Development of genomic resources in pigeonpea [*Cajanus cajan* (L.) Millspaugh]

Report Submitted to

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By

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CERTIFICATE

This is to certify that Ms. Anuja Dubey has carried out the research work on **"Development of genomic resources in pigeonpea [*Cajanus cajan* (L.) Millspaugh]"** for the degree of Doctor of Philosophy (Ph.D.) under joint-supervision of Dr. Ragini Gothalwal, H.O.D. Department of Bioinformatics and Biotechnology, Barkatullah University, Bhopal and Dr. Rajeev K Varshney Principle Scientist-Applied Genomics, International crops Research Institute for Semi-Arid Tropics (ICRISAT), Patancheru.

The research work is original and no part of this work has been submitted for the award of any degree or diploma of any other University or Institute.

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ABSTRACT

This study reports generation of large-scale genomic resources for pigeonpea, a so-called 'orphan crop species' of the semi-arid tropic regions. A set of 88,860 BAC (bacterial artificial chromosomes)-end sequences (BESs) were generated after constructing two BAC libraries by using *Hin*dIII (34,560 clones) and *Bam*HI (34,560 clones) restriction enzymes. A total of 3,072 novel SSR primer pairs were synthesized and tested for length polymorphism on two parental genotypes (ICP 28 and ICPW 94). In addition, Roche FLX/454 sequencing was carried out on a normalized cDNA pool prepared from 31 tissues and produced 494,353 short transcript reads (STRs). Cluster analysis of these STRs, together with 10,817 Sanger ESTs, resulted in 127,754 pigeonpea transcript assemblies (CcTAs). Additionally, Illumina 1G sequencing was performed on four parental genotypes of two mapping populations and a set of 7,453 SNPs were identified. Based on BES-SSR markers, the *first* SSR-based genetic map comprising of 239 loci was developed for this previously uncharacterized genome. In summary, while BAC libraries, BESs and CcTAs should be useful for genomics studies, BES-SSR, SNP markers, and the genetic map should be very useful for linking the genetic map with a future physical map as well as for molecular breeding in pigeonpea.

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1. INTRODUCTION

Pigeonpea (*Cajanus cajan* L.) is one of the major pulse crop of the tropics and sub-tropics. It is a major food legume crop in South Asia and East Africa with India is the largest producer (3.5 Mha) followed by Myanmar (0.54 Mha) and Kenya (0.20 Mha). It is the only cultivated food crop of the *Cajaninae* sub-tribe of economically important tribe Phaseoleae under sub-family *Papilionoideae* of *Leguminosae* family. It has a diploid genome with 11 pairs of chromosomes ($2n = 2x = 22$) and a genome size estimated to be 858 Mbp (Greilhuber and Obermayer, 1998). The revised genus *Cajanus* now comprises 32 species, with 18 species distributed in Asia, 15 in Australia, and one in West Africa. Of these, 13 are endemic to Australia, 8 to Indian subcontinent and Myanmar, and one to West Africa. The rest of them occur in more than one country (van der Maesen 1990). On a global basis pigeonpea can been considered as an under-exploited under resourced crop. The origins of pigeonpea have been a matter of dispute for a long time. Some authorities considered Africa to the center of origin due to evidence like presence wild species in West Africa (Rachie and Roberts, 1974). But inspite of this, several conclusions have been drawn in favour of India being the center of origin (van der Maesen, 1990). This is due to presence of large genetic diversity, several wild relatives, and presence of archeological remains and large scale usage of the crop in daily diet. It is believed to have traveled from India to Malaysia, then to East Africa and from there up the Nile Valley to West Africa. Historians believe that the crop then traveled to the New World from Zaire or Angola prior to the main slave trade.

Pigeonpea is the most versatile grain legume and its importance has been realized in India as a multipurpose crop. It is a hardy, drought-tolerant crop which often grows on poor soils. Pigeonpea has been used in numerous ways like for grain, fuel, wood, livestock feed. Apart from the many direct uses of pigeonpea it is a good crop to improve soil fertility. Pigeonpea forms nodules on its roots which contain nitrogen fixing bacteria and hence makes pigeonpea a crop which can be grown in poor soil conditions. These bacteria capture nitrogen from air and turn it into a form which the pigeonpea plants can use for growth. Pigeonpea contributes to the C, N and P economy of the soil (Rego and Nageswara Rao, 2000). Pigeonpea seeds have 20– 22% protein and are consumed as green peas, while grain or split peas. The seed and pod husks make a quality feed, whereas dry branches and stems serve as domestic fuel. Fallen leaves from the plant provide vital nutrients to the soil and the plant also enriches soil through symbiotic nitrogen fixation. Hence, fits into agroforestry and shifting cultivation system as a source of soil ameliorator. The protein content of pigeonpea ranges from 21% to over 25%.

India is the largest producer (2.30 mt) of pigeonpea followed by Myanmar (0.54 mt) and Malawi (0.16 mt) (FAOSTAT, 2009). The Indian sub continent alone contributes nearly 92 per cent of the total world production. Major states in terms of area and production are Maharashtra, Uttar Pradesh. Madhya Pradesh, Karnataka, Gujarat and Andhra Pradesh together contributes for about 90 per cent of area and 93 per cent of production of pigeonpea. Inspite of its importance very less attention have been paid either to crop production or technology development in case of pigeonpea. Although India leads the world both in area and production of pigeonpea, its productivity is lower than the world average. This is attributed to factors such as various abiotic (e.g. drought, salinity and water-logging) and biotic (e.g. diseases like *Fusarium* wilt, sterility mosaic and pod borer insects) stresses. Furthermore poor production practices such as low plant densities, low soil fertility, insufficient weeding and insufficient/inappropriate use of fungicides and herbicides are other constraints.

Diseases of economic concern include *Fusarium* wilt (*Fusarium udum* Butler), sterility mosaic disease (SMD), leaf spot (*Mycovellosiella cajani*) and to a lesser extent powdery mildew (*Leveillula taurica*). Apart from this the important pest which effect the crop production severely include the pod boring lepidoptera (*Helicoverpa armsigera* Hübner, *Maruca vitrata* Geyer and *Etiella zinkenella* Treitsche), pod sucking bugs (*Clavigralla tomentosicollis* Ståll and *Clavigralla horrida* Germar) and podfly (*Melanagromyza chalcosoma* Spencer) (Minja *et al.*, 2000). Furthermore, aboitic stresses like water logging and salinity also reduce pigeonpea production.

In pigeonpea, plant growth as well as flowering is highly influenced by the environment. Hence, breeding for wider adaptation, a complex phenomenon is a major issue to be tackled. Although related wild species are a rich reservoir of not only resistance genes against various biotic and abiotic stresses but also of genes responsible for yield components such as pods per plant, length of fruiting branches, and number of primary branches per plant, use of inter-specifics in pigeonpea improvement have been limited. This is due to the poor crossability of cultivated *Cajanus cajan* to species other than the closest species, *Cajanus cajanifolia* and *C. scaraboides*. Conventional breeding approaches which have been used for several decades offer limitation in overcoming various biotic and abiotic stresses (Varshney *et al.*, 2007). These breeding programs provide a limited amount of new diversity into the breeding gene pool, hence narrowing the genetic diversity within the elite gene pool.

Various advances in plant biotechnology and especially genomics together with traditional plant breeding technologies have led to the development of new improved varieties in a number of crop species with greater tolerance/resistance and higher yield (Varshney *et al.*, 2006, 2010a). In this context, molecular markers play a very important role as these are used for estimating diversity in germplasm, trait mapping, molecular breeding, genetic purity assessment of hybrid seeds, etc. Among a range of molecular markers starting with isozymes, RFLP (restriction fragment length polymorphism), RAPD (random amplified polymorphic DNA), AFLP (amplified fragment length polymorphism), SSR (simple sequence repeat), SNP (single nucleotide polymorphism) and more recently microarray-based DArT (diversity array technology). Among all the marker types, SSR and SNP markers are considered as the current markers of choice for plant genetics and breeding applications (Gupta and Varshney, 2000). While SNP markers have a promising future in plant breeding applications, and may augment or displace SSR based marker systems, SNP based markers and associated technologies are in their infancy in most crops, including pigeonpea, while SSR marker technologies are better established for wide spread use in molecular breeding. Utilization of substantial variability among pigeonpea landrace and germpalsm line for various morphological, physiological and agronomical traits using genomics-assisted-breeding can be an alternative approach to overcome the limitations of conventional breeding strategies. A revision of current breeding methods by utilizing genomics-assisted breeding is a must. Genomics-assisted breeding approaches have greatly advanced with the increasing availability of genome and transcriptome sequence data for several model plant and crop species (Varshney *et al.*, 2009a). This platform provides a broad range of applications including development of molecular markers, whole genome sequencing (Green *et al.*, 2006), transcriptome and gene regulation studies (Bainbridge *et al.*, 2006; Berezikov *et al.*, 2006), metagomics analysis (Krause *et al.*, 2006) and amplicon sequencing (Sogin *et al.*, 2006; Taylor *et al.*, 2007). These kind of platforms are available for many crops including, cowpea, common bean and soybean, pigeonpea being very important still lack these kind of studies.

Although efforts have been made in the recent past for development of molecular markers for this economically important crop but these were too elementary. In case of pigeonpea, until recently, only a few hundred SSR markers are available (Burns *et al.*, 2001; Odeny *et al.*, 2007, 2009; Saxena RK *et al.*, 2010a). A situation that is further hampered by low levels of genetic diversity within cultivated germplasm demands large scale development of genomic resources.

With advent of next generation sequencing technologies (NGS) like Roche FLX/454, Illumina/Solexa 1G Analyser and ABI/ SOLiD, it has become very easy to develop sequence data at very affordable prices. The sequence data produced can be used for large scale marker discovery. Furthermore, high-throughput marker genotyping platform and a very low cost associated to them calls for large scale development of genomic resource for this earlier called orphan crop.

Keeping the above in view, the present study was proposed with following objective:

1. Development of microsatellites markers from BAC-end sequences.
2. Development of transcript assembly for pigeonpea.
3. Large scale identification of SNPs.
4. Development of SNPs genotyping platform.

5. Genetic mapping of SSRs markers.

2. REVIEW OF LITERATURE

Pigeonpea (*Cajanus cajan* L. Millsp.) is an important grain legume crop of rainfed agriculture in the semi-arid tropics. Efforts have been made to improve production and to extend crop's adaptation beyond tropical and subtropical regions. However these efforts have very less contribution in productivity of this crop. Furthermore lack of high yielding cultivars has been the major factor underlying this bottleneck. In addition, other factors such as of biotic and abiotic stresses cause major yield losses every year. Unavailability of adequate genetic variation in germplasm collections is another bottleneck for successful breeding programme. An effective way to exploit the available genetic variation among germplasm collections would be development of genomics tools such as, ESTs (expressed sequence tags), molecular markers, genetic maps for molecular breeding (Varshney *et al.*, 2005). However, molecular breeding approach has not yet been initiated in pigeonpea primarily due to: availability of limited genomic resources and limited level of genetic diversity in majority of elite germplasm collection. Effort should be made for large scale development of genomic resources in pigeonpea.

2.1 Pigeonpea Genomics

Pigeonpea an important legume crops of India as well as other parts of the world is one of these kinds. Low availability of genetic resources is the major constrain in overcome various biotic and abiotic stresses which restrict the production of the crop (Saxena, 2008). Various studies have been performed to study the pattern of genetic diversity and development of molecular markers to enable marker assisted selection for improvement of this crop. Genetic diversity among wild species of the pigeon pea genus *Cajanus* has been studied using restricted fragment length polymorphism (RFLP) DNA as the specific nuclear probes (Nadimpalli *et al.*, 1994). In yet another study extremely high DNA polymorphism among wild species of pigeonpea was reported (Ratnaparkhe *et al.*, 1995). However, the DNA polymorphism among pigeonpea cultivars was very low (Sivaramakrishnan *et al.*, 1997). Amplified fragment length polymorphism (AFLP) has been used for analysis of DNA banding pattern among cultivars and wild species (Punguluri *et al.*, 2006). Diversity array technology (DArT) markers analysis also revealed low polymorphism among pigeonpea cultivars and high polymorphism between cultivated pigeonpea and its wild relatives (Yang *et al.*, 2006). Because of this low level of polymorphism in pigeonpea there was an urgent need of large-scale development genomic resources so as to undertake studies like germplasm characterization and molecular-mapping.

2.1.1 Marker repertoire in pigeonpea

The development of molecular techniques for genetic analysis has led to a great augmentation in our knowledge of crop genetics and our understanding of the structure and behavior of various crop genomes. Following are the molecular marker systems developed till date in pigeonpea.

2.1.1.1 *Restriction fragment length polymorphisms (RFLPs)*

Restriction fragment length polymorphism, or RFLP, refers to a difference between two or more samples of homologous DNA molecules arising from differing locations of restriction sites. In RFLP analysis the DNA sample is digested using restriction enzymes and the resulting restriction fragments are separated according to their lengths by gel electrophoresis. RFLP markers were used for diversity analysis of 24 genotypes belonging to genera *Cajanus*, *Dunbaria*, *Eriosema*, and *Rhynchosia*. This study showed that accessions of cultivated *C. cajan* shared more DNA fragments with *C. scarabaeoides* than with *C. cajanifolia* (Nadimpalli *et al.*, 1993). In yet another diversity study RFLP-PCR markers from 4 chloroplast gene specific primers were used to estimate diversity in 28 species belonging to five genera of the sub-tribe

Cajaninae; viz., *Cajanus* (15 species), *Rhynchosia* (10 species), *Dunbaria*, *Flemingia* and *Paracalyx*. This study showed very little variation in restriction patterns of five different genera indicating occurrence of limited evolutionary changes in chloroplast genome of these five genera (Lakshmi *et al*., 2000). RFLP markers from 3 maize mitochondrial probes were used to estimate diversity in 28 accessions representing 12 species of *Cajanus* and 4 species of *Rhynchosia*. 12 species of *Cajanus* were taken from 6 sections (*Cajanus*, *Atylosia*, *Fruticosa*, *Cantharospermum*, *Volubilis* and *Rhynchosoides*). Cluster analysis resulted in a clear-cut separation of two genera i.e. *Cajanus* and *Rhynchosia*. Species belonging to sections like *Cajanus*, *Fruticosa* and *Rhynchodoides* exhibited section specific grouping while species like *cajanifolius*, *volubilis*, *mollis* showed discrepancy in their positions (Sivaramakrishnan *et al*., 2002). Hence, RFLPs have been used in pigeonpea, to overcome the problems associated with phylogenic grouping such as inconsistencies in taxonomic relationships based on data from morphology, cytology and crossability.

2.1.1.2 *Randoml amplified polymorphic DNA (RAPD)*

Randomly amplified polymorphic DNA (RAPD) markers are DNA fragments from PCR amplified random segments of genomic DNA with single primer of arbitrary nucleotide sequence. Unlike traditional PCR analysis, RAPD (pronounced "rapid") does not require any specific knowledge of the DNA sequence of the target organism. RAPD markers were used for cluster analysis of 13 species belonging to the genera *Cajanus*, *Dunbaria*, *Eriosema*, and *Rhynchosia*. Results from cluster analysis indicated the proximity of *C cajan* to *C. albicans*, *C. sericeus* and *C. lineatus* than *C. acutifolius*, *C. grandifolius* and *C. reticulatus*. All the *Rhynchosia* species grouped together suggesting their origin from a common ancestor (Ratnaparkhe *et al*., 1995). Potential of RAPD in discriminating varieties of distinct characters was demonstrated in a study using 15 RAPD markers in 11 cultivated pigeonpea genotypes (Lohithaswa *et al.*, 2003). Cluster analysis resulted in separation of 24 genotypes into distinct clusters and sub-clusters suggesting RAPD as a good marker system for diversity analysis and cultivar identification (Choudhury *et al.*, 2008). Higher level of polymorphism (> 80%) was observed for 50% of 17 markers and cluster analysis resulted in formation of two distinct groups for 17 pigeonpea cultivars (Malviya and Yadav, 2010).

2.1.1.4 *Amplified fragment length polymorphisms (AFLPs)*

Amplified fragment length polymorphisms (AFLPs) is a highly sensitive PCR-based tool used in molecular biology to detect DNA polymorphisms. The technique includes i) digestion of total cellular DNA with one or more restriction enzymes and ligation of restriction half-site specific adaptors to all restriction fragments, ii) selective amplification of some of these fragments with two PCR primers that have corresponding adaptor and restriction site specific sequences iii) electrophoretic separation of amplicons on a gel matrix, followed by visualisation of the band pattern. AFLPs in 14 combination showed high level of polymorphism was observed between *C. cajan* and *C. volubilis* (62.08%) and *C. cajan* and *R. bracteata* (62.33%) while among cultivated types percentage of genetic variation was found to be very less (13.28%) (Panguluri *et al.*, 2006). A total of four combinations of AFLP markers were used for diversity analysis of 41 pigeonpea varieties of African (32) and Asian (9) origin. This study showed absence of major clustering pattern and population str atification and suggested that African and Asian pigeonpea were not genetically diverse (Wasike *et al.*, 2005).

2.1.1.4 *Diversity array technology markers (DArTs)*

Diversity array technology (DArT) is a cost effective hybridization-based marker technology that offers a high multiplexing level while being independent of sequence information. This technology offers molecular breeding programs an alternative approach to whole-genome profiling. DArT works by reducing the complexity of a DNA sample to obtain a 'representation' of that sample. DArT markers were used to estimate diversity in 96 pigeonpea genotypes representing 20 different species of *Cajanus*. Of the total 700 markers, only 64 were found to be polymorphic among *C. cajan* accessions supporting existence of narrow genetic base in cultivated pool. Most of the diversity was restricted to wild relatives or between the wild and cultivated species (Yang *et al*., 2006).

2.1.1.5 ***Microsatellites or simple sequence repeats (SSRs)***

Microsatellites or simple sequence repeats (SSRs) are stretches of DNA, consisting of tandemly repeated short units of 1-6 basepair in length. SSRs have been shown to be part of or linked to some genes of agronomic interest as a result since long time SSRs have been drawing attention of scientific research for crop improvement. The positive attributes coupled with their multi-allelic nature, co-dominant transmission, relative abundance, extensive genome coverage and requirement of only small amount of template DNA have contributed to the extraordinary increase of interest in SSRs in many organisms (Zane *et al*., 2002, Morgante *et al*., 2002). Traditionally, three approaches are used for identification and development of SSR markers: (i) construction of SSR-enriched library followed by sequencing of SSR positive clones (Gupta and Varshney, 2000), (ii) mining of EST (expressed sequence tag) transcript sequence generated by Sanger sequencing (Varshney *et al*., 2005) or short transcript sequences generated by next generation sequencing technologies (Varshney *et al*., 2009a), (iii) mining the BAC (bacterial artificial chromosome)- end sequences (BESs) (Mun *et al*., 2006). The development of SSR markers from BESs circumvents the limitations of the first two approaches, as a large number of SSRs can be rapidly identified and such genomic SSRs tend to display higher level of polymorphism relative to transcript associated SSRs. In addition, BES-SSR markers serve a useful resource for integrating genetic and physical maps (Mun *et al.*, 2006; Schultz *et al.*, 2007; Schlueter *et al.*, 2007). So far, the first two approaches have been used for developing SSR markers in pigeonpea with some success despite the labour-intensive and time consuming nature of the SSR enrichment and very low polymorphism levels of SSRs identified from the mining of transcript sequences.

First study based on these markers reported development of 20 SSRs, of which only half were polymorphic in cultivated pigeonpea germplasm (Burns *et al.*, 2001). Based on genomic DNA libraries another set of 20 SSRs makers was developed and used for diversity analysis of 15 cultivated and 9 wild relatives, as a result less diversity was detected in cultivated pigeonpea. Among different species least genetic distance and largest similarity coefficient was found between *C. cajan* and *C. cajanifolius* (Odeny *et al.*, 2007). A total of 113 SSRs were developed from SSR enriched libraries of pigeonpea. These were used for diversity analysis of 24 pigeonpea breeding lines (Odeny *et al.*, 2009). Similarly 23 SSRs were developed from SSR enriched genomic DNA library (Saxena *et al.*, 2010a). Furthermore in another study 84 EST-SSRs assosiated with biotic stress resistance were developed (Raju *et al.*, 2010).

2.1.1.6 *Single nucleotide polymorphisms (SNPs)*

Single nucleotide polymorphisms (SNPs) are highly abundant form of genetic variation present throughout the genome (Cho *et al.*, 1999; Rafalski, 2002). High frequency in genome makes SNP makers an attractive tool for mapping, maker-assisted breeding and map-based cloning (Batley *et al.*, 2003). SNP marker are markers of choice for various application (Rafalski, 2002) including marker assisted-breeding (Anderson and Lu¨bberstedt 2003; Varshney *et al.* 2007), genetic diversity (Nasu *et al.*, 2002; Varshney *et al.*, 2007), association mapping (Jander *et al.*, 2002), construction of high-density genetic map (Cho *et al.*, 1999), genome wide linkage disequilibrium (Ching *et al.*, 2002; Mather *et al.*, 2007). Due to progress in SNP genotyping platform and assayin technologies, these markers tend to be moat preferred marker system in plant genomics studies. In case of pigeonpea no study on development of these markers has been reported till date.

Among various marker systems, simple sequence repeats (SSRs) or microsatellites and single nucleotide polymorphisms (SNPs) are considered the preferred marker systems for the genetics and breeding community (Gupta and Varshney, 2000; Gupta *et al.*, 1996). The first set of 10 SSR markers however became available only in 2001 (Burns *et al.*, 2001). Subsequently, additional SSR markers have been generated at ICRISAT by using SSR-enriched library (Odeny *et al.*, 2007, 2009; Saxena *et al.*, 2010a) and about 200 SSR markers became available. Less than 10% SSR polymorphism in cultivated germplasm demanded the availability of large number of SSR markers for developing a useful set of SSR markers for pigeonpea breeding.

2.2 BAC-end Sequencing and SSR Mining

In past cloning and hybridization based procedures were used for identification of molecular markers. These procedures were low throughput, expensive and time consuming. In recent past bacterial artificial chromosome (BAC) library has proved to be a valuable resource for large scale development of genetic markers BAC based cloning was initially described by Shizuya and colleagues. Higher stability of BAC vectors over YAC (yeast artificial chromosome) makes BACs first choice for libraries construction in highthroughput genomic sequencing projects. The end sequencing of the BACs is proven to be a useful resource for selecting minimally overlapping clones. In past BAC-end sequencing approach has been used for whole genome sequencing of many species. BAC libraries have been constructed for a variety of species such as rice (Wang *et al.*, 1995), maize (Yim *et al.*, 2002), sorghum (Woo *et al.*, 1994), soybean (Shoemaker *et al.*, 1996; Salimath and Bhattacharyya, 1999; Tomkins *et al.*, 1999; Meksem *et al.*, 2000), papaya (Ming *et al.*, 2001), and apple (Vinatzer *et al.*, 1998). These libraries have made invaluable contributions to plant genomic studies including map-based or positional cloning of genes, genome-wide physical map construction (Mozo *et al.*, 1999; Klein *et al.*, 2000; Chen *et al.*, 2002; Han *et al.*, 2007), genome sequencing (The Arabidopsis Genome Initiative, 2000; International Rice Genome Sequencing Project, 2005), and comparative genomics (O'Neill and Bancroft, 2000; Ilic *et al.*, 2003). BAC-end sequences (BESs) are valuable resources for the development of genetic markers such as BAC-end sequence based microsatellite markers (Shultz *et al.*, 2007). BAC end sequence provides a random survey of the information contents (genes, transposons, repeats) of unsequenced genomes (Lai *et al.*, 2006; Hong *et al.*, 2007), and yields molecular markers useful for genetic mapping (Frelichowski *et al.*, 2006; Marek *et al.*, 2001 and Shultz *et al.*, 2007), and cloning of genes of agricultural interest (Coyne *et al.*, 2007; Liang *et al.*, 2007). Furthermore, in many agriculturally important species BAC clones and physical maps are being rapidly developed since they are essential components in linking phenotypic traits to the responsible genetic variation, to integrate the genetic data, for the comparative analysis of genomes, and to speed up marker-assisted selection (MAS) for breeding. It has been reported that analysis of BES data can provide an overview of microsatellites, of an unsequenced genome (Lai *et al.*, 2006). SSR markers have proven to be the best for this kind of analysis but where available in very low number, till date 156 SSRs have been for reported pigeonpea (Burns *et al.*, 2001; Odeny *et al.*, 2007, 2009).

2.3 Next Generation Sequencing Technologies

Genome sequencing is a robust method for gene discovery and for identifying transcripts involved in specific biological process. Over the past decade genome sequencing technology has become more efficient for complex genomes. Sequencing projects have provided not only the first insight into the gene complement for these tissue regions but also sets of genes involved in a number of biological processes. Several approaches were explored as a replace met to conventional Sanger sequencing technology these include sequencing by hybridization (Khrapko *et al.*, 1989), mass spectrometry resolution (Koster *et al.*, 1996), direct imaging of DNA sequence by atomic force microscopy (Hansma *et al.*, 1992), other approaches include techniques based sequencing by synthesis (Hyman, 1988; Brenner *et al.*, 2000) and microfluidics to sequencing (Woolley and Mathies, 1995). With the advent of reduced costs and higher throughput sequencing methods, expressed sequence tags (ESTs) can be economically generated for a wider range of organisms, thereby providing a more comprehensive assessment of an organism's transcriptome. In recent years, high-through expression profiling technologies like pyrosequencing have transformed molecular genetics approaches in legumes significantly (Margulies *et al.*, 2005). The advent of high throughput next generation sequencing technologies such as Roche FLX/454 sequencing developed by 454 Life Sciences (acquired by Roche), Solexa by Illumina Genome Analyser (Hayward, CA, USA) and SOLiD from ABI has created the potential for generating considerably increased amounts of information for many organisms including orphan legume crop like pigeonpea. Roche FLX/454 technology provide inexpensive, genome-wide information producing approximately 100Mb sequence data in a single run, contrasting to ~440 Kb sequence data generated by Sanger sequencing (Mardis. 2008). While Illumina/Solexa 1G sequencing technology allows to sequence millions of short cDNA of average length of 35 bp per sample tag (read), reducing the library construction cost, runtime and also increasing the sensitivity. Presently, the improvised Illumina/Solexa 1G technology generates 75+ bp reads for a total of > 33 Gb of paired-end data per run. Their efficient in-depth sampling of the transcriptome compared to Sanger sequencing has also been demonstrated (Hanriot *et al.*, 2008). But the relatively shorter reads produced by these technologies is a major drawback. However, the availability of various *denovo* assembly software programs such as CAP3 (Huang and Madan 1999), PCAP (Huang *et al.*, 2003), RePS (Wang *et al.*, 2002), and Phusion (Mullikin *et al.*, 2003). MAQ. SOAP, ELAND. MOSAIK, VALVET, EULER, SSAKE, SHARCGS can effectively assemble the shorter reads. Previously, combinatorial strategy involving cDNA normalization and FLX-454 deep sequencing platform has been employed in transcriptome characterization studies in *Medicago* (Cheung et al., 2006), Coral (Meyer *et al.*, 2009), Melitaea cinxia (Glanville fritillary butterfly) (Vera *et al.*, 2008) and many other non-model organisms.

Genomics-assisted breeding approaches have greatly advanced with the increasing availability of genome and transcriptome sequence data for several model plant and crop species (Varshney *et al.*, 2009b). This platform provides a broad range of applications including whole genome sequencing (Green *et al.*, 2006), transcriptome and gene regulation studies (Bainbridge *et al.*, 2006; Berezikov *et al.*, 2006). metagomics analysis and amplicon sequencing (Sogin *et al.*, 2006; Taylor *et al.*, 2007). Extremely efficient in-depth sampling of the transcriptome by these sequencing technologies as compared to Sanger sequencing has also been demonstrated in several plant species such as *Medicago* (Cheung *et al.*, 2006), barley (Steuernagel *et al.*, 2009), etc. Trancriptome assembly not only contributes to identification of potential novel genes associated with specific tissues but it also allows us to address the key issue of gene expression structure in tissues. Furthermore, it is possible to search for genes that are expressed in a wide range of tissues, including genes that are of importance to embryonic development, because all the libraries used in the study are from various developmental stages. Gene discovery and gene expression are key objectives of most genome projects (Jantasuriyarat *et al.*, 2005). A major current task in genomics is to characterize the functional importance of individual genes within the context of their interactions with other genes. The transcriptome of a particular species can be analyzed by sampling a large number of reads from normalized cDNA libraries constructed from different tissues or tissues from different developmental conditions or physiological stages (Gorodkin *et al.*, 2007). Compared with non-normalized cDNA libraries, studies of normalized cDNA libraries depleted the abundance of transcripts and optimizes discovery of novel genes (Flinn *et al.*, 2005).

2.3.1 Roche FLX/454 sequencing

Development of next generation sequencing technologies has significantly increased the volume of sequencing projects conducted by scientific community. Three main evolutionary improvements enabled genome sequencing projects in many species. These include, i) use of fluorescent tags instead of radioactive labels to detect the terminated ladders; ii) use of capillary electrophoresis in place of slab gels; and iii) development of paired-end sequencing protocols incorporating hierarchical template sizes (plasmids, fosmids and bacterial artificial chromosomes (BACs) to provide sequence context and orientation beyond the constraints of the actual sequence read-length in the conventional sequencing techniques (Meldrum, 2000). The 454 Life Sciences sequencing platform initiated the next generation sequencing by providing solution to three main bottlenecks of conventional sequencing faced by scientific community i.e. library preparation, template preparation and sequencing (Christensen, 1997). As direct incorporation of natural nucleotides seemed more efficient than repeated cycles of incorporation, detection and cleavage, technology based on pyrophosphate release with an enzymatic cascade ending in luciferase and is detection by emitting light was used for Roche FLX/454 platform. Roche FLX/454 sequencing was based on moving both the template preparation step and the pyrosequencing chemistry to the solid phase (Ronaghi *et al.*, 1996; 1998). Template DNA is nebulized and size-selected to produce a population of double-stranded fragments ranging from 400 to 600 bases. Two distinct oligonucleotide adapters are ligated onto the fragments, providing priming sites for subsequent amplification and sequencing. One of the adapters is biotinylated, permitting collection of single-stranded templates. The templates are amplified and immobilized by compartmentalizing individual template molecules and 28 μm DNA capture beads within droplets of an emulsion. PCR reactions conducted inside the droplets amplify the template molecules and complementary primers covalently attached to the DNA capture immobilize the product on the bead surface. Template-covered DNA capture beads are loaded into individual wells etched into the surface of a fiber-optic slide. The sequencing process uses an enzymatic cascade to generate light from inorganic pyrophosphate (PPi) molecules released by the incorporation of nucleotides as a polymerase replicates the template DNA (Margulies *et al.*, 2005). Individual nucleotides are provided to the open wells by flowing them over the fiber-optic slide. The number of photons generated by the cascade is proportional to the number of nucleotides incorporated by the polymerase and the release of the PPi generated by the individual sequencing reactions (Figure 1). Initially the system generated ~ 20 Mb of 110 base-read per 8 hrs run, subsequent released product generated an average of 100 Mbs of 250 base-reads. Using high density fiber-optic 400-600 Mbs of data is generated per run with an average size of 450 bps. Assembly of 148 Mbp of Roche/454 ESTs obtained for multiple genotypes was aligned and 23,742 SNPs were found in Eucalyptus (Novaes *et al.*, 2008) Roche FLX/454 sequencing of shoot apical meristem generated 261 000 ESTs of which 30% were novel; ~400 unique ESTs were also identified, for which 27 genes were validated using RT-PCR (Emrich *et al.*, 2007). A total of 292,465 ESTs were generated using Roche FLX/454 sequencing in *Medicago*, 184,599 unique sequences were identified. This study also include identification of 400 EST SSRs in *Medicago* (Cheung *et al.*, 2006).

2.3.2 Illumina/Solexa 1G sequencing

In contrast to the 454 and ABI methods which use a bead-based emulsion PCR to generate "polonies", Illumina utilizes a unique "bridged" amplification reaction that occurs on the surface of the flow cell. The flow cell surface is coated with single stranded oligonucleotides that correspond to the sequences of the adapters ligated during the sample preparation stage. Single-stranded, adapter-ligated fragments are bound to the surface of the flow cell exposed to reagents for polyermase-based extension. Priming occurs as the free/distal end of a ligated fragment "bridges" to a complementary oligo on the surface. Repeated denaturation and extension results in localized amplification of single molecules in millions of unique locations across the flow cell surface (Figure 2). This process is referred to as Illumina's "cluster station", an automated flow cell processor. A flow cell containing millions of unique clusters is now loaded into the 1G sequencer for automated cycles of extension and imaging. The first cycle of sequencing consists first of the incorporation of a single fluorescent nucleotide, followed by high resolution imaging of the entire flow cell. These images represent the data collected for the first base. Any signal above background identifies the physical location of a cluster (or polony), and the fluorescent emission identifies which of the four bases was incorporated at that position.This cycle is repeated, one base at a time, generating a series of images each representing a single base extension at a specific cluster. Base calls are derived with an algorithm that identifies the emission color over time. At this time reports of useful Illumina reads range from 26-50 bases. Illumina/Solexa 1G sequencing was used for identification of 8, 23,325 unique SNPs in Arabidopsis (Ossowski *et al.*, 2008). Illumina/Solexa 1G sequencing generated 574 Mbp data which was used to identify and mark repetitive regions and define putative gene space in barley (Wicker *et al.*, 2008).

2.3.3 Applications of NGS technology

NGS technologies have already been used for variety of applications, such as development of SSR and SNP- based molecular markers. Applications of NGS technology resequencing of well-characterized sp. (Ossowski *et al.*, 2008), *de novo* sequencing of crop sp. without reference sequence (Hiremath *et al.*, unpublished), association mapping using natural population, expression and nucleotide polymorphism in transcriptome, wide crosses and alien introgression, population genetics and evolutionary biology, organeller and genome-wide assembly (Varshney *et al.*, 2009a).

2.4 SNP Genotyping Platform

In contrast to other marker system, allele discrimination cannot be based on size difference on gel in case of SNP. Many SNP genotypying platforms have been developed over the past years. These technologies include i) allele specific hybridization, ii) primer extension, iii) oligonucleotide ligation iv) invasive cleavage (Sobrino *et al.*, 2005). The detection procedure for analyzing the products of these allele discriminating reaction include a) gel electrophoresis, b) fluorescence resonance energy transfer (FRET) c) fluorescence polarization, d) array or chips, e) luminescence, f) mass spectrophotometry. The KBiosciences PCR SNP genotyping system is a novel homogeneous fluorescent genotyping system which utilizes a unique form of allele specific PCR. This platform offers very high SNP to assay conversion rate, is flexible and offers ability to perform direct or indirect assays, works well in 96, 384 or even 1536-well plate formats. KASPar assay is the most cost-effective SNP typing system, accurate, reproducible and requires small amounts of sample material. The KASPar assay system relies on the discrimination power of a novel form of competitive allele specific PCR to determine the alleles at a specific locus within genomic DNA for SNP typing. Traditionally, allele specific PCR (ARMs) has been shown to work by a number of groups worldwide. A number of improvements to this technique have been made in the past few years. The most significant of these is the use of 3' - 5' exonuclease deleted Taq DNA polymerases. These deleted Taq's increase the discriminating power of the technique, however the technique can still suffer from extension of the incorrect allele, providing false positive signals. This technique employs a novel form of allele specific PCR that is distinct and different from ARMS. This increases the robustness and discriminating power of the technique. A novel fluoresence resonance energy transfer (FRET) homogeneous format is now available for this technique. The concordance rate has been shown to > 99.5% with an error rate and reproducibility to be < 0.3%.

2.4 Genetic Mapping

Genetic mapping is an important subject in biological research. Molecular markers and genetic maps are important pre-requisites for undertaking molecular breeding methodologies for crop improvement. Furthermore crop improvement programs has benefited from genetic diversity and mapping studies (Varshney *et al.*, 2006). A genetic map is based on the frequencies of recombination between molecular markers or gene loci during crossover of homologous chromosomes. The greater the frequency of recombination (segregation) between two genetic markers, the farther apart they are assumed to be. Conversely, the lower the frequency of recombination between the markers, the smaller the physical distance between them. This is the procedure of locating the molecular marker or gene loci/QTLs in order, indicating the relative distance among them and assigning them to their linkage group on the basis of their recombination value from all pair-wise combination. A genetic map acts like a road map of chromosome representing the recombination of loci derived from two different parents. Genetic linkage was first discovered by the British geneticists William Bateson and Reginald Punnett shortly after Mendel's laws were rediscovered. The understanding of genetic linkage was expanded by the work of Thomas Hunt Morgan. Morgan's observation that the amount of crossing over between linked genes differs led to the idea that crossover frequency might indicate the distance separating genes on the chromosome. Alfred Sturtevant, a student of Morgan's, first developed genetic maps, also known as linkage maps. It has been proposed that the greater the distance between linked genes, the greater the chance that non-sister chromatids would cross over in the region between the genes. A linkage map is created from analysis of many segregating markers, ideally avoiding having the inaccuracies that will occur due to the possibility of multiple recombination events. the construction of genetic map involves i) production of mapping population; ii) identification of polymorphism between parental genotypes for moleular markers and iii) linkage analysis of markers. By working out the number of recombinants it is possible to obtain a measure for the distance between the genes loci. This distance is called a genetic map unit (m.u.) or a centimorgan (cM) and is defined as the distance between genes for which one product of meiosis in 100 is recombinant. A recombinant frequency (RF) of 1 % is equivalent to 1 m.u. But this equivalence is only a good approximate for small percentages; the largest percentage of recombinants cannot exceed 50%, which would be the situation where the two genes are at the extreme opposite ends of the same chromosomes i.e 'unlinked' (Kearsey and Pooni, 1996). In this situation, any crossover events would result in an exchange of genes, but only an odd number of crossover events (a 50-50 chance between even and odd number of crossover events) would result in a recombinant product of meiotic crossover. A statistical interpretation of this is through the Haldane mapping function or the Kosambi mapping function, among others. A linkage map is created by finding the map distances between a number of genetic marker or gene loci that are present on the same chromosome, ideally avoiding having significant gaps between traits to avoid the inaccuracies that will occur due to the possibility of multiple recombination events. Linkage is calculated using odds ratios. This ratio is expressed in the form of logarithm of odds (LOD) value or LOD score (Risch, 1992). LOD is a statistical estimate of whether two loci (the sites of genes) are likely to lie near each other on a chromosome and are therefore likely to be inherited together as a package. A LOD score of three or more is generally taken to indicate that two gene loci are close to each other on the chromosome. A LOD score of three means the odds are a thousand to one (i.e 1000:1) in favor of genetic linkage. This LOD score can be lowered down in order to integrate makers within map constructed at higher LOD value. Software programs used for the generation of genetic maps include Mapmaker/ EXP (Lander *et al.*, 1987; Lincoln *et al.*, 1993) most commonly used software and MapManager QTX (Manly *et al.*, 2001). GMendel (http://cropandsoil.oregonstate.edu/Gmendel), MSTMap (Wu *et al.*, 2008). Another commonly used software is JoinMap which is used for map construction as well as combining maps developed from other mapping populations.

3. MATERIALS AND METHODS

3.1 Plant Material

With an objective of developing BAC- libraries pigeonpea accession Asha (ICPL 87119) was used. Seeds of Asha were grown under greenhouse conditions to the seedling stage and transferred to continuous darkness for 2 days prior to use. Developed libraries were used for end sequencing and identification of SSRs. Parents of an inter-specific mapping population ICP 28 and ICPW 94 were used for validation of identified SSR markers. Pusa Ageti (ICP 28) an early maturing pigeonpea variety was selected for cDNA normalization, library construction and transcriptome studies. Seeds were sown in pots (5 seeds per pot), maintained at glass-house. Four pigeonpea genotypes ICPL 87119, ICPL 87091, ICP 28 and ICPW 94 were used for identification of SNP markers using Illumina sequencing technology.

3.2 Identification and Validation of SSR markers

3.2.1 BAC-library construction and end sequencing

Nuclei were isolated and embedded in low melting point agarose, size selection by means of two rounds of pulsed field gel electrophoresis was carried out for *Bam*HI and *Hind*III digested DNA. Large size DNA fragments were ligated in vector pCC1BAC and transformed by electroporation in to Epicenter's *E.coli* EPI300-T1R cells. The insert sizes for each library were estimated based on pulsed field gel electrophoresis of *Not*I-digested BAC DNA. End sequencing was performed for the positive clones. There were 88,860 useful BES reads. Output sequence data was converted into FASTA format and vector sequences were masked. Terminal vector sequences were then trimmed and BESs shorter than 100 bp were discarded.

3.2.2 Mining of SSRs

BAC-end sequences were used for mining of microsatellite markers using Perl based *MIcroSAtellite* (MISA) search module (Varshney *et al.*, 2002) which is capable of identifying perfect as well as compound SSRs. All sequences with a size more than 100 bps were placed in a single text file in FASTA format, this file was used as an input for MISA. The criteria used for the identification of true SSR included minimum ten repeats for mono, six repeats for di and five repeats for tri-, tetra-, penta- and hexa-nucleotide for simple SSRs. Two SSRs separated by 100 nucleotide bases were considered under compound SSRs class. The sequence complimentarity was considered while classifying these microsatellites.

3.2.3 Primer designing

Designing of primer for identified SSR was done through standalone Primer3 program using MISA generated Primer3 input file. The criteria used for designing primer pairs included Tm range of 57°C – 60°C with an average of 59°C., amplicon size 100- 280bps, primer length 20 ± 5 bp and GC% 50 ± 5. Primers designed for Mononucleotide were excluded. M13 dye labelled primer pairs were synthesized for selected 3072 SSRs. The redundancy in the identified SSRs in terms of BAC clones was removed through cluster analysis. As result, from each clone single primer pair was selected for synthesis.

3.2.4 Screening on parental genotypes of mapping population

Amplification profile of 3072 BES-SSR primer pair was checked on two pigeonpea genotypes ICP 28 and ICPW 94. PCRs were performed in a 5 µl reaction volume [0.5 µl of 10X PCR buffer, 1.0 µl of 15 mM $MgCl_2$, 0.25 µl of 2mM dNTPs, 0.15 µl of 2 pM primer anchored with M13-tail (MWG-Biotech AG, Bangalore, India), 0.1 U of Taq polymerase (Bioline, London, UK), and 1.0 µl (5 ng) of template DNA] in 96-well micro titre plate (ABgene, Rockford, USA) using thermal cycler GeneAmp PCR System 9700 (Applied Biosystems, Foster City, USA). Touch-down PCR program was used for this reaction which included Initial denaturation at 94°C for 15min 5 cycles of denaturation at 94°C for 20sec touchdown from 60°C to 55°C (1°C decrease in each cycle) extension at 72°C for 30sec for next 31 cycles, denaturation at 94°C for 20sec annealing at 55°C for 20sec extension at 72°C for 30sec final extension at 72°C for 20min. Amplified primer pairs were initially visualized for amplicon bands using 1.2% agarose gel, capillary electrophoresis on ABI (3730) analyser was then used to further resolve fragment for better data analysis to assess polymorphic markers.

3.3 Development of Pigeonpea Trancriptome Assembly

3.3.1 Roche FLX/454 sequencing

Pusa Ageti (ICP 28) variety of pigeopea was used for construction of Roche FLX/454 sequencing based trancriptome assembly of pigeonpea (CcTA). In order to maximize the diversity of expressed genes in pigeonpea, different developmental stages of tissue samples were targeted for collection and construction of cDNA library. These tissue samples included embryo, cotyledon, root and shoot primordia, apical meristem, leaves, senescence leaves, flowers, stamen, and roots (Figure 3) harvested from several individual glass-house grown pigeonpea plants at different time intervals. This was done with an objective to induce gene expression associated with those developmental processes. Tissues were washed briefly with 0.1% DEPC water and then were frozen in liquid nitrogen. Total RNA was extracted from all the harvested tissues using modified hot-acid phenol method (Schmitt *et al.*, 1990). The integrity and purity of all the samples were assessed both on 1.2% formaldehyde agarose gel and UV Spectrophotometer at

A_{260}:A_{280}. An equal amount of each appropriate RNA sample was pooled to form a composite collection of total RNA sample for each tissue. Eleven cDNA libraries were constructed from each tissue sample to characterize specific stages of gene expression (Figure 4).

In order to minimize differences among the abundance of different transcripts (i.e., genes expressed at different levels), amplified cDNA was normalized employing the Smart cloning methodology (Ouyang and Buell, 2004; Zhu *et al.*, 2001) using the services of Evrogen [www.evrogen.com] and Sfi IA/B primers/adapters that permit directional cloning. Briefly, starting from RNA, reverse transcription was carried out using the pooled RNA samples. The primer annealing mixture (5 µl) containing 0.3 µg of total RNA; 10 pmol SMART-Sfi IA oligonucleotide (5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGC CrGrGrG- 3') and 10 pmol CDS -Sfi IB primer (5'-AAGCAGTGGTATCAACGCA GAGTGGCCGAG GCGGCCd(T)20–3') was heated at 72°C for 2 min and cooled on ice for 2 min. First-strand cDNA synthesis was carried out by the addition of PowerScript Reverse Transcriptase (BD Biosciences Clontech) in a final volume of 10 µl, containing 1X First-Strand Buffer (50 mMTris-HCl (pH 8.3); 75 mMKCl; 6 mM MgCl2); 2 mM DTT; 1 mM of each dNTP, incubated at 42°C for 1.5 hr and then cooled on ice. The first-strand cDNA was diluted 5 times with TE buffer, heated at 72°C for 7 min and used for amplification by Long-Distance PCR in a 50 µl reaction containing 1 µl diluted first-strand cDNA, 1X Advantage 2 reaction buffer (BD Biosciences Clontech), 200 µM dNTPs, 0.3 µM SMART PCR primer (5'-AAGCAGTGGTATCAACGCAGAGT- 3') and 1X Advantage 2 Polymerize mix (BD Biosciences Clontech). 18 PCR cycles were performed using the following parameters: 95°C for 7 sec; 65°C for 20 sec; 72°C for 3 min. Amplified doubled standard cDNA product was purified using QIAquick PCR Purification Kit (QIAGEN, CA), concentrated by ethanol precipitation and adjusted to a final concentration of 50 ng/µl. For cDNA normalization, 3 µl (about 150 ng) purified dscDNA plus 1 µl 4X Hybridization Buffer (200 mM HEPES-HCl, pH 8.0; 2 M NaCl) was overlaid with one drop of mineral oil, denatured 95°C for 5 min and then allowed to anneal at 68°C for 4 h. The following preheated reagents were added to the hybridization reaction at 68°C: 3.5 µl milliQ water;1µl of 5X DNAse buffer (500 Mm Tris-HCl, pH 8.0; 50 mM MgCl2, 10 mM DTT);0.5 µl double-strand nuclease (DSN) enzyme. After a period of 30 min. incubation at 65°C, the DSN enzyme was inactivated by heating at 95°C for 7 min. The normalized cDNAs samples were diluted by adding 30 µl of milliQ water and used for PCR amplification. The PCR reaction (50 µl) contained 1 µl diluted cDNA; 1X Advantage 2 reaction buffer (BD Biosciences Clontech); 200 µM dNTPs; 0.3 µM SMART PCR primer; 1X Advantage 2 Polymerize mix (BD Biosciences Clontech) and was amplified for 18 cycles of 95°C for 7 sec; 65°C for 20 sec; 72°C for 3 min. One part of the amplified, normalized adapter-ligatedcDNA population was digested with SfiI and directionally cloned into Clontech'sp DNR vector at the SfiA/B sites. For 454 sequencing, approximately, 3 µg of the final normalized, adaptor-ligated cDNA population was sheared via nebulization into small fragments a few hundred base pairs in length. The fragment ends were made blunt and short adaptors which provide the priming sequences for both amplification and sequencing of the sample library fragments were ligated onto both ends. These adaptors also provide a sequencing key (a short sequence of four nucleotides) which was used by the system software to recognize legitimate library reads. Next, the library was immobilized onto streptavidin beads, facilitated by a 5' biotin tag on Adaptor B, and any nicks in the double stranded library are repaired. Finally, the unbound strand of each fragment (with 5'-Adaptor A) was released, and the recovered single-stranded DNA library's quality is assessed.

3.3.2 Sequence data assembly and clustering

All the sequence analyses were conducted using publicly available software and custom Perl scripts. Quality trimming of the sequences was done by removing adapter sequences and short sequences (< 50 nucleotides) for the assembly process as this will lead to false joining of reads, and chimeras that were sequenced and reduced the quality of unique sequences. The vector trimmed high quality sequences were selected for further clustering and alignment into tentative unique sequences (TUSs) using the CAP3 program (Huang and Madan, 1999). The assembly included the publicly available 10,817 ESTs of pigeonpea along with the Roche/454 pyrosequencing reads.

3.3.3 Characterization of pigeonpea 454 trancriptome assembly

3.3.3.1 *Identification of paralogous*

The analysis was conducted, using both, the contig consensus sequences as well as the singletons following assembly. The longest open reading frame was identified using EMBOSS: getorf (http://emboss.open-bio.org/wiki/Appdocs) to identify all open reading frames and a custom script to retain only the longest. Clustering of these sequences followed using a virtual suffix tree generation with six frame translation using Vmatch (Beckstette *et al.*, 2006). Gene families of size 2 - 6 were clustered with the parameters i.e. subject percent match of 85 and query percent match of 70, a minimum length of 20 amino acids and an exdrop of 30. Pair wise alignments were obtained using ClustalW (Thompson *et al.*, 1994) and synonymous distances (Ks values) calculated using the method of Goldman and Yang (1994) as implemented in PAML (Yang 1997).

3.3.3.2 *Alignment of 454 pigeonpea sequence assemblies to soybean genome*

Alignment of pigeonpea TUSs with soybean genome was done using GMAP. This alignment was done by considering a stringency criterion of 90% identity and 80% coverage. For alignment, maximum intron length was considered as 20,000 bp and the number of introns per gene fragment was considered as 8. Poor and repetitive sequences were discarded. To get the best hit and multiple equally-good matches, the highest scoring alignment satisfying stringency criteria was taken as the best hit. Alignments within 1% identity and 1% coverage were considered as multiple equally-good matches.

3.3.3.3 *Functional annotation and similarity search*

Homology searches were performed against non-redundant (nr) nucleotide sequences of soybean (Glycine max- 351,935), Medicago (*Medicago truncatula*- 217,148), lotus (*Lotus japonicus*- 148,617), common bean (*Phaseolus vulgaris*- 21,807), wild soybean (*Glycine soja*- 18,419), red clover (*Trifolium pretense*- 37,860), grape wine (*Vitis vinifera*- 312,911), black cotton wood (*Populus trichocarpa*- 89,198), Arabidopsis (*Arabidopsis thaliana*- 616,064) and rice (*Oryza sativa*-1,169,591) available at the TIGR Plant Transcript Assemblies database using BLASTN algorithm at a significance threshold of ≤ 1E-30.

TUSs were compared with UniRef non-redundant protein database from UniProt knowledgebase using BLASTX algorithm to deduce a putative function. Sequence similarity was considered best at a bit-score greater than 50 and a significant e-value ≤ 1E-08. Each TUS was assigned a putative cellular function based on the significant database hit with the lowest E-value. Subsequently, TUSs that showed a significant BLASTX hit were used for functional annotation based on Gene Ontology categories from UniProt database (UniProt-GO). This process allowed assignment of TUSs to the GO functional categories of biological process, cellular component and molecular function. Distribution of TUSs was further investigated in terms of their assignment to sub-categories of the main GO categories. In each main category, the percentages of sub-categories distribution do not add up to 100% because some deduced proteins have more than one GO category.

3.4 Identification of SNPs

3.4.1 Illumina/ Solexa 1G sequencing and SNP identification

Pigeonpea genotypes i.e. ICPL87119, ICPL87091, ICP 28 AND ICPW 94 were subjected to Illumina/ Solexa 1G sequencing. A total of fifteen seeds from each of these genotypes were grown in green house. Total RNA from root tissue was extracted using modified hot-acid phenol method (Schmitt *et al.*, 1990). cDNA libraries of these four genotypes were subjected to Illumina/ Solexa 1G sequencing. Identification of SNPs from Illumina data was carried out using the Alpheus software system (Miller *et al.*, 2008). SNPs were identified on the basis of alignment of Illumina reads generated from each of the genotypes against a reference– in this case, the 454-based pigeonpea trancriptome assembly and respective counter genotype, allowing not more than two mismatches. Based on alignment results, variants at a particular nucleotide position were identified. Significant variants were selected based on two criteria i) allele frequency between two genotypes > 0.8, and number of tags aligned to the reference > 5.

3.4.2 Development of SNP genotyping platform

KASPar genotyping platform was developed using the identified SNPs. The selection of SNPs was done based on three criteria i) SNPs positions containing 60 bps flaking sequences, ii) Frequency difference between two alleles ≥ 0.8 iii) read depth ≥ 5.

3.5 Construction of Genetic Maps

Genotyping data were assembled for all segregating makers from 79 F_2 lines of ICP 28 × ICPW 94 mapping population and linkage analysis was performed with the help of Joinmap v 4.0 (Van Ooijen, 2006). Prior to linkage mapping, marker segregations in the populations were subjected to goodness of fit test to assess deviations from the expected Mendelian segregation ratio of 1:2:1. "Locus genotype frequency" function was used to calculate the chi-square values for all the markers. Distorted markers were also included for linkage analysis. Both the component maps were constructed using "Regression mapping algorithm" which relies on sequential addition of markers into a linkage group which starts from the most informative pair of loci (Van Ooijen, 2006). Linkage groups were determined based on "Independence test LOD score". Placement of markers into different linkage groups was done with "LOD groupings" and "Create group using the mapping tree" commands. Map calculations were performed with parameters like LOD value ≥ 2.0, recombination frequency ≤ 0.40 and a chi-square jump threshold for removal of loci =5. Addition of a new locus may influence the optimum map order, hence a "Ripple" was performed after adding each marker into map. Map distances were calculated using Kosambi mapping function (Kosambi, 1944) and third round was set to allow mapping of optimum number of loci in genetic map. Mean chi-square contributions or average contributions to the goodness of fit of each locus were also checked to determine the best fitting position for markers in genetic map. The markers showing negative map distances and large jump in mean chi-square values did not fit those map positions hence were discarded from mapping. Final map was drawn with the help of Mapchart 2.2 (Voorrips, 2002).

4. RESULTS

4.1 Development of Microsatellites Markers from BAC-end Sequences

With an objective to develop genomic recourses in pigeonpea and increase marker repertoire BAC-end sequencing approach was used to obtain a set of BAC-associated SSRs.

4.1.2 Development of BAC-end sequences and identification of SSRs

Development of BAC-end sequences based SSRs may provide a foundation for both genetic and physical map analysis. Under this approach two BAC libraries were constructed one using *Hin*dIII and other using *Bam*H1 restriction enzymes. The *Hin*dIII library is composed of 34,560 clones with an estimated average insert size of 120,000 bp, while the *Bam*H1 library is composed of 34,560 clones with an estimated average insert size of 115,000 bp. These clones combinely represent ~11X coverage of the pigeonpea genome. A total of 50,000 randomly selected BAC clones were subjected to end sequencing which resulted in generation of 88,860 BAC end sequences (BES) with an average read length of 620 bp. Most of the 50,000 BAC clones contain high quality sequence from both ends. The combined data represent ~ 56 Mbp of DNA sequences, which were submitted to the National Center for Biotechnology Information (NCBI) Genome Survey Sequence (GSS) database.

As a prelude to the comprehensive analysis these BAC-end sequences were analyzed for redundancy between clones and for sequence content as well as for removal of cytoplasmic organellar sequences using the annotation pipeline shown in Figure 5. Sequences were clustered using criteria of ≥ 95% identity and ≥ 200 bp overlap, producing a set of 41,736 singleton sequences and 10,711 sequence clusters. This non-redundant sequence set was filtered for rRNA, chloroplast and mitochondrial sequences using BLAST'N' against datasets of the corresponding sequence types, yielding a set of 41,329 singletons and 10,610 non-redundant BESs that were presumed to derive from the nuclear genome. In total this non-redundant nuclear genome dataset surveys 35Mb or ~ 4.3% of the pigeonpea genome.

4.1.3 Functional annotation of BESs

A series of parallel analyses were performed to annotate the features of singletons and clustered BESs. Similarity to transcribed sequences or known proteins was assessed by BLAST'N' and BLAST'X' of sequences against the TIGR plant transcript assemblies (http://plantta.jcvi.org/) and the National Center for Biotechnology (NCBI) information non-redundant protein database, respectively, using an E-value cutoff of $<1.00E^{-20}$. Further evidence of protein coding regions, as well as standardized nomenclature, was obtained by queries against the Interpro and GeneOntology Molecular Function databases. Similarity to known plant repeat sequences was assessed by BLAST'N' and tBLAST'X' against a database of plant repeat sequences (http://www.jcvi.org). Based on the compiled information, BESs were subdivided into five primary categories: (1) non-annotated, (2) gene-containing, (3) retroelement-containing, (4) transposable element-containing, and (5) organelle- or ribosomal rRNA-containing, as shown in Figure 6 and Table 1. Most sequence annotations were supported by multiple lines of evidence and a fraction of sequences were predicted to include both genes and either retroelements or transposable elements. Non-annotated sequences accounted for the majority of BAC ends, representing 53% of all non-redundant singletons and clusters, while nearly equal proportions of BESs were annotated as genes (21%) or retroelements (22%). It is likely that the retroelement category is an underestimate, because many of the most abundant Interpro descriptors within the "gene" category, such as "DNA/RNA Polymerase", are equally consistent with either "gene" or "retroelement". In the absence of additional annotation supporting classification as a retroelement, such sequences were classified as "gene".

Clustering of sequences as singletons or contigs provides a relative measure of sequence copy number (Table 1). As shown in Figure 7 a and b, greater than 80% of sequences annotated as either gene or non-annotated were associated with clusters of depth < 5 (Figure 7a) and their relative prevalence declined rapidly with cluster depth >1 (Figure 7b). By contrast, nearly 50% of all retroelement-containing sequences and 33% of all transponson-containing sequences were associated with clusters of depth > 5, and they accounted for the vast majority of clusters with depth > 10 sequences. Thus, sequence cluster depth supports the truism that mobile elements (i.e., retroelements and transposable elements) are often members of repetitive sequence families, while genes and intergenic regions (here we equate non-annotated sequences with intergenic regions) typically reside in less repetitive regions of the genome.

4.1.4 Identification of BES-SSR

With the goal of increasing genetic marker density we have used BAC- end sequencing approach to identify SSR markers in pigeonpea. A total of 88,860 BES sequences were generated and were used for mining of SSRs markers. As a result of this 18,149 SSRs (1 SSR per 3.11Kbp) were identified in 14,001 BESs representing 6,590 BAC clones. 3,124 BESs contained more than one SSR. A total of 2,111 SSRs were present in compound form (Table 2). Among these 6665 (71.53%) were defined as class II SSR ($10 \leq n < 20$ bp) and 2652 were class I SSR (≥ 20 bp). 2111 SSRs were found to be in compound formation. Maximum number of bases interrupting two SSRs in compound formation was 100.

4.1.5 Frequency and distribution of SSRs

Frequency of different SSRs identified during the present study revealed that mono and di-nucleotide were the most abundant classes with 8,827 mono-nucleotide repeats (48%) and 7,617 dinucleotide repeats (41%) of total SSRs, followed by tri- nucleotides sharing 8% (1,441) of total SSRs. Apart from this tetra-, penta- and hexa- nucleotide SSRs occurred at lower proportions which combinely account for arround 2% of total SSRs (Table 3). Among mononucleotide repeats A/T (8631) was significantly more abundant than C/G (196). These all mononucleotide were excluded from the present study. Among di-nucleotide repeat four types (AT, GC, AG and AC), AT was most common (4309) followed by AG (1953) and AC (1343) on the other hand GC (12) motifs were least common. All ten possible types of tri-nucleotide repeats were found in these BESs. Among these AAT/TTA motif was most common followed by AAG/CTT motif. Among the 11 different types of tetra nucleotide repeat motifs AAAT/TTTA was found to be most common. The total number of penta-nucleotide repeat motifs was eight and all of these were rare. Maximum numbers of different motif classes were recorded for hex nucleotide repeat motifs (total 21 types). Among these ACACCT/ATGTGG was most abundant.

4.1.6 Correlation between BAC end annotation and SSR occurrence

After excluding all mono-nucleotide repeat SSRs and SSRs with length <10 bp, the remaining 6,212 SSRs were selected for further analysis. These 6,212 SSRs were derived from 4,614 non-redundant BAC ends (singletons and clusters), 17 of which were annotated as organelle (15 chloroplast and 2 mitochondria).

The remaining 4,597 non-redundant BESs were divided among the four annotation categories, as shown in Table 1. Eighty-nine percent of these SSR-containing BESs (SSR-BESs) were either non-annotated or gene-containing, while 9.8% were retroelement-containing (Figure 8 and Table 1). The rate of SSR occurrence per 100 kb also differs considerably between annotation categories, consistent with the uneven discovery of SSRs between annotation categories. Thus, SSRs are twice as frequent per 100 kb in gene-containing (G) and non-annotated (NA) sequences compared to retroelement-containing (RE) sequences (Table 1 and Figure 8). Consistent with the likely pressure of purifying selection, BAC ends containing tri-nucleotide repeats were more likely to be annotated as genes (31%), compared to the remaining SSR-containing BAC sequences (22% annotated as genes).

For purposes of developing a uniform analysis of known pigeonpea SSRs, we obtained 457 SSRs submitted to NCBI GeneBank by researchers at the University of Bonn (Odney *et al.* 2007; Saxena *et al.*, 2009). Both of these publicly available SSR sets were generated using PCR-based microsatellite enrichment strategies. As shown in the Table 1, the relative distribution of SSRs between genome fractions differs substantially for SSRs obtained by means of genome enrichment compared to random BAC end sequencing. In particular, genome-enrichment methodologies produced approximately three times the rate of retroelement-associated SSRs and ~100-fold increase in the rate of SSRs derived from organelle or rRNA sequences, most of which were chloropast derived (data not shown).

4.1.7 Development of novel SSRs markers

Microsatellites are categorized into two groups based on length of SSR tracts and their potential as informative genetic marker: hypervariable Class I and potiantially variable Class II SSR. (Temnykh *et al.* 2001). All the microsatellites having a repeat length of ≥ 10 bp for di-, ≥ 15 bp for tri-, ≥ 20 bp for tetra-, ≥ 25bp for penta and ≥ 30 bp for hexanucleotide were selected for SSR marker development. A result a total of 6,590 primer pairs were designed. Out of designed primer pairs, a total of 3,072 primer pairs were synthesized (Table 4). Primer pairs were designed to amplify sequences containing both perfect and compound SSRs. These 3072 primers are designated as ''CcM'' markers prefix CcM indigating *Cajanus cajan* microsatellite. All primer pairs were first evaluated for successful PCR amplification on genomic DNA of two parental genotypes of mapping population i.e. ICP 28 and ICPW 94. Among these primer pairs 3026 (98.5%) showed successful amplification.).The tetra- and penta- nucleotide motifs had the highest success rate (100%) of PCR amplification followed by compound tri and di nucleotide repeats. Hexanucleotide repeats were having 97.67% amplification. (Figure 9). Of the all repeat motifs (AT)n repeats were having lesser level of amplification.

4.1.8 Polymorphism assessment of BES-SSR

BES-SSRs with successful PCR amplification were used for polymorphism assessment on the parental genotypes using capillary electrophoresis. As a result of this, 378 polymorphic SSRs were identified. Identified polymorphic SSRS were used for genotyping of 79 F_2 lines of ICP 28 × ICPW 94 mapping population.

4.2 Development of Transcript assembly for Pigeonpea

4.2.1 Clustering and assembly of transcript reads

A comprehensive set of 31 different plants developmental stages from early vegetative growth until development of reproductive organs (Figure 2) were collected for isolation of cDNAs. These cDNAs were pooled and normalized. Roche/454 sequencing of this normalized cDNA pool generated a total of 494,353 short transcript reads (STRs) were generated with an average length of 171 bp. In addition at the time of data analysis, 10,817 Sanger ESTs with average read length 527 bp were available in public domain. These two sequence datasets were analyzed separately as well as combinly. Based on analysis of 454 STRs, 52,827 contigs containing 354,131 STRs with an average length of 262 bp including 4,308 high confidence singletons were identified. Out of 48,519 contigs about 53.2% (25,850) were shorter than 250 bps. Remaining 140,222 STRs remained singletons. On the other hand Sanger ESTs analysis provided 746 contigs with an average length 637 bp and the remaining 5,553 Sanger ESTs were termed singletons. In order to develop a transcriptome reference in pigeonpea, 505,170 Roche/454 STRs and Sanger ESTs were assembled to yield a total of 127,754 tentative unique sequences (TUSs), with ~ 61.8% (79,028) singletons and the remaining 38.1% aligned to form 48,726 contigs with an average length of 273 bp (Figure 10) and maximum length of 2,067 bp (Contig 48542). A total of 3,006 (6.1%) contigs measured more than 500 bp in length. The detailed analysis of length distribution of 454/FLX STRs, Sanger ESTs and assembled 454 STRs and Sanger ESTs has been given in Table 5. Overall redundancy of the library was 25.2% which suggests that the normalization process was effective and the present generated library has the potential to uncover many more transcripts.

4.2.2 Identification of paralogous genes and genome duplication events

To identify potential signatures of genome duplication in pigeonpea, the transcriptome assembly (CcTA) was analyzed in detail using two approaches. In the first approach, sequence similarity was used to identify putative homologous gene pairs and pair-wise synonymous distances. Of the total 127,754 sequences (of which 48,726 are contigs), 9.8% (12,515) were clustered into a gene family. Of those, 3,098 are duplicates of family size 2; 537 are in families of size 3; 181 are in families of size 4, 89 are in families of size 5 and 68 are in families of size 6. Out of the above 5,778 pair wise synonymous distance measures were calculated that fall in the Ks range of 0 to 1.5 (Figure 11). Assuming that synonymous mutations occur in a clock-like manner following duplication and increase approximately linearly with time (Blanc *et al.*, 2004), we can use the synonymous distance between a gene pair to predict an approximate time of divergence between those two genes, or when a duplication event occurred. Figure 11 shows a histogram plot of the percent of pair wise distances to the synonymous distance value (Ks). There is a peak at roughly 0.06 and using the same clock as was used for soybean (Schumtuz *et al.*, 2010), this gives a divergence estimate of ~ 4.9 million years ago. While this might be indicative of a more recent duplication, it is much more likely to be the result of a segmental duplication given that only 9.8% of the sequences clustered into gene families. Another potential explanation for this peak is potentially an artifact of either the read length in contigs or the assembly process itself. Certainly this can and will be clarified with the genome sequence.

The chromosome number of pigeonpea (2n = 22) are the same as other phaseoloids such as common bean (*Phaseolus vulgaris*) and cowpea (*Vigna unguiculata*) are 2n = 22 while those of soybean (2n = 40) suggest an independent duplication in soybean following divergence from pigeonpea. With an objective to understand the pattern of genome duplication in cowpea and common bean also, similar analysis was conducted based on 16,791 Sanger ESTs for cowpea and 89,168 ESTs for common bean obtained from NCBI (Oct 2009). In the case of common bean, out of the 2,334 contigs, only 76 clustered into a gene family (or 3.26%) while 96.74% were remained as singletons. The breakdown of cluster sizes (or gene family sizes) is 27 clusters of family size 2, one cluster of family size 3, two clusters of family size 4 and one cluster of family size 11. Similarly, for cowpea, 11 contigs were found to form clusters (1.55%) while 98.45% are single copy contigs. The breakdown of gene families is four clusters of size 2 and one cluster of size 3.

In the second approach using BLASTN (<=1e-4) was utilized to align the, 37,170 pigeonpea sequences to the 46,430 soybean gene set (http://www.phytozome.net/soybean). Repeats such as large gene families, rDNA and other repeats were removed from the aligned dataset. Since soybean is highly duplicated due to past whole genome duplications, many of the pigeonpea contigs aligned to more than one gene locus. For best-hit alignments (first hit), 19,996 alignments had a mean sequence identity of 92.29%. The mean sequence identity for the 17,174 that had second good alignments was 91.56%. The most recent duplication event in soybean occured ~13 Mya, after the divergence from pigeonpea. If both alignments were to duplicates from the most recent duplication in soybean, we would expect approximately similar identity scores, however, a t-test between the first and second alignment values (% sequence identity) was significantly different (p-val< 0.00001). Thus, the difference in scores for the first and second best alignments is likely be a reflection of alignments to duplicated genes in soybean that have undergone asymmetric evolution or to duplicated genes from both the ancient (~59 Mya) and the more recent (~13 Mya) duplication events (Figure 12).

Based on analysis of detailed data on pigeonpea, limited data for cowpea and common bean and published results for soybean (Schmutz *et al.*, 2010), all four of these phaseoloid legumes, like most legumes, share the more ancient duplication at ~50-60 Mya. The pigeonpea genome shows slight evidence for another small-scale duplication, probably segmental, at 4.9 Mya, that does not appear to be shared with other phaseoloids. This indicates that recent the duplication in pigeonpea genome might have happened after separation of *Cajanus* from cowpea and common bean, but did not result in a change in chromosome number.

4.2.2 Characterization of pigeonpea transcriptome

4.2.2.1 Comparison with soybean genome

As an effort to validate gene structures in the newly developed assembly, the 127,754 TUSs were aligned to soybean using GMAP (http://www.icrisat.org/what-we-do/biotechnology/LegumeSequenceDatasets.html). The threshold for identity and coverage was set to 90% and 80%, respectively. As a result, 33,874 TUSs showed alignment and covered 10,857 genes of soybean. A total of 16,367 TUSs showed unique best matches with the soybean genome. TUSs were distributed across the chromosomes of soybean. An n average of ~1,693 loci on each soybean chromosome had significantly hits with an exception of chromosome 13 which had the highest number of loci (4,162) mapped (Table 6). The alignment results are uploaded to GBrowse. In GBrowse window, the direction of the arrows represents the orientation of the sequences. To give an indication about the confidence of location of pigeonpea TUSs in soybean genome, the sequences with single best hit are shown in green color and the sequences with multiple good matches are shown in red color (Figure 13).

4.2.2.2 Comparison with other legumes and model plant species at the transcript level

Detailed analysis of pigeonpea TUSs was performed using BLASTN (e-value ≤ 1E-30) similarity searches against plant EST datasets at JCVI. These results indicated that pigeonpea ESTs show highest percentage overlap with soybean (*Glycine max*) with 26,972 (21.11%), followed by *Medicago* (*Medicago truncatula*) 12,643 (9.89%), *Lotus* (*Lotus japonicus*) 10,472 (8.19%), common bean (*Phaseolus vulgaris*) 9,936 (7.77%), wild soybean (*Glycine soja*) 9,081 (7.10%), red clover (*Trifolium pretense*) 6,292 (4.92%), grape vine (*Vitis vinifera*) 5,394 (4.22%), and other model plant species such as *Arabidopsis* (*Arabidopsis thaliana*) 2,980, (2.85%) and black cotton wood (*Poplus trichocarpa*) 3,646 (2.33%) and rice (*Oryza sativa*)

2,714 (2.12%). Detailed results of BLASTN analyses are given in Figure 14. Of 127,754 unigenes, 735 (0.5%) were showed significant similarity across all the plant EST databases compared in this study and 82,100 (64.26%) did not show similarity to any plant species analyzed.

4.2.2.3 Functional annotation and gene ontology (GO) categorization

BLASTX (e-value ≤1E-08 and a bit-score value of ≥ 50) analysis of 127,754 TUSs against the UniRef non-redundant protein database enabled the putative identity assignment of these sequences into functional categories. A total of 32,719 (25.6%) TUSs showed significant similarity to the non-redundant protein database while 8,949 sequences (7.0%) had low similarity and 86,086 (67.3%) sequences had no significant matches. The 32,719 TUSs showing significant hit were analyzed further for functional categorization and to retrieve enzyme IDs as following: (i) Functional categorization was assigned by mapping the 29,921 (91.40%) out of 32,719. TUSs showing significant hit on BLASTX analysis onto the Gene Ontology categories using the UniProt Gene Ontology Consortium. TUSs with assigned putative roles were classified into three principle categories: biological process, cellular component and molecular function. As a result, 5,455 TUSs were successfully assigned under biological process (Figure 15a), 3,958 for cellular component (Figure 15b) and 6,491 for molecular function (Figure 15c). According to this GO schema, single protein corresponding to a TUS typically has more than one Ontology assignment. Furthermore under biological process, the sub-category metabolic process accounted for the highest percentage of TUSs at 4,080 (31%) followed by cellular process 3,904 (30%), biological regulation 865 (7%), localization 864 (7%), establishment of localization 846 (6%) and response to stimulus 702 (5%). The remaining sub-categories accounted to 21% of total significant TUSs (Figure 15a). In the cellular component category, the highest percentage of TUSs was assigned to cell part category 3,854 (44%), followed by organelle 2,379 (28%), organelle part 1,118 (12%) and macromolecular complex 886 (10%). The remaining 6% of TUSs were accounted to other defined sub-categories (Figure 15b). In molecular function, 45% (4,628) of TUSs accounted to binding, followed by catalytic activity 3,873 (38%) and transporter activity 481 (5%). The remaining sub-categories accounted to 12% of TUSs (Figure 15c). As expected, these libraries are derived from developing tissues, hence majority of the transcripts were involved in developmental categories like metabolic and cellular process (Zhang *et al.*, 2004).

Enzyme IDs were retrieved from the UniProt database and were distributed into one of the six major enzyme classes such as transferases- 31% (474), followed by hydrolases 28% (443), oxido-reductases- 25% (389) ligases 6% (98), lyases 5% (79), and isomerases 5% (79) (Figure 16).

4.3 SNP Discovery

Using Illumina/Solexa 1G sequencing in total 150.8 million tags were generated from four genotypes (ICPL 87119, ICPL 87091, ICP 28 and ICW 94). Number of tags generated per genotype varied from 16.84 million (ICPL 87091) to 18.64 million (ICW 94). For identification of SNPs, Illumina tags for two genotypes of a given mapping population were aligned with 127,754 TUSs (pigeonpea transcriptome assembly) and variants were identified using Alpheus program of NCGR (Miller et al 2008). The number of SNPs in an individual cross ranged from 6263 (ICPL 87119 × ICPL 87091) to 1,190 (ICP 28 × ICPW94) (Table 7). In total, 7,453 SNPs were identified.

4.3.1 Identification of disease responsive genes

Fusarium wilt (FW) is a serious disease that adversely affects pigeonpea production. With an objective to identify candidate genes for this disease, Illumina/Solexa tags of FW stressed genotypes ICPL 87091 and ICPL 87119 were used. Alpheus program of NCGR (Miller et al 2008) was used to achieve expression read count based on the alignment of Illumina/Solexa tags of ICPL 87119 (resistant) and ICPL 87091 (susceptible) genotypes to 127,754 TUSs (CcTA). Since the numbers of Illumina/Solexa tags mapped to the CcTA varied among genotypes, data normalization for more precise quantification was done by considering per million reads for discerning the expression values. A numerical comparison of FW-responsive reads generated from resistant and susceptible genotype representing a mapping population was conducted. The threshold log 2 for this analysis was taken as -2 to +2. The number of TUSs with significant differential expression was 1,869 (ICPL 87119 × ICPL 87091).

4.4 SNP Genotyping Platform

In order to design KASPar assays for detected SNPs, following criterion were used: i) Detected SNPs should contain at least 60 bp upstream and downstream sequences; ii) Frequency difference between the two genotypes of a mapping population ≥ 5; iii) read depth ≥ 5. KASPar assay were designed for 1,834 SNPs. A panel of 94 pigeonpea genotypes including parents of mapping populations, advanced breeding lines and wild relatives was used to validate 1,834 SNPs. As a result 1,616 SNPs were validated with a success rate of 88.1%. In case of ICP 28 x ICPW 94, 1,616 SNPs were identified and 1,094 could be validated.

4.5 Linkage Mapping

An inter-specific F_2 population derived from ICP 28 (*C. scaraboides*) × ICPW 94 (*C. cajan*) was selected for the construction of a reference genetic map. Consistent with a wide genetic cross, this pairwise comparison had the highest number of polymorphic SSRs. The mapping population was genotyped with all polymorphic markers and marker segregation data were analyzed by the goodness of fit test for a 1:2:1 segregation ratio. Only 138 (36.50%) markers showed good agreement with the exepected segregation ration 1:2:1 (at the threshold of $p = 0.05$). Among the 240 markers with deviation from Mendelian ratios we observed instances of complete absence or very low occurence of one parental allele, and instances of excess heterozygosity.

The genetic linkage map was constructed in a stepwise manner, beginning with the 138 normally segregating markers at LOD 5 and a minimum recombination fraction of 37.5. Subsequently, the 240 distorted markers were tested for integration with the help of Joinmap 3.0 software. The combined 239 markers yielded a genetic map of 930.90 cM (919 kb/cM) (Figure 17), with an average of 21 markers per linkage group and an average between marker distance of 3.8 cM. A total of 11 linkage group could be assigned, and these are presumed to correspond to the haploid chromosome set of *C. cajan* (n = 11).

5. DISCUSSION

The study deals with the large scale development of genomic resources of pigeonpea. This includes development of BES-SSR makers, development of pigeonpea transcriptome assembly using Roche FLX/454 sequencing, development of SNP makers using Illumina-1G sequencing and construction of genetic linkage map using developed SSR markers. The results of the study have been discussed in context of available studies.

5.1 Development of BES-SSR Markers

Presence of narrow genetic base of pigeonpea has slowed down the wide use of molecular marker technology for crop improvement (Saxena, 2008). The present study, focus mainly on the increase of genomic resources of pigeonpea, which will enable the use of marker-assisted-selection in this crop. With an objective of enriching SSR marker repertoire, two BAC libraries were developed with an estimated ~11X genome coverage of pigeonpea. Sequencing of 50,000 BAC clones from both insert ends provided 88,860 BAC-end sequences (BESs). Removal of cytoplasmic orgeneller BESs and cluster analysis facilitated the maximum possible recovery of nuclear genomic sequences comprising 41,329 singletons and 10,601 non-redundant contigs. With an objective to understand the constitution of SSR containing BAC clones, BESs were run through an annotation pipeline. Major proportion of the sequences remained non-annotated which may be considered as 'novel' *C. cajan* sequences. The overall repetitive fraction, resulting from BES analysis was found to be intermediate (22.15%) when compared with the percentage of repetitive elements in BESs of other legumes such as *Trifolium* (8.5%), soybean (33.5%), and common bean (49.3%) (Schlueter *et al.*, 2008). BES annotation analysis has shown a considerable variability in the amount of repetitive fraction in different crop species such as tomato (49.3%) (Budiman *et al.*, 2000), papaya (16%) (Lai *et al.*, 2006), banana (36%) (Cheung and Town, 2007), and citrus (25%) (Terol *et al.*, 2008). This variation in the amount of repetitive elements in BESs is an indicative feature of presence of repetitive elements in the genome of a species. A varying level of annotations in different species may also be responsible for difference in repetitive elements. Proportion of annotated genic fraction was found more or less similar as observed in the BESs analysis of other crop species such as *Phaseolus* (29.3%) (Schlueter *et al.* 2008), apple (10.9%) (Han and Korban, 2008), banana (11%) (Cheung and Town, 2007), *Brassica* (11%) (Hong *et al.*, 2007) and papaya (19. %) (Lai *et al.*, 2006).

BESs have been very useful to develop SSR markers in several plant species including legumes like soybean (Shultz *et al.*, 2007), common bean (Schlueter *et al.*, 2008) and *Medicago* (Mun *et al.*, 2006). In terms of SSRs abundance, overall density of 1 SSR per 5.64 kb seems to be in good congruency with the earlier reports in plant genomes (Cardle *et al.*, 2000). Similar results showing SSR frequencies of 1 SSR per 4 to 10 kb were achieved in different plant species like *Medicago*, soybean, *Lotus*, *Arabidopsis* and rice (Mun *et al.*, 2006). This discrepancy observed in different studies may be accounted to (i) amount of sequence data analyzed, (ii) criteria for SSR identification, and (iii) different sources of derived sequences. It is also important to note that after excluding non-annotated BESs, majority (70.21%) of SSRs fall belong to be associated with genes. These observations are in agreement of the comphrehensive study of Morgante *et al.* (2002) where SSRs were found associated mainly with genes.

In terms of distribution of SSRs, among the dinulcetoide repeats motifs $(AT)_n$ was found to be the most abundant followed by $(AG)_n$ and $(AC)_n$ repeats, which is in good agreement with the general finding in most plants (Gupta et al., 1996, Katti *et al.*, 2001, Temnykh *et al.*, 2001). In rice and other monocots CG/GC motif is very common, the least abundance of GC/CG motif in pigeonpea genome is consistence with previous observation in other legume species (*Medicago*, *Lotus* and soybean). Such low abundance of "CG" di-nucleotide repeats may be attributed to their tendency of forming secondary structures (hairpins), leading to a selective pressure against 'CG' accumulation in genomes (Eustice *et al.*, 2008).

While converting identified SSRs into genetic markers, though 3,072 SSR primer pairs were synthesized; of these 2,964 (96.48%) primers yielded scorable amplicons. This rate of successful amplification is quite higher than earlier reported in pigeonpea (Burns *et al.*, 2001; Odeny *et al.*, 2007, 2009; Saxena *et al.*, 2010a). All the repeat classes showed more than 98% amplification except di-nucleotide repeats which had comparatively lower rate of amplification (95.98%).

All the successfully amplified primer pairs were screened for polymorphism. The overall frequency of length polymorphism was found to be 12.75% which is lower than reported in earlier studies i.e. 50% (Burns *et al.*, 2001), 81.3% (Saxena *et al.*, 2010b), and 95% (Odeney *et al.*, 2007). Occurrence of a very low level of DNA polymorphism among pigeonpea cultivars is not unexpected as several studies have documented such results (Sivaramakrishnan *et al.*, 1997; Yang *et al.*, 2006; Saxena RK *et al.*, 2010b).

The frequency of marker polymorphism increased dramatically with SSR locus longer than 200 bp. PIC values for SSR markers were also analyzed in relation to repeat length and unit type. In terms of repeat length, Class I SSRs were more polymorphic as compared to the Class II SSRs which may be accounted to the hypervariable nature of Class I SSRs (Temnykh *et al.*, 2001) Among different type of repeat unit classes, tetra-nucleotide repeats, in general, showed the higher average PIC value (0.64) followed by di-nucleotide repeats (0.57). It was also observed that among trinucleotide repeat class, the 'TAA' repeat motifs, displayed higher polymorphism (average PIC value = 0.59). Similarly, 'TA' repeat motifs in di-nucleotide repeat class had a higher average PIC value (0.59) compared to the others. Similar trends were also observed in other legumes such as chickpea (Nayak *et al.*, 2010), *Medicago* (Mun *et al.*, 2006), and *Phaseolus* (Cordoba *et al.*, 2010) where the SSR markers with repeat motifs 'TAA' or 'TA' exhibited extensive abundance and polymorphism as well. Higher average PIC value of compound SSRs (0.58) can be attributed to the fact that the markers with compound SSRs have more than one SSR motif, which increases their chance to be polymorphic (Gupta and Varshney, 2000).

5.2 Development of Pigeonpea Transcriptome Assembly (CcTA)

A comprehensive study for development of CcTA was carried out using NGS based Roche FLX/454 sequencing technology. Based on phenology and utility of genotype in breeding programs PusaAgeti (ICP 28), a leading pigeonpea variety in India, was chosen for developing CcTA. Generated sequence data have been analyzed to understand the transcriptome architecture and genome organization with respect to potential duplication.

5.2.1 Clustering and assembly of transcript reads

Until recently, only 10,817 ESTs were available of which > 90% was developed during last two years. With an objective to generate a comprehensive transcriptomic resource, deep sequencing was undertaken on normalized pools of cDNAs from 31 tissues. Normalization of cDNA from the different tissues was done to optimize the discovery of novel genes. Unlike conventional sequencing, 454 library preparations involves random shearing of the normalized but un-cloned cDNA population, fragment-end polishing, adaptor ligation, library immobilization, single stranded DNA library isolation and sequencing (Cheung *et al.*, 2006; Margulies *et al.*, 2005). Therefore Roche FLX/454-based gene discovery projects represent a viable and perhaps favorable alternative to Sanger-based sequencing of EST libraries when a diverse sampling of genes is more important than obtaining full transcripts length contigs (Novaes *et al.*, 2008).

With an objective to compare assemblies, cluster analysis was done based on: (i) exclusively 494,357 Roche FLX/454 STRs, (ii) exclusively 10,817 Sanger ESTs, and (iii) combined dataset of 494,357 Roche FLX/454 STRs and 10,817 Sanger ESTs. Based on these analyses it was found that assembly of only Roche FLX/454 STRs had coverage of 12.73 Mbp with an average length of contig sequences as 262 bp. In contrast, though the coverage of the assembly based on Sanger ESTs was lower (0.47 Mbp), the average length of contig sequences was 637 bp. It is important to note that though number of Sanger ESTs as compared to Roche FLX/454 STRs is just 2.18%, the coverage based on Sanger assembly is 3.81% as compared to Roche FLX/454 assembly. Assembly based on combined dataset, however, provided higher genome coverage with 13.27 Mbp with and an average contig length of 273 bp. It is also important to note that 23,209 contigs of the assembly of combined dataset were longer than 600 bp while the longest contig based on only 454/FLX was 500 bp; and only 3,169 contigs were longer 500 bp. It is therefore evident that inclusion of Sanger ESTs in assembly has an advantage in masking the redundancy of sequence overlap and allowing improved assembly representing distinct transcripts and better coverage. Similar observations were made in some other recent studies in *Medicago* (Cheung *et al.*, 2006) and Atlantic salmon (Quinn *et al.*, 2008). In summary, this study provides a sufficiently high-quality assembly of 127,754 TUSs representing 1.53% pigeonpea genome sequence. This assembly has been referred as pigeonpea transcriptome assembly (CcTA) and was used for ensuing analyses.

5.2.2 Segmental genome duplication events

Within a genome, if a reasonably large group of duplicated genes with similar synonymous distances can be identified, this can be indicative of an ancient large-scale duplication event, or a polyploid event. Previous analyses in legumes have found evidence for an ancient duplication event roughly 50 million years ago (Ks ~.8) that occurred across a majority of the legumes (Cannon *et al.*, 2010). We were interested in determining if these were evidence for an independent duplication event in pigeonpea and whether or not they are shared by other close relatives. From the developed dataset it is evident that the duplication event which occurred in soybean ~13 million years ago was not shared by pigeonpea or any other member of the clade Phaseoloids. Clustering of the pigeonpea transcripts revealed that ~ 9.8% of the dataset represents gene families. While pairwise synonymous distances of these duplicated genes do present a peak at 0.06, this is not evidence for a major duplication event. Perhaps this peak represents a segmental duplication ~ 4.9 Mya ago based on a molecular clock. It is also possible that the peak at 0.06 may be the result of biases in the assembly process such as under-collapsed contigs. Nevertheless, the detailed picture about the extent of duplications and its sharing with other legume genomes will emerge only once the sequence data of the entire genome will be available (Varshney *et al.*, 2010b).

5.2.3 Gene structure, annotation and functional categorization

We aligned all TUSs to the soybean genome in order to predict gene structure and define exon-intron boundaries in the pigeonpea transcriptome assembly (CcTA). As a result, 33,874 TUSs were alignmed to 16,367 unique gene sequences of soybean. From this analysis, the structure and and putative order of 16,367 genes has been defined in pigeonpea assuming colinearity with soybean. These TUSs are distributed throughout the soybean genome with an average of ~1,693 TUSs/soybean chromosomes.

In order to understand relationships of pigeonpea genome with other legumes, a detailed comparison of the pigeonpea TUS was made against ESTs for other legumes as well as more distantly related plant species. As expected, TUSs showed higher similarity to the legume genomes than non-legume genomes. As pigeonpea belongs to Phaseoloid clade containing soybean and common bean, the TUSs should show higher similarity to the ESTs of these three legume species than others. While 21.11% TUSs have similarity with soybean, similarity to the common bean genomes is 7.77%. In fact, *Medicago* and *Lotus* show higher similarity as 9.89% and 8.19%, respectively than that of common bean. This can be attributed to larger EST datasets analyzed in *Medicago* (217,148), *Lotus* (148,617) than common bean (21,807). As expected, comparison of pigeonpea ESTs with monocot species like rice showed that the percentage of significance is much lower compared to any other legume species, despite the larger EST (Varshney *et al.* 2009b). Of 127,754 TUSs, 735 (0.5%) showed significant similarity across all the plant EST databases in this study.

In terms of understanding gene function, pigeonpea TUSs were analyzed using BLASTX analysis and GO categories of UniProt database. Putative functions could be inferred for 32,719 (25.60%) TUSs. Of these TUSs, 29,921 (91.40%) could be assigned to three categories- 'molecular function' (6,491) 'biological process' (5,455), and 'cellular component' (3,958). Highest number of TUSs corresponded to molecular function. Molecular functions generally correspond to activities that can be performed by individual gene products. Molecular function describes activities, such as catalytic or binding activities, that occur at the molecular level. Within this category sub-category 'binding' accounted for 45 % followed by 'catalytic activity' at 38% and 'transporter activity' at 5%. These categories have been recognized as more highly represented than any other classes (Zang *et al.*, 2004). Category 'biological process' accounted for second highest number of TUSs (5,455). The broad tissue and developmental stages sampling procedure used in this study can account for this kind of abundance. These libraries were derived from developing tissues, and hence contain high amount of transcripts involved in development. These libraries were derived from developing tissues, and hence contain high amount of transcripts involved in development. Under this sub-category 'metabolic process' accounted for highest percentage (31%). It was expected that functional categories (molecular function and biological process) mainly involved with general cell housekeeping activities like 'binding', 'catalytic activity' and 'metabolic process' would show the highest level of expression. These categories posses well characterized functions in common plant activities (Coram and Pang, 2005).

5.2.4 Identification of SNPs

Genetic markers are important tools for understanding genetic variation and identification of QTLs for the trait of interest for deployment in molecular breeding activities. However, until recently a very limited number of genetic markers in the form of SSRs were available (Raju *et al.*, 2010) and no SNP reports till date. Furthermore, not a single genetic map was published until 2010. One of the main reasons for this is the low level of polymorphism in pigeonpea germplasm. Therefore, it is desirable to develop a large set of molecular markers so that low level polymorphism constraint can be tackled. An approach to develop genetic markers is the mining of ESTs or transcript sequences for the presence of SNPs (Varshney, 2010c). Although markers developed from ESTs/transcripts are less polymorphic, they have been found useful for assaying the functional diversity in the germplasm collection (Eujayl *et al.*, 2002; Wen *et al.*, 2010), trait mapping (Zhang *et al.*, 2004) and comparative genomics studies (Stein *et al.*, 2007).

In several crop species, SNP markers are becoming more popular mainly because of their automation and less costs associated with genotyping (Kota *et al.*, 2007). In case of pigeonpea, so far, no SNP report is available. Therefore this is the first SNP discovery study in pigeonpea that reports 7,453 SNPs for two mapping populations. Majority of SNPs, however, were specific to the given parental combination of the mapping population. This fact, once again, underlines the availability of low polymorphism in pigeonpea germplasm collection (Odeny *et al.*, 2009).

For converting the identified SNPs into genetic markers, several choices are available for development of an appropriate SNP genotyping platform. These include GoldenGate assays (www.illumina.com/technology/goldengate_genotyping_assay.ilmn), KASPar assays (www.kbioscience.co.uk), cleaved amplified polymorphism sequence (CAPS) assays, etc. It is also important to note that as the SNPs identified are coming from exonic regions, they may exhibit low level of polymorphism in the germplasm collection. In summary, this study extends the existing marker repertoire to a great extent which will be very useful for pigeonpea genetics and breeding applications.

5.2.5 Candidate genes for FW

Although, FW is a serious production constraints, no serious effort has been made in past to identify the genes conferring resistance to FW. This is the first study that reports on identification of candidate genes associated with FW based on transcript profiling. For about a decade, microarray based analysis was used as a primary tool for gene expression profiling (Schena *et al.*, 1995; Brown *et al.*, 2000; Cooper and Shedden, 2003). However, it has been shown that these microarray analysis provide low sensitivity in quantitative measurements, non-specific hybridization and measures only known/ annotated transcripts (Git *et al.*, 2010). Recently "digital gene expression" by next generation sequencing technology has been introduced as a promising approach which provides a digital record of numerical frequency of the sequence in the sample. Here we have demonstrated the use of Illumina sequencing technology to identify differentially expressed transcripts. Higher number of tags produced through technology allows a deep coverage in detecting low-abundant transcript. Keeping in mind these advantages Illumina sequencing was performed for two FW responsive pigeonpea genotypes. Expression values generated in the experiment were used to study gene expression pattern among FW responsive genotypes that are parents of a mapping populations. This method of sampling enables us to study expression profile in contrasting parents which provides more evidence for genes involved in stress as well as their pattern of expression (up-regulated or down-regulated).

5.4 Development of a Linkage Map

To develop a reference genetic map, an interspecific cross was used so that a larger number of segregating loci can be integrated into the genetic map. Usually SSR markers are co-dominant and follow Mendelian inheritance (Bechman and Soller, 1990). However deviation from the expected segregation ratio for SSR markers is not an uncommon feature in inter-specific crosses and especially F_2 population. Significant distortion observed in the marker data may be attributed to several possible reasons such as the abortion of male or female gametes or the selective exclusion of a particular gametic genotype from fertilization, owing to incompatibility, incongruity, certation, or zygote selection (Kreike and Stiekema, 1997). Percentage distortion observed in the present study is comparable with previously reported studies performed on inter-specific crosses (Kianian and Quiros, 1992).

In the present study, the genetic map derived from an inter-specific cross ICP 28 × ICPW 94 included eleven discrete linkage groups corresponding to the basic chromosome number of the genus (x =11). Initial construction of a skeletal map with un-skewed markers and followed by integration of distorted markers helped in minimizing the possibility for spurious assignments of markers (Elangovan *et al.*, 2008). The final map comprised of 239 marker loci with a total map length of 930.90 cM having average spacing of 3.8 cM between two marker loci. This is the first report on the construction of SSR-based genetic map in pigeonpea. Therefore this map should serve as a 'reference map' for other future genetic maps of pigeopea. Moreover as the SSR markers are derived from the BAC-end sequences, these markers and the map should be very useful resource for linking the genetic map with a 'future' physical map of piegonpea (Varshney *et al.*, 2010b).

6. SUMMRRAY

Pigeonpea (*Cajanus cajan* L. Millsp.) is an important grain legume crop of rainfed agriculture in the semi-arid tropics. The Indian sub-continent, Eastern Africa, and Central America, in that order, are the world's three major pigeonpea producing regions. Being a legume, pigeonpea enriches the soil through symbiotic nitrogen fixation. A short day plant with a deep root system, pigeonpea tolerates drought, but is highly sensitive to salinity and water-logging. Diseases are major biological constraints to production. Genomics and biotechnological approaches have helped crop improvement in several crop species, especially cereals (Varshney et al. 2006). Similarly genomics tools will prove very useful to enhance the tolerance/resistance to abiotic/biotic stresses in pigeonpea. However, a very limited number of genomics tools in the form of molecular markers. ESTs (expressed sequence tags), and genetic maps are available for pigeonpea. A few microsatellite markers were developed in pigeonpea at ICRISAT. However because of the lower level of polymorphism in the cultivated pigeonpea germplasm, there is a need to develop genomics tools at the appropriate scale. Keeping all this in mind the present study entitled "Development of genomics resources in pigeonpea" was conducted with the following objectives- i) Development of microsatellite markers from BAC-end sequences, ii) Development of transcript assembly for pigeonpea, iii) Large scale identification of SNPs, iv) Development of SNP genotyping platform, v) Genetic mapping of SSR markers.

I. Development of microsatellite markers from BAC-end sequences

1. Two BAC libraries were constructed by using *Hin*dIII (34,560 clones) and *Bam*HI (34,560 clones) restriction enzymes. BAC clones were sequenced from both insert ends to yield 88,860 DNA sequences with an average read length of 620 bp.
2. Clustering based on sequence identity of BESs yielded a set of >52K non-redundant sequences, comprising 35 Mbp or >4% of the pigeonpea genome. These sequences were analyzed to develop annotation lists and subdivide the BESs into genome fractions (e.g., genes, retroelements, transpons and non-annotated sequences).

3. Analysis of BESs for microsatellites or simple sequence repeats (SSRs) identified 18,149 SSRs, from which a set of 6,212 SSRs were selected for further analysis. A total of 3,072 novel SSR primer pairs were synthesized and tested for length polymorphism on two parental genotypes of an inter-specific mapping population.

II. Development of transcript assembly for pigeonpea

1. Roche FLX/454 sequencing was carried out on a normalized cDNA pool prepared from 31 tissues produced 494,353 short transcript reads (STRs). Cluster analysis of these STRs, together with 10,817 Sanger ESTs, resulted in 127,754 pigeonpea transcript assemblies (CcTAs).
2. Comparison of the TUSs with the soybean genome showed similarity to between 10,857 and 16,367 soybean gene models (depending on alignment methods).
3. Functional analysis of these TUSs highlights several active pathways and processes in the sampled tissues.

III. Large scale identification of SNPs

1. Illumina/Solexa 1G sequencing was performed on four parental genotype of two mapping population of pigeonpea.
2. More than 70 million sequence tags were generated and wer used for identification of single nucleotide polymorphisms (SNPs). Sequence analysis of TUSs and the Illumina tags identified a large new set of 7,453 SNPs markers for use in genetics and breeding.
3. Differential expression of TUSs corresponding to genes involved in various pathways in response to Fusarium wilt (FW) was also identified.

IV. Development of SNP genotyping data

1. SNPs identified in this study have been used for development of SNP genotyping platform. The thresholds used in the selection SNPs include i) SNPs containing 60 bps flanking sequence, ii) frequency difference ≥ 0.5 iii) read depth ≥ 5. A total of 1,143 SNPs were selected for development of KASPar genotyping platform

V. Genetic mapping of SSR markers

1. Based on BES-SSR markers, the *first* SSR-based genetic map comprising of 239 loci was developed for this previously uncharacterized genome.

In summary, this study has generated i) sequence data interms of 88,860 BESs and 3,072 BES-SSRs, ii) trancriptome assembly of pigeonpea containing 127,754 TUSs iii) identified a total of 7, 453 SNPs for an inter-specific as well as intra-specific mapping population, iv) developed KASPar genotyping platform for 1,143 SNPs, v) the *first* SSR-based gentic map based on an intra-specific mapping population (ICP28 × ICPW 94). Large-scale genomic resource in the form of BESs, transcriptome assembly, SSRs and SNPs has been developed in an under-resourced crop species by deploying two prominent NGS technologies namely Roche/454 and Illumina/Solexa 1G sequencing. These data have been used for both basic as well as applied aspects in pigeonpea genetics and breeding. It is anticipated that SSR markers and the genetic map developed in this study should provide a reference resource for construction and comparison of genetic maps for new mapping populations, finger printing and cultivar identification, assessment of genetic diversity and gene flow among *Cajanus* species. New genetic maps, to be developed based on polymorphic markers identified in this study, will facilitate trait mapping and marker assisted selection. Furthermore, genomic SSR markers identified from BESs and integrated into genetic maps provide a valuable resource for anchoring future physical map or whole genome sequence to the genetic map. On the other hand the trancriptome assembly developed in the study will act as a reference for whole genome sequencing of pigeonpea.

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Table 1 BAC-end sequence characteristics

Annotation	RE	Genes	G + RE	TE	G + TE	NA	Totals
Total ends	14,659	20,579	2,572	327	148	43,644	81,929
Total sequence (bp)	9,088,580	12,758,980	1,594,640	202,740	91,760	27,059,280	50,795,980
Total unique clusters	6,670	12,022	919	201	44	31,877	51,733
Average cluster depth	2.2	1.71	2.8	1.63	3.36	1.37	1.69
Total unique sequence	5,131,626	8,897,905	764,163	154,620	44,218	20,029,073	35,021,605
Total clusters with SSRs	218	1,166	13	11	0	3,227	4,635
Total SSRs	406	1669	21	15	0	4145	6,256
SSRs/100 Kbp	4.5	13.1	1.3	7.4	0	15.3	12.3
Selected SSR loci	97	704	4	2	0	1974	2,781
Polymorphic SSRs	26	247	0	0	0	564	837
Average # of alleles	4.88±1.75	5.44±1.73	na	na	na	5.79±2.1	
Average PIC value	0.52±.21	0.58±.18	na	na	na	0.57±.19	

[a] Total unique clusters represent the total number of sequence clusters plus the number of singleton (non-clustered) sequences.

[b] Total unique sequence represents the sum of the nucleotide length of all unique sequence clusters.

[c] Three polymorphic markers are from BAC ends annotated as "chloroplast" and are not listed in this table.

Table 2 Distribution of polymorphic markers into different repeat classes

SSR type	Repeat classes	Number of markers synthesized	Number of markers amplified	Number of polymorphic markers	PIC value	Number of alleles
Compound Class I		657	626 (95.28%)	227 (36.26%)	0.08-0.88(0.58)	2-12 (5.74)
	NN	639	592 (92.64%)	236 (39.86%)	0.08-0.90 (0.60)	2-14 (6.55)
	NNN	200	194 (97%)	66 (34.02%)	0.08-0.85 (0.60)	2-13 (5.87)
	NNNN	62	61(98.38%)	14 (22.95%)	0.28-0.81 (0.50)	3-9 (4.71)
	NNNNN	10	10 (100%)	2 (20%)	0.52-0.76 (0.64)	5-7 (6)
	NNNNNN	43	43 (100%)	10 (23.25%)	0.52-0.76 (0.64)	2-7 (4.4)
	Total	954	900 (94.33%)	328 (36.44%)		
Class II						
	NN	1,006	987 (98.11%)	219 (22.18%)	0.08-0.83 (0.53)	2-9 (4.9)
	NNN	455	451 (99.12%)	68 (15.07%)	0.08-0.74 (0.48)	2-6 (4.4)
	Total	1,461	1,438 (98.42%)	287 (19.95%)		
	Grand Total	3,072	2,964 (96.48%)	842 (28.40%)		

Table 3 Frequency and distribution of different SSR motifs

Motif	Number (%)	Range (bp)	Average length (bp)
Mono-nucleotide			
A	8,631 (97.78%)	10-42	11.38
C	196 (2.22%)	10-18	11.86
Di-nucleotide			
AC	1,343 (17.63%)	10-64	11.87
AG	1,953 (25.64%)	10-82	12.75
AT	4,309 (56.57%)	10-98	21.55
CG	12 (0.16%)	10-12	10.33
Tri-nucleotide			
AAC	103 (7.15%)	15-37	16.68
AAG	159 (11.03%)	15-39	17.41
AAT	874 (60.66%)	15-102	21.91
ACC	49 (3.40%)	15-33	16.95
ACG	9 (0.62%)	15-27	18.33
ACT	95 (6.60%)	15-36	17.02
AGC	13 (0.90%)	15-21	16.61
AGG	21 (1.45%)	15-21	16.71
AGT	109 (7.57%)	15-36	16.34
CCG	9 (0.62%)	15-18	15.66
Tetra-nucleotide			
AAAC	3 (1.93%)	20-24	21.33
AAAG	13 (8.39%)	20-24	20.92
AAAT	101 (65.16%)	20-32	21.31
AATG	3 (1.93%)	20-20	20
AATT	10 (6.45%)	20-20	20
ACAT	15 (9.68%)	20-64	31.2
ACGT	1 (0.64%)	20-20	20
ACTC	2 (1.30%)	20-28	24
AGAT	4 (2.59%)	20-40	27
AGGG	2 (1.29%)	20-20	20
AGGT	1 (0.64%)	20-20	20
Penta-nucleotide			
AAAAG	3 (15.80%)	25-30	28.33
AAAAT	9 (47.37%)	25-30	27.22
AAACC	1 (5.26%)	35	35
AAGTT	1 (5.26%)	25	25
AATAT	2 (10.53%)	25	25
ACATC	1 (5.26%)	25	25
AGCAT	1 (5.26%)	25	25
AGCCC	1 (5.26%)	25	25
Hexa-nucleotide			

AAAAAG	24 (26.67%)	30	30
AAACTC	4 (4.45%)	30	30
AAAGAC	1 (1.11%)	36	36
AAATTG	1 (1.11%)	36	36
AACACC	1 (1.11%)	42	42
AACCAC	1 (1.11%)	30	30
AACCTG	1 (1.11%)	36	36
AACTTC	1 (1.11%)	30	30
AAGACC	1 (1.11%)	42	42
AATCAG	1 (1.11%)	36	36
AATGTG	3 (3.34%)	36-42	38
ACACAG	1 (1.11%)	48	48
ACACCT	39 (43.33%)	30-72	44.76
ACATCC	1 (1.11%)	30	30
ACCGTC	1 (1.11%)	30	30
ACCTCC	1 (1.11%)	42	42
ACTATC	2 (2.22%)	30	30
ACTATG	1 (1.11%)	42	42
ACTCTC	3 (3.34%)	30	30
AGCCTC	1 (1.11%)	30	30
AGGAGT	1 (1.11%)	30	30

Table 4 List of newly developed SSR markers isolated from BAC-ned sequences of pigeonpea

[a]Marker name	GenBank ID	[b]SSR motif	Forward primer (5'-3')	Reverse primer (5'-3')	Product size (bp)
CcM0001	FI188374	(GA)7	AGGCATGCAAGCTTTATTGG	TCCAAAATTTCGTCCAAAGC	166
CcM0002	FI188505	(AG)5n(AG)7	GCCTATAAATAGGGGCCAGG	AGAACAGAAACTCGGGCAGA	237
CcM0003	FI188508	(TTA)6	TGCAGCCAAATTATTTTGTTATGT	TTCAACAGCATCAGCACTCC	105
CcM0004	FI188513	(TA)8	TTAAATTGTCAGCCAAGGGC	TAAGAAATTTGGAGGTGCCA	228
CcM0005	FI188517	(AT)20	GGGGATGACAGTGTAACTGGA	TTGGAATCACAAACTAGTAATAGAACA	273
CcM0006	FI188554	(TA)8	GCACCAAATATGCAGTCAACA	TTTTGGATCGGTCAAGAAGC	280
CcM0007	FI188572	(TA)6	CCTAAGAAGAAGCGCTGTGG	TGCTTCTACAATGGACACGG	257
CcM0008	FI188611	(TA)19	CGGTGAAAAGGGTCAATGAG	CAAAATTAAAGCCTACTTATTTTACGA	182
CcM0009	FI188694	(GGA)5	CCATGATGTGTCACGTGGTT	TGCGAGGTGAAACTTGGTAA	189
CcM0010	FI188854	(AT)24	CCTTCAATGAGGACTTGTGTTG	CGTTTTCAATTTTTATATAATCGGG	260
CcM0011	FI188861	(CAA)5n(A)19	GAATTCCACGTGGTTGAGAAA	ATTGCAACCCCATGTTCATT	248
CcM0012	FI188879	(GA)6	AGAGCGAGCAATCACAGACA	AAGAATCCTCTACCGCAGCA	278
CcM0013	FI188884	(ATT)5	TGATAGTGGATGCTATAAAAAGAGGA	GATTCTGTGGGATTTTGTGGA	174
CcM0014	FI188947	(AAAT)6n(AT)7	AGTGAGGCCGAAAATCCTTT	TTTCCTACTCCTTTGAGTCCTTTC	244
CcM0015	FI188950	(AT)24	TTTCTTCATTATTGGTTGAATATCACA	CCGGTGTGTTCGAGCTATTT	276
CcM0016	FI188985	(AG)12	TCCAATGTTGGGTTAAAGGC	ATTTGGAACACCTCATTCCG	277
CcM0017	FI188997	(A)20n(AAT)5	CCAAAGGATGTGTCGTGATG	CATCCAAAGTTCAATAAGAGTTTGA	255
CcM0018	FI189023	(A)17n(TA)5	AAGCTGCCTGATGCATTTTT	CAGGGAAATGGAGAAAGCTC	279
CcM0019	FI189055	(TC)5(T)10	TAGAGTCGACCTGCAGGCAT	TAGCTCGGGTTCGAGGTAGA	210
CcM0020	FI189064	(AT)20n(AT)5	TAGAGTCGACCTGCAGGCAT	AATGGGGCATGAGTGATAGC	268
CcM0021	FI189072	(TTA)10	TGAATGTTTTCCAGGATTTTACA	GCGCAAATATAAGAGCCCAG	280
CcM0022	FI189103	(AT)5n(A)10	ACGTGACACACCATGTGGAT	AATCCATGCCAAACAAATGC	173
CcM0023	FI189142	(AAC)6	GCCAACTCCAAAGGGTACAA	ATTTGGTGAAGTGGGTGGAG	207
CcM0024	FI189144	(TA)9	GCTGTCAAAAGGTTCATCATTTC	CTCCTCCTGCACACAAGACA	279
CcM0025	FI189149	(T)16n(TA)22	TAGAGTCGACCTGCAGGCAT	GGATCAACAGTTAATGGTGAAAAA	234
CcM0026	FI189179	(TG)6	CAGGCATGCAAGCTTTTAGA	AACACAACAAAACTTGGGGC	269
CcM0027	FI189191	(AT)12	CCAAGGGAAAGATTCAACCA	ACCAAGTCAAATTTGCCACA	163
CcM0028	FI189231	(AT)15	CACCCAAACTCACTTCTTCCA	GAAATGTCATGTGGTTAATCTTTGA	257
CcM0029	FI189250	(AT)8	ACTTTTGGAGCTCATGGGG	GAAAACGTTTCCCAACCAAA	275
CcM0030	FI189258	(AAT)8	GCAATATCAATTCAATGGTGGA	TGACAGATGCACTCTCTCGTTT	218
CcM0031	FI189293	(TA)7	CTTCGAAGGCAAGAGAGAGC	GGATTCACGCTTAGTGCTGC	222
CcM0032	FI189299	(AT)6	CAGACCACAAACTCTTGCCA	AGAACGCACAGCAAGAAACA	236

CcM0033	FI189330	(TA)18	CTCAATACACCACTCAACCCA	TGCGTAAAATAATAGTGAAGACAAGT	280
CcM0034	FI189336	(TA)17	CGGATAAGGGAGTGGAATGA	TCCCTCTCTTTCTTGGACGA	278
CcM0035	FI189341	(GA)7	TTGTAGGTGCTTTGTGGCAA	GCCGTTGTAGGGTACGAAAA	259
CcM0036	FI189363	(AAAT)5n(A)10	GGGGGTGCTTTTAGGGAATA	AAAGAGGAGCAATGGGGAAT	256
CcM0037	FI189372	(ATT)6	TCAAAACCGTCAAAAATGACA	AATTTGAGATGAAATTTGTCGAA	183
CcM0038	FI189417	(GA)6	ATCACTGTCCGACTCAACCC	TACCCGAGATCATGAGGACC	238
CcM0039	FI189463	(AT)37	AGGAATAATGTTTGCTGCGG	TTGGTATGTGGAACGATTGC	261
CcM0040	FI189488	(GA)6	TCCGAGCAAAGGAGAAGCTA	GACGGCCAGAGAAATTTTGA	232
CcM0041	FI189508	(TAT)5	TGTGTTTTGCTTTTGATGGC	TGGCATCCAATGTCTGCTAA	252
CcM0042	FI189542	(T)10n(TA)5	AACTTTGAAAACTAAGGATTTGATTC	TTGGGTAACCATTGGTCTCA	262
CcM0043	FI189544	(TC)6	AACGACCATATCCAGAACGG	TGCCTCACAAATCTCACGAA	184
CcM0044	FI189547	(AT)22	TGCCCATCTGTTAAAACATCA	CAGAGCCTAAAGCACTTCGG	225
CcM0045	FI189573	(AT)5n(TA)5	TTTAATGGATTTGCATGAGCA	CTGCGTAATGCACGAACAAC	262
CcM0046	FI189581	(TA)7	ACTCAAGCTTTGTAAGCATTATGA	GGAGGAGGTTATTTTTGTTTTCG	100
CcM0047	FI189589	(A)12n(TC)5	TGTCTTTTGGATGAAAGTAGGGA	GTTGGGGATGGGAAGAGAAT	160
CcM0048	FI189606	(GA)7	TGGCAACCCTTCACACTACA	TCCAAAATTTCGTCCAAAGC	116
CcM0049	FI189635	(TTA)6	CTCGGTTCATGGTTGGCTAT	AGGTAGGGGCATATGGAAGG	168
CcM0050	FI189653	(ATC)5	GCGATTTTGCAGAGTCTTTGT	AAGGAACGAATTCACCTGGA	162
CcM0051	FI189688	(AT)8	ACCTTTATTTTGAGCAGGAAAA	TGAATCATTTTCTGTTGAAGGG	269
CcM0052	FI189710	(A)13n(AG)9	GCAGCAGAAAGCCCTGTATT	ATGCCTGCATCCATTAGTCC	277
CcM0053	FI189777	(AT)17	GGAATGAGATCATTAAATAAGGCAA	CGCCAAAAACCTTTGATGAT	250
CcM0054	FI189784	(TA)8	TCAATTTATGTCTCTATTGGAGTTGC	TGCATCATTGTCCACCTAACA	277
CcM0055	FI189791	(AT)16	CGTATCTAATTCAGCAATATGATTTTT	AGGAATGATTTTAAGGAAGAAATG	249
CcM0056	FI189800	(TG)6	TCATGCACGAACAATGTGAA	AACCCTTCAGACGCATTGAC	186
CcM0057	FI189804	(AAAT)6	CAATGTTGGCATAGGAACCA	GCTTAAAACTTGTGGGGCAA	269
CcM0058	FI189812	(AT)30	CCTTCTTCAATGTCAACAGTTCC	TGACGAGAAAGTGAATCGGA	181
CcM0059	FI189813	(GAA)5	GTTATGAAAACACGACACTCTCC	TGCATTTTTGGCCATTTGTA	186
CcM0060	FI189850	(AT)7	TGGAACAATGCCTATGGTGA	CTCAAAAACCTTTCTCCCCC	164
CcM0061	FI189855	(TAA)5	TTTGCATGTGCTTTTTGTCC	CATGGAGGGACCACTTCACT	272
CcM0062	FI189859	(TA)24	TCGCTTGTGCCTGTTCTTTA	CAGGTTTTGTGTTTGTTGCTG	241
CcM0063	FI189867	(TG)n(TA)5	ACTCAACCTGCACCTGTCCT	GCAAACTGCCCTCAAACAAT	218
CcM0064	FI189930	(AT)7	CATTTCTTTTCCCCTATTTTCTTTC	AAATAGGCTCAAATATTTTCACTGC	280
CcM0065	FI189944	(TAA)5	CGTGCTTCTGAGTGCGTAAG	GCCTTGTACTCCATCATGTTCA	178
CcM0066	FI190016	(GT)5n(A)20	TTGCTTCTTTTCTCGCTTGC	TCTTATTTTTGTGCAGCCCC	274
CcM0067	FI190029	(TG)7	CTTGGGAAGCATCTTCAAGC	TTTTGTTACACCAATCCTCGG	279
CcM0068	FI190044	(GAT)5	CCCTCTTCTCCATGGTCCTT	GACAAAGGTGAACTCTTGCCA	155

CcM0069	FI190059	(TG)6	ACCAAGCCTTTTCAAGTGGA	AGACTTCCACCCTAGGACCC	208
CcM0070	FI190076	(TA)9	GTGGATCTTGAATTGCCCAT	CAAATCCAACCTCAATTTCACA	254
CcM0071	FI190092	(TA)9n(AG)11n(AG)5	TAGCCCTAGTGGCCAACAAT	TTGTGAAATATGGTCATCAATCAA	222
CcM0072	FI190110	(AT)9	AGCGGGATAACCGCTATTTT	TTCAGCTGATTTTATTTTAATTTCTGA	250
CcM0073	FI190129	(TA)8	AATGAAACCCCAAATCCTGA	TTTTGACTCATCACGTAAATACACA	181
CcM0074	FI190130	(AT)16	AAGTACCCTTATTTTGAGCGG	TTCCGAACACTATTGAACATTGA	182
CcM0075	FI190136	(AG)7	TTTCCAAAGAAGTGTGTTGACC	GGTCAAAAGTGGATGTGGCT	233
CcM0076	FI190152	(TA)25	CAAAATTAAAGTCAAAGCTTAATCCA	TGTTCCTTCAATGGAAAATGA	280
CcM0077	FI190215	(AT)9	CCGGATAGCCAAACACAAAT	CCCGGCATGTACTCCTAGAC	260
CcM0078	FI190253	(TA)5n(T)10	TCAAAGGAAGTGGGAAATGC	AATTTTGTTTTTATTTGCATAAACC	193
CcM0079	FI190255	(AT)19n(T)11	AAGTCAATTGATTGTGCATTTTTC	TTGCACCAGTAAAAAGGATTG	244
CcM0080	FI190325	(AT)13(AG)11n(AG)8	TGCATGTTGTATGTTGGTTGG	GTAATGCATCTCAATAATTTCAACA	173
CcM0081	FI190370	(AT)16	GTGTGGGATGAGTGAAGCAA	CATCTATATGTAAAGCACATAAGGAAA	260
CcM0082	FI190371	(AT)16n(TA)7	TGTCAATGTCATGTTGGGCT	CATGCCATCTTCCTTTCTCC	245
CcM0083	FI190397	(GT)6	TGCACTATCAAGGGAGGTGA	CCGGACAATCTTAGGGGTCT	240
CcM0084	FI190448	(T)12n(TA)8	TTTGGTGATGGGAGCTTAGG	ATCATCAGTTCCCACAAGGC	279
CcM0085	FI190522	(TA)26	TGGCAAGCTTGAAAACTTATGA	CCCAAATGCAAAGGTCACTT	274
CcM0086	FI190523	(AT)8	GTTGGTCCCTCTTTTAACTTACAT	GGACCGGAATTGATCCACTA	272
CcM0087	FI190557	(CA)6	GGCATGCAAGCTTTTGGTAG	GCCTTTTCCACTTTTCTCACA	153
CcM0088	FI190562	(AT)19	GTGCTATATGGTGTGGCCCT	TCATCTTACGCAGCACCAAC	176
CcM0089	FI190571	(TA)6	TAGAGTCGACCTGCAGGCAT	GACGAAGCAACCTTGTGAGA	101
CcM0090	FI190623	(TA)6	TGCATATTGACCGTACACCG	TGCAGCATTGGTCCAAATTA	229
CcM0091	FI190671	(TA)6	GACCTCGATCGTGTTAACGG	TCACGATCCACCACAAAGAA	259
CcM0092	FI190692	(GA)6	GCCTATAAATAGGGGCCAGG	TCTCCTTAAGCAAGGACCGA	216
CcM0093	FI190703	(AT)27	TCATTGACCCCTCTGGAAAT	ACAATTGGAAAAATAAGTGAGTGAT	268
CcM0094	FI190715	(TA)15	TTGTAATTAGGATGCAATCGGA	TTAATCCCTTTCTGTTTGTCACT	265
CcM0095	FI190736	(TC)9	ATAATTAGTGGGCTGGGCCT	TGCCTCATAATCATGTTGCTTC	208
CcM0096	FI190777	(TTC)5	GAAGAAGGAGCTTGCACCAC	AAGAAACAACAATGGAGGCG	245
CcM0097	FI190782	(TG)6	AATGGGCAGGTTTTGTGAAC	ACCATGAACCGACCAAAGAG	243
CcM0098	FI190793	(AT)10	AACAACCGAGTGATTTGAAAAGA	AATCGGGTGATAAATATGAATAAAAA	257
CcM0099	FI190815	(ATC)5	AGCGTTTTTGTGGAGTCTTTG	AGGAACGAATTCACCTGGAA	162
CcM0100	FI190828	(TA)8	GGCCTCTAATTCTGCCAACA	GGTACAGTAGCAACCCCCAA	176
CcM0101	FI190833	(ATC)5	CCAAGAGAAAAACGTTTGTGAA	AAATGGAACGAATCACCTGG	111
CcM0102	FI190863	(ATC)5	CGTGTTTGTGAAGTCTTTGTGTC	TTCCTGACCACTTGAGAAACC	215
CcM0103	FI190912	(TTA)11	ATAGGATGTGACATTGGGGC	TCATAGGTTCACAAGTCTTGAAAT	237
CcM0104	FI190971	(TA)7	CAGGCATGCAAGCTTTCTAA	TTTTGTTGTTTTTAGTGGAATGTTTT	234

CcM0105	FI190981	(GCA)5	TGACAGGTAATTACGTTACACTCAAA	TTTCCCTTTTGGAGAACTCG	254
CcM0106	FI191007	(TAA)9	TAAAAATTGCGAAAATGCCA	AATTTTGATGATGGGCCAAA	260
CcM0107	FI191023	(ATT)5	GACTGCAAAATTCCAATGGC	ACGACAAATGGAACAAAGGC	244
CcM0108	FI191033	(AT)19n(T)14	TAGAGTCGACCTGCAGGCAT	TGCTCTTTGGTTTAGTTTGTAACG	187
CcM0109	FI191060	(TA)16	TGTGATAGTCCTTAAACCATTGAAA	AAAGCACCTTACCTTTTGTTTG	279
CcM0110	FI191118	(TC)6	CCGGACAATTTTAGGGGTCT	GAAAGTTCCCTTAGCCACCC	195
CcM0111	FI191119	(GA)6	GGAGGACGAACAGAAGCAAG	GGCATGGCTGTTTTGAATTT	136
CcM0112	FI191120	(TA)7	GCAGGCATGCAAGCTTATTA	GCGCGCCATCTTAATATCAT	148
CcM0113	FI191137	(TA)9	TCCGATGGAAACTTGTGTTG	TGATTTCTTCTTGCCACAAAT	230
CcM0114	FI191166	(AG)7	GGGAAATGAAAGTGGAGCAA	TGATTGGAGGGTCATTGTGA	152
CcM0115	FI191270	(TA)25	AAATCGAAGTACTTTACACAAAGCAA	TTTGGCTAGAGCTCTTCTATCACAT	273
CcM0116	FI191299	(AAC)5	ATTGGTTACGACGCCAACTC	GAATTCGAAAACGTGGCATT	271
CcM0117	FI191346	(AT)17	AAAGTTCTCTCCTCCTGGGC	AACATGCTTTGCACATCAACA	182
CcM0118	FI191373	(TC)6	TTCGAGCATTTCCTTCATCC	CCAACAGACATTTCAACCACA	194
CcM0119	FI191435	(GA)5n(AT)31	GAAATTTCCTTAGGTGACGCC	TTGACTCATTTTGTAGGAACTTCG	248
CcM0120	FI191497	(CA)7	GCTGATGATCACCTGCAACA	TGGGTCACCAGTGATGAAAA	278
CcM0121	FI191501	(TA)17	AGAAATTGGAGGCTTGGTCA	GGTATAAGGCTCAAACCCGA	273
CcM0122	FI191507	(AT)14	TGCTGCGATTATTTTTGCTA	GATTATGGGCGGAAATGATG	270
CcM0123	FI191522	(AT)15	CATGCAAGCTTAGGGGAAAA	TACTTGTCCTGCCTTGCCTT	201
CcM0124	FI191549	(AT)22	TGACACCCTATACCTTGCATAAAA	TGATGTTGATCATGTTGACGA	272
CcM0125	FI191561	(TTA)5	GCGCGTGACTCCTATAACATC	CGTACAAAATAATTGTCCAAAACAA	166
CcM0126	FI191618	(TAT)21	TGGTCCATGTTCCTCACTCA	CCAATGAAAATGAGAACCTTCA	218
CcM0127	FI191650	(AAGAAA)5	TTTGCTCAAGAGTGGAGCATT	TTGTAGGACATTGGGAAGCA	243
CcM0128	FI191673	(ATT)5n(AAT)9	CTGACCATTGTCATGCCCTA	TCCATAGGCCCAAGTGTTTT	188
CcM0129	FI191713	(TA)6	TGCAAGCTTGGGGAAATAGT	TCATCCACTTCAAGATTCAACC	190
CcM0130	FI191777	(TG)6	ACCAAGCCTTTTCAAGTGGA	TTCCACCCTAGGACCATACG	202
CcM0131	FI191778	(AT)21	TTTATAAAATCAAATCTAGCTTGTTCA	TGAAAGCTTTTAAGTTTGTTAAAGCA	212
CcM0132	FI191801	(AT)12	TCACTACCATGCCCAAACAA	TTGGGGAGAGTTGTAATGCC	217
CcM0133	FI191813	(TA)9	GTTGTCCCATTTTGACCTCC	CCATAATCCAATCCAAATCCA	176
CcM0134	FI191818	(AT)12	CTCTGCCCCGATGTCATATT	TTGGGATGTGAAGATGATGAA	240
CcM0135	FI191937	(ATC)5	AGCGTTTTTGTGGAGTCTTTG	CCCAAGAAAGCACCCTTGTA	250
CcM0136	FI191937	(ACA)5	GCTTGAAGCTTAAAAAGAGTTTTG	TTGCTCATGCACACAGCATA	189
CcM0137	FI191943	(ATA)8	GGGATGATCCAAAAACGAGA	TCACCGATGACTTGTTGCAT	225
CcM0138	FI191960	(TA)6	TTTTGGGTCATGCAATGAAG	TGTCCTCAAGCTCCTTTCGT	270
CcM0139	FI192023	(TG)6	GTGGGTTCTTGGTTGGAGAA	GGTGAAACTCCCAGACGAAA	202
CcM0140	FI192054	(AAT)5	CCAACTCCCCTTCTAGTGTCTC	TTTAAAGACATTTTCGTTTTCAAAT	205

CcM0141	FI192073	(AT)18n(TTA)6	TCATTGAACCTTGGTCAAACAC	AAAATAAAATTATGGGACCTAAATCCT	275
CcM0142	FI192081	(A)11n(GA)5	TAGAGTCGACCTGCAGGCAT	CCATCCAATCTCGAATCGTT	264
CcM0143	FI192084	(TAT)6n(TTA)8	GGACCCAACACGAAGCTAAC	AAGATCTCATCCAAAGAAAGTCG	271
CcM0144	FI192086	(TA)21	CACAAATTTTGATCGATCTTACCA	CAATCTTATTTTACACGGCAATCA	251
CcM0145	FI192134	(AGA)5	GACGCACATGGACTGCTAGA	CTGGTCACGTGGCTGTAGAA	220
CcM0146	FI192148	(CA)6	CCACCCTAGGACCCTACGAC	TGCACTATCAAGGGAGGTGA	243
CcM0147	FI192164	(TTA)5n(CT)6	GTTATTTTAACCGCCGCAAA	GAGGAAGAAGGGATTGGTGG	248
CcM0148	FI192212	(AT)6	TGGAATTTGACTCATTTAGAATAGGA	CCCACAGACAGCATATCAACA	279
CcM0149	FI192218	(CT)6n(CA)12	TCATGTGGGGTAGAGGGTGT	CAATGGACATGCACTTAGGG	270
CcM0150	FI192300	(TCT)6	CCTTTGGGAACGAAGATCAA	GATCCAGTTCGGGTTTTCAA	280
CcM0151	FI192372	(GA)6	CAGGCATGCAAGCTTTGTTA	CCCTCAAAAATTTCGTCCAA	161
CcM0152	FI192447	(TTA)7	AAGCATGGATGGATTGGAAC	AGCACGGTTAAGGCTAGCAA	256
CcM0153	FI192453	(CA)6	TTCATTTTCCTACCAGGGGG	TTTTCAAGGTGCAAGATTGG	196
CcM0154	FI192458	(AG)7	TTCACACTACAATTGCCTCACA	TTACACACAACGGCCATGTT	214
CcM0155	FI192473	(TC)6	AGAACGTGCCATTCTGGTTT	TTGCCTCACCAAATCTCAAG	245
CcM0156	FI192518	(TA)10	TCAAATTGAATCTTACAGAATTTTAGA	CTCTCCGGTTGAAGGCACTA	180
CcM0157	FI192539	(TCA)5n(CCTCAT)5	CTCCTGCCTGGAATCAAAAG	CATATCCATGGCAGTTGCTG	250
CcM0158	FI192554	(CA)5n(AT)11	CCTATCAGAGCATGCCCACT	TGCATGCATTTTGTGAGTCG	260
CcM0159	FI192564	(AT)7n(ATTT)5	TTAAATGGGTTTGATTGAATCTTT	CGTTCCGGGACTATGAAAAT	223
CcM0160	FI192601	(TA)6	AGGCAAGAAACATGGCTGAA	GGGTTGGAAATTTCGTGTTG	181
CcM0161	FI192608	(ATC)5	AGCGTTTTTGTGGAGTCTTTG	AGGAACGAATTCACCTGGAA	163
CcM0162	FI192640	(GA)6	TGTCCAACTCAACCCATTCA	TTAGGGATCAGACAGTCCCG	239
CcM0163	FI192647	(TGA)5	AACCACTTTCTTGACCCCAA	TGAAGTCTTGTGACGTCTGAGTG	278
CcM0164	FI192658	(AG)6	ATGCCCTTAATCGGTACCCT	CAAAGCTTGCTACAAGGTATTCAA	217
CcM0165	FI192686	(AAGAAA)5	TTCGAAAAGAATCCACTCCC	TGTAGGACATTGGGAAGCAA	203
CcM0166	FI192734	(TA)13n(T)10	CTCGACACATTCACATTCCCT	CCTGGGTTCAAATCCTACCA	141
CcM0167	FI192744	(AGT)6	TCAATGCCAACCTGACAAGA	TTTGAAATAGAACCTCCCCA	271
CcM0168	FI192798	(TG)9	CAACCTAGCTCTCAAAGATTCCA	TTGGCCACTAGGGCTAACTC	239
CcM0169	FI192804	(CA)6	TTCCACCCTAGGACCATACG	ACCAAGCCTTTTCAAGTGGA	206
CcM0170	FI192808	(AT)24	CAGGCATGCAAGCTTCTTTT	AGGGATGTCGCATTTTTCTG	208
CcM0171	FI192820	(TG)5n(T)11	TTGAATTATTGGCTGTTTCTGG	TCAATTCCATCGGTTAGGGA	234
CcM0172	FI192842	(AT)7	CATGTGCATTATTTACGTCGG	CCTCCAATTTATCATTTGTGTGA	274
CcM0173	FI192849	(TAAA)6	TTGTCAATGGGACCTCAACA	CTATCCCATGCCATCAACCT	278
CcM0174	FI192908	(AT)35	AGTCTTTGAAAAGAGGCCAAC	CAAAATGTAAGAAGATCAAACCAAAA	157
CcM0175	FI192915	(GA)6	GGAGCGAACAATCACAGACA	CCGAGATCATGAGAACCCTT	178
CcM0176	FI192943	(GA)10	GAAATTAAGAAGCGGCGATG	AACCTTATTGCCACGCAAAC	235

CcM0177	FI192947	(ATA)5	GAATGCCATTTCCCTTTTGA	TGGGAAGGACTGAAAGCAAG	239
CcM0178	FI192980	(AT)13	TCCACAAAATCGTACGGTGA	ATGCTTATGTCAGGGATGGC	258
CcM0179	FI193016	(TTA)6(TA)17	GCAAAATTGCACTAAAATTTGTTT	CCATCTTCGCCTGTCGTATT	189
CcM0180	FI193106	(AAT)5	TTGTGATACCATGTGCTTCTTG	GAAAAATTTCTCAAAATTCTCTTCTCA	236
CcM0181	FI193124	(G)13n(TG)5	TAGTTCACCGCCTGTCCTTC	TGCAGACGATAAACATTCGG	278
CcM0182	FI193170	(GTG)6	TTGGAGCAACAACAAAATGG	CAAGAGCATTTGATCCATGA	202
CcM0183	FI193187	(AT)10n(TA)8	GCCCATTTTGTCATCCCTAA	TTCAACAGTTGGATCGTTCA	236
CcM0184	FI193228	(CA)7	AAGCTTCACCACCAACATCC	TATAGGTGTGCCTTCGGGTC	278
CcM0185	FI193254	(TA)8	TTGATCATGACTTATGCCTTTGA	GGCTTGCTTTGAGTTCCTTG	232
CcM0186	FI193299	(AT)18	AAGATTTGATCCATATTTTCTGACA	CCACACTAATTAGGCAAATACGA	201
CcM0187	FI193316	(TG)6	GATTTTTCACTATAAAAGCAAAATGA	TTTGGCCTCAGAGTTTACATGA	247
CcM0188	FI193340	(TG)8	GAAGAAAAACACATAGAAGGGGG	AATCCCAGCCGCAAAAGTAT	173
CcM0189	FI193341	(TTA)7	TGTTAACCGTGTTGAAGGCA	ATCGAACACCAACCAAGGAC	221
CcM0190	FI193392	(CT)6	TAGTTGCACACTGTCCCTGC	TGACTCACAAAGTTGCTTTATCTT	190
CcM0191	FI193400	(AT)22	TCCGTTGCTTCTAAGTGTTCAA	CCCAAGTTAGGGTGAACCAA	212
CcM0192	FI193407	(TG)6	ACCAAGCCTTTTCAAGTGGA	CCACCCTAGGACCCTACGAC	202
CcM0193	FI193429	(TA)20	TAAATCACCACCCTTGAGGC	TGCAAAAACACATCCTGGAA	190
CcM0194	FI193432	(TGA)5	AGGCATGTGTTTGTGTTTGTTT	CCTTGAAAACTCTTGTTGGAATC	204
CcM0195	FI193462	(AT)11	CAACAATAAAGCATAAACCACCA	TGACGTAGATTGGGTAGTTAGGA	223
CcM0196	FI193495	(CT)7	ACACCGAATGGAAATGAAGC	ATTTGAGAGCCTAGTGCCGA	197
CcM0197	FI193525	(AAGAAA)5	GAGTTTTAAGAAGGAGGGCGA	TCTTCCTCGGAATCTATGGC	274
CcM0198	FI193529	(AT)9	TGCATTTTCAACCTTTCGTG	GGTCATGCAGACACTTCCCT	262
CcM0199	FI193620	(AAT)12	TGACCTCCTCCTCATGGTTC	GAAGGGAAGGAGGGACGTAG	200
CcM0200	FI193687	(AT)15	AGAGTCGACCTGCAGGCAT	CAATAAGCGTGCCATTTGTG	263
CcM0201	FI193693	(AT)13	GAGGCTTGCTGTGATACCCT	TAGGACATGTGACATCGGGA	273
CcM0202	FI193742	(AT)15	TTCTCCCCAGATTTCCACAG	TGCACTCAACTTTTGGCACT	214
CcM0203	FI193744	(AG)6	GGTTTGAGTCCTGGCATCAT	TTGTCAATATGCACTTTTAAGGATTT	216
CcM0204	FI193761	(AAT)5	TGGCTTAGATATCTCCCCACTT	TTGGTGAATGTCGTGTGGTT	259
CcM0205	FI193771	(GA)6	TGTCCAACTCAACCCATTCA	TACCCGAGATCATGAGGACC	233
CcM0206	FI193834	(AT)21	TGCCATATTTTGGTTTGAACA	CACAATACATTAGCCACATTGTCA	157
CcM0207	FI193838	(TA)15	TTTTGGCGGTCATTTTAACC	TTAGTCGGGAGCAACACTGA	235
CcM0208	FI193892	(TAT)10n(TTA)7	GCATCTAAATACAATTAATATTGTGGG	ATAGGGTGGATCTCTGGTGC	122
CcM0209	FI193903	(AC)7	TGTGCTCTCCAAGTTGTTGC	TTTTGATAATGCCAAAGGGG	278
CcM0210	FI193935	(ATG)5	CCAAGAAAGCACCCCTTGTA	TTGAGAAAAGCATTTTTGTGGA	262
CcM0211	FI193940	(TC)6	AATTCTCAATTGTAATCCCTCACTT	ACTGGATGTGAGGAGTGCCT	246
CcM0212	FI193974	(GAC)6	CTCATGGAGTGACCGAACCT	AAGTTCTAGGATTAAGGGAATGTCA	246

CcM0213	FI194037	(GA)6	GGGTGACTCTGGTTGCCTAT	GGGCAGAACCTTCTCCTCTT	253
CcM0214	FI194038	(GA)8	TGCGGCAACTTTTCACACTA	GCCTCAAAAATTTCGTCCAA	113
CcM0215	FI194054	(ATC)5	TTTGGGAAACTTCAGACATGAG	CACTTGGAATTCTTGAGGCA	199
CcM0216	FI194056	(TG)6	AAGGGAGGTGGACTACAAGGA	CGTTTAGAAGGCTTCAATTTTCC	157
CcM0217	FI194234	(TA)6	CGTGCTACCATTTTTCAAACG	AGCGTGCCAGATACATTCAA	105
CcM0218	FI194332	(TTA)5	TGCTTGTTTGGTTGTTGAGC	GGGCATATGGAAGGGTGTTA	175
CcM0219	FI194333	(GA)6	TAGGTGCTTTTTGGCAACCT	GGCCCGTTCCAATACACTAA	256
CcM0220	FI194351	(AT)15(ATA)5	GTGTGACACCCTCTACCCCA	TAGGACATGTGACATCGGGA	277
CcM0221	FI194360	(TA)17	AAAGTTATTGAGCGGCGTAA	TTTCATATTTGTGTGTTTCATGAGTT	231
CcM0222	FI194373	(AT)6	TGTGTTTGGTTTGGTTTTCG	TTGCACACATATATTGCATTTGA	105
CcM0223	FI194406	(AAT)8	AACATCAAGAAGGGTCCACA	GAGAGGATGTGACATTGGGG	263
CcM0224	FI194421	(TAT)7	TCACTGTGCATTTTCCGTGT	ACCCCGAGTCATCACTTCAC	267
CcM0225	FI194488	(A)10n(CA)6	AGCCAACCTTGCACAGTTCT	CCATTGTGGAGTTGTGTGAAGT	163
CcM0226	FI194492	(AAGAAA)5	TTCGAAAAGAATCCACTCCC	TGTAGGACATTGGGAAGCAA	203
CcM0227	FI194507	(TA)6	CACCGGTGTTAATTATAACCCTTATC	TTGGATCCCTCTCATTTTGG	263
CcM0228	FI194530	(TG)6n(GT)5(TA)10	TGAAAGGTCTGTTTGTGCCA	CATTGAAATTTGATGTAGAACATGAG	241
CcM0229	FI194594	(CTT)5	CGCTTTCTTTTACTTATTGCACG	CTCCAACGGGAAAATTTGAA	128
CcM0230	FI194646	(AAAT)5	CGCTTGGCTGTGAAAGTGTA	AGGAACGTGGTAAGTCGGTG	210
CcM0231	FI194690	(AAT)5	GGGGGTGCTTTTAGGGAATA	GGAGCAATGGGGAATAGGTT	223
CcM0232	FI194708	(CA)6	TTTGCCTACTAGGGGTTTCG	TCATTTTTGCAAGGGAAAGG	207
CcM0233	FI194715	(GA)6	GGTTTTAGGTGCTTTGTGGC	TAGACAGCTGGGGCTCATTT	158
CcM0234	FI194717	(AC)10(AT)29	GAGACCTTCACAACCTACCCA	TGGATCCTCTTATTCCAGTGTG	264
CcM0235	FI194736	(TTA)10	ATAGGATGTGACATTGGGGC	AACATCAAGAAGGGTCCACA	268
CcM0236	FI194751	(TC)7	AAATCTGGAATGGGCCTTCT	TCACAAATCTCAAGAAATACAATGG	151
CcM0237	FI194801	(AT)21	CAAAAATTAAAGGCTCATTAAACTG	TGAGAATCGGTAACCTAGCCA	277
CcM0238	FI194809	(AT)11(AG)6	TCCAGTGACAAGACCACCAA	TCTTAGAGTAAACGGATCATTCCC	183
CcM0239	FI194859	(AAT)9	AACATCAAGAAGGGTCCACA	ATAGGATGTGACATTGGGGC	265
CcM0240	FI194901	(AT)16	CCATTTTAAGTAGTTTAGGCATAACG	TTATCGTGAAAATCTCTCATGC	242
CcM0241	FI194917	(TAT)6	GGAACAAGGGAATGAGTGCT	TTGAAACAGGCTCCTAATCTCAT	109
CcM0242	FI194949	(AAGAAA)5	AGGGCCTCTCTTCCCTACCT	TCTTCCTCGGAATCTATGGC	262
CcM0243	FI194959	(TG)5n(TG)5	GGAGCCAAAGGTCTAGGGAG	TGCAAGCTCAATCTATGCAAT	246
CcM0244	FI195016	(AT)11n(TA)9	AGCATGTGCTTTGCATCAAT	TTTGGTGTATAAGATTACGAATGATTT	218
CcM0245	FI195087	(CA)6	TGGAAGTGTTCCAAGGGATT	ACCAAGCCTTTTCAAGTGGA	241
CcM0246	FI195094	(AT)16	ATGGAGCCAAAGTGTCCAAG	ATGAAAAGCAACTACGCGCT	226
CcM0247	FI195117	(ATA)5	CATCTCGACTCCTAAATTATCGC	TCAGGGATCTTGAGAGACCAA	236
CcM0248	FI195265	(TA)8	CAAACTCAACCCTACCAATGC	CATTCCTTGTCATCAATGAAGTTT	280

CcM0249	FI195279	(TC)10	TCAAATATTGTGTTCATCTCACG	GCCATATGGGAAGAGGATGA	260
CcM0250	FI195331	(CA)6	ATTTCCCCTCAAAAGGCAAC	TGATTAATGGATGTTGAAAGTGA	196
CcM0251	FI195376	(AAT)6	TTGCTGGAAGAAAAGGGTTG	ATGATTTTCCAACGCTCCTG	220
CcM0252	FI195409	(AT)23	CATAGAAGCCCACCTTCCAA	CTGCATGCAAAACGAAGAAG	234
CcM0253	FI195413	(TA)18	GGAAAGGAGAGAGTTCGCAA	CACACGTCAAGAAAAGAAAAAGG	197
CcM0254	FI195450	(AAC)6	GCTTGCTCACACCATCTGAA	AGCACAAAATCACCGGAAAG	191
CcM0255	FI195482	(GA)6	ATGAGAACCTACACCGCCAC	AGACCGCCAACAACGTATTC	252
CcM0256	FI195491	(AAGAAA)5	CGAAAAGACTCCACTGCCTC	TTCATCAAGTTCAGGCTCCC	195
CcM0257	FI195523	(AG)7(TG)15	GCCGTTACGAGGGTAATGAA	CTGTCTCAAAGGGACCCTGA	241
CcM0258	FI195532	(CA)6	CAGAGTCAGCGACTTTCGTG	GGGTAAGTTTTGTGAAAGTGTGG	192
CcM0259	FI195546	(TC)6n(CTT)5	CTTGCACCACAAGTTTCCCT	CCAAGAGCTTGAAGGAAGCA	240
CcM0260	FI195558	(AT)10n(A)16	TGGTTGTTCCCCTTTTCTACA	TCTGATCGTGTTGGTGGCTA	280
CcM0261	FI195595	(TA)12	AAGTGCCATCTTCAAGCACC	TTGTAATTCAAAATGATTGGACC	238
CcM0262	FI195598	(AAT)6n(ATA)11	AACCCAATTTCATTTGGAAAA	ACATCTCACTTGTTTTATCTCTTCAA	203
CcM0263	FI195617	(TG)7	AAAACCTTGTGCCACCTTTG	CGAGCATGGTTTTAAAATTCC	150
CcM0264	FI195643	(TA)24	TCAGTTACCTGAGGAGAAGTTTTTG	CACAAAGAATCAAGTCTTCCTATTCA	233
CcM0265	FI195693	(AG)7	TTCTAGGTGCTTTGTGGCAA	AACGTTCAAATCCAGAACGG	220
CcM0266	FI195700	(AC)6	TGCATTGGACGAAGAACACT	CCCCTGCATTGTTAGATGCT	155
CcM0267	FI195733	(ATC)5	AGCGTTTTTGTGGAGTCTTTG	CCTTGCCACTTGAGAAACCT	214
CcM0268	FI195757	(AT)24(GT)10	CCTTTTGGGTTAGGGTATCCA	CCCCTAACGTAGCCTGTCAA	210
CcM0269	FI195815	(GAA)5	GGGGAAATCACGAAGTTTCA	CACCTTCGTCTTCACCGTTT	274
CcM0270	FI195857	(AG)8n(AT)5	AGGCACAACAAATACTGCCC	ACATATACGAAAAGAACTGGTGG	235
CcM0271	FI195944	(A)23(AT)25	TGCTTCGCATTCCTCTTTTT	AGGAAAATGCTGCTTTGCAC	268
CcM0272	FI195981	(GA)6	GCTTTGTGGCAACCTTTCAC	CAACAGTTAGGGGACCTCCA	137
CcM0273	FI196032	(CTT)5	CAGGTATACGCTGCTCACCA	GCAGTTGCTGATGGAGTTGA	264
CcM0274	FI196038	(AT)27	GCTTTTAAAAATTTTGCAGACTTGA	AATATACTCCCTCTCGCGCA	254
CcM0275	FI196051	(AT)7	CTCAAGCTTCAACAATGACTATGA	TAGAGGAAACGCATTTTGGG	243
CcM0276	FI196076	(TC)6	TATTTGGTCCCAGGTCCATC	AAGAAATGACTGGAAGCCCA	118
CcM0277	FI196095	(AAT)8	TCCCACATAAAGGCAACTCC	TTTGTAACACCCCAATTTTCAA	280
CcM0278	FI196104	(GA)6	TGGATTAGGGGTGCTTTTTG	AAACAGGCCATTTTGGTCAG	191
CcM0279	FI196106	(ATC)5	GGAGTCTTTTTGACCATCTTGG	AGGAACGAATTCACCTGGAA	152
CcM0280	FI196123	(GA)6	CGGCAACCTTTCACACTACA	ACGGGTCATTCTGGTTTCAG	255
CcM0281	FI196136	(CACATC)5	GTGGCGTTGTTCTTCCATTT	CACCATTTTGTGTGGATTGTG	279
CcM0282	FI196138	(AT)8	GGGTTGTAATACGGTGACGG	CCCAAAACTAGTTCATGAGATAATAA	161
CcM0283	FI196144	(AAG)5	AGAAAGGTCAAACGAAGCCA	CATGCTTTGACTTTTGGGCT	269
CcM0284	FI196152	(AT)24	GGGTGTCATATTATAGCCAGGG	TTGATGTCAAATTGGTTGGA	210

CcM0285	FI196228	(AT)16	GGTGGCAGCTCCATTAAAAA	TGAGGAGTGAGAACAAATATCCAA	180
CcM0286	FI196245	(AT)6(AG)9	AAGGCTCTTTGATCAACTAACTCA	AATTCAGCGGTTGGATCATT	250
CcM0287	FI196256	(AT)6	GAATTTCAAGTGAGCATTCCG	TGCCATGTGAAAAAGACAACA	274
CcM0288	FI196318	(TA)8	TGAATGTGGGGTAGAGGGTG	TTGACTCATCACTTGTGTTTTCAA	262
CcM0289	FI196364	(TA)6	TTCCTTTGAGCCTTTGCACT	TCAAGTTTAAATGAAGGGTAGTTTTT	238
CcM0290	FI196431	(AAT)6	GAAAGAAAACCAGAAGAACCGA	TGGGATCAATTTCATAAATTTTACA	261
CcM0291	FI196506	(AT)40(AG)8	CACACAAAAACCACAATGACAA	TGTAGAACATGAGTTATCGAATGGA	229
CcM0292	FI196510	(TTA)6	ACCCATAGCAAGCAGAATGC	AGCTTGGGTTCAAAGGAACA	278
CcM0293	FI196516	(TA)11	GTTCCCGGCTACCAAATGTA	AAAAACACAAAAGATAAACATACATGC	231
CcM0294	FI196562	(AT)10	ACAAGTCAACCACACGAGCA	CACCAACATGCTTCTCATGC	100
CcM0295	FI196575	(AG)6	ATGATATGCGGGGTAGAGGG	AACCATGAGTTATTGAGCGGA	101
CcM0296	FI196633	(ATT)5	TTCACATTTTATCATTGCGGA	TCTTCGCGCTTATACGTTTG	242
CcM0297	FI196662	(AT)17	AATTTGTGGCAAAGTCGAGG	AGTGTACCCAGCGAATGAGG	265
CcM0298	FI196679	(TA)19	CGTAGCCGGATCTTCTTCAC	TGGTGTGGATTATGATGGATTG	245
CcM0299	FI196753	(ATT)5	CCAAGGAGGATTCCAATGAA	TGGATTTTGTGAGATTTTATGGAG	206
CcM0300	FI196755	(GA)6	ATGGAAAAGGTGCTTTGTGG	TAAATTGAAGCCTTGGGCAC	211
CcM0301	FI196778	(TAA)5	TTCCTTCTGAACAACGTACTCAA	GCTGAAACAAGGTTCTGGGA	270
CcM0302	FI196837	(TA)27	ACATGTGCAAACAATTGGGA	AAAACACTTTGCCTCGGATG	216
CcM0303	FI196859	(TA)7nt(GC)6	CAAGCTTTTGAGGTTCGACA	TCACGCAAGAAATTCACAGC	205
CcM0304	FI196867	(GGT)7	AACGACTCTCCAGCATGAGG	CAATTCCCCAAACCAAACAC	152
CcM0305	FI196881	(TA)11n(A)14	GAGCCTTTCCAACCTGCTC	TTTTTAGAGCATCCATCCCG	201
CcM0306	FI196910	(AAT)5	TCATTGTCTCTTTCTTTTCCATTT	GGCATGCTAACATGGCATTA	280
CcM0307	FI196915	(T)11n(AAAT)5	CCTACAACCGATCTCCGGTA	TGGGCTATAGCGATACCACTT	270
CcM0308	FI196918	(AAAT)5	TGTTCCCAAGGTTATCGACC	GCCTGCATCCTTTTGTAGTTG	257
CcM0309	FI196959	(TA)7	TCCGAGAACACACAAAGGTG	TGAATTTCAAAATTAGTTGAGTTGA	214
CcM0310	FI196960	(AT)29	CAACACCACAACACCACACA	TTTAGCCCCCAGATCTGACA	133
CcM0311	FI197026	(GA)6	TGTCCAACTCAACCCATTCA	TACCCGAGATCATGAGGACC	226
CcM0312	FI197054	(AG)n(A)10	TTAAAAGGAGGCCTCATCCA	AAACTTTCCGGTATTGTGCG	182
CcM0313	FI197094	(AT)11	TGGCACAATTGAACTCTTGG	TTAAACAGTTGGATCGTTGAAA	151
CcM0314	FI197125	(AT)13	TTTTTAAAATGATTGGTAACCTTATGA	AAAATTTAGTTGGTCCCGTAAAAA	213
CcM0315	FI197131	(GT)6	TTATTTTAGTTAGGGTCCATCTACCT	GTTGCTGAACCCATTCTTCG	124
CcM0316	FI197166	(AT)13(AC)5	CCGGACAATTTTAGGGGTCT	GCATGTTAGGCCACCTTTTG	227
CcM0317	FI197251	(AT)26	GGGTTTGAGACTATTGGAGGG	ATGAAATTGGGCGTGAAGAG	171
CcM0318	FI197271	(CA)7	CCCTAGGGAATCCGACTAGC	GGGAGGTGGACTACAAGGAA	258
CcM0319	FI197288	(TA)31	CTCGTGTCATTTTCATCCCA	AAAAGGTCACATGAAAGCCAA	178
CcM0320	FI197327	(AT)6	GTGATGGCCTCTTCATGCTT	TTTGTGATTGACCGGCATTA	273

CcM0321	FI197373	(TA)10	CGTTCAGAATTTGGTTTCCG	GGACCGTTCCAGATGCATAG	115
CcM0322	FI197418	(AT)21	AAAGACCACGATATGGGCAA	GAGTTGAAACTTTTATTTTCATCGAAT	276
CcM0323	FI197436	(AAT)8	CCCTTACCTGGATGAGTGGA	TATGGAAGGGGAAGGAAGGT	258
CcM0324	FI197444	(AT)5n(TTAT)5	AAATGAGTTTGATTGAATTTTTAAAGG	GCCCGTTCCAGATATACGAA	216
CcM0325	FI197528	(AG)5n(AG)5	TGGCGACCTTTCACACTACA	TTCACCCACAACGGAATAGC	269
CcM0326	FI197607	(TA)11	GTTCCCGGCTACCAAATGTA	TTTTGATTTTTCCAATCAACG	265
CcM0327	FI197614	(TA)12	TTGCCTTTTGCTTGTCCAAT	AAAACACACACCGACACACA	113
CcM0328	FI197632	(AC)5n(TA)14(CA)5	ATGAACTTTCAATCTAACGGTTG	TTTCTGCGTTTTGGGATTTT	264
CcM0329	FI197729	(GA)6	GCTTTGTGGCAACCTTTCAC	ACGATCGGATCCAGAATGAG	207
CcM0330	FI197758	(AT)27	CGTAGCCGGATCTTCTTCAC	TGGTGTGGATTATGATGGATTG	261
CcM0331	FI197782	(TA)21	ATGGCTTAGGCTCCCTCAAT	TCACCGTTACTTTCATCAAAACAT	212
CcM0332	FI197799	(CA)6	TGGTAAACCAAACCTGGGTA	TGAAACACATAGAAGGCAGGG	145
CcM0333	FI197853	(AT)22	CTTCACGAGACGGGAAAGTC	TGGGGGACAGATATAAACATGA	230
CcM0334	FI197879	(TC)8	TGTCCGGATTTGACACTTTG	ACACACTCCAGCGTGGTTTT	141
CcM0335	FI197912	(TTA)11	GACTTTGTTGTGGGTTTGCC	CGTTCAAAATAATTGTCCGAAA	271
CcM0336	FI197923	(A)10n(A)14(TA)11	GAGCATATGCGTGTTGCATT	TCCTAGGAGATGCATGATATTTATTTT	274
CcM0337	FI197970	(AAAT)6n(T)10	GATTTGCATAAGCCCAAGGA	GGTACAATAGCCCTCTAAACTGC	271
CcM0338	FI197972	(TA)9	ACAGTTGTTCTAGGTTCAATGTCA	TTGGGCCGTTTACCAGTATC	223
CcM0339	FI197976	(AT)6	CGGTTTCTTGAGAACCGATG	ACTTTTGTGGTGGCCAAGTT	217
CcM0340	FI197995	(TA)24	CCACTTTTATCTTTCCGATTCC	CATGATCAAAATCAAAACTCAATCA	256
CcM0341	FI197997	(CAT)5	AGGCTCTCCAACCCTTGAAT	GTGCAATGAGTGGTTTGTGG	135
CcM0342	FI197997	(CG)6(CA)6	TGCATTAGTTGTTAGATTAACGGG	ATTAAATCTGCCAAGTCCGC	195
CcM0343	FI198055	(AT)11	TGGCTCAACCACAACTTTGA	GGCACTTCGTGCCTCTAATA	268
CcM0344	FI198116	(AT)17	TGGCATGGTGTGAGATGAGT	AGCACATACAAACACACCACAA	263
CcM0345	FI198126	(AT)10n(TA)7	CAGGCATGCAAGCTTCTTTA	AATATATTCATTGGAACAAGAACCA	203
CcM0346	FI198175	(CAA)5	CCAACCAACAGCAACAACAC	GAGCGAGAACGACTTCTTGG	246
CcM0347	FI198208	(AT)12	TCTTTCCTTCGGTTCTTCCA	AGAATCAATCCAAAGCAAGCA	221
CcM0348	FI198224	(TA)6	TTACCCTCATTGGGCTTTTG	AAAATGTGAAAATCAAAGGGATG	272
CcM0349	FI198323	(GAC)6	CGCCAATTATATGCCATCGT	GATCCGAAGATTGCGTGAGT	163
CcM0350	FI198399	(AT)7	TCCCTGACACGAGTTTTGGT	TTGTTGGGGTTTAGTCCTGC	186
CcM0351	FI198406	(CAT)6	ACGAGCGATACCACTCAACC	AATCGGCCGTGAGTTATGAG	241
CcM0352	FI198421	(TTA)5	TGTTCGCAACAAGAGGAGTG	TCCTTGAGAAATTTGGCACC	192
CcM0353	FI198466	(AT)14	GATTCGCAAGTTGCTCCTTC	TTGTGATCACTTATCATCATTTTGG	189
CcM0354	FI198476	(GT)11	TCGCCAACTTCACTTGTCAG	TGTTGAGACTATCCTATTCTCTCTGTG	249
CcM0355	FI198527	(AT)13	ACATGAAATCGTGTTTTGTCC	TGATGAGTATCATCGATTTCCA	272
CcM0356	FI198531	(CAT)6	GCGATACCACCCAACCACTA	CAATCGGCCGTGAGTTATGT	276

CcM0357	FI198564	(TTA)5	TGGTTGGTCTAAATGCAGAAAA	TGATTGATGAGAAACTAAAACTCCA	209
CcM0358	FI198588	(TGA)7	TCATCCCCAACAATACCTGG	CATGCATCAAAATCCCAACA	274
CcM0359	FI198614	(AAG)7	CTCCAACGGGAAAATTTGAA	CAAGAAATGCTTTGAGAAGAAATG	170
CcM0360	FI198633	(AT)11	AAGATCTTGAGTTTGATTCTTGGA	TGGTCAATGTGAATTACCCG	169
CcM0361	FI198648	(TA)9	TCTTCCTGTCCTCATCCTCG	TGGAAACCAAAGTTGTGCAT	172
CcM0362	FI198657	(GA)6	TGTCCAACTCAACCCATTCA	TACCCGAGATCATGAGGACC	219
CcM0363	FI198683	(AAAAT)5	CCTTCAAAGAAAACACCCTCC	GCATACCAAGGTGTCTGTTTCA	222
CcM0364	FI198710	(AAT)5	TTGAAAGAAAATAAAGGGAGGA	TGGACATTAGTTTTGCGTGG	126
CcM0365	FI198723	(AG)8	TGTGCATCTCGATGATCTTTTC	GCAGTAAACGAAGGAGGCAG	118
CcM0366	FI198730	(AT)8	CCTATGCTCCACAACAAGAAAA	GCGATAGAAACATATTGCACACA	170
CcM0367	FI198767	(TA)5n(AT)9	AACATTGTGGAAATACCGAGC	ATTCATGCACACACATGCCT	268
CcM0368	FI198790	(GA)6	TCGTGGCAAGCTTTGTTAGA	CCAAAAATTTCGTCCAGGAT	151
CcM0369	FI198827	(AT)8(AC)5	GGGAAGTAAATTTCATATGGCCT	TGGGGAGTAAACCCCAATAG	228
CcM0370	FI198857	(AT)26	TGGTCCAACATCAATAGCAAA	TGATGATGACCGAGGGGT	278
CcM0371	FI198865	(CT)7	CACTCCGCACTCTCCTTCTC	CCAAATCGAAGATTCCCTCA	226
CcM0372	FI198887	(T)12n(AT)38	TCTCTTGCAGAATTATTGGCCT	TGGGGTAGAAATATTTTGAGAGTTT	216
CcM0373	FI198894	(TG)6	ACCAAGCCTTTTCAAGTGGA	TCCCAAAAAGCTTCAAGTGC	235
CcM0374	FI198903	(TA)11	GAACCGTCTTAAAATTTCTCATTT	CAATGGCACATTGTCAAAAA	161
CcM0375	FI198912	(TA)23	GTCAAGAGGGATCGATGCAA	TGATGCATTTTTATAGTGCGTT	280
CcM0376	FI198943	(TA)n(A)11	ATGGCTCATCCCATTAGCAC	TTTGCGAGCTGATGTTTCAA	208
CcM0377	FI198979	(CA)6	CCTTCAGCTAGGAAATCCGAC	GGGAGGTGGACTACAAGGAA	260
CcM0378	FI198997	(TG)6	GCTTGTAAACGTGATTGGGC	AGAGTCCCTCTGCGAAAACA	188
CcM0379	FI198999	(CA)6	TGTCACTTGGACTTCCACCC	ACCAAGCCTTTTCAAGTGGA	215
CcM0380	FI199160	(CA)6	GCTTCCTTGCCTACTAGGGG	ACCAAGCCTTTTCAAGTGGA	123
CcM0381	FI199172	(TA)21	CGATCCCTGCTTGAAATCAT	GGTTCAAGCGATGCACTACA	267
CcM0382	FI199187	(TC)10	TCTGACAATGAAACAACGCC	TTCAGTCACAAACACACATAAAGC	173
CcM0383	FI199225	(TA)6	TAGTGTGTGCCTGGTTTTCG	GAAATCATTAAGTGTACAAATTGGC	225
CcM0384	FI199243	(AT)13	CCTGTCAAACATGGTTAATTATAACG	TTTGCACACGTACGTCCACT	277
CcM0385	FI199264	(ATC)5	GACTATAGAATACTCAAGCTTGTGAGG	ACAGGAACGAATTCACCTGG	104
CcM0386	FI199277	(TAA)5	CGAGCAAATCAAATTAAAGGG	CATTGTGTCTTGTTCGTCTTTCT	210
CcM0387	FI199298	(AT)11n(TA)10	GGTTAAGCCTCCGACAACAA	TGGTGAGTTGTCCCTAATTTCA	258
CcM0388	FI199302	(AT)8(AC)5	TGCATATAACGCCAATTCAAA	CCTATTCGAGCATTTCCCAA	279
CcM0389	FI199318	(CAT)6	TGTCTTTCGGCCAAATTCTAA	GATCCAATCAGCCGTGAGTT	241
CcM0390	FI199319	(TA)23	CGATTGGATTAACAAAATTCACA	CACCACTGTAATTATAACCCCCTT	162
CcM0391	FI199344	(A)11n(AT)5	GGTTTAAAAAGTGAAATTTACGGA	AAATCTTTTGTTGCGGGTTG	212
CcM0392	FI199348	(AT)7	TGCTCCCTAATTTGAGACATTG	CAACATGAATCCATCATCATCA	143

CcM0393	FI199365	(AT)6	GTAGCCATGGTTTTGGGAAA	TTCATTTGTTCGTGCGTTGT	245
CcM0394	FI199377	(AAT)5(AT)5	TGGTTGAACACAACAGAAACAA	CATGGATTCCCTTTTGAAACA	251
CcM0395	FI199379	(CAT)5	CGACATCACTCATCCGCTAC	AATCGGCCGTGAGTTATGTACT	280
CcM0396	FI199408	(AT)7	TAGAGTCGACCTGCAGGCAT	CATTCGGATTTGAAAATGAAA	106
CcM0397	FI199413	(AT)5n(TA)10	TCATCTTGAATGTGTGCCAAA	CAATGATGTTTCACAAAATCACC	228
CcM0398	FI199483	(GAA)5	AGGCATGCAAGCTTCTTAGG	TCTCTCAAACCCACAAACCC	117
CcM0399	FI199533	(TA)16	AATTATAAACGGTTGAATTGAAAAA	TCGGCCTAGTCAGTCACCAT	247
CcM0400	FI199595	(AT)6	CCGTTGTCCAATTCTCATCA	TTTTATTGCACAATGGAAATTGA	244
CcM0401	FI199630	(AT)8	TTCATGGTCCAAAGATTAAAATGA	TTGTCAACTTGAGTTAAACCAAAC	228
CcM0402	FI199652	(TGA)6n(AG)5	CAGCATTTGAAGGAGAAGCC	GCAGATCCCTAACTCCTCCC	179
CcM0403	FI199658	(ATA)5	CACCATCGTTATTATCATCGTCA	CAATGAAAAACTACCCTATCGTGA	249
CcM0404	FI199672	(TA)11	GGGTGATGATTAACTCCTTTCA	TGTCAGTTGAACCCTCCTCA	271
CcM0405	FI199681	(TG)5n(AG)6	CTTCAGGGGTCACATAAGCC	GATGCCAAGCGTCCTAAGAG	270
CcM0406	FI199691	(CT)5(AT)5n(AT)12	TTGTCCATTGCACACACTAAAA	TTTTTAGGTTCTTTTAAAAATTTGCAG	262
CcM0407	FI199691	(TA)7(TG)14	TCAAGTGGTTGGGCCTTTAG	AAAGAAAATTCAAATAAATGGATACC	190
CcM0408	FI199796	(TA)8	AAGGGATGCAATCATGCAAT	TCACATTAATTTAGATGCAGATCCA	172
CcM0409	FI199804	(TTA)8	ATAGGATGTGACATTGGGGC	GAAAGGTCCACATAGGTTCACAA	235
CcM0410	FI199822	(AT)30	CACAGTGGCTCATACTGCAAA	TGAAAACCAAAAATATCAAAATAAGC	254
CcM0411	FI199828	(AT)21	TCCCTGCGTATGATTTCCTC	TGTGCTAATGAGCAGGTTGG	210
CcM0412	FI199866	(CA)7	CACAAAAATGACAAGGGAGTGA	TCGGGACACCAGTGATGTAA	267
CcM0413	FI199875	(T)10(CT)6	ATGCACTAAGCTTTGCCGTT	GGTTGAGCCTTCTTGTTGGA	256
CcM0414	FI199883	(TA)7	ATGGGACCAAGAAGCTTTCA	ATGCACCTGGGATCAAACTC	177
CcM0415	FI199973	(ATC)5	CCAAGAGAAAAACGTTTGTGAA	AATGGAACGAATTCACCTGG	111
CcM0416	FI200027	(AT)7	AAATTTAAAAATACTCATGTCGAAGAA	CCGTGAGTGTTAATGGACTAATATG	139
CcM0417	FI200049	(TA)22	CCCAAAAGTGGGATAGCAGA	TGACCTTAAACATTTTGTTTTCTTAAT	222
CcM0418	FI200079	(GA)6	GCTTTGTGGCAACCTTTCAC	GAACAGGTCGTTCCAGGGTA	245
CcM0419	FI200102	(GA)34	TTCTACGTTTTCAACATATCCAACA	GCTTGTACTTATCTCAGTGAATAGATG	280
CcM0420	FI200129	(ATT)8	CCACAGCAACAGCCAGATAA	AAGCATGAATTAGGCTTGGC	176
CcM0421	FI200154	(TG)6	GGGTTGCGACACACATTAGA	TGATGAAACTTCCAGACGCA	264
CcM0422	FI200158	(TTA)10	ATAGGATGTGACATTGGGGC	AACATCAAGAAGGGTCCACA	268
CcM0423	FI200162	(GA)8	CACACTACACAAATGCCTCACA	ACGATCATATCCAGAACGGC	205
CcM0424	FI200191	(GAA)5	CAATCGACTCTTGAGCATGG	GGACTTCCTCCTTTGTGCCT	133
CcM0425	FI200211	(A)15(AT)8	TCGATGTTACAATAAAGACCAGATG	TCCTCGTTTTTCACTTCCCA	189
CcM0426	FI200223	(CT)9	CTGGGACAAAGGCAGAATGT	CTATTGGTTGATGGGATGGG	252
CcM0427	FI200229	(TC)6	ATAGACAGCTCGGGCACAGT	TGGGGACTTTTAGGTGCTTTT	156
CcM0428	FI200285	(AT)8	TTAAATGGGTTTGATTGAATTTTT	CTTGTTCCCAAAGTGGAACG	244

CcM0429	FI200296	(AT)8(AG)7	TTACTTAGAGTAATGTGATCCCTCC	TGCCCTCTCATTGTCCATTT	196
CcM0430	FI200343	(TA)7	TCCCTAGCACAAAGAAAATCCT	GGGTTTAGGGTTTATAACCTTGTG	252
CcM0431	FI200348	(CATA)5(AT)9	CCATAATCCAATCCAAATCCA	TCACTGTAACGCCATCGAAA	126
CcM0432	FI200351	(CA)6	GGACTTCCACCTTACGACCA	TGCACTATCAAGGGAGGTGA	248
CcM0433	FI200365	(AT)11	TTGAAAGGAACTTTGGGTGG	AAACCCTGAATTCACATTTTTG	253
CcM0434	FI200389	(ATT)8	TAGAGTCGACCTGCAGGCAT	TTTAACGAGGCATACCCGAG	233
CcM0435	FI200416	(TTC)5	TGCATGCTTTTACTTTTGCG	CTGCCACACAAGCCTATGAA	141
CcM0436	FI200434	(TGA)5	AAGCACCTCTTGCAGAAACC	TGGAGTGTTTTCTTTGTGAAACC	241
CcM0437	FI200496	(TG)5n(TA)21	GGCATGCAAGCTTAGTCCAT	TCGGAGAATCAATTATGCAATC	260
CcM0438	FI200497	(ACA)5	TAGAGTCGACCTGCAGGCAT	ATCGATTTGCTCATGCACAC	234
CcM0439	FI200538	(AAT)5	GAAATTGGGAAAGAATACATTTACTG	TTTGGGGTATTTTTAAGATGTGC	238
CcM0440	FI200573	(TTC)5	TTCCACCCGAAGCATTTTTA	GCAACCCATCCAACTCAACT	185
CcM0441	FI200590	(T)10n(AT)28	TCTTATTTTTACTTTGATTTTCATGTG	TGATGTCGTAATGGATATATTAAAAAG	161
CcM0442	FI200617	(ACA)5	GTTCCAACGATGATGCCTCT	CACGGATGCTATTGTTGCTG	199
CcM0443	FI200654	(TA)17n(AT)5	TGACAAAATAATGCGGTCACA	CAAGCCAAAGTTTGTTTGAACT	261
CcM0444	FI200657	(TA)7	TGTCATGAGTGGCTGATCCT	TCAACCAAAATCCAAACCAA	184
CcM0445	FI200672	(TC)5n(CT)5	AAAGAGACAAAGGAAAGTAGGGAA	TATGGAAGGGGAGAGAGAGG	231
CcM0446	FI200675	(AAT)7	CTCATAACTCACGGCCGATT	TTCTGGATCCTTTCATTTTCTTT	255
CcM0447	FI200689	(TC)7	TTGGTGAGTGTCTCTGCTGC	CCTGAAGTAGCCAGTGGTCC	271
CcM0448	FI200708	(GA)6	AAAACTGCATTTATTTTGGGG	GTTGCAAGGAAGGAACGAAG	245
CcM0449	FI200744	(AT)24n(A)10	CGCCTAAATCCAAGGCTACA	CACAATCTCCTTGTTTGGCTT	261
CcM0450	FI200748	(AT)7	GCCAAGGTTGAGCTGAAAAG	GGTCGATTCATGTTTGGAGG	156
CcM0451	FI200787	(CAT)6	ACGAGCGATACCACTCAACC	AATCGGCCGTGAGTTATGAG	255
CcM0452	FI200803	(CA)6	CCACTTGGACTTCCACCCTA	ACCAAGCCTTTTCAAGTGGA	213
CcM0453	FI200828	(GAA)5	CATGGAGGCTCGGTTTCTT	CCATGGTTAGCCTAGCTTGC	235
CcM0454	FI200911	(TC)13	TTTGGCTGTGTGTGGAAAAG	GATTAGGCATCAGGAAAAGCA	214
CcM0455	FI200922	(TTA)9	TAGAGTCGACCTGCAGGCAT	CGTACAAAATAATTGTCCAAAACAA	206
CcM0456	FI200923	(AGT)5	TCAGCCTGATGTACTTTGCG	AGGCCACTAGTCATAAAGAGCA	230
CcM0457	FI200932	(TTA)5	GGCATGCAAGCTTCTTGTAA	TCCATTTACTGTGGCAGTGG	266
CcM0458	FI200938	(AATA)5	TGACGAATTTGGCAAAATGATA	CAAAAGGCTTACTTCAGAGGTTC	267
CcM0459	FI201000	(TA)20	TGCTATAACTTTTACTATCAAACTCCA	TTTCAATCAAACGTGATAAAAGTCTC	248
CcM0460	FI201029	(TG)7	TACCCGACACCGGCTTATAG	CGTCGAACACTAATCGCAAA	179
CcM0461	FI201160	(TA)8	GGTCAATCTTTACCTCAAGTCAAAC	CAAGAACTTTAACCTTAGCATTTTACA	268
CcM0462	FI201166	(AC)5n(T)10	CGTGCAAATCCTACCCATCT	TGCACTTCTCACCACCAAAC	161
CcM0463	FI201340	(GA)7	GGCAACCTTTCACACTACACAA	TAGACAGCTGGGGCTCATTT	143
CcM0464	FI201400	(AT)6	CCCGCTAATACCATTTCCCT	TTGCAATGGGGTATTTTTGA	263

CcM0465	FI201424	(AT)6	CCAAGGGAAAGATTCAACCA	TCCAGAGAAGATTTGCTTCACA	199
CcM0466	FI201555	(TC)6	AAGGGCTTGAGTCGTTCAGA	TCGTCAGAATCACCACCAAA	197
CcM0467	FI201578	(AT)8	TCGCAAAACCATGTTACTGAA	AACTCTACCGACAACTTCATGC	189
CcM0468	FI201580	(TAT)5	ATAAAAATATCCGCAACCGC	CGAAAGCAATGTCAAAGCAA	183
CcM0469	FI201583	(AT)11	TTTGCTTAAATTTGATAAGGCTATAA	CATAAAAACCAATTGATATGAAAAGAA	140
CcM0470	FI201627	(GA)7	TGCTTTATGGCAACCTTTCA	AACGGCCATATCCAGAACAG	224
CcM0471	FI201643	(AT)12	AAAATTTTTATCCACCCACTAAAA	TTTATGGCATTAATTGATTACACTTT	273
CcM0472	FI201676	(TG)6	AATCGATTACTGAAGTTAGCAAAAA	TCAAAAGTGCAGTGGACGAA	126
CcM0473	FI201688	(A)10n(A)10(AAT)6	GGGTGCTTTTAGGGAATGCT	AAAGAGGAGCAATGGGGAAT	261
CcM0474	FI201756	(CAT)5n(AC)5	AAGTACATCAACAACAACACAAAGAA	CCCCTATGTATGGTGGGGTA	200
CcM0475	FI201757	(TA)7	TTCTAAAATGAGAAGAAAATGGAGAAA	TGATCGAATAGAAAAGTGGAAAGA	180
CcM0476	FI201805	(AT)8	TGGCTTCTTGTTGTTGCTTG	AAAAATATGAGAGAGATCTCAACTGG	237
CcM0477	FI201839	(TA)23(T)16	AGCAATTTGAACCGACGAaT	CGACAATCAGCTAGCTCTTCAA	233
CcM0478	FI201848	(GA)6	TAGAGTCGACCTGCAGGCAT	GGAGTTTCGAGTTGAGGCAC	273
CcM0479	FI201854	(AT)16	AAATCAGTATATTTGATACTGGGAAAA	AGGGTTTAGGATTTATGTCTTCATT	239
CcM0480	FI201859	(GC)5n(AC)8(AT)6	TCCAACGACCACAAGCATTA	GTTGTTTAGCCCATTGGTGG	263
CcM0481	FI201912	(AT)42	CTCGCAAATTAGTCCTCCCA	TTTTTGGGGTTGTGAAGCAT	245
CcM0482	FI201925	(GA)7	TGGGGATTTTAGGTGCTTTG	CCGTTCTAGGGTGCAAATGT	260
CcM0483	FI201955	(AG)6	AGAGTTTAGGGGGAGGAGGG	CCCTATCTCGTCTCCTCTCG	272
CcM0484	FI201979	(T)12n(ATT)5n(AT)5	TGGAAATTAAACACCATGAAACA	TGCATGCTACCAAGGAATTG	248
CcM0485	FI201986	(TCA)5	TCCAACAATTTTGTAGTGCTGC	AGACGGTCTGAAACCGGAC	229
CcM0486	FI202042	(TA)25	CTTGAATTGCCCATAGGCTC	CAAATCCAACCTCAATTTCACA	280
CcM0487	FI202048	(AT)10	CAAATCAATCCAACCCGTCT	AGAATTCAAACCATTTGCACC	252
CcM0488	FI202075	(CAT)5	TTGCAACACAAGCGATATCAT	CAATCGGCCGTGAGTTATGT	278
CcM0489	FI202113	(TAA)11	AGGACTTTATGGCTGTTGGG	GGGAAAGAGAAGGAAAAGGG	186
CcM0490	FI202132	(AAC)7	CCCCGACTGAGATGGTTCTA	TGGCACGACATTGTGTTTTT	259
CcM0491	FI202143	(TC)7	GTGGTGGGGGATAGAGTGAA	GGTTGGGGCACTATCTTTGA	262
CcM0492	FI202198	(AT)21	AAAATTTACGAGCACTAAAATGAAAAA	TCAACAATAAATTGTCATATGTCTGG	271
CcM0493	FI202244	(A)11n(AAAT)5	ATCCTGCTCCCTCAAAGACA	AAGGTGCCCAAGTTGGTTTA	232
CcM0494	FI202253	(AT)21	ACGTGAAAAATCCGCAACTT	GCTTGTGTTTCAAAATCCAACTT	117
CcM0495	FI202266	(TA)7	TCACCTCTTGGATTCCTTGG	TAAAAGTGTAACGACCCGCC	250
CcM0496	FI202271	(TTA)5	CAAGCTTGAGGAATTAGAAATTGA	GGGGTCCAGTCAGCATTTTA	240
CcM0497	FI202277	(TA)7	TTCCATCATTCATTGTCTCTTCA	AATTCAATTCCCCGGTCTG	238
CcM0498	FI202283	(AT)7n(AT)9	GGCTCAACCCCTTACAACAA	ATTTACAAAATTGCCACCGC	276
CcM0499	FI202347	(TTA)7	ATAGGATGTGACATTGGGGC	AACATCAAGAAGGGTCCACA	258
CcM0500	FI202371	(ATA)14	GGTTAGACCCAACCCAACCT	CAATGCTATCAACTTGAAACACAA	229

CcM0501	FI202401	(GT)6	GAGGTGAGCTACAAGGAGCC	GTGAAAGTGTCCCAAAAGGC	268
CcM0502	FI202411	(TAA)19	CATCCTGCAAGACACGTGAA	TTGTCACGACTTGCACCTTT	240
CcM0503	FI202448	(AT)5n(TA)8	TAGAGTCGACCTGCAGGCAT	AATTGAATGAATGGCCAAGA	218
CcM0504	FI202475	(TC)6n(TTC)5	CCACAAGCTTCCCTCCACTA	CCAAGAGTTTGAGGAAGCAAC	234
CcM0505	FI202509	(ATT)5n(T)10	ACCAAGGAGGATTCCAATGA	GGATTTTGTGGGATTTTATGGA	206
CcM0506	FI202538	(TA)19	AATCTTGCACCAGAGAGCGT	TTTTAAATTGCTGAACTTCTTGGA	276
CcM0507	FI202566	(CA)6	CCACCCTAGGACCCTACGAC	ACCAAGCCTTTTCAAGTGGA	202
CcM0508	FI202590	(TA)19	TTCTCGGCTTTTACTTGCTCA	CAAAAGGCAAGTATCTTCTCTGG	124
CcM0509	FI202692	(ATA)5n(A)12	ATCGTTCGTGGGTGTACGTT	CGCAATGATGCATGGTAAAG	252
CcM0510	FI202723	(TTC)5	CTTCCTTTGTGCCTTGGTTC	GCAACCATGGCTCTGATACC	218
CcM0511	FI202793	(GA)6	TGCTACAGATGCATCAGGAAAT	TTCTTTGTGCTGTTAGTGAAAACA	276
CcM0512	FI202800	(AT)7	GCAGTCCGCAATTTAAAACC	GAAAATTTGCATATTCAAGTCATTAAA	258
CcM0513	FI202801	(AT)15	TTCTTCTCGGCTTTTCCTTG	GAAAAATTTGAAATCAAAAGGCA	130
CcM0514	FI202869	(TCT)7	CCATGGTTAGCCTAGCTTGC	CAACTCCAAGTGGTTCGGTT	248
CcM0515	FI202879	(TG)7	TCAATGGACTCAAACACGACA	TCGGTGATATCTGACCCCAC	260
CcM0516	FI202883	(TC)14	ATTGATGGTGTTGTGGCAGA	TTCGTGACACTCACTGGTCC	191
CcM0517	FI202884	(ATC)5	ATCCTCATCCTCATCCCCAT	GGAGCCCGTTATGAGTGCTA	202
CcM0518	FI202915	(AT)11	CACCATCATTTGGGTTTGTG	CAACCCTCATTGGAGATGCT	280
CcM0519	FI202926	(TA)7	ACACAAACACAGGCCCATTC	TTTGGAACCATACTATTGCCA	166
CcM0520	FI202954	(AT)17	GGAGGCAAAGATCTTCATCG	AGCTGCACGAGATTCAGTAGG	224
CcM0521	FI202970	(TAC)5	AAGATTGTGCACCAAGAGGG	TCTTCACTGAAATCCACCCC	139
CcM0522	FI202974	(TA)17	TTGTCTGTGGGTTCATGTGAG	AGAGGCACTCACAAATTCTCAA	190
CcM0523	FI202991	(TG)6	ACCAAGCCTTTTCAAGTGGA	GCTTCCTTGCCTACTAGGGG	122
CcM0524	FI203026	(GA)7	GCCTCACAAAACTCAAAAATACAA	TAGAAATCTCGGCCAGCAGT	119
CcM0525	FI203029	(AT)11	AAATGAGTTTGATTGAATTTTTAAAGG	GGGGCTATGACAATCCAAAA	219
CcM0526	FI203060	(AAT)7	AACATCAAGAAGGGTCGACAT	ATAGGATGTGACATTGGGGC	259
CcM0527	FI203115	(ATAA)5	GAAAAAGGGGAGGGTGAGAG	AATGATATAGGATGTGTTTGGCA	272
CcM0528	FI203143	(A)19n(CA)5	AAGGAGGATAGGGAGAGCCA	TGCCTCATGATAAGGTCTTTGA	125
CcM0529	FI203194	(AT)7(AG)5	TGATTTTTCTGTTTTGCCCTG	AAAAATATGATTGTTTGACGGTG	151
CcM0530	FI203211	(TG)6	TTTTGTGCTTGGTTCCACAA	TCTCTGGGCAGACAATGAAA	246
CcM0531	FI203247	(TA)8	GCTCCTTGGAATTCCTTCCT	TGTTGGCAACGAAAGTGAAA	215
CcM0532	FI203268	(AT)13	GCTTTATTTCGCTCCTTAATTTT	TCATGATCATCCTAATTCGTGAG	274
CcM0533	FI203277	(TC)8	GGCCATTCCAGGGTAAGAAT	TGCCTCACAAATCTCAAGAAA	220
CcM0534	FI203287	(AT)6	ATCCCCTCTCGTGCATGTAT	GGGTTTTGCACTGTGTGAGA	271
CcM0535	FI203335	(ATA)12	AGTCTTCTACCAATCCCCTTTATT	AGGACAAATGCGAAACTTGG	241
CcM0536	FI203355	(AAT)5	CCCCCAAAACCAACCTTAAT	CTCTTCAATTATGGCGGGAA	248

CcM0537	FI203404	(CTC)5	TATACTCGAGCTCCGCCAAC	GATCCTGATAACCCTGCCAA	244
CcM0538	FI203412	(AT)14(ATA)13	TGTCAATTTGAATTAATGGAATGAA	TTGGGGTAGTAAGGGTGTCA	275
CcM0539	FI203428	(TTAA)5	TGTACCATCCTGATTTTTCACAA	AAGTTTCCTTTTGCGAGTGC	239
CcM0540	FI203437	(AT)16	TCTTCACTTTGGTGTTATCGTCA	ACTCTTTAAATAATTCAATCCCCA	279
CcM0541	FI203441	(AT)6	TGTCAGGGATCAGACTGCTG	TGGTCAATCACCGAAGTGAA	130
CcM0542	FI203460	(AT)7	CCCAGTGAGCATTCAAAGGT	GGACCTACTGGTGGTAGGCA	264
CcM0543	FI203472	(A)11n(AT)18	CATCGGTTCTAGTGGAAATCG	CCGATGAGAGCATAGGAAAGA	250
CcM0544	FI203518	(ATA)7n(ATA)5	CGTACAAAATAATTGTCCAAAACAA	TGATGAATGTAACACCCCAGTT	164
CcM0545	FI203533	(AT)13	TGGTCATTAAAGTTTTTAAATTGGTTT	AGCAATGACAACAACAGTGGA	239
CcM0546	FI203538	(AT)11	CCAGTTCCGGGACTATGAAA	TGGGTTTGATTGAATTTTTAAAGG	221
CcM0547	FI203600	(AC)18(AT)15(TA)6	CCTTCAACTTAACCCCTTTCAA	CGAGGTTGGAAACTTAGTCCC	258
CcM0548	FI203606	(AC)8n(AC)8n(AC)7n(AC)5	GATGTAATCCCACCAAGGGA	TGGCCAAAGTGTAACGATTC	196
CcM0549	FI203637	(AT)35	CCGGACAATTTTAGGGGTCT	CTCTGTCTCGTGGGCTTGAT	262
CcM0550	FI203639	(GGA)6	TAACCTTTTCGATCATCGCC	GGTCTGAGTTTTGAGGTGCC	246
CcM0551	FI203655	(TC)11	GGCATGCAAGCTTTAAGTCA	AAGAATCAAAATTTAGTTCCAAACAA	235
CcM0552	FI203658	(AT)7	TGTATTTACCATTATGCAGCCA	TTGCATGGATCCTTCATGTC	171
CcM0553	FI203673	(AG)6n(AG)11n(A)11	TTTCTCCAACCTCCACCATC	TTGGAAGCACTCCTAGCTTTG	279
CcM0554	FI203694	(AC)6	TGCATTGGACGAAGAACACT	CCCCTGCATTGTTAGATGCT	155
CcM0555	FI203782	(CT)8	GGCATGCAAGCTTAAGCAAC	ATGCTACTCAAATCCGTGGC	200
CcM0556	FI203822	(AT)18	CGTAGCCAGATCTTCTTCACCT	TGGTGTGGATTATGATGGATTC	243
CcM0557	FI203898	(TTA)6	GCTTGCTGTAACACCCCAAT	AATACGTACAAAATAATTGTCCAAAA	146
CcM0558	FI203953	(TAT)6	CACTCCACTCCATGCAATCA	ATGCCTCGGACACTGAGACT	266
CcM0559	FI204036	(AT)34	TGTTTTTGAAATAGTCGGAGCTT	CCTGTTGGTTTCTCTTCCTCC	234
CcM0560	FI204127	(TA)6	GAAACCATGTGAACCCCATC	GCACCCTCTAGCTGTAACGC	280
CcM0561	FI204141	(TG)6	TGCACTATCAAGGGAGGTGA	CCACTTGGACTTCCACCCTA	254
CcM0562	FI204168	(A)11n(AT)9	GGTATACCGATTGGCAGCAT	TGCGTGTTTTCAAAAGTGAC	239
CcM0563	FI204232	(TAT)5	ATAGGATGTGACATTGGGGC	AACATCAAGAAGGGTCCACA	259
CcM0564	FI204250	(AC)6	TGTTATTTCCACTTCCAGACGA	TCAAACATAAAGCTTGCGTGA	191
CcM0565	FI204259	(ATC)5	TTTGTGGAGTCTTTGTGACCA	AGGAACGAATTCACCTGGAA	157
CcM0566	FI204295	(AT)9	AAAATGACACTTTGTGTCTTCATGT	TTTTTGTGGATAATTTTGTCCCT	208
CcM0567	FI204329	(TA)20	CCCTCGTTGAACCAACTCTC	TCTGCCTTTTAAGGGTCAATG	279
CcM0568	FI204384	(AT)6n(TA)6	CCAATATCTTGGTCATTGAATAGTAGG	AATAGGGGCGGTATTTGTCC	231
CcM0569	FI204391	(TA)9n(AT)11	TAGAGTCGACCTGCAGGCAT	GGTTTTGATCCCTGGTTGTG	159
CcM0570	FI204444	(AT)9	GGGACTAAATTTGCCACACC	GGACCCCAAGAGTTGATCCT	236
CcM0571	FI204461	(TA)7	CCAAAATCATTCCTGACTTTCA	TGGGTTGGGAACGATGTAAT	231
CcM0572	FI204523	(A)11(AT)8	GCTCACAATGAGTTGGAGCA	ATGACTCGGGAGCATCAAAC	274

CcM0573	FI204535	(CA)6	CCACCCTAGGACCCTACGAC	ACCAAGCCTTTTCAAGTGGA	202
CcM0574	FI204586	(AT)16n(TA)21	CACTATCGGAAGAATTGGTTTT	TTTGTTTCCACTTTTTAGTATACCATT	226
CcM0575	FI204593	(TC)6	CCTTTGCCCAAACAGGAGTA	GGAGCGAACAATCACAGACA	264
CcM0576	FI204713	(AAGAAA)5	AGGGCCACTCTTCCCTACCT	CCCCAATATGTCCTCTTCCA	144
CcM0577	FI204832	(TA)8	TAGAGTCGACCTGCAGGCAT	CCCTGTATATCAAACACCCCC	196
CcM0578	FI204862	(AG)6	TACCTTTTCCCCAGTGGTTG	GAGTGGAGAGTAGGGAGGGG	210
CcM0579	FI204875	(GA)6	CGACTCAACCCATTCATCCT	AGCCATAATAGGGCCTCTCC	280
CcM0580	FI204888	(TA)18n(T)10	TGTTTTTGAGATGGACTTTGAA	CCAATAAGCCCCTTGCTTTA	195
CcM0581	FI204919	(TA)24	ATGTTTGACCGGCACTTAGG	AAGATTCTCATGAAAGTAGTTCTTGG	258
CcM0582	FI204926	(TAT)5	TTGGGCTTCCATTAGGACAC	CCACCAAATTATGACCAAATACC	113
CcM0583	FI204939	(TA)21	AGTTGGAAGCGATTGGATAAA	ATCCCTAAAATAGGTCGATTAGATT	245
CcM0584	FI204953	(CTT)5	GAAGTTCCCCATTGTAAGGGT	AGGCCACATTGCTTCTCAAT	170
CcM0585	FI204986	(TTA)5	TCATACCCATCCCCTCATTT	GCTGTACTTTCCTCGTGGCT	157
CcM0586	FI205017	(GA)9	CAGGCATGCAAGCTTTGTTA	TTTTAGAACGGGTTGTTCCG	232
CcM0587	FI205045	(GTGGCA)5	AAGTTCCAATCCGAACCCTT	TTCCTACCCTGGAATTTGGA	221
CcM0588	FI205096	(ATA)19	AAAAACAATTATTGCGTAAGATTATCA	ACGTTAGGAGCAAAGCGTGT	266
CcM0589	FI205168	(TA)7	TAGAGTCGACCTGCAGGCAT	TTTTTCATAGACATATTTCACACAATG	274
CcM0590	FI205203	(ATC)5	TTGTGACCTTCTTGGAGTGTTTT	GGAACGAATTCACCTGGAAA	165
CcM0591	FI205206	(AT)20	TGGCATGCAAATATATCAATCA	CCTCTTGATCTTTCACACATGA	222
CcM0592	FI205217	(GAA)5	GCAAGCTTGTAGGAAGCCAC	GCCAATCATGGTTCTCTTGAA	280
CcM0593	FI205311	(AAT)7	AACATCAAGAAGGGTCCACA	AAAGGGAAAGGGTTCTGCTC	280
CcM0594	FI205393	(GA)9n(TC)9	GGCTTGGTTCTTTCTTGGTG	AAGTCCCTGACTTTCCCCAT	185
CcM0595	FI205395	(AT)10	TGAGGGAATTGAATTAGGAACAA	TGAATGCTATCGTGTTGTGAATC	227
CcM0596	FI205423	(A)13n(TA)6	GAAGTCATTGAATACAACATGCAA	TTGGGTGTTTAGGGATTGAGA	235
CcM0597	FI205454	(AT)9n(TA)6	TCGTCTCATGCGAGAATTAGG	CCCCAAATTGGTCAATCAAC	235
CcM0598	FI205472	(ATT)11	TGACAAATGAAGAATGAGAAGTTGA	TGCAATTTCAGTAATGGGTGTC	123
CcM0599	FI205498	(GA)7	AGCAATAAGGGAGGTTCGGT	GCCTAGCTTGCTCCATAAGC	231
CcM0600	FI205512	(AT)5n(T)10	ATGACGTGTGCATTTCGGTA	CCCTAAGCAAACCAAACCAA	269
CcM0601	FI205517	(TG)8	AGGAAGAAGCTCGTGAAGCA	AGACGGAAACCACACTCGTT	279
CcM0602	FI205600	(AT)14	TTTGCTCTATAACAAGGGATTCA	TGCTCTAATTCATGTCAAAACCC	216
CcM0603	FI205603	(A)21(AG)9	TGAGAGAGGATGTGTGGTGC	GTTGCACACACTGGCAAATC	232
CcM0604	FI205661	(TTAT)5	CATGTTTTACTGCAACTTTTATCATT	TGCATAACACATTGGTTGGG	280
CcM0605	FI205667	(TTA)5	CACCCCAGTTTTCAAAAAGGT	AATACGTACAAAATAATTGTCCAAAA	138
CcM0606	FI205697	(GT)6	TGTTGTTTTTGGACTGAACCA	AAACCCATAACCATGGAGCA	273
CcM0607	FI205709	(AT)17(AG)12	ATGCTCTACCTTGAGGGGGT	CGAGTTATTAAGTGGAGTAAATCTTGG	208
CcM0608	FI205717	(CA)6	ATTGCCTATTAGGGGTTCCG	ACCAAGCCTTTTCAAGTGGA	118

CcM0609	FI205740	(TA)7	GAAACCGCCATAAACCTTCA	TGCCTATCATGGCCTTCTTT	213
CcM0610	FI205765	(TTC)6n(T)12	AGAACAACCCAGAATGGCTC	GGAAAATTTTGGAAAAAGGCA	260
CcM0611	FI205771	(TA)15	AAGTGATGTCCAAATACATGATGG	GACCCCATCACACTTTCCC	259
CcM0612	FI205844	(CT)7	GCATGCAAGCTTGAAGAGAA	CAGCAGCTTCCATAACCCAT	185
CcM0613	FI205881	(TA)9	TCTCGCAATTCACAATCACA	ACGACTCCCCCAAACTTTTC	227
CcM0614	FI205907	(TTG)5	TTGCATGAATTGGTTCAAGG	TGGGTCAACAACAACCAAGA	218
CcM0615	FI205942	(AATT)5	GCTCCATTGGTCTCCAACAT	AATCATGGCATGGGGTAAAA	213
CcM0616	FI205951	(AT)13(T)12	TAGAGTCGACCTGCAGGCAT	ACCTTGGAAGGAGTTGCTGA	254
CcM0617	FI205981	(AT)6(T)10	CCAACCTCTCAGCACGGTAT	TTTCCCTTTTCACCCAAAAA	265
CcM0618	FI206052	(TC)6	ACCATTCTGGCCACTTTTTG	GGTGCTTTGTGGCAATCTTT	171
CcM0619	FI206055	(AC)6	TTTCATTCAAAGGCTATTTCCA	TAGGAGGTTGTTGTGATGCG	173
CcM0620	FI206116	(ACA)5	AAATTGAAATCACAGCATCACTG	CATTATGGCTGGTGTGCTTG	159
CcM0621	FI206119	(AT)15	GCATGCAAGCTTTTTCCACT	CTAAAATTTTGTTTTTCAACCGA	140
CcM0622	FI206122	(AC)7(AT)6	TAGAGTCGACCTGCAGGCAT	TGAACTTTCAATTTAATGGTTGGA	166
CcM0623	FI206133	(AT)6	ACCTTTTGATCGGAAGCACT	AATACCCGCGTGGATATGAG	271
CcM0624	FI206208	(TAT)10n(ATT)12n(ATT)10n(TTA)5n(TTA)14	TTGAAAAGACAAATAGTGTGCCTC	ACCTATCTTCCCCTCGCTTT	263
CcM0625	FI206209	(ATG)5	TTTGGATAAGTGGCGAGTGA	CCAAACCGCAACCTAGACTT	238
CcM0626	FI206225	(AC)6	TCGGATTCACCTTCTCTTGC	CAATCATTTTCCTAATTCTTGTGC	180
CcM0627	FI206311	(TC)10	AGCGAAAAGTTGCCCAAAC	ACGCCCTAAATTGGTACCCT	278
CcM0628	FI206427	(ACA)5	TGAACCAAAAATATGGAGTACCA	AATGGCGTCATTTGATCCAC	158
CcM0629	FI206513	(AATA)5	TCTTAAAGGCAATCAATCATATTCAC	CCGAAATGCACCTTCTTGAT	188
CcM0630	FI206514	(AT)5n(T)11	GAGTTCTGTAAAGTGTTTGGAAAGG	GAAACAGATAGGAATTGCTTCTTAAA	273
CcM0631	FI206556	(TC)6n(TC)10	GAATGAAAGGCTGCCAAAAG	CATACTTGATGTCTATATGATGGCA	198
CcM0632	FI206641	(AGA)5	TAGAGTCGACCTGCAGGCAT	TCGTGCTAACTTTGAACCCC	265
CcM0633	FI206705	(AT)19	GGGTGAAAGCATTGATAGCC	TTGAGCGGTGTAATGCTTAAT	238
CcM0634	FI206742	(TC)8	ATCCAGCTCAGCATCCACTT	TTTTCATTGGAGGGCATGTT	236
CcM0635	FI206784	(AT)10	CAGTAGCAGCACCAGTCCAA	GAAGCAAAAATTTTACAAGAACCAA	240
CcM0636	FI206907	(AT)18	TTGGTTTGTGCATGTAAATCG	TTTTCCGTTGCATTGTAAGTTG	272
CcM0637	FI206964	(AT)11	CCATCCACGTGGGTATTCTC	GGAGGCGTGAATCTGAAAAA	160
CcM0638	FI206984	(TA)6	GCGTACCCATAATTCAACCG	GGGTTTGATTGCGAATTATGA	237
CcM0639	FI207002	(AT)16	GCTTGCCATATAGGAGCTTCA	TGAGAACTAATCTCCTTCGAAAA	252
CcM0640	FI207059	(ATTT)5	TTTTTCAACGCAACAAATCG	TTTGGATAGTCATTCATCGTTCA	234
CcM0641	FI207090	(AAG)5	CTTGGAAAGGAGGAGGTTCC	GACTCCCCGTCAGGTCAATA	172
CcM0642	FI207100	(TC)5n(TA)16	AAGTCTTTTCCCCTTACCTTAAGAA	AAAGTTACATCAGTATCATTTGAACCC	277
CcM0643	FI207128	(TTA)7	AAAGGGAAAGGGTTCTGCTC	AACATCAAGAAGGGTCCACA	280
CcM0644	FI207156	(GA)6	CGGTCAGAGCGAGAAATCAC	GAGAAGGGCAAGCCATGATA	256

CcM0645	FI207207	(GA)6	ACACCAGCCAAACTGCTTTT	CAAAAGGGGAGGTTGTCTCA	159
CcM0646	FI207248	(ATT)5	AACATCAATCCGGTTCCAAA	GAGCAGACGAAGATGCACAA	280
CcM0647	FI207274	(AT)21	TCCGGATACAACAATTTATGAGA	TTTTGTTTTTGTTGTTGATATGTGA	130
CcM0648	FI207369	(AAGAAA)5	CAAGGGTGGAGCATCAATTT	TCTTGGTGGGACATTGTGAA	240
CcM0649	FI207461	(TG)6	TTGCATAAGGGTAAGTATATGAAAAA	GGAGCATACATCAAAGATTATTCAAC	279
CcM0650	FI207523	(ATC)5	AGCGTTTTTGTGGAGTCTTTG	CCAAGAAAGCACCCCTTGTA	254
CcM0651	FI207537	(TG)7	AACACGGCAAGTATACCGGA	TCGGTGATATCTGACCCCAT	252
CcM0652	FI207541	(AT)21	CGTCGCTCTATTTTACATCGG	TGCCACTACATTTCGGGTTT	253
CcM0653	FI207637	(TC)6	GGACGGTCAAGTTAAGCCAA	GACAACCATGGAGGTTCGAT	278
CcM0654	FI207725	(GA)6	TGTCCAACTCAACCCATTCA	TACCCGAGATCATGAGGACC	233
CcM0655	FI207731	(GAA)5	AAAATTCGATTTCGTGTCGTG	TCGCATTAAATAACCATGTTGC	146
CcM0656	FI207739	(AT)6	AGAACGTGGCGTAGCTGAAT	AGCCCTACCTAGCACTGAACA	226
CcM0657	FI207756	(TTC)6	ACCTCTTTTGTGGCTTGGTC	TCGTCCAATCTTGCTCTTGA	143
CcM0658	FI207804	(TG)6	GGAGGTAAGCTACAAGGAGCC	CCCAAAAGGCTTCAAGTGTC	253
CcM0659	FI207827	(TG)6	ACCAAGCCTTTTCAAGTGGA	GCTTCCTTGCCTACTAGGGG	122
CcM0660	FI207856	(ATC)5	TGTGTGACGTCTTGGAAAGG	CCAAGAAAGCACCCCTTGTA	240
CcM0661	FI207876	(AAT)9	CGAAATTATGAGAATATTGTTGGG	GGGTGAATCCTTTTGAATGC	245
CcM0662	FI207885	(CA)6	TTTGCCTAATAGGGGTTTCG	ACCAAGCCTTTTCAAGTGGA	118
CcM0663	FI207906	(GA)6	ATCACTGTCCGACTCAACCC	TACCCGAGATCATGAGGACC	236
CcM0664	FI207977	(A)13n(AT)13	CTTACAACACTAGGTTCCCGTG	CGTGTCATTTTGTTCCCGAT	255
CcM0665	FI207981	(GA)6	CCTTGGTTCAACACTTCGGT	GCACTCCTCAATTCATTCCAA	176
CcM0666	FI207996	(TTC)7	TCCAAACCTAGGAGAAAGCC	TCACGTCCAGTCTTCTCTGG	187
CcM0667	FI208037	(AC)7	CACTTTGTGCCTGCTTGTGT	TTTTGATAATGCCAAAGGGG	135
CcM0668	FI208061	(TA)28	TTCTTCTCGGCTTTTCTTGC	CCGGTTCTTGCTTCTTTGAG	179
CcM0669	FI208083	(TTC)6	ATTTTGCATGCCTGAGAGGT	CAGATTGCACCATTTGATCCT	123
CcM0670	FI208134	(TTA)9	TTCTGGATCCCTTTCATTTTTC	CTGTGACACCCTTCTACCCC	217
CcM0671	FI208169	(ATC)5	TGACCTTCTTGGAGCGTTTT	TGACCCCAAGAAATCACCTC	259
CcM0672	FI208208	(AT)12	ATCCACACCTCCAAATCCAA	CTCTGTAACGCCACGGAAAT	132
CcM0673	FI208212	(AT)6(AG)9	TGACCACCAACCATTACCAA	CATGCACCAGACCAGAATCA	272
CcM0674	FI208238	(AAAT)5	GGTGGAATTTGGAGGATGTG	TCCTGCATTAACTAGGGGACA	269
CcM0675	FI208256	(TAT)5	CAAGTGTAATGACGTGTCGGA	AAAAACGTGTAATTGATTTGCTATT	265
CcM0676	FI208260	(TA)19	TTCTGACTTTCCCAATGCCT	TAACTTGATCCGGTGCTTCC	180
CcM0677	FI208286	(AT)7	TATTGCAGTTTTTCCCCTGC	GCAGAGCAAGATGGTGTTCA	110
CcM0678	FI208312	(GAA)6	GCAAGCTTCCCTAACCTGAA	TGAGGAGGCGAGGTTTTAGA	258
CcM0679	FI208320	(TA)17	CACCTTACAACATTCGCCCT	AAGACATCTCTCCTATTGAGCCC	252
CcM0680	FI208353	(TC)9	AGTGCTCACTTCCACTCGGT	CCAATTCAAAAAGCAACATCA	109

CcM0681	FI208359	(TAT)5	AGGTTTGACAATGGCAGAGG	AATCGGTTAGTGGCAACAGG	166
CcM0682	FI208401	(AT)7	AGTAAGGAAGGGGGCGTAAA	TGTGCTTGACTGGCACTAGG	222
CcM0683	FI208427	(GA)7	CCTTTCACACTACAATAAGTCTCACAA	TCCAAAATTTCGTCCAAAGC	109
CcM0684	FI208563	(GAT)6	GTGCCTCTTGTTTCTGAGCC	TCATCATCCTCGGTTCTGTG	129
CcM0685	FI208588	(TA)16	GTTCAGTGGCGGATCTTCAT	GCCAGATTATTTTAGGGTGCC	253
CcM0686	FI208610	(AC)9	ATTAGTTTGGTGTTCGGGCA	TGCATAGTCTCTCCCCAAATG	201
CcM0687	FI208616	(TTA)6	GCATGATATTGCTTGGTTTGG	CGTGACTGTTCGTGGATGAG	276
CcM0688	FI208624	(TAT)6	GCAGAAGGCGTGTTTCATCT	TCAACTCCTGAATTATCCCTTAAAA	235
CcM0689	FI208659	(TG)6	ACCAAGCCTTTTCAAGTGGA	TCGTTAGAAGGCTCCTTTGC	132
CcM0690	FI208686	(AG)9	TGAAAACCATCTGGCAACAA	ACGTGTTTCTGGGGTGTCTC	250
CcM0691	FI208695	(AT)24	ACGACCCAGCTGGTCACTAC	GCAGCTCGCAGATGAAGTTT	238
CcM0692	FI208701	(AC)5n(A)10	GCTTCATTTGCCTACTAGGGG	CAAAAGGTTTTCAGGATGCAA	213
CcM0693	FI208712	(A)18(AAAC)5	TTTCCATTTTCATTTCCTGACA	TGATGTTGCTTGGAATATAAGGG	233
CcM0694	FI208714	(A)12(TA)10	CTCAGGGACGAAATTGGTGT	CACCGAAATTACTGTTCACATTTT	275
CcM0695	FI208731	(AT)29	GGGGACTCCTGATGTTAAAAA	ACACAATTGCTATGTGGGTAAA	276
CcM0696	FI208740	(TA)8	AGGTGGAATATCTTTTGGTTGGT	TCCAATAAATACAATAATTCGAACG	199
CcM0697	FI208747	(AT)8	GAGTACACCCCTACACCCTACAA	CTGGCACCCTGTTAAAATCA	188
CcM0698	FI208758	(AAT)17	CTCTTCTTGTTGTCCCTCGC	GCAGTTCTGGAATACCTCGC	188
CcM0699	FI208758	(TAT)5	AGTTTTGAGTTTGCGCGTTT	TCCAACTATTTATTGGTCCAGAAAG	180
CcM0700	FI208764	(TA)22	GCAACAGTGACAATGGGAAA	TGAAAACTGATGATGCACCC	178
CcM0701	FI208792	(AT)13	TCAAAGTCTAAGACACATAAGGATTGA	AACATCCAAAATACAACATCCG	280
CcM0702	FI208811	(A)11n(TA)6	CAAGACACCATTCTGTTCGG	AGAGTGGGATGGATGACTGG	267
CcM0703	FI208813	(AT)7	AACCCCAAATACTTCCCCAG	GCCCTCATCCATTCACAGAT	256
CcM0704	FI208833	(AC)6	AAGGTCACTTCAAGCTCCCA	CAAAGGGAGGTGAACTACAAGG	279
CcM0705	FI208838	(TA)8n(AG)6	TCTTCGTCTACACCCCTTGG	CGGTTGAATTGTTAAAATTTGATG	218
CcM0706	FI208854	(TTTA)5	TTCATTGCAAGTCCATGACC	TGCTCCCAATAGGAGAATGAA	249
CcM0707	FI208910	(AT)5n(A)10	AGCGGGATAACCGCTATTTT	GTGGGGGTGATGAATTTGAG	271
CcM0708	FI208931	(A)11(AG)5	TGAAATGGAATGGACAAAACA	AACGAAGTGAAATGAAAGGGAA	145
CcM0709	FI208942	(TA)11	CCCTCACTTGGTTCCATAAGA	AGGGTTCTTCCCCCAACTAA	280
CcM0710	FI208967	(TTA)15	TTTTATTAGGCATATCAAGCTATTTTT	AACAACAACCACAAAATAAGAGGA	276
CcM0711	FI208979	(AT)9	TCCTAGAAATCCTCTGCCCC	TGAATTCAGATGTGAAGATGATGA	260
CcM0712	FI209040	(CA)8	CATCACTCCTGTGAAAACGC	TTCACCTCCCCATTACCTTTT	242
CcM0713	FI209083	(GCT)6	ACCAAGTGATGCAATGTGGA	AGACATTGTTTGGACCTGGC	261
CcM0714	FI209093	(TTA)5	AGCTTGTGCTTCGTCCTGAT	GGAAGGGCGTTACACAAAAA	146
CcM0715	FI209127	(AC)5(AT)5	CATAGGGTCCTCCGTTTTCA	TGCAATTGTCACCAGGATGT	234
CcM0716	FI209142	(TA)6	CAAGAGACCCCAAATGAGAAA	TTTCAACAGGCATAATCATACAAAA	235

CcM0717	FI209169	(TA)8	GTGTTGCGCCCAATACCT	AAATAATGTTTGAAGTTATTATCCCTG	104
CcM0718	FI209205	(GA)6	GGTGCTTTGTGTCAACCTTTC	CGTTCTGGCCACTTTTTGAT	173
CcM0719	FI209208	(TA)19	AGATGCCACTCATAGCCAGA	TGTGTGGATTGTGATGGATTG	256
CcM0720	FI209266	(T)1n(ATCAC)5	CGTTTTCTTCTATCTCCTCACACTT	TGTCCTGTTTGGTAATGGCA	159
CcM0721	FI209310	(AT)19	ATCCAACCACGTGTTTCACA	TTTGAAATGGTATCGATGATTAAA	169
CcM0722	FI209340	(TC)8	CATTTCTCCGGACTCCAAAA	TGCTTTATGGCAACCTTTCA	126
CcM0723	FI209358	(GA)9	ATAGGTGCTTTGTGGCAACC	AACGTTCAGATCCGAAATGG	220
CcM0724	FI209362	(ATT)10	AGTTTTCCAATATACCTCAAAAGC	CAGTGCGGATTTGGATTTTT	275
CcM0725	FI209377	(TC)6	ATTTCCCTTTGTTGGAGCCT	TTGCCACAAGGTGAGTGAAG	225
CcM0726	FI209382	(TG)6	TCTCAACGGACTCAAACACG	CAAAATCACGATACCATTTTTATCC	233
CcM0727	FI209404	(AT)9	TTGATTATATGGACATATGTGTTGTGA	GAAAAGGAGGTTCATCAGTTCAA	237
CcM0728	FI209421	(TA)6(T)10	TCTGTATTGACCTTTAATTTGCGA	ATCATGTCACTCGATCCGAA	240
CcM0729	FI209430	(GA)7	GTGCTTTGTGGCAACCTTTC	CCTGAACGGGTTGTTCTGAT	272
CcM0730	FI209437	(CA)6	CCACCCTAGGACCCTACGAC	ACCAAGCCTTTTCAAGTGGA	202
CcM0731	FI209451	(AG)6	TTCACTTTCGGATCCCAGTC	AAAGAGGCATTTTTCACACATT	144
CcM0732	FI209457	(TTA)5	TCTATTGGGCCTGAGTTGCT	ATTCATCATGTTGCGGACAC	196
CcM0733	FI209480	(AAT)5	TGGTTTGAGGTTCAATGGTTG	TTCGGAATTTTATGTTTACTTTGAA	152
CcM0734	FI209484	(TA)23	TGCTCTTGAGAAAGAAGAGAAAGA	TCCCAACAAACAAGAATTTGG	270
CcM0735	FI209499	(ATC)5	TCTGTGTGACATCTTGGAGAGG	CCAAGAAAGCACCCCTTGTA	242
CcM0736	FI209504	(ATAA)6	GCAAATGGCTAATCATTAAACCC	GTGTTAGGTCGCCAAAAAGC	265
CcM0737	FI209536	(AT)17	TGTTGTTCCCAACTCTTCTTCA	ATAGCGGCTTATGGCAGATG	173
CcM0738	FI209601	(AT)7	CACATGGAAAACATGCAAGG	TGTGTGACTTGTTCTGATGTGG	214
CcM0739	FI209611	(AT)7	GGCTGCTGGACTGGATTAAA	TCGGTCACTAAAATCGGTCA	115
CcM0740	FI209630	(TA)8	GCGGACCTTGATAGGAAGAG	TTTATTGCAACCAGTGACGG	238
CcM0741	FI209649	(AT)41	TCGGACAGCACATGGAATAC	CGTGAGATTTTCAACTTTTAACTCTTT	216
CcM0742	FI209666	(TA)15	GAATTGATGCGAAGGGAAAA	CGTTTTTGATGGTGGTCACA	249
CcM0743	FI209678	(AT)12	TCAAAAATGACTTTTCTATGACCG	CGAACAACTTCGCTCGTGTA	251
CcM0744	FI209679	(TAA)16(AATA)5	ATCAGCCAAGCAAGGTGAAT	GATCGAGCCAACCAAACCTA	259
CcM0745	FI209679	(GA)5n(AG)13	ACTGCGGATTTGGAAAGAGA	GAGAAGAAGAAAAAGCGGGAA	255
CcM0746	FI209702	(AT)22	GTTTCGTTGTTTCATGGGCT	AACGGACACTTGTAATGGGC	159
CcM0747	FI209710	(AT)29	TTTTTACGGGCAATTATTCAAA	TGTTCTATATGATTCTCTGATGCTCAC	131
CcM0748	FI209720	(AC)6	TATCAGAGCATGCCCAACTG	GCATGCATTTACGAGTCGAG	264
CcM0749	FI209760	(TC)7	ACGAGCCATTCTGATTTTGG	GCGCTTTTTGGTTACGTTTC	198
CcM0750	FI209782	(TA)7	CAAGCTTGTGAAAAGAATCATCA	GGTGATTTGCATGACGACAC	198
CcM0751	FI209787	(ATC)5	TGTGAAACCAAGAAGTAAACCG	TCTTGACCCCAAGAAAGCAC	225
CcM0752	FI209832	(AT)10	TGAAGCCGGGATATCAAAAC	CATAGTACGCCAATTAGAATGTTCA	227

CcM0753	FI209923	(ATAA)5	TGTGATGGTTTAGACCCAAAGA	CCAACCAATGACTTTGATATCGT	177
CcM0754	FI209979	(ATA)6n(AT)5	AGTATCGGGGTACGCAATGA	CAGCCAACTAACAAACGGGT	144
CcM0755	FI210016	(GA)6	GGTGCTTTGTGACAACCTTTC	CGTCCAAGACTCCTCAGAGC	106
CcM0756	FI210065	(CA)7	AGCATGCCCAACTGAACTCT	TGCATGCATTTATGAGTCGAG	267
CcM0757	FI210079	(T)10n(TA)5n(A)10	TGCCTGCATGAATCTCTTTC	ACGCCTTCCTAACCAGAAAA	274
CcM0758	FI210104	(AT)6	CTCAAGCTTTGTCATCTCCAA	GTGTTTCGTCGCAATTCCAT	277
CcM0759	FI210127	(TA)8	GCTTGGAAATTGTTGCTTGG	TTGCATCCCCTTGTTCTCTC	256
CcM0760	FI210130	(AT)24	CCATAATCCAATCCAAATCCA	TGACGCCATGGAAATACTGA	142
CcM0761	FI210143	(GA)6	GGTGATTTGTGGCAACCTTT	CACATAACGGCCACATTCAG	228
CcM0762	FI210153	(TA)7(T)12	TGTTTTTCCTTCTCGGCTTT	TTCGGTTGATGTCCATTTGA	155
CcM0763	FI210167	(AT)8	CAACGCCTTTAAAACAAACCA	ATGGAGTGACCCACCACATT	149
CcM0764	FI210167	(GT)7	TCGGGGAAAATAAAAAGCAA	ATGCTCTCGCTGGAAAGAAA	230
CcM0765	FI210172	(TA)23	AATTAACCATCCGGGTAGGG	TGAAAAAGGATTGAGCCTGA	245
CcM0766	FI210233	(TGA)6	AAGAGTCCAACCATCCTTCG	TCGGTCTCACATTGACATCAG	225
CcM0767	FI210276	(TA)6	TTGAATGGCATATCTGGTGG	TCAAGAATAATTTTCAGTATTTCCCA	214
CcM0768	FI210321	(TC)6(T)12	TGTGGTCTTCTCGGCTTTTT	GGCATTTCATCTTCTCTGGAA	117
CcM0769	FI210347	(TA)8	GGAAGCATCGTTCCAATCAT	TGACCAAACTTGCTTTGCTTT	256
CcM0770	FI210384	(TGA)5	AGCACCCCTTGTAGAAACCC	TCTTGGAGTGTTTTCTTCGTGA	244
CcM0771	FI210421	(TC)7	ACGCCCTACACATTCGTTTC	TTCATGTTGTAACAAACCAATTCA	276
CcM0772	FI210422	(AT)15n(A)13	TCCAATTTCAGAGTTTGGGAC	GTGGGTGTGGCTAGTGGAAT	264
CcM0773	FI210461	(TA)8	TTGGCCAAGTTAAATTGATTCAT	TTCACTTCCATTACTTCATTCCA	188
CcM0774	FI210469	(AAT)8	TGTATGTAGGCTCAACTGCACC	TTGGTCCTTTGGGCATTTT	102
CcM0775	FI210476	(ATT)10	GTGGGTTTTGCATTGTGATG	CAATCCCTCTCATTCTCCCA	219
CcM0776	FI210476	(GCG)5	GAAGGTGTAGATTAGCGCCG	CATCACAATGCAAAACCCAC	277
CcM0777	FI210558	(AT)6	TCATTTAAAGTGAATGAGAGTTGCTT	TGGGTTTGGAAAGTGCAAAT	278
CcM0778	FI210611	(TC)8	CAAGCTTATTGAATTTCACCTCC	TCATGGAATGTCTTGATAAATGG	201
CcM0779	FI210617	(AT)6	CAAGCTTGGATACGTATTCTAATGAA	TTGAATGCAAAGCCAGTAGC	277
CcM0780	FI210710	(TA)25	TGTACAAAATGAACACCAATTCA	GCTTTCCCTATCCCATTGGT	251
CcM0781	FI210725	(CATC)5	CAATGGATACCCCTCCACAC	GTCGTTGTGAGCCCTCTCTC	211
CcM0782	FI210759	(TTC)5	TTGCCTTGTTAGCAGCTGTG	TCAATTGAATGCCCTCAACA	200
CcM0783	FI210759	(AT)26	GTTGCTTCGTGGGCTTGATA	AGGCAAAGAAGACTTCACGC	265
CcM0784	FI210799	(TA)17	AGTCAAGGAATTCACGCCAT	GATGTCATGCCTAATTGGTCC	280
CcM0785	FI210851	(AT)9	GCATGTGTTTTTACTTGAGTCGTC	TGGAGGCGATCTCTTTCTTG	277
CcM0786	FI210853	(ATC)5	TGTGAATCCAAGAAGAAAAACG	AGGAACGAATTCACCTGGAA	118
CcM0787	FI210863	(AATA)5(AT)10	TTTTGGTTACCTGGTCAATAGG	GCAGTGCACCTGATTTTCTG	229
CcM0788	FI210909	(AAATA)6	TGGCTTAGATATCTCCCCACTT	GGGATCATTTGGTTAATGTCG	275

CcM0789	FI210953	(TTC)6	CCTGTTTAAAGACCTTGCGTG	AGGCACCGTCTACGATCAAT	247
CcM0790	FI210955	(CA)6	TTGGGCTTCCATTAGGACAC	CAAAACAAATTTTTCACACAAACA	251
CcM0791	FI210959	(CA)6	GGAGAACATCACTGTTGCGA	GCCGGAAAAATAACAGACGA	219
CcM0792	FI211050	(TA)21	CATGCATGTGTGCACTTTGA	TCGGTGATATTGAATTATGGCA	158
CcM0793	FI211058	(GA)13	GCAACCCTACCCCTTAAACC	TTCTCTCTATCTCCCTACCTCCC	249
CcM0794	FI211099	(TAAT)5	CATGCACACGTTCACACAAA	TGTTGCATTTTAATCAATTATGCTT	260
CcM0795	FI211102	(TTA)5	CACCCCAGTTTTCAAAAAGGT	AATACGTACAAAATAATTGTCCAAAA	138
CcM0796	FI211119	(AT)7	ACATGGAAACATGCAAGGGT	GAGGCCAACATTGTGAGGAT	278
CcM0797	FI211242	(AT)9	TTTTTCCATGCCTCCAACAT	GCCAATTTTAATTCGCAGGA	240
CcM0798	FI211256	(TA)20(TG)6	GGCCCTTTATCTCTCCCAAA	TGTTTAAACCTTCGTTGCATCA	188
CcM0799	FI211287	(TAA)13	TTTGGAGTTTCACTAAGCCCA	AGCACGAGGAAAAGCAAGTC	238
CcM0800	FI211360	(TG)6	ACCAAGCCTTTTCAAGTGGA	TTCCACCCTAGGACAATTCG	204
CcM0801	FI211368	(AT)6	AGTGACGGAAATGAGGATGG	GTGACAATGCAGCACATGAA	224
CcM0802	FI211487	(TCT)7	TTGAAGGTGGCAATTGAAGA	ATGACCACAAACACAAGGCA	119
CcM0803	FI211487	(AT)5n(T)11	TGCCACTCCCATATGTTCAA	ACTTTTTCCTCAGCATATGTCC	194
CcM0804	FI211510	(TA)8	GCGACATAGGACACCTCCAT	AAAATCCTTTCTACCAAAACTTTTACA	157
CcM0805	FI211523	(AT)12	CGACAATGGTGGGTTGAAAT	CATTTTCCTTGTGCAGACGA	266
CcM0806	FI211549	(CA)6	ATTTGCCTACTAAGGGGACG	CCTTCCTAGGCATGATTCCA	209
CcM0807	FI211565	(GAT)5	GAGGATTCCCCACCATTTTT	TGTTTTCCATAGTATCATCTTGTGC	254
CcM0808	FI211659	(CAT)5	AAGCGATACCACCCAATCAC	TCGGCCGTGAGTTATGTACT	279
CcM0809	FI211662	(GA)6	AAAATCTCGGTGCTTTGTGG	ATAGACAGCTCGGGCACAGT	152
CcM0810	FI211663	(AT)19n(TA)6	TTTTTCCGGTCATTAACCATA	TTGGTCGGTCCTAAAACAGAA	202
CcM0811	FI211784	(CAT)5	TGCTCATCCTAAACAAGGCA	GATCCAATCGACCGTGAGTT	225
CcM0812	FI211795	(AC)6	TTTCTTTGTGCGCTTCTATTG	CAATGCAATTTTTCCCATCC	223
CcM0813	FI211835	(ATG)5	TTTGATGATGCTTTGCTTTGA	TCTCGTCTACCACTACTTGCACA	248
CcM0814	FI211859	(AG)6	TCATCCCACCATGTCAGAGA	CGAATCTGATCGAGCTCTCC	118
CcM0815	FI211860	(TA)8	TGAGTAGGAAATGGAGGTGGA	AAATACAATAATTCGAACGAATAAACA	208
CcM0816	FI211885	(AT)34	TTTGTTCAAAGATCTCCACTTCA	GAAAGGTGTGTACAACAATGGG	213
CcM0817	FI211896	(GA)7	TCTCCACGTATTGGGGACTC	GCTGCACAAGCCTCCTAAAC	203
CcM0818	FI211963	(TA)23	GGGCCACAACGGAGTTAAT	TTGTGTAATGACGCTGGTCAA	274
CcM0819	FI211985	(GA)6	TGCTTTTTGGCTAGCTTTCA	ACTTGGACATTGTTTTCGGG	133
CcM0820	FI212258	(AT)24	TGGAGACCTAAGTTTAATTCTTATTGC	CCTCGCTATCAAGGAAACGA	179
CcM0821	FI212269	(TG)6	TGATAGCACTTGCTCCAAACA	AACCAGTGAGGCAGTGACAA	105
CcM0822	FI212296	(TA)21	TTCCTCTCCCATTCTCCCTT	TTGCATCACGTGGAAGACTC	272
CcM0823	FI212386	(TGA)5n(T)11	GGCTTGTGTGTGTTTGTTTATG	GCTCACCAATCTTACTCGGC	228
CcM0824	FI212421	(TA)12	ACGCACGCATACATTGACAT	TGCAGTTTCCTCAGCTCTCA	171

CcM0825	FI212427	(AG)8	TGGATTTAAATTAGAAGAGCGAAAA	GAGAGGGTTCAACTTAAGTGATAAGA	122
CcM0826	FI212533	(AT)8	TTGTTCTTCTCGGCTTTTCC	CAAAAGGCAAGTATCTTCTCTGG	106
CcM0827	FI212544	(AT)13(ATTT)5	TGGTCATGCGATTATGGTTG	CGTACGTCTCACACAGGATCA	159
CcM0828	FI212567	(TC)9	GCTCCGGTCAAATGAACTTT	AGTTCTTTCTGCACACAGTTGTT	263
CcM0829	FI212652	(TA)14(T)13	ACGGGCGTATTGTTTTTCTG	TCTGGAGGAATGGCAAAATC	207
CcM0830	FI212672	(AC)7	TTTGGCATTTTCTTTCTCTCTC	CTTGCAGATCCCCCAATAAA	195
CcM0831	FI212710	(TC)6	GAATACTCAAGCTTCTCCCCA	AAGGAAACAACAATGGTGGC	227
CcM0832	FI212724	(TTC)6	TCAAGCTTAGGAAAGGCACA	TCGTGAATCTTCACTCGACG	186
CcM0833	FI212731	(TA)19	TCAGAAGGGGGTCTCACACT	TCGATCACAACGGTTTAAGAA	270
CcM0834	FI212739	(AT)10	GTCCGGCTTGCCTATAAGGT	AAGGCAACCTCCCCAGTATT	262
CcM0835	FI212752	(AG)6n(AG)5	GCCTATAAATAGGGGCAGGG	CGGAGCTGAAACTTAGGCAG	157
CcM0836	FI212753	(AAT)6	GAGCCAATTCCTTGGCATAA	AAAAATGGGAACCCTTCCTTA	226
CcM0837	FI212782	(TA)7	ACGGGCGTATTGTTTTTCTG	AGAAATCGGCAGAGCACAGT	220
CcM0838	FI212795	(CA)6	TGGACAAATGGACAGTGGTT	ACCCATGAAGCAAATCTTGG	266
CcM0839	FI212805	(TA)16	CGACGACGAGGTATAATTTGTG	TGCCAAAGTTAGACCAAATGAA	277
CcM0840	FI212812	(GAA)5(GAT)6	TCGAACAAAAAGGGTTTTGAG	ACCGTACAAACCCCTTACCC	174
CcM0841	FI212825	(AAGAAA)5	TGCTCAAGAGTGGAGCATCA	TGTAGGACATTGGGAAGCAA	237
CcM0842	FI212850	(AT)5n(AT)12	GTGCACCATTGGTTGTTTTG	TTGATCTTTCATGCCATGCT	266
CcM0843	FI212863	(AT)15	GAAACCGTGGGTCTTGGATA	CCCGGAAGGTTCCTTGTACT	279
CcM0844	FI212882	(TA)19	CGAGAGGCTGCACAAATTCT	GGCGCCCTTTTGTAAGTGTA	233
CcM0845	FI212904	(AT)15	ATAGCACCACCAACAGGACC	TCAATGTAGGACCTGGGTTTTT	211
CcM0846	FI212930	(TG)6	CTTTCTTGGTGGGCATTGAT	CGAATCAAATCATATTTGCGA	118
CcM0847	FI212938	(TTA)7	ATAGGATGTGACATTGGGGC	AACCTCAAGAAGGGTCCACA	259
CcM0848	FI212953	(AG)8	TGACAGTAGATTAGATTACCCCATGA	GTCGATTCAGCGGAGAAAAC	279
CcM0849	FI212955	(AT)11	AAAATCACCTGGTTTTTGCG	AACATGATCAAAATAATGACTTCCT	266
CcM0850	FI212963	(GA)6	GGAAAAGGTGTTTTGTGACGA	TAACGGATTAGCCCAGAACG	279
CcM0851	FI212982	(AT)25n(T)10	AAGCTTGTGTTTGTCCTTATTGC	TGACATCTTCAGGGTGAACCTA	275
CcM0852	FI213038	(AAG)12	TGAGATCAGTCACAAAAGAACCA	TTGAGCACAAGAGAACCACAA	148
CcM0853	FI213052	(TAT)5	GCTTGAACAAGCCCTAAGGA	AAAGCATGGAGAACTAGACCAA	261
CcM0854	FI213065	(TG)6	CGATCAATTGGAGAAAGGGA	GGACACAACAAACCCATCAA	236
CcM0855	FI213076	(AC)7	ATGGTGGTTGGGTGTTCATT	TGTAGGAACTAAAGTGGATTGAAAAA	280
CcM0856	FI213135	(TTC)9	TTCGCAGAGACCTAGGAACC	CGAAAACTGTCACGCAAGAA	255
CcM0857	FI213141	(TA)6	TCACTCAACAAAGCCATCCA	TGCATGCTTGAGATAATGCT	182
CcM0858	FI213145	(TAA)9	ATTTTTCCACGATCACCAAA	TTGGGATGACATTTATATCTTCATTA	171
CcM0859	FI213166	(AT)5n(A)27	TTTCAAATGTCCCCTTTTGG	GGCGGACCATATATCACGAC	247
CcM0860	FI213186	(AT)20	ACTTCCGTGCATTTTATTTGA	TGTTTTGGTTCTATTTGTTTGACG	232

CcM0861	FI213189	(CA)8	AGTTTCCTAATAAGGGGCCG	AAGGGAGGTGGACTACCAGG	147
CcM0862	FI213295	(AT)6n(A)10	AACCACTTATGCATGTTGATGT	TGAACTTGTGATGGTAATAGTTGTGA	243
CcM0863	FI213380	(AAT)8n(ATA)5	CCAACATTTGACTGACAACACA	GGCAATCCATAACCATGTCC	171
CcM0864	FI213384	(TA)9	TGCAGGATGGGTTCTACTCA	CCAATTCACCACCCCATTTA	214
CcM0865	FI213390	(TAT)10	ACGGAGAGCACTTTGGACTT	TTTAACCGTGTTCAACCTTGG	172
CcM0866	FI213427	(AT)19	GGAGGCAAAGATCTTCATCG	AGCTGCACGAGATTCAGTAGG	228
CcM0867	FI213462	(AT)21	TCCTAACGAGAACTAATCCTTGC	AACTTTTCATTTGCAACAAAGTGT	175
CcM0868	FI213477	(AT)9n(A)11	GATCGACTTCTGGGTTCTGG	TTGGAGGAACCAAAATTACACA	269
CcM0869	FI213514	(TA)5n(TG)6	CCAATTTTCCTGAGTGGGAA	GCATTACTCTTGCGAAAACGA	169
CcM0870	FI213624	(T)10n(AT)15	AAAAGATAAACATGCATACTGCAAA	TCTGTCAAACTTTTGAAGGAGATT	202
CcM0871	FI213641	(AT)28	GGGCCTCCTCCATCAATTAG	CACACACATATTCAACCCCC	257
CcM0872	FI213660	(TA)22	TTTTTGTTTTTATGGAAAATTTCTG	TCGTCCACTTATACCACATAGCA	274
CcM0873	FI213665	(GA)6	TGAGAACAAAGGCAATTCCA	TTCTTTGCCTATTGCAAATCTTC	185
CcM0874	FI213682	(T)10n(A)13	TCGGCTTGCTATGTTAACCC	GACACCCAACTCATCGCTTT	268
CcM0875	FI213721	(GA)9	GGTGTCTGCAGCAAGCATAA	AAGAAATTTCATGGTATTCTCAAAA	205
CcM0876	FI213790	(TTC)7	TCAAGCTTTGGAGGATATTTCT	CCATTTTTCCTATAACCCCGA	209
CcM0877	FI213810	(CA)6	TAGTGATGGTGGGTCCCATT	TGAGCAAAATCTTGGGCTTT	227
CcM0878	FI213859	(GA)8	GTGCTTTGCGACAACCTTTT	CTGGCACCCTTTTGATGTCT	168
CcM0879	FI213867	(TTG)5	TACTCAAGCTTCCTCGTGGG	GCAAGTCGATAAAAGCCGAA	208
CcM0880	FI213902	(TA)6	AAGCTTTTGAGCTTCTGAAGGA	TGAAACCTTCTTGGACCACC	271
CcM0881	FI213982	(CA)8	ATCACCAACATCCCCATGAT	TCACCAACGATGAATTGTGAA	279
CcM0882	FI213987	(TA)15	GCCATATTTGACCATATTAGGCTT	TATTTTGCAGCCTTGTGCAG	265
CcM0883	FI213996	(TA)5(AT)5	AGGTTTTTGCAACATTTATTTTAGA	TGGCCATTAAATTTATAATCACG	253
CcM0884	FI214000	(ATT)12	TAAATGGGTTCGTGGGTGAT	GGTGTGAAAATTTAAGAAAAAGGG	177
CcM0885	FI214010	(TA)35	GGGTTAGTGGGCCTTAGCTC	GCCCAAAATACACGGCTAAA	188
CcM0886	FI214016	(TA)5n(T)10	CGCTTGGAATCTTGGATTGA	CAGTTTTACTAACAACCGATGTAGATT	277
CcM0887	FI214043	(TC)10	CAACCTTAGACGGCTTTTGC	ACAGAAGGAACACGGTGGAG	165
CcM0888	FI214092	(TG)6	ACCAAGCCTTTTCAAGTGGA	TCCCAAAAAGCTTCAAGTGC	234
CcM0889	FI214100	(AT)7	TCCTTAGCCTGTTCCTTTAAATTG	TCTCTCCGGAAAAGTTGTCG	259
CcM0890	FI214119	(TAT)8	TTCCGCCGATAAATGTAAAA	TGTTGCTCGTTATTATGCTGG	231
CcM0891	FI214157	(TTTA)5	AAAGTTCAAACTCATGGCCG	AACAAACGGCCCAATATGAG	271
CcM0892	FI214168	(TA)6	TGATGCCTTATGTTGTGCTG	TGGAAACACACAAGGGTGAA	115
CcM0893	FI214234	(TTC)5	TTTCTTTGGAAACAAAAGCCT	AAAAAGGCCAAGAATGAATCAA	259
CcM0894	FI214271	(TA)11	AAGAGGTGAATTTTTCTTTTCCG	TCTACCCAAGCTGGGTCATC	248
CcM0895	FI214285	(AT)8	CGTTGACGTCGCACTTTATC	AGCTTGACCAGCACTAGGGT	278
CcM0896	FI214293	(TTG)5	CAAGCTTTGTGATTTGATTTGC	TCCAAGAGCACCTCTCAACA	119

CcM0897	FI214432	(AT)10	GGGGCTGTCATATTGGTGTC	CCCACTTTAGTCCTTGAATTTGA	259
CcM0898	FI214440	(AAAT)5	TCATTAAACCCCTGGAACCT	GCCAAAAAGCGCCTAATAGA	280
CcM0899	FI214455	(GA)7	GCTTTGTGGCAACCTTTCAC	CAGATTGGGCACATTTCTGA	145
CcM0900	FI214508	(TTAT)6	TGGGAAACTGTTATTGCTTGG	ATATGCCATCATTTGCTCCC	123
CcM0901	FI214527	(AT)8n(TA)5	GTTAAAATTGAACAATAACCTGAAAGT	TCATCGTTTCGGACACAGTT	251
CcM0902	FI214549	(CT)7(CA)6n(TA)26	ATGGGCACCCATAGGTAATG	TTGAACACTTCTTGAAAACATCTTA	279
CcM0903	FI214577	(TTA)10	CGGGAGCTCGAAACATTAAG	GGGGTCAAAGGTTGGAAAAA	229
CcM0904	FI214581	(TA)9	GAATACTCAAGCTTTCGTTGTCTG	TTTCAAGGAGCTTGCTTGGT	111
CcM0905	FI214603	(CT)8n(TG)5n(AAT)8	AAATCATGTGTCACAGGCCA	GTTGGTAATTTCCCGCTGAA	244
CcM0906	FI214612	(AT)20	CCAGGCCATCATAGCAGTTT	TATGGATTTTGGCACCATGA	217
CcM0907	FI214671	(T)10(CT)5	GACTCATGAGGTTGGCTTCC	TGCTTTATGGCAACCTTTCA	245
CcM0908	FI214674	(AAT)5	ATTGCATAACCGAAAGGGTG	ATGACTCCACCAACACGTCA	149
CcM0909	FI214688	(GA)6	AAACAGGGTGTAGTGGCTCG	TCAATTGGGCTATTTTTGCC	207
CcM0910	FI214738	(TTA)7	AAGGGAAAGGGTTCTGCTCT	AACATCAAGAAGGGTCCACA	280
CcM0911	FI214741	(AAAT)5	GGAATGGCCCGTTCTACTTT	TTTCGGGGACGAAATTTTTA	260
CcM0912	FI214749	(TG)6n(GA)7	ATCTCCCCAAGTGTGAAGCA	TGTGATTGTTTGCATAGATTACCAT	269
CcM0913	FI214755	(AG)6	GGGAAATGAAAGTGGAGCAA	TGATTGGAGGGTCATTGTGA	150
CcM0914	FI214800	(AT)12	ACACCTTGGTGGAGGACTTG	AAAACCTCCCACCTCACAAA	275
CcM0915	FI214826	(TA)8	CAAAGCAAAAGTAACCTTTTTAGTCC	TGTCTGTACTAGGCTGGTCCC	161
CcM0916	FI214851	(CT)6	GGAAATGGGGTGTGTTTGTC	CGAATTGGAGAAAGTGGGAA	110
CcM0917	FI214860	(ATTT)5	GCTTTTAAAATGTTTTTCCGCA	TGAGGATTAACGACAGTGTGTG	279
CcM0918	FI214876	(AAC)6	GAAACCTCGTTGGCATTGTT	CAGCGGAAGAATTGTTAGCC	139
CcM0919	FI214904	(AG)9	TGCCCATAAGGCCATAACTC	TTTGATTTTGTTTCCTGCCC	255
CcM0920	FI214908	(AT)22	TTGCAACCAACAATGCAAGT	TCCTTTAGGATCAACCGTGAA	254
CcM0921	FI214957	(TA)7	CAAATGAAACTCTCCGACCC	GGCATTGGAGGATAGGAACA	193
CcM0922	FI214972	(AT)18	CGTCGCATAACTTTTGATGG	TTCTAAAATTGCCTGATTTGACA	215
CcM0923	FI214992	(AC)6	CCCATCACTTAACCCAACAA	GAAGTTTGGAGGCTGAGCAC	200
CcM0924	FI215019	(TA)6	TATTGGGTACCAAAAGCCCA	CACATGGGCACACTTGAGAT	167
CcM0925	FI215036	(TTA)8	ATAGGATGTGACATTGGGGC	AACATCAAGAAGGGTCCACA	262
CcM0926	FI215137	(AATCAG)6	AGATCCATTTCACCCACTCG	TCCTCCAGATCCCTTCCTTT	237
CcM0927	FI215139	(TA)6	ACCAATGTACACCTCTCGGC	TTGGCTGATTTGTATTCTCGG	171
CcM0928	FI215150	(TTA)9	AGCACCTGTAACACCCCAAT	AATACGTACAAAATAATTGTCCAAAA	155
CcM0929	FI215185	(AAT)6(TAT)5	GGGGTCATTGGTACAACTCC	TTTGACTGCGATTCAAGCAT	276
CcM0930	FI215203	(AC)8	TGAGAGGCTGCATAGGTGAG	GTCAATCATTGTTCAATTTGAGTC	230
CcM0931	FI215208	(TA)24	CCATAAGCATCGTGTCCAGA	GGCATAAAAGCCATTCACAAA	280
CcM0932	FI215228	(AG)6	TTCTTTCATGGCCGAGAACT	AAAGGATATGTTTCCCAAACGA	247

CcM0933	FI215264	(AT)23	TGACAACCATTTTTATGTTGTGGT	CCTTGGCATGCTACAAGATT	241
CcM0934	FI215303	(AT)6	TTGGAACAATGCCTATGATGA	CCTGCAAAACAAGCTCACAA	160
CcM0935	FI215377	(TA)10	TGAAACTCTGAATCTGCCTCAA	TGCAGTTGAAAACCAAATATCAA	156
CcM0936	FI215381	(TC)6	TAGGGCCCCTCCATATTTTT	CTGTCCAACTCAACCCGTTT	280
CcM0937	FI215471	(CT)6	TTATCAGATAGAATGCCTTGCATA	TTGGCTTGAAAGATTGGAAAA	163
CcM0938	FI215571	(AT)13	AGCACTTGCCCCCACTACTA	TTAATTTCCTTTAAAAGTTTGACAGAT	214
CcM0939	FI215597	(T)11n(TA)5	TCACTTTTACTTTGGTATCATCCCT	ATTTTGGTCCACTTTAAAAACG	200
CcM0940	FI215621	(ATT)19	CCCAATCCAACATAGCGTCT	GGAAAATGTCTGAGGTGAGGA	242
CcM0941	FI215650	(ATC)5	CGTTTTTGTGGAGTCTTTGTG	TCACCTGGAATTCAGAAGCA	150
CcM0942	FI215656	(TC)5n(TC)5n(TC)7	AGGTGGAAATCCAACTTTCCT	GGGGGAGTGAGAGTGAGAGA	263
CcM0943	FI215717	(CT)5n(TC)5	TGCATTGTTTGGATGGAGAG	GGGATCGGAGAAAGAAAAGA	279
CcM0944	FI215749	(AAT)7	TTTAAGTGGTGAAGGCCTCG	TTGTGTCCAACAATTGACGA	218
CcM0945	FI215763	(AT)12	AGAACTCTTCGACCAAGGCA	CACATTTAATTGAAAGTTATTGAGCA	135
CcM0946	FI215791	(AG)12	AGTGAGAGAGTGCAGGCGTT	TGTGGAAAAGGCATGTTTGA	248
CcM0947	FI215852	(CT)9	CTCAAGCTTGCTTTGGAGGT	ACGCCCTAAATCGGTACCTT	252
CcM0948	FI215944	(AT)14n(AG)5(A)11	GCACAGGTCACGTCTGTACC	CATTTTCCCACCTTTCCTGA	221
CcM0949	FI215949	(CGC)5	ATCAGAAGCTTCCCGCTGTA	CGGTGCTATCTCTGTCCCTC	226
CcM0950	FI215949	(A)10n(AG)14(G)11	CTTCTTCACCACCCATTGCT	TTCAGAAACAGTGAACACACTGAA	188
CcM0951	FI215969	(ATT)5	AGACCAAGGAGGATTCCGAT	GATTCTGTGGGATTTTGTGGA	208
CcM0952	FI216072	(TA)20	GCCATGCCTTTGAATTTGTT	TATGCAACTCCCTGACCCAT	253
CcM0953	FI216092	(ATA)10n(AAT)5	TCACCCAGAAATAACACTGGAA	TGGTTCATGGCAAATCAAAT	280
CcM0954	FI216103	(GA)7	CAAGCTTTTTAGCATACGACGA	GACAGGTCTAATGGCGGTGT	236
CcM0955	FI216136	(A)11n(AAT)10	CTCAACATCAATCCGGGTCT	GCATGGATGCACATGAAAAC	249
CcM0956	FI216271	(AT)16	AGCCCCAACTCAATTATCAAA	TTCCTTGCGGTTTGAGCTAT	224
CcM0957	FI216286	(GA)6	GTACAGATCGCCCCAGGTAA	ATGGCTCATGGCTCATAGGT	225
CcM0958	FI216291	(AT)6	TGGTTGGATTGCATGTTGTT	CAAACCCACTCAACCCCATA	249
CcM0959	FI216314	(CGG)5	TCGGAGGATGATTCCACTTC	CCTCGGCTTCTCCTCCTC	122
CcM0960	FI216318	(AT)17	TGCTTTCCAAATTTACAGATCG	TTGATAAATCAATCGACATATAAAAGA	251
CcM0961	FI216340	(TA)9	AAGCTTACTGCTCGTTGGAA	ACGTGGAGTGATCACCAAAA	260
CcM0962	FI216360	(TCT)7	AGGACTTCCTCCTTTGTGCC	AGCATTGAAGGCCAATTGAT	221
CcM0963	FI216391	(AAT)7	AACATCAAGAAGGGTCCACA	AAAGGGAAAGGGTTCTGCTC	280
CcM0964	FI216408	(T)10n(TA)16	TGGCTTATTAATATTGTTCTCGTTTC	TTGAGAACTAATCGCGATACCA	164
CcM0965	FI216411	(AT)6	AAACGTTTAAGCCATGATTTTT	TTGTTGCTTGATATCCAAGGTG	273
CcM0966	FI216459	(TC)6	CGTTCTGGACCCTTTTTGAA	GGTTTTAGGTGCTTTGTGGC	180
CcM0967	FI216478	(TG)6	ACCAAGCCTTTTCAAGTGGA	CCACCCTAGGACCCTACGAC	203
CcM0968	FI216498	(AGA)6	CATGGCAATGGAAGGAATCT	TTTGGGGATTCTCATCTTGG	184

CcM0969	FI216506	(TTG)5	CCCAACCGTGAGTGCTTAAT	TTTGCAAGATTTGGACTGACC	276
CcM0970	FI216537	(TA)16	TTAAAATCACATCTTACGAAACATAAA	AGGACATACGTTCCAAAATTGA	187
CcM0971	FI216574	(TA)6	TGGACCATTGAGAGAAAGGG	TCAAGAGAGACCCTATGGCA	257
CcM0972	FI216601	(TA)15	ACTTTGGCTCAGGGCATAGA	TTGGAAAATCATTGTGAATGC	200
CcM0973	FI216602	(GA)6	TAGGTGCTTTTTGGCAACCT	GGCCCGTTCCAATACACTAA	256
CcM0974	FI216621	(AT)13	CGTCTTACAGACGATCTGCATC	CAAAGAAACAGACATGATAAAGAGAGA	161
CcM0975	FI216641	(AT)5(GT)7	GGAAACAAATCCTAAAATAATCAAAA	AACACACAACTTCCATGGGTT	137
CcM0976	FI216647	(TTC)5	GCAAGATGTCCCAAACACCT	TTTTCTTCAAACCTCAAAATCCA	194
CcM0977	FI216670	(AT)6n(AT)7n(AT)14	TAACTGCCCTAACTGCCCAC	CGTGTAGTATATATGTGCAGCCC	219
CcM0978	FI216682	(TTA)15	TTGGCTAAGTTATTATTGAATGTGTTT	GGTATGGAAGCGTCAAAAGAG	280
CcM0979	FI216692	(CA)7	CAGACGATGAAACTCCCAGA	TGAAAAACACATAGAAGAGGGG	178
CcM0980	FI216716	(GAA)6	TTCCATCAGGGTAGAGGACG	AAGTACGCACCAAACCCTTG	243
CcM0981	FI216723	(AT)6	GAGGGTGATTTGATCGCAGT	ACTCTTGCTCTTGGTTCCCA	255
CcM0982	FI216736	(AG)9	TCTTGCATACAAATGAAAAAGATCA	CTTTTGTTTCTTTGCGTCCC	154
CcM0983	FI216769	(ATT)5	CCATGGGTACCTGCACTTTA	ATCCACGGACATTCGTAAATA	259
CcM0984	FI216920	(TTA)18	TTTGCTTGGTGGCACATAGA	GGAAGGGCGTTACACAAAAA	273
CcM0985	FI216928	(AG)5n(TA)5	TCTTCGCCCATCCTTCATAC	GGAAGAAACAAAAGGCCACA	235
CcM0986	FI216991	(T)10n(AT)7	GATTATTGGAATTGTCGCTTCA	CGCGGGTACCCAATTAGTCT	134
CcM0987	FI217027	(ATG)5	CCAAGAAAGCACCCCTTGTA	TGGAGTCTCTGTGACATCTTGG	243
CcM0988	FI217035	(AT)11	CTTTGAAATGGAACAGCGAA	TTGTCCGCTTTGGGACTTAG	237
CcM0989	FI217073	(TC)8	CCATCTCCCTCTTCATCCAA	TTATCGCCAGTTCAACACCTT	234
CcM0990	FI217135	(TTAA)5	GCCAGCGTCATTACCACTTT	CGGTTCTCTGCTTTGTCTCC	269
CcM0991	FI217201	(AT)8	TGCATCCAATCTAGCTGGC	TTCCTTTTTAAAGTTTGTTTTTCCA	271
CcM0992	FI217213	(AT)20n(G)11	TGGTCTTAAACAGGCCCCTA	TTTCTGACGGAAAGTAGCACC	260
CcM0993	FI217222	(AT)6	TGAGCCTCATCATCCAAATG	TGGCATCCATGCATATCAAC	276
CcM0994	FI217264	(GT)6	TGCCAAACATTTCAACAATCA	TGTGTGGCTGAACATCTGCT	190
CcM0995	FI217274	(AC)7	GGACTTTTGGCCTCTTGATG	CGCATTGTTAGAGGGTTTGG	242
CcM0996	FI217333	(A)12(TA)8	CCGGATTATAAAGATAAGGTGCC	AACCACACGCTTGGAGTTCT	277
CcM0997	FI217374	(GA)8	AGTGGATGGTGTTGGAGAGG	TCCCTCTAGGGCTCACACAC	198
CcM0998	FI217450	(TG)7	GCCGGTCATGCTATGCTAAT	CCTGGGCAGTTCCAGTTTAG	265
CcM0999	FI217492	(TTA)6n(A)10	CTCAAGCTTTTACGCTTTTTAACT	CAGATGAGCTGATTCCAAAGG	238
CcM1000	FI217521	(AT)10	TCTGGTTTGGTCTGACTTGTTT	TCTGTTAAAGGGACAATTCATGC	280
CcM1001	FI217542	(TTA)9	TTTTAAATGGTTCAGAAATTGTGC	AGGGCGAGACTTTGTCTTCA	252
CcM1002	FI217552	(AAT)5	TTTAATGGATTCCGCGAGAC	CCAGGAACAAAAACGAAACG	263
CcM1003	FI217553	(GTT)5	TTGCCTTTTGAGATTCCCAC	ACAAGCAATCCGTTGCTACC	175
CcM1004	FI217577	(ATG)5	TTTGGTGATGCTTTGCTTTG	ATATGCTTGCAACACAAGCG	243

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CcM1005	FI217637	(CCA)5	CCACCACATTCAACCAATGA	GTTGCCCTCCAACATCAAGT	245
CcM1006	FI217663	(TC)6	AGACAGCTTGGGCACAGTTT	TGCCTCACAAATCTCCAGAA	111
CcM1007	FI217734	(CT)7	GTGGCGTTGTTCTTCCATTT	TTCTGGGTACGCCTAGATGC	215
CcM1008	FI217768	(TA)16n(A)11	GGGACTAAATCATCCTCCCA	TGTTTTCTTCACCTTAGTGCTCA	246
CcM1009	FI217803	(TC)14	GCCAATCCGACAATCAGACT	CAGTACAGGCCATTCCAGGT	267
CcM1010	FI217812	(TA)6	CCTTGTTTGAGAAGCCTTGC	TGTTGGAGTGAGAGGAGTGG	193
CcM1011	FI217823	(AT)6	TCCGAGCCATTTTCATAAGG	GGCTGCAAGCTTATCTCTTAGC	273
CcM1012	FI217859	(AT)31	TGGGATGTACCAACCTGGAT	GCATAAGCTTTACCTTTTAGAGAAGC	251
CcM1013	FI217866	(TG)6	TCCCATGGCAAGAGAAGAGT	AGTGCATTGGACGAAAAACA	217
CcM1014	FI217867	(AT)10	ACCCGATCATTTTGGACAGA	TGATGATCGATATTTGTAATATGAAGT	175
CcM1015	FI217872	(TG)8	GCCCTCTTACACTTTCTTACAAAAAC	CTTGTGGGAGTGGCTTGAAT	254
CcM1016	FI217873	(TTA)5	TCACCTGACGTAAAATAATGAAAAA	AATTTCATGAATCGACTTGACA	219
CcM1017	FI217896	(AT)6	TAGTGACGCCCAACAAATCA	CATATGTAACCCGTTAAGAGACTATCA	151
CcM1018	FI217942	(TA)22	GCAACTTTGGTATCTGAATTTAAAAG	ACTTCACCCTTGTCTCTAAAATAAAT	280
CcM1019	FI217978	(AT)15	TTGAAAGGGATATTGCAACAAG	AAATTCAGGAGTGACCGCAT	232
CcM1020	FI218093	(AT)7	GCTCAAACTCGAACTTATACATGC	ATGCGAATATGGGGACAAAA	220
CcM1021	FI218143	(TA)11	CAACCACATGCATGCAGTAAC	ATAAAGAGGGCAGGGGATGT	216
CcM1022	FI218149	(TA)12	TGCTAAGAGGGTTCTTCCCC	GAAAAAGGTGAAAGATGAAATTGA	143
CcM1023	FI218259	(TC)6	CTTCTTCCCTAATCCCAGCC	ACAAGCTATGTATTGGTGGACA	231
CcM1024	FI218293	(CTT)5	AAGGAGCAGAATAGCAGGCA	TTTCGCTTGTGGAAATCCTT	253
CcM1025	FI218381	(AG)8	GCTTTGTGGCAACCTTTCAC	AACGGCCAGATCCATAACTG	213
CcM1026	FI218404	(CT)9(AT)17	TCAGTGCAAAGAAGCCTCAG	GGAATGCATGATAGAGTAAACGA	221
CcM1027	FI218498	(TA)14	CAAAGGTAGCTTCTTGATTTGGA	CATGGCAATATATTTGCTCACAA	273
CcM1028	FI218510	(T)10n(AT)9n(T)13	TTTTAGATTTCCTTTGTGTTGATATTT	CAACCCAATATTATTATCTGTCACG	257
CcM1029	FI218539	(TTA)5	TGTGGGTTTGCCTAGGAAGT	CAAAATCAACCTTCTCTTAAAACAT	275
CcM1030	FI218565	(AC)6	TCATGAGGAATTAATTTGGGC	CCATACTTGCATGGTGGTGA	115
CcM1031	FI218675	(TA)11	GGAATTGTCATTGTGTTTTGCT	CGATCTATGGCGGACAAAAT	251
CcM1032	FI218727	(TGC)5	ACTCATCAGGCAACAAGCCT	CTCCAAATCGATCAATGCCT	279
CcM1033	FI218778	(TTA)9	TCGTTATTTGTCGTTTGAGGA	GTGTGACACCCTTCTACCCC	280
CcM1034	FI218785	(AG)12	CCTTCCCATTCACTCCATCA	TCTACCTAAGCCTGTTGCCG	104
CcM1035	FI218788	(AT)21	TTCTCGGCTTTTACTTGCTCA	GAAAAATTTGAAATCAAAAGGCA	136
CcM1036	FI218791	(GA)8	GCTTTGTGGCAACCTTTCAC	AGGGCCTCCAAAATTTCATC	117
CcM1037	FI218850	(ATA)8	CTCAAGCTTGCTTCTAAAGACC	GGAGAAATTTTGAATCATTTTCTATTG	232
CcM1038	FI218860	(TA)17	AACTCTTGCCCAACACAAGC	TGGAAAATGTAACACCATATTTTTCT	148
CcM1039	FI218869	(TC)6	AATAGACGACTCGGGCACAG	TGCCTCACAAAACTCAAGAAA	113
CcM1040	FI219004	(CCA)6	GACACCCAGAAGCTGCAAAT	TTGCCGTACATCGTTGGTAA	263

CcM1041	FI219060	(AT)9	TGAACAAAGTTCATATTGCTCCTT	AAGATAGCCAAATAAAAAGAGAGAGA	211
CcM1042	FI219165	(TA)17	CAAGAGTTCTTAAACGATCGAAA	AAAGAATTTTCAATCTAACGGTTG	221
CcM1043	FI219167	(GA)6	TGCTTTATGGCAACCTTTCA	GGCCCGTTCCAATACACTAA	253
CcM1044	FI219191	(ATT)7	AGCGTCTCGAGATGGAAAAA	GGAAAATGCTTGAGGAGAGG	193
CcM1045	FI219229	(AT)6	AACCTTAGTTGGTGATAGATTTCAGA	ACCGTCAAGTCCCAAATCAC	262
CcM1046	FI219233	(AGA)6	CAAAGAATGCCATGAAAGCA	CGTAGCTGTAGAGCGTTGTCC	205
CcM1047	FI219244	(TA)13	TTTTTCGAATTATCACAAAATAGGT	TCCAACCTGACTTAAACATACGG	228
CcM1048	FI219249	(TA)7	GGGAATTAGGCACGCTGTTA	TGTTTTGGTCTCTCCTTAATCAAA	272
CcM1049	FI219311	(AT)6	ATGCGCGTGAAGGAAAAATA	TTGCTGTTACATTTAGGAGGATAGG	162
CcM1050	FI219341	(CA)6	AGATTTCCCCATTCAAGCCT	GTGATACGGTTGGGTTCCAC	206
CcM1051	FI219381	(GA)7	GGTTTTAGGTGCTTTGTGGC	ATGCCACATAACGTTCGGAT	223
CcM1052	FI219400	(TA)13	AGAGGAAAAATGTGCGTTCG	GCTCCCATGTATGTTGGTCC	187
CcM1053	FI219413	(CA)5(CT)9(AT)21	TTTACCGGATCCATCAACAAA	GGAATGCATGATAGAGTAAACGA	147
CcM1054	FI219420	(TG)7	AACAGCTGCCTTCAGAATCC	AAGACAATGTCAAGCACCCA	270
CcM1055	FI219561	(AC)7	TCAGCTCCCCTAAGCTCAAC	TTTTGATAATGCCAAAGGGG	209
CcM1056	FI219565	(ATT)5	AAAGGGAAAGGGTTCTGCTC	TCATAGGTTCACAAGTCTTGAAAT	246
CcM1057	FI219637	(AAT)7	GGAGAAGGGTAAGGAAGTGGA	GGTTTGATGACAGGTCCGAT	191
CcM1058	FI219644	(TTA)8	ATAGGATGTGACATTGGGGC	AACATCAAGAAGGGTCCACA	262
CcM1059	FI219680	(CAT)5	TGAACAAAGAGTCTCCCACAAA	TCACTCTCAGCGGAAAAAGC	280
CcM1060	FI219705	(AC)6	CCAGCTTAGAAGGCTTGGTG	CCATGATTAGCCCACACTGA	240
CcM1061	FI219706	(AC)10(AT)9n(AT)21	TTTGAGTCCAATACCCTTTGTTT	GATGTACCCATGGACCACCT	272
CcM1062	FI219787	(TA)12n(TG)6(TA)7	AAATTGAGAACCCCTGCAAC	GAAACCAAAACATGTGCAAAGA	161
CcM1063	FI219843	(TGG)5	TTAATCGAAAGGATGGTGGC	GTACCAACACCACCTCGACC	175
CcM1064	FI219851	(TTA)8	ATAGGATGTGACATTGGGGC	AACATCAAGAAGGGTCCACA	262
CcM1065	FI219859	(TA)11	GCTGCCGCTAAGACAATCTC	TCGTAATGCACTCTTTTAACACAA	248
CcM1066	FI219874	(GA)6	AGAGCGAGCAATCACAGACA	AAGAATCCTCTACCGCAGCA	278
CcM1067	FI219900	(AGT)6	CAGGCATGCAAGCTTTGTAG	TTTGAAATAGAACCTCCCCA	240
CcM1068	FI219934	(CA)6	GGAGAACATCACTGTTGCGA	GCCGGAAAAATAACAGACGA	219
CcM1069	FI219941	(TA)9	AAGTCAAGTTGAACCTTTGCC	TTTAATCCATCGACTCACAATTT	280
CcM1070	FI220030	(TA)6	TGAAGCAAGGAACCAATGAA	TTTCTCGAAAAAGGCAAGTGA	180
CcM1071	FI220072	(GA)8	GCTGGTTGAGAAGAAGCACC	AGGTTGTTACCGCGTTTGTT	267
CcM1072	FI220105	(TAA)5	CCTTTCACAAAATTCCAAGTGC	CATCTTTTCATTAAAAATTATTCCCT	137
CcM1073	FI220134	(GT)5n(T)10	GGTGTACCTTTGGGTCACCA	AGCCTCATCACCAACATCCT	278
CcM1074	FI220139	(GA)8	TTTTAGGTGCTTTGTGGCAA	AACGGGTCGTTCTGATTTTG	210
CcM1075	FI220192	(AT)17	CCCTGGAGTGAAAGGATTTCT	GCCGGAATGAATTAAGCAAA	180
CcM1076	FI220196	(TC)12	GATCCTCATCAGCAAAAGCC	AACAGCCAGAAAAGCCTTGA	278

CcM1077	FI220235	(AT)18n(A)10n(AAT)11	TGGAGTAAGTTGACTCATGGGA	GCTAACAAGACCAAAAACCCA	240
CcM1078	FI220241	(A)11n(AAT)10	CTCAACATCAATCCGGGTCT	GCATGGATGCACATGAAAAC	249
CcM1079	FI220262	(TA)8(TG)6	TGAAGAAATGCTGACTCCAAAA	GCACATTATTTTACCCCTCCC	270
CcM1080	FI220284	(GA)6	GCCTCCTCCATCAAATGTGT	AGGCACTGTTCAAGGATTGG	242
CcM1081	FI220357	(ATT)5n(ATT)5	AAGGACGGGAAACTAGGCAT	GCAGTGAAGAATCACTGGCA	266
CcM1082	FI220366	(AT)24	CATGAAATCGTGTTTTGTCCT	TCTGGATGGTATCTTTTGAATTTATTT	214
CcM1083	FI220378	(GA)7n(T)11	GGCTTGACTTGCTTTTGGTC	TGAAGGTTGACATGGGTTGA	162
CcM1084	FI220393	(AT)24	TATTGAACCCCCTTCCAGTG	GCATTGGAACTCCAAAGACA	204
CcM1085	FI220395	(AC)6	TAGAGTCGACCTGCAGGCAT	ACTATTCCCGTGGGTCTCAA	130
CcM1086	FI220404	(AT)16	TTTGATGTTAGGTTGGTGTATTTGA	TCAAATTGAAGGAGATTTATTTTCTC	245
CcM1087	FI220413	(TA)14	GTTGTCCCATTTTGACCTCC	CCATAATCCAATCCAAATCCA	186
CcM1088	FI220423	(TTA)7	AGGCATGCAAGCTTTTAACC	TGTTTTATCTTTTGACATTTTAACCAA	200
CcM1089	FI220439	(TAT)6	GGGATAATTTGGGAGATGACAA	TGGGTCAACCCAACTCATCT	232
CcM1090	FI220466	(TA)5n(A)12	GCATGCAAGCTTAGCAAAATC	GCAACAACAATGACATTTGGA	278
CcM1091	FI220475	(CAA)5	TGGGTATGTTGGTGGTGAGA	TACCCAACACCACACCACTG	156
CcM1092	FI220497	(A)11n(TA)5	CATTTCACTTCTTCCTCCGTT	GTTTGTTTCAAAGACAAAAGTTAAAAA	166
CcM1093	FI220531	(TA)6	GCAGGCATGCAAGCTTTATT	GAAAATATTCCCTCGCGTCA	125
CcM1094	FI220565	(TTA)5	AAATTCAATCCATAACTATGAAATTCT	CGGTTCATGAATCAATGAGTTG	265
CcM1095	FI220645	(AG)5n(AG)7n(GA)7	CGAATTCAATACGGGTCGTT	TCTCCTTAAGCAAGGACCGA	267
CcM1096	FI220712	(CA)6	TTCCACCCTAGGACAATTCG	TGCACTATCAAGGGAGGTGA	245
CcM1097	FI220721	(TCT)5	TCAGGGTGAAGAATTCCCAA	ATCACCAAAACCCAGGTTGA	238
CcM1098	FI220734	(GA)10	CAGGCATGCAAGCTTTGTTA	ACAGGCCATTCTGATTTTGG	247
CcM1099	FI220751	(AT)9	TCCTAGAAATCCTCTGCCCC	TGAATTGAGATGTGAAGATGATGA	256
CcM1100	FI220754	(A)10n(TA)14(T)14	GCGCTCAAAAAGGAATGTCT	GAAAACTCACTTCTCTGGATTGG	256
CcM1101	FI220856	(TTC)5n(CT)14	TTGTGGCCTGATCTCACAAG	GGACTTTCTTTGCATTTGGC	170
CcM1102	FI220862	(AT)13	AAGCTGCGCTCCAAGTAGAC	ATTCGAAAATCCTTCCCTCG	208
CcM1103	FI220885	(AAG)7	GGCAGAGAAGGATTCGGTGT	GACGACTCAGCGTTTCACAA	148
CcM1104	FI220968	(TA)6	AAAAATAAGCTAATGAAGGCATCTT	GCACGGATGGACCACTTACT	156
CcM1105	FI220980	(AT)18n(TA)6	TCTTGCAAGGTCCTCAAAGG	CCGTTGAATCATTGAGATTTGA	233
CcM1106	FI221012	(TGA)5	TTTAATGCTGGCAAATGGGT	TCAAGTTCTTGATTTTAAAAGCTTCAT	229
CcM1107	FI221085	(TC)6	ACGAACCTCACTCATCCCAC	TTGTTGGTTGGCATACATGG	229
CcM1108	FI221110	(TG)5n(A)10	GAACGTGATCATTCACGGGT	GCAGATGATGCATGGTAAAGA	251
CcM1109	FI221111	(AC)6(AT)8(GT)10	CCCGTCATAGTTGTCACCCT	AGGAGTTGTTCTTGGCATGAG	212
CcM1110	FI221145	(ATT)10	TGCAGCAGAATCTTTGAAGG	CGAAGAACTCAATGTTGGACTG	240
CcM1111	FI221168	(TC)5n(TA)11	AAAGAACTTTCAATCTAACGGTTG	TGAATATCATTGAGAATGAAACAAAA	278
CcM1112	FI221168	(TA)16	GGTCCATCTTAAAAGTCATCCC	AATCAAAGATGATTTGATACTTCATTC	280

CcM1113	FI221175	(GAA)5	ACAAGGGTTTTGTTTCGTGG	ACGTGCCGTATTTGTTCTCC	207
CcM1114	FI221181	(A)10n(TA)18(T)10	GCGCTCAAAAAGGAATGTCT	GAAAACTCACTTCTCTGGATTGG	260
CcM1115	FI221219	(TA)6	CCAGTTTTGGTTGACGGTTT	TAGGACCCAAACCCGTGTAG	244
CcM1116	FI221254	(TC)9	CCATGTTTTGGGGTTTGTTC	TGTTGTAGCAATCAGCAAAATG	277
CcM1117	FI221260	(AAT)7	AACATCAAGAAGGGTCCACA	AAAGGGAAAGGGTTCTGCTC	280
CcM1118	FI221293	(TTC)5	TTCAAAGCTTAGAGACCCAAGAA	ACATGCAACCCGAAAAGTTC	276
CcM1119	FI221326	(CA)6	TGGAAGTGTTCTACGGGGTT	TTTGCAAATGAAAGCAAAGA	242
CcM1120	FI221338	(TGG)6	CAACGCAATCAACCCTAACA	CCAGCATCACCATAACCATC	171
CcM1121	FI221360	(AT)24	TGGCTAGATGTAGCGTGGAG	TAGTGGGTGGACACTCATGG	219
CcM1122	FI221388	(ATA)5	TGCAAGTATAACACATTATTGCCA	ATGGGCGAAAAATTAGAGCA	278
CcM1123	FI221395	(ATAA)5	CCTTATTTTGAGTGGGAAAAGAGA	GCAAGCTCTTTTAGACATCGG	232
CcM1124	FI221400	(TA)15	AACGCCATGGAAATATCGAG	ACAATGCAACCCAAATCCAT	145
CcM1125	FI221401	(TTA)7n(ATA)8(ATT)8	AAAAGACGAGAATGAGGGAGA	CTCTCAAACCTCAACCATGTG	236
CcM1126	FI221439	(TC)9	AGGGCAGAACTTCCACCTTT	TCCTTGGGGGTTAGATTTCC	232
CcM1127	FI221578	(AAAT)5	TGGGATGAAAATAAAATGAAAGA	GCAAGGAAGTGATACGAGAAAGA	102
CcM1128	FI221580	(AT)9(GT)9	ATTTTGTGTGTGCTTGACCG	GGAATGATCCGCTACCAAAA	277
CcM1129	FI221600	(AT)31	GGGGCGACATTTATGTGTTT	TCTCGAAGTCAATGCCCTCT	276
CcM1130	FI221613	(CA)6	CATAAAGGACGGCTTGTGGT	TCAAATGGTGATTGCACGTT	261
CcM1131	FI221637	(AT)6	AAAGAGTTGCGCCCTGACTA	GAAAACATAATATCTCTCAATGGGG	249
CcM1132	FI221643	(TTA)7	ATGGAAAGGGTTCTGCTCTG	AACATCAAGAAGGGTCCACA	279
CcM1133	FI221660	(AT)13	GCTTAACACTTTTTAACGCCTTTT	AGCAGCTGTCTTCTTTGTTGG	230
CcM1134	FI221673	(AT)12	CACTCGTAGCCGGATCTTCT	TGAATTGAGATGTGAAGATGATGA	183
CcM1135	FI221678	(AT)12	CGAATATTAAATGAGTAAATGTTGCTT	CACTTGCAGGAGTTTATTTTAAGG	276
CcM1136	FI221685	(CA)6	CCACCCTAGGACCCTACGAC	ACCAAGCCTTTTCAAGTGGA	202
CcM1137	FI221696	(AT)7n(AT)5	TTGTTGTTTTGTGGGCTTGA	GGAAGCAACATTCAATGCAA	227
CcM1138	FI221717	(CA)5n(TG)5	AAGTTGGCCTCATCAATGCT	CAAGCATGTCCAGCAAAAGA	248
CcM1139	FI221770	(ATG)6	CAGGGACAAATGCCTGAAGT	CCCACCAAGCTCTCAAAGAC	200
CcM1140	FI221838	(ATT)8	GCCCAATCCAACATAGCATC	GGAAAATGTCTGAGGTGAGGA	210
CcM1141	FI221891	(GTG)5	AAGTGATTTCGATGAATGACTTGA	ATGCAACAGCCACATCAAAA	201
CcM1142	FI221892	(AT)17	AGAATGAACAATTCATACATAACCAT	TCAAGTTTATGCTTTCCGAAGA	246
CcM1143	FI221908	(A)12n(T)11	TTCCACAAAATAGTTCTTGAAATGA	TTACTTTCCCAAAATAAACGGA	207
CcM1144	FI221943	(TA)6	AAAGCCCTTTATGGGGTTACA	ATAGCTTGGTTGGCTGGTGA	188
CcM1145	FI221945	(CT)7	ACATGCCTAAATCCAGTGGG	TAACCTCTCCAGGTCGATGG	237
CcM1146	FI221969	(TA)10(T)15	TGTTGTCCCTCAACATTTGC	TGAAAAAGACCAAGGGTAAAGG	169
CcM1147	FI221973	(AGA)5	GGTCACCTGAAAGTTGGCTC	CTGGGTCTGTGAGCTCGTTT	208
CcM1148	FI221991	(A)12n(AT)9	GATGTGCGTGAGAGAGAATAAGAA	AAAATCGCTGATGTGGGACT	222

CcM1149	FI222040	(AT)5n(TA)16(GA)12n(GA)6	GCCCCCTATATCAGATCAGTTT	TTGCCCTATTTCGTTGGTTG	185
CcM1150	FI222042	(TA)7	ACCCTCCATGGTCCCTACAC	TTTGTGCTTGATGACACTAGGAG	193
CcM1151	FI222095	(TA)7	GCATTTCCCAAATTAACGGA	ACTTGTGTCAGATGTGGCGA	263
CcM1152	FI222151	(TAAA)6	GCGTTAAATCGGGAGACGTA	TGGCCTTATCTTTTGGGTTG	219
CcM1153	FI222180	(TTC)5	AAGCCCCTTCACAAAGGAAT	AAGCAAGGTTCCAAGCTTCA	121
CcM1154	FI222188	(AT)24	TTCTCCCCAGATTTCCACAG	TCAAGAAGGGAAGTAAGAATTGG	240
CcM1155	FI222192	(AT)7	TGGTTGGAAATGAGTTGTGG	TGGCTTAATTCATGTGAAAAACA	110
CcM1156	FI222203	(AT)7	CCATGGATGTTGTTGCATGT	ACTTTACGCTTGTCGCCACT	270
CcM1157	FI222253	(TC)6n(TC)7(TA)27	CATGCAAGCTTTGGGTCATA	GATTTAAATTAGAAGAGAGGAGGATTT	178
CcM1158	FI222311	(TAGCA)5	AAGTTGAAAAGGCTGCGGTA	GCAATTTGCAAACAAACTCAA	103
CcM1159	FI222318	(GA)6	TTTTGGCAGCCTTTCTCACT	TGTGAGCAATCTCATGCACA	150
CcM1160	FI222321	(GA)6	GGTGCTTTTTGGCTACCTTTC	TCATTGTTATCAGGGCCACA	131
CcM1161	FI222437	(ATTT)5	TTGAGATAGGTTTGAGATAGTTGTTCA	CAAAATTATTTGATTTTCATTCTTGC	264
CcM1162	FI222449	(AT)22	TGATCGAACCTTGCTCTTGA	TGTAGTTTCACATTGGTTCTCCA	275
CcM1163	FI222468	(ATG)5	TCACCTCTTGGATTCCTTGG	GCAAGAAGTATCAAACAAATAAGCA	237
CcM1164	FI222564	(CT)19(AT)17n(T)11	TAGAGTCGACCTGCAGGCAT	TTTTTAAATTTTCTAACATGGCCC	277
CcM1165	FI222590	(TAA)5	GCTCGATTGCTCGTAGACCT	TGAACCCGTGAATGCTCATA	128
CcM1166	FI222612	(AT)9	CCCTTTCTAATTCGGTTTTGG	AACGATCCTGTGTAATGCCC	207
CcM1167	FI222704	(GA)7	AGCCAAAGGTCTAGGGAGGA	CACAGTTTAGGGGACTCCGA	182
CcM1168	FI222786	(TA)6	CATGCAAATTGCCTCCTTCT	TTCAAAACCATTGTTGTGCTTC	137
CcM1169	FI222826	(AT)5n(TA)9	TAGAGTCGACCTGCAGGCAT	TGTGGTCCTTTTACTTGCGA	205
CcM1170	FI222875	(TA)7	TAGAGTCGACCTGCAGGCAT	TGGTTGAAACCCAACAATGA	158
CcM1171	FI222881	(AT)7	TCAATAAATTAATGGGGGCAA	TGCCAAATCCATCTTTCATCT	260
CcM1172	FI222891	(AC)6	ACACCTTTGCACCTTCAACA	GATTCGGTAGGGTCAAACCA	263
CcM1173	FI222917	(TA)12	TTCTTTAAGTAAGCGGATCCTTC	TTTAATCTAACGATTGGATTTACAAAA	161
CcM1174	FI222926	(AT)14(GTAT)6	AATTGGTTGCCAGTGTAAAAA	CTTTGATTATCTTCAAATTGTTGTTT	222
CcM1175	FI222926	(TA)20	TTGTCCTTCATCATCCGACA	TGGCAACCAATTATATCTTTCAA	204
CcM1176	FI222973	(AT)6	GGCAACCCTGCAGACAATTA	TTCAATTCTACCGAGCCTGG	225
CcM1177	FI222996	(AT)24	ATGTGACACCCTCTACCCCA	TTGGAATTGTCGTTTCAATTTTT	130
CcM1178	FI223012	(AT)10	TCAATCGATCCACTTCGACA	CAAGTGCGAGAAAATTTGGA	230
CcM1179	FI223028	(TA)19	AGTGAGCGGGCATTATTTTT	GAGAGATAGGAAGCGATGCAA	263
CcM1180	FI223032	(CT)7	AGTCCCGAAAATTGGAGCTT	GATCGATTTTGTATTGCCCG	268
CcM1181	FI223047	(GA)6	TTTTTAGGTGCTTTGTGGCA	CGTTCCAATGCAGTTCGTTA	267
CcM1182	FI223049	(TAT)5	GGAGATCACTTCCTCGAAACA	GCACCCCTACAACGCTCTAA	234
CcM1183	FI223061	(AAAT)5	AGCTTCCAGCGGTATTCGAT	AGAGGGGTCTCTTTCACTTATGA	272
CcM1184	FI223082	(AT)9	GGAAGGGTGCTGCATGTAAT	CGAACTTTTCCACAGCCATT	272

CcM1185	FI223109	(TA)17n(A)10	AAAAATTGTGAAACACCCGA	AGAAGTGAAAGAAATAAATAATGGGT	199
CcM1186	FI223158	(AT)6	TGAAACACCGTAACTCGAGAA	ATGGTGGGAGATGCTAATGC	280
CcM1187	FI223159	(TC)6n(TC)5(TA)5n(TA)7	TGATTTCCATCAAAAAGTGTGA	GGTTATAATTCCATTGGGGGA	263
CcM1188	FI223192	(AG)5n(TTA)5	TTTCTTGATCTGCCCCAGAC	TTGAAAATTTGGCGAAAACG	255
CcM1189	FI223251	(TA)8	AAAGATAACTCTGGCAGAAAAAGA	AGCCACTCACGCAACATCTA	130
CcM1190	FI223272	(GA)7	ACCTCATGGCAAGCTTTGTT	AAATCTCGGGCACAGTTCTC	186
CcM1191	FI223292	(AT)7n(T)11	TGGCTATTTAATCCTTTTGTTGG	GTTATACGACGGATGGCGAC	252
CcM1192	FI223294	(ATG)5	TCCAATTCCCTTAGGCTGTG	GAGTGAGAAAGTGGCCAACC	182
CcM1193	FI223300	(TA)8	GCTTTCAAAATTAAGAAATGTTGGT	AAAATTACATCAATATCGTTTGAACTC	190
CcM1194	FI223308	(CAA)5	TCTTCATCTGCATCTGTGGC	GTTGCTGCTGAGAGTTTCCC	241
CcM1195	FI223333	(TC)6	TTTAAGGCCCCGTAACTCCT	GGCAGTTTTCGAAAGAACCA	102
CcM1196	FI223354	(AAT)5	TAGAAACACCCTTGTTGCCC	TGCTTACAATGGTACATTTGGC	263
CcM1197	FI223424	(AT)14	TCATTTGCTAACCCAAATTCC	TTCGGGAGTCGATTACGTGT	227
CcM1198	FI223437	(TC)10	TCAAAGAATCCGAATCCCAC	TCGGTGCTGAGAAGAGGAAT	267
CcM1199	FI223451	(CA)7	GAGAAACTTCTCACTCAGTTGCAG	TATAGGTGTGCCTTCGGGTC	199
CcM1200	FI223526	(ATC)5	TGTGAAACCAAGAAGAAAAACG	AAGGAATGAATTCACCTGGAA	121
CcM1201	FI223541	(TA)8	CAACGACACATGTCCTCCAC	GTGAAGCGAAATCCCACATT	266
CcM1202	FI223542	(TA)8	TAAGGTGTTTTGGGCAAAGG	CTGGAGCAAGCACAAGATCA	115
CcM1203	FI223595	(TA)10	GCCAATTCATAATGTGTTGAAAA	TTGGGCCAATGTGTTGTTT	259
CcM1204	FI223601	(ATA)6	GTTCGGCATTTGTGTTCCTT	TGTGTGTTTATGGTCCTGATGA	218
CcM1205	FI223621	(AC)6	CCCCTCTAGGAACCACATCA	ACATGTTTCACGTGGTTGGA	232
CcM1206	FI223643	(AT)26	AGACTTGCGCTCATAGGTGTT	TCATCTAGTGCTGGACACCCT	276
CcM1207	FI223661	(AT)17	TTCTCCCCAAATTTCCACAG	TTTTTGGCATTCTTTTTGGA	229
CcM1208	FI223689	(TTC)6	TGATGGTGAGTCTATGTCTGCC	AGCAAGTCATGATGGTCACCT	101
CcM1209	FI223746	(CAT)5	TTCACGGCCAACTATTTTCA	TTTTGAACTTGGGAGATGCC	273
CcM1210	FI223812	(AG)7	GGTTCCAAAGCAAGTTTCCA	CCATGTGAAGCGATTTTCCT	258
CcM1211	FI223819	(AATA)6	GATTCAAAAGATTTTTGGGGG	TCAATCTCTTGCCACCAATG	192
CcM1212	FI223834	(AG)11	GACACAATTGCTGATCAGGTC	TTCATGTAGAACGGCAGAAAAA	187
CcM1213	FI223857	(TG)7	ATTCGTTCTTTCATGGGTCG	CCGGACAATTTTAGGGGTCT	169
CcM1214	FI223871	(A)27n(AG)5	TCCCTGAGAAGAGAGGCTCA	CTCACCGTTACCGTCACCTT	264
CcM1215	FI223896	(A)14(TA)12n(AT)8n(AT)31	AAAAGTGTTACCTTATTTTCAACAAGT	CATTATTTCGGTTGTTTCCTATCT	277
CcM1216	FI223928	(TA)28	AATCCTTAACTAGTACCGGCAGA	GATATGCTCACATTTTATGTCTTCAA	159
CcM1217	FI224032	(AC)11(AT)16n(ATA)11	CCTCTCATCCAACATTAGCATC	TGAGAACATCACATGGCATAAA	279
CcM1218	FI224048	(AT)20	GTTTAAAGGTAGGAAAACGTAACAGT	GAACAGCCCGTTCCAATTT	278
CcM1219	FI224081	(GA)7	GCAGGCATGCAAGCTTTACT	TCTAGCGTCCGAACATTCCT	230
CcM1220	FI224086	(CT)14(AT)22	TCGAGTGCAATAAGTCAACCA	CGTGTACAAATTTCATCGACAA	188

CcM1221	FI224104	(ATC)5	CATTCATAGCATCTCCGGGT	CAAGAGCATGAAATGGAATTGA	272
CcM1222	FI224136	(GAC)6	CTCATGGAGTGACCGAACCT	AAGTTCTAGGATTAAGGGAATGTCA	246
CcM1223	FI224187	(GA)7	TGGGGATTTTAGGTGCTTTG	GACCTCCAAAATTTCGTCCA	139
CcM1224	FI224192	(ATT)8	AAAAAGGCACTTTGTACCTGTATTA	CTCCAAAAATGTTCAATAAACTTG	259
CcM1225	FI224216	(TA)29(GA)12	CATGTGTGCCATGTGTGTGT	GAGGGTTTAGACCGCACGTA	213
CcM1226	FI224219	(AT)36	CATTTTCAACCTGCTGGTCC	GGCCCACTGGAATAACATCA	277
CcM1227	FI224221	(TTA)8	ATAGGATGTGACATTGGGGC	AACATCAAGAAGGGTCCACG	262
CcM1228	FI224221	(ATG)6	TCAGAGCAGGTCGATCCAAT	AGCACAACACTAACAACACAAGG	130
CcM1229	FI224225	(TA)8	GCCACAATCATCTCCCAAAC	AAATAGGAAATAAATTCTTCTCATCAA	255
CcM1230	FI224259	(A)10n(AAT)6	TGGATTCTTTGGGATTTTGC	ACCCAAGAGCAAGAACGAGA	249
CcM1231	FI224357	(CA)6	AAGCCTCATCACCAACATCC	GTGAAACTTCCGTATGGCG	268
CcM1232	FI224405	(GA)6	GCTTGAGGCCTTGAGCTAGA	GCCCTCAGCAATTCTCATTC	270
CcM1233	FI224414	(AAT)9	GTGTGACACCCTTCTACCCC	TTCTGGATCCCTTTCATTTTTC	217
CcM1234	FI224427	(GT)6	GCAACAATAAGCAAAAACCGA	TTTGCAAAAGTGTGAGCAGT	259
CcM1235	FI224441	(ATA)15	TCCACCAGATGGTCAACAAA	GAAGGCTTTTTCAACCTCCC	226
CcM1236	FI224471	(AT)31	CCGATAGATTCAGTTCGTCTCC	AATCGGTTCTCCGTTCCTCT	254
CcM1237	FI224472	(TTC)5	CTGTCGGTGGATCATTCCTT	AGATATGCCGCGTCTCTCC	191
CcM1238	FI224477	(AT)10	TGAATGAAGAATCATAGGCAACA	TCAACAGTTGGATCGTTGAAA	231
CcM1239	FI224495	(TA)5n(T)13n(TA)11	TTAGTGTTTTGGGTGGGGAA	CACCGATATCGTTTGAATCCT	270
CcM1240	FI224501	(GA)6n(T)11	TAGGTGCTTTTTGGCAACCT	TTCTAAACGGGTCGTTCTGG	201
CcM1241	FI224524	(AAT)7(ATT)9	CGAAATCCAGAAGACAGGGA	CACGGGGAGGAGATAACGTA	246
CcM1242	FI224531	(AT)19	GGCATGCAAGCTTGTTGATA	CTGGTGTGGTTGATGGAGTG	213
CcM1243	FI224556	(GA)6	CAGGCATGCAAGCTTTGTTA	GTCGTTCCTAGGTGCGTGAT	264
CcM1244	FI224595	(AAT)5	TGCGAAAATGCCATCAATAA	TCGGGATTATGATAAAAGCTAGA	205
CcM1245	FI224694	(CTCA)7	TGTGGCATGTCTTGAATTGG	CAAGCTCAGCCAACAAAACA	214
CcM1246	FI224756	(TA)11	TGCTTGAACGATAACTTTGGG	TGGTGAAAACAACTAATTGCC	189
CcM1247	FI224759	(TGT)5(TAT)6n(TAT)5n(TAA)17	GCAAGAGTGACAAAGTGTATTATCC	TTTGACCAATGACCCATCCT	201
CcM1248	FI224822	(GA)6	CACACTACACAAATGCCTCACA	GCAGCTTGGGCTCATTTCTA	129
CcM1249	FI224835	(A)10n(A)10n(TA)18	TCCACAAACAGTTGAACGAGA	TTTCATAAAGATGTTTTTGTTCTTCA	222
CcM1250	FI224859	(AT)8	AAACATGTTAACAAGGTGACTTCAA	GGCATTGCATTTTCTAACTCC	251
CcM1251	FI224872	(CCA)9	CAAATGGCAGAACAGAGCAG	CGGAGATTGCATTGTTCCTT	228
CcM1252	FI224872	(GTC)5	CTCAGATCCTCGTCGTCTCC	CCGAGACGATTTCTCAGGAT	167
CcM1253	FI224892	(TA)6	GAGAACCATGTGAGTTCATCAAA	TGCAAATTTGAAAATCATTTCACT	270
CcM1254	FI224899	(AT)17	AAGTTATGGGTGGCAGCATC	TTTTAGTTCTGCTAGGAGTCTTCATT	163
CcM1255	FI224962	(AT)49n(AT)7	ACTACCTGAATGCTGACGCA	GAAAACAGGAAATATACAGTAGCAACA	240
CcM1256	FI224979	(TA)18	CCTCACCTAAGTTTGCCATCA	TGTGTGCCTCTGAGAACCAT	129

CcM1257	FI225059	(AT)15	ACACCTCCAAATCCAATCCA	CGCCATGGAATTATCGAGTT	136
CcM1258	FI225070	(TA)17	TCCTCTCGTGAGTCTTCAACTCT	TCAAACATAGGGGTTTCACGA	264
CcM1259	FI225089	(TG)6	TTGAAATCTTGGTTCACACCC	GAGGGCACAAGTCAAAGCTC	235
CcM1260	FI225092	(AG)7	TTAGGTGTTGTGCGTCAACC	TGGAACGGGTCATTCTAAGC	278
CcM1261	FI225101	(ACA)6	CCGCACTTGTCCTCTTCTTC	AACGTCATCCTCGAAAAACG	257
CcM1262	FI225134	(GA)6	GGCATGCAAGCTTTAATTTGA	CGATAACAAAGCCTTGTCCC	266
CcM1263	FI225136	(AT)28	CCCAAAATACACCCAATTCA	GCATATCCTGCTAATGTCGATT	226
CcM1264	FI225150	(TA)12	ATGAGAATTGCGTGCAACAG	CCTGGGATTTGTAAGCCTGA	204
CcM1265	FI225189	(AT)5n(T)10	AAAAACCTGCTTCATTCCAA	TCGTTCGGGACAACACATAA	259
CcM1266	FI225208	(ATTT)5	TTCATGAAAATGACTTCTTTTGG	ATTTGAAAATTGATGCCGGA	185
CcM1267	FI225212	(A)13(AT)9	GACCAGCCGTGAAGATTTGT	GGAAAAACAGCCACCAAGAA	186
CcM1268	FI225281	(GT)7	ACCAAGCCTTTTCAAGTGGA	TGAAAGTGTCCCAAAAAGCC	241
CcM1269	FI225285	(TA)9n(TTTA)6	TCCAAACTCGGTCAAATCAA	ATCCACGAACGAATTTCACC	235
CcM1270	FI225310	(AT)42n(A)10	GATTGATCACTCCATAACAAGCA	TCTCCATCTTCCACCACACA	266
CcM1271	FI225359	(AAAT)6	GGAGAGTTTAGGCTAGCAAATGA	CACCAAAAAGCGCCTAAGAG	277
CcM1272	FI225379	(TA)11	TGAGGGTTTTTAAAAGAAATGGA	TGCCCCCACTATCTAAAGTTTC	271
CcM1273	FI225446	(TAT)7	TTTCATTCATCTTCTTATTGGTTACA	CGTCGTTGCTTTCTTTACTTTG	207
CcM1274	FI225456	(GGT)5	TTCATACAAGGGCGTTAGTTCA	AAAAACATTTTTCTTCAAGATTTGG	273
CcM1275	FI225468	(TA)12n(T)12	TTTATACCTCAAAAATAAACCAAACA	GTAATACGCCGCCTCAAAAA	277
CcM1276	FI225540	(AAT)5	GAAGTTCCGCCACTGATTGT	TTCACAGGTTTGTGTGCTCG	240
CcM1277	FI225550	(AT)13	TACCTTTGGAGGCTTTGGTG	TTGCGACAACCCTGTCAATA	247
CcM1278	FI225563	(TC)13(TA)18	TCGATTACCAGAGAACATGGC	CCATCCACCTTCTATTTTCAGG	263
CcM1279	FI225625	(TA)13	GCAATGATGTCATGGACTCG	TTTTTCATCCAAACACACATGA	249
CcM1280	FI225660	(AT)6	CTACTGCTGGCCTACGTCCT	ATATAGCATTGCCCTGTGGC	230
CcM1281	FI225668	(CT)8	ATGGTTTCCGTTCTGTTGCT	CATTCACCAAACAGGCCATT	188
CcM1282	FI225677	(AT)18	TCAATGGTTACTATTCATTTGAAACA	CAGTCCTGCTTAAAACCGATG	257
CcM1283	FI225691	(AT)22	GCAGGCATGCAAGCTTAATA	AAACCCAAAAGTCAAACCAA	185
CcM1284	FI225715	(TTC)7	TAGAGTCGACCTGCAGGCAT	GGCTCTGAAAAGCCAAGAAC	115
CcM1285	FI225718	(AT)17	TTGTGACACCATCTACCCCA	GGACATGTTACATCGGGACA	279
CcM1286	FI225750	(TA)9	ATTGACCATTCACGCAATGA	CCAATGTCGTTTGAACTCTCC	190
CcM1287	FI225764	(AT)25	TTGAGTGGTCTCAACTTGGAAA	TTTTCCCCTCCTTCTTGTGA	261
CcM1288	FI225805	(AT)7	ACATGGAAACATGCAAGGGT	GAGGCCAACATTGTGAGGAT	278
CcM1289	FI225815	(AAT)8	TGTGCCATTTAATCGAAAATCA	CCATTCCATAAATTGACCGAG	244
CcM1290	FI225834	(GTT)5	TTGCCTTTTGAGATTCCCAC	ACAAGCAATCCGTTGCTACC	175
CcM1291	FI225898	(AG)10	CTGGGTCCAGTGTTGGACTT	CTTTGCTTGCTAGATCCCCA	201
CcM1292	FI225907	(TA)8	CTTTGCATCAAAATAAAGTAAAAATTC	TGCATTGGTGGTTAGCAAAG	266

CcM1293	FI225916	(AG)6	TGCTTTATGGCAACCTTTCA	AACACATAACGGCCAGATCC	231
CcM1294	FI225992	(AT)30n(G)13	TGAAGGAGAATTCAAAGCCAA	GGACGAGGACGGGTATCAT	276
CcM1295	FI226000	(TTA)7	ATAGGATGTGACATTGGGGC	AACATCAAGAAGGGTCCACA	259
CcM1296	FI226036	(TGT)5	TTGTTGTTGTGGCTGTGGTT	ACTTTCTGAACTGCCGGAGA	175
CcM1297	FI226078	(TA)6(A)12n(A)11	CATGCAGTGCCTAGGCTAGAA	CAAGAAACCGAATGCATCAA	212
CcM1298	FI226140	(GA)8	GGTGCTTTTTGGCTACCTTTC	CAGACTCAGGCACTGTTCCA	145
CcM1299	FI226141	(AT)5n(TG)5	GGGTGTTGAGATGTTAGAGATCG	AGCATTCATCATAATCATCAGACA	195
CcM1300	FI226162	(A)13n(AGA)8n(A)10	AGAGAGCCACCTTGGTTGAA	CATACATTCACACTTAACACTCTTTTC	259
CcM1301	FI226185	(AT)9n(TA)8	GATGCCACTCGTAGCCAGAT	TGGTATGGATTATGATGGATTGA	252
CcM1302	FI226212	(T)10n(CA)7	CCCTAGGGAATCCGACTAGC	TGAACTATCAAGGGAGGTGGA	270
CcM1303	FI226215	(AC)6	CACTTTGTGCCTGCTTGTGT	ATAATGCCAAAGGGGGAGAA	128
CcM1304	FI226250	(ATT)6n(T)11	CCAACTTAACTCATAAGGTGTCTGG	TTGGATGGAGTTTTGTTTTTCA	278
CcM1305	FI226284	(A)10(AAT)5	GAGCGACAGGAGGAGTGTTC	TTCGCGTTAGTGTGGTTTTG	211
CcM1306	FI226339	(TA)10n(AT)8	TCACTTCCAAATCCAGGAGC	TTTGAGCAAAAGGAGTGAACC	219
CcM1307	FI226364	(AAC)6	TAGAGTCGACCTGCAGGCAT	TTGCTCATGCACACAGCATA	205
CcM1308	FI226387	(TA)15	GCCCAATACAAAAAGTGATCC	CGCAAGTGCGTGTATTTTTG	206
CcM1309	FI226400	(AT)7	TAGTGCACTCAGCACCCAAG	TGTAGCTGCATGGCAATCAC	225
CcM1310	FI226421	(TG)9	CGGGCTCATTAATTTGTTCA	CGTAAATACCCCTTCACGGA	182
CcM1311	FI226421	(TA)7	TGGGAATTCTGGATCTGTGA	GGCAAGCCTACCCATAATCA	177
CcM1312	FI226432	(CA)7n(AT)5	AAGCCTCATCACCAACATCC	TTGTGAATCTTCCGTATGGC	270
CcM1313	FI226443	(AT)17	TGCTTTCCCTTTCTCCTTTTC	AAATGAACCACACTCGGACC	257
CcM1314	FI226455	(TC)6	TCCAAATATGCCTACGATCCTT	TAATCACACTTGCACGCACA	169
CcM1315	FI226501	(AAGAAA)5	AGGGCCACTCTTCCCTACCT	CCGGACAATTTTAGGGGTCT	263
CcM1316	FI226520	(TTC)5	GCATGCAAGCTTGAAGAGAA	GCCATTATAGCAGCAGCCTC	234
CcM1317	FI226560	(ACCTCC)7	GTACACGTCCACCTCCACCT	ATTGGGATTGGGTAGACCG	159
CcM1318	FI226584	(AT)8	GGCCTGGTCCTAGTTTTGTG	CTGGCCAATTTGACCTTGTT	238
CcM1319	FI226620	(G)10n(TG)5	GCATTGGTCCGAGATGAAGT	CGATGAAACTCCCAAACACA	254
CcM1320	FI226656	(TTA)12	CCAACAGGGTCAAAAAGCAT	AAAACGCACAAAATAATATTCCTC	261
CcM1321	FI226667	(GA)6	AGGCATGCAAGCTTTATTGG	AATTGAAATCTCGGGCACAG	198
CcM1322	FI226671	(ATC)5	TTTTGAAACTGAAGCCAACTGA	ATGGAACGAATTCACCTGGA	208
CcM1323	FI226680	(CT)6	AGAGTCCACATCATTCAGGGA	TTTCATTTGAGATGCCCTCTTT	115
CcM1324	FI226740	(TC)7	CAAGCGAGGTTTCTCACTCC	CGAATTCAATACGGGCTGTT	231
CcM1325	FI226766	(TA)6	TGTGTGTGGGTGGCTTTTTA	ACAAAAATTTGGGGCTTTCC	104
CcM1326	FI226771	(TA)18	CCTTGGCTTCTTTCCCTTTT	TTTTATCAAAATTTAACTGTGAACCG	273
CcM1327	FI226809	(TTC)6	TAGAGCGCTGTCCTTGTCTG	ACGAAGATTGCCATGAAAGC	199
CcM1328	FI226819	(AT)13	GCAGATAGCATCCTGGGAAA	TCCACACAAACACACACAAAA	107

CcM1329	FI226823	(TTA)6	GTACTGCGGTTTCAAGACCC	GCTGGCATCCCAACACTTAT	240
CcM1330	FI226847	(AT)14	TGAGAGTTTTGTCCTTGCATGA	CACACCAAAGAAAAGGGGAG	257
CcM1331	FI226849	(AAAAT)5	CCTGAGACAGATCCATGTTTACC	AGGGATCAATTGTGAATGTCG	250
CcM1332	FI226877	(TC)6	CTAGCACTCCAGAACGGGTC	TTGTAGGTGCTTTACGGCAA	275
CcM1333	FI226900	(AT)17	TGTGTTTGATTGAATTTTTAAAGG	GCCCGTTCGAGAACTATGAA	231
CcM1334	FI227006	(TTG)5(T)16n(T)10	GCATGTTGTGGATGTTTCAAG	CATTCGCCACTTACAATGAGT	280
CcM1335	FI227057	(AT)6	TCATACTACACTTTTTGACACTTCACA	AGAAAACAAGAACTCAAAGTAAACAA	274
CcM1336	FI227124	(ATC)5	TAGAGTCGACCTGCAGGCAT	AATGGAACGAATTCACCTGG	111
CcM1337	FI227155	(AAT)5	GATTCTGTGGGATTTTGTGGA	TTGGATTAAGGATGATTCCGA	209
CcM1338	FI227166	(TG)7(T)10	CGAAGGGAAGAACTCCTACCA	CCTTCCCTTTGGCCCTATAA	250
CcM1339	FI227173	(AT)6	ATTCATGCACACACATGCCT	GCCATGGAAATACCGAGCTA	253
CcM1340	FI227178	(TA)6	ACGCCATTCTAACCACCTTG	CCATAATCCAATCCAAATCCA	261
CcM1341	FI227223	(T)10n(A)10n(TA)6	AATTTGTGTCTCCATTCCCG	TCCTCGTCCCGCTTAATAAT	176
CcM1342	FI227291	(TA)8	GCACATGCCAGATCATTTTG	CGTCCCACATTCACTCCATT	268
CcM1343	FI227320	(CT)5n(AG)5	TTCATTTGCTTCTGCCACTG	GTGATGTGCTGCTGTGTGTG	165
CcM1344	FI227322	(TA)27	TAGAGTCGACCTGCAGGCAT	TGTTCTTAGAGAAATGCTAGCACAC	280
CcM1345	FI227326	(AG)6	GCTTTGCGGTAACCTTTCAC	ATAGACAGCTCGGGCACAGT	138
CcM1346	FI227369	(AAG)7	TTGTTGTGCTGAAAAGCAGC	GACAGGCACATCCACACAAG	271
CcM1347	FI227373	(GA)10	TCGTCGAGTAAATGCAGCAC	GGTTCTGTTGCAGTGAGCAA	220
CcM1348	FI227452	(T)10n(AT)18	TGAAGTCATTGCACCTTGACA	AAAGTGGCTAAACCAATTGCATA	280
CcM1349	FI227457	(TG)6	TGCACTATCAAGGGAGGTGA	CCACTTGGACTTCCACCCTA	255
CcM1350	FI227503	(GA)5n(A)12n(AG)6(A)14	AGAGAAATTGATGCGAAAGACT	TTTTCTCTTCTTTCTCGCCATC	186
CcM1351	FI227533	(TGA)5	CCGGACAATTTTAGGGGTCT	TGTGAAACCAAGAAGAAAAACG	227
CcM1352	FI227553	(TG)6	ACCAAGCCTTTTCAAGTGGA	GCTTCCATTGCCTACTACGG	123
CcM1353	FI227570	(TC)5n(T)10	ACATGTAGCATTGGGTGGGT	CACAGGGTACACGCAAGATG	165
CcM1354	FI227593	(TA)12(TG)6	AGTCAAGGAATTCACGCCAT	GGTTGATGTCATGCATAATTGG	278
CcM1355	FI227600	(AT)6	TGCTAGGGAGAAAACTCGGA	CCTGTCTTGCACCTTAAGCC	112
CcM1356	FI227645	(GA)10	CAGGCATGCAAGCTTTGTTA	AATCTCGGGCACAGTTCAAG	188
CcM1357	FI227664	(AT)15n(ATA)5	TCTAGCATCTCCATTAAACCATTT	ACACATATGACATTTAGCAAATAAAAA	280
CcM1358	FI227679	(A)11n(A)11n(AT)7	TCATGCATACTGTTCATCGG	TGCATGAAATTTAAGGAAGAACAA	273
CcM1359	FI227683	(GA)6	ATAGGTGCTTTGTGGCAACC	CATCTCTCAGGACCCCAAAA	129
CcM1360	FI227707	(AT)8	GGAAACACCAGGCAGAAGAG	ATGTATGGAGCAGAGCAGGG	221
CcM1361	FI227726	(AAG)5	CCATGCATAATGGCCTTACC	TTGAATTCCTTCTATTGGAAAAGG	224
CcM1362	FI227756	(TA)5n(TA)12	ACCAACTCCCACAATCTCCC	AACCCCATAAGAAGATTTATGACTTT	260
CcM1363	FI227814	(TA)6	TGGAAATACCGAGCTATTTGGT	ATTCATGCACACACATGCCT	251
CcM1364	FI227822	(TA)9n(TA)15	TAGAGTCGACCTGCAGGCAT	CAAAATAAACATGCGTGATAATGA	219

CcM1365	FI227823	(AT)20	AGCTCATTCCCCACATTGTC	TGCACTAAACAAGTCCAATGAAA	225
CcM1366	FI227825	(AT)16n(TA)7	TGCCAACTAATCTTGATCTTGAC	CAAATTCAATCTCAATTTCACATAAA	280
CcM1367	FI227868	(GCA)6	AGCAGATGCTGCAGAGTCAA	GACGCAAGATGTTGCTGAAA	238
CcM1368	FI227892	(GAT)5	CAACCTAAAAGGCAAGGCAA	TCTGTGTGACATCTTGGAAAGG	240
CcM1369	FI227920	(ATG)8	ACCCATGGAAGATTTTTGGA	TTCCCATGTTTCAACCTTAGC	192
CcM1370	FI227979	(CT)7	GGGATTCAGCCATATTGGAG	GCGGATCGAGAAGCTCTATG	238
CcM1371	FI227984	(T)12(GT)6	ATAATTGCGTCACGTTGCAC	TGATGGATGAAAAAGGTACGAA	164
CcM1372	FI227989	(TA)37	ATGGCTCATCCCATTAGCAC	TTTTGCTTGCTGATGTTTCAA	197
CcM1373	FI227996	(TG)7	AATCAACTCGGCCATTCTTG	TCCTTTCAAGCGGAAAACAT	255
CcM1374	FI227999	(TA)9	CAGGCATGCAAGCTTAAAAA	TCTTCTGAAAATTTCTTCCACGA	254
CcM1375	FI228026	(TA)8	AGGATTTTGGTTCTGACGGA	TGAAAAACTATAAGATGAAGTGTGAGA	191
CcM1376	FI228047	(ATT)6	TAGCTCTCTTACATGTCCCATTT	TCCACACATCTCCAACTTTCA	104
CcM1377	FI228061	(TC)7(TA)5	TAGAGTCGACCTGCAGGCAT	AATTAGGGGATTTAAAGTTATTCACA	180
CcM1378	FI228096	(AT)31	GCATGCAAGCTTTTGAGAGA	TTCTTTTTACATCATCTTTACCATTTT	199
CcM1379	FI228138	(TC)6	CATTCTTTGCCTATTGCAAATC	CCCATCAAAGGGGCATATTA	100
CcM1380	FI228157	(TA)27	AACCATGCAGCATCATGAGA	TGCATGTGCAAGAGTTCATGT	214
CcM1381	FI228166	(TA)9	AGCACACAGTACGGAAAGCTC	GGCAAATGTTTTCTCTGGAATC	243
CcM1382	FI228171	(AT)9	ACGAGGATGAAGGGAAAACA	TCCCAAGTGTATCCCTGGAG	207
CcM1383	FI228180	(TA)9	TTTTTGAATGGATTGATGATATTC	ATGACCCTTGCTCACCACTC	232
CcM1384	FI228198	(TTA)8	TCTGGATTCCTTTCATTTTTCTTT	TGGATCGACCTGCTCTGATA	240
CcM1385	FI228203	(TTA)10	TTTTAACGGGATCAATTAAATTCTG	AAAGGTGATGATGATTTAGTATGACA	257
CcM1386	FI228232	(TA)20	TCTTCTAACAAAGGAAAAGACAATGA	TTTCTTGTTACTCGACAATGCC	203
CcM1387	FI228245	(AG)8	ATTTGCCTATAACGCATGGC	CTCCCCCTCTAGATTCCCTC	181
CcM1388	FI228330	(TA)21	CCATTGTTCGGAACCAACTT	ACAATAACACACATCAGAGTTCAAA	273
CcM1389	FI228366	(TA)16	AAAATCAGTATATTCGACACTGAGAAA	CATTGCAATATCTAACTTTGTAGGG	253
CcM1390	FI228378	(TA)8	GCATGCAAGCTTGGGTATCT	CAAACGAATGTTAAAATGAACGG	274
CcM1391	FI228389	(AT)14	GGGTTAACATGCAAATAGTCCC	TTGCCTAAGTGTCATGCGAG	200
CcM1392	FI228390	(T)10n(AAT)15	CGTAGGCTTTTTGTTTTGCC	GGGGAGTTCCTTTCACCACT	199
CcM1393	FI228466	(TA)6	TGTTTGCTGGTGCATTAGAGA	AACCTTTCTCCCCTTTTGGA	270
CcM1394	FI228478	(AAT)5	TTTTTACTCTTTTTCTGCTTACACATT	TTGGTGTTGATGAATCAGTGG	133
CcM1395	FI228484	(AG)5n(CA)5	TGCCCAGAATAGAAAGATCCC	TGGGTGCATGTGATAATTTG	262
CcM1396	FI228507	(GT)6	CCTCATCAAGTTCAGGCTCC	GAAATTCAAGCATCCCTTGC	258
CcM1397	FI228529	(ATA)7	TTCCCAAATTTCTAACAAATACCC	GGTTATTTCACGGGCTTCAA	273
CcM1398	FI228539	(TAA)7n(TAA)11	TTTGTTTCTCTTTTAGAGGGCA	TCATATTCGAAATAGGCGGC	230
CcM1399	FI228630	(AT)8(TATG)7	TCATTTTGAGCTTGTGGCTG	TTTTAACACAAAGAAACATACCCA	163
CcM1400	FI228726	(AC)5(AT)6	ATTCATGCACACACATGCCT	TTTGAGAGGCTAGACGCCAT	280

CcM1401	FI228730	(AT)17	GCTCTCAACGCTATCCGAGA	GTACCCTGGTCACCATCGAG	269
CcM1402	FI228810	(TA)7(TATG)7	AACGCCATGGAAATATCGAG	CACCTCCATAATCCAATCCAA	120
CcM1403	FI228925	(GA)7	GCTTTGTGGCAACCTTTCAC	TTTCTGATTTCAAAACGGGC	253
CcM1404	FI228991	(TC)6	CATTCTTTGCCTATTGCAAATC	CTTGAAATCTACCCGGAGGG	275
CcM1405	FI229002	(TC)8	GCTCCTAATGAGACGCCACT	TTTGACAGGTACAATTACTATTTCAGG	275
CcM1406	FI229007	(AGA)10	AAACCCATTTTCCCCAAAAA	TCAAGAGTCAAGCTTTGGAGG	217
CcM1407	FI229015	(TTA)5	GACTCCAGCGGTATGGTTGT	AACGTCCCATTCCATCTTTG	194
CcM1408	FI229055	(AT)6	AAGGTTACAATCAATGGTAGACAAA	TGTTTATTGTACATGTGCGAGTCTT	249
CcM1409	FI229073	(TA)5n(TA)5	TGTCAAAAATAACGGATACACCA	TTGGTTTTGGGCGTTAAGTC	196
CcM1410	FI229083	(AT)6	TCCTTCAAGCATCATTACCAAA	GGTCAATCTGCAGACCCAAT	187
CcM1411	FI229103	(A)10n(A)19	AACGTAGGGTGTGAGTTCGC	GTTGATAGGGTTATTGCGCC	141
CcM1412	FI229118	(ATC)5	TTTGTGGAGTCTTTGTGACCA	CCACTTCTTGACCCCAGAAA	259
CcM1413	FI229155	(AAGAAA)5	TTCGAAAAGAATCCACTCCC	TGTAGGACATTGGGAAGCAA	203
CcM1414	FI229202	(AT)10n(TA)20	GGCATGCAAGCTTGAACATA	AATACTTAGTAAAAGTTACGCCGGT	275
CcM1415	FI229218	(ATC)6	TGTGAATCCAAGAAGAAAAACG	AGCACCCTTGTAGAAACCCA	206
CcM1416	FI229231	(AT)11(ATA)15	CTGTATCTCGCCCATTGTGA	TCACATGATTATTGGAATTGTCG	168
CcM1417	FI229275	(GAA)6	GAGAGGTGTTGTGGAGGGAG	CAAAGACGCAGAAAGCCTCT	204
CcM1418	FI229283	(AT)14	CCCTTGCCTCTCACATTTTC	GGAGACATCTTTGCGTGCTT	168
CcM1419	FI229291	(TA)6	TGGGACAATTTAATTTACACCATT	TGGTCCCGTCTCATTTCTTT	228
CcM1420	FI229298	(TTC)5	TAGAGTCGACCTGCAGGCAT	CTAGCTTCCCTTACCTCGGG	275
CcM1421	FI229312	(GTC)5	CCGGAGCTACCCATTATCAA	AAACATGTGCCCTATCGAGG	267
CcM1422	FI229325	(TTA)7	ATAGGATGTGACATTGGGGC	AACATCAAGAAGGGTCCACA	259
CcM1423	FI229404	(TA)11	TGGATCCTCTTTCAAGCACC	TCTGATTTGGTGTCCACAATTT	278
CcM1424	FI229406	(AT)27	TTCACACAGGATAACCGTTCA	TTTTAGGTGGAAAATTAAAAATCTCA	160
CcM1425	FI229436	(AAT)7(AATA)5	TGTGCTTTCTCATTACTGTCACAA	TCCCCAAAGTGAAAACCTCT	222
CcM1426	FI229449	(TC)5n(TC)7	CCTCAAATTCACCCAATGAA	TAGCACCAAGCTTCAATCCC	181
CcM1427	FI229464	(AGC)6	CAACCACATATTCTGCGAGG	GTTGCTGGCTTTCAGGTCTC	160
CcM1428	FI229466	(AT)31	GGCATGCAAGCTTAGTCTGA	GGGTCGGCAAGGTTTTTAAT	190
CcM1429	FI229493	(TCA)5	CCGAAAAGATTCCAGCAAAG	ATCTCCAAAGCCATTCATCG	271
CcM1430	FI229554	(A)12n(AG)6	AGCACTCCCAGAAAACAGGA	GCGAGAGCGTGTGTCAAATA	198
CcM1431	FI229574	(AT)19n(TGA)5	GGAATGTTGATACATGCTGAGG	TGTGTTAGGGTAGAGGGTGTCA	179
CcM1432	FI229586	(TA)6	GTGAATGGCATCAGCAGAAA	CATTTGAACACAGCATTCGG	215
CcM1433	FI229648	(TA)8	CAGGCATGCAAGCTTAACAA	TCATGCATCAATATATCATTTCACT	216
CcM1434	FI229683	(CA)7	TCGGTGATATCTGACCCCAT	AACACGGCAAGTATACCGGA	252
CcM1435	FI229687	(ATA)5	TGACACAAACAGGATAGAATTGAAA	TCGAATGTGTTTATCAAATGCC	236
CcM1436	FI229730	(TA)19	GCGTTATTTTGAGAGTTTAACGA	CACTCTGCACGCTTCTAAAAA	247

CcM1437	FI229769	(TA)7	GCAGGCATGCAAGCTTATTT	TCCCCTACCAAGAGGAGTTTC	267
CcM1438	FI229781	(TAT)8	ATTCAAACGGCGTAGCATGT	CCAACACGAGCAACAATGAT	213
CcM1439	FI229815	(TTA)5	TTTAATGGCCTTTGCACCTC	CTGCCTCCATTGCATTCATA	255
CcM1440	FI229833	(AT)6	GGGCAAAAGTTGGTGTCTTG	ACCCTTACGTGGTTGGAAAA	233
CcM1441	FI229861	(TA)5n(AT)9	AGGCATGCAAGCTTAAGGAA	TTTTACATTGACCCAAGTCGG	205
CcM1442	FI229912	(AT)12(T)12	TTCTCTGGGGGCATAAATTG	AACGGTAAAGCAGCAAATCC	259
CcM1443	FI229957	(ATC)5	GTCTTTGCGACATTCTTGGG	AAGGAACGAATTCACCTGGA	150
CcM1444	FI230046	(AT)15	TGGCTGTGGAATTTTGTCTTC	TTGGGGGAGTTGTTGAGTGT	224
CcM1445	FI230065	(AT)7	TTCATAATTACACAAGTTGTAGTGGA	TGTCAACTCATGACACATTTATTTTT	278
CcM1446	FI230122	(AC)5(AT)14	TAGAGTCGACCTGCAGGCAT	TCAAATGCCAATTTTTCAAGA	280
CcM1447	FI230144	(AT)10	CTTTCCACGGTCCAGTGAAT	TCCATTTGACATGTAAACAATGAAC	269
CcM1448	FI230149	(TTA)10	ATAGGATGTGACATTGGGGC	AACATCAAGAAGGGTCCACA	268
CcM1449	FI230155	(TATT)5	AATTCGTTGAGGCAAGTCAA	TCAAATTGGTTAGGCTTGGTG	162
CcM1450	FI230183	(CT)5n(TA)12	GGACGAAGATTGTGTGAAGAGA	AAAAGATATGATTGGTTGTCAGTG	276
CcM1451	FI230185	(TA)11	CCTTCCTTGCAATATCCAGC	TGCCTTGGTTATGTGCTTTG	115
CcM1452	FI230260	(AT)14	GGAGGCAAAGATCTTCAACG	AGCTGCACGAGATTCAGTAGG	218
CcM1453	FI230268	(ATT)21	CAGCTTGAGGGGGAGTGTTA	AAATAATGGCAGATCCCTCG	278
CcM1454	FI230275	(TAT)6	TGGGAGTGTAACACCCTATGC	AACCTCCCTTGAACCCATCT	273
CcM1455	FI230278	(C)13(CT)5	CCCCAAGACTTGACAACACA	CCAACAAGCCATCAAGGTAA	148
CcM1456	FI230413	(AT)13	AAATGACAGGCACACTCGTAA	AAATTCTTCCTTGAATTTTAGTGATGT	260
CcM1457	FI230443	(ATG)7	TGGGGTAGAGGGTGTCACAT	AAGAATGAAGAAGAGCGGTCA	273
CcM1458	FI230452	(TTA)9	ATAGGATGTGACATTGGGGC	AACATCAAGAAGGGTCCACA	265
CcM1459	FI230453	(CT)12n(TC)5	TTGGGATTGACCTTCCAAAG	CAAGATCAAGAAATAATAAGACACGA	171
CcM1460	FI230498	(ATT)9	TTACGTGCACCCGGAATACT	CGTTTAGCTCCTCTTTTGCG	262
CcM1461	FI230506	(TGT)5	GATGATATCTCCGACCTGAATTG	GGGTGTGCAACCTTTGTTCT	195
CcM1462	FI230540	(AT)6	TTGATCCAAATCAAATGAGGG	CGGTTAAATTTACAAAATTCACATT	156
CcM1463	FI230611	(TA)17	CACCTTACAACATTCGCCCT	AAGACATCTCTCCTATTGAGCCC	252
CcM1464	FI230618	(AAT)5	CGTAACATTCCTTTTAAAACACAAGA	TCAATTCAGGCATCTTGAAAAA	197
CcM1465	FI230635	(GT)7	TGAACTATCAAAGGAGGTGGG	CCAAGGTCACTTCAAGCTCC	274
CcM1466	FI230638	(GAA)5	GGTAGCCATGGCAGGAATAA	GAAGCAAATTTCGGGTTCAA	280
CcM1467	FI230645	(TG)6	ACCAAGCCTTTTCAAGTGGA	GCTTCCTTGCCTACTAGGGG	123
CcM1468	FI230710	(AAGAAA)5	TGGAGCATCAACTTCAACGA	TTGTAGGACATTGGGAAGCA	231
CcM1469	FI230754	(AG)7	GGTCGAGATCGTGTTCGATT	ATCCAACGCTCAAAAATTGC	229
CcM1470	FI230868	(TAT)6	ACGCAACGTTGGAAGAAGAT	GCTTAATCTAATTTGTTTTCACTCCT	217
CcM1471	FI230868	(AT)19	TGATGTTTGCTTGGTGCAAT	AACGTTGCGTCGGTTTTAGA	226
CcM1472	FI230895	(AT)8	ATGTCCAACCCCCTCTTTCT	TTCATGGGGCCAATGTAGTT	218

CcM1473	FI230902	(TTC)5	GTTTGCACCACAAGTTTCCC	CTCCAATGGCACGGTTATCT	220
CcM1474	FI230912	(CAT)6	ACATATGCTCGCAACACGAG	AATCGGCCGTGAGTTATGAG	270
CcM1475	FI230965	(GT)7	TGGTAGCCTCCTCGCTCTAC	GCTGAAAATGGTCCTTCCAA	273
CcM1476	FI230975	(AT)8n(AT)5	TTTATGGGGATTATTAAAATGGAAA	CTTTACTGCACCATGCCTCA	264
CcM1477	FI230978	(TTG)6n(TG)9	CGAGAAAACCCCAAAGTGAG	AACCTTCAACCAAAATCCCC	224
CcM1478	FI231001	(AT)13	GAGTCGACCTGCAGGCAT	GCCTTTAGCAACATCACACG	280
CcM1479	FI231081	(CT)6	TTGGGCAGATTAAGAATGGG	AAAAGTCAAAATTGGCAGGC	169
CcM1480	FI231083	(ATC)5	GGAGAGTTTTCTTTGTGAAACCA	CACCCCTTGTAGAAACCCAC	215
CcM1481	FI231167	(TA)32	TCTCTTTTAAAAATTATCAAACGGTAT	TTTGGCGGACATCTTTGAAT	268
CcM1482	FI231179	(TA)31	GCAGGCATGCAAGCTTATCT	TCAGGAAGACTAATTTCAGCCA	278
CcM1483	FI231188	(AG)7n(GA)7	GGAACCAAAGAGAGCTACTGC	CAAGGGTTGTTGAACCATGA	141
CcM1484	FI231217	(AT)7n(TA)13	GTGCACCATTGGTTGTTTTG	TGTGTTTTCGCATTTTGTTGA	173
CcM1485	FI231222	(AT)8n(TA)5	GATTATTGTAATGACCTTCCATGA	GCTGCGGGATGAGTAGTTTT	271
CcM1486	FI231224	(TAT)5n(TA)21	TTGGATTAAGGACATGAATGTAAA	AAATGTGACACCCTCTACCCC	190
CcM1487	FI231295	(TA)6	GAGGACCAAAAGTACAATTAAACCA	TCAACGACTTGTTTGTTTTACGA	243
CcM1488	FI231325	(TC)5(T)11	CGATAGGGGTTGTGATAAAGC	AACTTTAAGGTTTTCAAGGGCT	219
CcM1489	FI231358	(AG)7	TGAAAATTTTAGAGAAAGAAAGAAAAG	TCAGACAGAACAACGGCAAG	222
CcM1490	FI231394	(AT)14	CAATAATTAAGTAGAAAGCACAAAAGG	CAAACTTTTGAAAGAGATTAGTTCTCA	221
CcM1491	FI231436	(GAA)5	CCAAAACACAACATTTCCCC	TGAAAAGAAACACAATCCTTGAAA	100
CcM1492	FI231442	(AT)7	GAAACTTCCGGTTTCGGTC	TAGGACATGTGACATCGGGA	274
CcM1493	FI231459	(ATTA)5(TA)10	CAGATTGTCAAAGGAACCATTAT	CGAAGACATTTTCTTTTTGAAGC	161
CcM1494	FI231459	(AT)29	GAAATGGTGCAACCAATTTTCT	GTGCGTCATCCAATACGTCA	239
CcM1495	FI231485	(AC)15(AT)22	TGTCTGTTAAACTTTTGAAGGAGATT	AAAGGTAAACATGCATACTGCAAA	251
CcM1496	FI231497	(TG)5n(A)10(AAT)5	TACGATCGTTCGTGGGTGTA	TGACCTAAGAATGTACAAAGGGG	165
CcM1497	FI231498	(TA)5n(TA)6n(A)10	ATCCTCCTAGCGTCCCATTT	CCAATGCCAAAATAAATTTGAA	219
CcM1498	FI231528	(GAA)5n(GA)7	AAGCAAGGTTCCAAGCTTCA	TCCCTAACCTTTGTATTCACTTTTG	224
CcM1499	FI231541	(GAA)6	ACACGCAACCTACCCAACTC	GGCAGATTGAAGTCTGAGGG	196
CcM1500	FI231571	(AT)6	TGCAATTTTCGAACGTTTAGAT	AACTATTCATAATCAATTTCTTCAAGG	165
CcM1501	FI231579	(CA)6	TGGGATTAAGAAAAATGAGAGAAA	AATTTTCCATCAATGCCGAG	173
CcM1502	FI231617	(AT)10	ATTGTGATTCAAGCTTGGGC	AAAGATCATCCACCACCACC	255
CcM1503	FI231638	(TA)19	TCGACTTAAAAAGATCAAGTTCAA	AAATGGATTCAATTATTCAAGAGTGA	181
CcM1504	FI231673	(AT)11	GGCCCAAAAATTGGTTATCA	ACGGGATGATGTATTCCTTTT	144
CcM1505	FI231697	(ATG)5	CCAAGAAAGCACCCCTTGTA	GGAGTCTTTGTGACAATCTTGG	243
CcM1506	FI231721	(A)10n(A)10(TA)11	TGTTTTTGCAAAGGTTTCCC	CAACACAATGAAAAAGTAAACATCA	279
CcM1507	FI231773	(TA)6	TCTGCTTCAACGGACACTTG	ATTGCTTCGTGGGCTTGATA	127
CcM1508	FI231781	(TCT)5	CGTCTTCGGATGAGGAAGAG	ATCCCAAATCTCCAGCAATG	177

CcM1509	FI231801	(T)10n(ATT)5	CCCCTAGATCCCTCCATGAT	TTTCCCTTTTCACCCAAAAA	213
CcM1510	FI231808	(AG)7	CACACAAATCGTGATTTTAATTGG	CGTCAACTTATTTTGTCTTGCATC	168
CcM1511	FI231889	(A)10n(AT)7	TGCAGATGATTGGTGTGGAT	TCATCATTATCAAGTGTTCGGTG	219
CcM1512	FI231917	(T)12n(TA)10	ATACTCGCCGGGGATAAAAT	GGATGTTAATACCCACCCCG	280
CcM1513	FI231959	(CAA)5	AGATGTAGGAGGAGCATGAGC	GACCCCAAAACCTCATTCAA	240
CcM1514	FI231991	(AG)7	TACCTTATCCTGCCCTCCAC	AGTTACTTGACGGGGCTTTG	111
CcM1515	FI232036	(GA)6	GCTTATGAGATTGTTTCTTCATGAGT	TTACGGCATGAGCTGTGAAC	274
CcM1516	FI232057	(AG)9	TAAATAGGAGGCAGGGGTGA	TTCTCCTCCCCCTTACTTGG	189
CcM1517	FI232079	(AG)10	TAATGATCAACGCACTCCCA	TCCACTCTGCAATGCAATTT	157
CcM1518	FI232085	(TA)18	CCTGCCACCATTGAGTTTCT	TTTGCCATCAAACAACAAGG	114
CcM1519	FI232089	(TA)18	CAAAAGTTGATTTTTGGCCC	GCACCAAATCTTAAGCTCGC	271
CcM1520	FI232125	(AAC)6	CCCACAAGGAGAAGATCCAA	TCTTCCATTTGTCCCTCGAC	211
CcM1521	FI232145	(TA)6	AACAACCTGACATCATGAAAAGAA	TTGCCCTTAGCCTTTGTGTT	235
CcM1522	FI232171	(AT)14(TA)6	TGAAATGAGTCTACCAAAGCTTACTC	TTGATCTATGCACCAAGAACTTTT	207
CcM1523	FI232177	(AAG)11	AGCGCGTTAAAATAGCCAGA	CCAGGTCCCTTTTCTTCTCC	209
CcM1524	FI232185	(AT)14	TGATATCTACCAAACTTTTAAAGGAAA	ACAATAAAAAGAAAGCACAAAAAGT	226
CcM1525	FI232278	(AT)16	CCCTGATTTCATTTTCTTTTGG	TCGTCCCCATTTTAAACTAATTG	195
CcM1526	FI232316	(CT)6	TCAAAGCCAACTTTTCTCCTTC	ACGGAGATGCAAAGGAAATG	253
CcM1527	FI232350	(T)13(TAA)5(TTA)5	CCTCCAAGCCAAGGTGTATC	ATTCTCGAAAAGCATCCGAA	201
CcM1528	FI232371	(AT)16	AAATCCCATACAGTTATCAATGATTTT	CATGGATATGGTAAATTTCTAGGC	154
CcM1529	FI232390	(TCT)5	ACGGAGATAGGCTCAGACGA	ATGCATTTCTCTGACACCCC	272
CcM1530	FI232393	(AT)9	CACCGATCTTACCTAGCGGA	CCGTTAGTAATTTTCGACGGA	253
CcM1531	FI232395	(AT)39	TACCCTCGTGCAGGTACACA	CCACCCACTCATCATTTCCT	212
CcM1532	FI232427	(CAT)6	CATCATCATCAAACCTCAAACC	TCGCATTTAGTCCATATAATGTCA	165
CcM1533	FI232439	(CT)8(AT)8(TA)6(GA)7	TGAACTTTGAATCTAATGGTTGGA	CGATGAAATTCAACACACACC	253
CcM1534	FI232442	(GTG)5gn(GTG)5	GATTGGTTGGTATCGGTCGT	ACAAAACCAACCACCACCTC	209
CcM1535	FI232452	(TA)6(TG)6	TGGACAACCTTATCCAAGGAA	CCATAATCCAATCCAAATCCA	237
CcM1536	FI232499	(GT)8	GGGAGGTGGACTACAAGGAA	CCCTAGGGAATCCGACTAGC	260
CcM1537	FI232502	(AT)17	GACTGAAAGGTTAAACAATTAACAAAA	TTTGAATATGAATTTTACTCATTATCG	148
CcM1538	FI232534	(AT)17	AACAACAAACAAGCAAGGGC	TCAAGTAAATGAATAGCTCATCGAA	204
CcM1539	FI232595	(AT)20	CTTCACCAACTCGCCAAAAT	GACAAATTTATTCGATGGACCC	154
CcM1540	FI232617	(GA)9	GACGGTGGAGATGTTCCTGT	ACCTCGTTCCTTCCGTCTTT	189
CcM1541	FI232621	(TA)9	AAAGTTAATTATGCTTTGGTTATGATG	GCGACCAAACTCTTGTTCCT	107
CcM1542	FI232698	(AT)18n(A)10	CTAGTGAAGGAGGCTCACCG	TTGAGAAGGATAAGGTACGTACAGA	191
CcM1543	FI232716	(GT)9	CCTCCTCCATCAACAAGGAA	TGCATGCTTTAGTGCTTTGG	220
CcM1544	FI232842	(GTG)5	ATTGGGCCTCTTCACCTTCT	GTCATGCTCGAGAGAGACCC	192

CcM1545	FI232872	(ACTATC)5	GATTCCTCTCACGAGGTCCA	TTGCATCCATTTGATCCTGA	202
CcM1546	FI232978	(AT)24n(TG)5	TGATCAAAGACTATGAAAAAGTTCAA	ACACAGACACACAGACACAGACA	136
CcM1547	FI233006	(CA)6(TA)7	GGAAAGAGCAAAGTGATATCCG	TAGGGCTCTTTCATGATGGG	268
CcM1548	FI233020	(GA)9	CAGAGGCAACTAATTGGGGA	TACCCTGTTTTGCTCCCAAG	141
CcM1549	FI233021	(TA)27	TATGTTGAAATGGCCAAACG	TGCAAACTTGATTTGTGCAT	279
CcM1550	FI233038	(TTG)6	ATGCTTGCATGTTTGGGTTT	CAGGTATGTGGAACAGTGGAA	134
CcM1551	FI233069	(AT)28	TGGTTGCGTGTATGGAAAAA	ACATTTCCAGCACGTTGACA	256
CcM1552	FI233107	(TC)10	TTCAAACACCACAGCGTAGC	GCTTCACAGAAGAAGACGGG	161
CcM1553	FI233109	(TC)8	ATTGGCAACTTTCTGCAACC	GCTCTTCGAAAGAGACGGTG	273
CcM1554	FI233119	(TCA)6	AGGTGGAATGCTTTTGCAGT	GGTCCCTTTAGCGAACATGA	228
CcM1555	FI233136	(CT)5n(CT)5n(TC)14	GTTCTCCTCCCCCTTACCTG	TAAATAGGGGCATAGGGGGT	205
CcM1556	FI233143	(AT)8	GAAAACACAATAGGTAAACATACATGC	AGATATTCATTTATTTGATGTTTGTCA	216
CcM1557	FI233144	(TA)14	GGATAAAGGGCTTTCTCGCT	AGTGCAATAGGGCAAGCATC	242
CcM1558	FI233147	(TAT)6(T)14	GCATCGGATATGTGTTCATTCT	ACGCACGGAATTAAGTGGAC	148
CcM1559	FI233176	(AC)12(AT)8	TGCCAATTTTGACTTGAAAACA	TGCTTGTTTGGGAATAAGGC	260
CcM1560	FI233255	(AT)6	TTCAATTTATTCATTTATTTCCCAA	TTCCACAAAATAAACCAAAAGAA	224
CcM1561	FI233265	(AT)17	TCCAATTTTTCCAATTTTGATTTT	TTCAAATGAGATTAGTTTTCATACGTG	242
CcM1562	FI233294	(CA)11(TA)18	TTTTAATCCTTTTTGTTCTTTTCATGT	TTTCAAATAACGTAAATTTGGATAAAC	233
CcM1563	FI233370	(TG)5n(A)10(AAT)5	TACGATCGTTCGTGGGTGTA	TGACCTAAGAATGTACAAAGGGG	165
CcM1564	FI233373	(TC)7	GGCCCACATATGATGCCTA	TTTTAGGTGCTTTGTGGCAA	169
CcM1565	FI233424	(TA)23	TCCTCCTTTTTGGGATGTTC	TGGAGCTTGAGCCATCTGTA	279
CcM1566	FI233437	(AAT)8	TTGTAAGGGACCAAAAGAGGT	TTCAATTTAATGAAACGAAGTATCAAA	253
CcM1567	FI233440	(TG)6	TACCGGTTGTTCGTCTCCTT	TGCATTGGACGAAGAACATT	223
CcM1568	FI233441	(TA)8	TGCAGCTAGTAGAGGGTTCACA	GGGGAGAATAGGCACCTCTAA	189
CcM1569	FI233447	(GAA)5	ACCGCAAAATCAAATTCACC	TCGTCAAAGTGTGATCCTGG	238
CcM1570	FI233662	(TA)14	TGGTTTATAGAATGAAAAATTAACCAA	CAAATTTTCAACTCAACCATTG	280
CcM1571	FI233722	(AAGAAA)5	GGAGGCCCACTCTTCCTTAC	TTGTAGGACATTGGGAAGCA	161
CcM1572	FI233752	(TA)7n(T)10	ACTCTTGGAGTTATTTGATCCCT	AAATTTCAATGATCCAACCG	209
CcM1573	FI233902	(TA)12	AGGACCTGATGGCAGCATTA	CTCGTCGAAGGCTTGAATTT	196
CcM1574	FI233902	(A)14(TA)8	TCTTGGAGAAGTTGTTGGGAA	TTTATGTCTTTAAATATTATCCCCACT	251
CcM1575	FI233908	(TAC)5n(T)11	GAGGGGAAAAGTTGGAGAGG	CATGCAAAAGTAATAAAAGACAAATCA	254
CcM1576	FI233979	(GTT)6	TCTTGCACTCAAAGACACGG	TTGATGTTGCTTTCTCGTGG	100
CcM1577	FI233991	(AAT)7	CAAGAAGAAAAACAAACTCGTCAA	TGCGAAACAGTGTGAGGAAG	184
CcM1578	FI234002	(AT)25	CGTAGCCGGATCTTCTTCAC	TGGTGTGGATTATGATGGATTG	257
CcM1579	FI234004	(GT)7	GGGAGGTGGACTACAAGGAA	TCTCCAATTCCGTTTAGAAAGC	170
CcM1580	FI234035	(TA)9	CAGTTGAATCGTTGAAATTTGATG	CGAAACACCTAAGGGCATGT	270

CcM1581	FI234083	(TA)10	TGCATGGGTGTGATTCAAGT	TTTCTTTTTGGCCTTTTCTTTTT	267
CcM1582	FI234124	(AAT)5n(TGT)8	CCAACACCTTTCCTTAGCCT	CCTAACCAAGGATGACGTGG	202
CcM1583	FI234155	(GA)18	GCCTATAAATAGGGGCAGGG	GGACCTCCTCCTCTGGATTC	165
CcM1584	FI234160	(AT)24	AAGACGATCTTCAGTGGACCAT	TCCACTCACTAAAACCTCACCC	253
CcM1585	FI234162	(TG)6	CAGATCTGACCCAAAGTCATGT	CCCTCTTTCCGAATCAAACA	214
CcM1586	FI234195	(TA)9	CAACGGTTGAATTGTTGAAA	AAAAATTCCTCCACGACACTTC	240
CcM1587	FI234239	(T)10n(AT)10	GGGCATTTGCCTCCACTAA	GCCACCTAAAATCTATTTATTGACG	272
CcM1588	FI234332	(TC)5n(A)18	TTTTTGTCTATCTCTCCCCATCA	GCCGTATTCCTGTCATGTCC	225
CcM1589	FI234336	(ATG)5	GACCCCAAGAAAGTACCCCT	TTTGTGAAATCCAAGAAGAAAACA	215
CcM1590	FI234354	(AT)9	CGTCCATCCCCAACTAATGT	TTGTCCCAACCGGACTCTAC	223
CcM1591	FI234360	(TA)8	CCTAACCGAACACCTAAATGATG	GACTTTGTGTTGGACAGGCA	189
CcM1592	FI234385	(AG)8	CATGACAGCTTGCACCAAAT	TGCCAATGCCAACTAAAACA	265
CcM1593	FI234392	(AT)7	TCCCCCTTCCTAAGTTTCCA	TGCACATTTGTGTCATGTGG	151
CcM1594	FI234417	(TA)7	TTTCATACAAGAAATGTTACATGCAG	TTTCATGCAAAATCAACATTAAAA	137
CcM1595	FI234469	(TC)7	CTCATTTCAGAACGGGTCGT	GGTTTTAGGTGCTTTGTGGC	271
CcM1596	FI234470	(TA)6(TG)13	AGATCCAAAATTCACCAACCA	CACAAAGATTCAATAATGACACCA	270
CcM1597	FI234487	(TA)26	GAGAATGTGTTTTTCTTTCTGACTTG	AGAGAACCAAAATTCCCGATT	241
CcM1598	FI234499	(G)11(GA)10	GCCATGGTTGAGGATGTCTT	GGAGCTGGCTCTTATCATCG	255
CcM1599	FI234518	(TC)5(AT)5	CGACACAAATCCAAAAAGCC	CAAAGCTGAAAAGGTAGGGTT	280
CcM1600	FI234544	(CT)6	GTGGTTAGGAAACCTGCCAA	TGAGGGAGGAATCAGGAAGA	238
CcM1601	FI234750	(TA)24	GCTTGTTTGCTAGCACAATGTA	CCCACTCTCTATAAATAGATCCATCC	232
CcM1602	FI234782	(TA)18	TGACGATGTCGTCCTCAATTT	CCCAAGACTTGAACTCGAAA	248
CcM1603	FI234858	(TG)6	AAACATGAAATACATAGAAGGGGG	AACGATGAAATTCCCAGACG	180
CcM1604	FI234882	(TC)6	TGATAGGGCCCCTCCTTAAT	ATCCCGATCAGAACGAACAA	253
CcM1605	FI234972	(TA)37	TTGCAGATTTGATCTATGCATTAAG	TTTGTGTTGTAGTGTGTCTTTGC	239
CcM1606	FI234982	(AG)7	AAGGTTCTCAGCTGCTCCAA	TTCCTGAGAGGGTTTTGTGG	162
CcM1607	FI234984	(AG)12	ATAATTAGGGGCATCAGGGG	GTTCTCCTCCCCCTTACCTG	172
CcM1608	FI234986	(ATA)5	GACCTCTCAACGGGCTACTG	GCTGCATGCATTCTTTTCTTT	256
CcM1609	FI234996	(AT)26	TCATGGGAAGGACAACTTCA	AATACATTGGGGGAGGGACT	207
CcM1610	FI235025	(AT)16	ATTTACGCTGCCATGTGTGA	ACTCTGTCTGAGGCGTTGCT	151
CcM1611	FI235053	(AT)22	AAGAAAAATTCCTAAACCCGTG	GGAAGATCGTCCCTACGACA	250
CcM1612	FI235064	(AT)20	TGTGACATTTGACTGCATGTTT	TCACTGGAGTATCCATCGCA	243
CcM1613	FI235102	(GA)6	TTTGCCCCTTTACCTACGTG	ATGGCGGCTAAGCATACATC	133
CcM1614	FI235119	(CT)8	CCTCACACCAAGGTGGTACA	GAATGCTCCGAACTTGTTTCA	249
CcM1615	FI235124	(AT)23	TTCAAAGTTTGCATTATCGCT	GTTCTCAGCCGAGAGCATTC	237
CcM1616	FI235251	(TA)6	ACGACTTAGCACGACACCCT	GAATTCATTTGTTATTACAGATTTCAA	222

CcM1617	FI235258	(AC)5n(A)11	GACACACGGGCAAAAGAGTC	GGAGTTCTTTCAGACCGCAA	237
CcM1618	FI235293	(GA)7	TGAGTGAGAAGGTGAAATCTTAGAG	AAACAGAACAATGGCAAGGG	229
CcM1619	FI235358	(AT)18	AAAATTAATTATGCTTTGGTTATGACG	CCCTACTAACTTTGCGACCG	130
CcM1620	FI235377	(ATT)11n(T)10	ATGCCGAGGAAACACTTTGT	GGAGTGAATGCTCCCTTGAA	254
CcM1621	FI235381	(AT)7	TTAGTGGCATCCCTCTTATTTTT	CGGAATTGGATTTAGGAGGA	279
CcM1622	FI235382	(TA)26	TCCGGAAGATTCCTTATACCG	GGGTGATGATGTGGCAGTCT	279
CcM1623	FI235399	(GA)6	TCAGAGCGAACAATTACAGACA	TACCCGAGATCATGAGGACC	192
CcM1624	FI235433	(TG)6	TGAACTTTCAAGGGAGGTGG	CACCCTAGGCAAACCGACTA	265
CcM1625	FI235448	(TTC)12	TCATCCACCTCTTTCCATCC	TCAAAGGTGAGGGCTTTGTT	261
CcM1626	FI235486	(AT)15	TCGAAGAAAATGTTTATTTATTTGATG	AATAAATAGAAAACACAAAAGGTATGC	235
CcM1627	FI235535	(TAA)5	TTCAACAAAATAGAGATGAAAGTGA	TCCTCTCTTTTAAGCTCCCTCA	276
CcM1628	FI235548	(TA)22	TCCCTTTAAATTTTCCCATATATCA	TGTGGGGTAGGAAATATCACAA	273
CcM1629	FI235573	(TG)6	CATGGCAATCAAACTTTCCC	TTGCTCCTCCACTTATTCTCC	231
CcM1630	FI235613	(GA)9	TGTGCCCCAACCTTAAAATC	CCACTGTGACCCTTTCAGGT	280
CcM1631	FI235628	(AAT)5	AGTCATTAAACCCCAGGACC	GGTAGCCAAAAAGCACCTTC	278
CcM1632	FI235712	(AT)26	GTCGCGGTGCTCAATAAGAT	TTCCTTGCCACAGATATGGA	174
CcM1633	FI235714	(AT)7	CGATGCAATCTATAATCCATTTG	TGAATTGATTTTGGAGCAATTT	222
CcM1634	FI235728	(TCT)7n(CA)5	GTGTTCACAAGTGGTGGGTG	CGAACACGGTTGAGAGTTGA	236
CcM1635	FI235732	(TA)20	CGTGTAACCCGTCAACAAAA	TCGCTAACAGAAGGTATTTCTCA	275
CcM1636	FI235737	(AT)6	TCTTCAGGCTGGACCACTTT	CCTTATGATTTGGCCGGATA	136
CcM1637	FI235743	(A)10n(TTA)5	AAAGGAGTGAGATGGGGTCA	CTTAATGGCCACTGCAAACC	280
CcM1638	FI235748	(TA)5n(AT)5	TGTAGAATATGAGTTATTGAACGGAA	TGAGAATAATTAATGCAATGGAAAA	276
CcM1639	FI235782	(AT)8	AAATAGAAAGCAGAAAAGGTAAACA	CAAATTTTTGAAAGAGATTAGTTCTCA	207
CcM1640	FI235797	(TTG)6	TGTGGTGGGTTTTTGAGTCC	CAAGCAAACCAACCATCTCC	248
CcM1641	FI235806	(GA)5n(A)15	TATGGGTCCCCCACTTTGTA	GACAAAAATTTAAGCTTAGAAAAATGA	213
CcM1642	FI235865	(TC)5n(CT)5	AATTTTTGTGGGTTAGGGGG	GGGAGAGAAAGAGAGAGGGG	229
CcM1643	FI235962	(GTT)5	CTGACTTTGTTTTTGTGCTTCC	AGGGGGAGATTGTTGAGCTT	109
CcM1644	FI235980	(TA)19	TCATGATGAATCTCATTTAACCA	CACTGGTATCGTTTGAACCCT	265
CcM1645	FI236013	(A)11n(A)12(AAT)5	ATGTCGTGCATCAAGCAAAG	TGCAGGAAAATAAAAATGTTGG	222
CcM1646	FI236030	(AT)15	TGGATGCCACGTGAAAGTTA	TTTTTGGTGTTGTGCATATGAT	262
CcM1647	FI236063	(TC)9	ACACGTCGAATGTTCTGCAA	CATCATTCTCAGTGCAGATGG	251
CcM1648	FI236124	(TAA)5	TGAGATTTTATAAGGGAATCACGA	AATTTGCAAAGCAACCTAACG	243
CcM1649	FI236202	(T)13n(AT)22	TCCCCTAATAAACCAGATACGC	TGAGAAGTGTGTCTTTCTCCTATCA	278
CcM1650	FI236214	(AT)12	TCTGTCAAATTTTTGAAGGAAAT	AAAGGTAAACATGCATACTGCAAA	195
CcM1651	FI236262	(AT)7	TGTGTGGTAGTTGCCTCCTG	TTTGACCTCCAAACAAAGCA	229
CcM1652	FI236394	(GA)7	TTGGACTTTATGGTGTGCGA	GGCACCAATGACTTCGTTTT	120

CcM1653	FI236441	(AT)30	TCCATGCATTGTGTATGTCG	TGCATAGTCCTTAAAAACCCA	204
CcM1654	FI236465	(CT)8	CGCTCGAGTCTCAACAGACA	AGTATGTTTGGCAGCACTTGT	138
CcM1655	FI236487	(ATGTGG)9(ATGTGA)6	TTGGAACAATTGGGGATTTT	TCACATCCACATTCACATCG	275
CcM1656	FI236489	(CTT)6	TTTTGAGGAATTGTTTGGGC	ACCCTCCACCAAACACAAAA	212
CcM1657	FI236656	(TA)12	ATCGTCCCCATTTAAAAGCC	TTTTTGTCCCAAGAAAACTTGT	197
CcM1658	FI236664	(AAC)5	TGTAAATAGGTGTATGGTCCCTCA	TGTCTGAACTATTTTTCAGTTCAGTTT	149
CcM1659	FI236719	(TA)8n(TA)15	TTGCAAGCTTAATCTGTGTATTAAGAA	GGATCATCCCTACCTCGGAT	240
CcM1660	FI236735	(AT)14	CTGCACATTTCCTGCAAAGA	TCACTCAGTTTCACTGATTCGT	254
CcM1661	FI236737	(TG)6	TGGTATGAAAAGGCCTACGTG	GAAGGCCTTTCTTTTGCCTAC	185
CcM1662	FI236770	(AT)8	TCCCTTACCCAAGATTTTGAT	CCACATAAGGATGATCCAAAAGA	114
CcM1663	FI236807	(TA)5n(AT)5	AAGAGTGTTTTTGTTGGCGG	TTGCAGATACCAACCCCTTC	264
CcM1664	FI236845	(TC)6	GGCACAGTTCTCAGGACACA	AAGATCCGGCCTAAGCAAAT	198
CcM1665	FI236905	(TC)6	TAGGGCCCCTCCATATTCTT	GTCCAGCTCAACCCATTCAT	273
CcM1666	FI236922	(TG)7	CGTCCTTCGTTTTCCATGAT	CGATCAGTTTTACTGGACGC	261
CcM1667	FI236924	(TCTGTT)6	GATGTTTTGACGGAGCCATT	TTTTGGCGTTTCTTTGTTCC	157
CcM1668	FI236974	(TG)6	ATCGTGTCGCAAACATTCAA	GGTTGCTGGCTAAAACTGGA	140
CcM1669	FI237012	(AT)8	TGGTCATACGGTTTCCATGA	TTACACAGGTAAGAAAAAGGTATCG	136
CcM1670	FI237056	(TTA)7	TGTGTGTAGGTGGGACTTGG	CAGCAGAAGATTTAGGCACG	204
CcM1671	FI237091	(TC)6	AATTGAGGCAAGTAGTGTCTTTTT	CATTCCCAACCCACCTACAA	240
CcM1672	FI237092	(AG)7	ACGATTAGGCACGATTTTGG	TTTTTCCCTCTCATTTCAAACC	186
CcM1673	FI237096	(AT)34	TCCTTCGACATGCCTTTTCT	CCCTCCACAAGAATAAGAATCC	162
CcM1674	FI237111	(AAT)7	TTGAAAAGGATTCGTCCTCG	TTTCATTTTTCTTTAGAGACCTTGA	270
CcM1675	FI237126	(AT)9	TCAATTTATTTGCGGGCCTA	CATAACCATTGGTCCCCATT	279
CcM1676	FI237141	(TA)8	CAATGTGATGTTCTCATGGTCA	TTGTTCTTGCCGTCACTTACTC	244
CcM1677	FI237213	(AT)6	TGGATTGGATTGTTGAAGCA	GACTCCTTTTCCTTTGGATTTG	273
CcM1678	FI237251	(TG)6	GAAAAACCATGAGATCTAACCCA	TTGCAATCGGACTGTACCAA	231
CcM1679	FI237288	(TC)9	CCCTCTTTCTTCCCTCTCTTTC	AAATTTGCCCACGTTTGAAG	194
CcM1680	FI237316	(TA)13	AACGAATCAAATCTAATCCATTCA	TTCTTTATGGTTATTCAATTCATCCA	279
CcM1681	FI237319	(AT)25	AGATCCCCGAACCAAAGAAC	TTACCGAAAGGCTTGCAAAA	256
CcM1682	FI237364	(AT)6	TGAATAGAGATTATTTATTGACCGGA	CCAACCTAAAATCACATGAGCA	187
CcM1683	FI237365	(AG)6	CGCCAGAAAATAACCGCTAC	CCAATTTTATTAAGATCTCTCCTCTCA	258
CcM1684	FI237372	(AGA)5g(GA)8n(AG)9	TCAGCTATGACAAAACTTCCCA	ATGTGAGGCCCTTTCCTCTT	266
CcM1685	FI237384	(GT)6	GGGAGGTGGACTACAAGGAA	CAATTTGCCTACTAGGGGGTC	142
CcM1686	FI237408	(A)19(AT)15	GCAAGGACCTTTAAGTGCCA	TGTTGCTTTGTTTTGATGGCT	262
CcM1687	FI237410	(TA)7	GCTCAAGTAGACTGGTAAAATTGC	TGACTTTGGGTTTGATTGTTCA	240
CcM1688	FI237447	(AT)8	TCGTTTCAAAATGAATTATCCC	GCAAATTGAACATTTGCGG	239

CcM1689	FI237470	(ACCTGA)6	ACAAACACAATGCAACACCG	ATAGGCGAAGGACAGCAAGA	262
CcM1690	FI237485	(TA)14	CCATGGTCCCTTCCAAAAT	CTCCATCAATGGCGAAACTT	221
CcM1691	FI237486	(ATA)5	GGACCTCTCAACGGGCTACT	TTTTCACATCAAATTTAAAACCAGA	267
CcM1692	FI237505	(AT)27	AGTATAGGTGGCCCAACACG	GCGGGAGCTAGAGATGTTTG	149
CcM1693	FI237545	(TTA)7	CTTTCTTTTTCTTTAGAGACCTTGAT	AATGTGACACCCTTCTACCCC	201
CcM1694	FI237550	(ACC)7	GAGGGCATAATGGGAAACAA	CGAAACCCCTACTCTTGCAG	223
CcM1695	FI237576	(A)14(AAT)9(A)17	TTCAAGTCCCCCGTGTAAAG	ACGGTCGTGATTCTCTCTGG	268
CcM1696	FI237609	(AT)6	ACTTGTGTCAGATGTGGCGT	ATTCGAAGCCGAATCTTCCT	276
CcM1697	FI237641	(TGAG)5	GGCATCTCACAAAGCAAAAGA	TGACATCATTGAACAGAAGCAA	155
CcM1698	FI237648	(AAC)6	GGTTGAGTGGAGACATCAGC	TATGTGCTGCAACCAGTGCT	236
CcM1699	FI237666	(TA)7n(TC)8	CGGTATTTAAGCCCAACTCG	CGTTTATGTCCATGTCGCAC	275
CcM1700	FI237708	(CT)12(AT)27	CAGTTGGATTTACAAAATTCACATTTA	TCCACAACTAGGCCCAACTC	274
CcM1701	FI237736	(TC)8n(TC)5	CTCTCTGTCTTGCCTCATTCC	GAGAGAAAGGGAGGTGGGAG	149
CcM1702	FI237763	(AG)6	GCTTTGTGGCAACCTTTCTC	ACGTACAGATCCAGAACGGG	226
CcM1703	FI237809	(TC)7	CCTCCAAAAATTTCGTCCAA	GGTTTTAGGTGCTTTGTGGC	134
CcM1704	FI237810	(TA)11	GGTCAAAGGGATATGGCTCA	TTTTCTCAAAAATCCCCCAC	219
CcM1705	FI237830	(AG)29	CCCAAGGTGAAGCATAAACC	TGACGTTGAATCTCCAACAAA	244
CcM1706	FI237831	(TTC)5	GCAAGATGTCCCAAACACCT	TCTTCTTCAAACCTCAAAATCCA	194
CcM1707	FI237852	(TC)6	GGCCATTCCAACATAAGCAT	TGCCTCACAACACTCAAGAAA	280
CcM1708	FI237872	(TC)8	AGACCCCAAAAATTTCGTCC	AGGTGCTTTGTGGAAACCTT	121
CcM1709	FI237886	(CAA)6	AAAAATCAGTGCTGCTGCTG	GAACACCATCCCTATCACGC	209
CcM1710	FI237887	(CCA)5n(CCA)5n(CCA)5	ACAAAACCAACCACCACCTC	ATTGGGATTGGTTCGTATCG	263
CcM1711	FI237889	(TATT)5	GCAAGAATTATTTCATTCACTGCTT	TTCCCAGTAACATGGCAAAA	264
CcM1712	FI237911	(AT)18	AAAATTAATTATGCTTTGGTTATGACG	CCCTACTAACTTTGCGACCG	130
CcM1713	FI237925	(TG)5n(T)11	TGAAACAGATCTGCGTAGTGTC	CCCAATGCCCATTATCATTT	176
CcM1714	FI237955	(ATT)5	AGGGGAATGATGCATGGTAA	TCGTGGGTGTACGTTGATTG	235
CcM1715	FI237956	(TA)10	GAGGGTTCTTCCCCCAATTA	CACGTCAAGAAAAGAAAAAGGTG	144
CcM1716	FI237974	(AAT)8	AACATCAAGAAGGGTCCACA	ATAGGATGTGACATTGGGGC	261
CcM1717	FI238009	(CA)5n(T)10	GGGGTCTAGATTTAACACCTTTTG	TGTCATTTTTCTAGTTATGGCTTTTG	263
CcM1718	FI238020	(TA)6	ATTGACGCTTCCAAAACGAC	TTTTACATTGGCAACCAATCA	267
CcM1719	FI238047	(ATA)6	TCATTAAACCCCAGGACCTAA	GGTAGCCAAAAAGCACCTTC	279
CcM1720	FI238061	(TA)32(GA)13	TGGCTTAGCTGGTTGGGTAG	TCGACCATCTCAAATCAATCA	256
CcM1721	FI238114	(TC)6	CGACTTTTGGCTATTGGGAC	AAGAAAACCCCCTGATTGAA	261
CcM1722	FI238115	(GAA)6	GGATTCTAGCCCACAACCAA	GCTCTAAGGTTGGGAGACCC	260
CcM1723	FI238135	(GA)6	GGTATGGGTGTAGGTGGTGG	CATCACTCTCGCGCTCATTA	204
CcM1724	FI238138	(TGA)5	GCAAGAAAGCACCCCTTGTA	GGAGTCTTTGTGAAAATCTTGGA	244

CcM1725	FI238155	(AT)15	TGGACAACCCATCTTTTTCC	CAAGGAGTTGGATCCACGAT	233
CcM1726	FI238202	(TAT)5n(TTA)6	TTTTGCAATTGTTAAAGTTCGG	TTTTACTCTTGAATTAAAAGTGAGTGA	261
CcM1727	FI238224	(TC)5n(GA)5	AAGCAAGGTGCCTCTTTCAA	AAGAGGAGGGAAGCTTCTGG	168
CcM1728	FI238241	(TG)8n(AT)8(GT)8	TGCCTAGGACTGGAATTTGG	ACCCTGTGGCTTTTTCAGTG	268
CcM1729	FI238248	(AT)6	TCCGGTTCTTGTTTCTTTGA	TTCTTCTCGGCTTTTCTTGC	145
CcM1730	FI238253	(TC)12(TA)56	GTAATCAGATTCCCCCTCCC	GCACTTTAAATTCAATGGTTAGATCA	276
CcM1731	FI238324	(A)11(CT)5	ATTTAAGGGAAGGGAGGGGT	TTTCTTTTTGTGTTCTCTTATTGCAT	111
CcM1732	FI238336	(TA)15	CCATAAGCAAACCATCCCAC	TTGCAATGAATTTAGAGTTATTTTTC	215
CcM1733	FI238368	(AT)30	CGATTGGATTGTTGAGATTTGA	AAAAATTTGAGAAGTTCATCTATGC	189
CcM1734	FI238388	(TC)6	TCCAACGTAGCGAGGAGATT	TGTATACACTTGGCATGCATAATA	253
CcM1735	FI238409	(ATT)5	TGAATGTGTTACATGATGAGGTTG	TTCCTTCGCCTTAACCAAGA	110
CcM1736	FI238427	(CT)9	TGAAGAGAGGAAAGCAGGGA	TTTCAATGGTCTTGGCTTCC	193
CcM1737	FI238447	(CT)5n(TG)5(TA)5	TCAATGGTTGAATTGTTGAAATG	CCAGATGTGTTCACCAATGA	273
CcM1738	FI238450	(AT)28	TTTAATTTCAATGGTTGGATCA	TGTAAAACATGAGTTATTGAACGGA	198
CcM1739	FI238461	(ATG)5	TGGAACCTCATCAAACCCAC	TGGAGTCTTTGTGACATCTTGG	239
CcM1740	FI238497	(TA)12	CGTAAGATCCTTAGCCCGTG	CCTGCCTCTGGTAATCAATCA	183
CcM1741	FI238543	(TAT)5	CTGTGCTTCTTCCGGTCAAT	AGTGGGATGCATGCTTAGAGA	157
CcM1742	FI238567	(A)10n(TA)10(T)10	AGGCCCAACAAAGTTGAAAA	TCGCGAGGGAGATAAGGATA	223
CcM1743	FI238579	(CAA)6	CACGAAGTTGCTTTTGGACA	GGTTTTTGCAAGTTGGGAGA	189
CcM1744	FI238621	(TATC)10(TA)15	AATGGGCATAAGGATTGGAC	TGATGTAGAACATAATTTATTGAACGG	224
CcM1745	FI238653	(GTT)6	GCCTCGGAAAACTATAGGGG	TTGAAAGGGAACTTGAGCAGA	252
CcM1746	FI238693	(TA)24	TGATCGTTAAAGGTTCCTGTG	TCTCTTAAAAATTTGCAGATATAATCA	192
CcM1747	FI238722	(GA)5n(TA)21	GGAAGCAAATCAAAAAGAGAATTT	TTTCCCCTCCTTGTCTCCTA	280
CcM1748	FI238751	(TC)5(TA)7	AGTTGGACCGATGAAATTCG	AAAATTTGACAAAAATTGACAATCA	177
CcM1749	FI238753	(CT)13(AT)12(AG)9	TCATGGAGTATACAAATTCCTCATC	TCAAAGAGGTATCCAAGTCCC	148
CcM1750	FI238772	(TA)39	TTGGTCGCAGCTTTTTAGGT	TTTGATATCTGCACTTGTTGATGTT	161
CcM1751	FI238780	(AT)6n(TA)12n(AC)9(AT)20	GAAAGCACAAAAGGTAAATATGC	TTTGTCAAACTTTTGAATGAGATT	262
CcM1752	FI238790	(GTA)5	CATAAAACACGGATACCCCG	TTCTCCCTTTTTCTAAGTTTTGTACC	147
CcM1753	FI238797	(CAT)5	CCATCACCACCAAAAACACA	TTAATGATCGGACCACAACG	225
CcM1754	FI238800	(TA)6	TTGTGAGGCATCTTTTTGAGAA	CCACCAGATCAGTTCAGTTCAG	254
CcM1755	FI238814	(AAAT)5	TTTTCACACCCTCTCTTTCTGA	CGGAAAAAGTTATGTCTGCG	256
CcM1756	FI238823	(AT)6	TGCACATGCATGATGTCAAT	GGCCTCCTCTTCAGATCACA	230
CcM1757	FI238838	(AT)6	CTTTCTCCAGCCCTATGTGC	TTCCAAGAGTTGCTGAACCA	237
CcM1758	FI238871	(AT)16n(TA)9	CGTCAAGAAAATAGAAAAGTGAAAGA	TGAGAGAGTTCTTCCCCCAA	228
CcM1759	FI238933	(TTG)5	GGATGAGGCATGAGAAGAGG	ATGTTGTTCCGAAAGCCATC	130
CcM1760	FI238933	(T)10n(TA)5	AAGATGCTGGCTGGTTCACT	GCTAGCCTGGGAATTTATTTTTC	271

CcM1761	FI238937	(CT)17(AT)21	AGAATGTGAATTATTGAACGGAA	TTCCAAACCTAAGTTATGCATTAAGA	201
CcM1762	FI238965	(A)10n(TA)5	GAACCAAAAGAAAGAAAAGGCA	GTCCAACTTGAGGGGGACTA	280
CcM1763	FI238968	(AT)7n(TA)5	AAAAATTTTACACTAGCAGCCAA	TGATGTCAAAGTCTCCCACG	265
CcM1764	FI238977	(A)12n(AAAT)6	TTGCTAGAATGAAAACCCGC	TCAGCTCGAACAAACATTGC	112
CcM1765	FI238980	(AT)6	AAGGGAAGTGATGCATGGAG	TGAGGATATGTGTGTGCATTTG	203
CcM1766	FI238995	(TG)5n(TGA)5	TGTTTAAGCCTATGCAAAAGGA	CCTTGAAAACTCTAGTTTGAATCAAGT	252
CcM1767	FI238998	(AT)6	TTCCCGATCTTGATTAGCGA	GAATCCAATGCATCAAGTGATTT	280
CcM1768	FI239013	(TA)7	TACCACGTGTCATTGCCCTA	TGAAAAATTGGAAAATTTATTGGA	252
CcM1769	FI239114	(AG)6	TGAGACTTGTGCTTGGATGC	TGATTGGAGGGTCATTGTGA	239
CcM1770	FI239143	(AT)23	GCCAATTATATTGGTTCAAAGGG	TGAAAATGGGAAATCGCTTC	267
CcM1771	FI239193	(ATA)16n(ATA)5n(AAT)5	TCAGGTCTTATGAAAAGGGGAA	TTGTTCGAAACTTGACGTGC	249
CcM1772	FI239254	(AT)12	CATCAATCTGCCACATTTGC	GCACCAAAATTTTCTTTGGC	242
CcM1773	FI239303	(TA)10(AT)11	TGGATGGATTGACTTTTAGTCATAGA	TGGTGTAGTGAAATCATCTTGGA	244
CcM1774	FI239382	(AG)6	ATACAGGACCCAGGACACCA	GCAGGTTGGTTTAAAAAGATGAA	121
CcM1775	FI239386	(AG)7(AGAA)5(AG)5	TATAAATAGGGCCAAGGGGG	CCTTGAGCGAGGTTTCTCAC	225
CcM1776	FI239466	(ATAA)5	GCCATTCAGATTTCAGGCAT	GCTTTGAAACGGCAAAAGAG	212
CcM1777	FI239467	(AT)21	TCTTTTTCTCTTGCTGCGGT	TTTTCTCAGTTTCAAAAATTAACATCA	190
CcM1778	FI239478	(AT)16	AGAAGGAGGAAGCTGACCAA	TCATGAGTATGTGTTGAACGATTT	181
CcM1779	FI239479	(AAT)5	TGGGCATGACTAGAAACTTGG	AATTCGGCGCAAGAAATATG	270
CcM1780	FI239488	(TTA)6	ATCCAGTCGATGTGTGGTCA	CGACACACCCTAAACACGAA	255
CcM1781	FI239501	(AT)12	AAACATGCATATTGCAAATTTTATT	TGTTCATTTATTTGATGTCTGTCAA	208
CcM1782	FI239538	(AG)6	AAAGTATAGGAAATTAGGAACTGTTGA	GGTGTTGCTGACCCTGTTTT	165
CcM1783	FI239539	(AT)5n(TA)6n(TA)9n(AT)5	CGTAGCCGGATCTTCTTCAC	TGGTGTGGATTATGATGGATTG	273
CcM1784	FI239594	(AT)12	ATGGCGGACAAAAACAAAAG	TTGCTGCTTGTTATGCATTTTT	254
CcM1785	FI239598	(AT)22	CTGTGACACCCTCTACCCCA	TGGATTAAGGACATGAATGTGAA	167
CcM1786	FI239616	(TA)7	CTTTTTGGAGTAAGTGAATCGC	GATCCCTTCCACTAGCACCA	190
CcM1787	FI239627	(TG)9	GCTTTTCAGTCGGCTTTTTG	ACCAAACCTAGTTCCGCAAG	275
CcM1788	FI239667	(AAAT)5	GTCCACTGGATCGTTGAGGT	TTGAGCACTCCAACAATTTGA	210
CcM1789	FI239671	(TAT)5	CAGAGCACACGCGTAGAAAA	GAAGGGAAGGAGGGACGTAG	164
CcM1790	FI239692	(AAG)7	CGGAAAAGGAAATTGCTGAG	GCTTTCTTGCCGTTATTTGC	208
CcM1791	FI239700	(ACACCA)7	CGACGACGACTACAACGAAA	CTCTCTCGTCCACGACTTCC	176
CcM1792	FI239700	(ATC)5	TTTCCCACTGATGATGCTGA	AGCATTTGTTCAATGAGGGG	148
CcM1793	FI239708	(A)11n(ATA)5(ATT)5	TGCGAAATTTTGTGAACTTTG	CAGGAACATGAGCAAAAAGATG	272
CcM1794	FI239718	(CAA)5	TAAATGAGCATCCAGACGCA	ATTGACAGGAGGAGGCACAC	152
CcM1795	FI239750	(TC)7	TAAATAGACGGCTTGGGCAC	TTTTAGGTGCTTTGTGGCAA	155
CcM1796	FI239757	(AT)9n(T)11	GCCACTCTCGCTTATCATGC	CCCACAAAAGTCAATTTACTCCA	265

CcM1797	FI239782	(TA)7	TTTTTGGTTTCTAACAATGAGCAA	GGGGACTCATCGAAGAAGAA	144
CcM1798	FI239783	(CCA)5n(CCA)5	ACAAAACCAACCACCACCTC	GAGACTCGGATACGGAACCA	278
CcM1799	FI239799	(TA)9	TAGTGAACCGCGCAATGTAG	AAACGGGTCGACTGCATAAC	228
CcM1800	FI239810	(AC)5n(T)12	TTTGGATCCACTTCACTCACC	CTCTGAGAAGCATTGCAGTTT	242
CcM1801	FI239828	(TA)28	TGAACTTCGTGTAAACAACTCAAA	TTGAAGTAAGCTAGGATCAATTTTT	196
CcM1802	FI239839	(TCC)5	TTCGGGGTCAATAGTTGGAG	TATTGTGTAATCAACGGCGG	202
CcM1803	FI239870	(TTA)7	TTTCTTTTTCTTTAGAGACCTTGATAA	CTCATAACTCACGGCCGATT	245
CcM1804	FI239870	(ATG)6	AATCGGCCGTGAGTTATGAG	AAGAGTCTGACCATCGTCGC	242
CcM1805	FI239913	(GATGTG)9	TTTGGAACAATTGGGGATTT	AGGGAGAGGAACCACAATCA	263
CcM1806	FI239925	(AAT)5	ACTTGACTTGTGGAAGGGGA	GTTTGCTGATGGCAATGATG	234
CcM1807	FI239928	(AT)6	TTGCTGGATTACCATACGCA	TTTTTCCTCAAGAGAAAGTAGCG	248
CcM1808	FI239932	(TA)17	TGTCCATGTTAAGGATAGCGG	AGCACTCGAAAAACAAGCACT	226
CcM1809	FI239964	(TA)7	GTTCGAATCTCTCAGGCGAC	CTCCATCCTTTGGTTTGGGT	269
CcM1810	FI239978	(GA)6n(AG)6	GCCAAGCCTGAAAATCAGAA	TGCAAGTAAGTTCCTTCTTCCC	253
CcM1811	FI239994	(T)15n(AT)14	CAAATGTGGAATGTTAGTAGCAGTG	TTAGAGATCAATTTGAAGACCTTTTT	269
CcM1812	FI240054	(AT)21	TCTCTCACATGATGTAATGACTCG	TGGCTACTTTTTATTGCTTTCATT	201
CcM1813	FI240066	(AT)12	AACAAATCATGCAAACAAATCAA	CTCAGCTTGCTGTGATCTGG	161
CcM1814	FI240078	(AT)8	GGTTTCCTTGTTCGATGCTG	TCTAAATTCAAGTGCCTCTCTGT	171
CcM1815	FI240088	(AT)42	TGCCTCTTTGAATGTGTTAGGA	TTGTCACCAACTTTTTAAAGGAC	275
CcM1816	FI240099	(AT)14	AACAACCTATGACGCCCGTA	TGACGTTATTTGATTTTGAGGG	227
CcM1817	FI240143	(AC)7(AT)17	ATTGAGAAGGTTGTCACCGC	GAAAACAATGAAACCAAACAGAA	200
CcM1818	FI240154	(TA)10	TCTTTTGTCTCAAAAACAATTGACA	TTAACATTTTCGTCCCCACC	242
CcM1819	FI240192	(TAA)14	ACCTTCCTCCAATCCGTTCT	TGATTCTGTAACACTCTACACTTTCA	260
CcM1820	FI240205	(AT)14	GGCAGAAAATGGAGGGTACA	TTGGCTATCGGAAATAACGG	280
CcM1821	FI240220	(AT)7	AAACGCAAAAGGTAAACATGC	TGATATTTGTCAAACTTCTGAAGGA	208
CcM1822	FI240348	(TC)7	AGGGGCACATCAAACATCTC	TTCTAGGTGCTTTGTGGCAA	280
CcM1823	FI240384	(TG)6	TCCATCTTGCATGTTGGTCT	GGTCCCGAGAGTTGACAAAG	213
CcM1824	FI240408	(AC)7	TCGGGGAATGCAAAACTAAA	CCATTATCTTCCCGCACATT	234
CcM1825	FI240452	(G)13n(TG)5	TGAAGTTGGCGGAAAAACAT	TCGGACGAAAAACATACTTGC	263
CcM1826	FI240454	(TA)8	TCCGGACCGTGTTACCTATC	CATCTTCCCCTTCGAAAACA	215
CcM1827	FI240500	(AT)6	TTGGCATGCTCACAATGAAT	CTTGCACCGTTGCACTCTTA	153
CcM1828	FI240527	(TA)6	AAATAAAATTCTGCGTTGAGCA	TTGAGTCATTATGCAGTATCAACTT	259
CcM1829	FI240556	(TA)16	GCAAATTCTCAATTTAATCCTATGC	TTTGACCAATCACATCATCG	194
CcM1830	FI240565	(ATT)6	TGCAAAACAATCACACAATGC	AAATTGTATGGGATTGTGCCT	265
CcM1831	FI240572	(AAT)7(AATA)7	TGTGAAGGCACATGAATGGT	TTGTCAATTTGCACTTCAAGAAA	171
CcM1832	FI240593	(TA)6	ACGACTTAGCACGACACCCT	GAATTCATTTGTTATTACAGATTTCAA	222

CcM1833	FI240595	(TTA)10	CTGGACGGTTGGCATTATCT	CGAGGTTGAGTCAAGCACAA	267
CcM1834	FI240597	(TTA)5	TTTGACATAGTCATGTTAGCTTCC	TTGGTTAATCGTTAACATGTCATTC	226
CcM1835	FI240641	(AAT)5	AGTCATTAAACCCCAGGACC	GGTAGCCAAAAAGCACCTTC	278
CcM1836	FI240658	(AT)20	TGTTGTCTTCTCGCAAGTTTTT	GCCCCATTTTAGAGAATAGGAA	219
CcM1837	FI240658	(TA)5(A)16n(AC)6	TTCCTATTCTCTAAAATGGGGC	CAATTTCAATTGGAGATTTTTGG	258
CcM1838	FI240743	(TA)7	TTGGTGTGTCCAGACCGTTA	TTGAGCGGTGTAATACTTAGTAAAAG	278
CcM1839	FI240782	(TA)7	TTCAAATTGACGTATAAAATGCTT	TGCATATGGATGTTGTGACTAACT	267
CcM1840	FI240811	(TC)6	TCTGGTGACTTTCTGATGCCT	CACACTACAATGTGCCTCACAA	153
CcM1841	FI240815	(AC)8(AT)7(GT)8	CACCCTTTACTTGCCCCTTT	CAAAATTTGTTTCTTCTAATGCTTTT	215
CcM1842	FI240823	(AT)15	ATGCAAATGGAAGAATTGGC	TTGAGATTGGACCTGCATGA	257
CcM1843	FI240905	(TTAT)5n(T)10	TTCCTCTGTCCTGTCATGTTTT	TTTTTCTGTCATAATAAATGTCATCC	268
CcM1844	FI240915	(TA)9	TGAGTTATTGAATGAATTAAGTCTTGG	CGTGCAGTAACTCATGTTCTACATC	265
CcM1845	FI240947	(AT)21	TCGGTTGGCATAGGGAATAG	TTTTACGTGTCTTAGCCTTGAAA	262
CcM1846	FI240950	(AAT)18	CCAACTCGACCCAATCAATC	AACTCCAAAATCCAAAACTCG	160
CcM1847	FI240956	(AAT)11	AACATCAAGAAGGGTCCACA	ATAGGATGTGACATTGGGGC	271
CcM1848	FI240980	(A)12(GA)9n(A)15	CACGAATTGTTATTTTTGCAATG	ATTGTGCATGCTTTTCCTCC	215
CcM1849	FI241002	(TA)8	CAAATGCACGAGAACTTCCA	GACCACCATTGTGTTTTGCT	276
CcM1850	FI241056	(TA)15	GGGAGGAAAAATAATGATGATCTAA	GGGCCGTCCAACTTTTATTT	279
CcM1851	FI241137	(CATG)5	GCCTTCGTTTTCAATCTGGA	AACAGAAGGTGACCAAGAAAGAA	224
CcM1852	FI241192	(AATT)5	GATGGCCTTTTTCGATTTGA	CATCTCACTTTTGTATCTTTACCATAA	196
CcM1853	FI241192	(T)11n(AAT)5	TTATGGTAAAGATACAAAAGTGAGATG	AGGTCTTTATAGTAGTGGATTGAGGT	242
CcM1854	FI241242	(AT)24	AATCCTTACATTCTCGGGGC	TTTGAACAAAAACAAGTCAATCA	267
CcM1855	FI241320	(TTA)5	GCATGGATGCAATGAAAATG	TGTCCCTTAACGGAGTTTGG	279
CcM1856	FI241324	(AC)9	CAAGCAGATCCCCATCCTTA	GAAGAAAGGAAACTTGGGGC	206
CcM1857	FI241357	(A)11(AT)5	TGGGCTTACTTACCATGCAG	TGAAGATGGCATAAACGTATCA	214
CcM1858	FI241360	(TA)11	AAGTATAAGTATTCAGGTTGAATGCAG	TTTTAAAATAAATTTTGATGCCG	115
CcM1859	FI241443	(TTC)5	GCAAGATGTCCCAAACACCT	TTTTCTTCAAACCTCAAAATCCA	194
CcM1860	FI241463	(TA)9	CTGGGCATTATGGAAAGCAT	ATGGCAAGGATTGACAGACC	127
CcM1861	FI241479	(TTA)8	CTTTCTTTTTCTTTAGAGACCTTGAT	CCTAAGCATGGAGAGCTTGG	236
CcM1862	FI241501	(CT)5n(T)11	GCCCCAACTTGCATTTCTTA	ATCAATGACAAAATCCCCCA	219
CcM1863	FI241536	(GA)6n(TA)5	TGACACTTGCTCACCCAAAG	CACCTTTTCTTCAGCCCTTG	261
CcM1864	FI241553	(TC)6	AGAATGGCAAGCCACGATAG	TCCACTTTCAGATTCCGGTC	272
CcM1865	FI241584	(ATT)5	TGCCTAAGGAGGCAAACTGT	CAATTGATGGGGTTTTGGAG	178
CcM1866	FI241606	(TC)6	CAAGGCCTCAAAATTTCGTC	TTTTAGGTGCTTTGTGGCAA	127
CcM1867	FI241613	(TA)20	TTAAGAGGGTTTGTAGAGATGTTTTT	AGAACACGAGTTATTGAGTGGAA	266
CcM1868	FI241629	(AT)21	GGTTTTGAAACTCATCCCGA	GATCGTAGTGTGATAGCAGAAGTGA	251

CcM1869	FI241671	(TA)8	TCTTTCTCCTTTGGCCATTTT	TTTTTAATTTTTGGTCCTTGTTG	267
CcM1870	FI241680	(AT)14	TTCCCAACAAGGAGAAGTGG	TCAGTCCAATGAAACCAGCA	209
CcM1871	FI241707	(TAT)6	TGGCAAGATATTTTGGTATTTCC	TTTCCCATTCTTCAAGGTCAA	280
CcM1872	FI241727	(AT)10	ATTCTGTCGGAAACCCTGAA	GGCATACCTCACCCACTCAT	134
CcM1873	FI241751	(A)10n(T)10n(CA)5	GGAATGATGCATGGAGATGA	CATGGTTGTTCGTGGGTGTA	231
CcM1874	FI241752	(GTG)5gn(GTG)5	GAGACTCGGATACGGAACCA	ACAAAACCAACCACCACCTC	278
CcM1875	FI241776	(TA)6	TTGATTACCTTCAAGTTGTTGTTCA	AACGATTGTTGAAATTTAATGTTG	276
CcM1876	FI241805	(GAA)5	GCCGTGTTCGATTGTTGATA	AACGTAGGGTGTGAGTTCGC	155
CcM1877	FI241839	(CACTCT)5	GAAGCTTCTGGAACTCGGTG	GCAACAAGGAATCGGAAAGA	239
CcM1878	FI241946	(ATTT)5	TCAATAAAACAATGGAATCAGAGG	GCGGATGAAGTAGAAAGAATGTG	150
CcM1879	FI241951	(A)13n(AGA)6	GGATGTGCCAATGGTCCTAT	TCAAGGCCCAAAACATTTACA	169
CcM1880	FI241982	(TA)7	TCGCTTTCAGAAATGTTTTTGTT	TCCTTCTATTTTACACTTCAATAACGA	158
CcM1881	FI242007	(AT)6	CCCCTCACTTTTTGTTGCTT	TTTGAAGTTCATTGGGGACA	217
CcM1882	FI242058	(CCA)6	ACCATCACCATCACCTCCTC	TCTAGCTGGCGACATGTTTG	168
CcM1883	FI242060	(GT)6	CACAAATGGTTTTCAAGGTGC	TTAGAAGGCTTGCTTTTGCC	218
CcM1884	FI242073	(AG)8	AGTTGCCTTCTTGAAACTACCA	CATAAAATTTGGTGGGTCGC	279
CcM1885	FI242080	(TA)30	CCCACAACAAACAACAACCA	AAGGAGTATTTGAATTTGGGCA	254
CcM1886	FI242083	(TAA)24	CATGTATGTTCCCTGTATTTAATTTG	AGGCTTTTGTACCACCGTGT	273
CcM1887	FI242106	(AAT)6	CGTGGGTTTTTGACATTTGA	AGACGCTAATGCTTGGAGGA	203
CcM1888	FI242127	(TA)37	TTTGGTTCCAGACTTAGATTTGTG	TCTTCTAAATCTGCTTGGCATT	211
CcM1889	FI242165	(AT)20	TTTTAATGCTCAAATTAATGAACAA	GACTTGGTGGGTGAGGGTTA	156
CcM1890	FI242175	(AT)13	TGATCAAGAATTGGTCCAAAAA	TGAATTAATGAAATGAAGTATCAAATG	253
CcM1891	FI242182	(AT)6	AATGATTCAAGGTGCAAGGG	CCATCCAATCCAATTAAAGGC	206
CcM1892	FI242185	(TA)42	CTGCAAGTGACGAGATTCCA	CTGACTTGATCCCTCCTTGG	197
CcM1893	FI242200	(GA)10	CATCGACTCTGCAACGAAAA	GTGTTGTTGGTGTTTGTCGG	180
CcM1894	FI242263	(TA)8	TTGCAAAATGCTGCTAGGTG	GGGTTGGGATACCCCTTGTA	158
CcM1895	FI242267	(AG)12	GAGGAGAGGAGGCAGAAGGT	GTGTCCAGGATTGTAGGGGA	272
CcM1896	FI242276	(CAG)5	CGCAACAACAACAGCAAAGT	TTTTTGGAAGGGAGGGGAT	140
CcM1897	FI242278	(AG)7	TGTCCAACTCAACCCATTCA	TACCCGAGATCATGAGGACC	230
CcM1898	FI242288	(AG)5n(GA)5	ATTGCCTCGATGAAGGTGAC	AAAACCCTACGCAGCAACAG	264
CcM1899	FI242307	(TAT)5	TCAGCAATGCACATCATCAA	AGAAGCCCTGACTGGTGCTA	256
CcM1900	FI242314	(TGA)5	ACCTCAAGAAAGCACCCCTT	TGTGAATCCAAGAAGAAAAACG	212
CcM1901	FI242340	(CT)12n(CA)18(TA)19	AAGTCGGTTCATTTCATCACA	TACCGCCGTGTAAATCTGGT	256
CcM1902	FI242350	(TC)6	AGAACGGGCTATTTCCAGGT	CGGCAACCTTTCACACTACA	218
CcM1903	FI242379	(ATA)11	AAAATCAACCTTCTCTTGAAACA	TTTCAGAAATTCGAGGACGA	264
CcM1904	FI242419	(GAA)6	TGCAAAAGAACCAAAGAAACAA	AACGGAGCAACCAAACAAAC	262

CcM1905	FI242463	(AT)6n(T)10	TGTGGCAACCTTTTACATTTTT	GGAGAAAGGGATTGAAAACAA	167
CcM1906	FI242532	(T)11n(TTA)5	AGGGGAATGATGCATGGTAA	ATCGTTCGTGGGTGTACGTT	254
CcM1907	FI242563	(TA)17(ATA)10	TCCAACGCAAAGTAATTCACA	TCGAAACTTCGCTTTGAAGAA	198
CcM1908	FI242563	(CA)5(A)22	CGACATTTTCCAATGAACAAAA	TGGAACTGTGAATTACTTTGCG	204
CcM1909	FI242565	(TA)8	TTATACTGGTATCATTTGAACTCTCC	GGAGCACATATTTCAATTCCTTTC	108
CcM1910	FI242565	(CA)5(AC)10(AT)16	ACGATATTAAATTGTATTTTGTGTTGA	CATGCTCACCTATGAAACTCG	146
CcM1911	FI242572	(TA)35	TCGCAAAAATTAAGAAGAGATCAA	AAGGTGGTCAACTAAATTCATGG	261
CcM1912	FI242586	(TA)6	CATGCAGGTATGTGTCTCGG	AAACCATTCCAGCTCACCAC	231
CcM1913	FI242621	(TA)38	CTTGGGGACAATGGTCAAGT	TGAAAAGCAATAACAAAGTGGC	267
CcM1914	FI242628	(TA)8	TGTAGAACATGAGTTATTGAACGGA	TTGGGCTTTAGGCTTTCTGA	268
CcM1915	FI242631	(TTA)6	CTTTCTTTTTCTTTAGAGACCTTGAT	GTGTGACACCCTTCTACCCC	197
CcM1916	FI242637	(AT)6	ATATTGGGGCGTTTTGAAGG	TCTCGTGTTTGATTTTTGTCG	239
CcM1917	FI242661	(TA)6	ATTGACGCTTCCAAAACGAC	TTTTACATTGGCAACCAATCA	267
CcM1918	FI242668	(TA)8	TTGAATGTTGAAGGCTTAGGG	ACCTTGAGCCCACTCCTCTT	269
CcM1919	FI242725	(TATT)5	CAAACATATCAAAGCAAGGGC	GCTAAGGAGGATTAGGTTGTCG	155
CcM1920	FI242805	(AC)7(AT)10	AACAAGATAACTAGCATGCAACAA	TTGGCCGAGAACTCGTTTAT	140
CcM1921	FI242813	(TAA)8	TGAATCTTATCCTACCAACACACAA	AATTGAACGATTGAATACTTGATG	276
CcM1922	FI242823	(TA)6	AGCTGCAAAGTTAAGCTGCC	GGGGACGGGGATGTTAATAC	277
CcM1923	FI242835	(GT)6	GGGAGGTGGACTACAAGGAA	CCCTAGGGAATCCGACTAGC	256
CcM1924	FI242855	(TG)6	TGAACTATCAAGGGAGGTGGA	TCTTTTGCCTACTAGGGGGTT	150
CcM1925	FI242886	(TC)7	ATAGAGAATCTCGGCCAGCA	TGGCAACCCTTCACACTACA	148
CcM1926	FI242887	(TCC)6	CCACCCTTTTCACTGTGGTT	CCGTTAAAGAAGGCGTGAAG	139
CcM1927	FI242956	(T)15n(AT)22	TGGAATGTTAGTAGCAGTGAGATTG	TTAGAGATCAATTTGAAGACCTTTTT	279
CcM1928	FI243009	(TA)7	ATTCGCGTGACAAATTTCAA	AGGAGGGAATGAGGTGTGTG	237
CcM1929	FI243016	(TG)6	TCTTAAACCAGAACGACCCG	GTTCAACCAATCCTGCACAA	188
CcM1930	FI243028	(TG)8(T)13	CAATGAAATTGAATGCACCG	AGCCAAACACCGTGAAAATC	258
CcM1931	FI243063	(TA)6	TCAAAACTTACACATTTTACAAGGA	AATGGTGATTTTTCGGAACG	206
CcM1932	FI243064	(TA)15	AAAATGACCTGGAATCATTGG	TTGGTTGATATTGTGATGATGC	267
CcM1933	FI243066	(ATG)6	AATCGGCCGTGAGTTATGAG	ACGAGCGATACCACTCAACC	255
CcM1934	FI243141	(CAC)6n(CA)5	GCAACCTCATCTGGCTTCTC	CTTGGGGGCTTTTTCTTCAT	224
CcM1935	FI243156	(CT)14(AT)12	TTTATTAAAACTTTGCAGACTTGATCT	TGGCTAGAGAGCATTTATATGTGTG	192
CcM1936	FI243181	(TAT)5	CCAGTTGGGAGTTGGAAGAT	CCACCAAATTATGACCAAATACC	179
CcM1937	FI243194	(AG)6	ACACTTGCTGGCTTCACCTC	ATGCTCGCTTGAGATTGGTT	245
CcM1938	FI243200	(TA)12	TGTTGTAATTCTAAATTGTGGTCCAT	GACCATGGTGACAATGCAAG	151
CcM1939	FI243209	(AT)28	TCAGAATCAGGCACACAAGC	TGTGCGGATGACTTATAGGTTG	221
CcM1940	FI243209	(AT)13n(AT)8(TA)10n(AT)17	CGCACACAAGCTATAAGCCA	TGTGCCATGTGAATCAACAA	242

CcM1941	FI243238	(AAT)5(AAC)5	CACACCCCCAAGTGAGATTT	AAGAAGGGAACATGCAGTGG	260
CcM1942	FI243276	(TAT)6	TAAGTGAATTTTCGGGGACG	TAACCACCAAATTATGACCAAA	122
CcM1943	FI243329	(TTA)5	CTTCGTTTCGGAAATTCGAG	AGTCAGCCTAGCGAGAAACG	231
CcM1944	FI243338	(TTA)5	ACAAACGAGGCTACGCAGTT	CCGAAGATGGAAAAGAAGGA	121
CcM1945	FI243350	(TG)6	TGAACTATCAAGGGAGGTGGA	TTGCTTTCCTTTGCATGTTTT	233
CcM1946	FI243351	(TAT)10	TGCATACAAACAAAGAACCACA	TTCTGAAAGCAAACAACCCC	258
CcM1947	FI243367	(TC)7(TA)5	TAATCCGGTTTCGTCAAAGC	GGCAATCTTTCACCGTTTTC	259
CcM1948	FI243384	(TCA)11	TGAAGCATGTGTGAAAAGGG	AATGCACGATGACGATGATG	143
CcM1949	FI243438	(TGT)5	CACAATGGCCTAAGCCCTAA	AGCAAGACAAACTCCGCTGT	165
CcM1950	FI243455	(GA)9	TTGAATCAAAGGGCGAGAAG	CTTGTTGCAACTTTTGCAGG	267
CcM1951	FI243456	(TTA)5	AGGGGAATGATGCATGGTAA	TACGATCGTTCGTGGGTGTA	254
CcM1952	FI243486	(AT)6	TCTGGAGGAAAGGGTTACCA	TCAATTGCTTGGAAGGCTCT	223
CcM1953	FI243544	(AT)19	ACCTCATTGATATAGACAAAAATTGA	AACGCATAGATCAAATCTGCAA	270
CcM1954	FI243584	(TA)6	TTCTGCATCTTCAGCCACTC	TTGATAAAAGCATTGGTTTACGA	280
CcM1955	FI243600	(AT)26	TACCTGGCGGATCAGCTCTA	TGCATGAAATACCTCTTTTCCA	272
CcM1956	FI243674	(AT)23	TGGCTTTGGAGGAATTGTTT	CACTCCTCCACAAGAACCAAA	164
CcM1957	FI243680	(CT)6	CCACTCTCTCCGTTCTACGC	GTCAACGATGATGCATTTGG	182
CcM1958	FI243710	(TTA)6	TTTCATGCAACTCATCAGAACA	AGTGGAGTAAGCGGTTGGAA	152
CcM1959	FI243765	(CAA)6	ATGTAGCCCAACGAAGGATG	TCCTGTGGGTTTGAGAGATTG	145
CcM1960	FI243831	(AT)21	ATTTGGAAAGGGGGAAGTTG	CTCATACATGTACGGATATCAAGTCT	232
CcM1961	FI243832	(TA)10n(TA)8	GTTGGTGATTTATAAGAGGTAATTGA	TTCATGTCCTCCGATTTTCA	202
CcM1962	FI243859	(AT)16	TTTTTGACTTTTGTCTCACCAA	TCAGCAAAAGATTAAGTGACTATTTCA	215
CcM1963	FI243903	(AC)18(AT)10	TCCTTGTGCAAGTCTTGTTTT	TTCTAATGCAAGCAATTCCTGA	133
CcM1964	FI243931	(TC)5n(TC)7	GGATGCTATGGATATAGGGCA	TCCCTTTAGTGAAAGAATTTCCTG	145
CcM1965	FI243954	(TAA)5n(TA)24	GGAAATTATTCCATTTCATATACACA	AAAGAGAAAGAGTGGTTTGAGAGG	233
CcM1966	FI243973	(AT)27	GCTATTCTGTGATTTTTGTCCTGA	GGTTTACATTTGGTGTTAACGGA	167
CcM1967	FI244026	(A)10n(AT)5	GGGGACCGTAGTGAGAATGA	TTGTTGCTGTTTTGCGTTTC	244
CcM1968	FI244038	(GA)6	TTGATTCGGTTCTGTTTAGGTTT	TACCCGAGATCATGAGGACC	165
CcM1969	FI244059	(AT)22	TTGCGATTGGAAAGAAATCG	TGTTTTTGGAATCATCATGGC	165
CcM1970	FI244062	(TTA)5	AATTCACTCCACCCCCTACC	AGGCCATGGACTTTTGTCAC	230
CcM1971	FI244097	(ATA)5n(ATA)8	ATTAATCCATTGGGCCAGGT	TCGTGTTTTATATGGGCATGA	215
CcM1972	FI244105	(AAT)7	TCTGCGTGAGATTTCTCGAT	TCGTCCTTCAGGTTGCTTTT	148
CcM1973	FI244115	(AAT)5	ACACCTCTTCATTCCATTTGA	ACCCACATGATTTCGGTGAT	125
CcM1974	FI244129	(CA)6	TTTAGAAGGCTTCCATTGCC	ACCAAGCCTTTTCAAGTGGA	132
CcM1975	FI244169	(TC)8	CCATTCTGGCCATTTCTGAT	TGCTTTTTGGCTACCTTTCA	176
CcM1976	FI244199	(TA)8n(TA)5	TTGAACAAAGTAAATGAATGTCTCC	CCCAAAGCACAAATTAAATGC	183

CcM1977	FI244210	(AT)14	GGATGTTGCCAAAGAGAATG	TTCTCTGGGTTTTGAACATGAA	280
CcM1978	FI244293	(TC)6n(T)16	TGTGATAGGCTAGGTTGCCC	GTGGCTTTGGCTATGTGGTT	264
CcM1979	FI244356	(AAT)8n(TA)6	TTTTGGTTTTGGTTCCCTTG	CCATCTACAAAGAATGCGACC	213
CcM1980	FI244386	(GTG)5	GAGACTCGGATACGGAACCA	ACAAAACCAACCACGACCTC	277
CcM1981	FI244388	(AT)7	GCTGTGCAGCCTTTTAGTCC	TGCATGCACTATGCAGTTTTT	180
CcM1982	FI244391	(TC)17	TATCAAACCTGGCGATCACA	ATTCCGCAAACACATCACAA	246
CcM1983	FI244410	(TG)5n(TG)6	TTAGCCCATGCTCTTCCATC	AGCTCAACAATCTCCCCCTT	200
CcM1984	FI244429	(TAT)22	AATCAAGAGTGATAATGAGTATTGTCC	TATGGATAACCCGCGAACTC	279
CcM1985	FI244433	(AG)10	AGAAGCGAGAAAGAAAGGGG	GCAATGGTGATTGTGGAGTG	270
CcM1986	FI244448	(AT)9	TGATTGAATGTGAGACTGCGA	CCATTTACGCGTGTCTGAAA	217
CcM1987	FI244481	(T)10n(TG)6	TCATCTTCCACCTTCGATCC	CTTGAACCCTCCCACTTCAA	277
CcM1988	FI244503	(AT)18	TTGAACGGTTAGATTGTTGAAA	ACATGTAGGACGACAACCGA	202
CcM1989	FI244580	(T)13(TTG)5	TCAAGGATGGGATTGGTCTC	AACACCAATCAAGTTCCCCA	190
CcM1990	FI244608	(AT)34n(T)16	AGGATGAATTCAAAAAGATAAGAGAT	AAATTTAACGTCAAAACACCAAAA	247
CcM1991	FI244648	(TA)24	TTTTTCTAAAACTTTGCAGACATGA	AAAAATGGAGACGAAAGCAGTT	205
CcM1992	FI244651	(TTA)6	CCATTTCATGACAACCACCA	TTGTTGGTTTAGCGGAAAAA	245
CcM1993	FI244656	(AT)6	TGAATTTTGTAAATCCAACCG	AATTCAAGATGATTTGATACTTCATTC	181
CcM1994	FI244678	(T)10n(TA)8	AGTGCTTCTTTGGTCTGCGT	TTGTCCAGACCTGCAAAACA	252
CcM1995	FI244683	(AT)6	TTCAGATAAAGGAGATGACCCA	TGAAAAATCTCTAAAATGCCATCA	278
CcM1996	FI244685	(CT)6	TGGGTTGGAGGAGTACCTTTC	AAGCGTGTGTAGCCATTGGT	256
CcM1997	FI244702	(AC)10n(CA)7n(CA)32(TA)19	TGCACCTACAGGTACCCAAC	GCACAAGATATGTGTTGAAGTGC	224
CcM1998	FI244717	(TTA)7	CTTTCTTTTTCTTTAGAGACCTTGAT	CACCACCTACCAGCAATCCT	268
CcM1999	FI244760	(TAT)6n(TTA)16	TGAATCAAGTGATAAACATAAAAGTGA	GGGACGAGGGTCTCACATAA	159
CcM2000	FI244777	(AAATA)6	CAAGGCTCTTCCCAAACAAC	GTGGTGGTGGCCATATTTTC	240
CcM2001	FI244778	(GA)6	GCTTTGTGGCAACCTTTCAC	ATCTGGAATGGGTCGTTCTG	184
CcM2002	FI244784	(AT)11	CAGAATGGAAAAGAATGAACAAGA	TGGGAATTGTTTGTCGGAAT	276
CcM2003	FI244799	(TGA)5	TGACCTCAAGAAATCACCCC	AGCGTTTTTGTGGAGTCTTTG	259
CcM2004	FI244896	(CT)7n(AG)12	AGGAATGCGACATTTTGGAG	TCCCCATCCCTTTCTTTCTT	209
CcM2005	FI244913	(TC)6	CGATAGGGCCCCTTCATATT	TGTCCAACTCAACCCATTCA	276
CcM2006	FI244926	(AAAT)5	GCTTTTGGGATAACCGATCA	GTTGTGGAGTCCTTGCCTGT	272
CcM2007	FI244931	(TAT)6	CGACAAAGTGCATCCAAAAG	CCCTTCTCCTTTCCCCTAAA	267
CcM2008	FI244969	(AT)23	TTGTTTCCATTAGAAATGCCC	TACCGTTGTCATTTGAACCC	235
CcM2009	FI244970	(TTAT)6	AGGTGGTTATGCCTTGCTTT	GAGGAAAATAACTTGGAAAGCCT	251
CcM2010	FI244990	(AAGAAA)5	CGAAAAGACTCCACTGCCTC	TTCATCAAGTTCAGGCTCCC	195
CcM2011	FI244990	(TG)5n(AT)5	GGAGCCTGAACTTGATGAAATC	CCCTTACGTAGTTGGAAATTTGA	280
CcM2012	FI244997	(TA)10	TCCAAATTACTTTCTTTGATTTCAT	TATGTTGTAGCACCCGATGG	223

CcM2013	FI244999	(AC)6	TGTGGCTGAAACTTGTGCTT	TGTTGCCAAACATTTCAACAA	194
CcM2014	FI245003	(TG)6	GGAAGGTCCTTAGCCTTCCTT	TTGTTGAGCAAATCCTGCAC	243
CcM2015	FI245027	(AC)6	TGTTTTGGCTGAATCTTGTACC	TGCTTTTTAAACATGCATTGAAG	240
CcM2016	FI245040	(CT)6	GTGGTTAGGAAACCTGCCAA	TGAGGGAGGAATCAGGAAGA	238
CcM2017	FI245081	(GA)6	GCTTTGTGGCAACCTTTCAC	CAGGCCGTTCTAAATCCAAA	193
CcM2018	FI245104	(GA)7	GACGGTGTTTTGACTGGGTT	TCTTGTACTCTGTTTTCAGTGGG	263
CcM2019	FI245119	(GT)7	CCATCCATTGCTTCAACCTT	TTGCTTTCCTTTGCATGTTTT	260
CcM2020	FI245142	(TC)6	TAGGGCCCCTCCATATTCTT	TCACTGTCCAACTCAACCCA	273
CcM2021	FI245158	(AT)7	AAACTAAGGATATTGAAATGAAAATGA	TTGAACGGCGTAAGTTTAGGT	125
CcM2022	FI245220	(AAT)5	GATTTGTCTTGGCATGGGTT	TTAAACGAGCCCAATTCGTT	232
CcM2023	FI245230	(ATA)9	TCGGTGGTGGTAATCAATCA	ACACTATCCCAGTGGCAAGG	227
CcM2024	FI245249	(AT)31	CTGGATCATTGGTTTTCGCT	TGTGGCGTGAAAGTGTAGGT	234
CcM2025	FI245266	(AG)7	AACGTCAACGTCAACACCAA	CATGAAAACCATTCGCACAC	241
CcM2026	FI245281	(TC)6	TCAGGGCTCCAAATTTTGTC	TCGTGGCAAGCTTTGTTAGA	167
CcM2027	FI245348	(AT)19	CCACCCAACCACTAGGCTAA	TAACGCGGCTGCATACACTA	260
CcM2028	FI245431	(TA)7	TTTGCAGATTTGATCCTATGC	TTAATATGAAGTTATTGAGCGGTG	219
CcM2029	FI245442	(CTT)5	GATGATGAGTCTGCGTTTGC	GAATGTCCGGAACTGGAAAA	163
CcM2030	FI245492	(CT)6	GGCCTTGTGAATTGCAAGAT	AGGCAGTACCTGTTGGATGG	183
CcM2031	FI245501	(AT)16	TGAAAAACAACAACCAACACTCTT	TGCAGTATCAAATCATCTTGGA	275
CcM2032	FI245515	(ATA)8(ATT)7	CCACCATCCAGTGATGTGAG	TTGGAAACAGCAGTACGTGG	262
CcM2033	FI245554	(AT)12	TCATGGATAATGGTGAGGGG	TCAACTTCTGTGTTTGGCTTG	213
CcM2034	FI245589	(GATGTG)6	TTGGAACAATTGGGGATTTT	TCACATCCACATCCACATCC	249
CcM2035	FI245607	(TC)7	AGAACATGAGTTATTTGGTGGAG	GGAGGTGAATGGTGGTATGC	192
CcM2036	FI245623	(TA)11	TTGGTGGAATATTTGTGTGTCA	GCCATGGAGCAGAATGAAAA	262
CcM2037	FI245637	(ATAC)6(AT)26	ACTCCCTCCTGCATCCTTTT	GCAGAAGTCATCGCATAGCA	215
CcM2038	FI245660	(AG)20n(AG)5	ATAGGAGGCAGGGGGTAAAA	GCCAATCCGACAAACAAACT	259
CcM2039	FI245686	(GA)7	GCTTTGTGGCAACCTTTCAC	AACAGCCATATCCAGAACGG	212
CcM2040	FI245702	(TA)8	TTGGTCCAAGCTTCATAGTTTTC	TGAACAAATGGTTGTTTAAATGTC	279
CcM2041	FI245703	(GAT)5	TAATGGGTTTTTCCCACTCC	CCCAACCTCTGTCCTGAGAA	231
CcM2042	FI245715	(GAG)6	ACCGCATGACCCATAATCTC	CCGTTTCACCCAAAGTCATT	280
CcM2043	FI245728	(AG)9n(AG)5	ATAAATAGGGGCAAGGGGTG	CAGAACAACGGCAAAGGATT	267
CcM2044	FI245729	(TAT)9	ATCACTCCAAGCACCCAAAC	TGCAAATGGAAGGGAATAGC	212
CcM2045	FI245730	(AT)12	GCGAAAAGCATTTTCCTATTTTT	GGCCAGTAATCTTCCGACAG	149
CcM2046	FI245737	(TGA)5	TGGTCCTCCATCATTAAGCC	CCTTGAAAACTCTTGTTTGACTCAT	254
CcM2047	FI245794	(AAT)5	AAAGGGAACAAATCGTATTCAC	GAAAGGTAGCCAAAAAGCACC	191
CcM2048	FI245833	(TA)30	CGTGAATGTGATTAGACTTTTATCG	TGGCTCCATAAGGAAGCAAC	271

CcM2049	FI245893	(TAT)9	GCGACCAGGTACTTTCAAGC	CGAAAAGCGATTTCAGAATTT	260
CcM2050	FI245901	(CT)7	GATCGGACTCAAACACCCAC	AAAGACGCAATTGACGGTTC	120
CcM2051	FI245959	(TTA)5	TTTAATGGCCTTTGCACCTC	CTGCCTCCATTGCATTCATA	254
CcM2052	FI245994	(TTG)5	CGAATGGATTCTGTGTCGTG	TACAAGCTGTTGGCACTTGG	245
CcM2053	FI245994	(T)12n(AT)20n(AT)19	GCAAAAATGGGGGTTCAATA	CGACACAGAATCCATTCGAC	223
CcM2054	FI246021	(TA)11	TTTATATTGTGCACACATTTGCC	AAACTTAATCAATCAAACCATCAAA	106
CcM2055	FI246047	(TA)10	TGGCCTATCTCACTCAAGGC	TGGAATTATCAGGTTGGATTAAA	267
CcM2056	FI246055	(AT)7	TGGTTGGATCAGTTAAATTTGC	AGCACTTGGAGTAAATGGATCA	140
CcM2057	FI246070	(TC)6	TTTCCTCTCACCAATGACCC	CACGTTGGAGATGAATAGGGA	129
CcM2058	FI246086	(TG)8	TGTGAGCAACATGAAAGCAA	AAGCCAAACAATGAAGTGCC	236
CcM2059	FI246122	(AT)8	CCATTCTCATGTATTTGAGACCC	TTTTTCTTTCATCGTCCTAGACTTT	136
CcM2060	FI246133	(AT)21n(AT)6	TGGAGAAGAGATTCATTTATTTGATG	AGAAGCCAAACTTCCTTCGG	271
CcM2061	FI246161	(TG)7	TGCACATTGTCGCATAGTGA	GTCGGGCAGAAGAAGACTTG	199
CcM2062	FI246208	(GTA)5	CATTTTCATTGCATTGTGGC	TCATCCTTCCATCATTGTTGTC	143
CcM2063	FI246208	(AC)5n(AT)8	TCCCAGAATAAACGGATCTCTC	GCCACAATGCAATGAAAATG	200
CcM2064	FI246217	(CA)8	AGTTAAACATCACCGGGCAG	GGGATCATTCCAGGGTAGGT	252
CcM2065	FI246241	(TA)16	TTCAATGTTGGGAGTTACATGG	TTTCTAAATAGAGACATTGATGCAGT	268
CcM2066	FI246312	(TA)7	TTGAAAAATGAGGGATTTGGA	TGCGAAAGAAATAAAATACAAGTCA	105
CcM2067	FI246320	(TA)6	TGGTGAGAAGCTTTTCGGAT	CCTCTGTGGATGCTTGGTTT	279
CcM2068	FI246363	(TA)17n(AG)6	TGGAGTAATTTTATCCTTCTCCAT	AAGAACTTTTAATCTAGTGGCTGAA	174
CcM2069	FI246409	(T)11(TA)5	TTGTGGCATAGATGGAGTTGA	CACTCCTTAGACGCAGCTCA	255
CcM2070	FI246434	(CT)7	TGAGCTATTTCATCCTCTTGTCC	TCGGAAAAACTTTGAGTGGC	280
CcM2071	FI246446	(TA)10	CTTGTCAATGGTTTTGTCCG	TAATGCTAGTGCACCTCGTG	179
CcM2072	FI246492	(CA)6(TA)10	CTCTTACCTGCGCAACATCA	TACAGAATGCACCGTTGAGC	239
CcM2073	FI246503	(TA)12	CGGTCCCAAAAGATCAAAAA	TTTTTGCGGAGATTTGAAGG	259
CcM2074	FI246516	(A)12n(AC)7	GAGGACGAATCCCTCAAACA	TCAGCTCGAACAAACATTGC	184
CcM2075	FI246525	(AAT)5	TCAAACCACACCTCTTCATCA	TTTGGGAGTGAAATTACCCCT	129
CcM2076	FI246564	(AT)22	TTTGATCCACATTCAACCCA	CAAACTTTGATTTGTTAAGACATTGAG	165
CcM2077	FI246593	(TC)6	TAGGGCCCCTCCATATTCTT	CTCAACCCATTCAATTTCGG	255
CcM2078	FI246594	(CT)8	TCTTCCTTCGAATCACACCC	CTCGACCATCTCCTCGTAGC	183
CcM2079	FI246622	(AT)24	TTTTTGGTGTCTGATTTTGCTT	TGAGCTCTTGTGTTCTTGCG	193
CcM2080	FI246625	(ATA)5	TGATGGGTCCATTTTGGATT	CGAAATACGACGTGGAGGTT	210
CcM2081	FI246666	(TA)7	TCAACCAATTATGTCCATTTCC	TCATTTTGAGTGTCTCTTGTCCA	256
CcM2082	FI246686	(AAAT)5	GCGTGACATGGTCACATAGC	CGATCTTAGGAAGTTGAATTTGG	150
CcM2083	FI246687	(AT)13	TTTCCAACAAATTAAAATGGAAG	GGTGTTGGTACAACAACTGTAGATTC	259
CcM2084	FI246694	(AT)38	TGGTTGAATCGTTGAAAATTGA	GACGTTCTCTTTGTTGGATATTACTC	235

CcM2085	FI246732	(GAA)5	AACAAATGGGAGTGATTCGG	GATCTGAGAGAATGGCTCGG	266
CcM2086	FI246771	(TAA)6	CTCGCTTCACTTCTTGACCC	GGTGTAAACATCGTGTTTTTCATAA	179
CcM2087	FI246778	(AT)24	TGTCATTTAAGCTCCTCCTGAA	CCCCTCTCTTCGTGACTTTG	255
CcM2088	FI246798	(AT)21	TCAATCTATCGGTTGAATTTACAAAA	TTTCTATCGCACAAACAAACAAA	186
CcM2089	FI246827	(TG)6	TGAACTATCAAGGGAGGTGGA	AGAAGGCCTTTCTTTTGCCT	158
CcM2090	FI246879	(AT)14	AACAACCTATGACGCCCGTA	TGACGTTATTTGATTTTGAGGG	227
CcM2091	FI246883	(AT)17	CACCTTAAATGTTTATTTCGAATTTTG	GGGGAGTTGGGTTAGGAAAC	266
CcM2092	FI246898	(TTAT)5	TGAGTGCTGGACAAATCTGC	ATTAACGTCTCCGTTGCTGG	237
CcM2093	FI246900	(TTC)5	TCTTCCACTCCTTTTTCCCA	CTGTTGACCAGTGGGTAGCTT	195
CcM2094	FI246911	(AG)17	CGGTATAAAGCTCCTTGACCC	CAAAGGGATCCTTGGGAAGT	274
CcM2095	FI246919	(AT)24	TGGGTTAATTTTGTTTTTATGTATGTT	TTAAAATAAATTTTTCATGCTGTGA	231
CcM2096	FI246949	(AT)15n(AT)13	AGAACATGAGTTATTGAACGGAG	TGTGCGTGGGATGATAAAAA	279
CcM2097	FI246959	(CT)12	TGATAGGAATATTTCGGCGG	CCTTTGAAATTGAAGGCGAG	193
CcM2098	FI246975	(AAAAG)6	GGGCAAGAAATTTGTGTGGT	CTCATCCTCCATTGCCATCT	235
CcM2099	FI246983	(AT)28	TCTTCTAAATCTGCTTGGCATT	TTTTGTCATTGTTTCTTGGTTCA	207
CcM2100	FI246984	(AT)20	AGGTCACAGCCCATTTTGTC	ACCATAATCCCTCCTCACCT	176
CcM2101	FI247102	(AT)19(GT)17	TGAACGGTTGGATCATTGAA	AAAGTTATTGAGCGGTGTACCA	228
CcM2102	FI247144	(TAT)6	AAATTGATCTTTTGTGAGGGTCA	CGAGGGGTGTATTCCCAGTA	157
CcM2103	FI247153	(AT)6	AAACATCCGCCAAACAAGAC	TGCATTGATAAACCGTGTGG	258
CcM2104	FI247177	(TA)17	GAATCCAAATAATGGGGCCT	GAAGCATCACATCCTACCCG	237
CcM2105	FI247178	(AT)15	TTCGGAGAAAATGTTTATTTATTTGA	CACAAAAGGTAAACATGCATACTACA	233
CcM2106	FI247192	(GTT)5	GCGTTGAGAAGCCTCGAA	TTCCACTTCTGTTCCAACCC	261
CcM2107	FI247238	(CA)6	CCACAACAGTCTCAACCACG	TCGCTCATCAGATGGACAAG	224
CcM2108	FI247256	(TTAA)5	ACAAGGTCGACGAGGATGAC	AAGCCATGTCCACACAACAA	196
CcM2109	FI247328	(TTA)10	CATGTCATTTGGTGCTGAGG	TCAAATGTGCCTAGAAGGAGTG	241
CcM2110	FI247339	(T)10n(TA)6	GAACCTCAACCACCAAGGAA	TGTTGAGGTGGCACAGTCAT	182
CcM2111	FI247357	(TA)14	TCGCTTGTGCCTGTTCTTTA	CAGGTTTTGTGTTTGTTGCTG	221
CcM2112	FI247368	(CAT)5	TGCCGTCCCTTACTCAAGTC	TCATGCCTCCATAACCAACA	170
CcM2113	FI247382	(GATGTG)6n(TGAATG)7	TGGAATTGAGATGTGGATGG	TTCCAAGGTCACGTTATCCC	259
CcM2114	FI247428	(AT)8	CCCCAAAATCTGATGGAAGA	TTGCGAAGTTAACACTACCACA	116
CcM2115	FI247532	(TA)6	TCCTTGCCTTGTCCTCAATC	AGTGTGGGTTGCAAATGTGA	235
CcM2116	FI247554	(TA)19	TCAAGAACAACAATTGTCTCAGG	TTTCCAACACAAACCTCGTG	187
CcM2117	FI247638	(TA)23	CTTTATCATATCATTATTTGTTGCG	AAAAAGTGATGGATCGATATGAAA	251
CcM2118	FI247647	(TA)19	GTGTGGGGCTTCAAAGAAAA	AATCACCTAATAAATTCTTGTTGAGAA	248
CcM2119	FI247651	(TC)6	CACAGTTCTCAGGCCACAAA	GGTGCTTTGTGACAACCTTTC	104
CcM2120	FI247654	(AT)7	GGTTTAGCGTGCTAACCATCA	ATGGTCCCCCATGTTATTGT	132

CcM2121	FI247668	(TA)12	CAATGGGAGGTCATTTTATTTTT	TTCATGCAATAATTAATCAGGACAA	143
CcM2122	FI247679	(AT)16	TGAACGGTTGGATCGTTAAA	TTAGACGATTATTTATTTCAGCAAAA	185
CcM2123	FI247712	(TA)6	GGGCAAGGACGAGAATGTTA	TCATCTCTAGTGGGGTTCGG	249
CcM2124	FI247724	(ATA)7	GGATCAACTTGGATTTGCGT	TAATCTGCCCCAACTCGAT	257
CcM2125	FI247736	(AT)12	TGTTTATCGATTCATCCGTTG	AGTTACACCGGTGCCGTTT	171
CcM2126	FI247774	(ATA)6	CCTGGGAGCCAACACATAAT	GTGGGATGACATGCAAACAG	236
CcM2127	FI247777	(CA)6	TTTAGAAGGCTTCCATTGCC	ACCAAGCCTTTTCAAGTGGA	130
CcM2128	FI247783	(ATA)10n(TAA)6	CTCCCAGTCTCACAGAAGCC	AACCTCAAGGGAGGTTATTGC	212
CcM2129	FI247785	(TC)7	GGCTCTGTTTGGGTGTTTGT	AGCATTTGGAAGCATCAATGT	246
CcM2130	FI247830	(TG)6	CATTCCACTTTTGGAACGGT	TAACAGGACCTTGGCCTTTC	270
CcM2131	FI247836	(TC)6	GAAATCTCGGGCACAGTTCT	TGGAGAAGGTGCTTTATGGC	149
CcM2132	FI247888	(GA)7	GACGATGCAATTCCTTCATGT	TCATTTTTCAAATTTTAGAGTTGCTTT	115
CcM2133	FI247900	(TA)21n(A)12	GCGGGGTAAGTAAATCCCTC	TGTCTTGAAATATGGGATTTTTG	265
CcM2134	FI248016	(TA)7(ATA)7	TGGAAGGATTGTCTATGTTCAAA	GCCACAAAATATGTGTCAACTTC	125
CcM2135	FI248029	(TC)6	TACCCGAGATCATGAGGACC	ATCACTGTCCGACTCAACCC	237
CcM2136	FI248051	(TC)6	TACCCGAGATCATGAGGACC	CCATCAGAGCGAACAATCAC	194
CcM2137	FI248056	(AT)30	TGGAGTACGTGGATCCCTTC	TTTCACACCCCAAGTTTTCA	210
CcM2138	FI248130	(TA)21	TCATCCACCTTACTTAGTGGAAA	TTTACAGATACCTCATGAATACCCA	119
CcM2139	FI248147	(AT)34	CGAGTTTGGGAGTTTTCAATTC	TGGATGAAAGTTGTTGAGCTTG	261
CcM2140	FI248150	(T)15n(TA)5	TCATCGATATTTCATAGAAACAGTGTA	TCCGCAAAGATTTCTATCCA	260
CcM2141	FI248156	(TA)11	TTGAACCCACACCCTAGGAA	TCACATCTATATAAATTATGAGCAACG	276
CcM2142	FI248177	(AAT)7	TTTTGGTATGTTCAGACAGCTATAAAA	CACTAGTGTTATTTTAGCCCTTATCA	255
CcM2143	FI248198	(AT)27	TCCAACCTACCCTGAGAACAA	CATTTGTGGAACCAATATGGA	279
CcM2144	FI248214	(GA)6	GGTATGGGTGTAGGTGGTGG	CATCACTCTCGCGCTCATTA	204
CcM2145	FI248332	(CT)9n(TG)5	GCTCAGGATCGTTGGAAAAA	AGCTCAATCATCGCAGTCCT	191
CcM2146	FI248356	(GA)6	ATAAGGCATGGGGGATTAGG	CAACCCACCAATTAGAACCC	184
CcM2147	FI248445	(TTC)6	TCATTTCGTGGTTGCTTACG	CAATGAGGCTCTGGGAAGAC	126
CcM2148	FI248469	(AG)15(AGAA)6	TATAAATAGGGGCAAGGGGG	CCAACAATTATCCCCACACC	242
CcM2149	FI248494	(TA)22	TGTACAGGGCTGTAGGTTCG	TCATTTTGACCCTTTTTAGATTCC	235
CcM2150	FI248527	(GA)6	GGTTTTAGGTGCTTTGTGGC	GGCCGTTGTCATTTCAGAAT	270
CcM2151	FI248562	(TA)14	AGATCCCATCACCCCTTACC	TTCAATGATTGGGTCGTTAAAA	190
CcM2152	FI248567	(CTT)7	CAAGAGTCAAGCTTTGGAGGA	CCCTCACATGAAGATTGGCT	102
CcM2153	FI248569	(ATT)8	ATCCATGATCTTGGCCTGAG	GGAGTGAATGCTCCCTTGAA	280
CcM2154	FI248574	(AT)6	TCAAAGGTGTTCAAATCCTCG	TCACTCGCTTAATTTTTGGGA	171
CcM2155	FI248581	(CA)6	CTAAGCAACGTGCAATGGAA	TCTTGCTCACCATCATGTCA	280
CcM2156	FI248629	(GT)6	TCAAGGGAGGTGGACTACAAA	CCCTAGGGAATCCGACTAGC	254

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CcM2157	FI248633	(AT)17(T)16	GCCCATGCATCTCCTTAGAC	TTTCCCTTTTCACCCAAAAA	248
CcM2158	FI248658	(TA)6	CGGTAACCATTGGAAAACCA	AAGTGCAAAATTCATCAAGAAAAA	240
CcM2159	FI248713	(GAG)5	GTCGAGGGACAAATGGAAGA	CTCGTCCTCTTCCTCCTCCT	112
CcM2160	FI248722	(ATA)5n(CATA)16n(TACA)15	CACATTTAATTGAAAGTTACTGAGAAG	TTGGATGTACATTAGCAACAACC	276
CcM2161	FI248723	(TA)10	AATGCTTGCTCTTTGATGGG	AGGGACTTTCTGGTACGGGT	238
CcM2162	FI248725	(TC)7	GTTTGGGGGACCTCAAAAAT	TTTTAGGTGCTTTGTGGCAA	140
CcM2163	FI248726	(ATT)10	AATGTGATGAGTTTCAAGGCA	TATGATGAAGTAGGGGGCCA	259
CcM2164	FI248734	(TA)9	TCAATGACAATGTCCCAACAA	AAAGAAAAAGTCCATTCTCATTCAA	183
CcM2165	FI248753	(TA)6	AGCCATGCTCTCTTGTTGCT	TATGGGTAGTTGGGGATGGA	267
CcM2166	FI248767	(TC)8n(TA)10	GCCTCCCTCCAGTATTTTCC	AAAATATGTGACAACCATTTATTCG	235
CcM2167	FI248780	(GT)7	AAGGGAGGTGGACTACAAGGA	ATTGCTTTCCTTGCATGCTT	229
CcM2168	FI248790	(TA)23	GGGACCAAAAGAGGTATTTAACC	ATCCAACTCCAAGCATCACC	208
CcM2169	FI248798	(TA)7	AAAAATTGGAGACTTGATCTATGC	TCCATCGAGCCTATGCTAAAA	213
CcM2170	FI248816	(TTAT)5	GATGTCCAGGTGCCATCTCT	TTTCCATGGCCAGATTCATT	255
CcM2171	FI248833	(AT)6	AAACAACAACTTGAAGGTAATCAAA	CAATTATGTGAAACACATCTTGCAT	211
CcM2172	FI248838	(TA)20	TTGGATCGTTGAAATTTGATG	TCAATTCCGTGTTTGGATCA	277
CcM2173	FI248851	(TA)8	GGTGTCGTTTGAACCCTCCT	TCAATGGGATCCATGACAAA	275
CcM2174	FI248878	(TTC)5	GAGCTCCTTTCTCTGCCAAA	TTCCCTCACCTGAAAATTGG	194
CcM2175	FI248883	(A)13n(A)10n(ATT)9	CAGTCCTAACAATGATAAAAGGAAA	CCACTCTAAACGAGAGACAGACC	267
CcM2176	FI248915	(T)12n(AT)6	CATGAGCATGCATTAGGCAA	AGGTGGTTATGACAGCAGCC	257
CcM2177	FI248968	(TA)17	TCAAAATCTCAACTTCAACAACTTT	TTGTTTTGGGTGCTTAGGTTG	226
CcM2178	FI248975	(TC)6	TACCCGAGATCATGAGGACC	ATCCGGAGAGATGACCTCCT	254
CcM2179	FI249000	(TTA)7	TGTGTAACACCCCAGTTTTCA	CAAAATCATATAAAATCAACCTTCTCT	220
CcM2180	FI249003	(AT)31	CACCCTACAACGCCTGTAAAA	TGGATTAAGGATCCAACACAAA	223
CcM2181	FI249008	(ATT)6	GAGTCCGCGAGTCATGAAAG	TGGTGTAGGGAAAAGAAAGTCAA	235
CcM2182	FI249023	(TC)10	TGAAGACCCTTGTCTCCTGAA	CCCACCTCATCATCTCCCTA	155
CcM2183	FI249028	(TA)7	TTACATCACTCGTATGCGGC	TGAAAAATGATGACATGAGGTAA	142
CcM2184	FI249035	(AT)6	TGAGAATTTTCCTACTAAAAATAAGGA	TTTTGGATTACCCAATGGTTTT	230
CcM2185	FI249044	(AT)6(T)10	TAGATGTTTGTGCCATTGCC	TCGGTTTGTTTTGTGTTTTCTG	136
CcM2186	FI249067	(GA)6	ATTGGTTCTGTTTAGGTTTAGAGTTT	TACCCGAGATCATGAGGACC	161
CcM2187	FI249086	(AT)7	GCTTCTGAACCTCACCCAAA	TGGTTACTAGGGAAAGTGGGG	152
CcM2188	FI249114	(TG)6	GGTTTGATTGTTGAAATTTGATG	CAACGATGGTGCTAGTGGTG	252
CcM2189	FI249117	(TA)6	CGTGATAACGATGGAACCCT	CACCTCTTCTGAACCCCATC	118
CcM2190	FI249152	(AT)8	CAACTGCAAAATGATCTGGAA	TGGTTGATGTTATGATGATGCTC	274
CcM2191	FI249155	(TTA)7	AGCGACCTTGATAATTTTCTTTT	ATGTGACACCCTTCTACCCC	186
CcM2192	FI249170	(TA)10	GCCATTCAATAGTCACTCAAAAA	TTTGGGCTTTCATAAGGTGC	246

CcM2193	FI249172	(TTA)5	TGACGTGCATAAAAATTGGG	AACATGAAGTATTTCAACCTCAACA	280
CcM2194	FI249198	(GA)6	AGCTGGAGGACTACGTCGAA	TTTCTCACGGCTTGCACTC	139
CcM2195	FI249209	(AC)7	TGTGCATTTAAAACGGAGGA	GGTTGCTACACAAATTGCACA	169
CcM2196	FI249240	(TA)5n(AT)5	ACTCACGTTGGCCACTTTTC	CAGTGACCATGGGAAAACCT	146
CcM2197	FI249321	(T)10n(AT)9	GAAAACACAATAGGTAAACATACATGC	TTTGAGGAGATATTCATTTATTTGATG	225
CcM2198	FI249384	(TA)6	CCCAAGCTCACGGAATTGTA	TTTCGGATTGGCTGTCTTGT	274
CcM2199	FI249387	(T)10n(TAT)6	GGCCATACTGCCACGTAAGA	ACCAAACCACAACGACACAA	114
CcM2200	FI249413	(TAA)8	CACAAAGTGCCTTTTGTACGTT	AAAGAGCCACTGATTGGTGC	228
CcM2201	FI249429	(AT)8	CGGTTGAATCGTTGAGAATTG	AAGGAACTTTTAATGTAATGGTGAA	214
CcM2202	FI249438	(GGATGT)6	TTTGGAACAATTGGGGATTT	GTGCTCACCCCTGGTCATAG	276
CcM2203	FI249439	(GA)6	TTTACTGGTTCTGTTTAGGTTTAGAA	GAGAAGGGCAAGCCATGATA	221
CcM2204	FI249458	(AT)10n(AG)6	GGATAGGGGTGATCTTTCACA	CCATGAGTTATTGAGCGGAG	280
CcM2205	FI249487	(GTT)6	GCCTCGGAAAACTATAGGGG	CGTGGATCTTGCACTTGAGA	257
CcM2206	FI249503	(AT)31	GCCTTCAAACCCTCATGAAC	CGTGAATTTGGTTGAGAAGC	274
CcM2207	FI249534	(AGA)5	TGAACTCTTGAGTACAATGGTTTTG	GCCATAAGGCCCATAAGTCA	121
CcM2208	FI249577	(ATA)5	CCTAAAGGCACGAGTTGCTC	GCTGAAAGGGGTTCAACAAA	265
CcM2209	FI249608	(AAT)5	CCCACGATTTTTCTTTTGGA	TTGGCTAAAAATTTAAGAGGGA	257
CcM2210	FI249675	(CA)7	AACGTCAACTCTTAATCCAACTG	CTGCTGCTCCCATTTATTCC	234
CcM2211	FI249717	(AT)11	CCAATCCTTGGATTATGTTCCT	TGTTGAAAGTGGGGTGTAGG	280
CcM2212	FI249720	(CTC)5	TTTTCCCTCTCTTTCTCCCTC	TTAATTTCTCCAAGGTGCCG	161
CcM2213	FI249726	(TC)7	ATTTCATCCCCCTTGAGCTT	TGGACAACAATGCTTCATGC	253
CcM2214	FI249762	(TA)19(T)10	ATGTGGAAAAGATTGCGTGA	CCATAAATAATGATAAAATGTGCG	194
CcM2215	FI249835	(ATA)9	GGGACAAATGCCCTGACTAA	GGGTCGGTCCGGGTTTTA	260
CcM2216	FI249846	(AT)9	GCATGTTACCTTCCCCAGAA	TCTTGGGGTAGCAGTTTTCAG	158
CcM2217	FI249855	(TA)7n(AT)25	TCAACTTCCAAAAACACATTTCC	CCCATACTTGGTGAATCCAAT	272
CcM2218	FI249869	(AT)14	CCATTAAAATGGTCATTAAAGTTTTT	TGCCATGCCTAACAACGAT	277
CcM2219	FI249895	(AT)7	TTGAATGGTTGAAGTGGTTCC	TATTCCACCACCCCACAACT	173
CcM2220	FI249916	(AG)5n(GT)5	AGAATTGGAGGGAAAGGGAA	GCTCACAATTTGGCATCAGA	145
CcM2221	FI249952	(TTA)9	AGATTCGATGATGTGTTGCG	CCCATCACGGACCATTTATC	202
CcM2222	FI249970	(CT)6	TGAAATTCAACATTCACCATGAG	CAGTTTGATCGTTAAAATTTGATGT	185
CcM2223	FI249972	(TAT)5	AAAACATGTCAATGTGCCGA	TCATTCTTACCATTGTCATCGC	270
CcM2224	FI250002	(TG)6	CCGCTAGGTTACGGATTTGA	CCTCTTCAGGCTGTCCAAAA	139
CcM2225	FI250019	(TA)5n(A)10n(A)12n(AT)17	AGTGTTAAGGCCAAGCAAGC	TGAAAACCAAATCGATCTATTCCT	250
CcM2226	FI250109	(TA)33	CCAACTGCATTTAACAAATTGTACT	TTTAATTTGACGGTTGGATCA	200
CcM2227	FI250131	(CT)6n(AT)10	TGAACTTTCAATCTAATGGTAGAATTT	GAAAAAGTTGCTTCTAGAGTCATTTG	167
CcM2228	FI250131	(AT)13n(AT)6	TCGATTCAAAAGAAGAAAAGCC	GAATGAAGTATCAAATCATCTTGGA	278

CcM2229	FI250163	(CTT)5	TTGGTCTTGCGGTCCTTATC	AGGAGGGATGAAGGTTCGTT	101
CcM2230	FI250195	(AT)17	TTGATCATCCGGTGATTTTG	GGAGATTTAAAATGATTATCGCGT	190
CcM2231	FI250294	(TA)5n(A)11	TTTCAGAAAGAATTAAAAATGGTAACT	TGAGAATACTTGAAACTGGTGCTT	278
CcM2232	FI250328	(AAG)5	AGAAGGAGTGTGTGCGTGTG	CAACACCAACCACGTTGAAG	200
CcM2233	FI250438	(TA)6	ATATCTCGCGAAACCTTCCC	GGATGACTCGTTATTTGGATTTTC	279
CcM2234	FI250482	(AC)6(AT)37	TGTGTTTTCTAATCAATTTCAATCAA	TGAAGAGTTAAATAAATACATGTCTGC	260
CcM2235	FI250518	(AG)11	CGAATTCAATACGGGCAGTT	CCTTGAGCGAGGTTTCTCAC	225
CcM2236	FI250521	(TTC)6	GGAATCGAATGAAAGCCAAA	TGCAATGAAAGCACTTACGG	280
CcM2237	FI250563	(AT)25	TCAAAATTCACACAAGCGATG	TTTTTCCCATTAAATCCACCT	279
CcM2238	FI250568	(TAA)10n(AAT)8	TTGGTAGGCAATGGTGTTGA	GAACATGATCCATCCTCATATGTC	185
CcM2239	FI250575	(TTA)7	CAAATGGTAGATGATCGATTGC	GAAAAGCACACTAAAAATTTCCC	213
CcM2240	FI250580	(TA)7	GAAATAAAAACATCACATATCAATCG	TTGAATACGGTCAAGGTGGA	184
CcM2241	FI250619	(GA)12	TGCTGGTGTAAGTTGATCCCT	ATCTGCTATTCATGGTGGGC	130
CcM2242	FI250634	(AT)29	AGCTATATGCAGTCCCCAACA	GGGACCTTAGCCTTTCTTCAA	128
CcM2243	FI250703	(CCT)5	TAATGAGGGAAGGTTGCTGC	TGTTGGTATTGATTAAGTTTGGTG	136
CcM2244	FI250705	(TA)31	TCCCTTTTGCTTTCTACGCA	TTGTCTTGGCTTGGTTTGAA	250
CcM2245	FI250726	(ACC)5	GCAGCAACAGGCTTCTTACC	AACTCTCCCCTCGTTCGATT	171
CcM2246	FI250744	(AT)31	AAGTTGAACGGTTGGATCGT	TTGTTTTCTTAAAAAGGATTTTCATGT	229
CcM2247	FI250835	(ACTATC)5	AAATCAGGTGCAGCCATCTC	TGCATCCATTTGATCCTGAA	220
CcM2248	FI250869	(TA)14	GGATAAAGGGCTTTCTCGCT	AGTGCAATAGGGCAAGCATC	242
CcM2249	FI250875	(ATG)6	GATCCAATCGACCGTGAGTT	TCGGCTATTTCAAAATCGGT	252
CcM2250	FI250879	(T)11n(T)10n(TC)5	TGAGGAAGAAAATAGAGGAGAAAA	TCGTGCATCAAATTAAAAGTGC	195
CcM2251	FI250880	(TA)8	TCTCCATGTAGGATCAAGGCT	TCCGTGTGAGAGAGTTCTGG	194
CcM2252	FI250887	(TTA)5	ATTGGAACCCTTGGATCGTT	AGCCCAATATGCATTACCCA	192
CcM2253	FI250921	(TG)8	TCCTTGGATCCCAACAAGTC	TTGTAGCCCCACTAAAGGATTT	186
CcM2254	FI250933	(AAT)7	AACATCAAGAAGGGTCCACA	GGGAAAGGGTCTGCTCTGAT	272
CcM2255	FI250934	(CA)6	ATGTCATCATTCTCAGGGGC	TGATTGATAGAAACGATAAGGAAAAA	240
CcM2256	FI250982	(TA)26n(A)12	CGCCAAACTCGGTAAGGATA	AATGGAAATATTGCCTCCAGT	227
CcM2257	FI251002	(TA)26	TGAATGGCTCAGGAAGATGA	ACAGCACGTGGACACCAGTA	178
CcM2258	FI251011	(AT)27	TTTAATTTCAATGGTTGGATCA	TGTAAAACATGAGTTATTGAACGGA	196
CcM2259	FI251044	(ATT)10(TAT)5	ATAACGATGCCGAGGAAACA	GGAGTGAATGCTCCCTTGAA	271
CcM2260	FI251057	(AT)18	TTTTCCTTACAGCAAACCTGC	GTTTGGGTAGCATTGCACAG	165
CcM2261	FI251085	(TTTA)5(TA)5	CAACGGTTGAATTGTTGAAA	ATCGCAAGTAGACGGCAAAT	200
CcM2262	FI251090	(AT)8	TTACTGTGTTTTGGGTTTCGC	TTTCGGCTGGACCTTATACA	280
CcM2263	FI251108	(TTC)5	ATGCTTTTGCTTTTGTGTGC	ATGCTCAAACGGAGGTCAAG	182
CcM2264	FI251121	(AG)7	TCAAGAAATACAAAAGGGAGAGAGA	GTGCAAGGGGATCGAAGTAA	109

CcM2265	FI251144	(AT)7	TCAACATACGATGAAAACAAAGC	TGATGCAACTTAATCCAATTTTT	190
CcM2266	FI251146	(TG)5n(T)10	TGCACTTAAGAGTTGCATTTGG	AACTGCCACGTTGTTTGAAAT	179
CcM2267	FI251152	(TATT)5	AAATGAATGCAATGCAGAATG	TGCGCCATAAAGAAAAGTCC	232
CcM2268	FI251161	(TA)6n(A)10	GGACCAAATTAGATTTTTAACCCTC	TTTAAATTTTGCCAAGCAACTT	240
CcM2269	FI251228	(AAC)6	TGCCCGATATAGAATTTGCC	GATTTTCTCATGCACACAGCA	232
CcM2270	FI251231	(TA)18	CGACCCGACACACTTACACTT	TGATTAAAAATATCCTTCAATAGCTTG	259
CcM2271	FI251321	(T)10n(TA)5	AGATCAAGTGTGTGTTTGAATGTG	ATATGTGTGTGTACGCGGGC	280
CcM2272	FI251368	(TGA)5	TTAATGTTCCTCGGTTTCGC	AGCATCCTCATCAAAATCCG	230
CcM2273	FI251411	(GA)6	GCTTTGTGGCAACCTTTCAC	CAGGCCGTTCTAAATCCAAA	193
CcM2274	FI251435	(TA)6	TGAAAAGCAAGTTCCATTATGC	TCAAACCAAGCATAACTTCCTT	275
CcM2275	FI251474	(TTA)6	CTTTCTTTTTCTTTAGAGACCTTGAT	AATGTGACACCCTTCTACCCC	201
CcM2276	FI251499	(GA)7	TGAAACACCTTTTGAACGAGC	CGTTACGATTTTGAAACGGG	243
CcM2277	FI251552	(ATTA)5	CCTTCATCCTCGGAAGACAA	ACGAAGTGAAGGAGCGGTTA	195
CcM2278	FI251553	(AT)6	TTCAATCATTTCCTACACATATCAGA	TGCTCAGTAATTTTTAAGCCTGA	271
CcM2279	FI251563	(AT)20	TTGGTTCGGTAAATTAAGTTTGAA	CACTTTTCATATTTATGATTGGACA	192
CcM2280	FI251581	(ATGT)9	TTTAAGAGTTGGATTGTTGGAATTT	ATTGAGCGGGGTAGGTCTTC	188
CcM2281	FI251708	(TC)9	TCTCTCTCCGAACTTTCCCA	CTCACCCTGTTCGATTGGAT	227
CcM2282	FI251731	(TA)13	TCCTCTTTCTACTCACCCTCTCA	GAATTCATTTGTTATTACAGATTTCAA	267
CcM2283	FI251867	(AG)8n(AG)21	GAACCCCTGGATGCCTATAA	TCTCTCCCTCTTTCTTCCCC	161
CcM2284	FI251893	(TA)6	AGCTGCTTTGAGAAGTGGCTA	AGGCCGTCACATCAATAACC	269
CcM2285	FI251894	(TTA)6	GCAGCACTAGTACAGTTTGCATT	CTGGTATGGGGCACTTCATT	214
CcM2286	FI251934	(TTAT)5	TCTTAGAGTGCGGGCTTGAT	GGCATTAATAAGGCGTGTTTC	272
CcM2287	FI251959	(TG)7	TTGGTTGACCCACACAAGAA	TTCGAAAGTGCATTGGATGA	180
CcM2288	FI252005	(AT)6	CTCAAAAACCTTTCTCCCCC	TGCGGCATTGATTTTGAGTA	116
CcM2289	FI252028	(GA)6	CTGACCTTTGCAGGACTGGT	CCCAAAGAAGTGCAAGGCTA	239
CcM2290	FI252032	(AAT)11	TAACATCAAGAAGGGTCCGC	TTCCGGATTCCTTTCATTTTT	162
CcM2291	FI252064	(TA)12	CAATGGGAGGTCATTTTATTTTT	TTCATGCAATAATTAATCAGGACAA	143
CcM2292	FI252070	(AT)23	TTCATCGTTCACCAACATTCA	TAGATTTTCCACGCCCTACG	209
CcM2293	FI252096	(TA)8	TTTAAATTCAACGATTGTGTTGTT	AACGGATGATTTTCTTTACATCG	167
CcM2294	FI252109	(C)15n(AC)8	GCAGCATTAGCAAAAGCTCAA	CTGGATCCCTGGCTACAAAA	263
CcM2295	FI252132	(TA)6	TCAGGGTTTTTCGTTAATGTG	AAATCAGAGAAAGACATGAAGCA	205
CcM2296	FI252147	(TA)21	CGTCCTAATTATCACGAGTTTACA	GGGTAAAAGAAATATAAACCCCAAA	200
CcM2297	FI252170	(TA)8	GGTAGAGACCAAATGGAGCC	CCTGTCGTGTCGTTGTTGTT	280
CcM2298	FI252173	(GATGTG)8	TGAATCACCATTTTGTGTGGA	GAGTCATGCTCACCCCTGAT	276
CcM2299	FI252212	(TA)5n(AT)5	ACTCACGTTGGCCACTTTTC	CAGTGACCATGGGAAAACCT	146
CcM2300	FI252230	(A)13n(A)10n(GA)5	ACGTCTTCACCGGCATAAAC	TTTCAACCCTCTCGATTTGG	227

CcM2301	FI252241	(GT)6n(TC)6	TGCACCTCAAGTAGAGCAGG	CTGCAAATGCAATGAAGTGG	191
CcM2302	FI252259	(GAA)7	TGCATCTGATGGATTGTTCTG	AGCAGCCAGATTCGATGACT	273
CcM2303	FI252259	(A)11(AAAC)6n(T)10	AGTCATCGAATCTGGCTGCT	GTAACCGGCCTATTGACACG	183
CcM2304	FI252261	(GATGTG)9	GCGAATCACCATTTTGTGTG	CCAAGGTCACGTTACCCCTA	229
CcM2305	FI252313	(TA)29n(AC)6	CCTAACCAAATAAGTGTCAAGAAAAA	GGGGAAACTAGTTCGATTTGA	258
CcM2306	FI252371	(AT)6(AC)16(AT)21	TCAAATGCCATCCATCAAGA	TAAAGCTGGGTGTGGGTTTC	230
CcM2307	FI252377	(CT)8(AT)10n(TA)8	TGGATCGATGAGATTAAGTGGA	AGAATTTTTACGAAAATGAAAATCA	184
CcM2308	FI252399	(TA)21	GGGGTGGCACTTTTCCTATT	ACCGGCTAACGGCTTAGATT	192
CcM2309	FI252406	(AT)20(AC)5	GAAAAGGGAGAGGAGGAGGA	AAAAATAGATATGCCGCTGAAA	278
CcM2310	FI252423	(AT)6	AGCGCTATGTGAATGCCTAA	AAGAACCTTAAATTCAACGATTGG	168
CcM2311	FI252426	(AAT)5n(TAT)7	ACTTGTGACATGGATCGGGT	GGATGAAACAGTCCCGCTAA	182
CcM2312	FI252440	(AAT)7	AACATCAAGAAGGGTCCACA	ATAGGATGTGACATTGGGGC	259
CcM2313	FI252492	(T)11n(TTA)6n(CA)5	TCTAAAGAGAAATGATGCATGG	TGAATACGATCGTTCATGGG	274
CcM2314	FI252525	(TA)17	AATATTTGATGCTTCGTTTCATTA	GATCCCTTATTTCATTACTTCAACTT	280
CcM2315	FI252535	(TG)5n(TGA)5	TGTTTAAGCCTATGCAAAAGGA	CCTTGAAAACTCTAGTTTGAATCAAGT	252
CcM2316	FI252543	(AT)18	GGAACCAGATTAGGGACTTTCA	CAATTAAATAAATGGTAATTTTGGACA	177
CcM2317	FI252586	(GA)6	TGGGGCTAGTGAAGTTTGCT	CGTGGGATTCATTTGTCTCA	257
CcM2318	FI252589	(AT)17(T)1n	AGCATCACAAGTTCGCTTCA	TTCGATTTGATTTACCGATTGA	203
CcM2319	FI252593	(TC)6	AAAAGTTGGGTGGGACAACA	AAAAAGAGTGGGAGCGAAAA	186
CcM2320	FI252639	(T)10(CT)5	AATTGAAATCTCGGGCACAG	GGTTTTAGGTGCTTTGTGGC	164
CcM2321	FI252678	(TA)5n(TG)6	CGGATGACAAACCTTTTTGC	AATGATCCATTTTGACCGCT	275
CcM2322	FI252705	(AC)5n(AC)5	TCATCGTCCTCTTCAGACCC	CTCCCATCTCCGAAACAAAA	228
CcM2323	FI252744	(TA)19n(T)10	TTGAACGGAATAAGTCTCCTAAA	TCTGCCTTTTGTTCGTTGTG	255
CcM2324	FI252749	(TA)8(GA)8	AACTCTTTCGGTCCAATTCTTA	AAATTTCCTCTGCCCCTCTC	235
CcM2325	FI252763	(TA)9	TGGGTTGACTTCATTAAAGATTG	GCTGTGACCCACAACAACAC	160
CcM2326	FI252780	(T)10n(TATT)5n(T)12	TGGCTTGGGTAAATAACCCTT	TCGTGACTGTTTCGTGGATG	275
CcM2327	FI252805	(GCT)7	GGTTTCGGACTGCTGATCTC	TTTCCGAGAACTCGATTTGG	192
CcM2328	FI252840	(TA)32	GCATGCATGTTCAACTCTCC	TGCAGATAAGCCTATGCACAA	247
CcM2329	FI252908	(CA)6n(AC)5	TCTTGGAGTAAGTGTGGATTCCT	TCGAAGACTGTCATGCAAGC	160
CcM2330	FI252913	(TAT)12	CCTGAGTGTTTTCTTCTTTATTTGC	CCGGGTATCATTACAGGGAA	117
CcM2331	FI252977	(TTA)5	GCCGGGATATGTTCTTTTGA	CCCTTTTGAGAAAACCCCTT	259
CcM2332	FI252985	(ATA)13	TCCATTTTTCTTCTGCGGTG	TGCTATCAATCCAAAAACACAAA	239
CcM2333	FI252995	(TA)8	TTGGTCCAAGCTTCATAGTTTTC	TGAACAAATGGTTGTTTAAATGTC	279
CcM2334	FI253002	(AT)14	TATGAAGAGTGCTGCGTTGG	AGAAGAGGGAGGGGGATTTT	216
CcM2335	FI253009	(AT)6	CATCCTTCTCGCTTGTACCG	TACTCGGCCAACCATTCTTC	252
CcM2336	FI253061	(ATT)7	CCACTCTCCAACCCATTCAT	CAATAGCAAGAACCGTGCAA	185

CcM2337	FI253103	(AT)11	TTGTGATAATTTTATATGTGGAAACG	GGACCCAGCAAGAAATTTGA	130
CcM2338	FI253182	(TA)16	CCTTTGACATTTTTGTGTTCATTT	CATGGACCAAAATCAAAATTCA	253
CcM2339	FI253183	(ATG)6	TGTTTGGTAGGTGAATGATGGA	TTAGCAAGGCTTCGTCCACT	268
CcM2340	FI253187	(AC)6	TTGAATCTCTTGCATGGCTG	TTTCATGCCTTTTTCCAACA	254
CcM2341	FI253221	(TA)8	GAGCTATGACCAAGATTGATGG	TCAAAAGGATTAAAACTTTCCATTG	273
CcM2342	FI253238	(GATGTG)9	GGGGTGTGTGAATCACCATT	TTATCCCTAACCTAGGGCCG	236
CcM2343	FI253264	(AT)6	TTTAGAATAAATGAATCTTCTCCTCTC	AAGAAAACAAAATGAAACAGAATGAA	194
CcM2344	FI253322	(TG)6	CCCCTGCAGTGTTAGATGCT	GCCTGCACAAATTTTCAACA	194
CcM2345	FI253349	(AAT)11	GCTTGCAATGCTGAAGTCAA	CAGATTCGTTCCCGCATAAT	184
CcM2346	FI253437	(TA)20	TTGAGTGGTGTAATAGTTGGTAAAA	ACGACCCCTAAACACATCCA	273
CcM2347	FI253459	(TA)6	ACCAATGTACACCTCTCGGC	AAGGCAAAACACTCTCTGGAA	111
CcM2348	FI253474	(ATT)7n(TTA)5	ATGCCGAGGAAACACTTTGT	GGAGTGAATGCTCCCTTGAA	268
CcM2349	FI253516	(AC)7	ACTCTTGGAGTAAATGAATCCCT	CACTTTGATTACCTTCAAATTGTTG	215
CcM2350	FI253560	(AT)17	CGATAAGAACCAATTTAGTAGAAGAAA	CCATTCTGTGCCAACTCAAA	272
CcM2351	FI253600	(TA)7(TG)5	TTTTGCCTCTCCTATCTCAATTA	TGGGTATAATAATTTGATTTTCATCAT	205
CcM2352	FI253616	(AT)11n(A)17	TTTGCCGTTTGATAATTCTGTG	TGGACCTTTTTCCTTTCTGC	214
CcM2353	FI253711	(TGA)5	CACCACAATTTGGGTTGAGA	GCAGTTGCGGTCACATCTAA	132
CcM2354	FI253764	(TC)12(TA)21n(AT)10n(AT)10	ACGGTTGGATCGTTGAATTT	AAAACATGGGTGGGAGTATGTT	254
CcM2355	FI253782	(AAT)5	CGATGTCGAGAAGCTGTTGA	CCTTAGGGCTTCATCACCAA	203
CcM2356	FI253821	(TTA)7	TTTCTTTACCGAATTAACACGACA	TCTTGGAAATTTTGTTTCAGCA	207
CcM2357	FI253849	(ATT)10	AATTGGGCTTATGCATCGTC	TTTGCGTAACCTTCCCAAAC	199
CcM2358	FI253857	(TA)12	CAATGGGAGGTCATTTTATTTTT	TTCATGCAATAATTAATCAGGACAA	143
CcM2359	FI253858	(AT)7	CACACCTGCAAACAATTTCAA	CATGACTTGTTTCAACACTCAACA	237
CcM2360	FI253861	(TTA)5	GCATGGATGCAATGAAAATG	CACTGATGCTTGGCTCAAAA	266
CcM2361	FI253868	(A)18(CA)8	AGAATGAAAACCCGCAAAGG	TTGGATGTGGCACTTTGTGT	250
CcM2362	FI253913	(TC)6	TCTCTGCCACCAACTTTTCA	AAATCAACTTGGTTCCACGG	230
CcM2363	FI253963	(TCT)5	TCAGAGGGTGAGAAGTGGCT	TCGGTGCTAGAACCCAAAAA	172
CcM2364	FI254002	(TGA)6	TGGTGTTTGAGCCTATGCAA	CCTTGAAAAATATTGCTTGAATC	257
CcM2365	FI254022	(GAG)7	AACCAACGGTCGATGAAGAC	AAGGCAACAAGAAGGAACGA	254
CcM2366	FI254050	(GA)6	ATCGGAGCGACAATCACAG	TACCCGAGATCATGAGGACC	192
CcM2367	FI254089	(TC)13n(TA)30	TTGGATCGTTGAAATTTGATT	TCTCGGAGGTTTTGTGGAAG	228
CcM2368	FI254102	(CA)6	AAGCCTCATCACCAACATCC	ATGTGAAACTTCCGTTTGGC	264
CcM2369	FI254116	(GATGTG)5	GATTTTGGAACAATTGGGGA	CCCCTGGTCATAGGTGTGAA	277
CcM2370	FI254125	(AG)8n(TA)5	CAAAGTTTTCGCTGCCTCTT	GGAAGAAACAAAAGCCCACA	278
CcM2371	FI254150	(AT)16	TTCTTGGGTTCAGTCCCTTG	TCCCATACTTGGGCACTACA	279
CcM2372	FI254169	(AT)7n(A)11	CCACTCTCAACACACCCCTT	TTCTTCTTGCAGAACAGCCC	136

CcM2373	FI254204	(CAA)5	GGAGGTGGTACCAAACTTCCT	TTGGAACTCCTCTTTGGTGC	156
CcM2374	FI254229	(AT)24n(AG)6n(GA)5	TGAGTTATTAAGTGGGTAACTTTGC	TTGGTGGTGGTGATGTTGAC	257
CcM2375	FI254309	(TG)7n(TG)10n(TG)5	CAATTTTTCTGGATCCGTCA	AACATACACACACAGACATACACACA	120
CcM2376	FI254348	(CT)6	GGGGCCCTTATGATAAATTCTT	TGCTATGATTTGAGGAACCAAA	215
CcM2377	FI254354	(ATC)8(CATA)9	CAATTTTCACAACTTTATCAACACA	GAGGTCCCAGGGGTCTCTAC	250
CcM2378	FI254387	(TG)6	TGAAATATCAAGGGAGGTGGA	TTGCTTTCCTTTGCATGTTTT	234
CcM2379	FI254391	(TC)10	CCGGAAAAATTGCCTATTGA	TTCGATGACAGAATTTAGGTGC	151
CcM2380	FI254506	(T)10n(AAT)15	AGCTTTGGGCCTCTTCTTTT	TCATCGTCTTTCATGTGGGA	248
CcM2381	FI254593	(T)10n(ATT)5n(CA)5	TCTAAAGGAGAATGATGCATGG	ATCGTTCGTGGGTGTACGTT	253
CcM2382	FI254662	(TAA)5	CGACTCAACCTTTCTTTAACCC	TGTAACACCTTGTGTGATTTGC	273
CcM2383	FI254694	(GA)13(GAAA)5	AATTTGCCCATGTTTGAAGG	TACCTGGGTAAGCGGAGTTG	260
CcM2384	FI254722	(AT)8	AAAACACATGAAAGGGGTGC	GGATCTGAACACAATTCCTGC	259
CcM2385	FI254730	(GA)6	CTCAATTCTCCATGTGCAGG	GGGGACTGACTCGTCCACTA	263
CcM2386	FI254743	(TCT)6	ATTCGCGAGTTTTTGGAGAA	CAGTCCAGAACCAGAACCCT	157
CcM2387	FI254744	(AT)16(GT)22	TTCATCATTCACCAACATCCA	CGTAGGTTTCCAAGCTCGAC	256
CcM2388	FI254797	(TA)8	TTCTCCGTGAATGATATGTGTTG	TCTCACTTCCGGTGAGAAAAA	147
CcM2389	FI254867	(TC)8	ACGACGATCTCATCGATTCC	CACATCAAAATGTAACGGCG	127
CcM2390	FI254874	(TAT)5	TCCACTTTCTTCAATTGCCC	GTTTCCCTTTTCACCCAAAA	251
CcM2391	FI254895	(T)10(CT)6	GTACAATTCTCAAGGCCCCA	AGGTGCTTTGTGGAAACCTT	141
CcM2392	FI254995	(GT)6	GGGAGGTGGACTACAAGGAA	CCCTAGGGAATCCGACTAGC	256
CcM2393	FI255019	(TG)6	TGAGATTTTGCCTTTGGACA	TGCCCAACAGTGGGGTATAA	211
CcM2394	FI255036	(TC)12	TGGAAACGATTTCCTACCACA	ACAAGGGGAAAAGGGAAAGA	260
CcM2395	FI255041	(TTA)8	CGACTTTTAAGATTTCGTTTTAGAG	TGGCCATTCCTTTGCATATT	194
CcM2396	FI255047	(GATGTG)6	TGAATCACCATTTTGTGTGGA	CCAAGGTCACGTTACCCCTA	215
CcM2397	FI255060	(A)10n(CT)7	TGTGGTAATCTGGTGAACGAA	CTTACACCAATTACAAACTCTATTTGA	280
CcM2398	FI255202	(TA)20	AAAATCGTACGTGAGATATAAGAAGTT	CAATCAGAAAACAAACAAGACCA	280
CcM2399	FI255232	(TA)9	TTGAGGTTGATGCATTTCACA	TGGCACCACAAAACTTGATT	261
CcM2400	FI255247	(TTA)5	TGAAAAAGGCTACACCCACC	ACAACCAAAGAAGGCAGCAT	136
CcM2401	FI255257	(AT)10	CATTTGCACCCCCTAACATT	TTGCTACCTAAAATCTAACTACCGAAA	276
CcM2402	FI255286	(TA)30	GGATTCACTAGGTGGAACCTCA	CGGGTTGTAAACGAATTAGTGA	117
CcM2403	FI255319	(ATT)5	CTTTCTTTTTCTTTAGAGACCTTGAT	CACAGCAAGCACAACCAACT	223
CcM2404	FI255369	(GA)7n(TG)5	TGCAGTCACAGTGAAAACTGAA	TCATACACCCGTAGCACATGA	144
CcM2405	FI255460	(AT)11	GGTTGTTGGTGTAACGACCC	CCCTTCATAACGGAGGTCAA	215
CcM2406	FI255466	(AT)10	CCCCATGCAACCTTACAATC	CCTGGACAATTTTAGGGGTC	280
CcM2407	FI255572	(TA)23	CCAAGATCGATGCTTTGACA	TCAATTGGAAACAAGAAATCCA	275
CcM2408	FI255588	(GTT)5	CATGACATCTTCATCCACCG	CGGTGAAACTTTTCCTACGC	261

CcM2409	FI255641	(TTA)6	TGAAGGTTGATCCAAGGAGG	CGTGCAAAATAATTGTCCAAAA	186
CcM2410	FI255674	(TA)6	TTTTCTTCCATTCATTTTCTCTGTC	CGGCAAATTCCCAGTAAGAA	135
CcM2411	FI255684	(TA)7n(AT)5	GCAGATGAAGTGGTCAGGGT	TGGACTATAGTAAAGGACACTGAATTG	270
CcM2412	FI255688	(TA)27	ACCAAATCCTTGCCTCTGTC	AATAGAACCAACTCTACATTGAATTTT	277
CcM2413	FI255721	(TA)7	ATAAGAGGCTGTGTCCGTCC	TCATAGGGGTGAAAAACCAAA	260
CcM2414	FI255727	(AT)17	CGTAAAGATTTTGCCTCGGA	GCGTAGAACATGAGTTATTGAATG	147
CcM2415	FI255747	(TA)6	AGGTGACTGCATAATGAGACAAA	TGGTGAAGCATGTGCAGTCT	188
CcM2416	FI255757	(CAT)6	AATTGAAACAGTTGCGTCCC	TTTAACATGAGCGCAGATGAG	182
CcM2417	FI255838	(TA)6	CAACTACGCGCGTTTTGTAA	GCCAAGACAAGTCAAAAGCC	266
CcM2418	FI255882	(TAA)6n(TA)5	GGTGTGTCCGGACCGTTAT	TTGAGCGGTGTAATACTTAGTAAAAG	277
CcM2419	FI255900	(TA)27	AACAATTTGATGGCAAATGACTT	ATGTCCAAGATTGCATCCAC	232
CcM2420	FI255971	(TAT)6	AGGAAACTGAATTGGCCCTT	AGGCAAGAAGCTGCTGAAAG	122
CcM2421	FI256000	(AAG)7	GGCTCTGAAAAGCCAAGAAC	GTGCAGTTGAGGAGGAGAGG	153
CcM2422	FI256020	(TA)13	ATGGGTGGTGAACTCACGTT	CAAAACTCAACCCAAAATTTTATT	278
CcM2423	FI256047	(TCT)5	TTTAGGTCGATGGCTGTCAA	TTCTTGAATTTTCTCAAACGAAA	212
CcM2424	FI256049	(CT)9	GCTTGGGCATAGTTCTCAGG	TTGTGGCAACCTTTCACACT	139
CcM2425	FI256110	(AT)25	TCGGCCTGCATTTTAATTTT	TGCATTAACGTGCACTTGCTA	192
CcM2426	FI256123	(GCA)6	CAACTTGCTGCGAATCAAAA	CTGCTGCGAAGACCATCTAA	258
CcM2427	FI256124	(T)10(CT)5	CAAGGCTCTAAATTTCGTCCA	TCACACTTCAATGTGCCTCA	109
CcM2428	FI256282	(AT)10(AC)6	TGCTGCAAGTTACCAAAACAA	CATCAGATCCACCACTGCAT	280
CcM2429	FI256365	(TC)6	CCAAGACTCCTTAGAGCTTGAAA	CGGTACAGGTAAGAGGGCTG	160
CcM2430	FI256396	(TCT)5	AGTGGCATTTCATTCGGTTC	GATGCATTTCTCCGACACCT	262
CcM2431	FI256407	(AT)6	AACCTCTTCCCACTCAACCA	TCAAGAATAGGAAGTGATAAGGAAA	276
CcM2432	FI256551	(CCG)6	CACTTTTCCTCCTAACCGCA	GAAAATGGAAAGAATCGGCA	170
CcM2433	FI256555	(AT)12n(TA)13n(TA)9	TATCCACGGATTTTGGTCGT	CACATGATTATTGAAATTTTCGTTTC	202
CcM2434	FI256568	(TA)6	GGAGGCACATAGGCATAATAAGA	TGCAAAATAAATGAGGGAGC	280
CcM2435	FI256687	(AT)7	TGCCTATTAACGCTAGTGCAGA	TTGGGAGAGGGAAGGAGAAT	235
CcM2436	FI256721	(GAAT)5	TCACCCCAATTGCTATGACA	CCCTATCAACCAAACCCAGA	207
CcM2437	FI256765	(AG)6	ACCCTTACTTCCAAGGGCAT	ATGCATGCCCTCATCAAAA	234
CcM2438	FI256789	(TG)6	TGAACTATCAAGGGAGGTGGA	TTGCTTTCCTTTGCATGTTTT	234
CcM2439	FI256817	(T)14n(T)12	AGGTGGGTGCTTTTGAATTG	CATCCATCCTTTCCCAATGT	201
CcM2440	FI256846	(TA)26	TGTCGATAATGTTTGAACCACTG	TCATTTCTTGATTTGATTTACATGC	173
CcM2441	FI256917	(T)11(A)12	TGCATGCATGAACCTCATTT	TTTGATACCACTGCGTTTCG	229
CcM2442	FI256938	(GA)6	ATAACCGGAAACGACGATGA	CTTCGACTCTGACTTTCCCG	111
CcM2443	FI256981	(ATG)7	GCATCAATGATTGGCTTCAA	CCCCCTTTCCTATGTTGTTG	214
CcM2444	FI257032	(AT)6	GCACTTCATCTTCCGGTACAA	TTGACAATCCTCATTTGCCA	262

CcM2445	FI257060	(TTA)5	TTTAATGGCCTTTGCACCTC	CTGCCTCCATTGCATTCATA	254
CcM2446	FI257108	(TA)6	ACCTCCACCGACATTCAAAA	TCACACTCGTATTTTAGGACAGG	276
CcM2447	FI257109	(TTA)8	AGCACCATCAGGCAAGAGAT	AGGCACCACGAGCAAATTAT	192
CcM2448	FI257145	(AG)7	CTTCGAAGGGAGAAGAACCC	ACTCGCTGTCTCTAGCACCC	101
CcM2449	FI257153	(A)10n(TA)5	GGCTTACAATTAATGTCAATGGAT	TTTTTCTTCTCAATTGCGTTTTT	274
CcM2450	FI257222	(TC)6	TTTCAAAATGGGCCGTTCTA	TTGTGGCAACCTTTCACACT	245
CcM2451	FI257284	(AT)11	TCCATGATGCATGATTTGAAG	ATGATGGACCATGGCTTTCT	165
CcM2452	FI257316	(ATG)6	AATCGGCCGTGAGTTATGAG	CAGCCATATTCGGAGAAATCA	156
CcM2453	FI257332	(TA)12	CCACAAATTAGGGAGGAGACT	TGGTTCTTCCATGCACCTTA	229
CcM2454	FI257376	(AAG)5	TCAAAGTGGGAGGGTAGTGG	CACCCCAGTAAGTGGCTTGT	205
CcM2455	FI257386	(AT)16	CATCTCAGGGATTCTAAATTTCAT	GATGCGTAATTTGTTTGGGG	231
CcM2456	FI257443	(GA)8	CAACGAGTTATATATAGTGGGAACTCA	AGCCCTTGTGCAGTTATGCT	225
CcM2457	FI257452	(TAT)8(TGT)9n(TGT)5n(TTA)8	TCCGGTGTACAGTGGTGTGT	CTGTTATCCAACCTGACCCG	239
CcM2458	FI257476	(AAT)5	AGCTTGGGTGCGGATATAGA	TATAACTGGTGGTGGTGGCA	118
CcM2459	FI257513	(CT)5n(TG)5(TA)5	TCAATGGTTGAATTGTTGAAATG	CCAGATGTGTTCACCAATGA	273
CcM2460	FI257603	(TA)10n(AT)9	CGATAAAACATTTAGCGGCAA	AAGGGGGTCGACTATTGATT	279
CcM2461	FI257604	(AT)22	AACGGACACTTGTAATGGGC	GAAGCCTTCCTTCCAAGGTT	109
CcM2462	FI257641	(A)11n(TTTA)5	TTTGAATTTAATAGTGCAAGAAGATCA	TGTTTGTCTGGCCTGTTTTG	246
CcM2463	FI257642	(AT)11	AGCGCAAATGGAAGTTGTTT	CAATCCAACCCAATGTTTTGA	210
CcM2464	FI257649	(AG)11	ACGGCCTAGTTTCGTCACTG	TTCCCAGTCCCACGTTAGTC	279
CcM2465	FI257679	(TC)8(AC)6	CCAAACCCCACTTTTCTGTT	GTTGTGTGGGCAGTTTTCCT	205
CcM2466	FI257749	(ATT)5	GCTTTCAAATTGGGACGAGA	CCCACCCGTAGAATTTTTCA	230
CcM2467	FI257822	(AT)12	TGAACAACAACTTCAAGGTAATCAA	AAATATTTTGAAGGACCAAAGCA	274
CcM2468	FI257834	(AT)24	GTGTAACGATCTGGCAGGTG	GACATGTTTGCATGTTAACCCT	138
CcM2469	FI257855	(AT)17	CGGCATTTTGGTCAAGATTT	AGAACGCCAACTTCATGCTT	209
CcM2470	FI257870	(AT)6	TCCAGCATAGCAGAATGAAAAA	TGGTGTCAATGAATGGCTGT	192
CcM2471	FI257920	(ATT)6	CGGAGATATTTCATCCGAATAAT	ACCTGCAGTATCCGCAACTT	106
CcM2472	FI257931	(GT)6	GGGAGGTGGACTACAAGGAA	AAGGTCACTTCAAGCTCCCA	256
CcM2473	FI257969	(TA)11	TTCAAACTTCTTTTAATGTGCGA	AAGTGTTAGGAGATCAATTTTTCG	212
CcM2474	FI258061	(ATA)9	ACGCTGCTGCTACACTCTTG	TGCTTGAGTTACACACTTTCCAA	273
CcM2475	FI258066	(TGA)5n(AG)5	ATCAAGCTCTCCATGCTCGT	AGCGGTGAGAACGTTGAACT	195
CcM2476	FI258116	(AT)7	CACATGGAAACACAAAATACACC	CGAAGGAAGATCACTAGCCG	227
CcM2477	FI258145	(AAT)5	AAAGGGAACAAATCGTATTCAC	TGAAAGGTAGCCAAAAAGCA	184
CcM2478	FI258204	(AT)6	CCAACCTCTCAGCACGGTAT	TTTCCCTTTTCACCCAAAAA	264
CcM2479	FI258216	(AT)5n(AAT)5	CCCCAGGACCTAATAATGTTAAA	GCCAAAAAGCACCTTCTTGAT	279
CcM2480	FI258297	(AT)12n(TA)18	GGGTGCTTCAACTCACCTACA	GCACCCTTGTACTATCACCGA	256

CcM2481	FI258302	(TA)8	CACATCAATATACTTAAAGGTTCAACA	TGGTAGCAATGTTGCTTAATTGAC	200
CcM2482	FI258322	(AAT)5n(TAA)5	GCCCATTCTGGGCTACTAAA	CAAGCACGCTTAACTGTGGA	274
CcM2483	FI258410	(AT)11	CCGTCCTATTGTGTTAGTTCTCC	TTACCTTGCAATGCACGAAG	247
CcM2484	FI258446	(TA)6	ACCATTCTTTCCCCCAAAAC	GCTCACAAACATGAGTCTTTCAA	155
CcM2485	FI258491	(AT)18	TGTAGAACATGAGTTATTGAACGGA	ATTGGGTCCCAGTTTGATTG	227
CcM2486	FI258494	(T)10n(TA)28	TGCTAAAATTGGAATGAATGTTG	TTTCTTCTCACTTGATATCCTCCA	242
CcM2487	FI258499	(TC)6	GTCGTTTCTCAGGTCCCAAA	GTCCCAGCCTGAACAACATT	186
CcM2488	FI258515	(AGA)7	GTCAATAACTCGCCCCAAAA	TTCTTCGTTGCCCATCCTAC	251
CcM2489	FI258571	(AT)12	TGGTGCCCTCCAATTTCTTA	GTAAACACCAATTTTTGTTACATCA	248
CcM2490	FI258576	(CGT)5n(TCG)7	AAACTCTCCCTGTGGTCGAA	AGTACAACGCCCTCATGGAC	151
CcM2491	FI258625	(ATT)10	GAAAGGCTCCAGCAAAAGTG	GCATCATTCTTCTGTGGGGT	267
CcM2492	FI258675	(GA)9(CA)7	CTGAAGCAATGGAGGTTGGT	ACACCGTAATCATTCAGCCC	187
CcM2493	FI258693	(TTA)5	CTTGGCTCATGGTTGGCTAT	GAAGGGCGTTACACCAAAAA	164
CcM2494	FI258746	(TTA)5(TTG)5	GGAACCATCGGTTGAACATC	TAAGAATCGAACGCAACCCT	134
CcM2495	FI258762	(TA)18	TTCCGTGTCAATCAAACTCG	CTTCCAAATGTGTGGGTGAG	138
CcM2496	FI258783	(AG)6n(GA)5	GATCTGAGCTTCCACCGAAC	AAGCGCCATGTTTTAGTGCT	214
CcM2497	FI258870	(AT)5(AG)6	CGAGCCTTTCTATTATACCACCC	ACTTTGAAACTAAAAGGATCTCTCC	258
CcM2498	FI258879	(TA)17	GGCACACCTTTTATGCCCTA	GAAGTCCCATTTGGTGAGGA	239
CcM2499	FI258930	(AC)6(AT)6	CTACTCCCATTGCCACCCTA	TGGAGAAGTTGGAGACCATGT	263
CcM2500	FI258971	(CT)8n(CA)6	TGCGTACATGATCTCGTTGT	GATTTTCATGCAAGCAATACCT	132
CcM2501	FI259069	(AAT)5	AACCCCAGGACCTAATAATGTT	GGTAGCCAAAAAGCACCTTC	280
CcM2502	FI259078	(AG)13	TAAATAGGGGCAAGGGGTG	GAGGTTTCTCACTCTCCCCC	185
CcM2503	FI259221	(ATG)5	TCCACCTCCATCACTGGAAT	TGCATGCAAGACACAAATCA	154
CcM2504	FI259231	(AAT)8	TTTTCATCATCACACTCGGAA	TGCCCACTCATTATCAATCAA	241
CcM2505	FI259241	(GAA)8	CCTCGGAAGAGATTGCAGTT	TGATGAATTGGGAAGCAACA	201
CcM2506	FI259245	(TA)22	TTGTTAAGTCAAAAGACGATGTCC	GGAATGAAACATTCAAAGCAAA	273
CcM2507	FI259266	(AT)7	CAACCCCAGAGTTGCCTCTA	AGGGCTCTAGGCACAATCAC	109
CcM2508	FI259302	(AT)18	CAAGTCATCTTATGACCAGAGGG	TCAGGGTCAATACAAGAACAAAAA	264
CcM2509	FI259304	(TTA)8	CATGATGACATAACACGTGGC	GGTCATTAACTCGATAACTTTTGTT	254
CcM2510	FI259343	(ACTATG)7	CCCATGTTTTCTGTTTGGCT	TTTTGCACCCATTTGATCCT	175
CcM2511	FI259450	(AAT)5	AAAGGGAACAAATCGTATTCAC	GAAAGGTAGCCAAAAAGCACC	175
CcM2512	FI259472	(AAT)7	ATCAACCACAAGAGCTGCCT	TTCACATCTTGGTTGATGCC	263
CcM2513	FI259585	(TCT)5	GGAATGTCCTTGCACCAGTT	GGAGGCAAGTTCGTATGGTC	279
CcM2514	FI259602	(TATTT)5	AAACATATCGAAGCAAGGGC	GGAGGATTAGGTTGCAATACG	157
CcM2515	FI259617	(AT)12n(TG)8	CTCGATTCTTGGAGCGAAAC	ACAGCAATGACACCAAATCG	209
CcM2516	FI259637	(CT)6n(AC)7	AAATCCCACCCCATTCTCTC	AGGTCTCAGGGTCGAAGGTT	221

CcM2517	FI259645	(T)10n(T)10	TCTTCCCCCAAAAACAAAAA	TCCTGAATATGGTTAATTTATGGAC	224
CcM2518	FI259762	(ATG)12	CCAACGAGACCCTTGTTTTG	TTCAATTTCTCAACGCAGGA	260
CcM2519	FI259810	(CT)5n(AC)5	CCCGATATAAACGAATCCCC	GAAAACAAACGGGGCAGTTA	252
CcM2520	FI259969	(AAGAAA)5	GCTTTAAGAAGGAGGGCCAC	TCCTCGGAGTGTATGGCTTC	265
CcM2521	FI260009	(T)10n(T)10	ACGGCAACCTAATCCTCCTT	GGTCTGCATTCCATTAACATCA	218
CcM2522	FI260019	(T)10n(AT)5	GCGATTCATTTTTGGCTGAT	TGTTCGTAAGGAAATATGACGG	194
CcM2523	FI260036	(ATT)5	TTCACACAACTTTTGCGGAC	TTGGTGACAATGGTAGTAATGAAAA	271
CcM2524	FI260046	(GT)7	GGGAGGTGGACTACAAGGAA	GCTTGTTTCGTTTTGAAGGC	170
CcM2525	FI260126	(TC)9(TA)8	CAACGGTTGAATCCTTGAAA	CATGGTGCATTCATCTTGGT	145
CcM2526	FI260222	(TA)7	CCCGACTAAGTCCACCAAAA	AACGGCTCAACGGATAAACTT	125
CcM2527	FI260245	(AT)7	AGAAGGGTTCAAATGACACTAAGTA	AACCGATTTAAAAGAAAGGGTAA	265
CcM2528	FI260255	(AT)30	TTATTTCTTGCAGATTTTCTTGC	CAAATCGATGTGAGAATTGAGG	227
CcM2529	FI260289	(TC)7	AGAATCTCGGCCAGCAGTTA	TGGGGATTTTAGGTGCTTTG	163
CcM2530	FI260314	(AT)7	TTGGCTTTGTTGTTGAAAGC	AAAATATATTGTTGGGACTTCTTATCA	244
CcM2531	FI260334	(TTC)6	CGACTCACCCTCTGCTTCTC	TATCGTTGTGCAAAGGACCA	153
CcM2532	FI260364	(TCT)5	GTGGAATTGCTTGGGTTTGT	AACAAACCCTCCACCAAACA	201
CcM2533	FI260367	(TA)8	CACATCAATATACTTAAAGGTTCAACA	TGGTAGCAATGTTGCTTAATGA	199
CcM2534	FI260384	(CT)7	TTCCTCAATGAACCAACCTG	TTCTAATGTGACACAAGCCACC	100
CcM2535	FI260390	(GA)6	CGGCAACCTTTCACACTACA	AGAACGTGCCATTCTGGTTT	266
CcM2536	FI260426	(CGG)5	TACCCTTCGCAACAACAACA	CTGAGATAGTCCAGCGGCAT	227
CcM2537	FI260488	(AT)16	AAGTCTCTTAGATGAATTGCTTCG	GGACTTTGTGTGCTTTGAAGG	236
CcM2538	FI260519	(TA)19(TC)6	TCTCATCGCCTTCTCAGGTT	GCAGCATAGCTGAATGCAAA	137
CcM2539	FI260520	(AT)9	TTCCCTACGACACGTTCTCC	AAGGCGTGATTAAGTGGTGC	277
CcM2540	FI260584	(AT)19(GT)6	TCTATTTTGTTTGTTTTCTTTCCA	GTATGGTGGGGTATGCGAGT	266
CcM2541	FI260588	(AG)10n(AG)5	GCCTATAAATAGGGGCAGGG	TGGATAAGCGGAGCTGAACT	177
CcM2542	FI260641	(TA)8	AACCCGTAAATAATTCTTCTCACA	AAATTCGTTGGAATCTTTGCT	274
CcM2543	FI260662	(AT)20(T)1n	AAGCTCCTCACCAGCATTGT	TAAACAACGAAGAAAGCGCA	279
CcM2544	FI260678	(AC)7n(AC)8(AT)7	TGTTCCCCTAGATAAGCTCCA	TTGATAACTCACTGCACCACTTT	229
CcM2545	FI260689	(TGT)6	TGTTTTCCATCAAAACCAAGG	CCATTGCAATACTTTGAGTCCA	278
CcM2546	FI260706	(TA)8	GGTCGCTTGAGAATTTACTTCC	TGTTTGTTACCATGCCCAAA	163
CcM2547	FI260789	(AG)7n(AG)5(AGAA)6	GGCCTATAAATAGGGGCAGG	CAATTATCCCCACACCCTTG	239
CcM2548	FI260792	(AT)17	AAAGGTAAACATGCATAGTGCAAA	AATATAAATTTGAAGGAGATGTTCATT	243
CcM2549	FI260798	(TC)15(TA)20(GA)16	TGTAGAACACGAGTTATTGAGTGGA	GGAAGACTTACTCTTGGAATAAACAAA	177
CcM2550	FI260812	(TA)15	AAAATGACCTGGAATCATTGG	TTGGTTGATATTGTGATGATGC	267
CcM2551	FI260828	(T)11n(AAG)5n(A)10n(AG)14	AAAGGAAAAATCTCGCAGCA	TTGATCGATGAACACAAGAGAAA	253
CcM2552	FI260853	(AG)6	AGGAGTGGCCAAAGTTTGAA	TCCTATGGTGTTTGAAGGCA	215

CcM2553	FI260872	(A)14n(A)10	CACAAAATGCAAGCAATGGA	AAAAACTGTAGGCATATTAGGGC	180
CcM2554	FI260922	(AC)6	ATGGCCAAGGTACTGGGTTT	TCACCAGCAAAGCAAAAGTG	131
CcM2555	FI260992	(GA)6	CATGTTTTGTGAGGAAGCGT	TTCCCTCCCTTCTCACTTCA	179
CcM2556	FI260997	(A)14n(TA)22	CAAATGGATTTGACCAAAGTAAGA	TGCTGGAAAGAAGTTTTTGGA	210
CcM2557	FI261011	(GTT)7	TTTCTCCAAAGTGTCATGCG	TGACACCACCAACATGGACT	265
CcM2558	FI261023	(TAA)10	GACTCATTCGGGGCTCATAA	AAAAATGTTTGTGCATTTTCAA	255
CcM2559	FI261037	(GTT)5	TTTCCATCTTGTCCTCATGC	CGGAACCACACACAAAACTG	181
CcM2560	FI261052	(AT)12	TTTGCCTTTAGATTGACCCG	AAACCTAAGACACATGGGAAACA	272
CcM2561	FI261107	(AC)6n(AC)8n(AC)6n(CA)5	TGTATCAAAAACTGTAAATTCAACAA	TTGGAAGAAAGAAGGACGCT	274
CcM2562	FI261110	(AAT)7	AACATCAAGAAGGGTCCACA	ATAGGATGTGACATTGGGGC	259
CcM2563	FI261135	(TA)6(ATAA)5	GTGAGAGCCTTGTGCACTGA	GGCTTGCACTGAAGCAGTTT	267
CcM2564	FI261182	(TCC)5	TCGTCGTCGAAGTCTTGTTG	GGGAGGAAGCGAAAGCTAGT	242
CcM2565	FI261220	(TTA)10	CTTTCTTTTTCTTTAGAGACCTTGAT	CCATGTGAGCTCCAAATTCA	265
CcM2566	FI261257	(TC)6	CGACTCGGACACAATTCTCA	GTGGCAACCTTTCGCACTAC	131
CcM2567	FI261265	(TTA)8	CTTTCTTTTTCTTTAGAGACCTTGAT	TGGATCGACCTGCTCTGATA	230
CcM2568	FI261290	(TA)23(TAGA)6	GGATAAAGGGCTTTCTCGCT	GGGCTGTGTCTCTTGCAGTT	235
CcM2569	FI261463	(TA)21	TAAAAGTGTAACGACCCGCC	GGGCTGACGTTGTATTTAGTTG	242
CcM2570	FI261464	(TC)6	ATCAAAGAAACCACAACGGC	CCGATTGTTGTTCACGAATG	242
CcM2571	FI261486	(AT)8(AC)6	TTGCTTGAGAGCTACACCCA	CATGTTAGGCCACCTTTGGT	176
CcM2572	FI261501	(TG)6	TCCATGTTGCATGTTGGTCT	GGTCCCGAGAGTTGACAAAG	213
CcM2573	FI261505	(TC)7	TTGGGAAATAAGATCATTAGGGA	AGAAGAGGGACATTGTGAGTGA	180
CcM2574	FI261506	(AT)7	AACCCAACCCCATTGAGACT	GCCCTTCTCATTTCTTTTTCTTC	260
CcM2575	FI261567	(GATGTG)6	TGAATCACCATTTTGTGTGGA	TTATCCCTAACCTAGGGCCG	240
CcM2576	FI261578	(TG)6	ACCAAGCCTTTTCAAGTGGA	CCACTTGGACTTCCACCCTA	213
CcM2577	FI261622	(GT)7	AAGGTGTGTCTGTGTGTATGTTCA	AAAAAGATTCAAATTATCTTTGCTG	227
CcM2578	FI261626	(ATA)6	TTGTGTTACAGTTTCACTAAAAGACC	TGCAACACATCAGCATAAACC	276
CcM2579	FI261651	(TA)10	CTTAACATGGCCCGTGAAGT	CCGGTATTATTTGAACCCTGC	139
CcM2580	FI261718	(T)12(ATA)5	CTCCGTTGTGGTCCATCTTT	AAAAATGGCGGATACCAATA	269
CcM2581	FI261726	(AT)6	AAATGCCTAAAAATCCAATCGT	TGATTATCAATCCCATTTTCTTTT	159
CcM2582	FI261785	(GA)6	GGTGACTCAACTATTTCTCCGC	TTATATTTTCCGCGAGGGAG	127
CcM2583	FI261821	(AGAA)5cn(AGAA)5	TCCCTCGGCAAGTTAAGAAA	TTTGACGTGGTGAGAGTGTG	200
CcM2584	FI261836	(TCTT)5	GCAATCACCATCCCCAAATA	CTGGTGACCAATGCTGCTAA	232
CcM2585	FI261862	(TA)10	CCATTACATTCGGGCTTGAT	AGCCTTTCGAGAAGCTGTGA	121
CcM2586	FI261872	(AT)10	GCTCAGGACTCCATTTCACC	TTGGATTGTTGCAATGACTGA	205
CcM2587	FI261874	(TA)7n(ATT)5	CGTACACCAAATAAAGTAAACCCC	CCTGCAATAATTCATTAGATGTGC	251
CcM2588	FI261881	(ATAA)6an(A)10	ATTCCAAGGACCTCAAGCAA	TTTGAAGGGGAAATGGAAAA	278

CcM2589	FI261902	(TA)10n(AT)9	CGATAAAACATTTAGCGGCAA	AAGGGGGTCGACTATTGATT	279
CcM2590	FI261910	(GA)6	AGAGCGAGCAATCACAGACA	AGCAAGAATCCTCTACCGCA	280
CcM2591	FI261925	(TA)19	GCAACTACGCGTGTTTTTGTA	CACAATCTAATCCCCCACCA	273
CcM2592	FI262019	(GA)16	GCCTAATGCCTTCTCACTCC	GCACCGTTCTACCACCTCTC	162
CcM2593	FI262022	(TA)6	CTTGATCCATCTTCGCATGA	GGGAGTACATTAGCATTCCCC	136
CcM2594	FI262032	(TGT)5	GTGATAAAGCCCGCAACATT	AAAATGCAACAACGGTCACA	148
CcM2595	FI262092	(AT)14	CGCTCTGAAACCATGTCAAA	AAAAACTATATTGGTGTGAGTTGAAA	225
CcM2596	FI262172	(AAT)5	TCATTAAACCCCAGGACCTAA	GGTAGCCAAAAAGCACCTTC	279
CcM2597	FI262182	(AT)19n(AT)5	TGAAAGAGATTAGTTCTCATATGTGGT	GTAGAAAGCACAAAAGGTAAATACG	221
CcM2598	FI262190	(TA)5(AT)5	TCTCCTCCCAATTTAAGGGG	TCAACAATAAAATTGTGTGCG	253
CcM2599	FI262198	(A)11n(TA)8	GGGTTTGCTTCTTTGTCTCCT	TTGTTCACACACACACAAACCT	258
CcM2600	FI262334	(AAT)7	GAGCACTTGTTCAATACAAGACTCTAA	TGCATAAAACACGTTGCATAAA	211
CcM2601	FI262339	(AT)18(T)1n	CCGGTTATCCTTATTCGGGT	CATAAGACCCCCAATCCTCA	271
CcM2602	FI262360	(AT)7	ATAAAATCCCCACCCACGTT	GCACAAAACCAAAGGCTCTC	258
CcM2603	FI262410	(T)10n(AT)5	GCGTAACCATCTTCCTAACAGAA	AATGTTCCAAAAGTCATACAGATTC	280
CcM2604	FI262497	(CT)6	GTGGTTAGGAAACCTGCCAA	TGAGGGAGGAATCAGGAAGA	238
CcM2605	FI262506	(TC)8	TCTCCTCCAGACTCCTTAGAGC	CTTTGTGGCAACCTCTCACA	113
CcM2606	FI262526	(TAT)5	CTTTCTTTTTCTTTAGAGACCTTGAT	TGGATCGACCTGCTCTGATA	227
CcM2607	FI262538	(ATA)6	CCGTTGATCAATCATCTTGG	ACTGCCCGCCTCTACTCTTT	134
CcM2608	FI262548	(T)12n(A)11	TTTTGTAATGGTTGAGTTAGAAGAAA	AGCACTTTCCAACAGCAGGT	111
CcM2609	FI262590	(AT)24	TGAGTAGGCAGATTCCATTTGA	CAAGTGAGGGTCGAATTTCC	190
CcM2610	FI262592	(GT)8	GGGAGGTGGACTACAAGGAA	AAGGTCACTTCAAGCTCCCA	271
CcM2611	FI262611	(TA)9	TCCGTACTAGGTTCTTGTTCTTGA	GGCTTGTGGCTTTATTGCAT	228
CcM2612	FI262653	(ATT)5	TTTTATGAGAAAGGAATGAAGGATG	TGAATGTGTGAAATGACTCTCG	114
CcM2613	FI262667	(CT)6	GGGTTTAGGATGCAGAAGCA	GGTTGAAAAGGAAGAAGACGG	164
CcM2614	FI262698	(TTA)7	TTTGATAATCGTGAGCGGTG	TCCAAAACTCACCAAGTAAAAGC	217
CcM2615	FI262745	(AT)8	AGAGGCCATTGTTTGGTTTG	GCATGAGGGTGTGTTGAATG	180
CcM2616	FI262877	(TCT)6	TGAGAAGTGGCTAAAGCCTGA	GGGGGTGAAGAGGTTATGGT	149
CcM2617	FI262938	(TA)7	CAAATTTCATCGTAATTTTTGAACA	TGGATTAAATCGAGAATATTGAACA	150
CcM2618	FI263062	(TTA)5	TGGCGCACAGTTATTAAACTT	GCTCTTAAATGACAAATTGTGAGG	208
CcM2619	FI263093	(TC)12(TA)17	CGAGTTATTAAGTGGAGTAAATCTTGG	TGGAGGAACCTCAAATCCAG	262
CcM2620	FI263127	(GA)16	CAATTCAATTCACTTGACAACAAA	ACTAGACTCCGCCAAAGCAA	102
CcM2621	FI263134	(AC)7	TGCCCGACATATCAATAGCA	CTTTTGGGCTTCAATGTGGT	110
CcM2622	FI263138	(AT)5n(TC)5	AGAGAATGGCAAGCCACAAT	CCGGTCAAAGCGAACAATTA	259
CcM2623	FI263207	(GA)11	TGTGGGTTTGAGCCAATTTT	AACGGGTCGTTCCAAATTC	280
CcM2624	FI263230	(A)10(TA)8	TCCGGTTCTTGCTTCTTTGA	CAAAAACAAAATTTGGAAGCAA	248

CcM2625	FI263231	(TA)10	TTTTCTCCATTTCCCTTTCG	ATTCCACGGTTGAAGTTTGC	255
CcM2626	FI263241	(TA)22	GGATTCTGAAATATTTTGTTACGG	ACTGCCAATATAAATTACCATGTCT	198
CcM2627	FI263249	(GTT)5	ATTATCCGGGACATCGTCTG	AGGCGATCACTGCTTCCTTA	143
CcM2628	FI263269	(AT)6	AACACTTTTGGAGCTCGTGG	TCCCAAACCCAAAATCAAAG	253
CcM2629	FI263333	(TA)6	CATACGGCGTGTTCACAAAG	TGCATTGCATTGAAATCTAAGAA	165
CcM2630	FI263371	(A)10n(AG)11	TGACTGGTTTCGCACAAAAG	CGTAGGATTGGCCTCATGTT	211
CcM2631	FI263405	(AT)28	TCAGTAAATAGATTCCTCCCCA	ATGTTTTGGAGGGTGATTCG	184
CcM2632	FI263412	(AT)8	CCGCCATGATCCTTACATTT	TTGGAGCTGGTTGTTGTGAC	280
CcM2633	FI263442	(TC)6	CGATAGGGCCCCTTCATATT	TGTCCAACTCAACCCATTCA	276
CcM2634	FI263472	(TC)7	CCAAGACTCCTTAGAGCTTGAAA	TGGAGAAGATGCTTTATGGAAA	111
CcM2635	FI263498	(TACA)5	CATACAAAATGGAACCCAAGG	TAACCCTAAATTCGGCATCG	270
CcM2636	FI263563	(TA)5(TG)9n(AG)5n(GA)9	CCGTGGGCCCTTATACTCTT	TGGTTGAGTTATTGAAATCCGA	271
CcM2637	FI263609	(TA)12	CGATGAGATCGTTGACATTTG	TTTTACGATGTATTGCTCTTAAATAAA	230
CcM2638	FI263654	(TGT)8	AATCCAAATTGGGCAAGACA	TTCACCTACGAACCCACCTC	157
CcM2639	FI263655	(A)10n(T)10	GCCTGTTTGTTATCGGAGTTT	TCAAATCAAATAGATTAATGGGGA	131
CcM2640	FI263703	(AT)12	TGGGGTACTAAATTCCTTGAGGT	AACCAATGCCAAAACACCAT	195
CcM2641	FI263705	(AT)16	TTTTTGAAGATTAATTCTCTTGTGTGA	GGATTCGTCACTGGTTCCAT	243
CcM2642	FI263732	(AT)6	CCATGTTCCACCATACCTCA	GAACCTTAAATTCAACGATTGG	280
CcM2643	FI263762	(AT)8	CCTACCTTGGTCAGCCATTC	GAACTCGAGGTTTCAGTGGC	276
CcM2644	FI263791	(TG)6	GGTCGCAAGAAGAAGAGTGC	TGGAAAGCACCTTAAAGGGA	117
CcM2645	FI263798	(AAC)5	ATCCATGGCCAAAGAGAAAT	ACATCTACACCGGCTGAACC	184
CcM2646	FI263804	(GT)6	TCAAGGGAGGTGGACTACAAA	CCCTAGGGAATCCGACTAGC	254
CcM2647	FI263807	(TG)6	GGTGGAGACGGGGATAATTT	GAGGTATATTATTAATGGAGATAGGCG	165
CcM2648	FI263834	(AT)5n(C)10	TTTTTCTGTTGACTTCAACCTGT	TCAAAGCAAATATGTTCACAAAG	280
CcM2649	FI263840	(TC)8	TCCAAAATTTCGTCCAAAGC	ATAGGTGCTTTGTGGCAACC	131
CcM2650	FI263917	(AT)8n(AT)6	ACAACCATTCATTTTAGTACCAAGT	ATCGCAATTCAGCATTTTCC	175
CcM2651	FI263950	(TAT)9	GGATCAAGAGTTATTATTTTCGTGC	TGTTACAGCACAATCAAAACATGA	280
CcM2652	FI263958	(GA)6	TTTACTGGTTCTGTTTAGGTTTAGAA	TACCCGAGATCATGAGGACC	161
CcM2653	FI263980	(AT)21	TCAAAGGAGATGGACCAACA	AAGGGCATGTTTGAATGGAA	249
CcM2654	FI264014	(TC)6	TACCCGAGATCATGAGGACC	TGTCCAACTCAACCCATTCA	229
CcM2655	FI264016	(TA)31	CGGATAACCAATTAACAGCGA	GGTGGCTTGTTTTGATGCTT	252
CcM2656	FI264332	(AT)9	AAAGGGTCAAACATGGGACA	AACCCAATGGACATGGCTAC	225
CcM2657	FI264353	(AG)22n(GA)5	CGAAATCAGTACGGGTCGTT	TCCTCCTCTGGATTCCCTCT	203
CcM2658	FI264380	(TA)43	TTTCAAAAGGGGGATAACCA	CGTTTTTGCAATTGGACCAT	274
CcM2659	FI264410	(TA)22n(A)10	TCGTCAAAACAACCTTTGGA	TTTTCATCCACAAAAACAACAA	280
CcM2660	FI264458	(AAT)6	CCTTGCTCGGTGATTCATTT	CGGAGATATTTCATCCGAATAAT	255

CcM2661	FI264500	(ATT)5	CCGTTGGCCTAACTCACATT	TCGGTGTTATTCTCGATCAAA	242
CcM2662	FI264535	(TG)6	TGAAACTTCCGTATAGCGCC	GAAACATCTCACTCGGTTCCA	184
CcM2663	FI264545	(AT)7(GT)10n(GA)7	TCGCAGTCCAAACCACATAA	GTGTCGTTTGAACCCTCCTC	134
CcM2664	FI264568	(AGA)5	GGAGGCAGTGAGTGAGGGTA	CACGGATTGGATTTGGAACT	141
CcM2665	FI264613	(AT)20	TTCCAACCATAGCCAAGGTAA	ACGCATCGGTTGATGTTGT	177
CcM2666	FI264652	(AC)6	GCTCTCCCTCCACCTAATCC	TGTGTAAATTGTTCATGATGTTGC	263
CcM2667	FI264679	(AAAT)5	AAGCATGACGAGGAATGACC	GCGAAGGTCATGAGTTTTGAG	129
CcM2668	FI264688	(AT)12	TGCCACTCTCTCTGGGTTCT	CTCCTAGAGTGAACAAATCTCTCC	238
CcM2669	FI264867	(TA)26	TTGTAATCCGTGTCCATTGC	GGAGAGCCAAACACACACAA	117
CcM2670	FI264871	(TA)23	GCCAACTGCAAGCAATCATA	AACTCCAAATTTTCTCTCACTTGAT	280
CcM2671	FI264935	(TA)11n(A)11	TGACATTTTCAACGGCAGAA	GCGTCACAAAGCAAGTTTCA	271
CcM2672	FI265092	(TG)10	AGAGTAAACGGATCTCTCCTCA	TTTTCATGGGAGTAGGGCAG	229
CcM2673	FI265097	(TA)32	TTTTTGGTGAAATCATTTTGG	TGCACCTCCTGCTTTTACCT	271
CcM2674	FI265109	(TAT)7	CATTTTGCACACGTGCTTAT	TGGGAAGATAGGTAGAGACACGA	280
CcM2675	FI265110	(AT)29	GTTGTAGCGGTCGCATTTTC	TTTCCAATCTTTTTCCTCTCTCA	261
CcM2676	FI265182	(AG)7	ATTCAGTACAGGCCATTCCG	GTTCTCCTCCCCCTTACCTG	235
CcM2677	FI265237	(T)10n(AT)17n(AT)6	GTTTGGGCCGTTCTATTTCA	TTTGCGAGAAAAATTTGTGA	268
CcM2678	FI265286	(ACC)5	TTACACTGCAGAGTGCGGTC	TTGCGTGAACATGAGAGAGG	201
CcM2679	FI265305	(TC)7	ACCTAGCTAGCCCAGGCTTC	GCAAAAGCTAAACCGTTATTGG	217
CcM2680	FI265423	(TAA)6	AGACCCAACCTAACCCAACC	CGTTACCAAGTAAGAATGACAGTGA	176
CcM2681	FI265479	(TA)21	TTTAAATATTTTGAGGAATTAAGGTGT	TGCATGTTTTGTTTATTGTTCAGA	184
CcM2682	FI265483	(AT)6	TCCGATTCTTGCTTCTTTGA	TTCTTCTCGGCTTTTCTTGC	144
CcM2683	FI265496	(CA)8n(AC)8n(AG)5	GTGGTGAGCTATCGGGACAT	CAAGAATCAAACCATGGACCT	250
CcM2684	FI265498	(AT)6	CTGATCCTTGTTTGGCCATT	GAAACTCTCTCTTCTAAACTTGGAACT	280
CcM2685	FI265594	(AT)5n(TA)7n(TA)8n(AT)5	CGTAGCCGGATCTTCTTCAC	TGGTGTGGATTATGATGGATTG	273
CcM2686	FI265603	(AT)11	AATACTATGGTCGGGCCCTC	TGGTGAGTTCCACTTTTGCTT	147
CcM2687	FI265608	(TG)6	CCGGAGGTAGTTTTGTCCCT	CCTGAAACCTGACTAACAAACACA	246
CcM2688	FI265609	(TA)15	TCATCTAGTGCTGGACACCCT	AGACTTGCGCTCATAGGTGTT	254
CcM2689	FI265616	(AT)6	GCCCATGCATCTCCTTAGAC	TTTCCCTTTTCACCCAAAAA	223
CcM2690	FI265624	(ATT)10	TGACAATGAGTATCATCTTGAGCA	TCATTACCAATTCGACTCAACC	100
CcM2691	FI265637	(TA)7n(TA)12(T)16	CGCATAAAGGGACAATCCAG	GCTCAACCAATGTCGTCACA	202
CcM2692	FI265652	(TAT)5	CAACTTCCATTTCTCATAGTAGGG	ACGGGCAATGACTAACGAGT	270
CcM2693	FI265657	(TCT)5	GAGGAATTGCCTGGGTTTTT	ATGCCAATCCCAATTTCAAC	156
CcM2694	FI265670	(AT)22	CCATTATCCCTTTTAGCCTCC	TTAATGGGTTGACCAGGGAA	267
CcM2695	FI265676	(AT)14n(TA)5	TCTGGAATCCAAAGTAGATCCAT	TGATGATGCTCATTTATCCTGA	276
CcM2696	FI265677	(AT)28	GCCTTGGATGTGCTTCTACC	CAACATCGGTTGTGTAACAATTAAA	273

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CcM2697	FI265781	(CT)9n(T)14	AGAGTTCGGTGACGGTTACG	GATCTGTCGAGGTTGAGGCT	242
CcM2698	FI265827	(ATA)6	CCAAAAATGGTCCAAGCAAT	AACTCATGGGCGTGGTTAAG	165
CcM2699	FI265836	(GT)7(AT)8	AGATTTGAGGATCAAGCCCA	AAAAATTTGCAAACCTGACCT	241
CcM2700	FI265837	(T)16n(AT)5	AAACCTCACAGACGTGATCAAA	AATCCAAATTTCCTCCCACC	170
CcM2701	FI265850	(TTA)8	TTTCTTTTTCTTTAGAGACCTTGATAA	TTGTGACACCCTTCTACCCC	202
CcM2702	FI265871	(ATT)5	TTGTGAAGGAACCTAGGGGA	AGTCCCATCTTGTCGTTTGC	279
CcM2703	FI265894	(TTA)6	AAGCACATACCGATGTTAAAGAAA	CTCGGATTGGATCAGACGTT	203
CcM2704	FI265930	(AT)10	AAAAATGTTCAATGTCGTAGTATTTGA	TGCCATATATCATGCCCTCA	127
CcM2705	FI265945	(TTA)7	CCTTTCTTTTTCTTTAGAGACCTTGA	TTGTGACACCCTTCTACCCC	201
CcM2706	FI265945	(TTA)6(TA)1n	TCACATGATTATTGGAATTGTCG	TTTGTGACACCCTCTACCCC	141
CcM2707	FI265950	(TA)23(TAGA)6	GGATAAAGGGCTTTCTCGCT	GGGCTGTGTCTCTTGCAGTT	235
CcM2708	FI265969	(GT)8	ACTATCAAGGGAGGTGGGCT	CCCACCCTAGGGAATCTGAC	270
CcM2709	FI265995	(CAT)5	GGCGTGTGAGTATCGTATCGT	GCGAATTCGTAACTCGAAGC	235
CcM2710	FI266073	(ATA)13	TGAATTAACCTGGACCAGCC	ATTTTCGGAGCTGTAAGCCA	148
CcM2711	FI266125	(TTAT)5	CAACAATTTCACCCATAACAAAAA	TCTAGTGGTCCTCCATCGAA	200
CcM2712	FI266167	(AG)10	CACTTGAGCTGGAGGGATGT	AAGGATCCATGATTGCAAGG	105
CcM2713	FI266171	(T)12n(AT)5	TCGTTTAAATTACTACCACGTTTTCA	TTCATTTTCCATTACATTAATTCTTTG	275
CcM2714	FI266179	(GATGTG)7	TGAATCACCATTTTGTGTGGA	ACCCCTGACATGTTAACCCA	185
CcM2715	FI266188	(GCA)6	TCTTCGCCTTGGTAACCCTA	TGCTACACACGATTTCGCAT	272
CcM2716	FI266218	(TTA)6	TGTGTAATTAATGTAACACTCCGTTTT	CAACTTCCAAATTATCCCTTAAAGC	214
CcM2717	FI266246	(ATAA)5	AGCATCCCCAAACAGTGAAC	TTTTTCCGGTTAGAATTGAAGTTT	273
CcM2718	FI266253	(C)12n(AC)7	TTTGGTAGGAGAAGTCAGTTCCTT	ATCTCATTTTTGGGTGTGGC	148
CcM2719	FI266278	(TA)14	TTGACAGAATTAATGAGAACCAACA	GTTTGACCAACAACTTAGAATTTTATT	215
CcM2720	FI266308	(AT)16n(AT)8	TTGGTTCCTGAAAGTCGTGG	CAAGTCCGAGTGCATATTGAAA	263
CcM2721	FI266356	(TA)18	TTTTTGGTGCCTATCGAACC	TCGTGGTTCTCTTTTCCTTCA	203
CcM2722	FI266384	(GA)9	TGGAAGCTGTAAGTCCCAAGA	ATAGATCTCATCGGCGCAAC	141
CcM2723	FI266399	(AT)10	CGACAGAAAAATCCATCGGT	GAGTTGAGGAAAGAAATCAGAAACA	280
CcM2724	FI266405	(CT)5n(AT)5	CGCTTAAATCCTTCCCCATT	CATCACATTCGTCACTTGGG	232
CcM2725	FI266414	(TA)25	TGAAACACAAAAGGAAAGCAA	GAGAAAATGAGTTATTGAACGGA	141
CcM2726	FI266427	(TAA)5	ATCGAAGAAAAATATTAGCCACA	CACGATCATACTTATTATGGAATGG	204
CcM2727	FI266432	(AC)5n(A)13	AATGTGTAGCTCATGCCAAAT	AACAGAAGGCCTCCAACTGA	249
CcM2728	FI266483	(TA)6	GTGAAAACTTGCGGTCAGGT	ATTTGCGTATCGTGCTCCTC	192
CcM2729	FI266508	(TA)6	TAAATTTCGACCCGGCTACA	GCAAACTTGCTTTCACTTTCC	236
CcM2730	FI266542	(AT)16	TTTTCCACAAAATCATCGACA	TTTTGGTTAATTGGTTTTTCTTATCA	255
CcM2731	FI266548	(TTA)5	GCCTCGCTATACAAATTGCC	TTTTGTGTCACCATAGCTTATACC	245
CcM2732	FI266563	(AT)6(A)10	TTTGGTCATATAGTGGTTGGAGAA	CGAGAGCAAATGGGTCAAAT	173

CcM2733	FI266596	(TC)6	CCCAAAATTTCGTCCAAGAC	CGCTTTTTGGCTACCTTTCA	113
CcM2734	FI266617	(AATA)6	GGCTCCGTAAACTCGTATCG	CAGAGCCTTGTGCTTCAGTG	265
CcM2735	FI266684	(TC)10	GCCACGGACGGAAATTACTA	GTCCCCGTAAGTCAACCAGA	212
CcM2736	FI266707	(ATT)9	AGCGGTAACCATAACACCCA	TCCTCCCTCTAACCCATCCT	278
CcM2737	FI266828	(AAAT)5n(T)11	TCAAAGATATTATTTCCGGCG	TTGTTTGAGATCACCAAATCTGA	276
CcM2738	FI266879	(AT)10	TTCCTTGAAGGTAATATTTCTGAAAAC	AACCAATGCCAAAACACCAT	184
CcM2739	FI266883	(AT)13	CAGCTTGAGGGGGAGTGTTA	GGCAAAACTCAGCACACTCA	195
CcM2740	FI266889	(AT)11	TTCCAATCTTTCTTATTTTGGTTTTT	TTCAGAGGAGTTGTTCATTTATTTG	280
CcM2741	FI266916	(AT)8	GAAAACACAATAGGTAAACATACATGC	TTTGAGGAGATATTCATTTATTTGATG	223
CcM2742	FI266934	(AC)6	TTCAGACGCAATGACCTTGT	CATGAAACACATAGAAGGGGG	153
CcM2743	FI266949	(AC)7	TTGTAGGCTTGATCTCTGCATT	TGGTGTCATTTGATCCCTCTT	173
CcM2744	FI266998	(GATGTG)7	TGAATCACCATTTTGTGTGGA	TTATCCCTAACCTAGGGCCG	234
CcM2745	FI267039	(ATC)5	TGTGAAACCAAGAAGAAAAACG	TTCACTGGAATTCAAAAGCAAA	108
CcM2746	FI267087	(CT)7	GGCCTCAAAATTTCGTCAAA	TTTTTAGGTGCTTTGTGGCA	128
CcM2747	FI267126	(TC)6	TAGAATGGGTTGTTCCAGCC	CAGCAACCTTTCGCACTACA	183
CcM2748	FI267137	(AAT)8	CAGGGCGGAGACAGATTTAC	TGAAACCGCAAAATAATTGGT	216
CcM2749	FI267210	(ATT)8n(TTA)5	GTTTCCGGGAGCATATTGAA	TTGTATAACGAAGTTAAAAATTGGAAA	175
CcM2750	FI267252	(AG)8	TGGGAAAACGGATAAGCAAG	GTGGGGTTTGCAACAAGAGT	256
CcM2751	FI267305	(TA)13	CTGGACTTGATCGACCACAA	TAAAAGCCATCGAAAGTGGC	205
CcM2752	FI267336	(CT)7	TGGTTGAATCCTTGAATTTTGA	TTGGAATTCATCTTCCTCCAA	143
CcM2753	FI267354	(AC)6n(C)12	AGTGCATTGGACGAAGAACA	ACGTAGTCCCATGGTGGGT	277
CcM2754	FI267356	(AC)6n(C)12	CATTGTCCTTCAGCAGACGA	TGTGCACCAAGAATTGAAGTT	209
CcM2755	FI267395	(TA)8	TTTTTGGAGTAAGTGTATCCCTTC	ATCTGCAGAACCAACTGCAA	120
CcM2756	FI267496	(TA)25	CATTGAAATTTGATGTAGAACACAAG	TTTCCTCTTCCAATCACGCT	227
CcM2757	FI267534	(TG)6	TCCTAAATCCTAAACACCTACATGC	CCCTTCAAAGCTTTTGCACT	117
CcM2758	FI267553	(ATT)10	AGGGGAATGATGCATGGTAA	ATGTGTGCGTGCATTTGTTT	209
CcM2759	FI267564	(AG)6	TTTCTAGAAGCTTCGCGCTC	GCTTCGTTCACTCCAAGCTC	184
CcM2760	FI267580	(TA)6	CGGACGAAATTGGGTGTCTA	TTTCCCACGGATTATCTGTCT	247
CcM2761	FI267584	(TC)6	TTTTGTCCAAGACTCCTTAGAGC	TGGCAACCTTTCACACTACAA	101
CcM2762	FI267598	(ATA)6	GGTCGCATAATATTTCTTTTATGAGTT	TCAGTGAAAATAAAACACTTCATCCT	214
CcM2763	FI267598	(AG)9n(TCT)8	AGCACATCAAACAACAGGTAGA	CGCAGCCATTGAAGGAAGTA	268
CcM2764	FI267629	(TC)17	AGTTCTCCAGGCTCCCAAAT	TTTTAGGTGCTTTGTGGCAA	150
CcM2765	FI267670	(GAG)5	ATTGCCTCGATGAAGGTGAC	ATCGAGCAATCCAACAAACC	239
CcM2766	FI267680	(CT)6	CCAAACACGGTTTTAGATGC	TGAAATGCTCATACGGTATCCA	208
CcM2767	FI267691	(AAGAAA)5	GAGGGCTACTCTTCCCAACC	AAGCATGGTTTTCTTGGTGG	174
CcM2768	FI267695	(ATG)6	GATCCAATCGGTCGTGAGTT	ACGAGCGATACCACTCAACC	260

CcM2769	FI267743	(AC)6	TTTGTGCAAAAGTGTGAGCA	AAAATGCATTGAAGTCTCGGA	116
CcM2770	FI267789	(AAT)7	TTGTGACACCCTTCTACCCC	TCTGGATCCCTTTCATTTTCTT	207
CcM2771	FI267831	(AG)6	AGCAAGGAGGCATCACAAAG	ATCTCCTTTTCCACTCCGGT	235
CcM2772	FI267874	(TC)6	CACAATTATCAGGGCCACAA	CGGTACAGGTAAGAGGGCTG	188
CcM2773	FI267888	(CA)7(TA)5n(TA)5	CATTTGGATTGTTTAAATTTGATG	TGCTGGTCTTTAATGGTGTCTC	214
CcM2774	FI267891	(ATC)12	GCGATACCACCCAACCACTA	TTTGATGATGCTTTGCTTTGA	245
CcM2775	FI267894	(TA)6	TTTGCGAGACGAGGAATTTT	TGACCCGTTATGGTCTTTACA	260
CcM2776	FI267931	(GT)7	AAGGGAGGTGGACTACAAGGA	ATTGCTTTCCTTGCATGCTT	229
CcM2777	FI267955	(ATT)5n(TTA)5	TGATGTTAATGGAATGCTGACC	TGTTGATTGAGCATGTGTGC	157
CcM2778	FI267968	(GAT)5	TGCTGCTGTTTCAGACTTGG	TCAAGAATCGCGTGTGCTAC	250
CcM2779	FI267980	(GGA)7	GAAACCCAAAAGGGTGTGTG	TGCTCTGGTGCTTCAAAATG	217
CcM2780	FI267993	(GT)6	TCATTCTCGCGAATTCCTCT	ACACACGACGCAATGACAAT	276
CcM2781	FI268005	(CTT)5(T)1n	TCGTAGTCAAACCAAATCCCT	AAAGTGATTCATCCATAAAAAGTTTG	221
CcM2782	FI268013	(TC)6	TACCCGAGATCATGAGGACC	TCACTGTCCAACTCAACCCA	236
CcM2783	FI268067	(AT)31n(TA)10	AAAACTTTAAATTGAACGGCTGA	TCCAATTTTCATGTCGCAAG	224
CcM2784	FI268149	(TTA)6	CAACATGCACCTGTTTTTCG	AAAATCAACCTTCCCTTAAGACAT	267
CcM2785	FI268237	(TTA)7	CTTTCTTTTTCTTTAGAGACCTTGAT	CCTGATGTGGACATTTTCCC	280
CcM2786	FI268287	(TAT)6	TGCTATCAACTTAAAACATAAAACTCG	CAACCCTTTATCAAATCCAACC	149
CcM2787	FI268313	(GA)7	AGGTGCCTTTTGCCTACCTT	CATTTTGAAATTGGAACGGG	204
CcM2788	FI268322	(TC)8	ATCAGGGCCACAAAATTTCA	CACTACACAAATGCCTCACGA	102
CcM2789	FI268337	(TA)24	CGTTACAAGTATTCACCTTTTCCA	CCCAGACATATGCTCGTGAA	133
CcM2790	FI268356	(AAT)5	AAGGGAACAAATCGTATTCACTATG	GAGGAAAAATTTCGTCCGGT	280
CcM2791	FI268471	(TC)6	GGCTCAAAAATTTCGTCCAA	TTCTAGGTGCTTTGTGGCAA	108
CcM2792	FI268514	(TA)6	AAAGAAAAAGGAAAATAAAAGTGGTG	CATGGTAGGCTGGGTCAGAT	274
CcM2793	FI268551	(TA)6	TGAAACACCAGAAAGAGGATCA	TGAAAGGTAATAATGAAAAGATGAAG	221
CcM2794	FI268556	(AT)25	TCCGTTCAATAACTCATGTTCTACA	TCCCTCCTCACAAACACACA	242
CcM2795	FI268559	(AT)9	CCATAATTCATCCTTCCTAAACA	TGAGCAGAGGTTCAACTGTCAT	253
CcM2796	FI268569	(CAA)5(TAA)5	AACCACAACAACCACAACAA	TGCTTCAAAAGGTTTTACCAGA	176
CcM2797	FI268576	(AG)10n(AG)5	GCCTATAAATAGGGGCAGGG	CAACAATTATCCCCACACCC	234
CcM2798	FI268592	(TA)10(ATATA)5	CATGCATTAGAAACTTTCAGTCAA	TCAAAAGCCAATATATTATCCAAAAA	278
CcM2799	FI268616	(AT)26	AACACCTCGTGGTGGTCTTC	CGGATCATCCCTACCTCAGA	231
CcM2800	FI268639	(AG)9	GGGTCCTTCTTTTTGCATGA	GCATAAGGCCTTCCTCTGTG	264
CcM2801	FI268656	(AT)18	TGGTCTCATGTCTTTCCATCA	GAAAAGCCAATGTGGTGGTC	247
CcM2802	FI268723	(TAA)12	ACCTCCATTGGCATCAAGAC	GTTCGAGGACCTGAAAGCAG	275
CcM2803	FI268727	(TTA)5	TGGAATGCCTAAAATGCACA	TGCGAAAATGCCATCAATAA	178
CcM2804	FI268744	(ATG)5	CCAAGAAAGCACCCCTTGTA	TGTGAATCCAAGAAGAAAAACG	210

CcM2805	FI268771	(TA)14	ATATGGCACAAGGATGCACA	AGGCGTGATGCAGAGTCTTT	201
CcM2806	FI268830	(AT)6	TTTGAGTGGCTCTGGTGATG	ATGGAGGCAGTTGCTTTGTC	187
CcM2807	FI268929	(GA)6	GCTTTGTGGCAACCTTTCAC	ATCTGGAATGGGTCGTTCTG	187
CcM2808	FI268950	(AG)16	ATAAATAGGAGGCATGGGGG	GAGATGGAACTTGGGCAAAA	159
CcM2809	FI268956	(GT)5n(T)10	TTTGGAAAGTCTTGGGAGGA	CCTTGGCAAGCCACTAGAAG	129
CcM2810	FI269002	(TC)8	CAGTTCTCAGGACCCCAAAA	CTTTGCAGCAACCTTTCACA	125
CcM2811	FI269013	(AG)9	CTGGCTCTGATGCCACATTA	GCTCTTATGCTGAGCTTGCTG	248
CcM2812	FI269017	(GAA)5	AACTCCACAATGACAGAATTGAAA	GGAGAATGGGAGACACCAAA	253
CcM2813	FI269173	(AT)11	CAACAGCAGGTGAATCATGG	TCGGTATTATTATAACCCTCCTCG	195
CcM2814	FI269287	(TA)11	TCGACCCATTGCATTTAAGA	ATAAGCAATTGGAATTGGGG	255
CcM2815	FI269339	(TTC)5	TGACCTCCTTTCTTTCCCAA	TCCTCCAAAAACAAGCTTCC	113
CcM2816	FI269376	(CTT)5	AGAATACGTGGTGGGAGCAG	TCCAAGCTCCTTGAAGTGAAA	245
CcM2817	FI269380	(CT)6	CTGCAACAAGCCAAAAAGGT	GCCTTATTTCACCTCACCTCC	237
CcM2818	FI269418	(TA)16	AGTGATCCGCTTATTTCAACA	CCACTTAGCACCTTCCCAAA	249
CcM2819	FI269488	(A)13(AAC)5n(T)11n(TAC)5	CCATAATCCACACACACTTTTATAGTT	TTTGCAATCTAAATTGAACCAA	280
CcM2820	FI269537	(AT)6	TTCCTCATAATTCTCCTTAAATACCC	GATCCGTGCATAAGGAGAGC	135
CcM2821	FI269538	(GT)7	CACTTAAAAACCAAGCCTCTTCA	CCCTAGGGAATCCGACTAGC	238
CcM2822	FI269562	(AT)24	TGGAAAACTAAATTGATGAAATGG	AAAGAACCGACTCTTAAAAATCAA	179
CcM2823	FI269573	(A)15(TAA)11(A)13	CAAGTCCCCCGTGTAAAGAA	TCTGGGTTTTCCCAAAAATG	254
CcM2824	FI269703	(AGT)6n(TAA)9	AGGAGAAAGCTCTGGCACAA	GTGTGAAACTGCAAGGGGAT	154
CcM2825	FI269719	(GA)6	TTTTATTGGTTCTGTTTAGGTTTAGAA	GTGAGCAAGAATCCTCGACC	256
CcM2826	FI269765	(GT)10	ATTTTCCGTTACACCCACCA	AAGACAAGGCACATGTGATCC	222
CcM2827	FI269794	(CT)6	TCGTCCAACACTCCTTAGAGC	TTCGCACTACAATTGCCTCA	100
CcM2828	FI269808	(ATT)7	TTGTTGTTTGGTGGCTGGTA	GCTCACTAAGTAGAAAATGAAGTGAAA	241
CcM2829	FI269813	(TTA)7	TTTCTTTTTCTTTAGAGACCTTGATAA	TGGTTGATGTGACACCCTTC	205
CcM2830	FI269895	(AT)11	CGGGATGAGGGTGAACAAG	ATCGGTATTATTATAACCCTCCTCGT	100
CcM2831	FI270006	(AT)24	TGGTAACGGGACGACAGTTT	TGAGAGGATACATGATGCCAA	233
CcM2832	FI270227	(CT)9	TGCCTATTGACAATTTTCTCTCA	ATTGGTGGAGTGGAGTCAGC	161
CcM2833	FI270360	(AATTC)5	TCAGAGCACACCTGGACAAC	AACTTTGAGCAGAGCATTCCA	269
CcM2834	FI270411	(TA)19	GAGCCGCCACCAATATTTTA	CAAAAGAAGCATCTCTCACATTC	271
CcM2835	FI270479	(TC)7	TTCCGATTTTGGAACAGGTC	TTTTAGGTGCTTTGTGGCAA	203
CcM2836	FI270593	(TC)6	TCTAATTTTGGAACGGGTCG	GGTGCTTTTTGGCTACCTTTC	190
CcM2837	FI270601	(AT)6	AGCGCTAGCATTCTTTGCTC	GGATACTTGCAACGGGAAAA	279
CcM2838	FI270663	(TA)25	GACCTAGGATCGTGGCGTAA	TGGTTGTTAGAAAAGTTAGTTGAGTTG	223
CcM2839	FI270674	(AAGA)5(AG)10	GCCTATAAATAGGGGCAGGG	CAAGCGAGGTTTCTCACTCC	224
CcM2840	FI270693	(TA)8(GA)6	CGGTTGGATTTACAAAATTTACA	TTGAGCGGAATAACCTTACCA	180

CcM2841	FI270753	(AC)8(AT)7(GT)8	CACCCTTTACTTGCCCCTTT	CAAAATTTGTTTCTTCTAATGCTTTT	215
CcM2842	FI270776	(CT)10(AT)11	CCTCTAAGACATCATGTAGTTCAAACA	AAGCAAGGGTCAAGCTATCA	229
CcM2843	FI270794	(ATG)5	TGGAACCTCATCAAACCCAC	TGGAGTCTTTGTGACATCTTGG	239
CcM2844	FI270831	(AT)12	TAGTTGCAATTGCCTCACCA	AATAGCCGAACCTTGACCCT	247
CcM2845	FI270854	(AAT)5	AAAGGCAACAAATCCTATTCAC	AAAATCTGCGAGACACCTCTG	206
CcM2846	FI270870	(AT)7	ATGCACGCAATCCATAGTGA	CGCTGGATGAATGAAACAAG	185
CcM2847	FI270912	(CT)6	GGACTTTGGTGAGCCAGAAA	AGAGTTGCAGAGGGAGCGT	136
CcM2848	FI270953	(CT)6	TGAGAGACACGATGACCTCCT	ATGCAATTGTGTTGCAGGAA	175
CcM2849	FI270999	(A)11n(AATA)6	GCTAGAATGAAAACCCGCAA	TGGAAGGAGGAATCCATCAG	190
CcM2850	FI271005	(TAAA)5n(AT)5n(TA)5	TGCAAATAGTGGGTGGATGA	GGGGGTGTAGATCTGCAAAA	244
CcM2851	FI271104	(TTA)7	CTTTCTTTTTCTTTAGAGACCTTGAT	CACAGAATTTCCCACGGATT	223
CcM2852	FI271117	(TA)9	TCCCACACACCTTAAACCAA	GGATTCCAGATTTGTGCCAT	230
CcM2853	FI271145	(AT)6n(A)11	CCATAATTTTATTTCAAGGAGCCA	TGACCATAAAAATTGTCACTCAAA	279
CcM2854	FI271175	(TTA)7	TTTCTTTTTCTTTAGAGACCTTGATAA	GCACATGTTTTGTGACACCC	208
CcM2855	FI271212	(ATT)26	ATCCGGCTTCTGATGTATGC	GCTTCAGCTTCAGCATCTCC	270
CcM2856	FI271214	(TTA)5	ATGGGCACTGTTCTTTGGTC	TGTTCCAAAAGGAGGAATCAA	262
CcM2857	FI271272	(TA)11	TCCACGAATTCTCTATGCCC	CCCTTTTCTTGATTGGTTTCA	244
CcM2858	FI271285	(ATA)6	CCATTCATCAAAAGCCCAAT	TGATGGATAAGGGTATATTGATTGTT	240
CcM2859	FI271316	(AT)22	TTACAAGCATAGAGGGGTGG	TTCCAAGACTGAGGTCGGAT	267
CcM2860	FI271423	(TAAAA)5	GGGGGAAAAGAAAACTGCTC	TTCTATTCTTGATTGATTTGCCA	192
CcM2861	FI271457	(AGA)5	ACAATCCTCTCAAGGAGCCA	ACGTTTTGTTCATGCTTCCC	222
CcM2862	FI271460	(TG)5n(TA)16n(TA)21	TGAAGAACTTAAACCCAAAGTGG	GGAATGAAGTATTAAATCATCTCGAA	236
CcM2863	FI271478	(TA)21	AATCGATTTGGGCTTTGTCA	AGCATCATATAAATAGTTTCCTTTCC	257
CcM2864	FI271483	(TTA)8	TTTCTTTTTCTTTAGAGACCTTGATAA	TTGTGACACCCTTCTACCCC	202
CcM2865	FI271517	(AAT)5	CCAACTCAATTCCGACTCGT	TTTATTATATTTTTGGGGATGTAGAGA	136
CcM2866	FI271522	(GCC)6	CTCCATCTACATCCGCCACT	ATGCATTCAGGGTGGAAGAC	267
CcM2867	FI271587	(TA)7	TGGACAACCAATCCATAACG	GGGCCAGAATCGAGAAAGAT	262
CcM2868	FI271622	(AT)8	ACCAAGGGCGAACACATAAA	GACGACGTCGAGGATAGCTC	162
CcM2869	FI271653	(A)11n(A)14	GCAGCTTCCTGCCTCTAAAC	GGTGAAGCACGAGGTTCATATT	271
CcM2870	FI271767	(AT)29	ATGGCTAAAGTTTTACTATCCAGC	CATAGCAGGTGGTTGTGAGG	236
CcM2871	FI271821	(TA)12	AACGGAGTGCCCAAAAATTA	AAAGAAGAGGATATACAATTACCAAAA	194
CcM2872	FI271824	(AG)9	TTTTCTAATCCAGAAAACCAAAAA	TGAATATTGGCTCCCTGCTC	240
CcM2873	FI271857	(C)12n(CT)13(CA)13	TCACTTGGCCATAAAGGCTC	AGACATCAGGTGCATGTTCTG	264
CcM2874	FI271947	(GA)5n(GA)5	GAGAAATAAAGATATGGGAGGGG	TGTTTCTCTCACTCTCACTTCCTC	161
CcM2875	FI271956	(TTTA)5	ATACCGAAGTAAGGGCCCAA	TTACCATGCATCATTCCCCT	264
CcM2876	FI271971	(TA)13	TTCATCCAACGGTTTCAACA	TTCCATTCTCACTTTCTCATTCTG	270

CcM2877	FI271973	(TA)8	TCATTCAAAGTATCATTCATACCCA	CACATTCAACGATAATAAGAAATTTTG	258
CcM2878	FI272044	(CAGCCT)5	TTCGTTGCGATCTGAGACTG	AATGGAAGAACATGAAGCCG	272
CcM2879	FI272051	(AT)9	CCACGTGGGAGCTAGAAGAG	AGCTTCGCGGTACGGATA	279
CcM2880	FI272124	(AGTGAG)5	TGGAAGGCATTGTGTGAATG	ACACAAAGACCCAACCAAGC	120
CcM2881	FI272170	(T)10n(TTA)5	GAAATGATGCATGGTAAAGATGA	TTTCTTCTAATAAGAGTGGATTGAAA	202
CcM2882	FI272183	(GA)6	TCAGAGCGAACAATTACAGACA	GAGAAGGGCAAGCCATGATA	250
CcM2883	FI272196	(TAT)5	AAGGGGAAGGAAGAATGTCG	CCAATTCACCCTCTCTTGGA	108
CcM2884	FI272283	(AT)5n(TA)7n(AT)6	CACAAAATAACGAGGAGTGAGAAA	GGGGCAACGTAATGTTGATT	264
CcM2885	FI272289	(TAT)6	AGTTGATGTGAAGAAATGTTTGAA	ACTGATTCCTGGTTTGCCAC	115
CcM2886	FI272390	(AC)6	TGTGGCTGAACCTTCTGCTT	CATTTCAACAATCAACAAGAGG	184
CcM2887	FI272395	(TA)25	TGAAACACAAAAGGAAAGCAA	GAGAAAATGAGTTATTGAACGGA	141
CcM2888	FI272441	(AAT)13	TGCTCTTACAAAAACAAAAGCAA	TACACGCGATTGATTGGAAA	247
CcM2889	FI272453	(TTA)7	CTTTCTTTTTCTTTAGAGACCTTGAT	TTGTGACACCCTTCTACCCC	200
CcM2890	FI272469	(GCT)9n(TTCTGG)7	GACCACCTTGTACACCGTCC	GCCCAAAGAGGGATACCAAT	263
CcM2891	FI272476	(AT)15	TCCACGTGAAATGAATCGAG	ACAGTACACCACACCCACGA	214
CcM2892	FI272514	(GT)6	AGGGTTTTCAAGGTGCAAGA	AGGCTTTTGCCTACTAGGGG	205
CcM2893	FI272580	(AT)9	GGTTTGACAAATATGAGATAAATGAA	GAACGCCAACCAACATACAA	204
CcM2894	FI272616	(TC)6	TCCTTAGAGCTCGAAATTTCTCT	TTTTAGGTGCTTTGTGGCAA	104
CcM2895	FI272645	(AT)24	AATGATAATTGGACACTTCTTTTTC	TGCGTTAATTAAACAAGCAAGC	268
CcM2896	FI272699	(AT)6	GTATTTTGGAGCTCGTGGGA	CCCAACCAAATTCTAAACTCAAA	262
CcM2897	FI272858	(AG)5n(AG)8n(AG)15n(AG)5	GGTGCGTCAGATTGCCTATAA	TATCCCTACACCCTTGAGCG	276
CcM2898	FI272893	(TA)13	AAAAATGTTGGGTTACGAATACTCT	TTGAAACATTTTGATTTTACATCAGTT	248
CcM2899	FI272927	(AGA)8	TGTAAGCCCCACAATCCACT	TGGGTTCTAGGGGTTAGGTTC	262
CcM2900	FI272937	(TA)5(A)10	CAGGTTGGGTCCATCATTTC	TTTTGGCTGAAACGGACTCT	201
CcM2901	FI272989	(TA)21	CGCACTTGGGGTTACCATAC	TTGAAGGAAGGATTGTTGGG	236
CcM2902	FI273034	(AG)7	GCTTTGTGGCAACCTTTCAC	CGTTCTGGACCCTTTTTCTG	171
CcM2903	FI273099	(TA)19	TCCGTCACTGCCATTAATTT	CCCATAATTAAGGTCTCACATCG	151
CcM2904	FI273211	(TA)12n(AT)11	TCCATTTTGGACGGAAAGAG	GGTTGAACTTTCTTCCTTTAAACC	249
CcM2905	FI273233	(ATA)9	TGAGTGGTTAACAATCAAGAATTTG	TGAATGATGAGAGATTAGAAGGTTAAA	279
CcM2906	FI273286	(TA)5n(AT)21	AAATGTGGATCCCTTTTGTCTC	AATCCATGAGCAATCCAAGA	224
CcM2907	FI273299	(TA)17	TCAAAATCTCAACTTCAACAACTTT	TTGTTTTGGGTGCTTAGGTTG	226
CcM2908	FI273339	(AT)21	GTGTGCGATGCAGTTTATGC	CCGACAGTAATCAAGATTGGC	178
CcM2909	FI273455	(AT)13	TTGCAAAATTGATCTATCCATTAAA	TCGGAGGCTTGATCTAGGAA	166
CcM2910	FI273475	(TA)15(GA)17	CGTAGGAAAAATTATATTACTGATGGA	CACCATGAGTTATTGAGCGAAA	248
CcM2911	FI273494	(AAT)9	ATTGCAATCTTGGGAAATGC	TCATTGTGATAAAAGGGAGCA	188
CcM2912	FI273507	(TA)13	TGTTTTATGTTTTTAGTTCCCATCA	TCTGACACTCTTATTCATGGTGTG	205

CcM2913	FI273540	(TA)8	TGCAAAATACATTCAATCATATCACA	CCCCTGGGTAAGTGATGCTA	236
CcM2914	FI273631	(AG)8	ATAAATAGGAGGCATGGGGG	TCCTCCTTTGGATTCCCTCT	156
CcM2915	FI273715	(T)10n(ATTT)5	AAAATGCAAAGCAGGAATGG	TGACATGCATCCAATAAGCA	216
CcM2916	FI273771	(TC)6	TCAGGGCTCCAAATTTTGTC	AGGTGCTTTGTGGAAACCTT	131
CcM2917	FI273772	(TA)29	GGTTGAATCGTTAAAATTTGATGT	TGAGAATTTTCAAGCTGCGT	158
CcM2918	FI273794	(ATAA)5	GCCATATGGTCCATCACCTT	GCACGCGTTATATCATATCGTT	190
CcM2919	FI273796	(TC)13(TA)39	GGTTGGATCGTTGAAATTCG	ATCTCTTCATCTCGCGCTCT	224
CcM2920	FI273895	(TTA)5	TGCTTTGTCCTGATGACTGC	ATGCGCACAGGTTAATTTCC	226
CcM2921	FI273981	(GAA)6	TTGCGCGTTGTTAATTTGTT	AGAGTTTCTGGCGGAATCAA	190
CcM2922	FI274981	(ATT)7	GGTGTGCATTGAAGGGAAAG	AGCAAAGCAACGCATCTTAG	245
CcM2923	FI275005	(TA)5	TACACCGTCCACCCCTTTTA	TGGTGACAGGTTTCACGAAG	214
CcM2924	FI275007	(TA)11n(AT)9	CAACTTGATAAATTAATAACCGTGTTT	TTTGATGCTTAGGTTGATTCTGA	219
CcM2925	FI275011	(TA)11	CTAAGGACATTATCATGCTTTGAA	AATTTCTTCGGGCACAACAC	213
CcM2926	FI275020	(CAC)7	ACTTCTCCCTCCCCTTCTTG	AGATTGGAGCGGATTCCTTT	251
CcM2927	FI275042	(GATGTG)12	TGAATCACCATTTTGTGTGGA	CCAAGGTCACGTTACCCCTA	263
CcM2928	FI275046	(TA)6	GGTTACATGAGCTAATGATTCCTTT	GAAAGACATGCCTTCAATGCT	118
CcM2929	FI275048	(TTA)6	TGTTTGTTCATCAATTCGGC	CGTTCCCCACTCTTGTTCTT	263
CcM2930	FI275077	(TA)11	CTAAGGACATTATCATGCTTTGAA	AATTTCTTCGGGCACAACAC	213
CcM2931	FI275131	(TC)5	GTTCTTCGTACCTGCTTCCG	TGTGACTTATCATTAGGATTGACAAA	249
CcM2932	FI275131	(TC)6	TCTTCTGGGCAATGACCTGT	GAAAAATACTTCCCGGACCC	252
CcM2933	FI275136	(TA)10	CCTAAGACGTGGGACTCCTCT	TGCCATTAATTTTGTCTCCTGA	211
CcM2934	FI275140	(GATGTG)12	TGAATCACCATTTTGTGTGGA	CCAAGGTCACGTTACCCCTA	263
CcM2935	FI275163	(CT)5	GGTACCCATGGGGAATTTCT	ACTCCACCAACGTCAAAAGG	109
CcM2936	FI275173	(TG)5	CAAGGGGAGGTGGACTACAA	GCTTTCCATTGCATGCTTTA	227
CcM2937	FI275181	(TCT)5	TCTGTGAGCTCTTTTTCTCTCAA	GGGTCCGAGGTAGAAGAAGG	157
CcM2938	FI275194	(T)10n(TA)5	TCTCAGCATTAGGAGCTTTTAACTT	AAAGCATGAAAACTGGGGTG	184
CcM2939	FI275210	(GA)10	TAACGCGTCTCGAAGGAGAT	TTGGATTCTTGGAAGTTGGG	195
CcM2940	FI275223	(CT)5	TTGTGTCCCAACTTGCATTG	CAGCCTACACAGAGGCAACA	200
CcM2941	FI275230	(AT)12n(TA)14	AGCAACACTGAAAGCACCCT	TGAATGCATGATTGACTCACC	273
CcM2942	FI275236	(TG)5	TCCTGATAAGGCTCGAGGAA	GAAGCTTGGTTCCACACCAT	183
CcM2943	FI275249	(TC)5	TCTCTTCTCTCATGCAGCCA	TGAAGACGAACATCAGTCCG	142
CcM2944	FI275260	(TA)6	GGTTACATGAGCTAATGATTCCTTT	GAAAGACATGCCTTCAATGCT	118
CcM2945	FI275299	(GA)5	ATGGAATTGTGTGAAAGGGG	TCTTCCCTTCAAATCTCCCA	179
CcM2946	FI275326	(AG)5	AGGGTTCTGTCCAGTCCATCT	TCAATGGAGGATTACGAGGC	226
CcM2947	FI275350	(TC)6	TCTTCTGGGCAATGACCTGT	GAAAAATACTTCCCGGACCC	252
CcM2948	FI275371	(TAA)8n(ATA)5	CCAGAGACCTCTCAACAGGC	TTGAGAAATTTGCGGCTTCT	220

CcM2949	FI275373	(GA)5	ATGGAATTGTGTGAAAGGGG	TCTTCCCTTCAAATCTCCCA	179
CcM2950	FI275375	(TC)5	GCCACCGTCTTATAGGCAAG	GTGCGAATCATGTTCTCCAA	240
CcM2951	FI275410	(TC)5	GTTCTTCGTACCTGCTTCCG	TGTGACTTATCATTAGGATTGACAAA	249
CcM2952	FI275410	(TC)6	TCTTCTGGGCAATGACCTGT	GAAAAATACTTCCCGGACCC	252
CcM2953	FI275442	(CA)5	TGACCTAAGAATGTACAAAGGGG	AGGGACCACAGACCAAGGAT	197
CcM2954	FI275470	(GA)10	TAACGCGTCTCGAAGGAGAT	TTGGATTCTTGGAAGTTGGG	195
CcM2955	FI275477	(TA)11n(AT)9	CAACTTGATAAATTAATAACCGTGTTT	TTTGATGCTTAGGTTGATTCTGA	219
CcM2956	FI275495	(TA)7	CAACAATTTATACGGTGAGAAAAGAA	CCCCTGGGTAAGTGATGCTA	272
CcM2957	FI275504	(TA)5	TCTTGTGGTCATGTCAGTGCT	GGACAAAAGTTGAATTTAAGAAAAACA	112
CcM2958	FI275505	(CT)5	TCATATGTTTTTGTGCCCCA	ACGTCAGCCAAACATAAGGC	125
CcM2959	FI275512	(AT)12n(TA)14	AGCAACACTGAAAGCACCCT	TGAATGCATGATTGACTCACC	273
CcM2960	FI275537	(AT)26	CCTGGCTGTCACATAGCTCA	GCTGACAGATGCAGTGGATG	240
CcM2961	FI275542	(TA)5	TGAGAAGTAATCTCCTTCAAAAGTT	CCATGCACGGATCTATGTGA	189
CcM2962	FI275563	(TC)5	GCGCAGCATTCTCTTCTCTC	TGAAGACGAACATCAGTCCG	152
CcM2963	FI275594	(CT)5	TTCATAGGTTTTTGTGCCCC	ATCAATGACAAAATCCCCCA	238
CcM2964	FI275603	(AGT)7	AGCTTTGGTACCACTGACAGAA	TTTCCTCCATCATCCAAAGG	243
CcM2965	FI275607	(TA)19(T)11	GGATTGGTCAAGCTGATTGG	TTTTGGAGGTTTTGAATCTTGTT	280
CcM2966	FI275609	(AT)12n(TA)14	AGCAACACTGAAAGCACCCT	TGAATGCATGATTGACTCACC	273
CcM2967	FI275612	(TC)6	TCTTCTGGGCAATGACCTGT	GAAAAATACTTCCCGGACCC	252
CcM2968	FI275624	(TA)19	CTAAGGACATTATCATGCTTTGAA	AATTTCTTCGGGCACAACAC	229
CcM2969	FI275626	(AT)5	TAATGCATGTGGCATGTGTG	CCATCCTTCAAGGTTTGATGA	273
CcM2970	FI275630	(GA)5	ATGGAATTGTGTGAAAGGGG	TCTTCCCTTCAAATCTCCCA	179
CcM2971	FI275632	(GT)5	GCATGGCCGAAAGATAAAAG	GGCAATTATTGAGGCCAAGA	269
CcM2972	FI275633	(AT)6	CGGCACTACCAAATCAAGGT	GAATTCAAGTATGGAACTTGGGA	212
CcM2973	FI275654	(AGCCC)5	TAGTGGAACCTCCCATTTGC	TTCAAATCTGAATCCTCCGC	250
CcM2974	FI275657	(TA)11	CCTAAGACGTGGGACTCCTCT	TGCCATTAATTTTGTCTCCTGA	213
CcM2975	FI275677	(AT)5	GTTTATCCGCTGGGGATTTT	GACACTCAGCCGAACACTGA	197
CcM2976	FI275677	(CT)5	TACCCATGGGGAATTTTTGA	AAAATCCCCAGCGGATAAAC	192
CcM2977	FI275688	(TA)14	TTGATTTGAGTCTGCCCAATC	AAAAGCTCCAACGTGTGTCC	130
CcM2978	FI275694	(TTA)6	TCGTCAATCAACCGAAATCA	TTCATTTCGCTCTTCCGTTC	153
CcM2979	FI275705	(TTAA)5	CTTTGTCTCCTGCTGCCACT	GCCAGCGTCATTACCACTTT	278
CcM2980	FI275706	(TG)5	TCGCCAGGAAACTTGTGAAT	ACAATGCTGCAACCACAGAG	280
CcM2981	FI275716	(CT)5	TTCATAGGTTTTTGTGCCCC	ACGTCAGCCAAACATAAGGC	126
CcM2982	FI275720	(TAA)8n(ATA)5	CCAGAGACCTCTCAACAGGC	TTGAGAAATTTGCGGCTTCT	220
CcM2983	FI275728	(ATC)5	TCTGTGTGACATCTTGGAGAGG	TGAAACGAATTCACCTGGAA	145
CcM2984	FI275728	(TG)5	CATGCAACAACTTGGAGAACA	AGACAAGTTTTGCTCAATGCAC	149

CcM2985	FI275735	(GT)5	CCTCGATAGGGCACATGTTT	GGCACTTATTGAGGCCAAGA	229
CcM2986	FI275737	(TA)5	TCAAGCTTTAAACCAAATCCG	ACGCAAGATTCCTTGGTTTG	128
CcM2987	FI275756	(T)11n(T)10	TGCACAAAACCAAAACACTCA	AGGGTGACCGAGAATCATTG	257
CcM2988	FI275760	(CT)5	CCAAGCTCAAGCTACAAGGG	TCTAGGTGCCAAAATCGTCC	207
CcM2989	FI275782	(TA)5	CACCTCACGGCTTTTTCAAT	AGGCAAACACCTTCTCTGGA	100
CcM2990	FI275789	(AG)5	AGGAAAAGAGGGAGACTGGG	CTCTTCCCTTCCCTACCCCT	216
CcM2991	FI275803	(GT)5	CCTCGATAGGGCACATGTTT	ATGACGGCACTTATTGAGGC	234
CcM2992	FI275816	(TA)9	TTATTAGAGTTGATGTTTATTTCATGC	TTCCTAACACAAGTTGTTCGAAAT	117
CcM2993	FI275817	(TA)5	CCTGCAGACAAGATTGGGAT	TTGCTCTTACAAAAGGATGGC	134
CcM2994	FI275825	(A)10n(TA)8	AAAATCTCACAATCCGGTGC	CAAGAGACCGAAAATTTCAAAGA	210
CcM2995	FI275827	(AT)8	TGTAATTCAGCCCTCTCGCT	CCACTAGCCTACCTCGACCA	269
CcM2996	FI275844	(GT)5	CCTCGATAGGGCACATGTTT	TGGCACTTATTGATGCCAAG	230
CcM2997	FI275853	(AC)5	AAGCAATCATCATCAAACATAAGC	AGCCTCCTAACCATGGACCT	164
CcM2998	FI275872	(GA)6	TGTCCATCCCTCAAAAATCA	TGGCTTGTTTCTCGATTGTG	260
CcM2999	FI275878	(GT)6n(TA)7	GGTAGAGAGGGGGCAACAAT	TCTTGCAATCTCCATCCCTC	208
CcM3000	FI275893	(AT)22	CCATGTTGGGGAGGATGTAA	AAGTGCAATAAGTCTCCCAAGA	203
CcM3001	FI275905	(ATC)5	GCATTTTTGTGGAGTCTTTGTG	AGGAACGAATTCACCTGGAA	161
CcM3002	FI275912	(AC)6(AT)8n(T)10	TGGTTTTGGTGTAGAAGGTGG	GGACAAAAGCACTCGGATTC	239
CcM3003	FI275916	(AT)6	TAGGCCTCAACACCACCTTC	TGCGACACAAAAAGGCACTA	270
CcM3004	FI275937	(TGT)5	TCTTGCTTGCTTTGATTTGC	TTCGCTTTCTGTGTGTGTATGA	240
CcM3005	FI275945	(GT)5	CAGATGTTGCTGTCATTGGC	GCAATGAAATAGGCCAACAAG	263
CcM3006	FI275950	(A)12(AAC)5n(A)10	GTTAGGGACGGTGTCTCACG	TATTCGTGTTTCTCGCAGCA	158
CcM3007	FI275960	(GT)5	CCTCGATAGGGCACATGTTT	GGCACTTATTGAGGCCAAGA	229
CcM3008	FI275968	(AT)21	TTGGAACAATGCCTATGATGA	AACCTTTCTTCCCCTTTGGA	166
CcM3009	FI275977	(AC)5	TCAAAGCAAACCCTTTGACA	GTGGATGATTGGAAGGATGC	230
CcM3010	FI275980	(AT)7	ACCCTCTTTTCAGCCCAGAT	AGACCATGACCCTCCTTGTG	135
CcM3011	FI275984	(CA)6	GCTTCATTTGCCTACTAGGGG	ACCAAGCCTTTTCAAGTGGA	124
CcM3012	FI275995	(AT)5	CATGCACTACGCGATGAAGT	CCATTTTCACAGAAATGGGTC	209
CcM3013	FI276053	(CA)15(TA)5	TTGTTTGTCATGCATCACCTT	ACAATCCTCAAACCATCCCA	241
CcM3014	FI276065	(TG)6	ACCAAGCCTTTTCAAGTGGA	CCCAAATAGCTTCAAGTGCC	231
CcM3015	FI276092	(A)10n(A)10	TGAAGACCAAACGTGAGCAG	AGAAGATGTGGCAGTGCAAG	223
CcM3016	FI276101	(TA)26	GGTCAGTTCCATAATTTGATGC	GACGTTAATTTCAACCCAGCA	280
CcM3017	FI276127	(GA)5	CAACACAAGGAGGTTCGGTT	AGCTTGCTCCACAAGCTACC	228
CcM3018	FI276142	(AT)8	TTGTGTCCGGCACTCAATTA	ACCCATTTGTCATTGCCATT	203
CcM3019	FI276159	(AG)5	AGGAAAAGAGGGAGACTGGG	TCTTTCTCCTTCCTCCCCTC	271
CcM3020	FI276159	(AG)6	GGGAGTGAGAGTGCGAGAGA	TTTTGCGGGTGTCTATAGGG	177

CcM3021	FI276175	(A)10n(A)10	TTCATCCTTTGTCTCCTTCACA	TGACACTGAAGCATTCCTTTACA	244
CcM3022	FI276181	(AT)22	TCTCACGAGTCTTGTCAGCAA	CAACACTCCGGAGGAAAGAG	197
CcM3023	FI276183	(GA)5	GGTTTTAGGTGCTTTGTGGC	GTTCCGATTTCAGAACGAGC	278
CcM3024	FI276201	(T)11n(A)12n(A)12	TGGAGTAAAATTCGCCAAAAA	TTTGAATGATGACCAAAAATAAAAA	130
CcM3025	FI276203	(ATC)5	AGCGTTTTTGTGGAGTCTTTG	AGGAACGAATTCACCTGGAA	163
CcM3026	FI276203	(AAC)6	CAACTTATGATGTCAAGGGCAA	TGCACACAGCATACACAACAA	148
CcM3027	FI276204	(CT)5	CAAGATTCCCAAAACCGATG	CCAATGGTGAAGGAAGCATT	137
CcM3028	FI276205	(TC)5	GCACTTCAAGCTTCTCCACC	CCAATCGAAAAGGAAACCTC	269
CcM3029	FI276207	(CA)5	TGCATGCTTTAGTGCTTTGG	AAGATTTTCAGGGTGCGAGA	275
CcM3030	FI276284	(AG)17	CTGCTTTTTGAGAACGAGCC	CCCTCTGGATTCCCTCTTTC	224
CcM3031	FI276296	(AC)7	GCACGTTGGATTTAGTCCGT	GCACAGGGAATGTTCAAGGT	162
CcM3032	FI276315	(T)11n(A)12n(A)12	TGGAGTAAAATTCGCCAAAAA	CGAGTTATGTATGAAAGAAAGCG	263
CcM3033	FI276322	(AT)6	TGCCTCTCTTTTTGTCACCC	TGCATTGGAAGCTATAGGGG	226
CcM3034	FI276330	(GGC)5	CGGGGAGACTCACCTTGATA	CTTCTCCGCACTCTCCACTC	204
CcM3035	FI276344	(AT)5	CTTTCTTCAGTTGCCCTTGC	TTTCCCTTTTCACCCAAAAA	233
CcM3036	FI276352	(AAC)6	GGCATGCAAGCTTAAAGGAG	TTGCTCATGCACACAGCATA	186
CcM3037	FI276384	(TA)5	TGCCTTCTTGGATCCACTTT	TGTTTTCTTTGGTTCTCAACCC	132
CcM3038	FI276428	(AG)6	TGTCCAACTCAACCCATTCA	TACCCGAGATCATGAGGACC	228
CcM3039	FI276430	(AT)5	TGCTGTCCACTATGTCTTTCTAGG	TCCTGGAGTAAACGAATCCC	278
CcM3040	FI276430	(TA)5	TGCTGTCCACTATGTCTTTCTAGG	TCCTGGAGTAAACGAATCCC	278
CcM3041	FI276433	(AG)5	GAGCAGCAGAAGGCTGCTAT	CCCATTCCATGCAAATTACC	145
CcM3042	FI276441	(TC)5	AAGCTTGCTTTGCAAATTCC	CGGCCCATTCCAGTATAAAA	275
CcM3043	FI276443	(TC)6	ATCCCTTTGTTGGAGCCTTT	TGGCTACCCTTAGCTTCCAA	188
CcM3044	FI276484	(GA)5	ATATCAACATCACCCGGCAT	GGATTCCACGACCTAGCTGA	185
CcM3045	FI276500	(TTA)5	TTTCAGAAATTCGAGGACGA	AATACGTACAAAATAATTGTCCAAAA	186
CcM3046	FI276501	(AT)7	ACCCTCTTTTCAGCCCAGAT	AGACCATGACCCTCCTTGTG	135
CcM3047	FI276521	(CA)5	TAGAGTCGACCTGCAGGCAT	TGAACTATCAAGGGAGGTGGA	231
CcM3048	FI276529	(GA)7	TTGTAGGTGCTTTGTGGCAA	GGCCGTTCAAGGGTTAAAAT	251
CcM3049	FI276530	(GT)6	TAGAGTCGACCTGCAGGCAT	CAAAAATATTGGTGCCCAGC	253
CcM3050	FI276570	(TG)6	TAGAGTCGACCTGCAGGCAT	AGCCCAAAACCCTTATCCTC	100
CcM3051	FI276589	(TC)6	AAGAATCCTCTACCGCAGCA	AGAGCGAGCAATCACAGACA	279
CcM3052	FI276617	(TC)6	GCTTAGCTTCCTCCACAAGC	AGCCTCCTAACCATGGACCT	260
CcM3053	FI276622	(TA)5	GGGTGGAGTGATCGACTGTT	CCAAACATCTCAACACCTCAAA	267
CcM3054	FI276633	(AG)5	ATCAATGACAAAATCCCCCA	CCCATGGAGAATTCTGACTCC	195
CcM3055	FI276638	(AAGAAA)5	TTCGAAAAGACTCCACTCCC	ACGGCCAAGACACTTGAAAC	176
CcM3056	FI276652	(AT)7	ACTTGTAACGACCCGACTGG	CAGCTGGCAGATGACGTTTA	208

CcM3057	FI276656	(AT)25	AAACGTTTTCCAACCAAATTC	AAGCTCTAGGGTTGGGATTGA	211
CcM3058	FI276659	(CT)5	GCTCTCGACAACTGGGTAGC	ACGACAGCCAAACATAAGGC	278
CcM3059	FI276668	(AC)10	CAGCTGCAAAATGGAATGTC	CAAATTGGGGTTTGATCCTG	243
CcM3060	FI276671	(GT)6	TGCAATGTTATGGAGGCAAG	CCCCTCTTTTAAAATTGGTCA	274
CcM3061	FI276682	(TA)11	GCAAGCTTTGAAGGACCAAG	TGTGTCATTTGAAGCATAGAGGA	257
CcM3062	FI276686	(TTC)5n(AG)6	CACACGCGTTCGGAATAGAT	GCAAACGGTTTCAGCTTTCT	268
CcM3063	FI276702	(TG)5	GGTGCTTTGAGAAGCCAACT	GCCATTTGACTACCCTCCAA	223
CcM3064	FI276706	(TA)8	TAGGACATGTGACATCGGGA	TCTGTGACACCCTCTACCCC	260
CcM3065	FI276710	(TC)6	GCTTAGCTTCCTCCACAAGC	AGCCTCCTAACCATGGACCT	260
CcM3066	FI276712	(GT)5	CCTCGATAGGGCACATGTTT	ATGACGGCACTTATTGAGGC	234
CcM3067	FI276724	(A)12n(A)14	AACCCAAGCAAAGGAAGGAT	TTGTCCCAAAGTCCACAAGTC	175
CcM3068	FI276741	(CA)8	GTATTGTCCGCTTTGGCAGT	TTGGAGTAGTTGAGCTGCTTTG	269
CcM3069	FI276753	(ATC)5	CCAAGAGAAAAACGTTTGTGAA	AACCACTTTCTTGACCCCAA	220
CcM3070	FI276760	(AT)18	CCAAATGTCAATTTTATTGTGGAA	TTTTCTCTTGAATATTTTATGTTCGTG	177
CcM3071	FI276765	(TA)5	ACCAATGTACACCTCTCGGC	AAAAGGCAAAAACACTCTCTTGA	111
CcM3072	FI276777	(AG)8n(AG)38n(GA)17n(GA)12	GGTGAAGGAAATCATTGTGGA	AGTCACTCCTCGTCTTCCTCC	270

Table 5 Sequence length distribution before and after assembly of Roche/454 STRs and Sanger ESTs

Range of Nucleotide Length	**Raw 454 Reads**	**Raw Sanger ESTs**	**Assembled 454 reads**	**Assembled Sanger ESTs**	**Assembled 454 + Sanger ESTs**
50	31,876 (6.4%)	44 (0.4%)	0	0	0
51-100	61,172 (12.3%)	180 (1.6%)	2,282 (4.7%)	5 (0.6%)	2,253 (4.6%)
101-150	84,878 (17.1%)	420 (3.8%)	4,854 (10.0%)	4 (0.5%)	4,829 (9.9%)
151-200	88,806 (17.9%)	449 (4.1%)	5,934 (12.2%)	17 (2.2%)	5,874 (12.0%)
201-250	185,863 (37.5%)	658 (6.0%)	12,780 (26.3%)	24 (3.2%)	12,561 (25.7%)
251-300	41,758 (8.4%)	630 (5.8%)	9,224 (19.0%)	20 (2.6%)	9,015 (18.5%)
301-350		401 (3.7%)	4,960(10.2%)	21 (2.8%)	4,821 (9.8%)
351-400		603 (5.5%)	3,415 (7.0%)	42 (5.6%)	3,349 (6.8%)
401-450		666 (6.1%)	1,901 (3.9%)	37 (4.9%)	1,879 (3.8%)
451-500		573 (5.2%)	3,169 (6.5%)	57 (7.6%)	1,124 (2.3%)
501-550		740 (6.8%)		58 (7.7%)	3,021 (6.1%)
551-600		575 (5.3%)		65 (8.7%)	
601-650		621 (5.7%)		51 (6.8%)	
651-700		887 (8.2%)		45 (6.0%)	
701-750		1590 (14.6%)		79 (10.5%)	
751-800		682 (6.3%)		42 (5.6%)	
801-850		1,098 (10.1%)		74 (9.9%)	
851-900				24 (3.2%)	
901-950				18 (2.4%)	
951-1000				12 (1.6%)	
1001-1050				11 (1.4%)	
1051-1100				40 (5.3%)	
Total reads	494,353	10,817	48,519	746	48,726

Table 6 Mapping of pigeonpea 454-Sanger assemblies on soybean genome

Total number of TUSs	127,754
Total number of TUSs with Hits on soybean chromosome	33,874
Total number of genes covered	16,367
chromosome1	1,450
chromosome2	1,773
chromosome3	1,359
chromosome4	1,563
chromosome5	1,643
chromosome6	1,643
chromosome7	1,702
chromosome8	2,160
chromosome9	1,563
chromosome10	1,711
chromosome11	1,535
chromosome12	1,459
chromosome13	4,162
chromosome14	1,241
chromosome15	1,542
chromosome16	1,096
chromosome17	1,654
chromosome18	1,605
chromosome19	1,515
chromosome20	1,499
Average number of TUSs mapped on each of the twenty soybean chromosomes	1,693

Table 7 Illumina sequencing based SNP discovery in five parental combinations

<table>
<tr><th>Genotypes</th><th>ICPL 87119</th><th>ICPL 87091</th><th>ICP 28</th><th>ICPW 94</th></tr>
<tr><td>Number of reads (in Millions)</td><td>18.4</td><td>16.8</td><td>18.01</td><td>18.6</td></tr>
<tr><td>Number of SNPs in parental combination</td><td colspan="2"></td><td colspan="2"></td></tr>
<tr><td>Substitution</td><td colspan="2">5965</td><td colspan="2">1115</td></tr>
<tr><td>Insertion</td><td colspan="2">176</td><td colspan="2">42</td></tr>
<tr><td>Deletion</td><td colspan="2">122</td><td colspan="2">33</td></tr>
<tr><td>Total SNPs</td><td colspan="2">6263</td><td colspan="2">1190</td></tr>
</table>

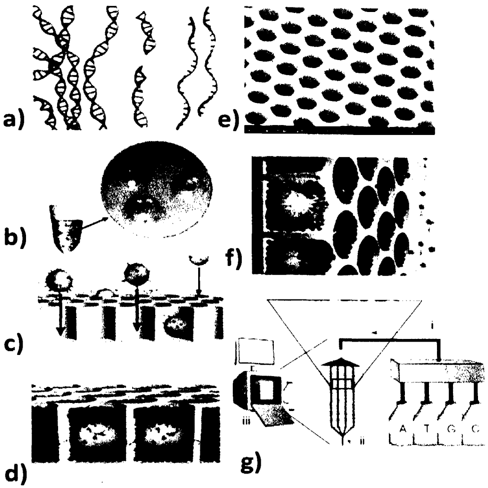
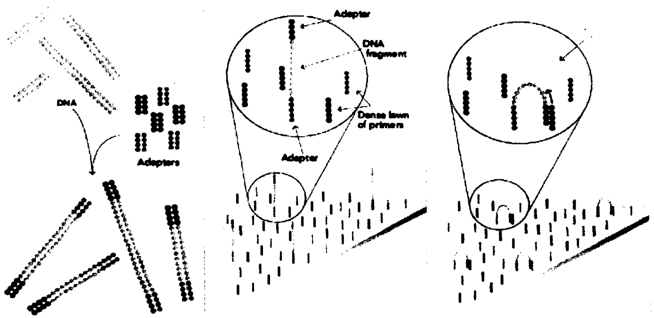


Figure 1 Overview of the 454 sequencing technology.

(**a**) Genomic DNA is isolated, fragmented, ligated to adapters and separated into single strands. (**b**) Fragments are bound to beads under conditions that favor one fragment per bead, the beads are isolated and compartmentalized in the droplets of a PCR-reaction-mixture-in-oil emulsion and PCR amplification occurs within each droplet, resulting in beads each carrying ten million copies of a unique DNA template. (**c**) The emulsion is broken, the DNA strands are denatured, and beads carrying single-stranded DNA templates are enriched (not shown) and deposited into wells of a fiber-optic slide. (**d**) Smaller beads carrying immobilized enzymes required for a solid phase pyrophosphate sequencing reaction are deposited into each well. (**e**) Scanning electron micrograph of a portion of a fiber-optic slide, showing fiber-optic cladding and wells before bead deposition. (**f**) The 454 sequencing instrument consists of the following major subsystems: a fluidic assembly (object i), a flow cell that includes the well-containing fiber-optic slide (object ii), a CCD camera-based imaging assembly with its own fiber-optic bundle used to image the fiberoptic slide (part of object iii), and a computer that provides the necessary user interface and instrument control (part of object iii).

(Source- Rothberg and Leamon, 2008)



1 PREPARE GENOMIC DNA SAMPLE

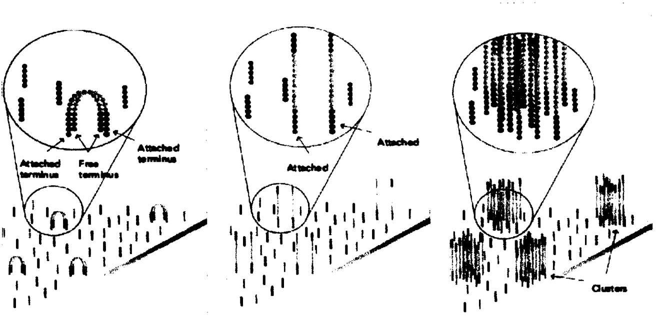
Randomly fragment genomic DNA and ligate adapters to both ends of the fragments.

2 ATTACH DNA TO SURFACE

Bind single-stranded fragments randomly to the inside surface of the flow cell channels.

3 BRIDGE AMPLIFICATION

Add unlabeled nucleotides and enzyme to initiate solid-phase bridge amplification.



4. FRAGMENTS BECOME DOUBLE STRANDED

The enzyme incorporates nucleotides to build double-stranded bridges on the solid-phase substrate.

5. DENATURE THE DOUBLE-STRANDED MOLECULES

Denaturation leaves single-stranded templates anchored to the substrate.

6 COMPLETE AMPLIFICATION

Several million dense clusters of double-stranded DNA are generated in each channel of the flow cell.

Figure 2 Overview of Illumina/Solexa 1G sequencing

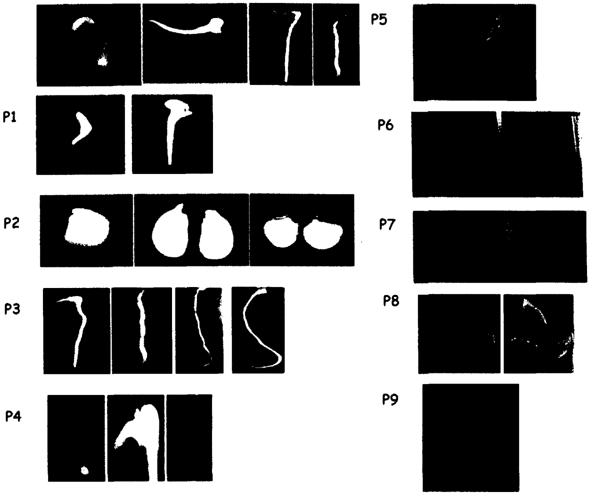


Figure 3 Plant tissue samples for FLX/454 sequencing. P1- 1-3 embryo; P2 - 1-3 days old seedlings; P3- 4 & 5 days old seedlings; P4- 4 & 5 days old seedling ; P5- 10, 14, 17, 22 & 24 days old plant ;P6- Young, Matured leaves; P7- Flower buds, Unbloomed flower & Bloomed flower; P8- Early senescence; P9- 4, 5, 6, 8, 10, 14, 17, 22 & 24 days roots

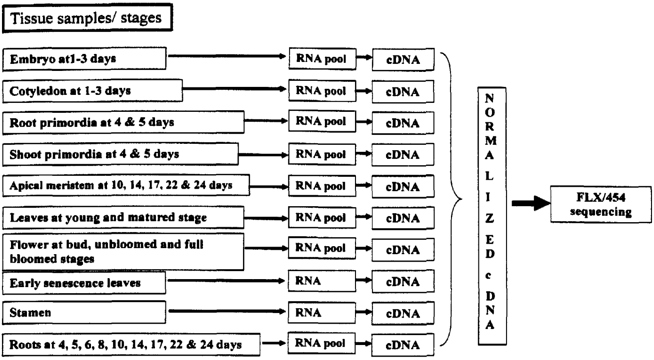


Figure 4 Graphical overview of cDNA normalization for FLX/454 sequencing. Flowchart of the experimental design to obtain a normalized cDNA pool enriched for genes specifically induced at various developmental stages from different tissues of pigeonpea (PusaAgethi).

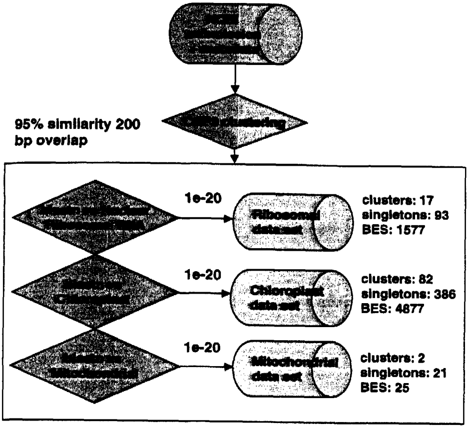


Figure 5 Annotation pipeline for analysis of BESs. This pipeline resulted in selection of non-redundant genomic BAC-ends which excluded organeller sequences, and further identification, annotation of non-redundant sequences together with SSR discovery, selection and primer designing.

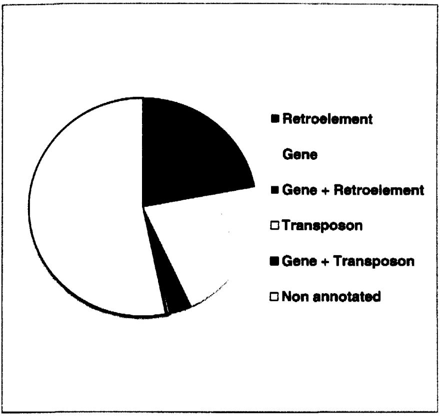


Figure 6 Distribution of BESs according to annotation. Major proportion of non redundant BESs remained non-annotated followed by nearly equal percentage of genes and retroelements.

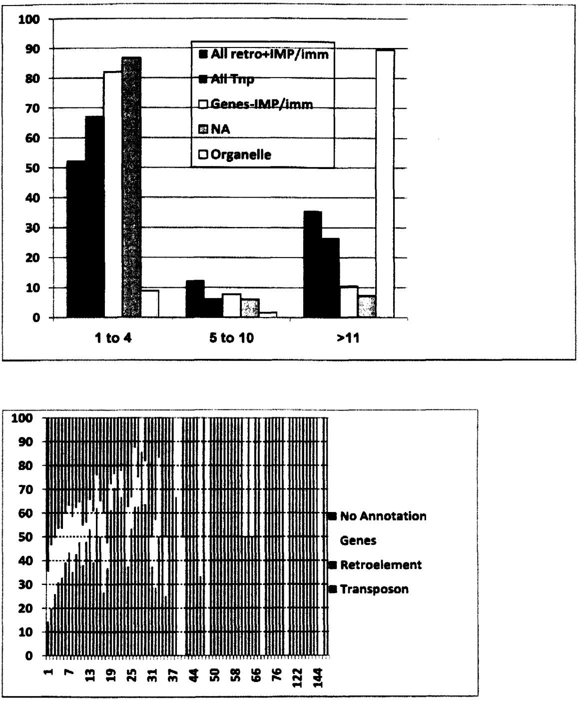


Figure 7 a) and b) Distribution of BAC end categories according to BES cluster depth. Cluster depth supported the repetitive nature of mobile genetic elements while genic regions were mostly associated with less repetitive sequences.

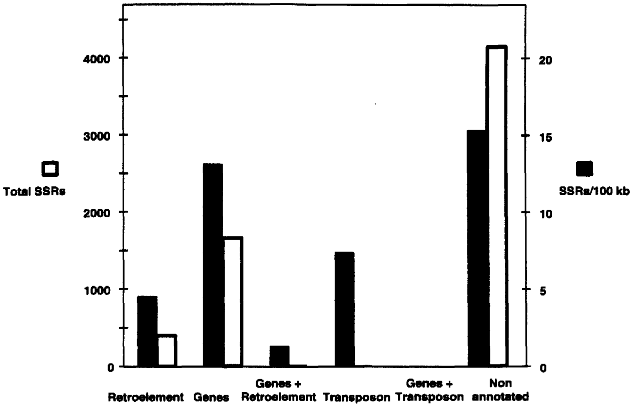


Figure 8 Distribution and frequency of SSRs in differing genome fractions. Maximum frequency and maximum amount of SSRs was exhibited by non annotated regions followed by the regions containing 'genes'.

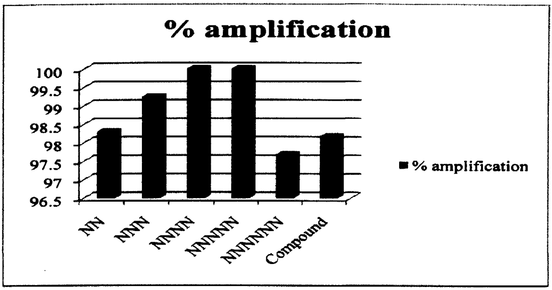


Figure 9 Percentage amplification pattern of different SSR motifs

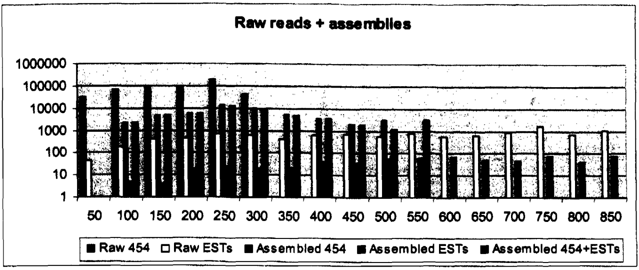


Figure 10 Sequence length distribution before and after assembly of short transcript reads (STRs). Read size of FLX/454 STRs ranged from 50 to a maximum of 300 bases, with the highest number of STRs having read size between 201 and 250. Read size of high quality Sanger ESTs varied from 50 to 850, maximum number of reads had 700-750 bases. A size comparison between raw FLX/454 STRs and assembled FLX/454 reads (contigs) showed that majority of sequences in each case had size range between 201 and 300, while similar comparison between raw Sanger ESTs and assembled Sanger ESTs (contigs) showed a range of 600-650. However, maximum number (18.16%) assembled of FLX/454 STRs and Snager ESTs (contigs) are ranged between 550-600.

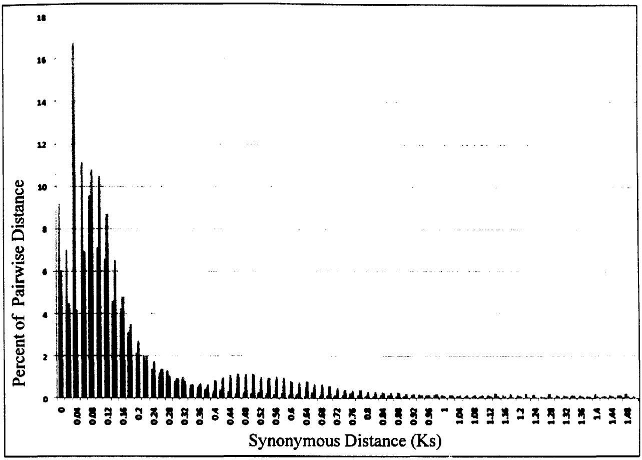
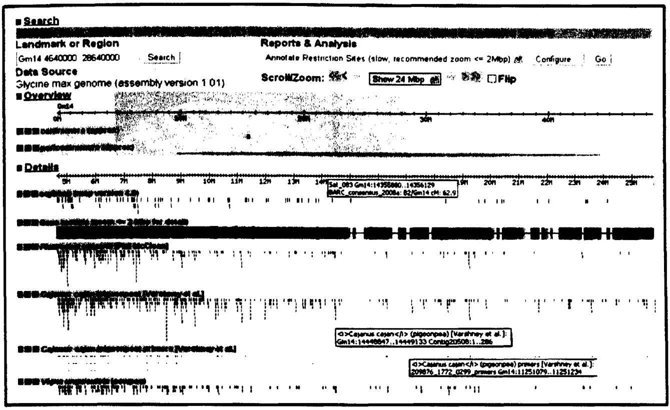


Figure 11 Histogram plot of pigeonepea TUSs based on alignment to soybean genome. Histogram plot of percentage pairwise distance to the synonymous distance value (Ks) a peak at 0.06 which gives a divergence estimate of ~4.9 Mya. This is an indication of recent segmental duplication in pigeonpea post to its separation of *Cajanus* from cowpea and common bean, but did not result in a change in chromosome number.

Figure 12 Distribution and alignment of pigeonpea TUS against the reference genome of soybean. All the TUSs of CcTA were BLASTed against the gene set of soybean. Soybean chromosomes are arranged in a circle and grey indicates pericentromeric regions (bar is putative centromere) and colours indicated gene rich regions of soybean chromosomes. First alignments for pigeonpea contigs are shown as green hashes on the outside of the soybean chromosomes and second alignments as red hashes. Black lines in the middle connect the first and second best hits



Landmark or Region: Gm14 4640000 28640000

Data Source: Glycine max genome (assembly version 1 01)

Sat_083 Gm14:14355880..14356129
BARC_consensus_2008a: 82/Gm14 cM: 62.9

<i>Cajanus cajan</i> (pigeonpea) [Varshney et al.]:
Gm14:14448847..14449133 Contig20508:1..286

<i>Cajanus cajan</i> (pigeonpea) primers [Varshney et al.]:
209876_1772_0299_primers Gm14:11251079..11251234

Figure 13 Gene structure prediction based on comparison of CcTA and soybean genome. The figure shows three alignment paths with directional arrangement of few TUSs', their position and their overlapping pattern predicted using GMAP, a standalone cDNA mapping and alignment tool. To give an indication about the confidence of location of pigeonpea TUSs in soybean genome, the sequences with single best hit are shown in green color and the sequences with multiple good matches are shown in red color

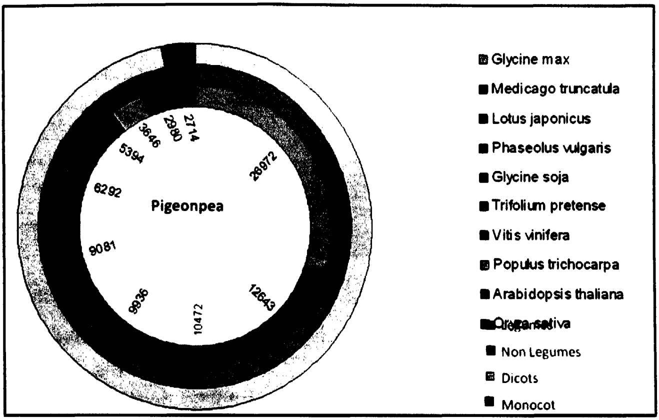


Figure 14 Similarity search of TUSs across different plant EST databases. Significant similarity of the pigeonpea TUSs against different plant EST databases has been conducted using BLASTN algorithm at an e value of =1e-30. The figure also represents the similarity coverage by the TUS among legume species and non-legumes and across dicots and monocots.

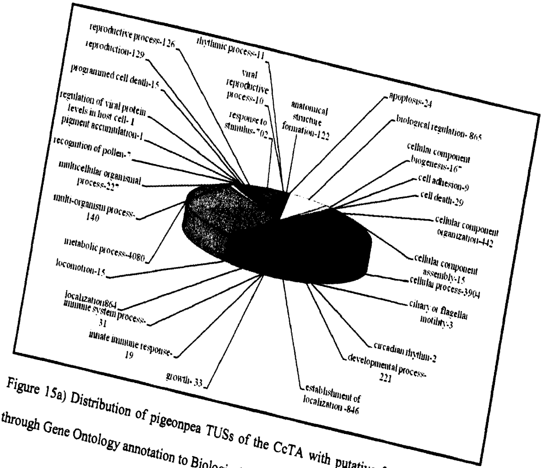


Figure 15a) Distribution of pigeonpea TUSs of the CcTA with putative functions assigned through Gene Ontology annotation to Biological process.

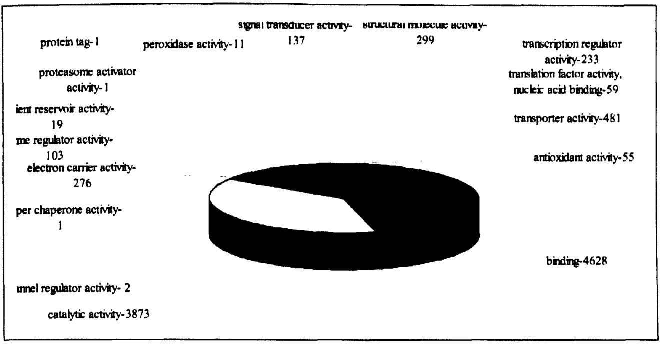


Figure 15b) Distribution of pigeonpea TUSs of the CcTA with putative functions assigned through Gene Ontology annotation to Molecular function.

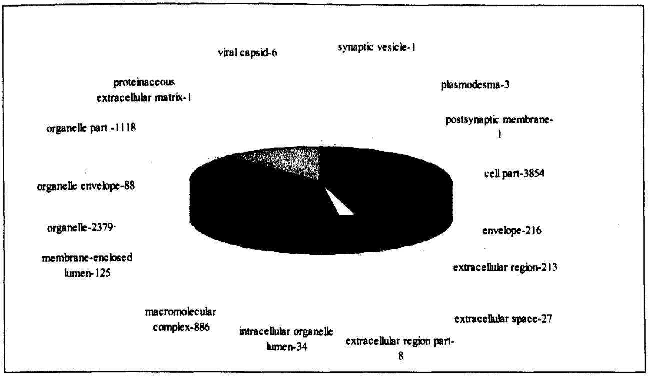


Figure 15c) Distribution of pigeonpea TUSs of the CcTA with putative functions assigned through Gene Ontology annotation to Cellular component.

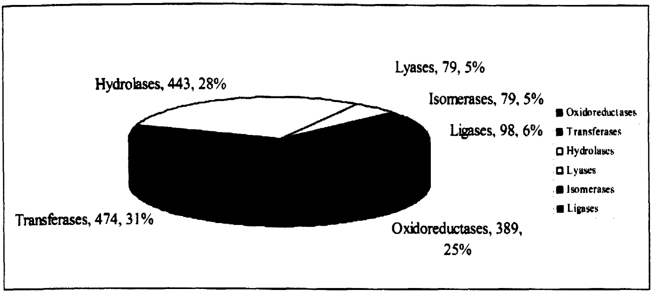


Figure 16 Distribution of pigeonpea TUSs onto GO assignment showing coverage of major enzyme classes. The details on distribution of pigeonpea TUSs onto GO assignments covering six major enzyme classes such as oxidoreductases (389) followed by transferases (474), hydrolases (443), lyases (79), isomerases (79) and ligases (98)

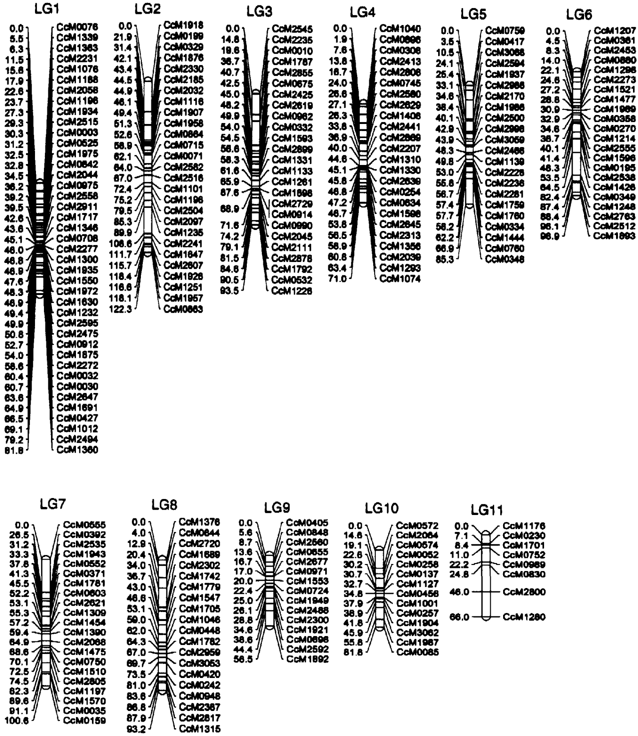


Figure 17 Reference genetic map of pigeonpea derived from an inter-specific F2 population (ICP 28 × ICPW 94)