaffold_20_#_86_#_Contig	Phyca_SSR140	(GGCAAG)3	ACCAAGGAGCAGAAGATGGC	CTGGTCGTACAGCACCTTGT	114	_No FA Found
>jgi|Phyca11|507739|fgenesh2_kg.PHYCAscaffold_30_#_8_#_Contig1	Phyca_SSR140	(TGCAGG)3	ACGGACACGAAGAACAAGGA	GTTGTCCAACCGTACCGAGT	282	_No FA Found
>jgi|Phyca11|508273|fgenesh2_kg.PHYCAscaffold_33_#_132_#_40999	Phyca_SSR141	(TGACGA)3	AGGACGACGACGATGACATG	AGTTTCTCCATCCGCAGCTC	284	_No FA Found
>jgi|Phyca11|508666|fgenesh2_kg.PHYCAscaffold_37_#_41_#_409687	Phyca_SSR141	(CGATGA)3	TGCCACGATGGAAATGAGCT	GTCTCCGTCGTCTTTGTGGT	106	_No FA Found
>jgi|Phyca11|509101|fgenesh2_kg.PHYCAscaffold_42_#_8_#_Contig2	Phyca_SSR141	(AGACTC)3	CGTCAACTGGCAGAAGGTCT	GGGCCTTGTCCTTAGCCAAT	227	_No FA Found
>jgi|Phyca11|509580|fgenesh2_kg.PHYCAscaffold_47_#_71_#_40977	Phyca_SSR141	(CAGATG)3	ATGGTCCTATGGGCTACGGT	CATGCCGTACATAGGGGGTC	272	_No FA Found
>jgi|Phyca11|509696|fgenesh2_kg.PHYCAscaffold_48_#_99_#_Contig	Phyca_SSR141	(GAAGAC)3	TTCCGAGGCAAGGAAGTGTC	CGTCGTAGCCGAATACGTCA	295	_No FA Found
>jgi|Phyca11|510085|fgenesh2_kg.PHYCAscaffold_53_#_70_#_Contig	Phyca_SSR141	(TGGAAG)3	CGGTGGAGAAGTGCTAACGT	TTCATGCGGTAGGAGCGATC	285	_No FA Found
>jgi|Phyca11|511130|fgenesh2_kg.PHYCAscaffold_76_#_31_#_Contig	Phyca_SSR141	(AGTGCC)3	AGAACAACAAGGAGGCGCTT	GAACCACAGTGGACGCACTA	291	_No FA Found

>jgi|Phyca11|511509|fgenesh2_kg.PHYCAscaffold_87_#_15_#_410115	Phyca_SSR141	(CAAGGA)3	TGCCGCCAGTATTGAGAAGG	TCCGTCTCGATAGCTTTCGC	117	_No FA Found
>jgi|Phyca11|525145|estExt2_fgenesh1_pm.C_PHYCAscaffold_20084	Phyca_SSR141	(TCCTCG)3	CTGGGTCTTTCCTGGTCGAC	CAGCCGATGACAAAAGCGAG	271	_No FA Found
>jgi|Phyca11|527838|estExt2_fgenesh1_pm.C_PHYCAscaffold_230063	Phyca_SSR141	(CGACAG)3	CCGTCTCAGACCTTGCAGTT	TGTATAGGCGCTTCGTCGTC	187	_No FA Found
>jgi|Phyca11|529544|estExt2_fgenesh1_pm.C_PHYCAscaffold_440060	Phyca_SSR142	(CTCAGA)3	AAGTACCAGCAGATCGTGGC	CGTCTTCTGCTGCATGAACG	150	_No FA Found
>jgi|Phyca11|5314|fgenesh1_pm.PHYCAscaffold_5_#_117	Phyca_SSR142	(CAACGT)3	TGACACCGACACGTCAGAAG	CCAATTCAAACACCGCCTGG	282	_No FA Found
>jgi|Phyca11|531719|estExt2_fgenesh1_pg.C_PHYCAscaffold_20066	Phyca_SSR142	(AACAGC)3	TCCGTCTTACTATCGCGTGC	AGAGTGTCATCCGTCTCCGA	229	_No FA Found
>jgi|Phyca11|532496|estExt2_fgenesh1_pg.C_PHYCAscaffold_50257	Phyca_SSR142	(CGTCGA)3	CACTGGAGTCCGACAACGAA	CAACTTGCTTTCCATGCGCA	194	_No FA Found
>jgi|Phyca11|532660|estExt2_fgenesh1_pg.C_PHYCAscaffold_70065	Phyca_SSR142	(AGATCG)3	TACGAAGCCGAAGCAGATCC	CTTGGCAAAGCTTCGATCGG	286	_No FA Found
>jgi|Phyca11|533691|estExt2_fgenesh1_pg.C_PHYCAscaffold_160072	Phyca_SSR142	(CTCGTC)3	AACAACAGCAGCAGCAACAG	CCAAAGTCTTCACGGTTGCG	290	_No FA Found
>jgi|Phyca11|535315|estExt2_fgenesh1_pg.C_PHYCAscaffold_340034	Phyca_SSR142	(AAGCTC)3	AGAACAAGGGCGAGGACTTG	CGGCGTAGTTCAGCAGTTTG	262	_No FA Found
>jgi|Phyca11|537167|estExt2_fgenesh1_pg.C_PHYCAscaffold_760035	Phyca_SSR142	(CAGAAA)3	CCGTCAGAGACTGTGGAACC	GAAAATGTCTACCGTCGCGC	240	_No FA Found
>jgi|Phyca11|538155|estExt2_Genewise1Plus.C_PHYCAscaffold_1051	Phyca_SSR142	(CGGCTT)3	ACGGACAAGTACGGTGGTTC	AGCCATGACAATGCCCTTGA	300	_No FA Found
>jgi|Phyca11|541576|estExt2_Genewise1Plus.C_PHYCAscaffold_7029	Phyca_SSR142	(AGCAGT)3	CTCTGGCTCAAGCAATTCGC	TTCTTCCGTTGCCTCCTGAC	268	_No FA Found
>jgi|Phyca11|548630|estExt2_Genewise1Plus.C_PHYCAscaffold_2903	Phyca_SSR143	(GTGCTC)3	CGACTTTTTGTGCTGTGCGA	GACTGGATGCAAGCTGGACA	227	_No FA Found
>jgi|Phyca11|549364|estExt2_Genewise1Plus.C_PHYCAscaffold_3201	Phyca_SSR143	(CAAGGA)3	AGGAGGGAGTCGGTCTTCTC	CTTCTTTGCCTCCGAGCAGA	270	_No FA Found
>jgi|Phyca11|562574|estExt2_Genewise1.C_PHYCAscaffold_90628	Phyca_SSR143	(CCAACA)3	CCCCGAGACACCAATTCCAA	GCGTTGGAGTTGGTGTTGAC	113	_No FA Found
>jgi|Phyca11|574796|estExt2_Genewise1.C_PHYCAscaffold_650156	Phyca_SSR143	(GCAGTG)3	TCTGACTGGCAAGATGGCTG	GAGCTAAAAGCCGTTGCGAG	269	_No FA Found
>jgi|Phyca11|99832|e_gw1.4.1163.1	Phyca_SSR143	(GGCAAG)3	GCGAAGACTCCCTCCAAGAA	CTGACGCAGCACCTTGTAGA	111	_Histone-fold
>jgi|Phyca11|131593|e_gw1.108.36.1	Phyca_SSR143	(G)20	AGGAGCAAACACACTCACTGT	CGTGTGCTTGATCACCTCCT	172	_No FA Found
>jgi|Phyca11|15430|fgenesh1_pg.PHYCAscaffold_13_#_118	Phyca_SSR143	(CAG)7	TTGGGAAGCCAAAACCAGGG	CTTGGCTGTCCTGCTGCT	277	_TonB box, conserved site

>jgi|Phyca11|21986|fgenesh1_pg.PHYCAscaffold_331_#_1	Phyca_SSR143	(AGA)7	GAGAGGCTGTCAGGAACACC	AGTTGGTGTTGGCTTGGGAA	243	_No FA Found
>jgi|Phyca11|506991|fgenesh2_kg.PHYCAscaffold_23_#_122_#_Conti	Phyca_SSR143	(GTA)7	TGTGTCGTGGGCGGATTAAA	AGGCATGCTGCATGAAGACT	213	_No FA Found
>jgi|Phyca11|534570|estExt2_fgenesh1_pg.C_PHYCAscaffold_250064	Phyca_SSR143	(GAA)7	CACGGGGAGGATTTGGAACA	TCCAGGAACGAAGGCATGTC	266	_No FA Found
>jgi|Phyca11|543759|estExt2_Genewise1Plus.C_PHYCAscaffold_1300	Phyca_SSR144	(GCA)7	CCTGTGACGTCTTCGGAACA	CTGGTGTCACCACTGCTGAT	164	_No FA Found
>jgi|Phyca11|548293|estExt2_Genewise1Plus.C_PHYCAscaffold_2802	Phyca_SSR144	(CAC)7	GGACTGGAATCCAACACGGT	CGTACGTGTTGGTGCCATTG	130	_No FA Found
>jgi|Phyca11|551706|estExt2_Genewise1Plus.C_PHYCAscaffold_4301	Phyca_SSR144	(AGA)7	TTATGGATGGCAGTGTGCGT	TTTTGAACGACTCCTCCGGG	297	_No FA Found
>jgi|Phyca11|557962|estExt2_Genewise1.C_PHYCAscaffold_10148	Phyca_SSR144	(AGG)7	GAAAAACCTGCGGTCGATCG	CCGATACCTGGTCGCACTAC	171	_No FA Found
>jgi|Phyca11|572324|estExt2_Genewise1.C_PHYCAscaffold_470314	Phyca_SSR144	(AGA)7	AGGAGCTCAGTGGGAAGGAT	GGTCGTGTGCATTTGGTACG	175	_No FA Found
>jgi|Phyca11|505072|fgenesh2_kg.PHYCAscaffold_11_#_18_#_40983	Phyca_SSR144	(AG)5(GAA)4	ATATTCCAGGCGCACACACA	ACAAGCAGAGAGGCAATGCT	293	_No FA Found
>jgi|Phyca11|532912|estExt2_fgenesh1_pg.C_PHYCAscaffold_90071	Phyca_SSR144	(AC)5(ACAAG)	CAGCAACAACAAGCAGAGGC	GAGTAGGTTGTGCCGAGGTC	120	_No FA Found
>jgi|Phyca11|531315|estExt2_fgenesh1_pm.C_PHYCAscaffold_108000	Phyca_SSR144	(AGA)4(GGA)4	GCTGCCATTGAAGCCATCAG	GCCACTCGTTGTAGCTCTCC	205	_No FA Found
>jgi|Phyca11|505215|fgenesh2_kg.PHYCAscaffold_12_#_3_#_Contig1	Phyca_SSR144	(CAG)4t(GGC)4	GCTCGTCAACGCGATACAAC	CTGCTTGACTGGGGTCTCTG	188	_No FA Found
>jgi|Phyca11|558170|estExt2_Genewise1.C_PHYCAscaffold_10741	Phyca_SSR144	(GAA)4c(AAG)4	GACAAGGTGCACTCGGAGAA	AGTCTCTCTCCGTCCAAGCT	176	_No FA Found
>jgi|Phyca11|505466|fgenesh2_kg.PHYCAscaffold_13_#_116_#_Conti	Phyca_SSR145	(CAG)5(CAA)4	TACCCCCACAAACAACCAGG	TCGAACTGCAGCTGGTACTG	138	_No FA Found
>jgi|Phyca11|525868|estExt2_fgenesh1_pm.C_PHYCAscaffold_50187	Phyca_SSR145	(GAA)4gag(GA	TGAATTGCGGCGCTATTGTG	CAAACTCCACCTCTGCCTCC	285	_No FA Found
>jgi|Phyca11|126140|e_gw1.61.140.1	Phyca_SSR145	(GAA)4cagg(A	TGGCTGTCGGTTCAAATGGA	ACCCAGCCAGAGATTCAACG	263	_No FA Found
>jgi|Phyca11|533179|estExt2_fgenesh1_pg.C_PHYCAscaffold_110054	Phyca_SSR145	(GAA)4gaga(A	GACGCAGCAACCAACGTATC	GGCTGCAGGTGTAACTGAGT	283	_No FA Found
>jgi|Phyca11|509827|fgenesh2_kg.PHYCAscaffold_50_#_28_#_41016	Phyca_SSR145	(CAA)4cggaga	TCTGCTTGTGCTGGTCTCAG	GTAGCCGAGGATTCCAGTCG	289	_No FA Found
>jgi|Phyca11|509882|fgenesh2_kg.PHYCAscaffold_51_#_9_#_Contig2	Phyca_SSR145	(AGA)4aacgtcg	AGGAGGCAGAGACACAGGAA	AAACCGGTGGAAACGTACGA	280	_No FA Found
>jgi|Phyca11|507351|fgenesh2_kg.PHYCAscaffold_27_#_25_#_41017	Phyca_SSR145	(CAG)4tacggcc	GTAAGCCACAACAACCAGCG	CGTACTGCTGCTGAGGTTGA	271	_No FA Found

>jgi|Phyca11|17710|fgenesh1_pg.PHYCAscaffold_30_#_21	Phyca_SSR145	(GGA)4agaagtg	CGAGGAAGACGAGATGGTGG	CCCCGCCTTAAGCATCATCT	283	_No FA Found
>jgi|Phyca11|506688|fgenesh2_kg.PHYCAscaffold_21_#_60_#_410327	Phyca_SSR145	(GA)5aagcaatga	TTCCCGTACCAAGTGAGTGC	ACAGCATCGCTTCTTCTCCT	271	_No FA Found
>jgi|Phyca11|557744|estExt2_Genewise1Plus.C_PHYCAscaffold_3640	Phyca_SSR145	(GAG)5gaagaa	GACATCCCCAGCTCTAACGG	CTTCAGGGGTGGCTTGAGTT	172	_No FA Found
>jgi|Phyca11|547097|estExt2_Genewise1Plus.C_PHYCAscaffold_2303	Phyca_SSR146	(AAG)4ctgccaa	ATGCTTTGGTGCAACGTGAC	ATCACCGTCTTCCTTGGCAG	216	_No FA Found
>jgi|Phyca11|530554|estExt2_fgenesh1_pm.C_PHYCAscaffold_680016	Phyca_SSR146	(ATG)4aagaaga	CATGCACAACAGCCAGGTTC	ACCGATTGCACACGATGTCT	182	_No FA Found
>jgi|Phyca11|532798|estExt2_fgenesh1_pg.C_PHYCAscaffold_80088	Phyca_SSR146	(ACT)5aca(ACT	CGTGGAAACTTACCGGGTGA	CACTCCACTCTTGAGGCTCG	266	_No FA Found
>jgi|Phyca11|19812|fgenesh1_pg.PHYCAscaffold_52_#_64	Phyca_SSR146	(GAA)4gaggaag	GACCACCTAGCTGCAGTTGT	CGTCCTCCTCGTTCAGATCG	280	_Chromo domain-like
>jgi|Phyca11|4546|fgenesh1_pm.PHYCAscaffold_2_#_142	Phyca_SSR146	(CTCCTG)3cac	GGAAAGTGATGCCACCTCCA	GTCTCGTAGTCGGTGGTGTC	246	_No FA Found
>jgi|Phyca11|575408|estExt2_Genewise1.C_PHYCAscaffold_730104	Phyca_SSR146	(AGC)4agtgaag	ACTATCAGCGAGCGAAGACG	CGTAGAACCTCAGAATCCCGT	149	_No FA Found
>jgi|Phyca11|548666|estExt2_Genewise1Plus.C_PHYCAscaffold_2903	Phyca_SSR146	(GC)5gtcagtcga	CATGCCAGTCTGGTCGAGTT	CAAAAGCACACGAGGCTTCC	221	_No FA Found
>jgi|Phyca11|22110|fgenesh1_pg.PHYCAscaffold_736_#_2	Phyca_SSR146	(CACGAC)3cac	ACAACGACTACGGACACCAC	CATAGCATTCCGGCCGTAGT	206	_No FA Found
>jgi|Phyca11|531297|estExt2_fgenesh1_pm.C_PHYCAscaffold_106001	Phyca_SSR146	(AAG)4agaagaa	CACGGTGGTTGAGTGGAGAA	ATGCAACGCCCCTTCAATTT	248	_No FA Found
>jgi|Phyca11|507377|fgenesh2_kg.PHYCAscaffold_27_#_51_#_409681	Phyca_SSR146	(CGC)4acatgtcc	GGGGAGGCAGCAATAACAGT	AAATGGTGCTCTCCACGGAG	243	_No FA Found
>jgi|Phyca11|126376|e_gw1.62.19.1	Phyca_SSR147	(AAG)4acgaaaa	GCTGTCACGGGTGAAGAAGA	TCATGGGCGTGAAGTTCTCC	220	_No FA Found
>jgi|Phyca11|12860|fgenesh1_pg.PHYCAscaffold_1_#_312	Phyca_SSR147	(AAG)6agttcatc	GGAAGCGGTTTGTATCCCCA	GATCCTGCAAAGCCATGAGC	225	_Zinc finger, C2H2-type
>jgi|Phyca11|506640|fgenesh2_kg.PHYCAscaffold_21_#_12_#_gi|1890	Phyca_SSR147	(AGA)5cgctgtaa	AGTCGCTGTTCTGGCTCTTC	AAGATACACTTGGGCCAGCC	257	_No FA Found
>jgi|Phyca11|111343|e_gw1.20.542.1	Phyca_SSR147	(GGC)4atcacgtc	GTGCAACAACAGACAGCACC	TGCACTGCGAATGTCCTCTT	237	_No FA Found
>jgi|Phyca11|116045|e_gw1.30.427.1	Phyca_SSR147	(ACGA)3ggagcc	CGGAGCAGGTCTCACTTGAG	TTCGTCCGTCCAAAGAGTCG	244	_No FA Found
>jgi|Phyca11|553774|estExt2_Genewise1Plus.C_PHYCAscaffold_5501	Phyca_SSR147	(GCA)6aaatagc	TCGAGGTCCTAGTGGCATGA	GGGTTTCGCTGTTGTTGAGG	159	_No FA Found
>jgi|Phyca11|504290|fgenesh2_kg.PHYCAscaffold_7_#_42_#_Contig3	Phyca_SSR147	(GCA)5acaactc	CGTCCCTCAGCAGTCACTTT	TGTCAGACTGTGCACTCGAC	254	_No FA Found

>jgi|Phyca11|502988|fgenesh2_kg.PHYCAscaffold_2_#_104_#_gi|1890	Phyca_SSR147	(CCA)4gagccta	TGCAGAGAACACCCCAATCC	GTACTAGGTGCAACAGCGGT	207	_No FA Found
>jgi|Phyca11|504813|fgenesh2_kg.PHYCAscaffold_9_#_204_#_Contig	Phyca_SSR147	(CAG)4tacagttc	AGCATGCCGTGTACTTCACA	CTGACCTCCATCTCGAGCAC	233	_No FA Found
>jgi|Phyca11|572504|estExt2_Genewise1.C_PHYCAscaffold_480242	Phyca_SSR147	(TTC)4cactgact	CGTCCGACGATTCAGGTAGG	ACTACCGAGAAGTGGGTCCA	256	_No FA Found
>jgi|Phyca11|509662|fgenesh2_kg.PHYCAscaffold_48_#_65_#_Contig	Phyca_SSR148	(GAA)4gaggcca	ACTACCGAGAAGTGGGTCCA	CGTCCGACGATTCAGGTAGG	256	_No FA Found
>jgi|Phyca11|16300|fgenesh1_pg.PHYCAscaffold_19_#_47	Phyca_SSR148	(GTG)5aaccggt	TGCTGGTGGTAGTGACGAAC	ATCGGTATCATGAGCAGCGG	250	_No FA Found
>jgi|Phyca11|12083|fgenesh1_pm.PHYCAscaffold_95_#_9	Phyca_SSR148	(CGA)4cgtggac	CAGAATTTGGGCTTCGCACG	GAGCCGCGACGATCATCATA	206	_RNA recognition motif, RNP-1
>jgi|Phyca11|535674|estExt2_fgenesh1_pg.C_PHYCAscaffold_400035	Phyca_SSR148	(CCG)4cctcccc	GAACGAGTCGGCTTCGGAC	TGGACTCCTCGTGGAAAAGC	167	_No FA Found
>jgi|Phyca11|505093|fgenesh2_kg.PHYCAscaffold_11_#_39_#_Contig	Phyca_SSR148	(GGA)4cgagctc	GTGTCGAGAACGTTGGGTGA	GATCTCCGAAGACGCTGGAG	286	_No FA Found
>jgi|Phyca11|542968|estExt2_Genewise1Plus.C_PHYCAscaffold_1005	Phyca_SSR148	(AGA)4agcacaa	GGCAAGGTGAACGACAACAC	ATTCCGAGTCGCTTGTCTCC	295	_No FA Found
>jgi|Phyca11|19814|fgenesh1_pg.PHYCAscaffold_52_#_66	Phyca_SSR148	(ATC)4gttcaagg	ATTACGGAGATCACGCGTCC	ACACCTCCTTGTCCATGAGC	286	_Acetyl-coenzyme A carboxyltransferase, C-terminal
>jgi|Phyca11|532077|estExt2_fgenesh1_pg.C_PHYCAscaffold_30269	Phyca_SSR148	(CAG)4tttgagtct	CCCCAACCCAAATGGCCT	CGAGTCTCCGTTGGTGGAAA	290	_No FA Found
>jgi|Phyca11|548193|estExt2_Genewise1Plus.C_PHYCAscaffold_2704	Phyca_SSR148	(GAACAG)3gag	GCTGGAGAGGATAGCAGCAG	CAACGTTTGCACCTTACGCA	228	_No FA Found
>jgi|Phyca11|100397|e_gw1.4.666.1	Phyca_SSR148	(GAG)4tacgtgg	GAGCAAGAAGAAGGTGGTGC	TTGTAGCAGTCCGCAGTGTT	170	_No FA Found
>jgi|Phyca11|110522|e_gw1.18.429.1	Phyca_SSR149	(GAA)4gtcgaag	CACTGTGGTAAACCCGGACA	TGCCACAATCCAGCATCCAT	286	_No FA Found
>jgi|Phyca11|114698|e_gw1.27.299.1	Phyca_SSR149	(GAA)4ggcgaag	CACTGTGGTAAACCCGGACA	GTCGTCCTCTTCCTCTCCCT	219	_No FA Found