HIGH DENSITY GENETIC MAP OF *MISCANTHUS SINENSIS* REVEALS INHERITANCE OF ZEBRA STRIPE

BY

SIYAO LIU

THESIS

Submitted in partial fulfillment of the requirements
for the degree of Master of Science in Crop Sciences
in the Graduate College of the
University of Illinois at Urbana-Champaign, 2015

Urbana, Illinois

Master's Committee:

Assistant Professor Erik J. Sacks, Chair
Assistant Professor Patrick J. Brown
Professor Brian W. Diers
Professor John A. Juvik

ABSTRACT

Miscanthus is a bioenergy feedstock crop that has only recently become the subject of modern breeding efforts. It also has more than a 100 year history as an ornamental crop in the U.S., with many cultivars currently sold by the horticulture trade. *Miscanthus* is a perennial, self-incompatible, C_4 grass, with some genotypes capable of maintaining high rates of photosynthesis under cold temperatures, which makes it a good choice for biomass production in the Midwestern U.S. The efficiency of breeding improved *Miscanthus* biomass cultivars would be greatly increased by using marker-assisted selection, because phenotypic selection for yield traits must typically be done in the second and third years of field trials. Thus, high-density genetic maps will be useful for identifying marker-trait associations that could facilitate mapping and breeding efforts in *Miscanthus*. Recently, a framework genetic map for *M. sinensis* was developed at the University of Illinois based on 658 single nucleotide polymorphism (SNP) markers using a GoldenGate genotyping array. However, sequencing of restriction site associated DNA tags (RAD-seq) is a promising approach for obtaining thousands of SNPs at lower cost than with GoldenGate. A major goal of the current research was to develop high density genetic maps of *M. sinensis* that integrate thousands of new RAD-seq SNPs with previously mapped but less numerous GoldenGate SNPs. In the present work, a mapping population consisted of 261 F_1 progeny was developed from a cross between two diploid *M. sinensis* cultivars, 'Strictus' and 'Kaskade'. SNP genotyping included 138 previously mapped GoldenGate SNPs and 3,044 single copy RAD tags assayed by high-throughput sequencing and called via the UNEAK pipeline in Tassel 3.0. Separate high-density genetic maps were produced for both the female parent ('Strictus') and the male parent ('Kaskade') using the regression mapping algorithm in JoinMap4.1. A composite genetic map was constructed for *M. sinensis* using the maximum likelihood mapping algorithm in JoinMap4.1. Zebra stripe mutants, characterized by horizontal yellow-green/white crossbands on the leaves (perpendicular to the leaf axis), have been found in many grasses, and a number of zebra stripe genes have been mapped in maize and rice. However, only one study on zebra stripe in *Miscanthus* has been published; a single locus model was suggested for this striping trait but it was not mapped. In the present study, segregation of zebra striping was observed in the F_1 mapping population and mapped as an example to confirm the utility of the new map. Quantitative trait loci (QTL) analysis identified three QTL for zebra stripe presence/absence and three for zebra stripe intensity. Two of the zebra stripe intensity QTL may be the same as two of the zebra stripe presence/absence QTL, or tightly linked. We determined that the inheritance of the trait was recessive but incomplete penetrance was observed for each zebra stripe presence/absence QTL. Epistatic interactions were important to the expression of the trait. Three-loci models explained up to 63% of the total variation for zebra stripe presence/absence and 68% for zebra stripe intensity. Comparative mapping indicated putative correspondence between QTL detected in *Miscanthus* and previously cloned genes conferring zebra stripe in maize and rice.

I dedicate this thesis to my dearest family
and friends for their love and support.

ACKNOWLEDGEMENTS

This work would not have been made possible without the support of many people. First, I would like to thank my major advisor Dr. Erik Sacks for his guidance and mentorship throughout my master’s program at the University of Illinois, Urbana-Champaign. Dr. Sacks has helped me grow so much and challenged me in ways I never thought I would in my field of study. His meticulous attention to detail and pursuit of excellence will always serve as a standard to which I hope to achieve. I thank my graduate advisory committee members: Dr. Patrick Brown, Dr. Jack Juvik and Dr. Brian Diers for their insightful advice and helpful feedback. I would also like to thank all the members in the Sacks Lab for their expertise and invaluable help along every step of my research project. I’m deeply thankful to Dr. Lindsay Clark for her time, patience, and tremendous help. Lindsay trained me to work in a molecular lab and taught me genetics data analysis. She has provided me with knowledge, expertise and thoughtful advice on graduate school, and for that I will forever be in her debt. Thanks are in order to Mr. Chris Kaiser for teaching me how to take plant measurements in the field, and to our lab undergraduate helpers and farm crew for their assistance in DNA extraction, field data collection, and trials maintenance. My appreciation extends to Dr. Donald Bullock for giving me the opportunity to serve as a TA for his statistics and experimental design class. He helped me realize my potentials and inspired me to believe in myself. I’m truly grateful for his trust, guidance and encouragement. Lastly, I thank my parents for their unending support and love throughout my life. I thank my friends for their company and friendship throughout the years.

Table of Contents

CHAPTER I: LITERATURE REVIEW

Miscanthus

Miscanthus is a perennial, self-incompatible, C_4 warm season grass. Taxonomically, *Miscanthus* is classified in the tribe Andropogoneae within the Poaceae family, which includes several species of high agricultural and economic value such as maize, sorghum and sugarcane (Clifton-Brown *et al.*, 2008). The number of species within the genus *Miscanthus* is still a subject of debate, and continuing investigation. Clayton and Renvoize (1986) classified the genus *Miscanthus* into approximately 20 species, most of which are native to eastern or southeastern Asia (China, Taiwan, Japan, Korea and south), with two species found in the Himalayas and four in southern Africa (Hodkinson *et al.*, 2002a). Recent molecular marker data and phylogenetic analysis showed that 5-6 species were defined within *Miscanthus sensu stricto* (*s.s*.) on the basis of DNA sequence and fingerprinting data (Chen & Renvoize, 2005; Hodkinson *et al.*, 2002a, b). Three *Miscanthus* species, *M.* × *giganteus*, *M. sacchariflorus*, and *M. sinensis* have been identified as having high potential for biomass production (Jones & Walsh, 2001).

Miscanthus s.s. species are native to eastern or southeastern Asia, and widely distributed from about ~ 50˚ N in Siberia, throughout the temperate zone to ~ 22˚ S in the tropical zone of Polynesia (Hodkinson *et al.*, 1997; Hodkinson *et al.*, 2002a). Adaptation of *Miscanthus* populations to cold and temperate climates makes this crop well adapted to Europe and the U.S. The native distribution of *M. sacchariflorus* is limited to temperate regions of China (e.g. Hunan, Hubei provinces to the border of eastern Russia), Korea, Russia, and Japan (Sacks *et al.*, 2013), whereas *M. sinensis* is found in temperate, subtropical and tropical areas of southeastern Asia, including China, Korea and Japan, and it is the most broadly distributed *Miscanthus* species in Asia (Lee, 1993; Shouliang & Renvoize, 2006; Sun *et al.*, 2010; Sacks *et al.*, 2013).

Miscanthus species have traditionally been used for grazing and burning in China and Japan for thousands of years (Stewart *et al.*, 2009), and recently have become the focus of sustainable biomass production to meet renewable-energy needs (Clifton-Brown *et al.*, 2004). Unlike most C_4 warm-season grass, some *Miscanthus* cultivars can maintain high photosynthetic rates at low temperatures, which occur naturally early and late in the growing season (Beale *et al.*, 1996), explaining why its canopy can be rapidly formed in the spring and maintained over a long growing season (Dohleman & Long, 2009).

So far, the most promising biofuel candidate for *Miscanthus* feedstock production in the emerging U.S. bioenergy industry is a single genotype of *M.* × *giganteus* (Heaton *et al.*, 2010). In 1935, a sterile triploid individual of *M.* × *giganteus* was brought from southern Japan to Denmark by Aksel Olson and has been cultivated and distributed since then (Linde Laursen, 1993; Greef *et al.*, 1997; Lewandowski *et al.*, 2000; Głowacka *et al.*, 2014). High biomass yields of this genotype and its broad adaptation to temperate agricultural regions made this single genotype an excellent feedstock candidate for biofuel production in the Midwest U.S., along with its remarkable sustainability via perennial growth, efficient nutrient recycling, and below ground carbon sequestration compared to maize and switchgrass (Heaton *et al.*, 2004; Heaton *et al.*, 2008; Heaton *et al.*, 2010; Somerville *et al.*, 2010; Purdy *et al.*, 2013). Dohleman and Long (2009) demonstrated that this *M.* × *giganteus* genotype is 60% more productive than maize in the US ‘Corn Belt’; Propheter and Staggenborg (2010) observed in Kansas that it yielded about twice as much as maize. Naidu *et al.* (2003) discovered that this genotype can maintain 80% higher photosynthetic yields at 14/11˚C (day/night) than maize. Further research has shown that the two enzymes involved in photosynthesis, pyruvate phosphate dikinase (PPDK) and ribulose-1,5-bisphosphate carboxylase oxygenase (RuBisCO) are most likely responsible for the recovery and maintenance of photosynthetic capacity in *M.* × *giganteus* at low temperature (Naidu & Long, 2004; Wang *et al.*, 2008). Moreover, perenniality is another advantageous trait for bioenergy feedstock, because it contributes to several environmental benefits such as nitrogen use efficiency, water use efficiency and soil erosion control, especially compared to annual crops. However, the limitations of using this single sterile *M.* × *giganteus* genotype for biomass production include slow and expensive vegetative propagation, high field establishment costs, and potential risk of disease or pest damage due to lack of genetic diversity. Given the lack of genetic diversity available to *Miscanthus* farmers, an understanding on *Miscanthus* genetics would facilitate the much-needed breeding of additional *M.* × *giganteus* cultivars.

The basic chromosome number in *Miscanthus* is 19 (Adati *et al.*, 1962). The ploidy level in *Miscanthus* species ranges from diploid to hexaploid but diploid and tetraploid are common (Clifton-Brown *et al.*, 2008). *M. sinensis* is typically diploid with a monoploid genome size of about 1.5-2.8 pg (Clifton-Brown *et al.*, 2008; Rayburn *et al.*, 2009; Sacks *et al.*, 2013), whereas *M. sacchariflorus* is usually diploid in China and Russia, but only tetraploids have been observed in Japan with a monoploid genome size of about 2.1-2.3 pg (Hirayoshi *et al.*, 1957; Rayburn *et al.*, 2009; Sacks *et al.*, 2013; Li *et al.*, 2013; Moon *et al.*, 2013; Chae *et al.*, 2014). The strong candidate for high biofuel production, a sterile *M.* × *giganteus* genotype, is an allotriploid (3n=57) hybrid produced from a cross between a diploid *M. sinensis* (2n=38) and a tetraploid *M. sacchariflorus* (4n=76) (Greef & Deuter, 1993; Hodkinson & Renvoize, 2001; Hodkinson *et al.*, 2002c). Because this genotype is unable to produce viable seeds, it has a low risk of becoming invasive plant, but sterility imposes limitations on improving this genotype through conventional breeding methods.

A number of approaches have been used to increase the genetic diversity of *M.* × *giganteus* so that more than just one sterile triploid genotype will be made available to farmers. Collection of naturally occurring triploid *M.* × *giganteus* from areas where sympatric populations of *M. sinensis* and tetraploid *M. sacchariflorus* exist is one solution (Nishiwaki *et al.*, 2011; Stewart *et al.*, 2009). Petersen *et al.* (2002) and Yu *et al.* (2009) restored fertility of *M.* × *giganteus* by manipulating ploidy levels in order to circumvent reproductive barriers between species. Yu *et al.* (2009) applied methods that were used to double the chromosome number in maize callus (Wan *et al.*, 1991) in order to regenerate the fertile hexaploids from triploid *M.* × *giganteus.* Chromosome-doubled plants were obtained from their study and pollen was shown to be viable but no seed was produced, which may be due to the obligate outcrossing nature of *Miscanthus* species. Furthermore, genetic modification of *Miscanthus* by *Agrobacterium tumefaciens* (Engler & Chen, 2009) and by particle bombardment (Wang *et al.*, 2011) has been reported.

Despite the success in doubling the chromosome number and genetic transformation of the sterile triploid *M.* × *giganteus*, depending on a single clonally propagated genotype for biofuel production poses inherent risks because a new disease or pest could result in severe damage to plantings. Moreover, breeding additional *M.* × *giganteus* cultivars with improved winter hardiness, and high yield-potential for the Midwest U.S. is critical because the current cultivar is insufficiently hardy to establish well during cold winters in central Illinois. Based on the reasons above, superior *Miscanthus* cultivars should be bred by choosing parents with desired traits. Substantial genetic variation has been found among the parental species of *M.* ×*giganteus*, *M. sacchariflorus* and *M. sinensis* (Jorgensen & Muhs, 2001, Clark *et al.*, 2014a; Clark *et al.*, 2014b; Głowacka *et al.*, 2014). Thus, future breeding strategies for *Miscanthus* will be directed towards the improvement of the parental species followed by interspecific crosses to remake *M.* × *giganteus*. Improvement of *M. sacchariflorus* has been limited in the U.S. because there have been only one diploid and two tetraploid genotypes commercially available. Recently, collection of *M. sacchariflorus* germplasm by the University of Illinois and others has circumvented this barrier to progress. On the other hand, because *M. sinensis* is adapted to a diverse range of environments and many ornamental genotypes have been available commercially in the U.S. and Europe, considerable genetic variation within this species has been available for plant breeders to make genetic gains for key traits towards breeding improved *M.* × *giganteus* cultivars.

Interspecific hybridizations in *Miscanthus* can be a useful approach to increasing genetic diversity of *Miscanthus* grown for biomass. Martin Deuter, the breeder at Tinplant Biotechnik und Pflanzenvermehrung GmbH, a German commercial breeding company, developed a number of selections from crosses between *M. sacchariflorus* and *M. sinensis*. In 2006, Tinplant released two cultivars named *M.* × *giganteus* ‘Amuri’, and ‘Nagara’. ‘Amuri’ consisted of multiple selected diploid *M.* × *giganteus* genotypes produced from a diploid *M. sacchariflorus* crossed with a diploid *M. sinensis,* whereas ‘Nagara’, is a triploid *M.* × *giganteus* genotype derived from a cross between a tetraploid *M. sacchariflorus* and a diploid *M. sinensis* (Sacks *et al.*, 2013). Transgressive segregation can be captured and exploited from such interspecific crosses. Hirayoshi *et al.* (1960) made a cross between a diploid *M. sinensis* var. *condensatus* and a natural tetraploid *M.* × *giganteus* (Japanese Ogi) and obtained both triploid and tetraploid progenies. Both types of progenies showed transgressive segregation for biomass traits (Hirayoshi *et al.*, 1960), however, the tetraploid progeny yielded higher than its parents and the triploid progeny (Matumura *et al.*, 1985, 1987). Recently at the University of Illinois, new triploid *M.* × *giganteus* individuals have been bred from the cross of diploid *M. sinensis* by tetraploid *M. sacchariflorus* (Chae *et al.*, 2013). One of the genetic maps recently published was based on a diploid *M. sacchariflorus* × *M. sinensis* interspecific cross population (Kim *et al.*, 2012). Thus, hybrids produced from these interspecific crosses suggest that crossing diploid *M. sacchariflorus* and diploid *M. sinensis* may also be a useful strategy for breeding superior *Miscanthus* cultivars. Selections of *M. sacchariflorus* and *M. sinensis* can be used as parents to develop improved *M.* × *giganteus* genotypes.

Genetic markers and genetic mapping

Genetic markers

Genetic markers are specific locations on a chromosome, representing differences between individuals of the same or different species (Staub *et al.*, 1996; Tanksley, 1983). Genetic markers can be classified into two major types: morphological markers, also known as visible or classical markers and molecular markers (Kumar, 1999). Morphological markers themselves are phenotypic traits or characters that can be visually monitored. Molecular markers have been developed to detect and track the polymorphisms at the protein level (known as biochemical markers) and at the DNA level (called DNA markers) (Jones *et al.*, 1997; Kumar, 1999; Winter & Kahl, 1995). Isozyme markers are the most commonly used protein markers, which are allelic variants of the same enzyme detected by electrophoresis and specific staining (Vodenicharova, 1989). DNA markers can be divided into two categories: hybridization-based markers and PCR-based markers, depending on how the polymorphism is revealed.

Unlike traditional phenotypic markers that are limited in number and may be influenced by environmental factors and/or developmental stage of the plants (Winter & Kahl, 1995), molecular markers are advantageous for plant breeders, because they are detectable in all stages of plant growth development and are not affected by the environment (Winter & Kahl, 1995). Moreover, using molecular markers decreases time to produce crop varieties with desirable traits and improves breeding efficiency and precision. Thus, many agricultural research institutes as well as private plant breeding companies have been striving to develop useful markers to facilitate the application of molecular breeding of crops.

DNA markers can also be divided into three major groups based on their detection method and throughput (Winter & Kahl, 1995; Jones *et al.*, 1997; Gupta *et al.*, 1999; Joshi *et al.*, 1999): 1) hybridization-based markers including restriction fragment length polymorphisms (RFLPs) (Botstein *et al.*, 1980) and variable number tandem repeats (VNTR) loci (Nakamura *et al.*, 1987; Rogstad, 1993); 2) polymerase chain reaction (PCR)-based markers, including random amplification of polymorphic DNA (RAPD) (Williams *et al.*, 1990), sequenced characterized amplified regions (SCARs) (Paran & Michelmore, 1993), amplified fragment length polymorphism (AFLP) (Vos *et al.*, 1995), and microsatellites (Hamada *et al.*, 1982; Litt & Luty, 1989) or simple sequence repeats (SSRs) (Jacob *et al.*, 1991); 3) DNA sequence-based markers: single nucleotide polymorphisms (SNPs) (Berger *et al.*, 2001).

RFLP markers were first used for human genome analysis (Botstein *et al.*, 1980), and widely used in plant genetics in the late 1980's (Lander & Botstein, 1989). The basic protocol for using RFLP markers is first digest genomic DNA by restriction enzymes, then separate the restriction fragments on gel and transfer them to membrane, and finally hybridize radio-labeled probe for visualization. RFLPs are co-dominant and reproducible markers, and have the advantage of detecting gene duplications. They were used to detect the metalloprotease MMP23 gene duplicates in human but not in chimpanzee (Puente *et al.*, 2005). Moreover, compared with PCR, RFLPs are more robust for detecting distantly-related sequences. Genetic maps based on a common set of RFLP probes provided a basis for linking tomato and potato genomes and locating the conserved regions of both tomato and potato chromosomes (Bonierbale *et al.*, 1988). However, the disadvantages of using RFLP markers include that they are labor intensive, costly and time consuming.

With the development of PCR technology (Mullis *et al.*, 1986), new generations of PCR-based markers were developed in the early 1990's. RAPD, SCAR, AFLP, and SSR markers are the major PCR-based markers. Williams *et al.* (1990) generated RAPD markers by using PCR amplification of random genomic DNA fragments with single arbitrary 10 base oligonucleotide primers. RAPD markers are used to identify polymorphisms simultaneously in various regions of a genome (Williams *et al.*, 1990). However, these markers are dominant, thus heterozygous individuals cannot be distinguished from both homozygotes. Other disadvantages of RAPD markers are poor repeatability and sensitivity to experimental conditions (Karp *et al.*, 1996). The low repeatability of RAPD is mostly due to its short primer as well as its random sequence, which allows it to anneal to different parts of the genome even when the genomic sequence is not an exact match.

SCARs were developed by sequencing RAPD bands to allow development of longer and more specific oligonucleotide primers, which resulted in less polymorphism but more reliability (Paran & Michelmore, 1993). In contrast to RAPDs, SCARs have the advantage of being more specific and reliable in detecting polymorphisms. In lettuce disease resistance breeding, Paran and Michelmore (1993) were able to increase the reliability of RAPD markers linked to an insect resistance gene by converting them to SCARs. Similar results were obtained in tagging gall midge resistance genes rice breeding (Nair *et al.*, 1995; Nair *et al.*, 1996).

AFLP markers detect fragment length polymorphisms by using both restriction enzymes and PCR amplification of fragments (Vos *et al.*, 1995). The use of two enzymes, a rare cutter such as *Pst*I and a frequent cutter such as *Msp*I, double digest the genomic DNA into fragments of different length (Jones *et al.*, 1997). AFLP bands can be detected by silver staining, florescent dye or radioactivity (Mohan *et al.*, 1997). Although running vertical polyacrylamide gels is to some extent challenging, the ability to detect large number of polymorphisms and produce DNA fingerprints with AFLPs makes this marker system useful for developing high resolution maps (Menz *et al.*, 2002).

Microsatellites, also known as SSRs are short nucleotide sequence repeats flanked by unique sequences (Hamada *et al.*, 1982; Tautz & Renz, 1984).SSRs offer several advantages: they are abundant in plant genomes, highly polymorphic, highly reproducible, and able to distinguish between closely-related individuals based on the number and frequency of alleles detected (McCouch *et al.*, 1997). Developing SSR markers may have been expensive and laborious because it involves library construction and clone sequencing, however, SSRs have been considered cost effective to use (Smith *et al.*, 1997). SSRs have been used in mapping many plant genomes such as soybean (Akkaya *et al.*, 1992), rice (Zhao & Kochert, 1993), and maize (Senior & Heun, 1993). Another advantage of SSRs is their transferability across species or genera, especially among species within families, such as the grass family (Gramineae) (Cordeiro *et al.*, 2001; Holton *et al.*, 2002; Thiel *et al.*, 2003) where synteny is a common feature (Gale & Devos, 1998). Thus, markers developed in one species may be used to predict the linkage relationships in closely related species and therefore facilitate genetic linkage map construction in species with less informative maps or markers. For example, the synteny between sorghum and sugarcane genomes facilitated the development of a sugarcane map because linked loci on the sorghum map provided useful information predicting their location in sugarcane genome (Dufour *et al.*, 1997; Grivet *et al.*, 1994). Similarly, SSR markers from sugarcane were successfully applied to *Miscanthus* (Cai *et al.*, 2005). Kim *et al.* (2012) also applied SSRs designed from sugarcane expressed sequence tags (ESTs) to *Miscanthus* and successfully constructed EST-SSR-based genetic maps for *Miscanthus*. In addition, Yu *et al.* (2013) indicated that 46.6% of the rice SSR markers they investigated were transferable to *Miscanthus sinensis*, and useful for genetic analysis in *Miscanthus*. Zhao *et al.* (2011) successfully transferred 86.0% of the *Brachypodium distachyon* SSR markers to *Miscanthus sinensis*.

A SNP marker is a single base variation in a DNA sequence. Usually, a SNP has alternative of two possible nucleotides at a given position, which makes it a simple bi-allelic co-dominant marker (Brookes, 1999). SNPs are the most abundant type of markers in both plant and animal genomes (Gupta *et al.*, 2001). They are highly polymorphic, evenly distributed in genomes, and amenable to automation and high throughput sequencing platforms. Compared to the gel-based markers such as RFLPs, RAPDs and SSRs, SNPs are sequence-based markers and the methods used to discover SNPs save much time and cost (Gutpa *et al.*, 2001). Different methods have been used in SNP discovery such as locus specific-PCR amplification (LSA), whole genome shotgun sequences (Weber & Myers, 1997), overlapping regions in bacterial/P1 artificial chromosomes (BACs and PACs) (Taillon-Miller *et al.*, 1998), and reduced representation shotgun (RRS) (Lander *et al.*, 2000). Sequencing methods for detecting SNPs evolved from traditional Sanger sequencing method (Sanger *et al.*, 1977; Lander *et al.*, 2001) to next generation sequencing (NGS) technologies (Wheeler *et al.*, 2008) such as Illumina, 454 Life Sciences/Roche, and Solexal/Illumina and Applied Biosystems (SOLiD). The development of new sequencing platforms has advanced SNP genotyping at low cost with large amount of sequence data and also facilitated SNP identification in whole genomes (Van Tassell *et al.*, 2008).

Genetic mapping

One of the major applications of DNA markers is to develop genetic linkage maps (Mohan *et al.*, 1997). In the early 1900's, T.H. Morgan and his student, Alfred Sturtevant, published the first genetic map for a common species of fruit fly, *Drosophila melanogaster*. In Morgan's experiments, they showed the locations of sex linked genes on the sex chromosome (Morgan, 1910). The principle of genetic linkage mapping is to order and assign genetic markers to their linkage groups, and indicate the relative genetic distance between the markers along the chromosomes based on the recombination frequency (Jones *et al.*, 1997). In plant breeding, the main reason to develop genetic linkage maps with DNA markers is to locate genes associated with traits of interest by using the mapped markers, and therefore facilitate marker-assisted breeding.

In genetic mapping with molecular markers, two major factors are critical to success: marker types and population types (Staub *et al.*, 1996). Choice of marker system has potential impact on the map density, informativeness, cost, and time required to develop markers. Choice of mapping population affects the efficiency of developing a genetic map and its later informativeness in quantitative trait loci (QTL) studies. Also, both the number of markers (marker density) and size of populations (meiotic events) sampled for mapping are of importance. For preliminary genetic mapping, generally 100 to 200 markers are mapped (Mohan *et al.*, 1997). Large numbers of makers are needed for high-resolution fine mapping. SNP markers hold promise to higher map resolution because they are abundant, highly polymorphic in the plant genomes, and automated to high throughput sequencing platforms (Gupta *et al.*, 2001; Rafalski, 2002). A range of 50 to 250 individuals is used in preliminary genetic mapping (Mohan *et al.*, 1997) but a larger population size is required for high-density map construction. Even if an infinite number of markers are used in map construction, it is possible to produce a poor low-density map if there are few progeny in the population.

The marker system used in genetic map construction is determined by several factors such as project objectives, population structure, genetic diversity of the species, time and cost (Staub *et al.*, 1996). Each marker type has its pros and cons and its potential utility needs to be assessed before use. In the case of grass species, since conservation of gene order is common in grass genomes (Gale & Devos, 1998), comparative genetic maps were developed based on RFLP markers (Whitkus *et al.*, 1992; Grivet *et al.*, 1994). However, the resolution of these maps with hybridization-based RFLP markers is generally insufficiently high for detecting microsynteny (Kilian *et al.*, 1997). Sequence-based markers have recently been used in comparative genetic mapping and considerably enhanced map resolution (Klein *et al.*, 2003; Sorrells *et al.*, 2003). In *Miscanthus,* due to its high degree of genetic similarity with sugarcane (Amalraj & Balasundaram, 2006; Heaton *et al.*, 2008; Jensen *et al.*, 2008), SSR markers derived from sugarcane have been used to study *Miscanthus* and improved our understanding of the *Miscanthus* genome (Cai *et al.*, 2005; Kim *et al.*, 2012).

Choice of mapping populations depends on a number of factors such as experimental objectives, marker type (Tanksley *et al.*, 1988), population, species, and time required for analysis. Populations from two inbred parental lines such as F_2 (McCouch *et al.*, 1990), backcross (BC) (Causse *et al.*, 1994), doubled haploids (DH) (Zhang *et al.*, 2008) and recombinant inbred lines (RIL) (Mansur *et al.*, 1996) have been used extensively for genetic mapping studies in self-compatible species. However, it is difficult or impossible to develop mapping populations from inbred parents for obligate outcrossing species, such as *Miscanthus.* Due to the self-incompatibility and consequently a high level of heterozygosity, the genetic mapping approach used in *Miscanthus* is more similar to forest or fruit tree species (Głowacka, 2011) than for inbreeding crops.

Grattapaglia and Sederoff (1994) proposed a two-way pseudo-testcross mapping strategy for outcrossing species, and constructed two parent-specific linkage maps in *Eucalyptus* by applying this strategy. The pseudo-testcross mapping strategy uses markers that are heterozygous in one of the parents only, and calculates dominant markers following testcross configuration in F_1 progeny; thus, it is a fast and simple approach to construct genetic linkage maps in obligate outcrossing species. Genetic linkage maps of different marker types using the pseudo-testcross strategy have been developed in several grass species such as sugarcane (*Saccharum spp.*; Al Janabi, 1993; Grivet *et al.*, 1996; Ming *et al.*, 1998), ryegrass (*Lolium spp.*; Inoue *et al.*, 2004; Jones *et al.*, 2002), switchgrass (*Panicum virgatum* L.; Missaoui *et al.*, 2005; Okada *et al.*, 2010), meadow fescue (*Festuca pratensis* Huds.; Alm *et al.*, 2003), orchardgrass (*Dactylis glomerata* L.; Xie *et al.*, 2011) and *Miscanthus* (Kim *et al.*, 2012; Swaminathan *et al.*, 2012; Ma *et al.*, 2012).

Genetic mapping in Miscanthus

To understand the genetics of important agronomic traits and enhance breeding efficiency of *Miscanthus*, a genetic linkage map is needed. A genetic map would be useful for locating genes that control traits of interest by using the mapped markers. A preliminary genetic linkage map of *M. sinensis* was published by Atienza *et al.* (2002) using 257 RAPD markers. They identified 28 linkage groups (LGs) on this initial map, which was more than the expected 19 LGs. Moreover, the density of this map was not sufficient for identifying markers tightly linked to traits of interest. In addition, the low reproducibility of RAPD markers was also disadvantageous. To identify highly repeatable marker-trait associations in *Miscanthus*, a complete linkage map with higher density is needed. Kim *et al.* (2012) developed SSR-based genetic maps for *M. sinensis* and *M. sacchariflorus*. A total of 261 loci were mapped in *M. sacchariflorus,* covering an estimated 72.7% of the genome; in *M. sinensis*, a total of 303 loci were mapped, covering 84.9% of the genome. Moreover, the SSR-based maps provided a framework for aligning *Miscanthus* LGs to those of the closely related species, *Sorghum bicolor*, revealing a whole genome duplication event in *Miscanthus*. The development and utilization of SSR markers in *Miscanthus* mitigated the problems in the initial linkage map by Atienza *et al.* (2002) due to the abundance and reproducibility of SSRs. However, a higher density map would be useful to further facilitate marker-assisted selection in breeding.

SNP markers have become widely used in plant molecular genetics due to their genome-wide abundance and amenability for high-throughput detection platforms (Mammadov *et al.*, 2012). Recent advances in new sequencing technologies have enabled the economical discovery of SNPs on a large scale in many species (Davey & Blaxter, 2010). Next-generation sequencing (NGS) has been used to discover SNPs in the genomes of important crops such as maize (Gore *et al.*, 2009), rice (Deschamps *et al.*, 2010), soybean (Hyten *et al.*, 2010), and sorghum (Nelson *et al.*, 2011). For example, over 34,000 SNPs were recently mapped in barley by using the genotyping by sequencing (GBS) approach (Poland *et al.*, 2012).

A framework genetic map for *M. sinensis* was recently developed at the University of Illinois using a GoldenGate genotyping array (Swaminathan *et al.*, 2012). Deep transcriptome sequencing (RNA-seq) from two *M. sinensis* accessions was employed to define 1,536 single nucleotide variants (SNVs) for a GoldenGate genotyping array, of which 658 SNPs were validated via segregation in a full sib F_1 mapping population (Swaminathan *et al.*, 2012).

Ascertainment bias and modest density were limitations of the Swaminathan *et al.* (2012) map. Another research group at Aberystwyth University in the UK constructed a high-resolution linkage map of *M. sinensis* using the GBS approach (Ma *et al.*, 2012). This complete and high-resolution linkage map contained 3,745 SNPs, spanning 2,396 cM on 19 LGs with 0.64 cM average resolution, providing a resource for QTL detection as well as serving as a reference for future *Miscanthus* genome sequence assembly (Ma *et al.*, 2012). However, the methods used in the Ma *et al.* (2012) paper were proprietary, and therefore it is not possible for others to repeat their work.

In this present study, sequencing of restriction site associated DNA tags (RAD-seq) was applied to discover SNPs in *Miscanthus*. Sequencing of RAD tags is a new method that uses Illumina NGS to simultaneously identify and genotype thousands of SNP markers in a large number of individuals at low cost (Baird *et al.*, 2008; Davey & Blaxter, 2010; Miller *et al.*, 2007; Peterson *et al.*, 2012). RAD-seq targets a fraction of the genome for sequencing by using flanking restriction enzyme cut sites and produces a reduced genome representation. Genome complexity reduction may be achieved with a two-enzyme system (Poland *et al.*, 2012), which includes one infrequent-cutter and one frequent-cutter. This type of library construction provides a robust and efficient approach for obtaining thousands of SNPs at low per sample cost in diverse species with large genomes (Elshire *et al.*, 2011). Moreover, the RAD-seq approach also works for species that do not have a reference genome (Hohenlohe *et al.*, 2012). Thus, RAD-seq should be a useful method for developing a high-density map containing numerous mapped markers for *Miscanthus*.

Quantitative Trait Loci (QTL) analysis for plant improvement

Introduction

The term, quantitative trait loci (QTL), first coined by Gelderman (1975), refers to regions of the genome that contribute to variation in a trait of interest. QTL mapping has provided a useful tool for studying genetic architecture of complex trait variation (Falconer *et al.*, 1996). Complex traits, such as biomass yield in agriculture are usually quantitative, which are typically influenced by the environment, multiple genes of small effect, or both. The work of Sax (1923) on seed size (a complex trait) associated with seed-coat color (a simple trait) in common bean (*Phaseolus vulgaris*) firstly revealed the importance of QTL analysis in agriculture. In the Sax (1923) study, the basic concept was to detect QTL by using the segregation of simply inherited phenotypic markers linked to factors affecting the quantitative trait of interest. QTL analysis identifies marker-trait associations based on the phenotype of the trait and the genotype of markers. A significant difference in the phenotypic values between two individuals suggests linkage between a QTL and a marker locus that is being used to classify the genotypic groups (Tanksley, 1993; Young, 1996). If a QTL is tightly linked to a marker, the chance of recombination between the QTL and marker is low, and therefore, the QTL and marker tend to be inherited together. The development of molecular markers and statistical software packages during the 1980’s provided useful tools for detecting QTL, and since then, numerous QTL underlying different traits of interest have been identified in many crop populations and environments (Reviewed by Xu, 1998; Collard *et al.*, 2005).

Types of mapping populations

To efficiently map traits in bi-parental populations, it is advantageous to choose parents that differ greatly for the traits of interest (Semagn *et al.*, 2010). F_2, BC, near-isogenic lines (NIL), DH and RIL are populations developed by crossing two inbred lines, and are commonly used for QTL mapping in self-pollinating species. Among these population types, F_2 and BC are the simplest to develop in self-pollinating species in terms of time and money. Compared to a BC population, F_2 is more powerful to detect QTL with additive effects and estimate degree of dominance (Carbonell *et al.*, 1993). Both F_2 and BC populations are temporary populations because they are highly heterozygous and cannot be propagated indefinitely through seeds (Burr *et al.*, 1988); thus they are not frequently used for evaluation in multiple locations and over multiple years. RILs, NILs and DH populations produce homozygous lines that can be multiplied by seeds and reproduced without genetic change, thereby making available an 'eternal' resources for collaboration among different QTL mapping projects. DH populations are quicker to develop compared to RILs and NILs but only possible for a few species following a haploid production protocol, which may be complex and laborious.

Analysis methods

Single locus association, also known as single marker analysis (SMA) is the simplest QTL mapping analysis method (Collard *et al.*, 2005). Statistical models such as *t*-test, ANOVA (Soller *et al.*, 1976), linear regression (Haley & Knott, 1992) and maximum likelihood (Weller, 1986, 1987) were used in SMA. The advantages of ANOVA at the marker loci are: it's simple, no genetic map is required for markers; and multiple loci can be accounted for (Broman, 2001).

However, SMA fails to separate QTL position and QTL effects. ANOVA detects smaller QTL effect at a marker than the true QTL effect due to recombination occurrence between the QTL and marker (Broman, 2001). Linear regression has the advantage of providing the coefficient of determination (R^2), which indicates the proportion of variance accounted for by the markers. However, if a QTL is distant from a marker, the power to detect a QTL will be decreased.

Interval mapping (IM), proposed by Lander and Botstein (1989), analyzes linked markers on a genetic linkage map. IM is more powerful to detect QTL than SMA because the intervals between the linked makers on the chromosomes are analyzed simultaneously (Lander & Botstein, 1989). However, IM assumes the presence of a single QTL located on each chromosome, and the interactions between multiple QTL are not considered in this model.

Composite interval mapping (CIM) overcomes the weakness of the IM method, which detects only a single QTL at a time (Zeng, 1993, 1994). CIM extends the IM method and can detect linked or interacting QTL in the genomes (Doerge, 2002) by including additional markers as cofactors and therefore, CIM is more precise and accurate in QTL mapping. Both IM and CIM methods present the test statistic results in a logarithmic (base 10) of odds (LOD) score profile, which indicates the likely location for a QTL in relation to the linked markers. The LOD score shows the ratio of the likelihood of obtaining the evidence for the presence of a QTL at the location to the likelihood of no QTL detected from the same evidence. The significance threshold for a potential QTL is determined using permutation tests (Churchill & Doerge, 1994).

The goal of QTL mapping is to identify loci that affect the phenotype. In the past, QTL mapping has been considered as a hypothesis testing problem and much of the effort has been focused on adjusting multiple tests; however, QTL mapping is best viewed as a problem of model selection (Broman *et al.*, 2003). Multiple-QTL mapping (MQM), originally introduced by

Jansen (1994, 2007) is a model selection procedure that identifies multiple QTL using both forward selection and backward elimination (Kao & Zeng, 1997; Kao *et al.*, 1999; Zeng *et al.*, 1999). Compared to the hypothesis testing approach, MQM has the advantages of increasing power in QTL detection, separating linked QTL, and identifying epistasis among QTL (Broman *et al.*, 2003). Unlike in the hypothesis testing, both types of errors (false positive and false negative) can be made at the same time in MQM (Broman *et al.*, 2003).

QTL mapping in outcrossing species

Designed line crosses are required in most QTL mapping methods, and F_2 and BC are common simple line crosses used in mapping QTL. Complex mating designs involving multiple crossed lines are also used in both animal and plant breeding (Yi & Xu, 2002). Complex mating designs can be more informative than simple line cross as there are more alleles segregating but more difficult to conduct the analysis. The statistical power of QTL searching can increase when using a multiple line crosses design and therefore, there is improvement of precision in estimating QTL positions and effects (Rebai & Goffinet 1993; Muranty, 1996).

Several statistical approaches have been used for QTL mapping in multiple line crosses, such as weighted least square (Xu, 1998), the fixed model and random model (Xu, 1998), regression-based QTL mapping method (Rebai & Goffinet, 1993, 2000), and expectation-maximization (EM) algorithm (Liu & Zeng, 2000). Yi and Xu (2002) proposed a Bayesian approach implemented via the reversible jump Markov chain Monte Carlo (MCMC) algorithm for mapping QTL in multiple line crosses. This approach allows searching for multiple QTL simultaneously in the genome, and more importantly, provides inference on the posterior distribution of the number of QTL (Yi & Xu, 2002).

Mapping and identifying QTL in obligate outcrossing species is more complex than self-pollinated species because inbred lines can be produced from the autogamous species, whereas this is typically not possible for obligate outcrossing species. The strategies such as two-way pseudo-testcross, half-sib and full-sib families derived from controlled crosses are commonly used in QTL mapping for outcrossing species (Grattapaglia & Sederoff, 1994). Maximum likelihood method was used for QTL detection in both full-sib and half-sib designs (Knott & Haley, 1992, Mackinnon & Weller, 1995).

Software for analyzing outcrossing species

Several statistical programs have been used for mapping QTL in outbred populations. MapQTL (Van Ooijen, 2009) is a software program based on windows operating system, and can map QTL in different experimental populations, from inbred lines such as $BC_{1,}$ $F_{2,}$ to lines produced from non-inbred parents such as full-sib family. MapQTL program performs QTL mapping using different methods such as interval mapping, multiple quantitative mapping (MQM), and a nonparametric method. MapQTL is also compatible with JoinMap4.1 (Van Ooijen, 2011).

MCQTL is a statistical program that performs QTL analysis in multi-cross design (Rebai *et al.*, 1997). In addition to mapping QTL in populations derived from non-inbred lines (Jourjon, 2000), this program also performs analysis that links multiple families, assuming the same QTL locations in all of the families. Moreover, a connected modeling of the QTL genotypic effect is allowed in multiple related families. MCQTL runs on the UNIX system. Billotte *et al.* (2010)

conducted a QTL analysis on multi-parent populations in oil palm using a new package of MCQTL called *Outbred*. This *Outbred* package was designed to analyze more than one related crosses between diploid heterozygous parents, and takes into account that parents can be shared between families, and therefore a connected model is allowed. A 2 × 2 complete factorial mating experiment involving four parents was designed in Billotte *et al.*'s study. Two types of QTL search, within-family analysis and across-family analysis were performed and compared using the new extension of the MCQTL software. A set of 76 QTL involved with 24 quantitative traits were identified. Across family analysis proved to be more efficient due to the interconnected families.

R/qtl (Broman *et al.*, 2003) is an add-on package to the free statistical software R and has been widely used for QTL mapping. Similar to MCQTL, R/qtl performs QTL mapping in simple line crosses as well as multiple line crosses. Previous studies have shown that the power of detecting QTL increases when combining different line crosses (multiple families) compared to using simple line cross (single family) alone (Muranty, 1996; Xie *et al.*, 1998; Xu, 1998, Rebai & Goffnet, 2000). R/qtl performs single-QTL genome scans, which assumes only one QTL segregating when searching for QTL. Several methods have been implemented in single-QTL model in R/qtl such as simple marker regression, standard IM, Haley-Knott regression, and multiple imputation method. In addition to one-dimensional genome scans, R/qtl also performs two-QTL, two-dimensional genome scans, which considers each pair of positions in the genome as putative QTL locations. The two-QTL model was first proposed by Haley and Knott (1992), and has the advantages of gaining power in detecting QTL of modest effect, separating linked QTL, and exploring epistasis between QTL. Moreover, a fully automated multiple-QTL model method is also implemented in R/qtl, which provides a powerful approach to dissect the genetic architecture of complex traits. The main computational method used for QTL mapping in R/qtl is the hidden Markov model, which deals with missing genotype data and genotyping errors. R/qtl runs on Windows, Linus, and MacOS systems.

QTL mapping in *Miscanthus*

Developing a marker assisted selection (MAS) program for *Miscanthus* would be beneficial to improving breeding efficiency, because the lengthy establishment period of at least one year is an impediment to rapid selection. Phenotyping most biomass traits for *Miscanthus* in the first year is not worthwhile because the first year yield is much less than the subsequent years, and moreover it is not representative of yield in subsequent years. A MAS program would allow selection of promising individuals during the seedling stage, which will shorten the breeding cycle and save resources. Successful examples of applying MAS in plant breeding have been reported in rice (Huang *et al.*, 1997; Singh *et al.*, 2001; Suh *et al.*, 2013). In Huang *et al.*'s work, MAS was used to pyramid disease resistance genes in rice so that a large population can be screened quickly at an early stage of development with the aid of appropriate markers. In addition, MAS has also been successfully applied in some outbred forage species such as white clover (Barrett *et al.*, 2009) for selecting seed yield gain and alfalfa (Castonguay *et al.*, 2009) for selecting freezing tolerance. Thus, MAS is an advantageous strategy for complex trait improvement of perennial crops like *Miscanthus.*

Mapping QTL associated with complex traits is expected to facilitate MAS and is considered as the first step towards developing a MAS program. This is particularly essential when interaction among QTL, between QTL and environment, or between QTL and genetic background are significant (Falconer, 1981). Conventional phenotypic screening for complex traits is difficult, costly, and labor intensive. However, MAS allows selection based on tightly linked markers that reliably predict a trait phenotype, as MAS relies on the linkage disequilibrium (LD) between a marker and a QTL. Once the linkage between a QTL and marker is established and its general utility across populations is verified, an effective MAS program can be implemented.

To date, five QTL studies on *Miscanthus* have been published, of which four were conducted on the same population by Atienza *et al.* (2003a, b, c, d) and one on a different population by Gifford *et al.* (2014). Atienza *et al.* (2003a, b, c, d) identified QTL associated with a variety of traits but the QTL analysis in all four studies was based on the first linkage map of *M. sinensis* (Atienza *et al.*, 2002), which consisted of 257 RAPD markers covering 28 LGs, more than the 19 LGs expected for *M. sinensis.* In Atienza *et al.*'s population, 89 F_1 progeny were studied over two years for a variety of traits including yield, yield components, height, stem diameter, chlorine and potassium content, and combustion-related traits. However, there were significant limitations to the Atienza *et al.* (2003a, b, c, d)'s QTL studies. First, the genetic map used was incomplete. A complete genetic map saturated with markers would be advantageous for detecting QTL. Second, a larger population size is needed to reduce the Beavis effect and increase power of identifying QTL. The Beavis effect is a phenomenon in which the average estimates of phenotypic variances associated with correctly identified QTL are overestimated if few progeny are evaluated (Beavis, 1994, 1998; Xu, 2003). In a recent *Miscanthus* QTL study, Gifford *et al.* (2014) phenotyped an *M. sinensis* population that consisted of 221 F_1 progeny over 3 years, and identified a total of 72 QTL on 14 different chromosomes across 13 traits important for biomass production. Of the 36 QTL detected in year 2 (year 1 was establishment year), 22 were detected in year 3 and 6 detected in year 2 were mapped close to the same region as QTL in year 3, but didn’t share overlapping confidence intervals. Moreover, to account for the variation caused by the establishment effect from year 1, Gifford *et al.* (2014) used spring emergence and vigor rating as covariates in their QTL analysis. Although the use of spring emergence and vigor rating as covariates increased the power to detect QTL in year 2 & 3, Gifford *et al.* (2014) indicated that appropriate covariates may vary for different populations, and additional covariates should be explored. Gifford *et al.*’s study set the foundation for QTL fine mapping, gene positional cloning and marker assisted selection. However, limited number of QTL identified for certain traits suggested that phenotypic data collection methods can be improved and the variation caused by establishment effect in certain traits can be more effectively accounted for. Moreover, for *Miscanthus* QTL to be useful for MAS, they will need to be validated for multiple populations and over multiple environments. Finally, the marker density of the genetic map used in Gifford *et al.*’s study can be improved. To identify robust marker-trait associations, a genetic map saturated with numerous markers will be desired. Thus, the present genetic mapping study is expected to be useful for future *Miscanthus* QTL work.

References

Akkaya MS, Bhagwat AA, Cregan PB (1992) Length polymorphisms of simple sequence repeat DNA in soybean. *Genetics,* **132**, 1131-1139.

Al-Janabi SM, Honeycutt RJ, Mcclelland M, Sobral BWS (1993) A genetic linkage map of *Saccharum spontaneum* L. 'SES 208'. *Genetics,* **134**, 1249-1260.

Alm V, Fang C, Busso CS, Devos KM, Vollan K, Grieg Z, Rognli OA (2003) A linkage map of meadow fescue (*Festuca pratensis* Huds.) and comparative mapping with other Poaceae species. *Theoretical and Applied Genetics,* **108**, 25-40.

Amalraj VA, Balasundaram N (2006) On the taxonomy of the members of ‘Saccharum complex’. *Genetic Resources and Crop Evolution,* **53**, 35-41.

Adati, Adachi S, Shiotani I (1962) The cytotaxonomy of the genus *Miscanthus* and its phylogenetic status. *Bulletin of the Faculty of Agriculture, Mie University,* 1-24.

Atienza SG, Satovic Z, Petersen KK, Dolstra O, Martin A (2002) Preliminary genetic linkage map of *Miscanthus sinensis* with RAPD markers. *Theoretical and Applied Genetics,* **105**, 946-952.

Atienza SG, Satovic Z, Petersen KK, Dolstra O, Martin A (2003a) Identification of QTLs associated with yield and its components in *Miscanthus sinensis* Anderss. *Euphytica,* **132**, 353-361.

Atienza SG, Satovic Z, Petersen KK, Dolstra O, Martin A (2003b) Identification of QTLs influencing agronomic traits in *Miscanthus sinensis* Anderss. I. Total height, flag-leaf height and stem diameter. *Theoretical and Applied Genetics,* **107**, 123-129.

Atienza SG, Satovic Z, Petersen KK, Dolstra O, Martin A (2003c) Identification of QTLs influencing combustion quality in *Miscanthus sinensis* Anderss. II. Chlorine and potassium content. *Theoretical and Applied Genetics*, **107**, 857-863.

Atienza SG, Satovic Z, Petersen KK, Dolstra O, Martin A (2003d) Influencing combustion quality in *Miscanthus sinensis* Anderss.: identification of QTLs for calcium, phosphorus and sulphur content. *Plant Breeding,* **122**, 141-145.

Baird NA, Etter PD, Atwood TS *et al.* (2008) Rapid SNP discovery and genetic mapping using sequenced RAD markers. *Plos One*, **3**(10): e3376. doi:10.1371/journal.pone.0003376.

Barrett B, Baird I, Woodfield D (2009) White clover seed yield: A case study in marker-assisted selection. *Molecular Breeding of Forage and Turf*, 241-250.

Beale CV, Bint DA, Long SP (1996) Leaf photosynthesis in the C4-grass *Miscanthus* × *giganteus,* growing in the cool temperate climate of southern England. *Journal of Experimental Botany,* **47**, 267-273.

Berger J, Suzuki T, Senti K-A, Stubbs J, Schaffner G, Dickson B (2001) Genetic mapping with SNP markers in Drosophila. *Nature Genetics,* **29**, 475-481.

Beavis WD (1994) The power and deceit of QTL experiments: lessons from comparative QTL studies. In: *Proceedings of the Forty-Ninth Annual Corn and Sorghum Industry Research Conference,* 250-266.

Beavis WD (1998) QTL analyses: power, precision, and accuracy. *Molecular dissection of complex traits,* **1998**, 145-162.

Billotte N, Jourjon MF, Marseillac N *et al.* (2010) QTL detection by multi-parent linkage mapping in oil palm (*Elaeis guineensis* Jacq.). *Theoretical and Applied Genetics,* **120**, 1673-1687.

Bonierbale MW, Plaisted RL, Tanksley SD (1988) RFLP maps based on a common set of clones reveal modes of chromosomal evolution in potato and tomato. *Genetics*, **120**, 1095-1103.

Botstein D, White RL, Skolnick M, Davis RW (1980) Constructionof a genetic-linkage map in man using restriction fragment length polymorphisms. *American Journal of Human Genetics,* **32**, 314-331.

Broman KW (2001) Review of statistical methods for QTL mapping in experimental crosses. *Lab animal*, **30**.7

Broman KW, Wu H, Sen S, Churchill GA (2003) R/qtl: QTL mapping in experimental crosses. *Bioinformatics*, **19**, 889-890.

Brookes A (1999) The essence of SNPs. *Gene*, **234**, 177-186.

Burr B, Burr FA, Thompson KH, Albertson MC, Stuber CW (1988) Gene mapping with recombinant inbreds in maize. *Genetics*, **118**, 519-526.

Cai Q, Aitken KS, Fan YH, Piperidis G, Jackson P, Mcintyre CL (2005) A preliminary assessment of the genetic relationship between Erianthus rockii and the "Saccharum complex" using microsatellite (SSR) and AFLP markers. *Plant Science*, **169**, 976-984.

Carbonell E, Asins M, Baselga M, Balansard E, Gerig T (1993) Power studies in the estimation of genetic parameters and the localization of quantitative trait loci for backcross and doubled haploid populations. *Theoretical and Applied Genetics*, **86**, 411-416.

Castonguay Y, Cloutier J, Michaud R, Bertrand A, Laberge S (2009) Development of marker-assisted selection for the improvement of freezing tolerance in alfalfa. *Molecular Breeding of Forage and Turf*, 221-227.

Causse MA, Fulton TM, Cho YG *et al.* (1994) Saturated molecular map of the rice genome based on an interspecific backcross population. *Genetics*, **138**, 1251-1274.

Chae WB, Hong SJ, Gifford JM, Rayburn AL, Widholm JM, Juvik JA (2013) Synthetic polyploid production of *Miscanthus sacchariflorus*, *Miscanthus sinensis,* and *Miscanthus* × *giganteus*. *Global Change Biology Bioenergy,* **5**, 338-350.

Chae WB, Hong SJ, Gifford JM, Rayburn AL, Sacks EJ, Juvik JA (2014) Plant morphology, genome size, and SSR markers differentiate five distinct taxonomic groups among accessions in the genus *Miscanthus*. *Global Change Biology Bioenergy,* **6**, 646-660.

Chen SL, Renvoize SA (2005) A new species and a new combination of *Miscanthus* (Poaceae) from China. *Kew Bulletin*, **60**, 605-607.

Churchill GA, Doerge RW (1994) Empirical threshold values for quantitative trait mapping. *Genetics,* **138**, 963-971.

Clark LV, Brummer JE, Głowacka K *et al.* (2014a) A footprint of past climate change on the diversity and population structure of *Miscanthus sinensis*. *Annals of Botany*, **114**, 97-107.

Clark LV, Stewart JR, Nishiwaki A *et al.* (2014b) Genetic structure of *Miscanthus sinensis* and *M. sacchariflorus* in Japan indicates a gradient of bidirectional but asymmetric introgression. *Journal of Experimental Botany* (in press).

Clayton, WD, Renvoize, SA (1986) Genera Graminum: grasses of the world. Kew Bulletin Additional Series XIII.

Clifton-Brown JC, Stampfl PF, Jones MB (2004) *Miscanthus* biomass production for energy in Europe and its potential contribution to decreasing fossil fuel carbon emissions. *Global Change Biology,* **10**, 509-518.

Clifton-Brown JC, Chiang Y-C, Hodkinson TR (2008) *Miscanthus*: genetic resources and breeding potential to enhance bioenergy production. *Genetic improvement of bioenergy crops. Springer, New York*, 273-294.

Collard BCY, Jahufer MZZ, Brouwer JB, Pang ECK (2005) An introduction to markers, quantitative trait loci (QTL) mapping and marker-assisted selection for crop improvement: The basic concepts. *Euphytica,* **142**, 169-196.

Cordeiro GM, Casu R, Mcintyre CL, Manners JM, Henry RJ (2001) Microsatellite markers from sugarcane (Saccharum spp.) ESTs cross transferable to erianthus and sorghum. *Plant Science,* **160**, 1115-1123.

Davey JL, Blaxter ML (2010) RADSeq: next-generation population genetics. *Briefings in functional genomics,* **9**, 416-423.

Deschamps S, La Rota M, Ratashak JP *et al.* (2010) Rapid genome-wide single nucleotide polymorphism discovery in soybean and rice via deep resequencing of reduced representation libraries with the Illumina genome analyzer. *Plant Genome,* **3**, 53-68.

Devos KM, Gale MD (1997) Comparative genetics in the grasses *Plant Molecular Biology,* **35**, 3-15.

Dohleman FG, Long SP (2009) More productive than maize in the Midwest: how does *Miscanthus* do it? *Plant Physiology,* **150**, 2104-2115.

Doerge RW (2002) Mapping and analysis of quantitative trait loci in experimental populations. *Nature Reviews Genetics,* **3**, 43-52.

Dufour P, Deu M, Grivet L *et al.* (1997) Construction of a composite sorghum genome map and comparison with sugarcane, a related complex polyploid. *Theoretical and Applied Genetics,* **94**, 409-418.

Elshire RJ, Glaubitz JC, Sun Q, Poland JA, Kawamoto K, Buckler ES, Mitchell SE (2011) A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. *Plos One,* **6**(5): e19379. doi:10.1371/journal.pone.0019379.

Engler D, Chen J (2009) Transformation and engineered trait modification in *Miscanthus* species. *World Intellectual Property Organization*.

Falconer DS (1981) Introduction to Quantitative Genetics (2nd edn). Longman, New York.

Falconer DS, Mackay TF, Frankham R (1996) Introduction to Quantitative Genetics (4th edn). *Trends in Genetics,* **12**, 280.

Geldermann H (1975) Investigations on inheritance of quantitative characters in animals by gene markers I. Methods. *Theoretical and Applied Genetics,* **46**, 319-330.

Gifford JM, Chae WB, Swaminathan K, Moose SP, Juvik JA (2014) Mapping the genome of *Miscanthus sinensis* for QTL associated with biomass productivity. *Global Change Biology Bioenergy*.

Głowacka K (2011) A review of the genetic study of the energy crop *Miscanthus*. *Biomass and Bioenergy,* **35**, 2445-2454.

Głowacka K, Kaczmarek Z, Jezowski S (2012) Androgenesis in the bioenergy plant *Miscanthus sinensis*: from calli induction to plant regeneration. *Crop Science,* **52**, 2659-2673.

Głowacka K, Clark LV, Adhikari S *et al.* (2014) Genetic variation in *Miscanthus* × *giganteus* and the importance of estimating genetic distance thresholds for differentiating clones. *Global Change Biology Bioenergy*.

Głowacka K, Adhikari S, Peng J, Gifford J, Juvik JA, Long SP, Sacks EJ (2014) Variation in chilling tolerance for photosynthesis and leaf extension growth among genotypes related to the C_4 grass *Miscanthus* × *giganteus*. *Journal of Experimental Biology,* **65**, 5267-5278.

Gore MA, Chia JM, Elshire RJ *et al.* (2009) A first-generation haplotype map of maize. *Science,* **326**, 1115-1117.

Grattapaglia D, Sederoff R (1994) Genetic mapping of QTLs controlling vegetative propagation in *Eucalyptus grandis* and *E. urophylla* using a pseudo-testcross strategy and RAPD markers. *Genetics*, **137**, 1121-1137.

Greef J, Deuter M (1993) Syntaxonomy of *Miscanthus* × *giganteus* Greef et Deu. *Angewandte Botanik*, **67**, 87-90.

Greef J, Deuter M, Jung C, Schondelmaier J (1997) Genetic diversity of European *Miscanthus* species revealed by AFLP fingerprinting. *Genetic Resources and Crop Evolution*, **44**, 185-195.

Grivet L, Dhont A, Dufour P, Hamon P, Roques D, Glaszmann JC (1994) Comparative genmoe mapping of sugarcane with other species within the Andropogoneae tribe. *Heredity*, **73**, 500-508.

Grivet L, Dhont A, Roques D, Feldmann P, Lanaud C, Glaszmann JC (1996) RFLP mapping in cultivated sugarcane (*Saccharum* spp): Genome organization in a highly polyploid and aneuploid interspecific hybrid. *Genetics*, **142**, 987-1000.

Gupta PK, Roy J, Prasad M (2001) Single nucleotide polymorphisms (SNPs): a new paradigm in molecular marker technology and DNA polymorphism detection with emphasis on their use in plants. *Current Science*, **80**, 524-535.

Gupta PK, Varshney RK, Sharma PC, Ramesh B (1999) Molecular markers and their applications in wheat breeding. *Plant Breeding*, **118**, 369-390.

Haley CS, Knott SA (1992) A simple regression method for mapping quantitative trait loci in line crosses using flanking markers. *Heredity*, **69**, 315-324.

Hamada H, Petrino MG, Kakunaga T (1982) A novel repeated element with Z-DNA-forming potential is widely found in evolutionarily diverse eukaryotic genomes. *Proceedings of the National Academy of Sciences of the United States of America-Biological Sciences*, **79**, 6465-6469.

Heaton EA, Voigt T, Long SP (2004) A quantitative review comparing the yields of two candidate C_4 perennial biomass crops in relation to nitrogen, temperature and water. *Biomass and Bioenergy*, **27**, 21-30.

Heaton EA, Dohleman FG, Long SP (2008) Meeting US biofuel goals with less land: the potential of *Miscanthus*. *Global Change Biology*, **14**, 2000-2014.

Heaton EA, Dohleman FG, Fernando Miguez A *et al.* (2010) *Miscanthus*: a promising biomass crop. *Advances in Botanical Research*, **56**.10

Hirayoshi I, Nishikawa K, Hakura A (1960) Cytogenetical studies on forage plants. VIII. On 3x and 4x hybrids from *Miscanthus sinensis* var. *condensatus* × *M. sacchariflorus*. *Gifu Daigaku Nogakubu Kenkyu Hokoku= Res. Bull. Fac. Agric. Gifu Univ.*, **12**, 82-88.

Hirayoshi I, Nishikawa K, Kubono M, Murase T (1957) Cytogenetical studies on forage plants (VI). On the chromosome number of ogi (*Miscanthus sacchariflorus*). *Res Bull Fac Agric Gifu Univ*, **8**, 8-13.

Hodkinson TR, Chase MW, Lledo MD, Salamin N, Renvoize SA (2002a) Phylogenetics of *Miscanthus, Saccharum* and related genera (Saccharinae, Andropogoneae, Poaceae) based on DNA sequences from ITS nuclear ribosomal DNA and plastid *trnL* intron and *trnL-F* intergenic spacers. *Journal of Plant Research*, **115**, 381-392.

Hodkinson TR, Chase M, Ranvoize S (2002b) Characterization of a genetic resource collection for *Miscanthus* (Saccarinae, Andropogoneae, Poaceae) using AFLP and ISSR PCR. *Annuals of Botany*, **89**, 627-636.

Hodkinson TR, Chase MW, Takahashi C, Leitch IJ, Bennett MD, Renvoize SA (2002c) The use of DNA sequencing (ITS and *trnL-F*), AFLP, and fluorescent in situ hybridization to study allopolyploid *Miscanthus* (Poaceae). *American Journal of Botany*, **89**, 279-286.

Hodkinson TR, Renvoize S, Chase M (1997) Systematics of *Miscanthus*. *Aspects of Applied Biology*, **49**, 189-198.

Hodkinson TR, Renvoize S (2001) Nomenclature of *Miscanthus* × *giganteus* (Poaceae). *Kew Bulletin*, **56**, 759-760.

Hohenlohe PA, Catchen J, Cresko WA (2012) Population genomic analysis of model and nonmodel organisms using sequenced RAD tags. *Methods Mol Biol*, **888**, 235-260.

Holton TA, Christopher JT, Mcclure L, Harker N, Henry RJ (2002) Identification and mapping of polymorphic SSR markers from expressed gene sequences of barley and wheat. *Molecular Breeding*, **9**, 63-71.

Huang N, Angeles ER, Domingo J *et al.* (1997) Pyramiding of bacterial blight resistance genes in rice: marker-assisted selection using RFLP and PCR. *Theoretical and Applied Genetics*, **95**, 313-320.

Hyten D, Cannon S, Song Q *et al.* (2010) High-throughput SNP discovery through deep resequencing of a reduced representation library to anchor and orient scaffolds in the soybean whole genome sequence. *BMC Genomics*, **11**, 38.

Inoue M, Gao ZS, Hirata M, Fujimori M, Cai HW (2004) Construction of a high-density linkage map of Italian ryegrass (*Lolium multiflorum* Lam.) using restriction fragment length polymorphism, amplified fragment length polymorphism, and telomeric repeat associated sequence markers. *Genome*, **47**, 57-65.

Jacob HJ, Lindpaintner K, Lincoln SE *et al.* (1991) Genetic mapping of a gene causing hypertension in the stroke-prone spontaneously hypertensive rat. *Cell*, **67**, 213-224.

Jansen RC (1994) Controlling the Type-I and Type-II errors in mapping quantitative trait loci. *Genetics*, **138**, 871-881.

Jansen RC (2007) Chapter 18- Quantitative trait loci in inbred lines. *Handbook of Statistical Genetics*, 3rd edition. Wiley.

Jensen E, Thomas-Jones S, Farrar K, Clifton-Brown J, Donnison I (2008) Unravelling the genetic control of flowering time in the bioenergy grass Miscanthus. *Comparative Biochemistry and Physiology a-Molecular & Integrative Physiology*, **150**, S181-S181.

Jones E, Mahoney N, Hayward M *et al.* (2002) An enhanced molecular marker based genetic map of perennial ryegrass (Lolium perenne) reveals comparative relationships with other Poaceae genomes. *Genome*, **45**, 282-295.

Jones MB, Walsh M (2001) *Miscanthus for energy and fibre*, James & James, London.

Jones N, Ougham H, Thomas H (1997) Markers and mapping: we are all geneticists now. *New Phytologist*, **137**, 165-177.

Jorgensen U, Muhs HJ (2001) *Miscanthus* breeding and improvement. In: *Jones MB, Walsh M (eds) Miscanthus for energy and fibre*, 68-85.

Joshi SP, Ranjekar PK, Gupta VS (1999) Molecular markers in plant genome analysis. *Current Science*, **77**, 230-240.

Jourjon M (2000) MCQTL: Software For Mapping QTL in simple or composite design. In: *Proceedings of the Plant and Animal Genome Conference VIII, San Diego, California. Available at http://www.intl-pag.org/pag/8/abstracts/pag8060*.

Kao CH, Zeng ZB (1997) General formulas for obtaining the MLEs and the asymptotic variance-covariance matrix in mapping quantitative trait loci when using the EM algorithm. *Biometrics*, 653-665.

Kao CH, Zeng ZB, Teasdale RD (1999) Multiple interval mapping for quantitative trait loci. *Genetics,* **152**, 1203-1216.

Karp A, Seberg O, Buiatti M (1996) Molecular techniques in the assessment of botanical diversity. *Annals of Botany,* **78**, 143-149.

Kilian A, Chen J, Han F, Steffenson B, Kleinhofs A (1997) Towards map-based cloning of the barley stem rust resistance genes *Rpg1* and *rpg4* using rice as an intergenomic cloning vehicle. In: *Oryza: From Molecule to Plant*, Springer, 187-195.

Kim C, Zhang D, Auckland SA *et al.* (2012) SSR-based genetic maps of *Miscanthus sinensis* and *M. sacchariflorus*, and their comparison to sorghum. *Theoretical and Applied Genetics,* **124**, 1325-1338.

Klein PE, Klein RR, Vrebalov J, Mullet JE (2003) Sequence-based alignment of sorghum chromosome 3 and rice chromosome 1 reveals extensive conservation of gene order and one major chromosomal rearrangement. *The Plant Journal,* **34**, 605-621.

Knott SA, Haley CS (1992) Aspects of maximum likelihood methods for the mapping of quantitative trait loci in line crosses. *Genetical Research,* **60**, 139-151.

Kumar L (1999) DNA markers in plant improvement: An overview. *Biotechnology Advances,* **17**, 143-182.

Lander ES, Botstein D (1989) Mapping mendelian factors underlying quantitative traits using RFLP Linkage Maps. *Genetics,* **121**, 185-199.

Lander ES, Altshuler D, Pollara V, Cowles C, Van Etten W, Baldwin J, Linton L (2000) An SNP map of the human genome generated by reduced representation shotgun sequencing. *Nature,* **407**, 513-516.

Lander ES, Linton L, Birren B *et al.* (2001) Initial sequencing and analysis of the human genome. *Nature,* **409**, 860-921.

Lee YN (1993) Manual of the Korean grasses. *Ewha University Press*, Seoul

Lewandowski I, Clifton-Brown JC, Scurlock JMO, Huisman W (2000) *Miscanthus*: European experience with a novel energy crop. *Biomass & Bioenergy,* **19**, 209-227.

Li X, Hu D, Luo MM *et al.* (2013) Nuclear DNA content variation of three *Miscanthus* species in China. *Genes & Genomics,* **35**, 13-20.

Linde-Laursen I (1993) Cytogenetic analysis of *Miscanthus* 'Giganteus', an interspecific hybrid. *Hereditas,* **119**, 297-300.

Litt M, Luty JA (1989) A hypervariable microsatellite revealed by in vitro amplification of a dinucleotide repeat within the cardiac-muscle actin gene. *American Journal of Human Genetics,* **44**, 397-401.

Liu Y, Zeng Z-B (2000) A general mixture model approach for mapping quantitative trait loci from diverse cross designs involving multiple inbred lines. *Genetical Research*, **75**, 345-355.

Ma XF, Jensen E, Alexandrov N *et al.* (2012) High resolution genetic mapping by genome sequencing reveals genome duplication and tetraploid genetic structure of the diploid *Miscanthus sinensis*. *Plos One,* **7**(3): e33821. doi:10.1371/journal.pone.0033821.

Mackinnon M, Weller J (1995) Methodology and accuracy of estimation of quantitative trait loci parameters in a half-sib design using maximum likelihood. *Genetics,* **141**, 755-770.

Mammadov J, Aggarwal R, Buyyarapu R, Kumpatla S (2012) SNP markers and their impact on plant breeding. *International Journal of Plant Genomics,* **2012**, 728398

Mansur LM, Orf JH, Chase K, Jarvik T, Cregan PB, Lark KG (1996) Genetic mapping of agronomic traits using recombinant inbred lines of soybean. *Crop Science,* **36**, 1327-1336.

Matumura M, Hasegawa T, Saijoh Y (1985) Ecological aspects of *Miscanthus sinensis* var. *condensatus*, *M. sacchariflorus*, and their 3x-4x-hybrids, 1: Process of vegetative spread. *Research Bulletin of the Faculty of Agriculture Gifu University*, **50**, 423–433.

Matumura M, Hasegawa T, Saijoh Y (1987) Ecological aspects of *Miscanthus sinensis* var. *condensatus*, *M. sacchariflorus*, and their 3x-4x-hybrids, 3: Aboveground standing crop and response to cutting. *Research Bulletin of the Faculty of Agriculture Gifu University*, **52**, 315–324.

McCouch SR, Chen XL, Panaud O *et al.* (1997) Microsatellite marker development, mapping and applications in rice genetics and breeding. *Plant Molecular Biology,* **35**, 89-99.

McCouch SR (1990). Construction and applications of a molecular linkage map of rice based on restriction fragment length polymorphism (RFLP). Cornell University, Ithaca, New York. (Ph.D. thesis)

Menz MA, Klein RR, Mullet JE, Obert JA, Unruh NC, Klein PE (2002) A high-density genetic map of Sorghum bicolor (L.) Moench based on 2926 AFLP (R), RFLP and SSR markers. *Plant Molecular Biology*, **48**, 483-499.

Miller MR, Dunham JP, Amores A, Cresko WA, Johnson EA (2007) Rapid and cost-effective polymorphism identification and genotyping using restriction site associated DNA (RAD) markers. *Genome Research,* **17**, 240-248.

Ming R, Liu SC, Lin YR *et al.* (1998) Detailed alignment of *Saccharum* and *Sorghum* chromosomes: Comparative organization of closely related diploid and polyploid genomes. *Genetics,* **150**, 1663-1682.

Missaoui AM, Paterson AH, Bouton JH (2005) Investigation of genomic organization in switchgrass (*Panicum virgatum* L.) using DNA markers. *Theoretical and Applied Genetics,* **110**, 1372-1383.

Mohan M, Nair S, Bhagwat A, Krishna TG, Yano M, Bhatia CR, Sasaki T (1997) Genome mapping, molecular markers and marker-assisted selection in crop plants. *Molecular Breeding,* **3**, 87-103.

Moon YH, Cha YL, Choi YH *et al.* (2013) Diversity in ploidy levels and nuclear DNA amounts in Korean *Miscanthus* species. *Euphytica,* **193**, 317-326.

Morgan TH (1910) Sex limited inheritance in *Drosophila*. *Science,* **32**, 120-122.

Mullis K, Faloona F, Scharf S, Saiki R, Horn G, Erlich H (1986) Specific enzymatic amplification of DNA in vitro: the polymerase chain reaction. *Cold Spring Harbor Symposia on Quantitative Biology,* **51**, 263-273.

Muranty H (1996) Power of tests for quantitative trait loci detection using full-sib families in different schemes. *Heredity,* **76**, 156-165.

Naidu SL, Long SP (2004) Potential mechanisms of low-temperature tolerance of C-4 photosynthesis in *Miscanthus* × *giganteus*: an in vivo analysis. *Planta,* **220**, 145-155.

Naidu SL, Moose SP, Al-Shoaibi AK, Raines CA, Long SP (2003) Cold tolerance of C4 photosynthesis in *Miscanthus* × *giganteus*: adaptation in amounts and sequence of C_4 photosynthetic enzymes. *Plant Physiology,* **132**, 1688-1697.

Nair S, Bentur JS, Rao UP, Mohan M (1995) DNA markers tightly linked to a gall midge resistance gene (*Gm2*) are potentially useful for marker-aided selection in rice breeding. *Theoretical and Applied Genetics,* **91**, 68-73.

Nair S, Kumar A, Srivastava MN, Mohan M (1996) PCR-based DNA markers linked to a gall midge resistance gene, *Gm4t*, has potential for marker-aided selection in rice. *Theoretical and Applied Genetics,* **92**, 660-665.

Nakamura Y, Leppert M, Oconnell P *et al.* (1987) Variable number of tandem repeat (VNTR) markers for human-gene mapping. *Science,* **235**, 1616-1622.

Nelson J, Wang S, Wu Y, Li X, Antony G, White F, Yu J (2011) Single-nucleotide polymorphism discovery by high-throughput sequencing in sorghum. *BMC Genomics,* **12**, 352.

Nishiwaki A, Mizuguti A, Kuwabara S *et al.* (2011) Discovery of natural *Miscanthus* (Poaceae) triploid plants in sympatric populations of *Miscanthus saccariflorus* and *Miscanthus sinensis* in southern Japan. *American Journal of Botany,* **98**, 154-159.

Okada M, Lanzatella C, Saha MC, Bouton J, Wu RL, Tobias CM (2010) Complete switchgrass genetic maps reveal subgenome collinearity, preferential pairing and multilocus interactions. *Genetics,* **185**, 745-760.

Paran I, Michelmore RW (1993) Development of reliable PCR-based markers linked to downy mildew resistance genes in lettuce. *Theoretical and Applied Genetics,* **85**, 985-993.

Peterson B, Weber J, Kay E, Fisher H, Hoekstra H, Orlando L (2012) Double digest RADseq: an inexpensive method for *de novo* SNP discovery and genotyping in model and non-model species. *Plos One,* **7**(5): e37135. doi:10.1371/journal.pone.0037135.

Petersen KK, Hagberg P, Kristiansen K, Forkmann G (2002) In vitro chromosome doubling of *Miscanthus sinensis*. *Plant Breeding,* **121**, 445-450.

Poland JA, Brown PJ, Sorrells ME, Jannink JL (2012) Development of high-density genetic maps for barley and wheat using a novel two-enzyme genotyping-by-sequencing approach. *Plos One,* **7**(2): e32253. doi:10.1371/journal.pone.0032253.

Propheter J, Staggenborg S (2010) Performance of annual and perennial biofuel crops: nutrient removal during the first two years. *Agronomy Journal,* **102**, 798-805.

Puente XS, Gutiérrez-Fernández A, Ordóñez GR, Hillier LW, López-Otín C (2005) Comparative genomic analysis of human and chimpanzee proteases. *Genomics,* **86**, 638-647.

Purdy SJ, Maddison AL, Jones LE, Webster RJ, Andralojc J, Donnison I, Clifton-Brown J (2013) Characterization of chilling-shock responses in four genotypes of *Miscanthus* reveals the superior tolerance of *M.* × *giganteus* compared with *M. sinensis* and *M. sacchariflorus*. *Annals of Botany,* **111**, 999-1013.

Rayburn AL, Crawford J, Rayburn C, Juvik J (2009) Genome size of three *Miscanthus* species. *Plant molecular biology reporter,* **27**, 184-188.

Rebai A, Goffinet B (1993) Power of tests for QTL detection using replicated progenies derived from a diallel cross. *Theoretical and Applied Genetics,* **86**, 1014-1022.

Rebai A, Goffinet B (2000) More about quantitative trait locus mapping with diallel designs. *Genetical Research,* **75**, 243-247.

Rebai A, Jourjon M, Goffinet B, Mangin B (1997) QTL mapping in multiple crossing designs using MultiCrossQTL. In: *Advances in Biometrical Genetics: Proceedings of the Tenth Meeting of the EUCARPIA Section Biometrics in Plant Breeding, Poznań, Poland.* pp 225, Institute of Plant Genetics, Polish Academy of Sciences.

Rafalski A (2002) Applications of single nucleotide polymorphisms in crop genetics. *Current Opinion in Plant Biology,* **5**, 94-100.

Rogstad SH (1993) Surveying plant genomes for variable number of tandem repeat loci. *Molecular Evolution: Producing the Biochemical Data,* **224**, 278-294.

Sacks EJ, Juvik JA, Lin Q, Stewart JR, Yamada T (2013) The gene pool of *Miscanthus* species and its improvement. *Genomics of the Saccharinae. New York, Springer*, 73-101.

Sanger F, Nicklen S, Coulson AR (1977) DNA sequencing with chain-terminating inhibitors. *Proceedings of the National Academy of Sciences of the United States of America,* **74**, 5463-5467.

Sax K (1923) The association of size differences with seed-coat pattern and pigmentation in *Phaseolus vulgaris*. *Genetics,* **8**, 552-560.

Semagn K, Da Silva CGM, Montenegro Stamford T, Cardoso De Andrade SA, De Souza E, De Araújo J (2010) Production of ethanol from mesquite (*Prosopis juliflora* (SW) D.C.) pods mash by *Zymomonas mobilis* and *Saccharomyces cerevisiae*. *Electronic Journal of Biotechnology,* **13**(5), 12-13.

Senior ML, Heun M (1993) Mapping maize microsatellites and polymerase chain reaction confirmation of the targeted repeats using a CT primer. *Genome,* **36**, 884-889.

Shouliang C, Renvoize SA (2006) *Miscanthus*. Flora Chin **22**, 581-583.

Singh S, Sidhu JS, Huang N *et al.* (2001) Pyramiding three bacterial blight resistance genes (*xa5* , *xa13* and *Xa21*) using marker-assisted selection into indica rice cultivar PR106. *Theoretical and Applied Genetics,* **102**, 1011-1015.

Smith JSC, Chin ECL, Shu H *et al.* (1997) An evaluation of the utility of SSR loci as molecular markers in maize (*Zea mays* L): comparisons with data from RFLPS and pedigree. *Theoretical and Applied Genetics,* **95**, 163-173.

Soller M, Brody T, Genizi A (1976) On the power of experimental designs for the detection of linkage between marker loci and quantitative loci in crosses between inbred lines. *Theoretical and Applied Genetics,* **47**, 35-39.

Somerville C, Youngs H, Taylor C, Davis SC, Long SP (2010) Feedstocks for lignocellulosic biofuels. *Science,* **329**, 790-792.

Sorrells ME, La Rota M, Bermudez-Kandianis CE *et al.* (2003) Comparative DNA sequence analysis of wheat and rice genomes. *Genome Research,* **13**, 1818-1827.

Staub JE, Serquen FC, Gupta M (1996) Genetic markers, map construction, and their application in plant breeding. *HortScience,* **31**, 729-741.

Stewart JR, Toma Y, Fernandez FG, Nishiwaki A, Yamada T, Bollero G (2009) The ecology and agronomy of *Miscanthus sinensis*, a species important to bioenergy crop development, in its native range in Japan: a review. *Global Change Biology Bioenergy,* **1**, 126-153.

Suh J, Jeung J, Noh T *et al.* (2013) Development of breeding lines with three pyramided resistance genes that confer broad-spectrum bacterial blight resistance and their molecular analysis in rice. *Rice*, **6**, 1-11.

Sun Q, Lin Q, Yi Z, Yang Z, Zhou F (2010) A taxonomic revision of *Miscanthus s.l.* (Poaceae) from China. *Botanical Journal of the Linnean Society,* **164**, 178-220.

Swaminathan K, Chae WB, Mitros T *et al.* (2012) A framework genetic map for *Miscanthus sinensis* from RNAseq-based markers shows recent tetraploidy. *BMC Genomics,* **13**, 142.

Taillon-Miller P, Gu ZJ, Li Q, Hillier L, Kwok PY (1998) Overlapping genomic sequences: A treasure trove of single-nucleotide polymorphisms. *Genome Research,* **8**, 748-754.

Tanksley SD (1983) Molecular markers in plant breeding. *Plant molecular biology reporter,* **1**, 3-8.

Tanksley SD, Miller J, Paterson A, Bernatzky R (1988) Molecular mapping of plant chromosomes. In: Gustafson JP, Appels RA (eds) *Chromosome structure and function, Plenum Press, New York*, 157-173.

Tautz D, Renz M (1984) Simple sequences are ubiquitous repetitive components of eukaryotic genomes. *Nucleic Acids Research*, **12**, 4127-4138.

Thiel T, Michalek W, Varshney RK, Graner A (2003) Exploiting EST databases for the development and characterization of gene-derived SSR-markers in barley (Hordeum vulgare L.). *Theoretical and Applied Genetics*, **106**, 411-422.

Van Ooijen JW (2009) MapQTL® 6. Software for the mapping of quantitative trait loci in experimental populations of diploid species. *Kyazma BV, Wageningen, Netherlands*.

Van Ooijen JW (2011) Multipoint maximum likelihood mapping in a full-sib family of an outbreeding species. *Genetics Research*, **93**, 343-349.

Van Tassell CP, Smith TP, Matukumalli LK *et al.* (2008) SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. *Nature Methods*, **5**, 247-252.

Vodenicharova M (1989) Use of proteins as molecular genetic markers in plants. *Genetics Selection*, **22**, 269-277.

Vos P, Hogers R, Bleeker M *et al.* (1995) AFLP: A new technique for DNA fingerprinting. *Nucleic Acids Research*, **23**, 4407-4414.

Wan Y, Duncan DR, Rayburn AL, Petolino JF, Widholm JM (1991) The use of antimicrotubule herbicides for the production of doubled haploid plants from anther-derived maize callus. *Theoretical and Applied Genetics*, **81**, 205-211.

Wang D, Naidu SL, Portis AR, Moose SP, Long SP (2008) Can the cold tolerance of C4 photosynthesis in *Miscanthus* × *giganteus* relative to *Zea mays* be explained by differences in activities and thermal properties of Rubisco? *Journal of Experimental Botany*, **59**, 1779-1787.

Wang X, Yamada T, Kong FJ *et al.* (2011) Establishment of an efficient in vitro culture and particle bombardment-mediated transformation systems in *Miscanthus sinensis* Anderss., a potential bioenergy crop. *Global Change Biology Bioenergy*, **3**, 322-332.

Weber JL, Myers EW (1997) Human whole-genome shotgun sequencing. *Genome Research*, **7**, 401-409.

Wheeler D, Srinivasan M, Egholm M *et al.* (2008) The complete genome of an individual by massively parallel DNA sequencing. *Nature*, **452**, 872-876.

Weller J (1986) Maximum likelihood techniques for the mapping and analysis of quantitative trait loci with the aid of genetic markers. *Biometrics*, 627-640.

Weller J (1987) Mapping and analysis of quantitative trait loci in Lycopersicon (tomato) with the aid of genetic markers using approximate maximum likelihood methods. *Heredity*, **59**, 413-421

Whitkus R, Doebley J, Lee M (1992) Comparative genome mapping of sorghum and maize. *Genetics*, **132**, 1119-1130.

Williams JGK, Kubelik AR, Livak KJ, Rafalski JA, Tingey SV (1990) DNA polymorphisms amplifed by arbitrary primers are useful as genetic markers. *Nucleic Acids Research*, **18**, 6531-6535.

Winter P, Kahl G (1995) Molecular marker technologies for plant improvement. *World Journal of Microbiology and Biotechnology,* **11**, 438-448.

Xie C, Gessler DD, Xu S (1998) Combining different line crosses for mapping quantitative trait loci using the identical by descent-based variance component method. *Genetics*, **149**, 1139-1146.

Xie WG, Zhang XQ, Cai HW, Huang LK, Peng Y, Ma XA (2011) Genetic maps of SSR and SRAP markers in diploid orchardgrass (*Dactylis glomerata* L.) using the pseudo-testcross strategy. *Genome*, **54**, 212-221.

Xu S (1998) Mapping quantitative trait loci using multiple families of line crosses. *Genetics,* **148**, 517-524.

Xu S (2003) Theoretical basis of the Beavis effect. *Genetics,* **165**, 2259-2268.

Yi N, Xu S (2002) Mapping quantitative trait loci with epistatic effects. *Genetical Research,* **79**, 185-198.

Young N (1996) QTL mapping and quantitative disease resistance in plants. *Annual Review of Phytopathology,* **34**, 479-501.

Yu CY, Kim HS, Rayburn A, Widholm JM, Juvik JA (2009) Chromosome doubling of the bioenergy crop, *Miscanthus* × *giganteus*. *Global Change Biology Bioenergy,* **1**, 404-412.

Yu J, Zhao H, Zhu T, Chen L, Peng J (2013) Transferability of rice SSR markers to *Miscanthus sinensis*, a potential biofuel crop. *Euphytica,* **191**, 455-468.

Zeng ZB (1993) Theoretical basis for separation of multiple linked gene effects in mapping quantitative trait loci. *Proceedings of the National Academy of Sciences of the United States of America*, **90**, 10972-10976.

Zeng ZB (1994) Precision mapping of quantitative trait loci. *Genetics*, **136**, 1457-1468.

Zeng ZB, Kao CH, Basten CJ (1999) Estimating the genetic architecture of quantitative traits. *Genetical Research*, **74**, 279-289.

Zhang KP, Zhao L, Tian JC, Chen GF, Jiang XL, Liu B (2008) A genetic map constructed using a doubled haploid population derived from two elite Chinese common wheat varieties. *Journal of Integrative Plant Biology,* **50**, 941-950.

Zhao H, Yu J, You FM, Luo M, Peng J (2011) Transferability of microsatellite markers from Brachypodium distachyon to Miscanthus sinensis, a potential biomass crop. *Journal of Integrative Plant Biology*, **53**, 232-245.

Zhao X, Kochert G (1993) Phylogenetic distribution and genetic mapping of a (GGC)n microsatellite from rice (*Oryza sativa* L.). *Plant Molecular Biology,* **21**, 607-614.

CHAPTER II: HIGH DENSITY GENETIC MAP OF *MISCANTHUS SINENSIS* REVEALS INHERITANCE OF ZEBRA STRIPE

Abstract

Miscanthus is a perennial C_4 grass that has recently become an important bioenergy crop. The efficiency of breeding improved *Miscanthus* biomass cultivars could be greatly increased by marker-assisted selection. Thus, a high density genetic map is critical to *Miscanthus* improvement. In this study, a mapping population of 261 F_1 progeny was developed from a cross between two diploid *M. sinensis* cultivars, 'Strictus' and 'Kaskasde'. High density genetic maps for the two parents were produced with 3,044 newly developed single nucleotide polymorphisms (SNPs) obtained from restriction-site associated DNA sequencing, and 138 previously mapped GoldenGate SNPs. The female parent ('Strictus') map spanned 1,599 cM, with 1,989 SNPs on 19 linkage groups, and an average inter-marker spacing of 0.8 cM. The length of the male parent ('Kaskade') map was 1,612 cM, with 1,821 SNPs, and an average inter-marker spacing of 0.9 cM. The utility of the map was confirmed by locating quantitative trait loci (QTL) for zebra stripe trait which was segregating in this population. Three QTL for zebra stripe presence/absence (*zb1*, *zb2* on LG 7, and *zb3* on LG 10) and three for zebra stripe intensity (*zbi1*, *zbi2*, *zbi3* on LGs 7, 10, 3) were identified. Each allele that caused striping was recessive. Incomplete penetrance was observed for each *zb* QTL, but penetrance was greatest when two or more *zb* QTL were homozygous for the causative alleles. Similarly, the intensity of striping was greatest when two or more *zbi* QTL were homozygous for alleles that conferred the trait. Comparative mapping indicated putative correspondence between *zb3* and/or *zbi2* on LG 10 to previously sequenced genes conferring zebra stripe in maize and rice. These results demonstrate that the new map is useful for identifying marker-trait associations. The mapped markers will

become a valuable community resource, facilitating comparisons among studies and the breeding of *Miscanthus*.

Introduction

Miscanthus has more than a 100 year history as an ornamental grass in the U.S. (Anonymous, 1876; Bailey & Miller, 1901), with many cultivars currently sold by the horticulture trade, but it has only recently become the subject of modern breeding efforts as a bioenergy feedstock crop (Scurlock, 1999; Clifton-Brown *et al.*, 2004; Somerville *et al.*, 2010; Sacks *et al.*, 2013). *Miscanthus* is a perennial, self-incompatible, C_4 grass that is closely related to sugarcane but can produce high biomass yield in temperate climates, making it a good choice for much of the U.S. (Lewandowski *et al.*, 2000; Clifton-Brown *et al.*, 2008). So far, the most promising *Miscanthus* biofuel candidate for the emerging U.S. bioenergy industry is a single, high-yielding, sterile genotype of *M.* × *giganteus* (2n=3x=57), a nothospecies derived from cross between diploid *M. sinensis* (2n=2x=38) and tetraploid *M. sacchariflorus* (2n=4x=76) (Linde-Laursen, 1993; Hodkinson *et al.*, 2002; Heaton *et al.*, 2008; Głowacka *et al.*, 2014). Dependence on a single clonally propagated genotype for biomass production poses risks because a newly emerged disease or pest strain could result in severe damage to plantings. Moreover, there is need to breed new cultivars with improved cold tolerance and high yield-potential for cold-temperate environments such as the Midwest U.S.

Substantial genetic variation has been found among the two parental species of *M.* × *giganteus*, *M. sinensis* and *M. sacchariflorus* (Jorgensen & Muhs, 2001; Clark *et al.*, 2014; Clark *et al.*, 2015; Głowacka *et al.*, 2014). By choosing parents with desired traits, we expect that superior *Miscanthus* cultivars may be bred. Thus, an understanding of the genetics behind key traits in *Miscanthus* is critical to enabling selection of parents. For many crops, genetic maps have provided a useful tool for identifying associations between traits of interest and molecular markers, and such associations have enabled marker-assisted selection (MAS; Collard & Mackill, 2008). MAS would be especially valuable for increasing the efficiency of breeding *Miscanthus* because phenotypic selection for most of this perennial crop's traits must typically be done in the second and third years of field trials, whereas MAS can be completed on 1-2 month old seedlings before they are transplanted to the field.

Genetic mapping in *Miscanthus* is challenging due to its obligate outcrossing nature that results in high levels of heterozygosity. However, the two-way pseudo-testcross mapping strategy (Grattapaglia & Sederoff, 1994) has provided a useful approach for outcrossing species and has been applied to construct genetic maps in grass species such as sugarcane (*Saccharum spp*.; Al-Janabi *et al.*, 1993; Grivet *et al.*, 1996; Ming *et al.*, 1998), ryegrass (*Lolium spp.*; Inoue *et al.*, 2004) and switchgrass (*Panicum virgatum* L.; Missaoui *et al.*, 2005; Okada *et al.*, 2010). To date, several genetic maps for *Miscanthus* have been published using this approach (Atienza *et al.*, 2002; Kim *et al.*, 2012; Ma *et al.*, 2012; Swaminathan *et al.*, 2012). The first *Miscanthus* genetic map, published by Atienza *et al.* (2002), used 257 randomized amplified polymorphic DNA (RAPD) markers spanning over 28 linkage groups (LGs); however, these maps were incomplete because *Miscanthus* has a basic chromosome number of 19. Moreover, the low reproducibility of RAPD markers would be disadvantageous to applying MAS in breeding, though quantitative trait loci (QTL) mapping was performed with this map (Atienza *et al.*, 2003a, b, c, d). Kim *et al.* (2012) developed simple sequence repeat (SSR)-based genetic maps of *M. sinensis* and *M. sacchariflorus*, which mitigated the low repeatability problem in the initial map, and allowed them to identify a whole genome duplication in *Miscanthus* relative to sorghum. However, the Kim *et al.* (2012) maps remained incomplete (23 LGs detected for *M. sinensis* and 40 LGs for *M. sacchariflorus*). A framework genetic map for *M. sinensis* was recently developed at the University of Illinois, using 658 single nucleotide polymorphism (SNP) markers from

GoldenGate assays and 210 SSR markers derived from sugarcane expressed sequence tags (Swaminathan *et al.*, 2012). This map (Swaminathan *et al.*, 2012) successfully identified all 19 LGs, confirmed the recent genome duplication in *Miscanthus,* revealed substantial synteny between *Miscanthus* and sorghum, and identified the chromosome fusion that resulted in n = 19 for *Miscanthus* from the n = 10 that is typical of the Andropogoneae; however, modest marker density of GoldenGate SNPs was a limitation to QTL mapping and MAS. Moreover, the ascertainment bias of GoldenGate SNPs in Swaminathan *et al.*'s study (2012) limited the usefulness of the markers for other populations. The most marker-dense map for *Miscanthus* published previously, included 3,745 SNP markers on a composite genetic map of *M. sinensis*, obtained from genotyping-by-sequencing (Ma *et al.*, 2012), which also supported the conclusions of genome duplication and synteny with sorghum. However, the methods and markers in Ma *et al.*'s study were proprietary, which prevents others from repeating their work. Thus, a high density genetic map with numerous publicly available SNP markers is needed.

Zebra stripe is a leaf trait characterized by transverse yellow-green or white bands (perpendicular to the leaf axis). Zebra stripe has been observed in many grass species, including maize (*Zea mays* L.), rice (*Oryza sativa* L.), and sorghum [*Sorghum bicolor* (L.) Moench] (Demerec, 1921; Hayes, 1932; Quinby & Karper, 1942; Kinoshita & Takemure, 1984; Kinoshita & Takahashi, 1991). In the ornamental horticulture trade, the alternating pattern of yellow and green is considered desirable, with *M. sinensis* 'Zebrinus' among the first *Miscanthus* genotypes to be imported into the U.S. in the 1870's (Anonymous, 1876). In *Miscanthus*, zebra striped ornamental cultivars differ in the intensity of striping, with the most highly striped cultivars, such as 'Super Stripe' and 'Gold Bar' especially valued. This non-uniform pigment-deficiency has also been observed to be affected by environmental factors such as light, temperature, and the diurnal light/dark cycle, as well as developmental stage (He *et al.*, 1999; Kusumi *et al.*, 2000; Huang *et al.*, 2009; Lu *et al.*, 2012). In maize, three types of zebra striping have been described: zebra striping only in mature plants, zebra striping only in seedlings, and zebra necrosis (Demerec, 1921; Stroman, 1924; Hayes, 1932; Giesbrecht, 1965); all three produce yellow-green transverse stripes on the leaves as a result of the chlorophyll deficiency, but they differ in timing of appearance. In rice, zebra phenotypes can appear in a variety of colors, from pale green, yellow-green, white-green to albino (Kusumi *et al.*, 2000; Zhao *et al.*, 2014). Natural zebra striped mutants have, to the best of our knowledge, not been reported in sorghum but have been induced by X-rays (Quinby & Karper, 1942), with the zebra striped sorghum plants less vigorous than wild type green plants, perhaps due to lower photosynthetic capacity. The incomplete, often temporal, chlorosis in zebra stripe expression provides a valuable opportunity to study the genetics of chlorophyll and plastid development because complete knockout mutations would typically disable photosynthesis and thus be lethal.

Where studied, a single recessive gene model has been proposed for the inheritance of zebra striping, in maize, sorghum and rice (Demerec, 1921; Quinby & Karper, 1942; Wang et al., 2009). Only four genes for zebra stripe, two from maize and two from rice, have been cloned and their function and mechanism understood. A recent map-based cloning study has shown that *zebra crossbands7* (*zb7*) gene in maize encodes 1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate reductase (IspH, also called HDR or LytB), a key enzyme essential for early stage chloroplast development (Lu *et al.*, 2012). Huang *et al.* (2009) characterized maize *camouflage 1* (*cf1*) mutant, which displays a zebra banding pattern of nonclonal yellow-green sectors on the leaves and the yellow sectors can progress to bundle sheath cell-specific death. Huang *et al.* (2009) also cloned the *cf1* gene and determined that it encodes porphobilinogen deaminase, an enzyme in the tetrapyrrole biosynthesis pathway, which is responsible for producing heme and chlorophyll. In rice, *zebra2* (*z2*), the first cloned gene responsible for yellow and green striped leaves, has been shown to encode carotenoid isomerase (CRTISO), which serves a key role in the carotenoid biosynthesis pathway (Fang *et al.*, 2008; Chai *et al.*, 2011; Zhao *et al.*, 2014). Previous studies have reported seven mutations in the CRTISO gene in rice, and all had unique mutation sites but each affected chloroplast development and photoprotection (Fang *et al.*, 2008; Wei *et al.*, 2010; Chai *et al.*, 2011; Han *et al.*, 2012; Liu *et al.*, 2013; Zhao *et al.*, 2014). Map-based cloning of *zebra necrosis* (*zn*) gene in rice revealed that *zn* encodes a thylakoid-bound protein that protects developing chloroplasts from photodamage during early stages of leaf development (Li *et al.*, 2010).

In *M. sinensis*, Touchell *et al.* (2007) studied phenotypic segregation in F_1, F_2 and backcross populations of ‘Strictus’ (yellow striping perpendicular to the leaf axis) × ‘Variegatus’ (white striping parallel with the leaf axis) and concluded that zebra stripe presence/absence from the ‘Strictus’ parent was likely conferred by homozygous recessive alleles at a single locus, though variation in expression of the trait was likely due to other genetic and environmental factors. Until the present study, zebra stripe has not been mapped in *Miscanthus*, though selection by horticulturalists for *Miscanthus* cultivars that differ in zebra stripe intensity may have unintentionally provided grass geneticists with a useful trove of mutants.

In this study, we report on using restriction-site associated DNA sequencing (RAD-seq) to develop high density genetic maps for *M. sinensis*. High-throughput sequencing of RAD tags is a genotyping method that integrates SNP discovery and genotype calling into one step (Baird *et al.*, 2008). RAD-seq has been used to construct high density genetic maps for many crops, such as barley and wheat (Poland *et al.*, 2012), rice (Spindel *et al.*, 2013) and perennial ryegrass

(Pfender *et al.*, 2011). The objectives of this study were: 1) to identify thousands of SNP markers for genotyping *M. sinensis*, 2) to construct high density genetic maps of *M. sinensis* that integrate new SNPs from RAD-seq with the previously mapped but less numerous SNPs from GoldenGate assays, and 3) to confirm the utility of this map by locating QTL for zebra stripe in *Miscanthus*. This high density genetic map for *Miscanthus* provides a community resource, enabling others to reproduce the mapped markers for their own research purposes. Moreover, this map is useful for identifying robust marker-trait associations, which will facilitate genetic improvement of *Miscanthus*.

Materials and methods

Mapping population and growing conditions

A cross between two diploid (2n=2x=38) *M. sinensis* cultivars, 'Strictus' (sourced from Emerald Coast Growers, Pensacola, FL) and 'Kaskade' (sourced from Digging Dog Nursery, Albion, CA) produced 293 individuals that were used in this study. The cross was made in an isolated greenhouse bay at the University of Illinois in 2010 with 'Strictus' as the female parent. To initially confirm the parentage of the progeny, 30 random individuals along with the two parents were screened with 12 SSRs derived from sugarcane expressed sequence tags and intergenic sequences (Swaminathan *et al.*, 2012), and the test result confirmed that 'Strictus' and 'Kaskade' were the true parents of this population. Because *Miscanthus* is self-incompatible, the female parent was not emasculated; however, infrequent progeny from selfing are possible, as the self-incompatibility system has been shown to be leaky (Hirayoshi *et al.*, 1955). Analysis of GoldenGate and RAD-seq SNPs confirmed that 261 of the seedlings were F_1 progeny but 32 seedlings were identified as the product of self-pollination. Typically, *Miscanthus* individuals are highly heterozygous due to self-incompatibility and thus F_1 progeny are expected to segregate for many traits. 'Strictus' was characterized by its yellow zebra striped leaves, whereas the leaves of 'Kaskade' were entirely green.

Seeds were germinated in trays containing a peat-based potting mix (Metro-Mix 900, Sun Gro Horticulture, Agawam, MA; 15-25% Canadian sphagnum peat moss, composted bark, perlite, vermiculite, dolomite lime, and ureaform fertilizer) in a greenhouse. When the seedlings reached sufficient size, each individual was divided into ramets and grown in 36-cell plug trays (PL-36-STAR*, T.O. Plastics, Clearwater, MN) for subsequent planting in a replicated field trial. The field trial was a randomized complete block design with three replications. Plots consisted of single plants on 1.5 m centers. The trial was planted at the University of Illinois' Energy Farm in Urbana, IL (40° 3'57'' N, 88° 11'43'' W; USDA hardiness zone 6) in Flanagan silt loam (fine, smectitc, mesic, Aquic, Argiudolls, 4-5% organic matter) on 9 June 2011. Irrigation was provided on an as-needed basis during the first (establishment) year to prevent drought stress. No supplemental irrigation was provided in subsequent years. In the spring of each year, 100.8 kg N ha^{-1} fertilizer was applied. Pre-emergence and post-emergence herbicides were applied at planting and in the spring of each year (Atrazine, 2.8 kg ha^{-1}; S-metolachlor, 1.5 L ha^{-1}; and 2, 4-D, 1.8 L ha^{-1}), and additional hand-weeding was done as needed.

Marker development and genetic map construction

Genomic DNA was extracted from freeze-dried leaves via a CTAB (cetyltrimethylammonium bromide) protocol adapted from Kabelka *et al.* (2002). Extracted DNA was quantified with a Quant-iT^{TM} dsDNA Picogreen® kit (Life Technologies) and DNA concentration was normalized to 100 ng/ul for GoldenGate™ and RAD-seq analysis. RAD libraries for Illumina sequencing were prepared based on a protocol for sorghum, barley, and wheat (Poland *et al.*, 2012), using 96 barcoded adapter sequences from Thurber *et al.* (2013). In brief, each DNA sample was digested with the rare-cutting enzyme *Pst*I-HF (High-Fidelity; New England Biolabs) and the common-cutting enzyme *Msp*I (New England Biolabs), then ligated to a unique barcoded adapter and a common adapter. Samples were pooled and the 200-500 base pair (bp) size fraction was extracted from a 2% agarose gel after electrophoresis and purified using a Qiagen Gel Extraction Kit. The purified DNA was PCR amplified using Kapa-HF Master Mix (New England Biolabs) and the PCR product was extracted as above to eliminate primer-dimers. All RAD libraries were sequenced on an Illumina HiSeq 2000 with 100 bp single-end reads at the DNA Sequencing Unit of the Roy J. Carver Biotechnology Center at the University of Illinois. Most F_1 individuals from this mapping population were duplicated in a second round of libraries to obtain at least 500,000 read counts per sample, except for 36 individuals with low concentrations (less than 50 ng/ul). Both parents were included in four libraries to obtain high read depth. All sequence data from this study have been deposited in the NCBI Sequence Read Archive (BioProject SRP053003).

To discover SNPs and call genotypes from RAD-seq, we used the Universal Network Enabled Analysis Kit (UNEAK) pipeline in TASSEL (version 3.0 standalone), due to its ability to distinguish heterozygous SNPs from paralogous loci in organisms lacking a reference genome (Lu *et al.*, 2013), especially given the recent genome duplication in *Miscanthus* (Ma *et al.*, 2012; Swaminathan *et al.*, 2012). Additionally, three *M. sinensis* doubled haploid lines (Głowacka *et al.*, 2012; Swaminathan *et al.*, 2012) were used to further distinguish paralogous loci from heterozygous loci. To ensure that genotypes were called accurately, a minimum of five reads was required to call a homozygote for a given SNP if only a single allele was detected for a given individual. If fewer than five reads were present, a missing genotype was assigned to that individual to avoid the possible error of calling a genotype a homozygote when in fact it was a heterozygote.

RAD-seq yielded 1192.6 million sequences reads, with each RAD library of 96 DNA samples yielding close to 200 million reads. With no more than 10% missing genotype calls allowed per SNP, 10,398 SNPs were discovered via the UNEAK pipeline. The average read depth per F_1 individual was 52 read counts per SNP and each parent had 129 read counts per SNP. A total of 672 previously identified GoldenGate SNP markers, including 658 previously mapped SNPs (Swaminathan *et al.*, 2012), were designed in an oligonucleotide pool assay (OPA) on the Illumina website. The 658 SNPs were used to link prior *Miscanthus* genetic maps with the new RAD-seq SNPs maps. The two parents and 76 F_1 individuals were genotyped with this OPA at the Functional Genomic Unit of the Roy J. Carver Biotechnology Center at the University of Illinois. Genotypes were called manually based on signal intensities using Illumina Genome Studio software. Only markers showing clear polymorphism were used in the linkage analysis.

Because heterozygote under-calling was anticipated within parental genotypes, we confirmed RAD-seq SNP genotype of the parents based on the allele frequency distribution in the F_1 population. Specifically, expected allele frequencies (0.25, 0.5, or 0.75) corresponded to segregation ratios that resulted from one of three possible combinations of parental genotypes: 1) the crosses of AA×Aa with 1:1 segregation of AA and Aa progeny, 2) Aa ×Aa with 1:2:1 segregation of AA, Aa and aa progeny, and 3) aa × Aa with 1:1 segregation of Aa and aa progeny. The coding scheme for both RAD-seq SNP and GoldenGate SNP markers followed the cross pollinator (CP) population type in JoinMap4.1 (Van Ooijen, 2011).

Among the 10,398 RAD-seq SNPs identified, 2,229 were eliminated from the data set because they appeared heterozygous in at least one of the three doubled haploid lines evaluated. In addition, 263 SNPs were removed due to missing genotypes in either of the two parents. To maintain the missing rate for each SNP of less than 10% (via fewer than five reads for a given SNP if only a single allele detected), 1,892 SNPs were eliminated, with 6,014 SNPs retained for further filtering. Segregation of each SNP was tested for goodness-of-fit using x^2 values from the Locus Genotype Frequency calculation in JoinMap4.1 to identify departure from expected ratios of 1:1 or 1:2:1 depending on the marker class. SNPs that showed segregation distortion with $P <$ 0.05 were eliminated from map construction. An additional 2,634 SNPs were eliminated due to segregation distortion ($P < 0.05$), with 641 markers from the marker class AA × Aa, 1,265 markers from the marker class aa × Aa, and 737 markers from the marker class Aa × Aa. In all, 3,371 non-distorted SNPs were retained, of which the marker class was compared with the two parental genotypes. Among these 3,371 SNPs, 86% matched their corresponding parental genotypes, and among the mismatched SNPs, 32% can be explained by heterozygote under-calling in the parental genotypes. Thus, a final set of 3,056 RAD-seq SNPs were retained for genetic map construction. Of the 672 SNPs in the GoldenGate assay, 241 were informative (segregated in one or both parents) in our population. After 32 segregation distorted SNPs ($P < 0.05$), and 38 SNPs that had similarity greater than 0.99 were eliminated, 171 GoldenGate SNPs were retained for map construction.

Map construction was based on the 261 F_1 individuals. The set of 3,056 RAD-seq SNPs and 171 GoldenGate SNPs (3,227 total) were separated into three segregation types: 1) 1,399 SNPs heterozygous in 'Strictus', 2) 1,219 SNPs heterozygous in 'Kaskade', and 3) 609 SNPs heterozygous in both parents. Separate maps were produced for the female ('Strictus') and male ('Kaskade') parents. Genetic maps were constructed using JoinMap4.1 with CP population type (Van Ooijen, 2011). A minimum of independence logarithm of odds (LOD) score of 11 was used to define linkage groups. The use of GoldenGate SNPs from a previously published *Miscanthus* genetic map (Swaminathan *et al.*, 2012) allowed for direct identification of linkage groups on the newly developed RAD-seq SNPs map. To ensure markers were assigned to the correct linkage groups, markers in suspect linkages (pairwise recombination frequency estimates larger than 0.6 calculated in JoinMap4.1) were not used for marker ordering, and thus 10 RAD-seq SNP markers and 13 GoldenGate SNPs were eliminated. Maternal and paternal maps were first constructed using the regression mapping algorithm in JoinMap4.1 (Van Ooijen, 2011). Marker orders in both parental maps were calculated using the Kosambi mapping function. A composite map was subsequently generated using the multipoint maximum likelihood mapping algorithm implemented in JoinMap4.1 (Van Ooijen, 2011), and map distance was estimated using the Haldane mapping function.

Phenotyping of zebra stripe and QTL analysis

Two sets of phenotypic data were taken on 2 June 2013: 1) zebra stripe presence/absence, and 2) zebra stripe intensity. Zebra stripe intensity was visually scored with the following scale: 0, 0.05, 0.1, 0.3, 0.5, 0.7, 0.9 (Fig. 1); the two parents were used as controls with the green-leafed parent 'Kaskade' scored as 0, and the highly striped parent 'Strictus' scored as 0.9. The zebra stripe intensity score estimated the relative leaf area that was striped rather than green; it does not refer to any differences in color saturation, or hue of the stripe, which was typically yellow, though late in the season sometimes included brown areas (presumably damage from exposure to full sun over the course of the growing season). Analyses of variance (ANOVAs) were conducted and least squares means (LS-means) were calculated using SAS Procedure GLM (SAS® 9.3, SAS Institute Inc., Cary, NC, USA). Mean separation among genotypic classes was performed using Tukey-Kramer Honest Significant Difference (HSD) test in JMP Genomics Version 7.0 (SAS® 9.3, SAS Institute Inc., Cary, NC, USA).

QTL analysis was performed on the LS-means for both zebra stripe presence/absence and zebra stripe intensity data. Single marker analysis (SMA) was initially conducted using a customized R script, then interval mapping (IM) using Haley-Knott regression algorithm (Lander & Botstein, 1989; Haley & Knott, 1992) was conducted with a step size of 1 cM using R/qtl (Broman *et al.*, 2003); both methods are based on a single-QTL model, which assume a single QTL segregating in each genome scan. Additionally, IM approach assumes the residual variation in the phenotype follows a normal distribution, though regression based interval mapping method is robust against non-normal trait distribution (Rebai, 1997) and application of interval mapping will still provide reasonable results for non-normal traits if the significance threshold was determined via a permutation test (Churchill & Doerge, 1994; Doerge, 2002). Thus, nonparametric interval mapping that uses the Wilcoxon rank-sum test was performed in R/qtl for both zebra stripe presence/absence and intensity given that the residual variation of the phenotype did not follow a normal distribution (Fig. A1); non-parametric results were consistent with the IM method. Subsequently, composite interval mapping (CIM) was conducted (Jansen, 1993; Zeng, 1993; Jansen & Stam, 1994; Zeng, 1994) with the QTL detected by IM via R/qtl. The "addqtl" function was used to search for additional QTL. If a second QTL was detected by CIM, then it was added to the model until no more significant QTL were identified. Finally, multiple-QTL model (MQM) analysis (Zeng *et al.*, 1999), which used an automated stepwise search for model selection, was conducted in R/qtl (Broman *et al.*, 2003). MQM provides a powerful search for additional QTL that is independent of the CIM method by controlling for QTL already in the model. The genome-wide significance threshold ($P < 0.05$) to call QTL was determined based on permutation tests with 1,000 permutations (Churchill & Doerge, 1994). The interaction among QTL was explored using scantwo function in R/qtl, which is based on a two-QTL model, assuming two QTL segregating when searching for QTL (Fig. A2, A3). Significant interactions among QTL were tested in R/qtl after fitting all QTL terms in the model. The position and effect of significant QTL were refined using Haley-Knott regression method and percent variation explained was calculated in R/qtl by fitting a model containing all QTL identified with their interactions if existed. Confidence intervals were calculated using the 1.5-LOD support interval method (Lander & Botstein, 1989; Dupuis & Siegmund, 1999).

Results

Genetic maps

The female and male maps each had the expected 19 LGs but to resolve LG 15 on the male map it was necessary to include 14 segregation distorted markers (P < 0.05). The female map spanned 1,599 cM, with 1,989 markers (102 GoldenGate SNPs and 1,887 RAD-seq SNPs) and an average inter-marker spacing of 0.8 cM (Fig. 2a). There were only two gaps greater than 10 cM on LGs 3 and 9 of the female map, with between marker distances of 16.6 cM and 10.6 cM, respectively. Length of the male parent map was 1,612 cM, with 1,821 markers (90 GoldenGate SNPs and 1,731 RAD-seq SNPs) and an average inter-marker spacing of 0.9 cM (Fig. 2b). Two gaps greater than 10 cM were found on LG 2 and LG 4 of the male map, with between marker distances of 10.9 cM and 14.4 cM, respectively. A composite genetic map was constructed from 3,044 RAD-seq SNPs and 138 GoldenGate SNPs (3,182 total) with all 19 LGs successfully resolved at a minimum LOD score of 11 (Fig. A4).

Phenotypic analysis

Zebra stripe presence/absence segregated approximately 1:1 in the F_1 progeny (138 striped plants: 123 non-striped, $x^2 < x^2_{0.05}$= 3.84; P > 0.05, Fig. A2a), which indicated that inheritance was recessive and suggested a single locus. The 32 individuals that resulted from self-fertilization of the striped female parent, ‘Strictus’, were all striped, further confirming recessive gene action, as a hypothetically heterozygous dominant striped parent would have been expected to produce some non-striped progeny from selfing but this was not observed. Thus, we determined that the striped female parent, ‘Strictus’, was homozygous recessive for the striping trait whereas the non-striped male parent, ‘Kaskade’, carried a recessive allele for striping on at least one locus. QTL mapping for zebra stripe was done entirely on the male parent (‘Kaskade’) map.

QTL mapping for zebra stripe

An initial SMA for zebra stripe presence/absence identified the most significant SNP on LG 7 (Fig. 3a). After accounting for this significant SNP on LG 7 in the model, a significant SNP on LG 10 was detected. When both SNPs on LG 7 and 10 were included in the model, a second significant SNP on LG 7 was identified. Based on a permutation determined LOD threshold, IM using Haley Knott regression algorithm also identified two peaks above threshold on LG 7 and one on 10 for zebra stripe presence/absence (Fig. 3b). However, IM method makes the assumption that only one QTL is segregating when searching for QTL and doesn’t account for QTL elsewhere in the genome. CIM was subsequently applied based on the IM results. After controlling for the major peak on LG 7, a slight increase of the LOD score was observed in the peak of the QTL on LG 10, suggesting that the QTL on LG 10 was real (Fig. 3b). Then, by taking into account both QTL on LG 7 and 10, a small second peak on LG 7 and a peak on LG 14 were observed just above the significance threshold (Fig. 3b), suggesting additional QTL needed to be accounted for. To explore whether or not a second QTL on LG 7 existed, a two-dimensional two-QTL genome scan was conducted on LG 7 while controlling for the QTL on LG 10, and the second QTL on LG 7 was confirmed to be significant (Fig. A2a). Including the second QTL on LG 7 increased the LOD score by 6 if epistasis was allowed and by 4 if no epistasis was allowed (Fig. A2a). After controlling for the two QTL on LG 7 and one on LG 10, the peak on LG 14 disappeared and no more additional QTL appeared to be significant (Fig. 3c), which suggested the three-QTL model for zebra stripe presence/absence was sufficient.

Independent from the CIM method, the automated selection procedure of MQM analysis also identified three significant QTL (*zb1*, *zb2*, and *zb3*) for zebra stripe presence/absence, with two of them (*zb1* and *zb2*) detected on LG 7 at position 51 cM and 36 cM, respectively, and one on LG 10 (*zb3*) at position 4 cM (Fig. 3d,e). A significant interaction between *zb1* and *zb3* was also detected by MQM (Fig. 3d, Fig. A2b). The 1.5-LOD support interval for each QTL extended to a 2 cM, 8 cM and 3 cM region around the point estimates of *zb1*, *zb2*, and *zb3*, respectively (Fig. 2b). An additional interaction term between *zb1* and *zb2* was detected after the model was fitted and therefore was included in the final QTL model. The final three-QTL model for zebra stripe presence/absence explained 63% of the phenotypic variation (Table 1).

For zebra stripe presence/absence, each QTL could independently confer the zebra stripe phenotype but penetrance was not 100%, and it was often low for single loci (Table 2). For example, *zb1* (on LG 7) alone had only 18% penetrance and *zb2* (on LG 7) alone had only 25% penetrance. Moreover, there were significant interactions among some of the QTL and different combinations gave greater penetrance than others (Table 2). For example, the combinations, *zb1* and *zb2*, or *zb1* and *zb3*, or *zb1*, *zb2* and *zb3* had greater than 90% penetrance. In contrast, the combination of *zb2* and *zb3* had 64% penetrance, which although not as high as other combinations, exceeded the penetrance of any single locus.

For zebra stripe intensity, a series of single marker analyses also identified three significant SNPs on the male parent map, with two on LG 7 and one on LG 10 (Fig. 4a). IM identified two peaks above the significance threshold on LG 7 and 10, respectively (Fig. 4b). CIM was subsequently applied based on the IM results and showed an increase of 8 for the LOD score in the peak of the QTL on LG 10, after controlling for the major QTL on LG 7, which strongly suggested that the QTL on LG 10 was real (Fig. 4b). However, after taking into account the QTL on LG 7 and 10, an additional QTL on LG 3 appeared to be significant, and a weak peak on LG 7 exceeded the significance threshold (Fig. 4b). Because the QTL on LG 3 was more significant than the one on LG 7, the QTL on LG 3 was taken into account along with the QTL on LG 7 and 10, and no more additional significant QTL were found, suggesting the weak peak on LG 7 was probably an artifact and the three QTL model was sufficient (Fig. 4c) for zebra stripe intensity. In addition, a significant interaction between QTL on LG 7 and 10 was detected in the two-dimensional two-QTL genome scan (Fig. A3). Consistent with CIM results, MQM analysis identified three significant QTL (*zbi1*, *zbi2*, and *zbi3*) on LG 7 at position 47 cM, LG 10 at position 6 cM, and LG 3 at position 24 cM, respectively (Fig. 4d,e). However, no significant interaction was detected in the MQM automated selection procedure (Fig. 4d). The 1.5-LOD support interval for each QTL extended to a 4 cM, 6 cM and 21 cM region around the point estimates of *zbi1*, *zbi2*, and *zbi3*, respectively (Fig. 2b). The final three-locus model for zebra stripe intensity explained 68% of the phenotypic variation (Table 1). ANOVA results for zebra stripe intensity indicated that only *zbi1* and *zbi2* (on LG 7 and 10) interacted to give a greater intensity than would be expected from additive effects alone, but *zbi3* (on LG 3) was a modifier with only additive effect (Table 3, Fig. 5). The best combination was all three QTL, which gave more than 50% of the leaf area striping (Table 3, Fig. 5).

Discussion

High density genetic map

High density genetic maps for two *M. sinensis* cultivars, “Strictus’ and ‘Kaskade’ were produced with more than 3,000 newly developed RAD-seq SNP markers. We have made these mapped markers available for use by others (Table A1, A2, A3), and we expect that they will become a valuable community resource, enabling comparisons of QTL across populations, environments and studies. Moreover, we linked our RAD-seq SNP maps with the previously published maps of *M. sinensis* ‘Grosse Fountaine’ × *M. sinensis* ‘Undine’ (Swaminathan *et al.*, 2012), and all four maps had similar lengths. The maps developed from the current RAD-seq study will enable detection of markers tightly linked to QTL, which is a first step towards applying MAS and thereby improving breeding efficiency. Given the especially high marker density in some regions of the current maps, and the high degree of synteny between *Miscanthus* and sorghum, it will also be possible to hypothesize causative (candidate) genes underlying traits of interest. In addition, the sequenced and mapped RAD tags in this study will facilitate ongoing efforts to obtain a whole genome assembly of *Miscanthus* by resolving uncertainties in assembling large scaffolds caused by high heterozygosity and the recent genome duplication.

Mapping zebra stripe QTL

To confirm the utility of the new high-density genetic map, we mapped QTL for zebra stripe in *Miscanthus*. Consistent with the study of Touchell *et al.* (2007), we confirmed the recessive inheritance of zebra stripe in *Miscanthus*. However, we identified three loci for both zebra stripe presence/absence (two on LG 7 and one on LG 10) and intensity (one each on LGs 3, 7 and 10), which differed from the Touchell *et al.* (2007) conclusion that a single locus conferred zebra stripe presence/absence, based on the segregation ratio in a ‘Strictus’ (striping perpendicular to the leaf axis) × ‘Variegatus’ (striping parallel with the leaf axis) backcross population. The different QTL mapping methods we employed showed consistent results, indicating strong evidence for the identified QTL (Fig. 3). To further test if the second QTL on LG 7 (*zb2*) was real rather than a false association caused by the heterozygote under-calling of genotypes within *zb2* QTL region, graphical genotypes were evaluated to identify suspect heterozygote under-calls, and modified QTL analyses were conducted using two approaches: 1) eliminate the individuals which had suspected heterozygote under-called genotypes; 2) correct the suspected heterozygote under-called genotypes. The second QTL on LG 7 was still detected as significant using both approaches, which suggested that there were more than one QTL on LG 7 associated with zebra stripe presence/absence.

The apparent discrepancy between the conclusion of Touchell *et al.* (2007) and our QTL analyses can be reconciled by the observations of incomplete penetrance for each of the three zebra stripe presence/absence QTL (Table 2). Without the marker data and the subsequent discovery of incomplete penetrance, phenotypic data alone could also have led us to the erroneous conclusion that only a single locus conferred the trait. Segregation of the F_2 in the Touchell *et al.* (2007) study was also inconsistent with a single recessive locus, as only about half of the expected number of horizontally zebra striped plants were observed. Penetrance for zebra stripe presence/absence was greatest when two or more *zb* QTL were homozygous for the causative alleles (Table 2). Similarly, the intensity of zebra striping was greatest when two or more *zbi* QTL were homozygous for alleles that conferred the trait (Table 3). Notably, two pairs of QTL for presence/absence and intensity on LG 7 (*zb1* and *zbi1*) and on LG 10 (*zb3* and *zbi2*) had overlapping1.5-LOD support intervals (Fig. 2b), so it was not possible to determine if the QTL within each pair were in fact the same locus or tightly linked loci. Though we might expect that individuals with multiple mutations for zebra striping would be rare and at a selective disadvantage in nature, horticulturalists appear to have preferentially selected *Miscanthus* individuals with multiple zebra stripe mutations because their phenotypes were more consistent and more visually striking than single mutants (Fig. 1,5). Lastly, the three-locus models explained 63% and 68% of the total phenotypic variation for zebra stripe presence/absence and intensity, respectively (Table 1), which suggested that other genetic or environmental factors affected zebra striping. Chai *et al.* (2011) and Lu *et al.* (2012) have shown that many of the zebra mutants in maize and rice are temperature and/or light dependent, which would be consistent with our observations of incomplete penetrance of *zb* QTL in *Miscanthus*. Additionally, the average zebra stripe intensity score among the selfed progeny of 'Strictus' was not significantly different from the average score among F_1 progeny with all three homozygous zebra stripe intensity loci, indicating that there was no evidence that the female parent contributed dominant alleles from one or more unmapped zebra stripe loci. Thus, the unexplained phenotypic variation in the current study may have been due to the environment and/or yet to be identified genes.

Comparative mapping

Genes controlling zebra stripe in maize and rice are critical to chlorophyll and/or carotenoid biosynthesis and chloroplast development, which are of fundamental importance for plant growth and crop productivity (Chai *et al.*, 2011; Lu *et al.*, 2012; Zhao *et al.*, 2014). In prior studies, at least 12 genes controlling zebra stripe have been found in maize and 16 have been found in rice (Table 4, S1; Szalma *et al.*, 1999; Hayes, 1938; Singh, 1934; Hayes & Chang, 1939; Lu *et al.*, 2012; Nelson, 1991; Horovitz, 1948; Giesbrecht, 1965; Neuffer & England, 1995; Huang *et al.*, 2009; Zhao *et al.*, 2014; Li *et al.*, 2010). Genomic comparisons among species within the Poaceae have demonstrated that synteny and collinearity are a common feature of this family (Devos & Gale, 1997; Gaut, 2002), and recent comparisons of the *Miscanthus* and sorghum genomes were consistent with this broader finding (Kim *et al.*, 2012; Ma *et al.*, 2012; Swaminathan *et al.*, 2012). Thus, we would expect to find correspondence among loci underlying zebra stripe across *Miscanthus*, maize and rice by using sorghum as a bridge to enable cross-species comparisons between the *Miscanthus*, maize, and rice genomes.

In maize, *zb7* is a recessive mutant of the IspH gene on LG 1 that confers transverse green/yellow striped leaves in young plants (Lu *et al.*, 2012). Intriguingly, the IspH gene on sorghum LG 1 was found to be 0.2 Mb from a RAD tag that mapped to *Miscanthus* LG 10 within 15 cM (or 0.9 % of the 1,612 cM genome) of *zb3* and *zbi2* detected in the present study (Table 4). This finding suggests that *Miscanthus zb3* and/or *zbi2* may be a mutant of IspH or part of a cluster of genes involved in chloroplast development that includes IspH. However, it should be noted that sorghum LG 1 does not typically correspond with *Miscanthus* LG 10 but rather LGs 1 and 2; the closest RAD tags to IspH were on *Miscanthus* LGs 1, 13 and 10 (0.1, 0.1, and 0.2 Mb, respectively), whereas the closest tag on LG 2 was 3.0 Mb distant (Table 4). It is possible that a translocation of this genomic region has occurred in *Miscanthus* with respect to sorghum, or alternatively that the alignment position of this marker was incorrect. Lu *et al.* (2012) found that the maize *zb7* gene has a single nucleotide mutation in a highly conserved region, and gene silencing of IspH results in a complete albino phenotype, indicating that *zb7* is important for chlorophyll development. Lu *et al.* (2012) also noted that the expression of *zb7* is under 16-h light/8-h dark cycle regulation, and low temperature inhibits the mutant expression. This is consistent with our observation in *Miscanthus* that zebra stripe plants usually do not develop transverse yellow bands on the leaves during early spring in central Illinois, and the number and area of the horizontal yellow bands increase later in the season as the temperature becomes warmer and days gets longer (data not shown).

In addition, maize *zb6* gene on LG 4, mapped to sorghum LG 4 between 51 Mb and 57 Mb, which corresponds to *Miscanthus* LG 7 (as expected) within the genomic region that includes the 1.5 support intervals for *zb1*, *zb2* and *zbi1* (Table A4). The finding suggests evidence for co-localization between *Miscanthus zb1*, *zb2*, *zbi1* and maize *zb6* gene, however, this correspondence merits further investigation since maize *zb6* gene has not been fine mapped or cloned.

In rice, *z2* is a zebra stripe gene that was mapped to rice LG 11 (Chai *et al.*, 2011), and the subsequently cloned gene was found to be a mutant of CRTISO, a carotenoid biosynthesis gene. Based on syntenic relationships across rice, sorghum and *Miscanthus*, *z2* was found to be on *Miscanthus* LG 10 (as expected) within 60 cM (or 3.7 % of the 1,612 cM genome) of *Miscanthus zb3* and *zbi2* (Table 4). No other genes mapped in maize or rice were found near any of the identified loci in *Miscanthus*. However, different *Miscanthus* populations may have additional zebra stripe QTL that correspond to some of the other genes mapped in maize and rice. Thus, multiple lines of evidence, including QTL mapping in *Miscanthus,* and cloned genes for zebra stripe in maize and rice, indicate that LG 10 in *Miscanthus* likely has several genes that are important for chlorophyll development, and some alleles of these genes can result in the zebra stripe phenotype.

Leveraging the extensive gene annotations available for sorghum, maize, rice, and *Arabidopsis* (http://www.maizegdb.org; http://www.gramene.org/; The Arabidopsis Information

Resource (TAIR); http://www.phytozome.net/), we also identified candidate genes in genomic regions of these grasses that corresponded to RAD tags in the 1.5-LOD support interval of each *Miscanthus* QTL for zebra stripe presence/absence and intensity (Table A5). In total, 44 genes related to chloroplast development, or chlorophyll biosynthesis were found from sorghum, maize, rice, and *Arabidopsis*, that corresponded to the QTL regions identified in *Miscanthus*. Of these 44 genes, 4 genes were identified in the *zb3* & *zbi2* region on LG 10, 6 in the *zb2* region on LG 7, 1 in the *zb1* & *zbi1* region on LG 7, and 33 in the *zbi3* region on LG 3. Notably, the *zb1* & *zbi1* region harbored a gene in *Arabidopsis* that encodes 2-C-methyl-D-erythritol 2,4-cyclodiphosphate (IspF) synthase, which is an especially promising candidate for zebra stripe because *Arabidopsis* plants defective in this gene display an albino lethal phenotype (Hsieh & Goodman, 2006). Moreover, homologs to the IspF gene in sorghum, maize and rice have a conserved function (Table A5). A similar candidate gene approach using synteny has been employed in fava bean (*Vicia faba* L.) by Khazaei *et al.* (2014) to identify a ribose-phosphate pyrophosphokinase gene from the sequenced model legume, *Medicago truncatula*, as a candidate for QTL underlying canopy temperature under water-deficit.

Some of the QTL for zebra stripe that we found in *Miscanthus* corresponded to genomic regions in maize and rice that have not previously been associated with genes for this trait but which in intriguingly contained genes for chlorophyll, carotenoid and plastid development. At least 32 maize genes associated with photosynthesis were found on maize LG 2 within corresponding *Miscanthus* QTL regions, of which, 5 genes were found in the *zb2* region, 2 genes in the *zb3* & *zbi2* region, and 25 genes in the *zbi3* region (Table A5). In rice, 15 genes associated with photosynthesis were identified on rice LG 9 in the *zbi3* region and 2 were found on rice LG 12 in the *zb3* & *zbi2* region (Table A5). To our best knowledge, there have not been any zebra stripe genes mapped to maize LG 2 or rice LG 9 & 12. Thus, past selection for zebra stripe in *Miscanthus* by horticulturalists has likely provided geneticists and physiologists with novel mutants for studying photosynthesis in the Poaceae. Zebra stripe genes in *Miscanthus*, maize, rice and sorghum offer a valuable research opportunity to elucidate the complex mechanism of photosynthesis and productivity in humanity's most important crops.

References

Anonymous. 1876. The zebra-striped Eulalia. *The American Agriculturalist* **3**, 460

Atienza SG, Satovic Z, Petersen KK, Dolstra O, Martin A (2002) Preliminary genetic linkage map of *Miscanthus sinensis* with RAPD markers. *Theoretical and Applied Genetics,* **105**, 946-952.

Atienza SG, Satovic Z, Petersen KK, Dolstra O, Martin A (2003a) Identification of QTLs associated with yield and its components in *Miscanthus sinensis* Anderss. *Euphytica,* **132**, 353-361.

Atienza SG, Satovic Z, Petersen KK, Dolstra O, Martin A (2003b) Identification of QTLs influencing agronomic traits in *Miscanthus sinensis* Anderss. I. Total height, flag-leaf height and stem diameter. *Theoretical and Applied Genetics,* **107**, 123-129.

Atienza SG, Satovic Z, Petersen KK, Dolstra O, Martin A (2003c) Identification of QTLs influencing combustion quality in *Miscanthus sinensis* Anderss. II. Chlorine and potassium content. *Theoretical and Applied Genetics,* **107**, 857-863.

Atienza SG, Satovic Z, Petersen KK, Dolstra O, Martin A (2003d) Influencing combustion quality in *Miscanthus sinensis* Anderss.: identification of QTLs for calcium, phosphorus and sulphur content. *Plant Breeding,* **122**, 141-145.

Bailey LH, Miller W. 1901. Cyclopedia of American horticulture. *New York: The MacMillan Co.*

Baird NA, Etter PD, Atwood TS *et al.* (2008) Rapid SNP discovery and genetic mapping using sequenced RAD markers. *Plos One,* **3**(10): e3376. doi:10.1371/journal.pone.0003376.

Broman KW, Wu H, Sen S, Churchill GA (2003) R/qtl: QTL mapping in experimental crosses. *Bioinformatics,* **19**, 889-890.

Chai CL, Fang J, Liu Y *et al.* (2011) *ZEBRA2*, encoding a carotenoid isomerase, is involved in photoprotection in rice. *Plant Molecular Biology,* **75**, 211-221.

Churchill GA, Doerge RW (1994) Empirical threshold values for quantitative trait mapping. *Genetics,* **138**, 963-971.

Clark LV, Brummer JE, Głowacka K *et al.* (2014) A footprint of past climate change on the diversity and population structure of *Miscanthus sinensis*. *Annals of Botany,* **114**, 97-107.

Clark LV, Stewart JR, Nishiwaki A *et al.* (2015) Genetic structure of *Miscanthus sinensis* and *M. sacchariflorus* in Japan indicates a gradient of bidirectional but asymmetric introgression. *Journal of Experimental Botany,* (in press).

Clifton-Brown J, Chiang Y-C, Hodkinson TR (2008) *Miscanthus*: genetic resources and breeding potential to enhance bioenergy production. *Genetic improvement of bioenergy crops. Springer, New York*, 273-294.

Clifton-Brown JC, Stampfl PF, Jones MB (2004) *Miscanthus* biomass production for energy in Europe and its potential contribution to decreasing fossil fuel carbon emissions. *Global Change Biology,* **10**, 509-518.

Collard BC, Mackill DJ (2008) Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. *Philosophical Transactions of the Royal Society of London, Series B: Biological Sciences,* **363**, 557-572.

David M. Goodstein, Shengqiang Shu, Russell Howson *et al.* (2012), Phytozome: a comparative platform for green plant genomics, Nucleic Acids Research. 2012 40 (D1): D1178-D1186.

Demerec M (1921) Heritable characters of maize — X. Zebra striped leaves. *The Journal of Heredity,* **12**, 406-407.

Devos KM, Gale MD (1997) Comparative genetics in the grasses *Plant Molecular Biology,* **35**, 3-15.

Doerge RW (2002) Mapping and analysis of quantitative trait loci in experimental populations. *Nature Reviews Genetics,* **3**, 43-52.

Dupuis J, Siegmund D (1999) Statistical methods for mapping quantitative trait loci from a dense set of markers. *Genetics,* **151**, 373-386.

Fang J, Chai C, Qian Q *et al.* (2008) Mutations of genes in synthesis of the carotenoid precursors of ABA lead to pre-harvest sprouting and photo-oxidation in rice. *The Plant Journal,* **54**, 177-189.

Gaut SB (2002) Tansley review no. 132 on evolutionary dynamics of grass genomes *New Phytologist,* **154**, 15-28.

Giesbrecht J (1965) A second zebra-necrotic gene in maize. *The Journal of Heredity,* **56**, 118,130.

Głowacka K, Adhikari S, Peng J, Gifford J, Juvik JA, Long SP, Sacks EJ (2014) Variation in chilling tolerance for photosynthesis and leaf extension growth among genotypes related to the C_4 grass *Miscanthus* x*giganteus*. *Journal of Experimental Biology,* **65**, 5267-5278.

Głowacka K, Clark LV, Adhikari S *et al.* (2014) Genetic variation in *Miscanthus* × *giganteus* and the importance of estimating genetic distance thresholds for differentiating clones. *Global Change Biology Bioenergy*.

Głowacka K, Kaczmarek Z, Jezowski S (2012) Androgenesis in the bioenergy plant *Miscanthus sinensis*: from calli induction to plant regeneration. *Crop Science*, **52**, 2659-2673.

Grattapaglia D, Sederoff R (1994) Genetic mapping of QTLs controlling vegetative propagation in *Eucalyptus grandis* and *E. urophylla* using a pseudo-testcross strategy and RAPD markers. *Genetics,* **137**, 1121-1137.

Grivet L, Dhont A, Roques D, Feldmann P, Lanaud C, Glaszmann JC (1996) RFLP mapping in cultivated sugarcane (*Saccharum* spp): Genome organization in a highly polyploid and aneuploid interspecific hybrid. *Genetics,* **142**, 987-1000.

Haley CS, Knott SA (1992) A simple regression method for mapping quantitative trait loci in line crosses using flanking markers. *Heredity,* **69**, 315-324.

Han SH, Sakuraba Y, Koh HJ, Paek NC (2012) Leaf variegation in the rice *zebra2* mutant is caused by photoperiodic accumulation of tetra-cis-lycopene and singlet oxygen. *Mol Cells,* **33**, 87-97.

Hayes HK (1932) Heritable characters in maize XLIII — Zebra seedlings *The Journal of Heredity*.

Hayes HK (1938) Zebra seedling, *zb4*, has been located in chromosome 1 by the following studies. *Maize Genetics Cooperation Newsletter*, **12**: 1.

Hayes HK, Chang MS (1939) Recent linkage studies in maize. II. Zebra-striped 6 (*zb6*). *Genetics*, 24: 60.

He R, Ding Y, Yu J, Gao W (1999) The changes of chlorophyll content and several enzyme activities in zebra-leaf rice. *Journal of Wuhan University (Natural Science Edition),* **46**, 761-765.

Heaton EA, Dohleman FG, Long SP (2008) Meeting US biofuel goals with less land: the potential of *Miscanthus*. *Global Change Biology,* **14**, 2000-2014.

Hirayoshi I, Nishikawa K, Kato R (1955) Cytogenetical studies on forage plants. (IV) Self-incompatibility in *Miscanthus*. *Japanese Journal of Breeding,* **5**, 167-170.

Hodkinson TR, Chase MW, Takahashi C, Leitch IJ, Bennett MD, Renvoize SA (2002) The use of DNA sequencing (ITS and trnL-F), AFLP, and fluorescent in situ hybridization to study allopolyploid *Miscanthus* (Poaceae). *American Journal of Botany*, **89**, 279-286.

Horovitz S (1948) Zebra-necrosis. Maize *Genetics Cooperation Newsletter*, **22**: 42-43.

Hsieh MH, Goodman HM (2006) Functional evidence for the involvement of *Arabidopsis* IspF homolog in the nonmevalonate pathway of plastid isoprenoid biosynthesis. *Planta,* **223**, 779-784.

Huang M, Slewinski TL, Baker RF, Janick-Buckner D, Buckner B, Johal GS, Braun DM (2009) Camouflage patterning in maize leaves results from a defect in porphobilinogen deaminase. *Molecular Plant*, **2**, 773-789.

Inoue M, Gao ZS, Hirata M, Fujimori M, Cai HW (2004) Construction of a high-density linkage map of Italian ryegrass (*Lolium multiflorum* Lam.) using restriction fragment length polymorphism, amplified fragment length polymorphism, and telomeric repeat associated sequence markers. *Genome,* **47**, 57-65.

Jansen RC (1993) Interval mapping of multiple quantitative trait loci. *Genetics*, **135**, 205-211.

Jansen RC, Stam P (1994) High-resolution of quantitative traits into multiple loci via interval mapping. *Genetics,* **136**, 1447-1455.

Jorgensen U, Muhs HJ (2001) *Miscanthus* breeding and improvement. *In: Jones MB, Walsh M (eds) Miscanthus for energy and fibre*, 68-85.

Kabelka E, Franchino B, Francis DM (2002) Two loci from *Lycopersicon hirsutum* LA407 confer resistance to strains of *Clavibacter michiganensis* subsp *michiganensis*. *Phytopathology,* **92**, 504-510.

Khazaei H, O'sullivan DM, Sillanpaa MJ, Stoddard FL (2014) Use of synteny to identify candidate genes underlying QTL controlling stomatal traits in faba bean (*Vicia faba* L.). *Theoretical and Applied Genetics,* **127**, 2371-2385.

Kim C, Zhang D, Auckland SA *et al.* (2012) SSR-based genetic maps of *Miscanthus sinensis* and *M. sacchariflorus*, and their comparison to sorghum. *Theoretical and Applied Genetics,* **124**, 1325-1338.

Kinoshita T, Takahashi M-E (1991) The one hundredth report of genetical studies on rice plant: Linkage studies and future prospects. *Journal of the Faculty of Agriculture, Hokkaido University= 北海道大學農學部紀要,* **65**, 1-61.

Kinoshita T, Takemure I (1984) Inheritance and linkage relationship on zebra chlorosis and zebra necrosis in rice. Genetical Studies on Rice Plant. *LXXXVIII. Journal of the Faculty of Agriculture, Hokkaido University = 北海道大學農學部紀要*, **61**, 445-455.

Kusumi K, Komori H, Satoh H, Iba K (2000) Characterization of a zebra mutant of rice with increased susceptibility to light stress. *Plant Cell Physiology,* **41**(2), 158-164.

Lander ES, Botstein D (1989) Mapping mendelian factors underlying quantitative traits using RFLP Linkage Maps. *Genetics,* **121**, 185-199.

Lewandowski I, Clifton-Brown JC, Scurlock JMO, Huisman W (2000) *Miscanthus*: European experience with a novel energy crop. *Biomass & Bioenergy,* **19**, 209-227.

Li J, Pandeya D, Nath K *et al.* (2010) ZEBRA-NECROSIS, a thylakoid-bound protein, is critical for the photoprotection of developing chloroplasts during early leaf development. *The Plant Journal,* **62**, 713-725.

Linde-Laursen I (1993) Cytogenetic analysis of *Miscanthus* 'Giganteus', an interspecific hybrid. *Hereditas,* **119**, 297-300.

Liu S, Wei X, Shao G, Tang S, Hu P (2013) Map based cloning of a ‘Zebra’leaf mutant gene *zl2* in Rice. *Chinese Journal of Rice Science (Chinese Version),* **27**, 231-239.

Lu F, Lipka AE, Glaubitz J *et al.* (2013) Switchgrass genomic diversity, ploidy, and evolution: novel insights from a network-based SNP discovery protocol. *PLoS Genetics,* **9**, e1003215.

Lu XM, Hu XJ, Zhao YZ *et al.* (2012) Map-Based Cloning of *zb7* Encoding an IPP and DMAPP Synthase in the MEP Pathway of Maize. *Molecular Plant,* **5**, 1100-1112.

Ma XF, Jensen E, Alexandrov N *et al.* (2012) High resolution genetic mapping by genome sequencing reveals genome duplication and tetraploid genetic structure of the diploid *Miscanthus sinensis*. *Plos One,* **7**(3): e33821. doi:10.1371/journal.pone.0033821.

Monaco MK, Sen TZ, Dharmawardhana PD *et al.* (2013) Maize metabolic network construction and transcriptome analysis. *The plant genome,* **6**(1).

Ming R, Liu SC, Lin YR *et al.* (1998) Detailed alignment of *Saccharum* and *Sorghum* chromosomes: Comparative organization of closely related diploid and polyploid genomes. *Genetics,* **150**, 1663-1682.

Missaoui AM, Paterson AH, Bouton JH (2005) Investigation of genomic organization in switchgrass (*Panicum virgatum* L.) using DNA markers. *Theoretical and Applied Genetics,* **110**, 1372-1383.

Monaco MK, Stein J, Naithani S, Wei S *et al.* (2014). Gramene 2013: comparative plant genomics resources. Nucleic Acids Research. 42 (D1): D1193-D1199. PMID:24217918.

Nelson OE Jr (1991) Locations of new mutations on 9S. *Maize Genetics Cooperation Newsletter,* **65**, 86.

Neuffer MG, England DJ (1995) Induced mutations with confirmed locations. *Maize Genetics Cooperation Newsletter*, **69**, 43-46.

Okada M, Lanzatella C, Saha MC, Bouton J, Wu RL, Tobias CM (2010) Complete switchgrass genetic maps reveal subgenome collinearity, preferential pairing and multilocus interactions. *Genetics,* **185**, 745-760.

Pfender WF, Saha MC, Johnson EA, Slabaugh MB (2011) Mapping with RAD (restriction-site associated DNA) markers to rapidly identify QTL for stem rust resistance in *Lolium perenne*. *Theoretical and Applied Genetics,* **122**, 1467-1480.

Poland JA, Brown PJ, Sorrells ME, Jannink JL (2012) Development of high-density genetic maps for barley and wheat using a novel two-enzyme genotyping-by-sequencing approach. *Plos One*, **7**(2): e32253. doi:10.1371/journal.pone.0032253.

Quinby JR, Karper RE (1942) Inheritance of mature plant characters in sorghum induced by radiation. *The Journal of Heredity,* 323-327.

Rebai A (1997) Comparison of methods for regression interval mapping in QTL analysis with non-normal traits. *Genetical Research,* **69**, 69-74.

Sacks EJ, Juvik JA, Lin Q, Stewart JR, Yamada T (2013) The gene pool of *Miscanthus* species and its improvement. *Genomics of the Saccharinae. New York, Springer,* 73-101.

Scurlock J (1999) *Miscanthus*: A review of European experience with a novel energy crop. pp26, Oak Ridge National Laboratory, Oak Ridge, TN (US).

Singh, S (1934) Zebra5 (*zb5*) which shows in seedlings as a virescent and in mature plants as a zebra stripe (transverse bands of green and yellow tissue) shows no crossing over with *d7*. *Maize Genetics Cooperation Newsletter,* **8**, 1.

Somerville C, Youngs H, Taylor C, Davis SC, Long SP (2010) Feedstocks for lignocellulosic biofuels. *Science,* **329**, 790-792.

Spindel J, Wright M, Chen C *et al.* (2013) Bridging the genotyping gap: using genotyping by sequencing (GBS) to add high-density SNP markers and new value to traditional bi-parental mapping and breeding populations. *Theoretical and Applied Genetics*, **126**, 2699-2716.

Stroman GN (1924) The inheritance of certain chlorophyll characters in maize *Genetics*, **9**, 493-511.

Swaminathan K, Chae WB, Mitros T *et al.* (2012) A framework genetic map for *Miscanthus sinensis* from RNAseq-based markers shows recent tetraploidy. *BMC Genomics*, **13**, 142.

Szalma S., Stinard P.S., Cone, K.C. (1999) Allelic relationships among the zebra mutants in the Coop's *zb1*, *zb2*, and *zb3* stocks. *Maize Genetics Cooperation Newletter*, **73**, 23.

The Arabidopsis Information Resource (TAIR): improved gene annotation and new tools. Nucleic Acids Research 2011 doi: 10.1093/nar/gkr1090.

Thurber CS, Ma JM, Higgins RH, Brown PJ (2013) Retrospective genomic analysis of sorghum adaptation to temperate-zone grain production. *Genome Biology*, **14**, R68.

Touchell D, Smith J, Ranney T (2007) Inheritance of leaf variegations in *Miscanthus*. *Southern Nursery Association Research Conference*, **52**, 349-351.

Van Ooijen JW (2011) Multipoint maximum likelihood mapping in a full-sib family of an outbreeding species. *Genetics Research*, **93**, 343-349.

Wang Q, Sang X, Ling Y, Zhao F, Yang Z, Li Y, He G (2009) Genetic analysis and molecular mapping of a novel gene for zebra mutation in rice (*Oryza sativa* L.). *Journal of Genetics and Genomics*, **36**, 679-684.

Wei J, Xu M, Zhang D, Mi H (2010) The role of carotenoid isomerase in maintenance of photosynthetic oxygen evolution in rice plant. *Acta Biochim Biophys Sin (Shanghai)*, **42**, 457-463.

Zeng ZB (1993) Theoretical basis for separation of multiple linked gene effects in mapping quantitative trait loci. *Proceedings of the National Academy of Sciences of the United States of America*, **90**, 10972-10976.

Zeng ZB (1994) Precision mapping of quantitative trait loci. *Genetics*, **136**, 1457-1468.

Zeng ZB, Kao CH, Basten CJ (1999) Estimating the genetic architecture of quantitative traits. *Genetical Research*, **74**, 279-289.

Zhao J, Fang Y, Kang S *et al.* (2014) Identification and characterization of a new allele for *ZEBRA LEAF 2*, a gene encoding carotenoid isomerase in rice. *South African Journal of Botany*, **95**, 102-111.

TABLES AND FIGURES

Table 1 Quantitative trait loci (QTL) identified for *Miscanthus* zebra stripe presence/absence and intensity.

Trait	**QTL**[*]	**LG**[†]	**QTL peak (cM)**	**Closest marker to QTL peak**	**1.5-LOD support interval (cM)**		**Flanking markers**		**LOD**	**PVE**[‡]
					Left border	Right border	Left	Right		
Zebra stripe presence/absence	*zb1*	7	51.0	TP107979	50.0	52.0	X83	TP107979	19.5	19.8
	zb2	7	36.0	TP78983	34.0	42.0	TP47894	TP57806	4.9	6.9
	zb3	10	4.0	TP74459	2.0	5.0	TP79286	TP65474	22.3	18.6
	zb1: *zb2*								4.8	3.3
	zb1: *zb3*								12.6	9.2
	*zb*_Model									63.0
Zebra stripe intensity	*zbi1*	7	47.0	X83	46.0	50.0	TP28957	TP107979	26.7	45.5
	zbi2	10	6.0	TP65474	3.0	9.0	TP74459	TP4584	27.4	47.3
	zbi3	3	24.4	TP75257	7.0	28.0	TP43225	TP25237	7.0	8.3
	zbi1: *zbi2*								10.8	13.8
	*zbi*_Model									68.3

[*] The numbering of QTL was based on the linkage group number first, and then LOD score from largest to smallest.

[†] Linkage group.

[‡] Percent variation explained calculated from the drop-one-QTL-at-a-time ANOVA analyses (at α = 0.05) in R/qtl.

Table 2 Number of striped and non-striped F_1 progeny of *Miscanthus sinensis* 'Strictus' × 'Kaskade', and penetrance (proportion) within each genotypic class[†] among three loci[††] for zebra stripe presence/absence (*zb1*, *zb2*, and *zb3*).

			zb1 zb2			
			1 1	2 1	1 2	2 2
zb3	1	Striped[‡] (count)	0	2	3	39
		Non-striped[‡] (count)	58	9	9	2
		Penetrance[§] (Prpn)		0.18cd	0.25bcd	0.95a*
	2	Striped (count)	28	10	7	46
		Non-striped (count)	30	1	4	2
		Penetrance (Prpn)	0.48bc	0.91a***	0.64ab	0.96a

[†] Genotypic classes: 1 = heterozygous; 2 = homozygous recessive.

[††] *zb1*, *zb2* are on linkage group 7, and *zb3* is on linkage group 10.

[‡] Counts based on nearest markers to the QTL.

[§] Penetrance estimated as number of striped F_1 progeny divided by total number of F_1 progeny within each genotypic class. Means separation by Tukey-Kramer HSD; means with the same letter were not significantly different. Interaction between QTL indicated, where *, **, *** = significant at $P = 0.05$, 0.01, or 0.001, respectively.

Table 3 Average zebra stripe intensity score, standard error and sample size (n) for F_1 progeny *Miscanthus sinensis* 'Strictus' × 'Kaskade' within each genotypic class[†] among three loci[††] for zebra stripe intensity (*zbi1*, *zbi2*, and *zbi3*).

			zbi1 zbi2			
			1 1	2 1	1 2	2 2
zbi3	1	Average score[‡]	0.09bc	0.12c	0.10c	0.38b*
		Standard error	0.01	0.02	0.02	0.04
		n	2	14	19	26
	2	Average score	0.10bc	0.24bc	0.14c	0.56a
		Standard error	0.00	0.05	0.03	0.04
		n	3	24	15	29

[†] Genotypic classes: 1 = heterozygous; 2 = homozygous recessive.

[††] *zbi1*, *zbi2*, *zbi3* are on linkage groups 7, 10, and 3, respectively.

[‡] Means separation by Tukey-Kramer HSD; means with the same letter were not significantly different. Interaction between QTL indicated, where *, **, *** = significant at $P = 0.05$, 0.01, or 0.001, respectively.

Table 4 Cloned zebra stripe genes in maize and rice, and their corresponding orthologous regions in *Miscanthus*.

Gene name	Gene symbol	Species	Linkage group for the species in which gene was identified	Orthologous region(s) in sorghum based on sorghum physical map		Expected linkage groups in *Miscanthus* based on Swaminathan *et al.* (2012)	The three markers that that were nearest to the zebra stripe gene in sorghum and mapped in *Miscanthus* (*Miscanthus* LG[*] shown)			
				LG	Range (Mb)		LG	Marker	Distance to gene[†] (Mb)	Distance to QTL[‡] (cM)
zebra crossbands7	*zb7*	*Zea*	1_long arm	1	7.894-7.897	1	13	TP42765	0.100	
						2	1	TP94641	0.132	
							10	TP54034	0.236	13.2 (*zb3*) 11.2 (*zbi2*)
camouflage1	*cf1*	*Zea*	5_short arm	4	4.443-4.447	7	8	TP105102	0.064	
						8	1	TP122214	0.067	
							8	TP40456	0.084	
zebra2	*z2*	*Oryza*	11	5	53.890-53.895	9	10	TP27302	0.001	57.9 (*zb3*) 55.9 (*zbi2*)
						10	9	TP20195	0.496	
							9	TP112083	0.684	
zebra necrosis	*zn*	*Oryza*	6	10	1.129-1.131	18	19	TP742	0.013	
						19	18	TP86555	0.050	
							19	TP90066	0.263	

[*] Linkage group.

[†] Physical distance of marker to the zebra stripe gene in sorghum was calculated based on the marker position in sorghum to the mid-point of the corresponding genomic region of the gene in sorghum.

[‡] Genetic distance of marker to the *Miscanthus* QTL if the marker was found on the same linkage group where QTL was located.

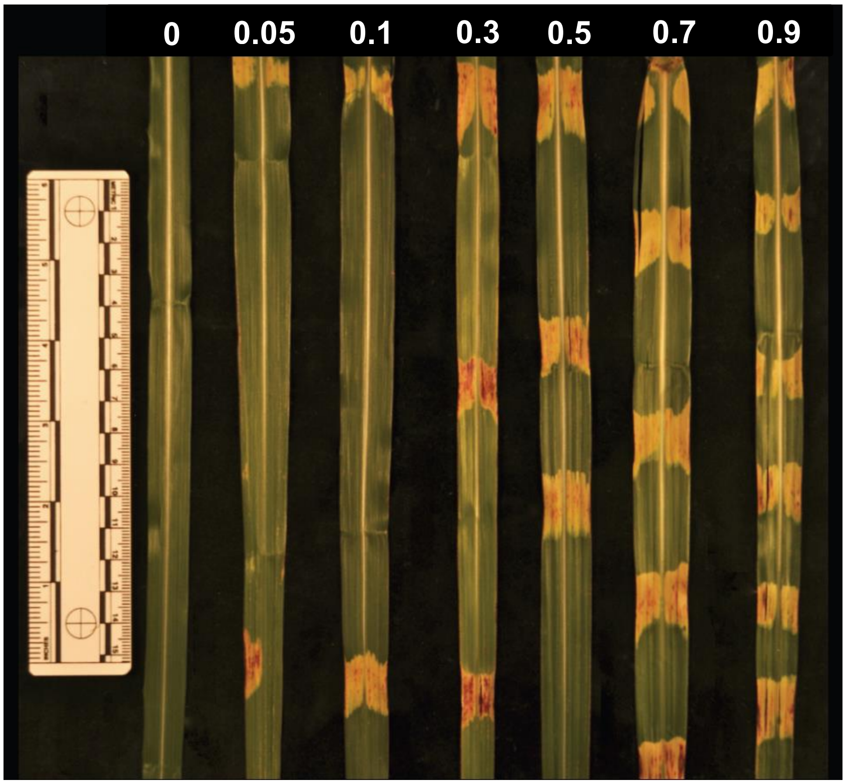

Fig. 1 Zebra stripe intensity scale in *Miscanthus sinensis*. The score was visually rated based on the relative leaf area that was striped rather than green.

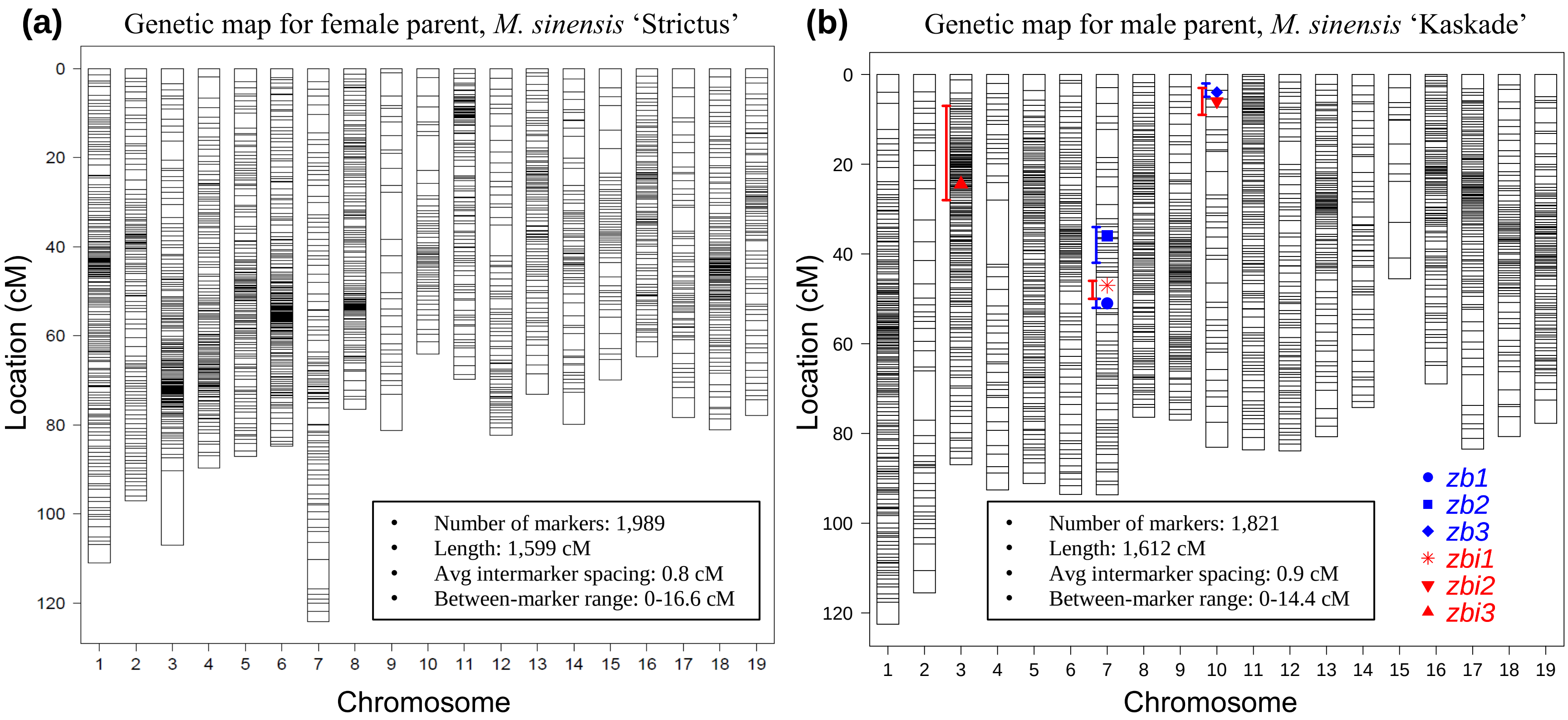

Fig. 2 Genetic maps for two *Miscanthus sinensis* genotypes: (a) the female parent, 'Strictus', (b) the male parent, 'Kaskade', and the locations of QTL for zebra stripe presence/absence (*zb*) and intensity (*zbi*). QTL mapping for zebra stripe was done entirely on the male parent ('Kaskade') map because this parent had heterozygous zebra stripe loci whereas the female parent ('Strictus') had only homozygous loci for zebra stripe. Genetic distance is shown on the left in centiMorgans (cM). Linkage group numbers, based on the genetic map from Swaminathan *et al.* (2012), are shown at the bottom. Horizontal lines represent estimated positions of the genetic markers, and red and blue symbols represent the peak LOD scores of QTL for presence/absence and intensity, respectively. The numbering of QTL was based on the linkage group number first, and then LOD score from largest to smallest. Bars indicate the 1.5-LOD support interval.

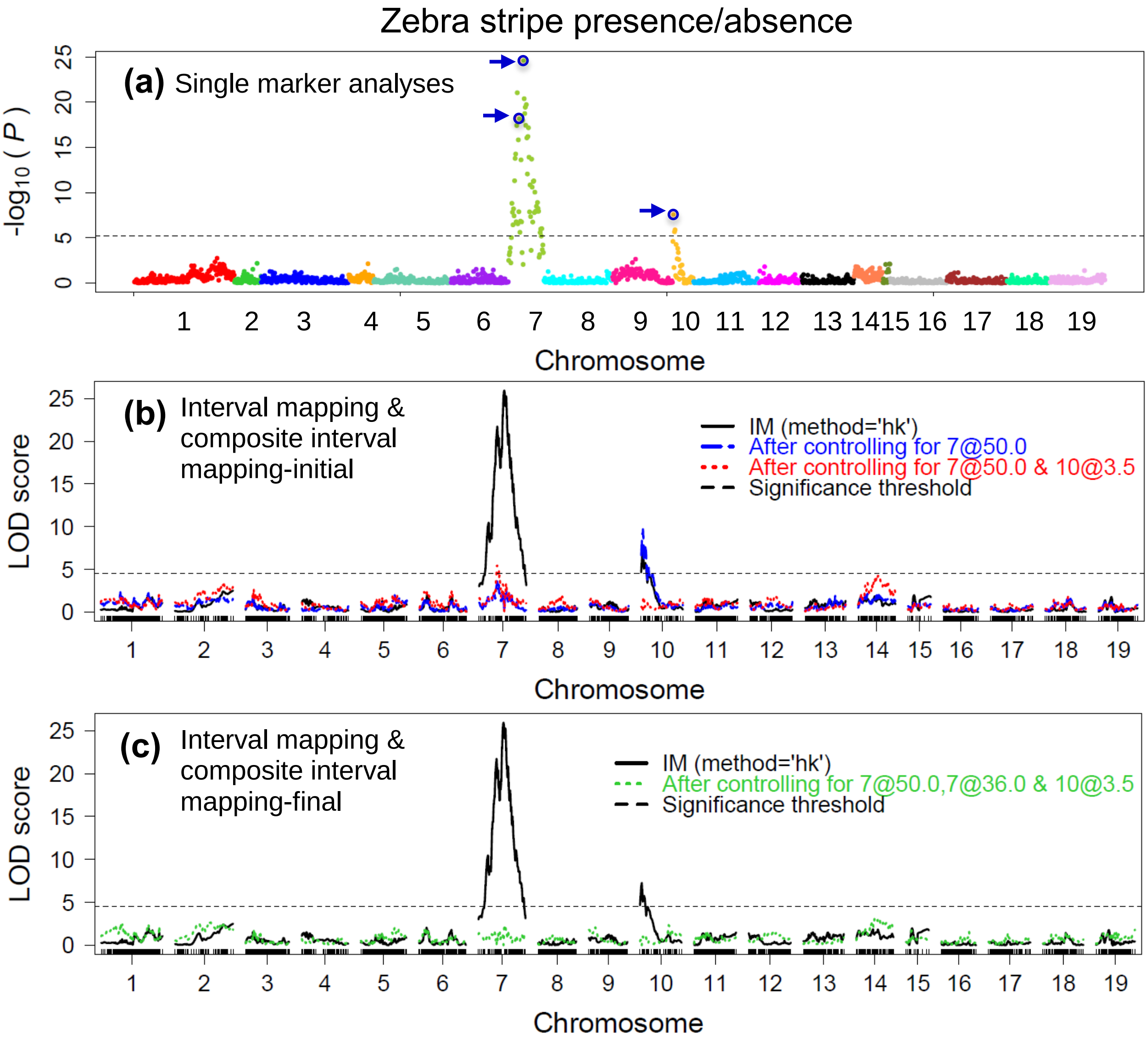

Fig. 3 QTL results for zebra stripe presence/absence in a *Miscanthus sinensis* 'Strictus' × *M. sinensis* 'Kaskade' population: (a) Manhattan plot of single marker analysis. Each of the 1,821 SNPs is plotted. The x-axis represents the chromosomal location on the male parent map, and the y-axis represents the -log10 *P* values in the first round of single marker analysis. The horizontal dotted line represents the Bonferroni-corrected *P* value significance threshold via 1,000 permutations. The arrows indicate significant SNPs associated with zebra stripe presence/absence, which were detected in three rounds of single marker analyses after controlling for the significant SNPs the previous rounds. (b, c) LOD curves from interval mapping (IM) and composite interval mapping (CIM) methods, controlling for the first two QTL in (b), and all three QTL in (c). The horizontal dotted line represents the significance threshold via 1,000 permutations.

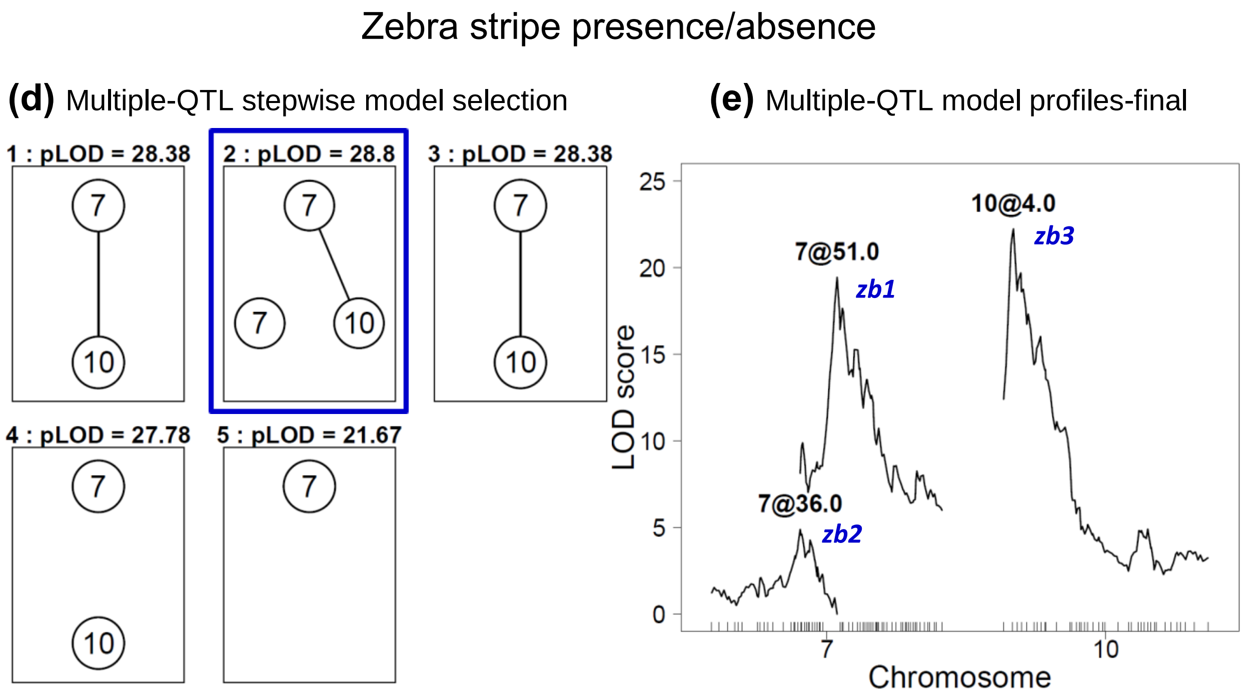

Fig. 3 (cont.) (d) The sequence of models tested by the automated stepwise procedure in multiple-QTL model (MQM), with circles corresponding to QTL (chromosome number indicated within circles) and line segments between QTL indicating interactions. The best model was identified at step 2 with the largest penalized LOD score (pLOD). (e) Profile LOD score curves for a three-QTL model for zebra stripe presence/absence. The numbering of QTL was based on the linkage group number first, and then LOD score from largest to smallest.

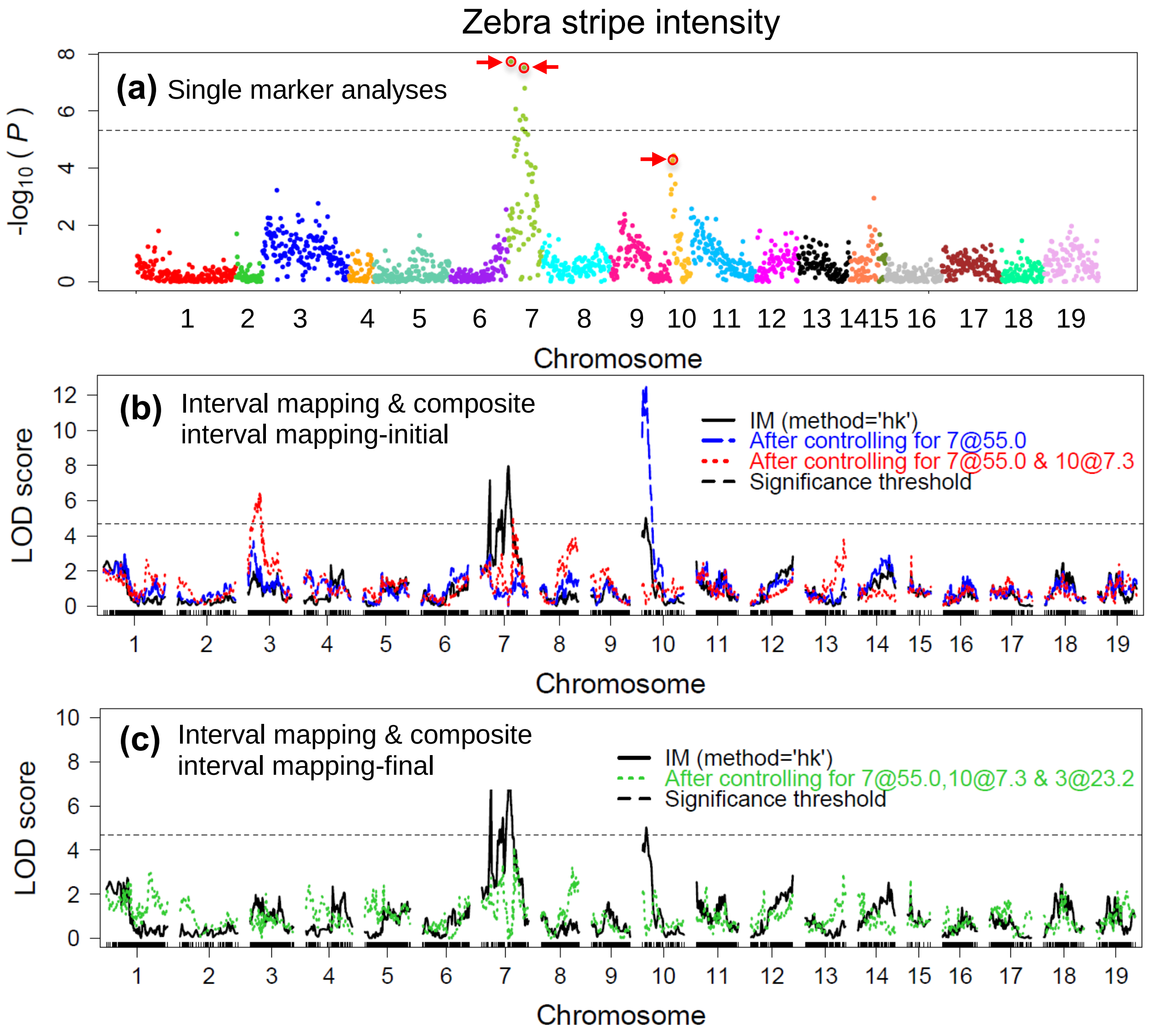

Fig. 4 QTL results for zebra stripe intensity in a *Miscanthus sinensis* 'Strictus' × *M. sinensis* 'Kaskade' population: (a) Manhattan plot of single marker association analysis. Each of the 1,821 SNPs is plotted. The x-axis represents the chromosomal location on the male parent map, and the y-axis represents the -log10 *P* values. The horizontal dotted line represents the Bonferroni-corrected *P* value significance threshold via 1,000 permutations. The arrows indicate significant SNPs associated with zebra stripe intensity, which were detected in three rounds of single marker analyses after controlling for the significant SNPs from the previous rounds. (b, c) LOD curves from interval mapping (IM) and composite interval mapping (CIM) methods, controlling for the first two QTL in (b), and all three QTL in (c). The horizontal dotted line represents the significance threshold via 1,000 permutations.

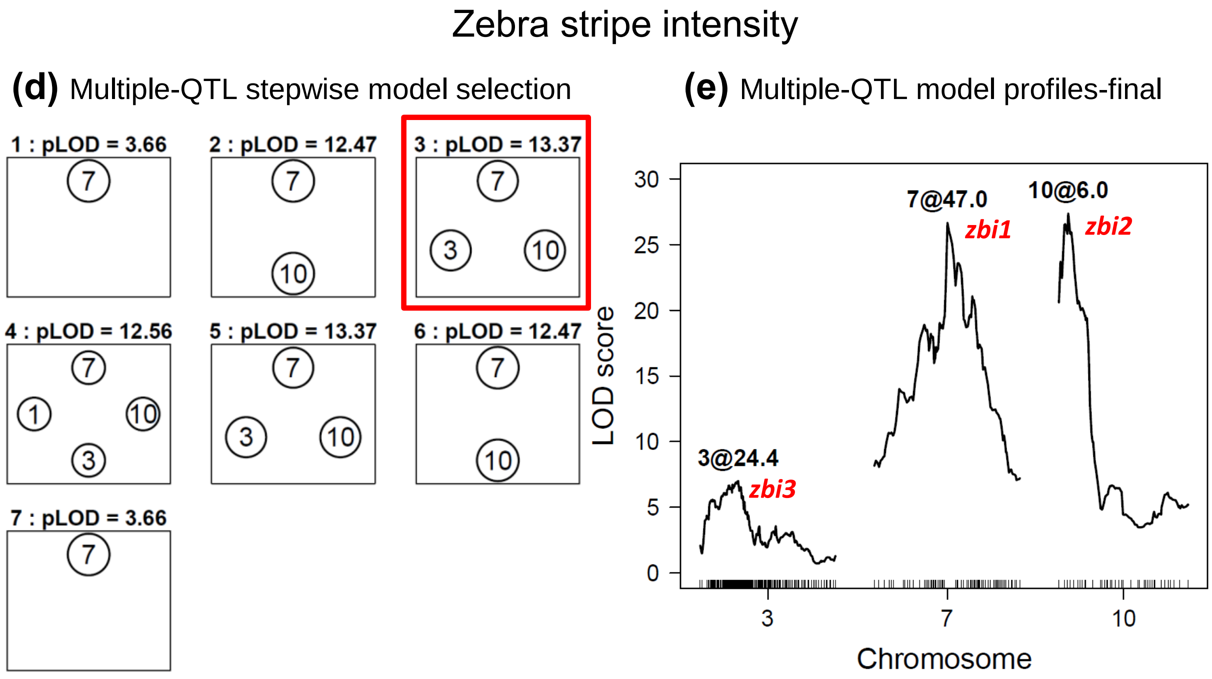

Fig. 4 (cont.) (d) The sequence of models tested by the stepwise procedure in multiple-QTL model (MQM), with circles corresponding to QTL (chromosome number indicated within circles). The best model was identified at step 3 with the largest penalized LOD score (pLOD). (e) Profile LOD score curves for a three-QTL model for zebra stripe intensity. The numbering of QTL was based on the linkage group number first, and then LOD score from largest to smallest.

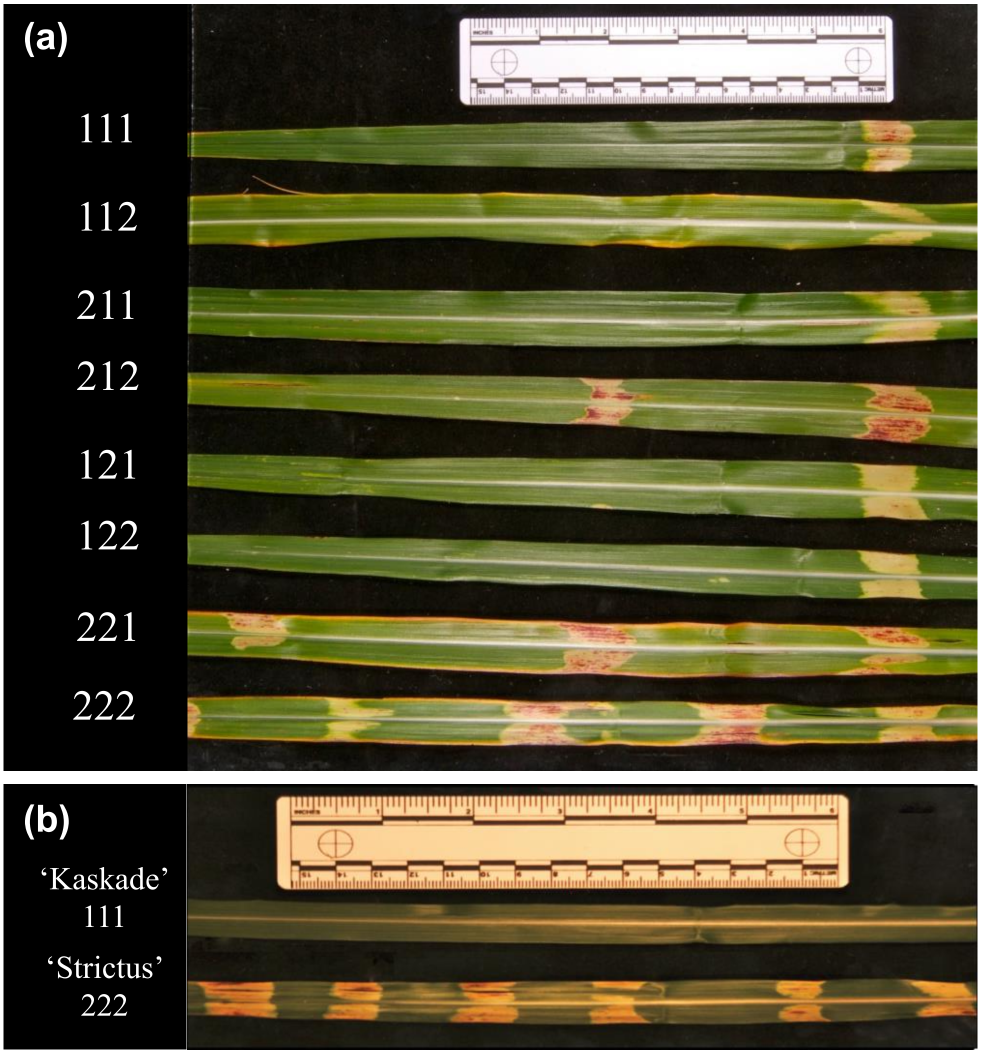

Fig. 5 Segregation for zebra stripe intensity in a *Miscanthus sinensis* ‘Strictus’ × *M. sinensis* ‘Kaskade’ population: (a) Typical leaves of the F_1 offspring within each genotypic class among *zbi1*, *zbi2*, and *zbi3* on linkage groups 7, 10, and 3, respectively. 1 = heterozygous; 2 = homozygous recessive. (b) Representative leaves of the parents of the mapping population.

APPENDIX

Supplementary figures and tables

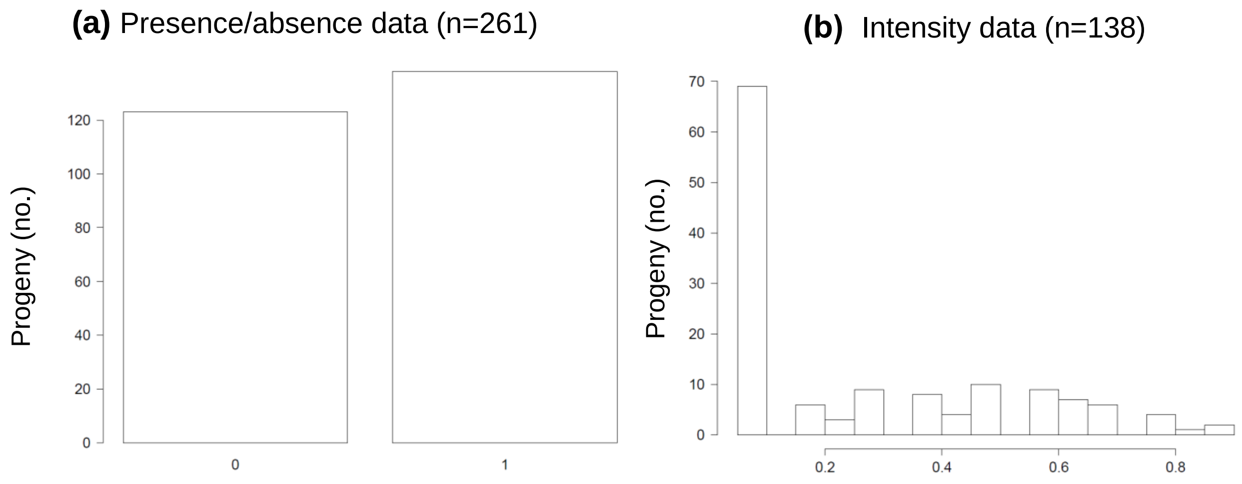

Fig. A1 Frequency distribution of the zebra stripe trait in F_1 progeny of a cross between *Miscanthus sinensis* 'Strictus' and *Miscanthus sinensis* 'Kaskade': (a) zebra stripe presence and absence, with 0 representing absence of striping and 1 representing presence of striping. (b) zebra stripe intensity based on a 0.05, 0.1, 0.3, 0.5, 0.9 scale. Data are expressed as the least squares mean of the three replicates.

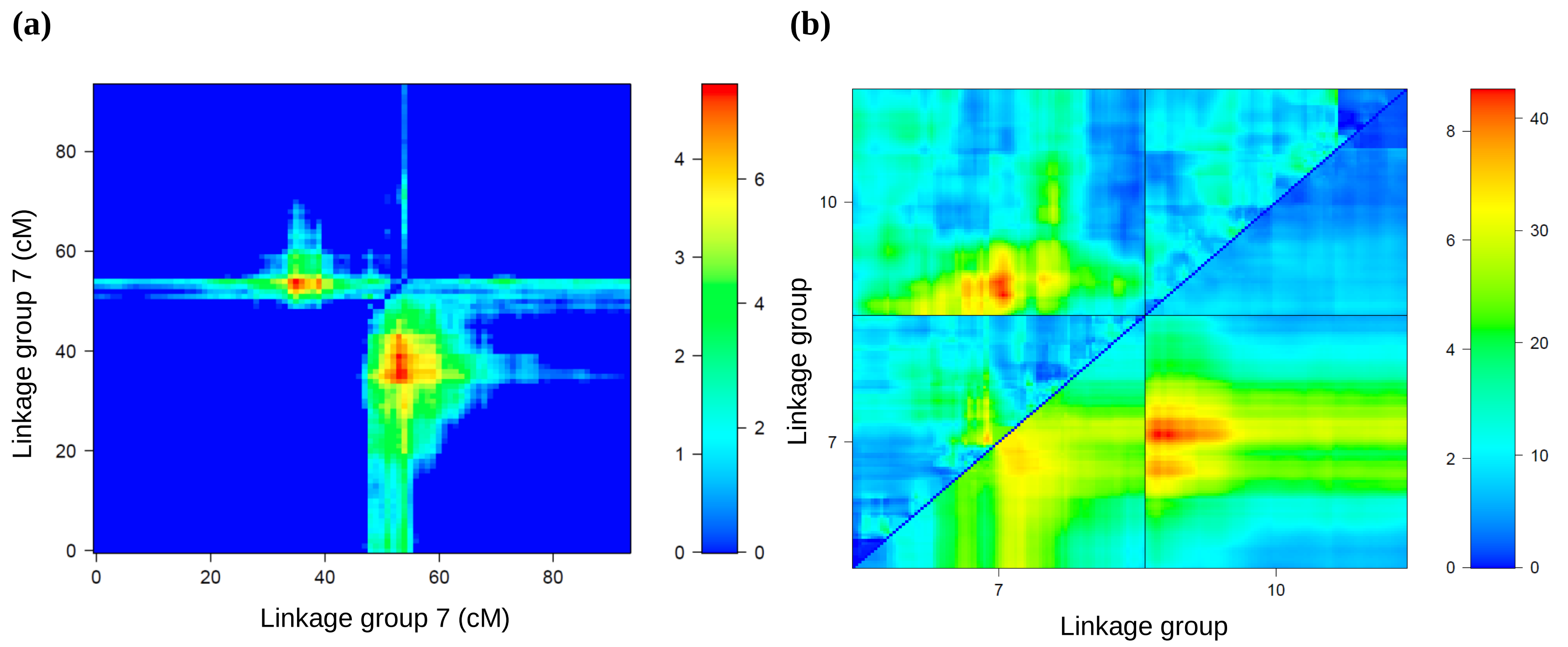

Fig. A2 Two-dimensional, two-QTL genome scans with the zebra stripe presence/absence data: (a) LOD scores on *Miscanthus* linkage group (LG) 7 after controlling for the QTL identified on LG 10. LOD$_{av1}$ score (indicating evidence for a second QTL with no epistasis allowed) is displayed in the upper left triangle; LOD$_{fv1}$ score (indicating evidence for a second QTL with epistasis allowed) is displayed in the lower right triangle. In the color scale on the right, numbers to the left and right correspond to LOD$_{av1}$ and LOD$_{fv1}$, respectively. (b) LOD scores on *Miscanthus* LG 7 & 10. LOD$_{i}$ score (indicating evidence for interaction between QTL) is displayed in the upper left triangle; LOD$_{f}$ score (indicating evidence for full two-QTL model) is displayed in the lower right triangle. In the color scale on the right, numbers to the left and right correspond to LOD$_{i}$ and LOD$_{f}$, respectively.

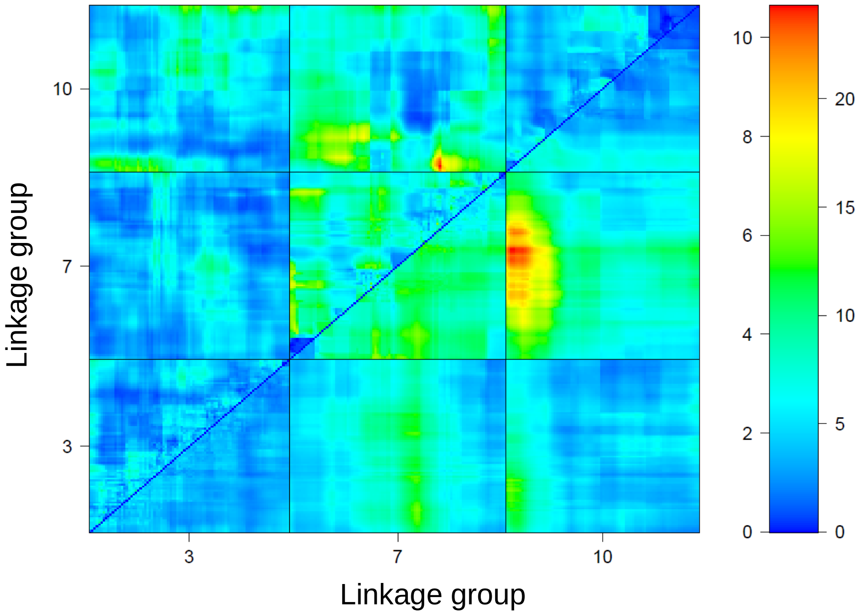

Fig. A3 Two-dimensional, two-QTL genome scans on *Miscanthus* linkage groups 3, 7 & 10 with the zebra stripe intensity data. LOD_i score (indicating evidence for interaction between QTL) is displayed in the upper left triangle; LOD_f score (indicating evidence for full two-QTL model) is displayed in the lower right triangle. In the color scale on the right, numbers to the left and right correspond to LOD_i and LOD_f, respectively.

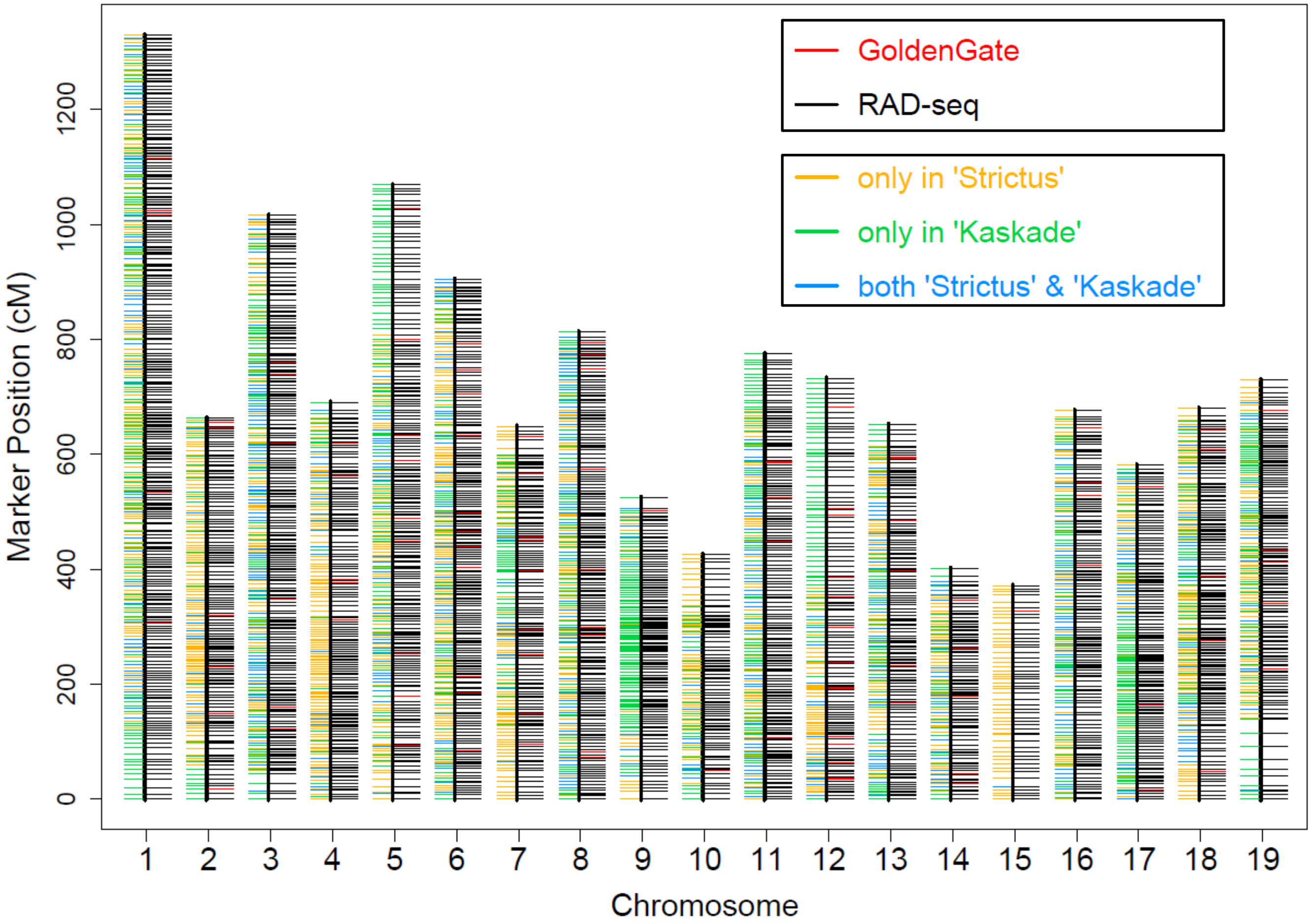

Fig. A4 Composite genetic map for *Miscanthus sinensis* with 3,044 RAD-seq SNPs and 138 GoldenGate SNPs (3,182 total). Genetic distance shown on the left in centiMorgans (cM). Linkage group numbers shown at the bottom (linkage group numbers based on the genetic map from Swaminathan *et al.* (2012)). Horizontal lines represent estimated positions of the genetic markers. Marker type is shown by color (red, GoldenGate SNPs; black, RAD-seq SNPs; gold, heterozygous in *M. sinensis* ‘Strictus’ only; green, heterozygous in *M. sinensis* ‘Kaskade’ only; blue, heterozygous in both *M. sinensis* ‘Strictus’ and *M. sinensis* “Kaskade’).

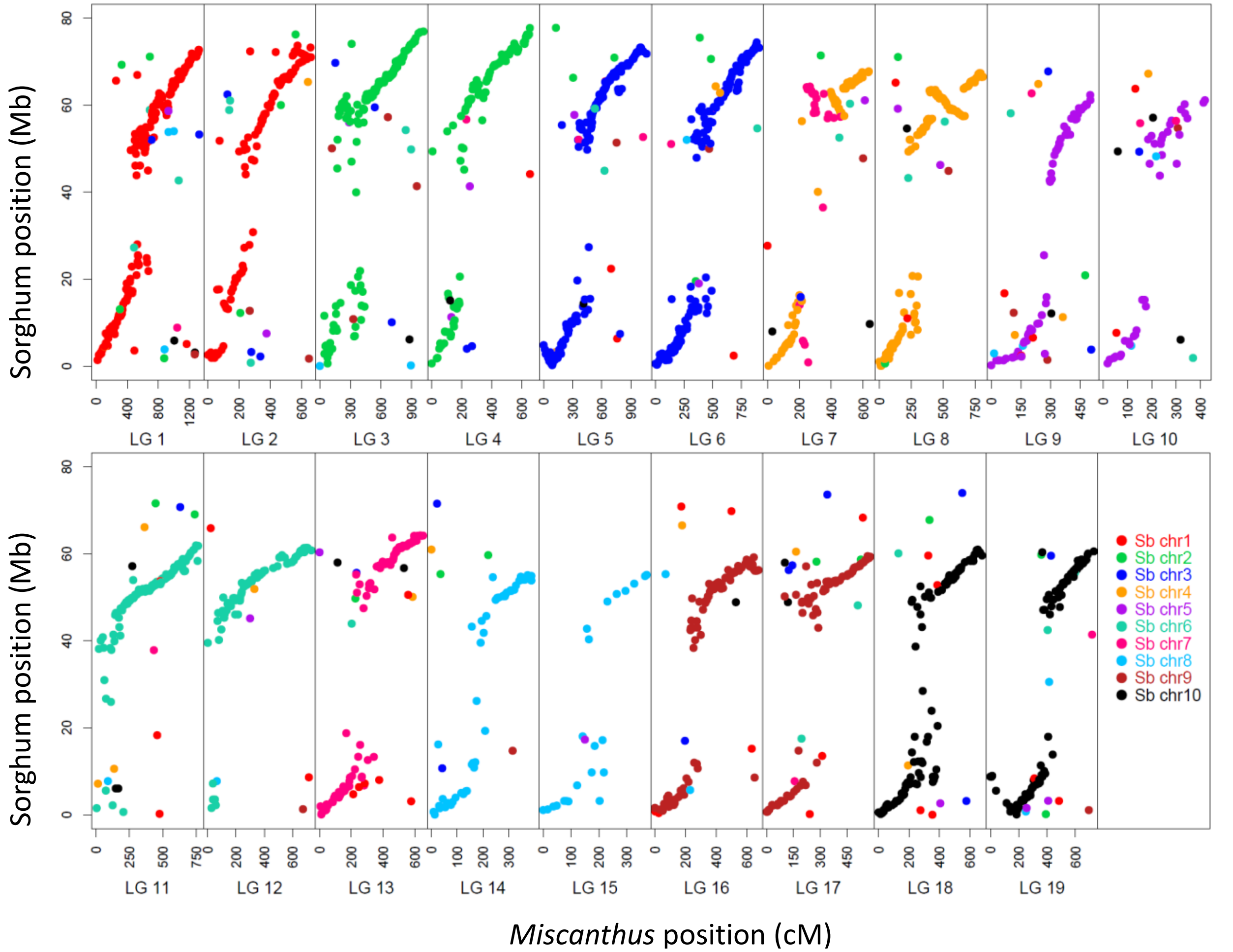

Fig. A5 Scatterplots of positions of mapped *Miscanthus* markers relative to their positions on *Sorghum bicolor* v1.4 physical map. Horizontal axis shows composite genetic map position of markers on the 19 *Miscanthus* linkage groups (LG), in centiMorgans (cM). Vertical axis shows physical map position of markers aligned to the 10 sorghum chromosomes (Sb chr) in megabasepairs (Mb). Each dot corresponds to a single marker, and is colored by different sorghum chromosomes.

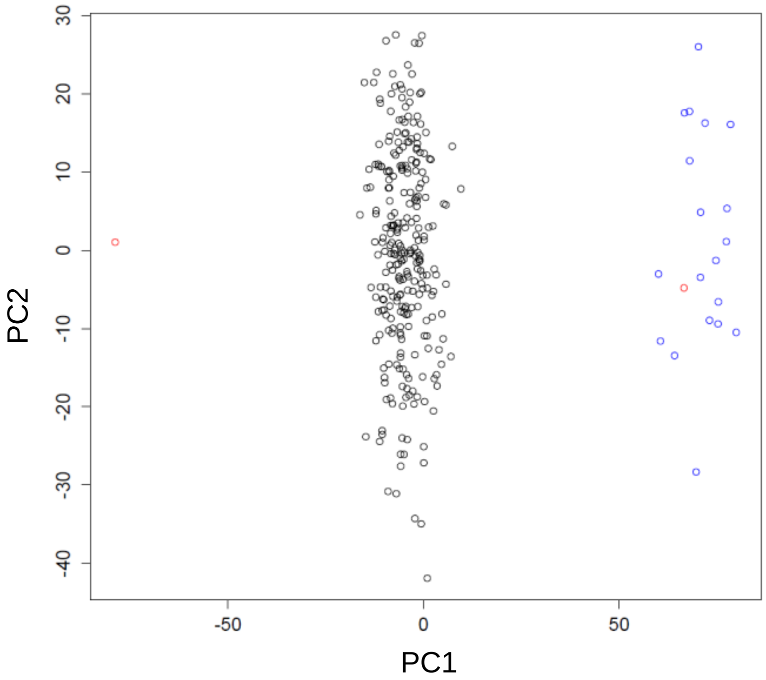

Fig. A6 Principal component analysis plot demonstrating 19 individuals (blue circles) appeared to be the product of self-fertilization of the female parent *Miscanthus sinensis* 'Strictus' (red circle on the right). 6,014 RAD-seq SNPs polymorphic between the two parents, *M. sinensis* 'Strictus' and *M. sinensis* 'Kaskade', were used to show the variability of the 293 individuals and the two parents explained by the first two principal components (PC). Each circle represents an individual.

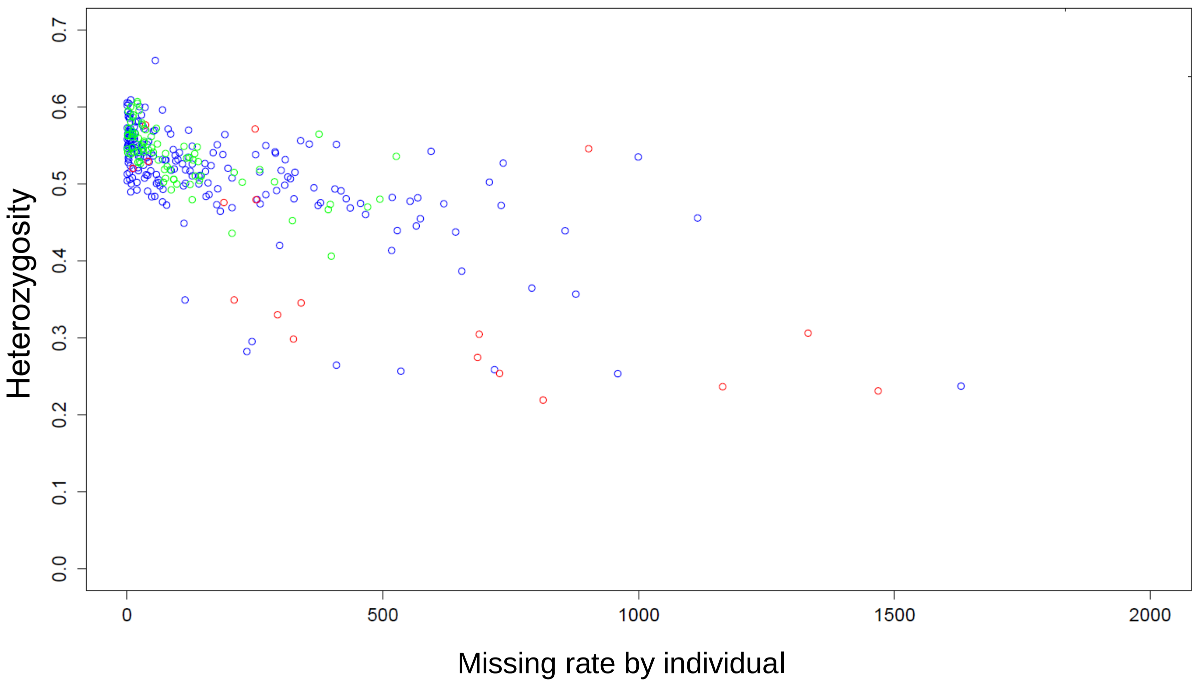

Fig. A7 Plot of average heterozygosity against the proportion of missing data by individual across 6,014 RAD-seq SNPs. Each circle represents an individual. 18 selfed individuals and 75 F_1 individuals, both identified by GoldenGate markers are indicated in red and green, respectively; 201 individuals indicated in blue are the ones to be tested whether or not a true F_1 or self.

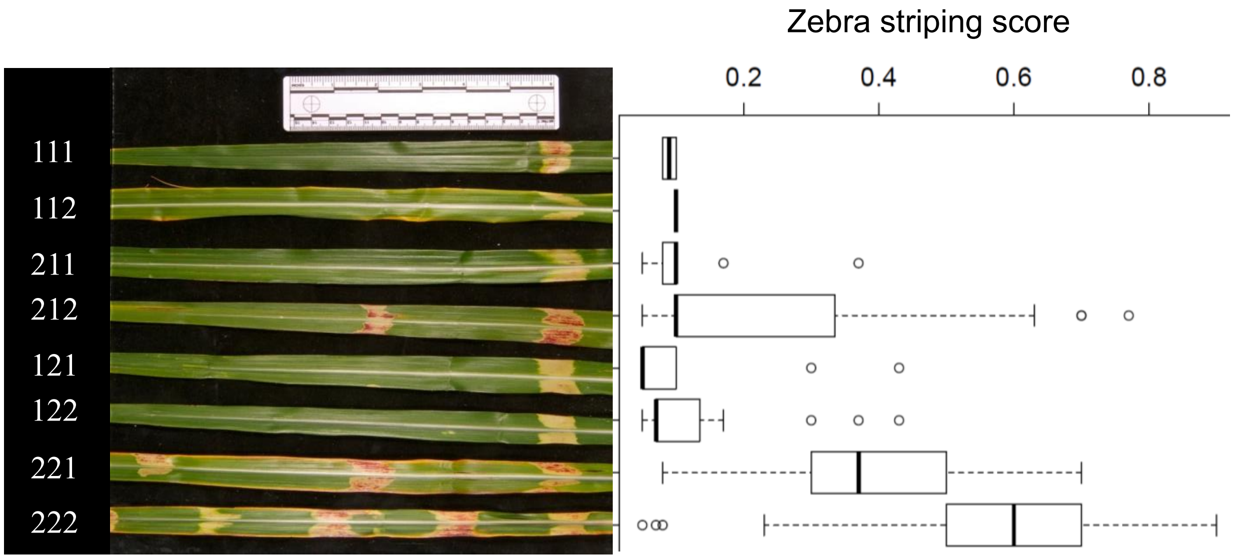

Fig. A8 Boxplots of zebra stripe intensity distributions for all genotypic combinations (*zbi1*, *zbi2*, *zbi3* on LG 7, 10 & 3, respectively). 1 = heterozygous; 2 = homozygous recessive.

Table A1 The 241 GoldenGate SNPs that are polymorphic in an F_1 population of *Miscanthus sinensis* ‘Strictus’ × ‘Kaskade’.

Marker Name	Locus Name	Ilumina ID	Sequence	Sorghum LG*	Position on sorghum LG (bp)
X2	GFSSContig18404_380	GFSSContig18404_380-0_T_R_1890479701	TGCACCGCCTATTGGTGTGATAGACTCCAGCAGTTCTGCAATGCCTGAGCAAGAGCTTG[T/C]AGCTACCCAAGCAAACTCCCATGGAGATAAACCAGTGCCTAAGCAAGAGCTTGCAGCCACC	2	73079176
X8	GFk35ctg648025_353	GFk35ctg648025_353-0_B_R_1890481331	CTGTCATTCCCAACAGGTTTTGTTTTAGACCTCTCAAGTTCCACATGAATAGGAGTCCT[A/C]GAACTTTTGGGCTCCAAGACAACAGATGCAGCTGCTTGGGGAATGCTACTGTCTTCAACCT	7	58207132
X19	GFSSContig18994_311	GFSSContig18994_311-1_B_F_1863900892	GCCAGTCTGTCAGCCACATCATTTGTCCATTGGAAGAACCGTGTCAACTGACGAGTAAAT[A/C]TCAATACCGCAACAGGGACAGTGGTTACATTGGCATCTTGCCCAGCTAACCTCTCACACA	7	59460069
X28	GFSSContig16759_1172	GFSSContig16759_1172-0_T_R_1890482149	GTCCACCATGGCTGCCAAGTCTAATGGAGGCAGTGGTAAGCACAGCATACCTAGTAATG[T/G]TGGTGGTGTCGTGGCAACGAAGCAGCACAATGCGTCATTGTCAGGAACGAGTACAAGGGGC	2	66101587
X52	GFSSContig16380_877	GFSSContig16380_877-1_B_F_1863900973	CAACACCTGGACCTCCCTCTGGCCTGGCACCGGCAAGCCCGGCCTCTGGGTCACCTCTAG[T/C]TCCCGCATGGGCGCACTCTACACCCTCATCATCCGCGAGGAGGAGATATACATCACGCAA	4	67583451
X57	GFSSContig473	GFSSContig473-1_B_F_1863901167	GCTGAGGCCCACTGTTGACATCTCAGTGACTGCTGATGCAGATTTCGTGCGCCCGGAGCT[T/G]CGACAGTCTTCATAAGCTTGTATGGATCTGCAGCGTGTACTGCAATGGTTAGTTTGTAAG	3	58592304
X59	GFSSContig18771_265	GFSSContig18771_265-0_B_R_1890481084	CTCATCTGACCCAGGTTGTCCATCACTGTCAGCCCTGATCCAGACCCAAGCAAAAGTGA[T/C]AGCCAAATAAGCCAAAAATCAGCCTTCACAAATGCTTGCATCAGGGTGAAGTTGTCCCCTC	6	38333670
X62	GFSSContig15731_680	GFSSContig15731_680-0_T_F_1890480641	CATCTCCCGCAACAGCAACTACACCTTCTGAGCACTGATCAGAAGAAAATGATGCTGCA[C/G]ATTCGAGCGTATCACAGGACAATGGTGTCAAGAGAAAATGGCCTTGATGTATATAACCCAG	NA	NA
X63	GFSSContig7649_1236	GFSSContig7649_1236-1_T_R_1863899573	GAGGTGCTGGCGCTGCTGGGCGCGCTCAACTTCTGGCCGCTGGCCATCTACTTCCCCGTG[A/G]AGATGTACTTCATCCAGCGGAACGTGCCCCGGTGGTCCGCCCGCTGGGTCGTCCTGCAGA	6	46044287
X65	GFSSContig20421_1653	GFSSContig20421_1653-1_T_F_1863899785	GCCCAGGAGATGCCACCAGGAACCTCTCCCAGCAGTGCTTGAATGCACTT[A/G]CTAATGTTGTGCCTGGTCTTATTGGAGGTAGTGCTGATCTTGCGTCCTCC	10	1924546
X70	GFSSContig11850_777	GFSSContig11850_777-0_B_R_1890482288	TTTTGATCATCGCTTCTGGACATCAATGTGTCAAAGTTTGGAAGTTCTTCAACAGTACA[T/G]GATTCTAAAGTGCCTATTACATTCTGATCCCCAACATTTGCAAGTGAAATATCTGACTTCA	3	2045071

Table A1 (cont.)

X73	SSk50ctg157713_198	SSk50ctg157713_198-0_B_R_1890482082	TGTTGTGGTTAGCATAGCGATCTGATGGATCAATGCCCTCAAACCGCTG[T/C]GGGAACTGAACATAACCAATACGGTCGCCACCACGGTCCATCATGAAGCAC	10	723372
X80	GFSSContig18167_254	GFSSContig18167_254-0_B_F_1890480280	TTCTCCAGTTTCATCGTTTCCAGGCAGAGCGACAAGAACCAACTTGGGCTCGCGGAATC[A/T]ATGATCTTGTTTGAAGTTGCCAAGTACACAAAGCCATCCCTGACTGCCACAACCAGGAGCT	3	54629654
X97	GFSSContig17622_639	GFSSContig17622_639-1_B_F_1863899745	GCGTACCACGCCATCGCGGTGCTCACGTGGGAGGAGGTCCTGCTCCACGG[T/C]ACCAAGCACTACAGCGACGGGCTCAGCCGTTTCTGCGACGCCAAAATGAG	1	64057697
X118	GFSSContig9469_613	GFSSContig9469_613-0_B_R_1890481123	TAGAGGAACCCATTTGCCATACTTTGGTGGCAAGAGGTCCCTCGTCAGATTGGCTGCCA[A/C]TGCAAATCCGAAGAATCCATAGCACAGCTGCAAACAATGTCGGGGCAGAGCAGAGAAGCCC	6	53147886
X119	GFSSContig18297_1609	GFSSContig18297_1609-1_T_R_1863900293	CCCACTGCATTCGGAAGCAGGTGTTCATCTCTAGCACGGGGCGACCGCTCCAGTCGCCAC[A/G]GAGCCGCGGGTTGAGGTGGAGTATCCTCGGCGGCTCCTCGCCGTCGGCGGCGCGCAGGCC	8	53137669
X120	GFSSContig10709_686	GFSSContig10709_686-1_T_R_1863898303	TCAAGCTGGCGAGTGCGCTCTCCGACCCATAGGAAGTGGGCAGAGCAGTC[A/G]TAATAGAGGCCACTGGTGGAGTCTTCACGTGTGAGTGCTTGCTCATAAGG	7	64135545
X123	GFk50ctg18383_265	GFk50ctg18383_265-0_B_F_1893112201	CTTGCATGTGAATATCCCTGAGCAGGACCCTGAGGATGCAAAAATCGTGGAGGTCATTGA[A/G]GCTGAGTTCCACAAGCTTGGTGTGCAGAACGGGTCCGCCAATGGCATCGACCAAGCATAG	10	52518354
X126	GFSSContig2648_373	GFSSContig2648_373-0_B_R_1890480681	GTGCCGAATTGAGGCAGAGGAGCTATCTCTTGACGCATCTGAGATTGTC[A/G]TTGCAAGCACTAGGCAAGAAATAGAAGAGCAGTGGAACTTGTATGATGGTT	4	5621401
X127	GFSSContig18538_1416	GFSSContig18538_1416-1_B_F_1863901079	GCTCGAGGACGCCATGGCCGGGAAGGAAGCCGTCTGGGCGGAGATTGTCA[T/G]GGAGAATGACCTCATAGCGACGGAGCTTGACGAGATCACCAATTGGTGGT	1	54706743
X130	GFSSContig20175_2257	GFSSContig20175_2257-1_T_R_1863899790	GCTGAACCTGGGAAGGCTGATTGGGAGCTTGCCCTTGTAGAGACAGCAAG[T/C]AACTTGTCCAAGCAGAAGCCAGCAATGTCAGGTGGTATGGACCCGCTGCT	NA	NA
X132	GFSSContig6639_712	GFSSContig6639_712-1_T_F_1863899658	GATGCAGAGCCGGACAAGTACGTGGTGACAGCCTTGGCCATCACATGACG[T/C]TGCTGGTTGGCACTTCCATCTGCAAGATAAGAAGCCATCTGGACCATGAA	7	18758696
X153	GFSSContig13612_465	GFSSContig13612_465-1_B_F_1863898177	CAGGCCACAGGTACAATGACCACCGTCCCTGCACCCTTGAGGAACTGGAG[T/C]CCGTCAGAGAGGATATCAGTCAGGCCGCTTGACCTGAAGCCTTCAGCAAT	7	62997760

Table A1 (cont.)

X164	GFSSContig12418_570	GFSSContig12418_570-0_B_F_1890479695	ATGATCAAGATTAAGTGTATCTGCCAATGTTTGGCTCAATTCATCAGTTGAACTTGCAG[A/G]TGGTGCCTGAGGTGGTTCGAAGCCAAGATGAGTAAGCAATTTTGTCCGTGCAAAATCCCCG	2	75485266
X166	GFSSContig12816_576	GFSSContig12816_576-0_T_R_1890479773	GCTGCAGCATTTCTATCATAGTCAACAAGCCTCTTTGCATAAGCTTCAGCTGCAGCTTC[T/C]GCTTCGGAAAGAGGTAACCCGGCATCACTTAAACCAGCATAAGTGCTACTTTCCTTCAAGA	2	59003882
X167	GFSSContig19882_825	GFSSContig19882_825-1_B_F_1863899567	GGATGTTGAAGATCTTGTGGTGCCCCGCCGCGATGGCGTTCCACATCGCCGTGTTGCCCT[T/G]CGCGTCCTTGATGTTCACGTTGCACGCGTGCTTGAGCAGCACCAGCACGCAGTCCTCGTA	9	50579186
X170	GFSSContig17760_1517	GFSSContig17760_1517-1_B_R_1863899214	GTGGGCTATCATGCGCTCATGGGTATTGAGTTGAGTCCTCTGTATGAAGA[A/G]TTCCTGAGGGAGAAGAAGACAATTGTTCGTGGCATGGCTCATCCATTTTT	3	19964030
X172	GFSSContig19146_697	GFSSContig19146_697-0_T_R_1890479768	CATGCCAAGGACGAAGATGGTGTGTTGAAGGCGACGTGGATGGCTGACGGTACGCAGTG[C/G]CCTGGGACATGGATCGAGCAGGCTGAGAACCATAGAAAAGGACAGCACGCTGGAATTGTTA	2	69030163
X182	GFSSContig11849_357	GFSSContig11849_357-0_T_R_1890481760	ATTTCCTCTTCAAAAACCTTGGCAGCAGCACTGGCATTGAAGCCATCCAGTGCCTTTGC[A/G]GTGAGTTTCTCACTTTCATTAACAAGCCCATTTGGATCTAACAGAACCCTTTCTTCCGGAG	9	48023744
X185	GFSSContig10862_580	GFSSContig10862_580-0_B_F_1890479765	CGCCGAACGGCACCACGCTGTGGCAGAGCTTCGACCACCCGACGGACACGTTCATCCCG[A/G]ACATGAAGGTCGGGCTGCGCTACCGGACGCACGACGGCGTGCGCATCGTGTCGTGGAGGGG	2	67072885
X186	GFSSContig14798_161	GFSSContig14798_161-0_B_F_1890480595	AAATTTCAGCAGCAGGTAAGCTACACACCCATGGCTGCCGTTTTCTTGT[A/G]CTGGATGAAGTCGACCAGCTTTTGTCTTTTAATTACCGTGAAGATATGCAT	4	56909879
X188	GFSSContig10367_393	GFSSContig10367_393-1_T_F_1863900216	TGTCAAATCTCCAAACTGATTTATTGACCATCCATGTTTACCAGGTGATAGACCACTAAA[T/C]GTGGCTTCAACTCTAGCCAACTCCATGTTTACTTGGGCCAAACGAACAACACCAAATACA	6	55049847
X189	GFSSContig18119_1138	GFSSContig18119_1138-1_B_R_1863898271	CAGCCATGACTTGTGCGAGACTGGGCGCGCCATTTCCCTGAAGCATGGCTACACCATAGT[T/C]GTTCCTCATTCTCTTTGACACTCCACCTTGCATGTAAGATGCTGGTATAACATTATTGGG	2	60452753
X201	GFSSContig19372_585	GFSSContig19372_585-0_B_R_1890481508	GCTTTGATCAGTGGTACTGCCCATTCCACAATGTTCCCTTCCTCGAACTGCATGTCAAT[T/C]GCTTTCCTGCCACTCAGTATCTCCAGGAGAACAACCCCGAAGCTGTAGACATCAGATTTTG	8	3643181
X202	GFSSContig18384_1020	GFSSContig18384_1020-0_B_F_1890481289	GTTTCAGCTTTCACAAGGGGCGGATAAGTGGGTTAGCGAGTTCTCTAGTCAACATAATC[A/C]AGGTGCGCTAAATGAGAACTGGGTTGATGAGTTCTCAAAATTAAATGTCACTGATGAATGG	7	63329978

Table A1 (cont.)

X203	GFSSContig9469_436	GFSSContig9469_436-0_T_F_1890481142	AAGATCCAAAGCCCATCACCACATATCAACCCAGATGCAACTGCTGGCA[A/C]CATTAAAGATGCTTTACTTTTGTCAATCATGTGCCAGATGAAGACTATCAA	6	53148094
X209	GFSSContig16948_270	GFSSContig16948_270-0_B_F_1890482177	GTCTTGACATCAGGTAAAGGGAATTCAATCTTTCTGTCAATTCGACCTGG[A/G]CGAAGCAAGGCTGGGTCAAGACTTTCAATGCGATTTGTTGCTAGAATAAC	2	77647679
X214	GFk50ctg97419_270	GFk50ctg97419_270-0_B_R_1890482600	TGCTGTCGCTTTGGCAGACCTTGATGCAGCAAAACAGGAGCTTAGAAAG[C/G]TCAAGAAGGATTTTGAAACATCTTTGGATATGAGGTTGTCTGCTGCCCAGC	super_11	984549
X219	GFSSContig18265_294	GFSSContig18265_294-1_T_R_1863899416	AACGAAGACGAGCACCACCACCATCTCCCCCTCCGACTCCGATTTCCACGAGGCCTCCTC[T/G]ATCCGCCACTTGTTGCCCCCGTCCGTCGCCCCCGCCTCCACCAGCGCGTACACCCGTCGC	3	54801988
X225	GFSSContig17916_723	GFSSContig17916_723-1_B_R_1863900087	CCCAAGATAATGACGAAGAACCGTCTGATTCGCCTCTCCGAGATGGATAC[T/C]CCTATTCTGACCATTGTTTCCAGCAACCGTCCTCTGATGATCAAGTGCAG	2	8732472
X226	GFSSContig20159_876	GFSSContig20159_876-1_B_F_1863899662	GCACCAATCCTTTCAGAATATAGACCAAGGTTCTTGCTGTAAGATTGTGC[A/G]ACAAACACTTCCATGCCACGCTTAACAAAAAGCCTGACAGAAAATGCATC	4	65842476
X229	GFSSContig18533_925	GFSSContig18533_925-1_B_R_1863898348	GCCTGCGGGTAACGCAGAAGGGTCATGCTGTAGCTGAGCTTGGTGAAGAA[A/G]TTGGGCTCAAATGCAGTGGTGGGTGATGAGCTGCTGGGCCTGTTTGTGAA	10	953256
X235	GFSSContig17750_1212	GFSSContig17750_1212-1_B_F_1863901041	CAAGATCGAGAGCAGGCCGCACCGCCACCGGCCCATCCGCCTCGTCGACGACGCCAACGT[T/C]GGCACCGCCAAGCACTTCGAGTACATGTTCTACGTCGACTTCCAGGCGTCCCTCGCCGAG	6	42610199
X239	GFSSContig12282_763	GFSSContig12282_763-1_T_F_1863900275	GCAATCCCTGCAGGACCTTCATCGATCTTGCAGGTCCAGTCAGGCTGGCTCAGTGACCAA[A/G]CCTGCACCATGGGCCGCTTGTAAAGTCCACATAGAATATATTCTGAATCCGGTGCCCACT	1	50563125
X242	GFSSContig17936_728	GFSSContig17936_728-1_B_F_1863900879	TGTAAATCGACACCAGAATCGTGTATGCATAGAGGTTTGGTTTGATGCCAACCTTGCACA[T/C]GTGTTCCCAGACCTTCAATGCCTCATCATATAGCTTGCCTTTCTCAAGTGCACTCAGCAA	10	58642427
X243	GFSSContig15832_782	GFSSContig15832_782-0_B_U_1890482342	CAGAGAGCGTTCCCGATCGAGATCCCCCGGAAAGCTTTTAGGCTTAACGA[T/G]CATATTACAACCACGGCTATCACCCTCGGAGGTGAAGGTGGCACCATGGG	8	16168782
X253	GFSSContig12642_472	GFSSContig12642_472-0_B_F_1890481797	GAGAGCCTCGGTTTGGGATGCAGATTGAGTAGCCACATGAGTGTGATGA[A/G]GAAGGATCCCGATGCGAAGTGGAAGGTAGTGATGGTGTAAGGGAAGGGTAT	9	6672742

Table A1 (cont.)

X256	GFSSContig6268_272	GFSSContig6268_272-1_T_F_1863898930	TGAGGGCAAGTGATGCACTTGATGTCCTTTATTTCTCTGTAACATATCTC[T/C]GATGTTTCCGCTAGCAGACCAATGATCCTCTTGAAAAAATCTTCCTTTGT	2	3991673
X271	GFSSContig2383_483	GFSSContig2383_483-0_B_F_1890479801	CACTTTGTTCCTCAGATGGTCAACTCTCTTAGCCGCCTTGGATTGCCATACAACACAAC[A/G]GCGGAAAATAGAAGGCTTGCAATTGAACTTGCTGGGTTGGTAGTGGCATGGGAAAGACAGA	NA	NA
X273	GFSSContig20378_1618	GFSSContig20378_1618-1_T_R_1863899655	CTCTACGCGTATACGATCTTGGTGTCGATTTACATCGGCAAGGGCAACCATGCTATGGTG[A/G]ATGCTGTACTTCATGACATGCTATCGAAACAGATCAAGCCGACTGTTGTCACATTCAATG	10	58642342
X274	GFSSContig7317_190	GFSSContig7317_190-0_T_F_1890479356	GGAAGCACAGGGGATCTAGAACAGAGCAATGGCAGAAGCAGCAGCGTCTGGAGGAACCC[A/G]CAAGCTTTGTCCAAGACAAGATATATGGACGACTCTGATATTGAGGAAGGGCTAAGCCTGC	super_186	9044
X275	GFSSContig15224_1725	GFSSContig15224_1725-1_T_R_1863899349	ACAATAACAAGCTGCAAAGTTTTGATGAAAGTAATGGACGTGCAATGAATGGTCGGTCAC[A/G]TTCCAGTTTTCTTCAGATAACAAATGCACTAGGCAGCAGTGGTATAGTTTCTGCCAAGGT	2	62336662
X278	GFSSContig12512_154	GFSSContig12512_154-1_T_R_1863898900	TTCTGCTCCCAGGTTTCATTTAACCCCTGCAAGGCCTGATTAATCATCTG[T/C]TGCACCTGCTCCTGTGTGAATTTCTGCCGTTGCCCATTTTTACCAAAACA	6	56933712
X280	GFSSContig26_215	GFSSContig26_215-0_T_R_1890480576	AGCCTTCGCACCTTCTCATAGATATCCGAGTAGGTGCAGTTCTTCCTGACGAGGCGGTC[A/T]CGAACACTAGCAAGAAGTAAATCAGTCTTTGGCAGCTCACCCTCACTCTTGACATGCGCCG	4	16571044
X298	GFSSContig18443_1437	GFSSContig18443_1437-1_T_R_1863900739	TGATGCAGCAAGGGAGAAGTTCTTTGTCCCAGAGTCTGACCACCTGACACTCCTGAACGT[A/G]TATCTTCAGTGGAAGTCTAATCAGTATCGAGGCGACTGGTGCAACGACCACTTCCTCCAT	2	68775145
X304	GFSSContig2301_308	GFSSContig2301_308-0_B_R_1890480638	TTCTGTGAATAAACTGGCACACTGGACATGCGTGAACCTTCAGCAGCTA[T/G]ACCATGAGGATGCTCTGATCTTCTCTTATGCACATCCATGGCACCTGTGCC	4	13081476
X310	GFSSContig1614_738	GFSSContig1614_738-0_B_R_1890480184	GGGGAAGAGAATGTTCTCGTCATTGATTTGCTGGGGCCGAGTTTGGAGGACCTGTTTTG[T/C]TATTGCGGCAGGAAATTCACGCTGAAGACTGTCCTGATGTTGGCTGACCAGATGATTACAA	3	637355
X316	GFSSContig12441_604	GFSSContig12441_604-1_B_R_1863898150	CAGTACGAGGCGTACGCCGAGAAGCTGGGCACCCTGATGACCTACTACTC[C/G]GCGGAGGGCGAGGACGAGGTCCTGACGGGCAACATCCGGAACAAGCTGGT	6	48887495
X320	GFSSContig7695_1043	GFSSContig7695_1043-0_B_F_1890479676	TGTTGAGAGGAGGACACGGCCCTTGAGTTGTTCAGGTGATGGGAATTCTTTGAGGTGAT[T/C]GGAGTCAGGCGGGTAGTACAGTATGTCACCAAATACTTCAAGAACCATCTTGGCAACTTTT	2	77441080

Table A1 (cont.)

X333	GFSSContig5058_327	GFSSContig5058_327-0_B_F_1890479362	GAGGAGTACAGCGATGAAATTTTCAAGCTTCTGGATGGTGGCGCGCACATCTACTTCTG[T/C]GGTTTGAAGGGGATGATGCCTGGAATTCAGGACACCCTTAAGAAGGTGGCAGAGCAGAGAG	1	5084866
X340	GFSSContig16376_214	GFSSContig16376_214-0_B_R_1890481755	ATCGCTAACAGTAACTATTTGTGTTTGTGTGTCTAGTTTAAATCTCAGT[A/G]TGGTTTAGAGCAGAACATCATTGTCGTCCCCAAGAATTGACAGAGAGAATG	9	6664433
X343	GFSSContig15044_1090	GFSSContig15044_1090-0_B_R_1890480538	GCTCCTAGATTTGCTTCGATTGCCAGTTAGAACAGGCATGACAGCTGCATTCCTTTCAA[A/T]TTTTGATTCATTAACACCATTTGTATGGATTTCCCCGTTTTGCAGGGGGGAGACATCTTGT	4	7207664
X347	GFSSContig19618_2015	GFSSContig19618_2015-0_T_F_1890482202	GATCATCTTTAGGAATTTCAACATGCAGCTGCTTCCCACTGGCACTGGGA[A/G]GACCTATGACAAATTGTTCCTCTGCATTTTCAACTGGTTTAGCACCCATT	NA	NA
X358	GFk35ctg340610_63	GFk35ctg340610_63-0_B_R_1893112220	AAGGAGGCAGGCAGAGGGAAGCGGAGCTTCGAGGAGGAGAGGGCGGAGGA[T/G]GAAGAGAGAGCGTAGGCTGCGGCAGCTGCTGCGGGCACAGCGGAAGCGGC	6	55047642
X360	GFSSContig10511_296	GFSSContig10511_296-1_T_F_1863900768	GTAGACGCCGAAGTTTCCGACGCAGAGCATGGCGAGCAGCCAGAAGAAGTAGTCGAGGTG[T/C]GCCCGGTTGATGTCGTCGGGGATCCAGCCGTCCCGGCCGCCCCGCGCGGTGGCGCGCGCC	3	70432267
X365	GFSSContig20589_1320	GFSSContig20589_1320-1_T_R_1863899408	CATGATGCGGTTCTGGGATGAGAAAGCAGTTATGGTTCGAAGATTAGAGA[T/C]GGCCTCAGCAGCTAGCTTACTACATTCGGCTTGTGCTTGTGTTGATTTCT	4	5961562
X369	GFSSContig17173_502	GFSSContig17173_502-1_B_R_1863899026	CAACCAGAATGACAAGAACTAGGTCCTGCTGCATTATGAGAGTGGCCTGT[A/G]TGTCCTCGAGCATAGGCATCAGAATGACTGAAACTGACACCATCTCCAAA	6	56441152
X372	GFSSContig2984_879	GFSSContig2984_879-0_B_R_1890479253	AGCTTCACAACATATGGGACCTTCCCAGTTGAGAAGGTCGAGATCACCTGCCCTGTCTC[A/G]GTATCCCAGTACTGTATATTCCTGTCATACCCAGCACTCAAGAATTTAGTTCCATCATTGG	1	56428774
X381	GFSSContig18408_1087	GFSSContig18408_1087-1_T_R_1863898314	ATGGCAAATTAAGGAGCTTGCTAATGATCTCAGCACAGTGGAGAGGACGCTAGGACAGTC[T/C]GGGTTGAAGGAGCGGGAGAGGTCGGCATTGTCGCACAAGCAAAGGCAGCTCAAGGCTCAG	6	377030
X382	GFSSContig16519_974	GFSSContig16519_974-1_T_F_1863898241	TGGGCAGCTCTCCACCTGTGGCTCTTGAAGTAGAACCCAGCACCAGACAC[A/G]AATAGGCAGATTATGAACCCAAGCAGCTGCATGCGAACAGCGTCAGCACG	10	953541
X388	GFSSContig4415_344	GFSSContig4415_344-0_B_R_1890482155	CAAACTTTGCCAGATCACTGGAGAGATTGACTCAGTAAGGAAAGGTCTC[A/G]ATGCTGTATCTGAATTGCTCTTAGCTCATCCACCCAAGGAAACTGATGCAG	3	406901

Table A1 (cont.)

X393	GFSSContig3855_930	GFSSContig3855_930-1_T_R_1863899390	GTCCAGTGCAGATCACCTGTGGAGCTGCACACACTGTTCTTGTTGCTGGTGATGGGTATA[T/G]GATGTGGGCATGGGGCAGAGGCCGCAGTGGTGTGCTTGGGAGAGGCCAGACTGCTGACAG	3	61682675
X400	GFSSContig20092_371	GFSSContig20092_371-1_T_R_1863899857	GGCAGCGGCCACCAATGCACCACCGCCGGGGGCCAGACCCAGACCTGCGC[A/G]CCGTCCACCCTGAAGGTGACCTTCTTCTACGTCTCCCTCTACATCGTGGC	9	50806686
X405	GFSSContig15832_1407	GFSSContig15832_1407-0_T_U_1890482386	TTGACATTAAGGGCAAAAGAATACAGTCACTGGCTGAGTTCAGCACTGAC[A/G]GAAACTTGGTCCTGTCCCATGAATATTGCCCTAGTAGTATATCCAGTTAT	NA	NA
X410	GFSSContig17760_1991	GFSSContig17760_1991-1_T_F_1863899629	GTAAAAGGGGAGGATGGAAATCAAGACATGTACTTGCCAGCTCTTCTCCC[A/G]AAAGTACCTGGTCGATTCTACTACCTATTCGGGCAACCGATTGAAATGAA	3	28482311
X414	GFk40ctg123299_208	GFk40ctg123299_208-0_T_R_1890481791	AGAAAGCTCGTGAAGGGAGGGACTATGTGCACAAGAACTTCAACTGTGAGGACTTGCTC[A/T]TGAATTTTCTGTATGCGAATGCAAGCTCCACAAGGACCGTGGAGTATGTCCACCCCGCATG	9	56100690
X420	GFSSContig9469_821	GFSSContig9469_821-0_T_R_1890482214	TAGAACAGAAAAAATGTCAGCGGTCCAATGACACAGCCCATGGCAGTGCCAATAGCCTG[A/T]GCAGTAATCATTGATTTAGGTGATGTTAATGTAAGATGTCCAGTCTTGAAGTCATGCATCA	6	53147719
X421	GFSSContig19131_53	GFSSContig19131_53-0_B_F_1890480449	AATGGGAGGTTGGCAATGGTAGCCATGCTTGGTTTCATGGTGCAAGCATC[A/G]GTAACTCATGCCGGCCCTATCGACAATCTTTTGACACACCTTTCGGACCC	4	63977438
X426	GFSSContig12968_306	GFSSContig12968_306-0_T_R_1890482156	CGTCAATCCGGGCATTTGGAAGGACAACAACTACGGCTCGGACTTCATCCGCAACGCCA[A/T]GATCCCAGACATCGACTTCGCTTCCATCCACCTCTACCCTGACACCTGGCTGCAGCAGCAG	3	62638623
X440	GFSSContig2913_283	GFSSContig2913_283-0_T_R_1890480251	CGGAACTGTTGTCTGGTGTCATCCAGCGATCCAGAGTTGTCGATCACTATGTCGGCTTC[T/C]GACTTCTTCAAGTCCAGCGCGAGTTGTGCGTTGATCCTGTTCTGCGCTTGCTCTTCAGAGC	NA	NA
X453	GFSSContig11545_976	GFSSContig11545_976-1_B_F_1863898135	TCAATCAGGTATTCAATGTCAACAAGAGGAATGGGAACAGGGTTCGGGTT[T/C]GCAATAAGGACATCAACAATAAGCTCTATCTTCTCCAGGCTGACTTGGGG	2	12301307
X458	GFSSContig20530_102	GFSSContig20530_102-0_T_F_1890479198	TGTGGCAGGATGCACCTGCCCATCTAGCACTGAACAAAAATCCATGGCATGTAAGCCTC[A/G]TTGCAGTATCAGGTTAAGTGTCTAATGCGACAACATTGACCATGGAGCTGACAAATCAGTA	1	21022213
X464	GFSSContig18335_922	GFSSContig18335_922-1_B_R_1863900601	CTGTTCGCCATGCCAGAGATCACTGCAACTGGCAACAACGCAACACTCTT[T/C]AACTCTGGTGTCATGGTCATAGAGCCTTCCAACTGCACATTCCAGCTGCT	9	52112939

Table A1 (cont.)

X470	GFSSContig20403_1940	GFSSContig20403_1940-1_B_R_1863899229	AATGCTGGAGACGGTACAGCCATAACGACATATGGAAAGAGGGATCCCAA[T/C]GATGCCTTGGACGATGAAAATATCGCATCCTCATTCCAATTGATGTCCAA	9	58044029
X472	GFSSContig8940_858	GFSSContig8940_858-0_B_R_1890481054	AAAGATAGCCTGCAAGGCCCGTATGCCCTCGTTCAGAAGCCAGGAAAGC[T/C]GCTGTTTTACCCACTGGGTCTTGTGCAGTGGGATCAGTAACTGCTGTTGCC	NA	NA
X483	GFk40ctg445731_197	GFk40ctg445731_197-0_B_F_1890479813	GCAGCCTAACGGCACTGTGCAATCCTTCTCCGTCTCCTTTGTGTTTGCAATCCTCTCTG[A/T]CCATGCTGACATTAGTGCCGATGGCATGGCCTTCTTTGTTGCCCCAACCAAGAACCTCTCA	2	13073677
X492	GFSSContig11918_395	GFSSContig11918_395-0_B_F_1890479702	ACCATTCAAGCTGCAGAATGGATGGCTTTTGTGGGCTGGAGTTGGCCTCTTTGGAGCAA[T/C]AATTTCTATTGCTTTAGCCGGAGCTGCTATGACTTATCTGAATGGTGAAACTCCAGAGAGA	2	58999396
X502	GFSSContig19084_575	GFSSContig19084_575-0_T_F_1890482141	TCAGGGAGTTCCCAGTCAAAACAGTGAAGCAGGTTGGCCAAGATGAACTC[C/G]ATGTTAGTCACAGCCATGGCCATCCCCGGGCAAATCCGGCGACCTGAGCC	1	1042529
X520	GFSSContig17577_1399	GFSSContig17577_1399-1_B_R_1863898262	GAGTTCCGGACGGAGATCGAGCTGCTCTCCCGTGTCCACCACAAGAACGT[A/G]GTCAGCCTCGTGGGGTTCTGCCTGGACCAGGCGGAGCAGATCCTCGTCTA	8	10778664
X523	GFSSContig18309_474	GFSSContig18309_474-0_B_U_1890482655	ACTTCTCTTGATAACCTGGTCCATCTGGAATGTGTGATTTGCGATAGAGTCCAAGATCA[A/G]TGCCATCAGCATCGATAATGGCCACCGAATTATAATGTGCATTGTTTGCTTCTTCGAAAAA	4	50906248
X527	GFSSContig18881_588	GFSSContig18881_588-1_B_F_1863899798	AGGATGGCGACCATGATGGTGGAGAGGGGGTTGAACATGGTGACGAAGAC[A/G]GGGCCTTTCTTCTCGGTGCACCACAGCTGCACGAACACCGTGAAGCCGTT	1	70053618
X528	GFSSContig7525_157	GFSSContig7525_157-0_T_R_1890480618	CAGTCGATGCTGGATTATGGCCTGTCGATTGCCCTTGATGCCATATGGTTCTTGCGGAC[A/G]AAACGGGATCTTGAGGGGCTCAACAGTCTGATAGCGAAGATTGTGGCCTCAGGGGCAAAGG	4	52866469
X536	GFSSContig18290_1509	GFSSContig18290_1509-1_T_F_1863900172	GGCTGCGTCATCAGCCCCGTCGTGTTCTGGATCTTCTACAAGGCGTACGA[T/C]GTCGGGCTGGAAGAAGGGTACCCGGCGCCGTACGCCAAGATCTACCGGGG	4	1000853
X540	GFSSContig16463_305	GFSSContig16463_305-0_B_R_1890480611	CCAGGGTTAGATTTGATCAGAAGCTGCCGGCCATCAAGATGAGTAAGAACAAACTGGAA[A/G]CCACACAGTGCCTCAGTGAGAGAGATTGTGTGCTCAACGTACAAGTCATCATACTTCCTCT	4	62928686
X548	GFSSContig17456_751	GFSSContig17456_751-1_B_F_1863898123	GACTACTAAGATGAGTGTGACCATTGCTCCTCTCAAGATGTCCAAACCCA[T/C]GAGGCCACTTATCTTAACAACATACAACCTATCAACAGTGCTCATAGACC	2	2409894

Table A1 (cont.)

X559	GFSSContig8870_238	GFSSContig8870_238-0_T_R_1890482183	TTTCCTGTCCATGCTACCGCCCTTCGCCACCGCCGGCGCCACCTTCTCGCTAACATCCT[T/G]CTTCCTCCCCATGACGCTGGCCTTGTCAAGAAGCCGAACCACCTTGGACTTGCCCGCGGCG	1	12017508
X568	GFSSContig1840_351	GFSSContig1840_351-0_B_R_1890481113	TGTGTAGGAGCACCATGAGATGTGGTGGAAGCAGGTGGCACAGAGGATATGACAGATTT[A/G]CCCTTACTGCGAGCATCGGTTTTTATCTTTATTTCATTATCAGCACTCCGCTTGAGTTCAG	NA	NA
X584	GFSSContig12698_1019	GFSSContig12698_1019-1_B_R_1863898535	TTCAGGCTACCTTTGGTGAAGAGCATCAATGTCAGTGGGCACAAGTATGG[T/C]CTTGTCTATGCTGGTGTTGGTTGGGTCATTTGGCGGAGCAAGGAGGATTT	7	57312732
X595	GFSSContig15605_1353	GFSSContig15605_1353-1_T_F_1863899324	TTTCAGCTTGCTCATGCATCCTTCCGTCTATATTGTGTAAGAAACAATCA[T/C]GTGCAAAGTGTTAAGCTTGGTCCTCGTCTCCTTGGGGATGCTCCAAAAAT	2	60431545
X596	GFSSContig8643_492	GFSSContig8643_492-0_T_R_1890481266	TTCGCACATTGCACAACGTATTCGGCAAGATGGTGGGACTGCGGATGCATCTCTTCGCC[A/G]TGAGATCCAAACTGAATCTGTTCAGCTAGGAATTTCGATGCAACATTTGGGTGCTATGTTT	7	60495814
X612	GFk50ctg34159_526	GFk50ctg34159_526-0_T_F_1893112198	GTTAGGAAGCAGTGCAGGGCTGAATCATGTCAATGGAGCTCCAAGGATTA[A/G]ATCAGTTGTGAGCATACCCAATAGGGAAAGGCTTGATGGTAGCACACATA	2	613145
X624	GFk40ctg9752_150	GFk40ctg9752_150-0_B_R_1890481093	GAAGGGGAAGTTTACATGTTGCCTGCTGACTTGATGAGAGCAGTAGTCCCTGTTTTTCC[A/T]CCATCAGAATCCACCATAGTTCGTGAAGGAAGATTAAGGGGGGAGCGGAGCCCTGGAGAGT	6	50812497
X633	GFSSContig15477	GFSSContig15477-1_B_R_1863901147	GCCATTGATGCCTTCTCTTGTAGTAACTCGTGGAGGAGAGAGTCGTCATT[T/C]GGCAATCTAACATCCCATTTCCGGATAGCTGCAACAATGACTTGGAAAGC	NA	NA
X638	GFSSContig17850_1447	GFSSContig17850_1447-1_T_F_1863898691	GATGAGCTGGAGAAGAACCTGGAGCTCACCGACTGGCACATGGAGCCATC[A/G]AGGATGACCCTGTACAGGTTTGGCAACACATCAAGCAGCTCACTCTGGTA	10	51803309
X642	GFSSContig15237_626	GFSSContig15237_626-1_T_F_1863899425	CAGATTGCCGCGGCGGCCATGCCGATGATGGAGAGGACCAGGCCGATGCC[A/G]ATCTTCTCCAGGTTTGTGAACCCCTGACGGCCGGTCACGAGGCTCCGGCA	3	19176478
X647	GFSSContig8083_743	GFSSContig8083_743-1_T_F_1863899554	CACCATCGCCATCCTCCTCTCCATCCCGGTCTTCGCCGCGGGATCCAGGCTGTACCGGAA[C/G]AAGGTGCCCACGGGGAGCCCGCTCACCACCATCGCCAAGGTCCTCGTCGCTACCGCGCTC	10	50564913
X664	GFSSContig18615_2488	GFSSContig18615_2488-1_B_R_1863898868	AATGGTGTCCAAAATAAGGCCCTCAAGAGGGTGGTTGTATAGAGCTCCAAAGGAATAAGG[A/G]ACTACAAGAGTGTGGTGCTTGGAATGGATGTGTTTATACAGGAACTTGTTAATGTGCATG	4	58811382

Table A1 (cont.)

X665	GFSSContig10130_795	GFSSContig10130_795-1_B_R_1863900508	CATGATGGCATCAGCACCTTCCCGGACTGCAATAGCTATGTCAGAAACCTCTGCCCTAGT[A/T]GGAGTAGGATGGTCAATCATGCTTTCCAACATATTTGTAGCGACAATGACTGGTTTCTCC	1	49673720
X668	GFSSContig2033_278	GFSSContig2033_278-0_B_R_1890481481	TCGCCAGGAGCCCCGTACTGGAGATCCTCAACATCCAAGGGACCATTAAGGGGTTGCGT[A/C]TCGTCGGCCAGAGCCTTCGGTGCGTGCAGATCTGCGCTTCCGTGGTGGAGAACATCGCCGT	8	37504427
X6	GFk50ctg127857_253	GFk50ctg127857_253-0_T_R_1890480274	TAAAGTTCGACGCACTTGAGCAATTGGTTCCTGTTATGGATCAAAAGACATATTGGGCC[A/G]TTGTGTCGAAAAATTTTGCTTCAAAGCCCAGGATAGATTCGATAAAGTACTACCTGAATGT	3	67658158
X26	GFSSContig9726_926	GFSSContig9726_926-1_B_R_1863899728	TACATGCCGGCGTGTCTGTCGGGCAGTAAGATCGGCAACTACGAGTGGTTCGAGTACTGC[A/G]CGCGCCGCCTCATGGACACCAGCGGCATCATCATCAACTCCTCGGTCGAGCTGGAGCCTG	2	68655608
X37	GFSSContig3933_570	GFSSContig3933_570-0_T_F_1890481710	TTATGCTGTGCAAAAATCAAAACTCTGTGTTGCCCGACAGCTGTCGAAGCATCAGGACT[A/T]GATATTTCTGATCCTATACCACATTCTTGAAGTATTTCTTGAAGAGCAACAAGCTTAGGTG	9	59196167
X45	GFSSContig16360_390	GFSSContig16360_390-1_T_F_1863900630	GCGAGGATTCAGCATTCCTCTTATAAGATCTTTTGCACTATCAGATATGA[T/C]GGGCCACGGGTCAGAATCAAAATCAATGACACCTTTCAATACAGCATCAA	6	55594981
X46	GFSSContig11847_583	GFSSContig11847_583-0_B_F_1890480778	GGGTACCTAATTCCTGCTTTTATACATCTGAGGAGATGCCACAATAATCCGATGTTGGG[T/C]CCTACGGTATTGGTTTTGGCCCCTACTCGCGAGCTTGCTTCACAAATACAAGACGAAGTAG	5	61159244
X50	GFSSContig12663_1010	GFSSContig12663_1010-1_T_F_1863898371	CTGAAGAAGAGAACAAGTGTTGTGCCCTTTGCTGCGATTCTTGATGGACG[A/G]CAGAAACTGCCCAAAGATTATCACAAGGAGTTCTTTCGGTTACCATATGT	8	33994953
X51	GFSSContig18253_1408	GFSSContig18253_1408-1_T_R_1863899939	GAAGAGGTCCTGAGAGAGCAGATAGCTGGTGGTCAACCACGGACACACAG[A/G]CCATGGAAGAAGATCATTGTCATTGTTGAGGGTATCTATAGCATGGAAGG	5	45707101
X55	GFSSContig14690_690	GFSSContig14690_690-0_B_R_1890481103	ACTTTGTGGTAAAGGTGATCTCTTCAGGGGTTAGATCATCAGACTCCTG[A/G]GCCAACCACCCACCACTCACCTGCCTAAGTGAAAGCATCCCTTTTCCACTT	6	57160241
X61	GFSSContig6638_165	GFSSContig6638_165-1_B_F_1863899208	GGTGGCGCGGGGCTTCCTGAGCCTGTACAAGACGGCCGGGGAGAAGGTCAAGAGCCTGTC[C/G]GAGGAGGTGATGGACGAGGTGCGGCGCCTCATGGACAAGTACAAGGGCGAGGAGCTCAGC	4	63070853
X66	GFSSContig19719_251	GFSSContig19719_251-1_T_R_1863898636	AAGAGTGCCACAACTTCTTCCAGCCTTTTTAGGTTTGAAACCCCTCTCTCTGTGCACAAC[T/G]TCATCACCTTGCCATGCCCTGACAGAAACCACAAGCTCCCCATTCACTTCAACAGATGCT	6	62045851

Table A1 (cont.)

X79	GFSSContig10620_634	GFSSContig10620_634-0_B_F_1890480156	GGTTTTCTCCACGTTTTCTTGGAGCTGGTCTTTTAAATCTCAGCAGGCTAACAGCGAAT[T/C]CTCAGTTCTGAATTCTAGTGATTCCTCTGGATATGGTTACCATGGCAAGACACTGGAGAAG	3	52816333
X86	GFSSContig20006_1334	GFSSContig20006_1334-1_T_F_1863898131	GCTTGCAAAGAAGGAAGAAATCTACTCTCAGTTGCAAGCGAGTTTGAAAA[A/G]GATTTCTGACACTGTGCCCTTAGCACCAAGGATGTTAAAGGATATAATAG	10	57906816
X89	GFSSContig14473_841	GFSSContig14473_841-0_B_F_1890479209	TGGTTTAAAACTCGGAAAATCAGAACATGGGTGCTTTCTCCTGATAAAAAAGATGTCAG[A/C]CCACGCATTTTATTTGACCGATCTTCAGAAGATGTATACTCTGACCCTGGCTCACCAATGT	NA	NA
X98	GFSSContig10741_1216	GFSSContig10741_1216-0_B_F_1890480145	CTAGACCTTCCAGGAGGACTTGCCGTCTTCGCTTCAGTTGGAAAATGTT[A/G]TCCTGTGACTGGCTAGACTGCAACAGACGGTCAGTGTCATCAACCTCAAGA	3	63773120
X99	GFSSContig7996_485	GFSSContig7996_485-1_T_F_1863898980	ACAAGGATGTCAAGCATCCAATGCAGGTTGTCAGCCTGCCTAGCAATCTG[T/C]GCCACCTCTGAGTGATCACCCTCTGAAGCCCTCACAAATTGCTCACACAG	6	55296845
X104	GFk45ctg342913_247	GFk45ctg342913_247-0_T_F_1893112180	TGGAAATTGCTTCTATCCGGTGACAGTGACAGCAACCGCTGAGGATGTTGCTAGTGGAGG[A/G]TTGCTTGATGTGATTAGGATGATACGGGATGGGAAGGCTAGGCTTCCTTTGGAGTTTGCC	8	7977535
X105	GFSSContig16458_1714	GFSSContig16458_1714-1_B_R_1863898111	CGAGCTTAGCAAGCTCACGATCATAGCTACCCTTGCAAAACAGGCACATG[T/G]CTGGCTTAGCCATCAGAGGATGGTCACTCCCTGCCCCAGGTGGCCATCGG	7	13309964
X122	GFSSContig19978_2050	GFSSContig19978_2050-0_B_R_1890479306	CAGAAGAATGGTTTCAAATGAATGCTGTTCTTCGTGTAAGCCTGGGGAA[T/C]TTCTTGTTTTTTGCAATATTGGCTCTCATGATGATTGGTGTGAAAGACCAG	1	17032984
X131	GFSSContig19351_2904	GFSSContig19351_2904-1_T_R_1863900029	TGAGCAAAGCCCAAAGCATTATACAATGCCCGTGTAGCTGCAAGCCTCACATCAGAGTTT[A/G]CCTCAGAAGCATTCATACCCTGAACAACAGCTGTAAGTATTTTATTGACTTGGTCTTGGT	NA	NA
X134	GFSSContig12703_673	GFSSContig12703_673-0_T_F_1890480237	TCTGTATGGCTTCTCGCAGGCCATTGCCACGCATAAGGCACTGCAAGGG[T/C]TGCAGGGGAAGAGGCCGTTCATTCTGACCCGCTCCACGTTCGTCGGGTCGG	3	7500246
X138	GFSSContig11701_739	GFSSContig11701_739-1_B_R_1863900984	GCTCTCAACAAATCAGAATACACTCACAGTCGGTGGACTGTACACAGTTGATCCTCAGAC[A/G]GCCGTGAAGGCAAGGCTCAACAACACTGGAACGCTTGCCGCGCTTCTTCAGCATGAGCTT	1	66841447
X143	GFSSContig5092_390	GFSSContig5092_390-0_T_U_1890482420	AAGGAGGACAAGAAGGAGGGCGACAAGAAGGAGGGCGACAAGAAGCAGCA[A/G]CAGGTCGTGTGGTACGGCCCGCCGCACCCGTGGTACGCCGCCGCGCAGCA	6	60362521

Table A1 (cont.)

X151	GFSSContig15396_715	GFSSContig15396_715-1_T_F_1863899371	GACGCTGTACGCGAAGTGCATCACGTCGGCGCCGTCCACCTGGTCGCAGGTGCAGGGCAG[A/C]GGGATCCTCAGCTTCTGCCCCGATCTGGATGAGGTTAACGTTGGTGATGTTGTTGGCGGTG	9	1722376
X152	GFSSContig19723_735	GFSSContig19723_735-1_B_F_1863898462	AGATAAGTTTGATCAGATGCTCATGAGAAAGGAGTATGAGTACTCAATGAATGTCCTTGC[A/G]TTTGGAATTCAGAGCTCAGACATCACCCCAGCTTTCCCATATGTTGCACCGTTTTCATGC	3	49752585
X154	GFSSContig9387_726	GFSSContig9387_726-0_B_R_1890481706	GTCCTCAATATAAATGGCTGCTCCAGCTTAGGTGGAACAACATCCCCAAATAGAGAAGC[C/G]TCATGTGCCAACTTCAGTAAAATTCTTCGCACAATCTCTCCCAGATACATGCCAGAAATCA	9	55414507
X157	GFSSContig14161_1141	GFSSContig14161_1141-0_T_F_1890480629	CGGGCGCTCCATGCTGACCAGTATGATGCACAAAGAATGGTACCAACTGCCATAAGCCA[T/G]AGAAACACCTCTGCAGTATCAACCAGAGGACGATCTGGAGAGTACAGCTCCACTAAGACTT	4	67352063
X165	GFSSContig11002_434	GFSSContig11002_434-0_B_R_1890482002	GTGCCTCCATGATCTGCTTCTGAGCACATGGATGATCTATATCAAGAAGAGAGGGCATC[T/C]GTGTCAAGAGGTCATCCAATGACTCCAGCAAAGCTTTCCTTTTTGATTTTCTCATAGGTCT	10	7176784
X174	GFSSContig19603_1415	GFSSContig19603_1415-0_B_U_1890482376	CGCCCAATCCACGGACATCTTGCCGGCGTCGCTGTACGTCGTCAGGCGGC[T/G]GAGCTTGCTGTACGGAATCATGGGCGAAGCTTGCAGCAAAATATGGATCT	4	60492701
X176	GFSSContig11465_504	GFSSContig11465_504-0_T_F_1890480245	CTCAATGGAGGTGACAGTGTGAATCCAGTTCAAATGGGTAATAAGATGGTTGAAAGGGT[T/C]GTGAACATGAGAAGGCTAGTTCCTCCAAAGCATGATGATCAAAGATCCAGCCTCAACAGTC	3	6683212
X177	GFSSContig18986_1716	GFSSContig18986_1716-0_B_F_1890482088	ACAGGTTCTTCAACTACGAGACATGCTACGGCAATGATAGATCGTCAGT[T/C]GACTGGGTAGAAAAGTTTCAGTTCACTGCAGCAGAGATCCTGACTGTGGCC	10	48867712
X199	GFSSContig13400_323	GFSSContig13400_323-1_B_R_1863899761	AATTCTTCTCTTCAGAGAAGACGGTTCGCGCCCCAAAGGCAAGAACTGCTGCTCGCGCCA[T/C]GGCTGTAGTGGTCAGCATTCTACTGACAAAGCCAAAGGCAAGGAGGTGCACAGGGTGGCG	6	56462968
X200	GFSSContig14911_734	GFSSContig14911_734-1_B_F_1863900904	AATTATTGCAATTGGCCGAAGCCCTACCATGCGGCAGCCATTGATCCATGCCCAAAATGT[A/G]CCTGCCACTGGTGTTCCTGTCCCAACACTCGATCAGCGTGCAAGTAGAAATGATGCCTGG	1	49703657
X217	GFk40ctg349904_126	GFk40ctg349904_126-0_B_F_1890482044	CATGCCATCAACTTCTGACCTTAAATTTATGAGTTCCTGATTCTGGCGTTCTAAATCTG[T/C]TCTTTCTTTCAACAAGTCTGCTAGTTCCTCTTCTCTGTCTGTCCTCTCATTTGCAAGCTCA	10	20423246
X222	GFSSContig5034_412	GFSSContig5034_412-0_B_F_1890481325	ACTAAGCCTGTTGAAATTCAAGTGGGTGGGAGGAGTGTCGTGAACAAAGATATCACACA[A/G]CTGGTCGAGGTGCGACCAGACACCGAGAGGTTCTTCAGGCTGTTAGAGTTGCTTGGTGAAT	7	5138627

Table A1 (cont.)

X237	GFk25ctg762174_247	GFk25ctg762174_247-0_T_F_1890479212	CAAGTGGCTACACATGGAGAAAATACTGGCTATGAAGTTCCTTGCTTGATAGTTGCTGC[A/G]AAAGATGATCTTGACCAATCTTCACAAGCTCTACAAGAATCAACTAGAGTGAGCCAAGACA	1	3149279
X267	GFSSContig7729_683	GFSSContig7729_683-0_T_R_1890479329	TCTGATAGAAGAGATGAAGATGGTTGGATGAAGGGGCTTCAGAGGCATATTGCTTTGCT[T/C]CAGTTCCGCAGGCCACTATGTAACACCAGTCTGGGATGTCAGTGGTGCCAATCATCAGTGA	1	26686745
X277	GFSSContig17910_1353	GFSSContig17910_1353-1_T_R_1863899914	GTGAGCGGCGAGGGGCTGAGACCCTTGGCGACAGCGGTGATCACCTCTGC[T/C]GTGAGGTCCAGCACCTCGTTGGCAGTTTGCGCCTGGACGATGGAGCGATT	3	2814495
X290	GFSSContig19787_956	GFSSContig19787_956-1_T_R_1863900656	TGGGCCACCATTACCAGTAGGCAGGATAGAATTGCCAGGCATTCTGAACTTGACGCTATA[T/C]GGTATCCCACATTCGCCCCCACCGTCCTTTCCATATGTAGCCCACCATGGTTTCCAAGGT	2	766164
X305	GFSSContig18231_1011	GFSSContig18231_1011-1_B_R_1863899643	CGAGAAGCTCCTGCCGCAGCTATCAAATCAAGAAAAGGCCAAGAAATCGGAGAGGAGCAC[T/C]GTGTGCCTCTACTTCTCCACCGACCGGGCGCCGGTCCAGGACCCCATCCTGCTGCTCAAC	2	74081417
X308	GFSSContig20360_172	GFSSContig20360_172-0_T_R_1890480226	ATTTGCTGGCATCAGCATATTCTTCTACTTGTGGCACCACTGGATTGTTTTTGTTTGAA[A/G]TAGCTGAAGCAGTGTTATCCTCATCTGCTTTCAGTGCTTCTTCAACTTGTGGCACCTCTGT	3	59642734
X327	GFSSContig8648_564	GFSSContig8648_564-0_T_F_1890481768	CTTGGACGAGCTGCGGTTCTGAAGCATGTTAATTTCCTCACAGCTTGTGGATTTATGCT[A/C]TCTCAAGTGAGCAAAATGGTTGTGGCATGCCCCCAACTGCTCGCACTAAATATGGATATAA	9	48738773
X329	GFSSContig14866_659	GFSSContig14866_659-0_B_F_1890481793	TCCACTGCGGATGCAGGGGCTGTGCCAGCGGTGATTAAAGTTGATATCCTGTGGTTGTG[A/G]GATAACCTCAAAACTGTTCAAAATGTGTCCTTATATTTGAGCCCGTATGCTGTGAACAAGC	9	52399520
X331	GFSSContig20039_958	GFSSContig20039_958-1_T_F_1863901063	GGTGTTCTGGGTGGTGCCCCGCTCCTCGTCCATCAAAATCCGGTGGGCGA[A/G]CCTCAAGAACCGGCTCATGTCCATGTGCCCTTCCTCCTACTCCATCCCGT	9	1318926
X332	GFSSContig11100_445	GFSSContig11100_445-1_B_R_1863900383	CATCCCCCGGGGTACACATCAGGGACATTTTCTTTGTCCATGTTCTTGGCCCTTGAGTTG[T/C]TCCGAACTGATTTTTCTGAAAGAGATGGTATAACTGTCGCAAAGCTTCTCTCCTTGCTTC	1	9710866
X341	GFSSContig19145_875	GFSSContig19145_875-0_T_F_1890482093	ATGTTGTTCTAATTTGCTCGTATAGCTGTACTTAATAAGCAGATGTACC[T/G]TCATGGACTCGTAAGACTATTCAGATGTATATAATTATACTTAGTGCACAC	10	60084282
X355	GFSSContig18577_871	GFSSContig18577_871-1_T_R_1863898993	GTCACAGAATTCTGGCCAGTGGAAGTTTAAAAAGGGTCCTGAATATGGTAATGGTGTTTC[A/G]GCTCTTTCTGTACCCAAACAGTACAGTTCTAACACTAAACAATCATCTGGGAACAAGTTT	10	5972378

Table A1 (cont.)

X356	GFSSContig451_367	GFSSContig451_367-0_T_U_1890482307	ATGTATAGTTGGCCCTGATAGATCTGACGTGTCGTCGCTGTAGCCTGTGT[T/C]TGAGGTATGCGCTGCGTGGTAGCAAGTGCCGTACGTATTACATGTTTACA	NA	NA
X379	GFSSContig13511_179	GFSSContig13511_179-1_B_R_1863898130	ATACAAACAACCAAGCACCCAACACTCCAGATCTCAAGGTCCTTGGTGAG[A/G]ATGCTCTCCCTCCCTCAGTCCAGCACATCATCACCTAGAAGTAGCCCTAG	1	73247705
X387	GFSSContig15156_860	GFSSContig15156_860-1_B_R_1863898710	GTCGCCGTTGGACTTGCAGCTCCACAGCTGCACCTGCTTGCCGTTGTAGTAGTAGCCGTA[C/G]GGCACGTCCACGCACCTCCCTTCCAGGCCGACGAGGCGCACCGTCGGCTCGGCCTGGCCG	NA	NA
X402	GFSSContig12104_510	GFSSContig12104_510-1_T_F_1863901026	GAGGGCGATGAGCCACTTGGGTTTCCTGAGGGTGACAAGGATGTTCTCGT[T/C]GACGCCGTTGCCGAAGGCCCAGTAGCCGACGAGCGCGGCAGGGAAGTAGC	7	2468184
X403	GFSSContig17910_784	GFSSContig17910_784-0_T_R_1890482233	GTGTACGGGCACTGCTAGTGCTACCACCCTCTCCACCAGAAAGTTCTTCTGCTGAGCTC[T/G]GATGCGCGCTTGATTTTAAATCAGATACATGGCACTGAAAACTGGTATCATTCTGAAAAGC	NA	NA
X409	GFk40ctg540920_180	GFk40ctg540920_180-0_B_F_1893112187	GAAATGCATGGGTCAAATCTCAAATAGCTTTTGTTTGGACAAAATCCCTAGGTGAAAACT[A/G]CCACCTGCTTGATGGCCAAATGTCTATTCATAAACAAGGATGCCGTGGAGCAGTCTGGTT	3	55380139
X411	GFSSContig15624_913	GFSSContig15624_913-0_B_R_1890480764	GTAAAAGCCAGAGATGATTCTGTTACTTTTTCTCTAGTACAAGAAAATCCATCTGTACG[T/C]ACTAGAAACATCTCTGCTTTTCTTCTTGACTGGAGTCTAACGACACCAGTTGAAGAAGCAC	5	8108879
X432	GFSSContig18538_955	GFSSContig18538_955-1_B_F_1863901091	GGCCATCGGCAAGGTGCAGACCCCGGACCCGCCCTTCAACGAGGACATGCCGCGCCTCGA[T/C]TGCCCCAACTTCTACTACGACATGGAGGACATCCTCTTCGACCAGGTCTCCCGCCGCGAC	1	54707213
X434	GFSSContig11847_520	GFSSContig11847_520-0_T_F_1890480790	CCTGTTGCACTGCAAAACCGGGACATAGTAGCTATTGCCAAGACAGGGTCTGGAAAGAC[A/G]CTGGGGTACCTAATTCCTGCTTTTATACATCTGAGGAGATGCCACAATAATCCGATGTTGG	5	61159307
X437	GFSSContig19736_4089	GFSSContig19736_4089-1_T_R_1863898539	TGGACTGCATGATCTGAGATCCAGACTGAGCATCATTCCACAAGAGCCGACGATGTTCGA[A/C]GGAACTGTCAGAAGCAACCTTGACCCCCTAGGGGAGTACTCTGATGATAAAATCTGGGAG	1	69014234
X445	GFSSContig15281_3466	GFSSContig15281_3466-1_B_R_1863898181	TGTTAAGCTCGTCAATGCTCTTAGGACGATACCAGCCATCGTCAGAAACAGGAACTGGAG[T/C]ACTGTTAACCTGCTCAATCGAGGACTTTATCTCAGATTTGAGAAACTCAGGGAAAGTGCA	1	4622525
X467	GFSSContig6446_373	GFSSContig6446_373-0_T_R_1890480233	TCTGCTTCAGGTACTGTGGCCCGAACCGTAATGTCTTTACGGGATGATGGGGGTCGCCG[T/C]TGGTTTCGAATTCGGAGTCCATGTAGCGATCCCCTGGCTGTTCTTCTTGCAAAAACAGCTC	3	72353041

Table A1 (cont.)

X469	GFSSContig20506_2030	GFSSContig20506_2030-1_T_R_1863899276	TATTATGTTCACAATGTCATATGCAGGCTGGATAAGATTACCATCTGAAT[T/C]CAACTTTACAGGGCCAGTTGCACCCATGAAATTTACTTTGCGGATTTTTT	NA	NA
X482	GFk50ctg100382_211	GFk50ctg100382_211-0_B_F_1890479168	CTAACACCTGGCCAATCTGCCAGGAGGAAATTAGCACTGGGAGAGAGTGCAAGTAGGCG[A/T]GTAAGGGATAATCAACTGCCTGAACCCACTGGACAGTTCTCACGAGGTTTAAATACAACCA	1	17063499
X488	GFSSContig4096_351	GFSSContig4096_351-0_B_F_1890481784	GCATCTTCAAGGGCAACAGGCAGGCCATCTTCTTCTAAGTCCGGAGGAA[T/C]AAAAACATTTTTCACGAGTGGAATCGGACCTTGGACATCATACAACCCAAT	9	51331309
X496	GFSSContig18202_1355	GFSSContig18202_1355-1_B_F_1863899741	GGCCTGCAGGAGTTCTTCTACGATCAGGTGCCGGACAAGCTGCGCAGCCT[T/C]GGGCTGGCGCTCTACCTCAGCATCTTCGGCGTCGGCAGCTTCATCAGCAG	9	50807789
X513	SSk40ctg20422_195	SSk40ctg20422_195-1_B_F_1863899074	AAGTCGACGTAGACGATTCCGAACTTGGACGTGTAACCTGACTGCCACTC[A/G]AAGTTATCAAGGAGAGACCAAGCGAAGTAGCCAGCCACGTTTGCACCATC	1	9729690
X532	GFSSContig13472_457	GFSSContig13472_457-0_B_R_1890481753	GGTGTTGCTTCCCATCCAGCAGCCCAGAGAGAGAATAATGATATGGCAAATGCTGCCAC[A/G]TCAGAAAGAAGATGTGCTGCATCAGTTAAGATGGCAAGACTGTTTGCTTTGATGCCCCCAA	9	2669340
X544	GFSSContig19690_2175	GFSSContig19690_2175-1_B_F_1863899708	CGCCACCGACCCGCGGCTGCCCAAGAACGCCAAGGCCTTCTTCAACATCCTCGACTTCTC[A/G]GTGTTCAGCTGGGACAACAAGCTCCCGGGCGCCCAGCTGCTGCTGTCGCGGCTGCGCATG	6	62202181
X551	GFSSContig15887_1200	GFSSContig15887_1200-0_T_U_1890482365	GCGCTCTGTTATCTAGCTAAGGTACTCTCCAGGTTTGTTGTCAGACTCCA[T/C]GATTCTATCAGGGATGAGCGCTATCTCATCGGGCAGAGGTTGCAGAACTA	10	54238449
X571	GFSSContig16407_724	GFSSContig16407_724-1_T_R_1863898359	GGCTGCCTTAAAGATGCGAGGGCTGTATAGGACCACGGCCTCGATTCCCGTGAGGTGCTG[A/G]AAGAAGTGGACTCCGAAGGCCGCGACGAGGATACGCCGGACGGGGGGCGTCGGGTGCAGG	6	30264069
X589	GFSSContig15224_746	GFSSContig15224_746-1_B_F_1863898498	TTCTTGTGAAGGCATGGTGTGATCAGAGAAATCTTGAGGAGGCCTGGGGC[A/G]TTGTGGGCAAGATGCGAGCAGGTGGTGTTGAGCCTGATATCGTCACTTAC	2	62305422
X593	GFSSContig11785_150	GFSSContig11785_150-0_B_U_1890482642	CGCCGCCGCCGTCACCACCGCCATTGCCGTCGACCATCTTGCTGATGAACTTGGGGATG[T/G]GGACCTCGTACCCAAACAGCGAGAAGTTGGGCGGCAGCTGCGGCATCTTAGGCCCCGATGG	2	2833060
X594	GFSSContig14923_586	GFSSContig14923_586-0_B_F_1890481047	CTAATGCATAGCTTATCCACAGCAGCAAGTGCTATCCTCCTCTTCAATATATTGGCATC[A/G]GGGTCAACAAGGTATAGAGCAAAGTCTGTGATCACTAGGATGCGCCTTTTCATCTTTCCTG	6	59145596

Table A1 (cont.)

X598	GFSSContig7988_209	GFSSContig7988_209-0_T_U_1890482373	AACGCCAGAACAGAGAAGAACGAATCGCGCCACAACAGAGAAGAACGAAT[T/C]GCAGTCCTCAGATGCCGCAACAGCCGGATGCGCCGCCTGCGATGCCCCCT	NA	NA
X607	GFSSContig10350_450	GFSSContig10350_450-1_B_R_1863898885	CCACGGCGCCGATGATTGGCGACAACGCCGCCGAAGACATCAGAGCCCCC[T/G]CCTCGCTCTCCTCCATCTCATCCCGCACCTAAGCATGCAGACGCATCCTT	1	65309889
X608	GFSSContig12124_870	GFSSContig12124_870-1_B_R_1863899909	GAGATCCTTGATTGCCTCGACGAGGACAATGTCATTGGCAGTGGCGCGTC[T/C]GGAAAGGTGTACAAGGCCGTGTTGAGCAACGGCGAGGTGGTGGCGGTGAA	3	219836
X617	GFSSContig17839_594	GFSSContig17839_594-0_B_U_1890482551	CTCTCTCAGCTAGTGTCCTGTGGTGGCCACCATGCACACCGAGACAGCTG[A/G]CAATAATGGCATCCGGCGGCGGCGCCATGGCGCCGTCGCGCTGCTGCTCG	8	55144546
X641	GFk45ctg106126_165	GFk45ctg106126_165-0_T_R_1893112213	GAAACATGTGGGGAGGAGCCAGAGTTGTGTCACCTACAGCAGGTGGATCT[T/C]TCCAAGGACCTCATCAATGCAGAATGGAACCTTGCGAAAGCAGCATACAC	3	71053730
X643	GFSSContig16256_300	GFSSContig16256_300-1_B_F_1863899696	CACCGGCACGGACCACCCGTACGCCGGCTCCGTGAGCATCACCTGGAAGA[C/G]GACGTCGTAGCTGGCCCCCGGCGTGAGGTGCGACAGCTCCAGCTTCCCGT	3	5530709
X662	GFSSContig17986_981	GFSSContig17986_981-1_T_R_1863898328	TACTCCTTCCTTCCCTCCATGGACGCCCCCCGAGAGAACACCTTGATGGC[T/G]ACATCGAGGCCGGACTCCTTCAGGTGGCCGCGGTACACCGACCCCGACCC	8	7737343
X667	GFSSContig9542_144	GFSSContig9542_144-0_T_U_1890482520	ACCACAACGTGTAACGTGAGCGCTTATCCGGTGGCTCCAAAACCTTTCCT[A/G]CCTTTGATGCAAAAGAAAAAAGAAAGAAAGATATGTAGATGCTGAAATGT	1	65161268
X11	GFSSContig10593_69	GFSSContig10593_69-1_T_R_1863900201	AAGGATATCCCGCAAGGATGAGATTATGAAGGCCATTGGGAAGAAGCTAGACCGCTACAA[A/G]AACCCATGGTTAGAGTTGAAAATTCAGTATGGCCAAAATAAAGGGAAGTTCTATAATGAG	3	20393360
X21	GFSSContig20569_1650	GFSSContig20569_1650-1_B_F_1863899033	TGGGTTAAGAAGGTAGATGTCACAATGTCTGCGCAACCCGCACAGCCAAC[T/G]TATGGAGGGGAGCTTCCAGAAGGACTACAGAAGATTTCCAACATCATAGC	NA	NA
X67	GFSSContig15931_175	GFSSContig15931_175-0_B_U_1890482647	GGTGCACCTGACACTCTTCCCTTGGAGCAGCAGGTCAAAAGCTTCGTTGATGTCCTTGA[A/G]GCCGACTTCATGGGTTATGAACTTGTCAAGCTCCAACTCCTTGTTCAGGTACTTATCGGCG	1	67724596
X76	GFSSContig14158_427	GFSSContig14158_427-1_B_R_1863900355	GAAACGTCGTGCCGAGGCAGCTGCTCAATTTTGATCCCCAAAGGCTCAAA[T/G]ATCTCCTCCACCTTTTCTTCTGGGACAGGAACGGCTGCTGTCGACGACTC	6	57253680

Table A1 (cont.)

X83	GFSSContig17337_2234	GFSSContig17337_2234-1_T_R_1863900852	GTGGACTGCAGTCCATCGGTGCCTTCGACGATCAGGAACTGCGTCTCGAAGGGGATGTCG[T/C]GGCCTGATGAGCCCATCCTCTGCGTCATCCACCACATCTTGAATCGGAACGTGCACATGA	7	63617802
X87	GFSSContig17942_483	GFSSContig17942_483-0_B_U_1890482384	TCCAGAAGACCCGGCAGTCGCAAGCACAGCTCGCCAGGTCCTGTGCCCAT[T/C]GGATCCGTGTCAAAAAGATCCGGCAGTCGCAAGCACAGCTCGGCCAGCTG	6	49592234
X92	GFSSContig11810_723	GFSSContig11810_723-1_B_R_1863898417	CAGCGCCGGGTCTGCCATCATGAAGAACAGGTACGTCTTCACCGGCGCGTCGTGGGTCAC[T/C]GGTGCATTCAACAAGGTCGCCAAGGCTGCCACGGACGTCGGGACGATGACCAAGGAGAAG	10	658457
X116	GFSSContig16289_1017	GFSSContig16289_1017-1_T_R_1863899283	CATATCGCCCTTCATGCCACTCTGAGCAGTCGGGACGTTGACTGCTGCTTGATCCCAGAG[A/G]TTGATTTCCACCTGGAAGGTAAGGGTGGCCTGTGTGAGTTTCTGTATGAGCGGATTAAGA	6	49174455
X137	GFSSContig1362_140	GFSSContig1362_140-0_T_F_1890481109	CTGTAGTCACCACCGTGGTTCCGCCGCGAGCGGGCGTTACGAATACCACGCTCATCATC[C/G]ACCTGCCGCCGGCCATTCCTGCCGCCATAGTATGCTGGGGCTTCCTGTGTCACCGAAAGCG	6	49960123
X141	GFSSContig14117_827	GFSSContig14117_827-1_B_F_1863898152	AGAACTCTACAGGCACGCCAGTCCTACGAAGCCGCTCCACTGCAAAATACACAACACGTC[A/G]GTGAGTGTCATCCTCGTGTCCGATGCCACCGGTCGTTGCATCGTCAAGATGTGCGGGGAC	7	58043595
X169	GFSSContig19031_267	GFSSContig19031_267-1_T_F_1863900407	TTCCTCTCTGCGAAGTAAGCCGGCTGTTCCGGCGCCGGCAGAGACACGCT[A/C]CCGTTCTCCAGGATGGACACCACGGACGACATGAGCGGCCTGCCGTTCGG	2	66891104
X184	GFSSContig3212_326	GFSSContig3212_326-0_T_F_1890479828	TATAGTGGTAGAGGACACCACTCAGACAGATATAGGCATTATAGTCCTGAAAGGCGTTC[A/G]TATTCAGATAATCATTCTCGCCGTCACCGCTCTATTGATGTTGAAGAAAGGCATACTTCTG	2	17325216
X187	GFSSContig15802_503	GFSSContig15802_503-1_T_R_1863899495	AGGTTCAGGCTTCTTGTCTTCCCTGCCTTTCCCCCTAGCTCGCAGCTGTG[A/C]TTGAACCCTTTTAAAGAGCTCCACAATCTCCTTCTCTCTTTCCCCAGGAG	NA	NA
X190	GFSSContig12763_195	GFSSContig12763_195-1_T_F_1863899985	CCAACATAGGGTAGCCTGAATTTTGTGTTGCCAACGAACACAATGCTCTG[A/C]AGATGTCGATCATGGCAGGGAACATAACTCTATTTACCCCCTCTTTCAGA	6	52537823
X195	GFSSContig18985_1909	GFSSContig18985_1909-1_T_R_1863898628	CCGTCGGGGTTGCCGAGGTCGTTGTAGACGTCGTAGCGGTAGACGCGGTC[C/G]TGCTCCTGGTATGGCCCCTGCTGGTCGTCGCCCCTCAGGTTCCGGAGCTC	3	69865284
X196	GFSSContig16654_1653	GFSSContig16654_1653-0_B_F_1890480580	CCTGCATTATATCTGTTATGGGTTTTAGAGAAGATACAAACAATACAAGGGGTGCTACC[T/G]CAGAATCTATCAATGCTTTGCCTACATATAAATTCAAAACCAAGAAACGCCGCCATGGTTC	4	65210644

Table A1 (cont.)

X220	GFSSContig2426_408	GFSSContig2426_408-1_T_F_1863899428	TTCATCCTGGCAACACTTGGTTGCTAGTGATAGGAACCTCCTGATGCATT[T/C]TGGGGGGCACAAGCCCATCCGGCCATCGATTATTTCAGAAACTGTGCCCG	9	53272693
X233	GFSSContig19389_58	GFSSContig19389_58-0_T_F_1890478804	GAGTGCCCATTCATGAAGCTCCTCAGCTGCATCTTCCCCAGGGCATTCTC[A/T]GGCCGCTCCTTAAACACCCACATGTACATGTTCTCCATGTCGTGCTGCAC	1	62822153
X244	GFSSContig10720_700	GFSSContig10720_700-0_B_F_1890479688	CCCTGCGTCGGTGGGGGCGACGGGGGTATCCAGCGTCGGAGACCTCAGGACCGTCGTCG[T/C]CTCACAGATGGAGAACCTCAAGCGCCGACTCGACGCACTCCATTCCCGCGCTCACGCCGAC	2	17104859
X247	GFSSContig2952_216	GFSSContig2952_216-0_T_R_1890481279	ATGGACATTGCACAATCAACACGAGAAGAGTTACTGCTGCTATCAGAGACTTGTGCTCT[T/C]GTGGATGAGTTTTGGGAGGCAAGATTACGTGTCACCTTTCAACTGTTGTTCTCTTCTATTA	3	55633219
X252	GFSSContig18963_787	GFSSContig18963_787-0_B_F_1890479370	TTCAAGAGCAGTCTCAGAATCCAATTCATCCGGCCTCACTTCGATAGCT[T/C]GTACACTCTTGTCCACCAATCCCACGTCAAGAACATCTTCAGCAGGAGCAA	1	64629127
X264	GFSSContig17278_2352	GFSSContig17278_2352-0_T_F_1890482189	ATGAAGGACAAGCATACTAAGATGCCTCGTGGATTTGGATTTGTTACATTTTCTGATCC[A/T]TCTGTTATAGACAAGGTTTTGGAGGATGATCACGTTATAGATGGCAGAACGGTTGAAGTCA	4	8350554
X265	GFSSContig4757_256	GFSSContig4757_256-0_T_R_1890481254	TTGTCAATCTGGTCACCCATCAGAAGCTCACCCAGATTCTCAGCACTCTTCTTGATGCC[A/G]CCCTTGGGACGGCAGTAGGGCAGGCTGTAGTAGTTGAAAGGCATCTCCGTCTCGATGGACG	7	63556087
X269	GFSSContig15731_814	GFSSContig15731_814-1_B_F_1863900350	AGCATTGCTTGCCTGTGGCTAACTATACAAGGGAATAGCTTTGGAGGTCT[A/C]AGGCCAAGGAATCGAGAACGTGTGTCCGATAGCTGACCCGTAACCATGTC	4	2809730
X294	GFSSContig18320_993	GFSSContig18320_993-0_T_F_1890481689	GCTAATGAAGCATCATCACAAGTGACTCCAGCAGCTAATAGTTCTGCTAAAGCATCGAG[T/C]AGCCGCCCCATGACTGCTGCTGAGAGGCAGCGAGAAAAGCTGCAGAAAATGTTGGATGAAA	9	48979028
X309	GFSSContig14516_517	GFSSContig14516_517-0_T_F_1890481495	GTGGGCAAGTATGAGCTCGGCCGCACCATAGGTGAAGGCACATTCGCAAAGGTCAGGTT[T/C]GCGAGGGACACGGTGACCGGCGAGGCCGTAGCCATCAAGATCCTAGATAAGGAGAAGGTAC	5	2202238
X311	GFSSContig18342_909	GFSSContig18342_909-0_B_R_1890482015	AGAAATCTGTTCCAACAGCCAGGGCAGAAGTGGTTGATTGGACTATGAACAATAGTACA[A/G]TTCAGTCAGTAGAATCCCCACCTAAGTACACGTCAGAGGAAAGCCCAACACTTCTGCAATC	10	3193258
X319	GFSSContig5486_299	GFSSContig5486_299-0_B_R_1890482125	ATTGTGACCCGTCGCCATAAGTTTAATCTAATTGCTGATATGATGTTGG[A/C]TGAAGCCACTGAAATGCAATTTGATTTGATTGTCATGCCGGGAGGTTTGCA	3	1569586

Table A1 (cont.)

X321	GFSSContig11691_448	GFSSContig11691_448-0_B_U_1890482419	GATAGCTTCTGGTGTAGCGGTGGTGTGGCGAGTGGACCTGGGTCTCTTCT[A/C]CGGCGCTCTCCGGCGACGTGCCATGGTCCTGGGCCAGGTGGGCGTGGAGT	NA	NA
X346	GFSSContig19229_860	GFSSContig19229_860-0_T_U_1890482537	CCTCCAGCTGCACCCAGGCATTCCTACCCGTGAAAAACACGTCGTCCAGA[T/C]CGAGCTTGGCTAGCCTGTGGAACCCCGTGAAGTCGGCAGGCGCCGCCGGG	2	11583438
X349	GFSSContig20112_1572	GFSSContig20112_1572-1_B_F_1863899440	CTGGGCGCCATCGCCTTCTGGCCGCTCACGGTTTACTTCCCGGTGACCAT[A/C]TACATCGCGCAGGCCAAGGTGGAGCCCGGCAGCCGGAAGTGGGTGGCGCT	3	69100803
X368	GFSSContig16734_2201	GFSSContig16734_2201-0_T_R_1890479785	TCTCTGCTTTGGTTATTATCCGGGATATGACCTTGTTCCAGAGTAGATGGTTCCACCTG[A/T]GTTTGAGATGGTGTCCCATCAACTAATTCAATATCTGAACTGTTAGTTATCTGTGCAGAGT	2	37109270
X415	GFSSContig13900_299	GFSSContig13900_299-0_T_F_1890480763	ACCTCGACACCTTCTTGGGCACCAGGTCTCTGATCAGGTTGATGATGAT[T/C]GCTGCAGCGAAGAACACGTAACAGAGAGTGAGGCAGTTCTTGGGAAGCGAG	5	45152706
X423	GFSSContig14643_563	GFSSContig14643_563-1_T_R_1863900544	GTGGATATCTCTGACATCCCTGGTGGACCTTCAGCATTTGAAATATGTGC[T/C]AAGTTCTGCTATGGCATGATTGTAACACTCAATGCATATAATGTCCTCGC	1	14076523
X428	GFSSContig16441_703	GFSSContig16441_703-1_B_F_1863899359	TCCGCTCGAATCCCAGATTGATTGAGTGTGTAAACAGTTGATTCACAGGC[A/T]CCCTTTATGGCAGTTGTGTCAGCATCCTTATAAGGCACTGCAATCACAAT	7	60132867
X448	GFSSContig16218_668	GFSSContig16218_668-1_B_R_1863899387	TTGGCGAGGCCGAAGTCGGAGATCTGCGGCTGCAAGTCGTCGGTGAGCAG[T/G]ACGTTGGAGGCCTTGATGTCCCGGTGGATGATCCGCCTCCGGCACCCCTT	10	58153817
X454	GFSSContig20494_844	GFSSContig20494_844-1_B_R_1863899625	ATCCATAGAGGCAGACAAGCTTATTTGCATTGTTGATGGCCAAATATTTGATGAGCATGG[T/C]CGAGTCAATCGTTTTATGTCTATTGAAGAAGCAGATATGTTGATCAGAACACGTGCTAAG	1	54126459
X476	GFk50ctg317996_319	GFk50ctg317996_319-0_B_R_1890482142	TTCTGAAATGCCTCGGTTGCTACTGGTCGGCTGGGGTGGGCTCAATGAATCTCCACCAA[T/C]GGACAGTGAACTTGATGGCTCCAGGATATCACCAGTGGAGTACTGAAAAGAGTATGCATCT	10	180868
X485	GFSSContig12527_197	GFSSContig12527_197-1_B_F_1863900123	GAAGAGGAGCCCTTGGCAGCTACAGGCTGGAAGAGTGACCCTCCCGCCCCGTAGTAATCC[T/G]ATAACCAGCCAGATATGATCTTCAGTTCTGATTCTCTTAGGGCCACCAGCCAATCTGGGT	3	63680821
X493	GFSSContig3155_328	GFSSContig3155_328-1_B_R_1863899856	CCTGAGCTTCATGGTCCGGCTGCACCAGAAGTCCGCGATCGGCGAGGAGACGAGCGTACC[A/G]GACTCGTTCCGCTGCATCCCGCCCGACCGCAGCATCGAGGCGTCCCGGCAGGAAGCCGAG	6	3509617

Table A1 (cont.)

X497	GFSSContig14390_1376	GFSSContig14390_1376-0_T_R_1890481734	GCGTCGGAGGCCGGGGCAGCGTCAGCAGAGACGAATGCATTGTCGAGCGACTGGTGGGG[A/G]AAGTACTTCTTCTCCAGGCGGTAGAGCATACGGTAGTGCTTGTCCTTCTCCCACGGCATAG	NA	NA
X499	GFSSContig19230_886	GFSSContig19230_886-0_T_R_1890479218	AAGCTGCCGAAGCTGCCTCGCATCGGCCCAAAGCCCCGGTCCAAGGCGCTGACCATCGC[A/G]CTGCCGATAGTCACCACAGTATCCGTCCTCGCGGCGGTCGCCGTCGCGTTCTTGCTGCTGC	1	24003332
X506	GFSSContig20436_3127	GFSSContig20436_3127-1_T_R_1863899006	TAGAGCTTCTCCGAATTGGTGAAGGCGAAAATCTTCCGGATCCCATTCTG[T/C]AGCGCGACAAGCAGCCCATCCATGAGCGCGAGGTGCTCAGCCACCAGCTC	8	54748793
X517	GFSSContig19193_773	GFSSContig19193_773-1_T_R_1863900143	CACAACAATTTCTCCGGCGTGGTTGACGCCGCCACCGTCCTTAAGTTCGG[A/G]AAATCCTCCTTCTTCCAAGCCGGCAACATGTTGCGAGTGATCGCGGAAAT	4	10118087
X576	GFSSContig10844_1430	GFSSContig10844_1430-0_B_U_1890482354	CTCCAGCAGTACTGGCTGCATGATGCTCAGTGCCGCAACCTCATCGAAAA[T/C]CTTCTCTGCGTACTTCTCAGTGCTATTGCTGTCGGTGCCTTTGGAGTAGC	NA	NA
X582	GFSSContig10035_1071	GFSSContig10035_1071-0_B_F_1890481727	ACCTTTTTGCAAAAACGTTCTTCCATATCAGTTGTCACGGCACTAGTGCACTCATCAAG[A/G]ATGGCAAACTTTGGCTTATGGTAGAATAACCTGGCCATTCCCAATCTTTGCTGCTCGCCGA	NA	NA
X592	GFk45ctg342913_370	GFk45ctg342913_370-0_B_R_1893112193	ATGGTCCACGGGCGATGTGAAGGTAGACCCATATCAACTGACATTCAAGCACAATGTTCT[A/G]TTTGTGTCTGATTGGACGAGGCTTGGATTCTTTGAGGTTGACTATGGGTGGGGTGTACCA	8	7977658
X601	GFSSContig13754_1668	GFSSContig13754_1668-0_B_R_1890481121	ACCAACTCTGCATGGTGGGGAGCTGACAAATAGCTCTTTTCAACAACCTGCAGAACTTG[A/G]ATGCCCTTGGAAAATTCTGGAAGTAGTGCTCTAGCTCGAGTGAGGAAAACAGGAGGTAAAA	6	49212265
X625	GFSSContig15381_363	GFSSContig15381_363-1_B_F_1863898183	GGCATGGTCAAGATCGCCGACGCGGAGCATCACCTGGCACAAGGGCTCTGGAGTTCCAGG[T/C]CTCTCAATGATCTCAAACTTGTAGCCATCAGGGTCCTCCACGAAGGCGATGACGGTCTTG	4	15759507
X628	GFSSContig20127_221	GFSSContig20127_221-0_B_U_1890482557	AAAATTAAGATACAAGATGGCTTCAGTAAACTGGTGCTGAGCGCGCTCGA[A/C]GTGGGCGCAGTCACCACGGCTCCAACTGCTCCCGCAACTGTCGCCATCAT	NA	NA
X635	GFSSContig9550_549	GFSSContig9550_549-0_B_R_1890481721	GGAAGAAATTTAAAAAGAAGGTACCACGACAAGCAGCAGGTGTATCGTC[A/G]TCTGCTCTGCAAGAGGCCCAAGACATATTTGGTGATGTTGATGAGCTGCTA	9	53798708
X637	GFSSContig14160_179	GFSSContig14160_179-0_B_U_1890482414	CAGAAAGCAAGAGAAAAAATGAGGCTTCGCGTCGGAGCTCTTGCTCTGCT[T/C]TTGCTCCTGTTCGTCCATGGAGGCGGCCAACAGGCAGCGGAGGCCGGCGG	3	58594809

Table A1 (cont.)

X646	GFSSContig10419_989	GFSSContig10419_989-1_T_F_1863900193	GCTACCCATTCCTCAACTACAATTGTATCATCAAAGCCAGCAGGAATCTG[A/G]GCAAACACTGAGGCAAGTTGGTGAACAATCACAGCTTCAGAACCAGGGTA	1	17065308
X658	GFSSContig15731_268	GFSSContig15731_268-0_T_R_1890480586	GTGCAAATACTGACAGCAGCCTCATTTTCCTGCAATTCCAGCAGACAGGTTGTGTCCCT[A/C]CTCCTTGGATCAAGGATCCTAATGCAGGAAACCCACCTCTCAGATTCAGCCTTTGGATAAC	4	2809192

[*] Linkage group.

Table A2 The 10,398 RAD-seq SNPs discovered via the UNEAK pipeline for an F_1 population of *Miscanthus sinensis* ‘Strictus’ × ‘Kaskade’.

RAD tag name	**Sequence**
TP29	TGCAGAAAAAAAAAGAAAAAGAAATA[A/C]TCCGAGTCTCCGACACACAAGAACAATTACTCCCACG
TP37	TGCAGAAAAAAAAAT[A/C]TCATTCTTGTAAACGATGTGCAAAGAATATATACATGGGAGGAACATA
TP42	TGCAGAAAAAAAACGCTCGATGCCCCCTAATCCGTTTTCCCCATTCCGCTCGCCCCAT[C/T]GGAGT
TP52	TGCAGAAA[A/T]AAACTTGAGAAAGGCCGTACTTTTAAAGTGTATTATAGAAAAATCTTAGGTGCAT
TP58	TGCAGAAAAAA[A/G]TAGTGAGAAATGGGCCCGATAGCCATGGAACTTGGTCACTTGGAAGAATTGC
TP86	TGCAGAAAAAAGATATGTCCCCTCTCATTCTTGCCTCTAGAAGACGTACCAGAGAAGAAG[A/G]GGG
TP110	TGCAGAAAAACAACACCCTAGGTAACAACCATATCTTATATTGCCGAATAAAAAA[C/T]AACACCCC
TP111	TGCAGAAAAACAACCGCAAGGACA[A/G]GCGTCGAGAGGAAGGTAAACAACGACAAACTCATTCTCG
TP116	TGCAGAAAAACATGCAATTCTTTCGAACCTGATGATGGAAGAATTAGGCAACTACTGAC[A/G]TGAC
TP154	TGCAGAAAAAGAGG[C/T]GGTGAGGCTGCGCTTATACCTGTCTTGCTGTTTTCCTTCGGTTCTCCCG
TP164	TGCAGAAAAAGCTGTAGGCTGGACATAGGGTTGGGTCTGTGATTCATTTGG[G/T]CTGGCAACTTTG
TP173	TGCAGAAAAAGGTAAAAATAGAGCCCACTATTTATTCATTGGCAAAA[C/T]CATTTGTTTAACCAAA
TP174	TGCAGAA[A/G]AAGGTAGAAGCCTGCTATCAGCAGCAACAGGCAGATGAGCCTAAGGTAATAGAGGA
TP270	TGCAGAAAACACATGGGAAGGAAGCGGAAGAACATGGTGGCTACCC[A/G]CTCGAGCCTACGCCTCA
TP316	TGCAGAAAACATGGAGA[G/T]GGAGATGGCACGGCAGCACCACCGCTGGTCCGCTGCCCGTTTGCGG
TP329	TGCAGAAAACCACCAAATCATCAGTACTCTCTCCCTCTTTCGCTTCACCAGCCTAGTTCG[A/G]GGA
TP351	TGCAGAAAACC[C/G]TGAATGCTCCTGCTTCAGTCATTGCGTGATCTTTTTTCAGATTAATCTAGAA
TP359	TGCAGAAAACCTGATTTATATATTTTGTAACATTTATATATGTCCT[C/T]CAAAAAGACAAAGATAA
TP362	TGCAGAAAACCTTGCTCAATAATCTGTGTTCTTGTTTGTTGCAACTCTGTCGTATGTTT[A/G]CTCA
TP403	TGCAGAAA[A/G]CTGCCGTCTTCCAACCAATCGGGACCCCAATGACGCCTTTCGGCCTCCAGATTTG
TP422	TGCAGAAAAGAAATAATCACATTTGGCAGTTCTTGGAAAAACCGACG[A/G]AAACAAAGCAACATCC
TP427	TGCAGAAAAGAAGAG[C/T]GAATCATTTGCATCTGCCTGAACCACACATGACATGGACAATCGTTAA
TP446	TGCAGAAAAGAGGCAAAAAACGCTTGAAAAACAGATGGAACCAGTACTAAAA[A/T]TTTCCTCACCA
TP493	TGCAGAAAAGGGACTCCTCTGTTTTGTTGTTTTTT[G/T]AGGGCAAAGAGGCTGTTTATGTCATTAT
TP503	TGCAGAAAAGGTCGCTGCCGAGCGCCGCGGCAGAGTGCGGGCCCAGCAGGTGAGGTCGCCGC[A/C]G
TP505	TGCAGAAAAGGTTCTTCCTTA[A/T]TGGCTTATTGCAGAAAAGGTTCTGACCAAGAAACTTAGCAGG

Table A2 (cont.)

TP519	TGCAGAAAAGTC[A/G]CAAGCAACGTTTGACCACCAAGTGGCCTTTTGGGCAGCTCCATGATGAAAC
TP521	TGCAGAAAAGTC[C/T]CATCCGTACAGTGGTGGATATTGTAATTGACCGCCACAGGGTGATGTGGCG
TP523	TGCAGAAAAGTCTTTCTTGCAATATTTACAAGTTGCAGAAACTAAAAC[A/G]TTATTACCATCATAG
TP543	TGCAGAAAATAAATC[A/G]AATGGAACAGGCGCTGCTGGCGTGGCAGTTTAGATGGAATATATATAG
TP559	TGCAGAAAATAGACAAAAACGCTTGAAAAGCAGTTGGAACCAGTACTAAAAA[A/T]TTGCTCAGCAA
TP566	TGCAGAAAATAGCCCAGGTGAAGAGACAGCCCACCAGCACGGCAACGAGGCC[A/G]ACGGCGGCCGC
TP579	TGCAGAAAATATAGGAG[C/T]ACTTGCTTAGTGATTAGAGCGTTCCGTTCATGCGATACACGCTACA
TP583	TGCAGAAAATATGTGGGTGCAGGGGTGGCCACTGCCC[A/T]CTGGCCAGCGACGACGACGAGCCTGC
TP593	TGCAGAAAATCAGAGTCTTTGATACTAACATAATCGATTCCCACACATT[G/T]ATTTAATAATTTAT
TP601	TGCAGAAAATCCCATGATCTCCTTTTAACATTCGAGGAACCGATTAT[C/T]GCCACCACTTGAGGAA
TP608	TGCAGAA[A/T]ATCTACAGCTCGGGAGTGTGGCAGTTCGAGGGCGACATGTACGTGCCCTCGGGCAC
TP622	TGCAGAAAATGAGAGGGCACGGCACCGATGCCGCAGTCTCCCCACCGCCCTGTAGGAATAGGC[A/G]
TP637	TGCAGAAAATGGATAAAACCAAGTACACACTTGACACGA[A/G]CTCATGGGACTCCGCTAGTGTCTC
TP645	TGCAGAAAATGGTGCGTGGGAAACGTACGTGTGTGTGCCGTGTGC[A/G]TTGCCTAGCACTCACAGT
TP652	TGCAGAAAATGTTGCTGCTGAATCAGCTGTTGGGCACTGAGATGTGGATGCTGTTGTTGGA[C/G]TT
TP672	TGCAGAAAATTGAAGAGCTAA[A/T]GCTTCGTGATGGCGGAGGGTGCAATGAGCCCAACTGGGATGG
TP695	TGCAG[A/G]AACAAAAGCAAAGGTGACGTGGACTTGAAAGAGCTGCCTGTACGTCCTGGAACGAAAG
TP697	TGCAGAAACAAAATGCTCCAGTTCCCACGA[A/G]GTTGGTGGGTACGCGGCAGTGTCGGTTGCACAC
TP702	TGCAGAAACAAACTGCTTGCCGCCAGGATAACCACCGTGGCCACCAACAGCAGTGA[C/G]CATGTGG
TP706	TGCAGAAACAAAGTTGAAGCACACGCCCCAAGCAACAGCATCATGAAGGACCTGACA[G/T]GTTAGG
TP732	TGCAGAAACAATCATCGCC[A/T]GATTCCGAAGCAGCTCAGGCAGCAGGGGCGGATCCATTAAAGGG
TP742	TGCAGAAACA[A/G]TTTCGACCGCTGTCATCAGAACACGCCAAGCGTGATTGGAGAAGCAAACAGAA
TP751	TGCAGAAACACAGATATTCGCTTTCAGG[A/G]CATATCGTCAGAGCAAGTTCAGTCAGATGTTGAAT
TP768	TGCAGAAACACGGCAATGAAGGGCGTCCCAAACCTTCCTTG[C/T]GCGAGGACAGGCAGTGAAGATG
TP780	TGCAGAAACAGAACACGCAAATGTGGCCGATTAGCCGCG[G/T]CGGGAAACAGGGGACCGAGGAAAC
TP783	TGCAGAAACAGAAGCAGAG[A/G]CAGAGTCAAATTCACAGTCCCAATCCGAACCATGGTGCTACCCG
TP794	TGCAGA[A/G]ACAGAGTTGCAGCAGCTGCTGCCTTGGAACTTGGAAGCGTTCCAAGAAACCCCTCCT
TP808	TGCAGAAACAGGAGAAGAAAACTCACTCGCTGTTGCATGATGCTCGTC[A/G]TCTCGCGTCGTTCTG

Table A2 (cont.)

TP823	TGCAGAAACAGTAGTAAGA[A/G]ATGTTTACGAAACTAAGTAAAAAAAAAGTATATGAATTTGACCA
TP848	TGCAGAAACATCTAGGTAAGCATGTACAA[G/T]AAAATAGATTCAAGAAAATATTATTCATATGCCC
TP869	TGCAGAAAC[A/C]TTTTGCCAAATCCCCCATGGCATGCCAATTGCCAGAGCCGCGGTCACGAAAACG
TP877	TGCAGAAACCAAACCAAG[A/C]ATGAACTTGTCAGCCTATACGCTGCTGGCCAGTCATCAGCTGGCA
TP897	TGCAGAAACCAGACAACACAGATGTAATTTCCATTATTTTAAAACACAAGAGAAATTA[A/G]CAGCT
TP928	TGCAGAAACCCAGCCCGATCGACATTCAGTTTCTTTTGTGCCTGTG[C/T]ACGCACGTACCTCTTCT
TP929	TGCAGAAACCC[A/G]TGAAACCCCCTCTTTACGGCATGAGCATGAACCTGAGTAGCCTCGTTTGCTG
TP941	TGCAGAAACCCTTGAGAAGTATGTTGTATGAAA[C/G]TACATCTGGCGTGCATCCATGCTCAGGCAT
TP944	TGCAGAAA[C/T]CGAACAGGCAAACAAACAACCGCTGCTCCATGCCTCGCAACGCGTCCGCGCGACG
TP966	TGCAGAAACCTCAAAACCCCAACGA[C/T]GCCGCAACCGCAAGGGGACAAGGCGGGAGGGGTTTCTG
TP974	TGCAGAAACCTGGG[A/C]ACGGTTATTTAGTTAGTAAAAAAAATGTTGTAGAGGCAAATCACCGACA
TP980	TGCAGAAACCTTCTATGCGGCTTTCAATCTTCTCAGGCAAATCACGCCCTAGTTTAAAAT[G/T]AAT
TP981	TGCAGAAACCTT[C/T]TGCCAAATCCTCCATGCCATGCCAATTGCCAGAGCCCAGAGAGGCGGTCAC
TP999	TGCAGAAACGATACTCAGCGACATGCCA[A/G]TCGCATTGGGGTGATTGGTGTCCGCCTCGTGTTGT
TP1028	TGCAGAAACGGACGCCAATGCT[A/G]ATGCCGCTCATTTGCAGACAGTGTCAAAGCGCCAGCCATCC
TP1043	TGCAGAAACGGGAATGATCGCTTGGTTAATTTGGCGAGC[A/G]ATAGCCATGTTGCTTGCTAGTTTC
TP1061	TGCAGAAACGTAAACAAGATTCGCATCGCATGCA[A/T]TTCGCACGCGCCGCGCCCAAATCGGCCAC
TP1086	TGCAGAA[A/G]CTAGAGCCGAAGGTTTACACTGACACCATGATCACGGCTTTTTGCTCGGTGAGGGA
TP1102	TGCAGAAACTCATAATCTCTC[A/G]TGTGTGTTTTGATAGGTGCCACTGGCGACTCGTGGCAAAAGA
TP1103	TGCAGAAACTCATTTACA[A/T]GTGGCCACCTGCCTTCACTGTATTTCTGGCGTGTAGTAGTGTAGT
TP1145	TGCAGAAACTGTGCTGATCGC[C/T]ATCACTGCGAGGAGCTTGAGGTGCTCCTCTCAGCACAAGGCG
TP1167	TGCAGAAACTTCTCTCGCGCTTCACATGGGCTGTTGCATCTACCAC[C/T]ACAGTTTAGAGGCAGCT
TP1197	TGCAGAAAGAAGCCAGAGGCCGCGGCAGGCACGGACACTTCACGCAGGCCGCGCACTAG[A/C]GCCA
TP1200	TGCAGAAAGAAGG[A/C]ACCCGAACCCATCTCTCTCGGCTCTGGCACTTTAATGTCCCGTTCGTTTG
TP1228	TGCAGAAAGAGAAAACGAC[A/G]ACGTCGCTGTCCCATACAGACCAGGAGGATCCTTCATACTTATC
TP1243	TGCAGAAAGAGGGCGGCTTGCCCAT[C/T]GAGCTCACCGACGACATCGTCATGGCGCTCATGTTTGT
TP1248	TGCAGAAAGATAAACAGCAGAAGAGAAGATAAAGCTAAATGAGAGCTGGTTTGA[A/C]TATGATCAT
TP1250	TGCAGAAAGATACATATAT[A/T]GAAGACAATCTCATAGTCAGCAGCGAGCGGGTCGTTTGTATGTT

Table A2 (cont.)

TP1263	TGCAGA[A/C]AGATGCATAACACTATGGGTTAATTAACAGATGCAAACCTTGCTAATGTTTGTTCAC
TP1300	TGCAGAAAGCAGC[A/C]CGCGCGGGGCACAATGAAACTGTTGAGTTTGAACTGCTGGGGCTTGGGGC
TP1336	TGCAGAA[A/C]GCCGCGACGAGCGTGTTGTAAGTCACGGCATTGGGGTCGCAGCCCGCGCCGCGCAT
TP1345	TGCAGAAAGCGGCGATGGACACCATCTTCGCCGTCACCTTCGG[A/T]TCGGACCTCGACACGCTGGG
TP1371	TGCAGAAAGCTGTCATGAACATGTTCAGGTTGCTAGACTGGATTTCCATTCTA[C/T]GGTCACTAGC
TP1374	TGCAGAAAG[G/T]AAAATAATTACGTACTAATCAGCAAACGTATTCATGCAGCAAATATATATAAAA
TP1380	TGCAGAAAGGAAGATA[C/T]GTGCGCGGGTAGATAGGAGTTGAGGAGAGTAGATCGAGAAAGACGCA
TP1389	TGCAGAAAGGAGCAGGAGGAGCGTTGCAGTAGCCAGCAGGGTGCTGCTAG[A/C]AGAAACCATCTTG
TP1413	TGCAGAAAGGCACATTTTAAATTTGAT[C/T]AGCATTGGCATTTGACCAGAAGGGCGGACCTAGTGT
TP1415	TGCAGAAAGGCAGGCTACTCTGTCGA[C/T]CCACGCGGTGATCGTCCTGTATGTGCCCCCCTCCCGC
TP1435	TGCAGAA[A/C]GGCGGCGGCACTTCTGAGAAAGGCGACGGACCCGAGGGCGGCGTCCACTGAGCCCG
TP1442	TGCAGAAAGGGAAGAAAAGAAAACCACACTCATCTGTGA[C/T]TAGAGCATGGACAGGAAAGGTGGA
TP1469	TGCAGAAAGGTGGGCATGTTTATTTGGTTAGGAACAAACATTGTTGTACAGG[C/T]AAATCATCGAG
TP1473	TGCAGAAAGGTT[A/G]GCAATCGCTACGTGCCCACGACGCGGCAGATACGGTTCGACCTGGGCCGTG
TP1475	TGCAGAAAGGTTGG[C/G]CAGGAAGCCGTGCCAACAACATGGCAGATACGGTTCAGTCTGGACAGCG
TP1481	TGCAGAAAGTACAACAGTTTCATGTGTCGAGCACACCCAAAAGTGTCCCTTGGTCCCCCTA[A/G]TA
TP1482	TGCAGAAAGTACAATGGCTGCTTCAGCTGGTAAGCGTTGTATTGCTCACTTAGCC[C/T]TCCCCTCA
TP1489	TGCAGAAAGTAGTAAATTTTGGATGGAAATACTCTTTTAATTTTGTTTTCGGACGTTACGC[C/T]AA
TP1534	TGCAGAAAGTTTGGTAGCGCAGCGCGCATCCCAAGGCCGTCAGCTCGCC[A/G]CTGCATCCAGGCAC
TP1539	TGCAGAAATAAAAACTTCACAA[C/G]AAGATATTTAGAAGGTCCAGTTGCTAATTTAAAATGGGTAC
TP1553	TGCAGAAATAACCACTGTT[A/T]ACTGCATGTTCTAGTGCAAATATGTACCAAGTAATGAGCCAATG
TP1578	TGCAGAAATA[C/T]AGGCTGCACACGCGGCGCACGTCGTCGGACGTCGGCGGCGTCGACCAGCACGT
TP1589	TGCAGAAATACTATCTTCAGCAGCAGCA[A/G]CAGCAGAGTCAGTACGGGCTTGAGCAGACTTTCCC
TP1640	TGCAGAAATCAAACGCAAGGTAAGCTTTTCAATTAGGCCATGATTTC[C/T]AGCCGAGAAACAAGTA
TP1653	TGCAGAAATCAGAATGGACTGTCTCGTGTGTGGTGTCCGATCGGCTAATGGGCGTC[A/G]TGGTGGT
TP1658	TGCAGAAAT[C/T]AGTGTAGAAAGGGAATTAGAGAGCCAACAGTGTTTTCCATTGATCTCTGATGTA
TP1708	TGCAGAAATGAAAAGGAAATCGAGCAGGTGAGGGCGGCACGCTGC[A/G]CTGAGGCCGAGCGACGCC
TP1719	TGCAGAAATGAAGCAAACGCCTCGCGTCAGATTACGAACCCGCAAGCTAAATGTGAA[C/T]GGAATG

Table A2 (cont.)

TP1752	TGCAGAAATGCAGAATGCCAGCGTTG[C/G]CCGTTTCTTGCCCACGCAGACGGCAGACGCAGGCAGC
TP1757	TGCAGAAATGCAGCCGTGCTGGGAGCTCCAAAGCCCTGCCGCTGGCTGTCATCAGCTG[A/G]TTTCT
TP1782	TGCAGAAATGCGGCGCGGACAGGCCGACGAGCGATGACC[A/G]ATCAGCTTGCAACCGAAACAACGG
TP1785	TGCAGAAATG[C/T]TCTCTCTGTTCACTAGTGGCCAGAATTATGTAGATGCTGTTTATTGAAAGAAG
TP1794	TGCAGAAATGGAGAGTATAATGCATGTACAAATCTGTCAAATATATCGTGGAGCATTTAGGTA[C/T]
TP1802	TGCAGAAATGGCTGTTCCTGCTATTAAAGGAGGTCCAGCTCCAGGTCGGGTAGTCACGAAAC[C/T]A
TP1819	TGCAGAAATGGTTCACC[A/T]GCTACTGGAATGGAGGCCAGCTCTGGCCGACCAAGTCGACAGCAGC
TP1828	TGCAGAAATGTACTGCACCACAAGTAGTAATAAACACATATAGGAAGCGTCCGCCGTTACA[C/T]GA
TP1864	TGCAGAAATTAAGCCACAGCAGTTGCATGTTACT[A/G]TTAAAAGACACGCGCCGTCTCCAGCGGGA
TP1901	TGCAGAAATTCACTGTGGCTTTTTTTTTGAGAGGAAACTCCGCCTATTGTGGGAC[A/G]TCTTTGGT
TP1904	TGCAGAAATTCAGAG[A/G]GAAAGGATCCAAGATAAAAAGAAATCAAGCCATGTTTCCAACCAATGA
TP1905	TGCAGAAATT[C/T]AGCACGGTAATAGTATAGTAATCTCGAGATAAGGATCCCAATACACGGCCATG
TP1912	TGCAGAAATTCTTTTTAGGCCCACGTATAGCAGG[C/T]TGATTGCCCAACCAGGATTCACATGGGTC
TP1923	TGCAGAAATTGGACGG[C/T]TTTGTCTCCCCTGTTTTTGCAGTTGGTATATCATTCATTCATTTAAT
TP1955	TGCAGAAATTTCAGGCAAGTTGCTATA[G/T]TTAGATAGCTACCAAACTATAGAAAGAAGGACGCTC
TP1968	TGCAGAAATTTGCATATTTCTTTTGCTACGACCCAATTTACATGCAA[C/T]AGAATCTCTATCTACC
TP1997	TGCAGAACA[A/C]AACTAGCAACCTAGCGCGTCGTAACAAGCAAAACAAAAGGAAACAAACAGAAAT
TP1999	TGCAGA[A/G]CAAAAGCAACAACACAAATTCTGTCAGTTGGTGACATGGCGACGACAAAACCAAACA
TP2010	TGCAGAACAAACCCGTTGCTGGTTTGGACCTGCACGGCAGCAGGGGACTGCATCCC[A/G]TTAACTT
TP2030	TGCAGAACAAATCCTATGTGCTGCTACCATCCCTGCACTTTTCTTGTGCCCAGC[C/T]GCTTGTGCA
TP2045	TGCAGAACAACATCAACTACGCCTGTGGCT[A/C]TGTCGACTGTAAGCCGATCCAGAGCGGCGGCGC
TP2053	TGCAGAACAACCCCTCGTAGACGCCGAGCATGGCGTCGAAATCGACCACGGCG[C/G]CCGCCACGCC
TP2086	TGCAGAACAAGACGGCCTTCACGACGAAGAAGAACTACGG[C/T]AGGGAGGAGCGCGAGGCGCAGTG
TP2087	TGCAGAACAAGAGAAATCTGTTTCTTACTGGGCTGCGGC[A/G]TAGAGATTCTGTGCCTTTGCCCAA
TP2094	TGCAGA[A/G]CAAGCAAGGCATCCTCCATCAACGACCCATTCCAATGGCGCCCGCCTTCGGCCGCTC
TP2098	TGCAGAACAAGCATTCGTTCGTCTCGTCGGCCCAGC[G/T]ACGCTCCATGCAGCCCAATCCGACGCA
TP2099	TGCAGAACAAGCGTGAGCCC[A/C]AGTGGCCCCTCTTCTCCTTGCGATGGCCACGCCACTCATCGTC
TP2137	TGCAGAACACA[A/G]CACAGAAAGCATTGTTCAGCATGTCAAATGCCACAGAATCTTGTTGCCTGCG

Table A2 (cont.)

TP2138	TGCAGAACACAACACAG[C/T]GATGGACGGCCAGCCAGGTGCTGCGACGTCGAGTCTTGGTTCAAGA
TP2146	TGCAGAACACACACACGATAAAGGTA[C/T]GATGAACACATATGGATCCAATAAAGGTATGATGAAC
TP2171	TGCAGAACACCACTGCGCGGTACAGCAGCGCGCCTTTGCGGCTCTGCATAAGTACCCACCAGT[C/T]
TP2186	TGCAGAACACCTGCCTCAAGACCTGGGGCGGGCAGCCCGAGAAGGTCAAGGC[C/T]GCGCAGGACGC
TP2198	TGCAGAACACGCACGCACCGA[C/T]CTCAGGAGTCAGGTTCTTCAGAAAATTACAACGTGATATTGA
TP2204	TGCAGAACACG[C/T]GGCTGATTGCCAAGGAGAGCCACCCCATGCACCTCCACGGCTTCAACTTCTT
TP2222	TGCAGAACACTAGAATGAAAGGCAGCTGAGAAAATGG[G/T]ACTTGACACAAGACAATGGCAGTATT
TP2236	TGCAGAACAGAACACAGAAAGCATTGTTCAGCATGTCAAATGCTACAGAATCTTGTTGC[C/T]TGCG
TP2239	TGCAGAACAGAAGA[A/G]TCAACCTCAACCTGAATGCGTGATATACCATAATCAGTGGCCGCTTGGA
TP2241	TGCAGAACAGAAGCGCATGGG[A/G]TGGGAGTGCAAGCTGCGACGATGCTGCACCTCGCCGCGGGCG
TP2243	TGCAGAACAGAAGTGGGAAAGAGCGCGAGCGAGCCGACATCAGGTTTTGGGCCTT[A/G]GTGTAATA
TP2246	TGCAGAACAGAATGAATACCCTCCTTTCACTGGCTCCAGCACGTCGCTCCTCCGA[C/T]CCCGACGA
TP2260	TGCAGAACAGAGATCGT[C/T]GGCATAGAGCTCGACGACGGAACGGAGGTTGGCAGCGGCGCGGAGC
TP2270	TGCAGAACAGATGACAGGTTGCTCC[A/G]TCTGACAAATAGATTGTATGACTGAAATATAGATGTCT
TP2282	TGCAGAACAGCAATGAGCGGAACCAACCTTGTCGACTGCGTGCAGGGCGGCGCCGTG[A/G]CCAATG
TP2301	TGCAGAACAGCCGATAGGTGGTCCCAGATGTCTAGTTGATCTTGTGA[C/T]GAGTGGCTTGAGATGA
TP2302	TGCAGAAC[A/C]GCCGCCACGGCCCACGGGAGAAGACGACTGACTAGGCGCGGAAGGAAAGAAAGGA
TP2311	TGCAGAACAGCGTGGACGCCGTGTTCAC[A/G]TTGCACAGGCCGAACGCACCGCACATGGCGTAGTC
TP2312	TGCAGAACAGCGTTAGTACAGCGTTGGAGGTAATTGCAGGACTCGGCTGG[A/G]TCCATGGGCCATG
TP2344	TGCAGAACAGGTCATGAAGAAATGTGATGGTCTACCGCTTGC[A/T]CTTGTCACCACCGCCCAGCTC
TP2364	TGCAGAACAGTTTCGTCTAATGCCGTATTAACAAATTCCACTTGCACTGAACTAGTATA[A/C]GAGA
TP2396	TGCAGAACATCAGCGCAAAACTGATAGTGTGTACTATCTATATTG[A/G]TGAATAACTGAAACTGCA
TP2414	TGCAGAA[C/T]ATCTACTTCTCCTACGGGATGGCGTACGGCGGCGGCGGCTTCGCCATCAGCCGCCC
TP2416	TGCAGAACATCTCTGGAAGATACAGCACAAGCACCTAATAACATAAAAAAATAT[A/G]CATAGCTCA
TP2417	TGCAGAACATCTGAGATGCAAAATAGCCATTGCAGTGGTAATCAGAGTCAAGAGGATGCAG[C/G]AA
TP2421	TGCAGAACATCTTCCTGATGAACAACCTCTACTACGTGGTGCAGAAGGTGCGGGAGTC[C/G]CCGCC
TP2430	TGCAGAACATGACGGGGCT[C/G]GCCACGCTGTACGACTACGCGAAGCAGCGGGCGTACGCGACGGA
TP2486	TGCAGAACCAA[C/T]AACTCGTAGTCTGTGTTTAAAGGGGATCAGTGTCTGAAGCTCAATGACCCTG

Table A2 (cont.)

TP2512	TGCAGAACCACACGCCACCGC[A/G]AGATCAGCACCACGCGCGATCCCAGGAATGGAAAGCATTTTA
TP2519	TGCAGAACCACCTAGTGGCGCCCCAGCCAGGCGCGAGGGGGCCGCGGGGAGGCGGCGGCGAT[C/G]C
TP2526	TGCAGAACCACGCA[C/T]AGTACGTTACACGCTCGCATCGTCCTAAGCTCGTGCCGCGACACTTCTG
TP2556	TGCAGAACCAGGCCAACCGCTGGCTCGAGTGCCTCCA[C/T]GCCGCCGCCGAGCTCGAGAGGAAGGA
TP2560	TGCAGAACCAGGTCCGCGCGCGATCGGTA[C/T]GGCGATTCAGTGCCTCAACGAAAGCTGCATCTAC
TP2570	TGCAGAACCAGTTTCAGTGCTACTACTAAACTGGAGTTCAGAACTTCAGATTCAAAATG[G/T]ATAT
TP2584	TGCAGAACCATTAAGGTACGTGCAGTGATCTATCCG[A/T]TGCATGCCAGGACTGCATTATATTAAT
TP2601	TGCAGAACCCAATCGAGAGTCGCCGC[A/C]CGCTTTGCTCCGCCGTCTCCTCCTCCGCGGAGTAATT
TP2606	TGCAGAACCCACATCAGAAAAGAATAAAAAAAATAAACAATCA[A/G]ATAAATAAACTGGCAAAAAC
TP2613	TGCAGAACCCATCAAACAACATCG[G/T]CTCCCTTGCGCGTTGCTCTTCAGTGTGCCCTACGCAGCG
TP2616	TGCAGAACCCATGTCCTC[C/G]GAACAGAACTGTAACTGTAACTCTGCACAGCTCAGAGCGCAACTG
TP2617	TGCAGAACCCATGT[C/T]CTCCGAACCGAACTGTAACTCTGCACAGCTCGGAGCGCAGATGCTGCCT
TP2642	TGCAGAACCCGTCACAGGTCTACAAAATTCAGA[G/T]ATATCAAAAGATCAGGCGCAAAGTAGTCAA
TP2643	TGCAGAACCCGTCACCGCG[C/G]TCGCGCCGATTTGGAGGGGTTAATGCACTAGAAACTGACCTTTC
TP2646	TGCAGAACCCTAGACCCCCACCCGACCCACCGT[C/T]CCTCATCGACATGGCCGATGCCTCCGACCA
TP2655	TGCAGAACCCTCTCACGCCGCTTCCTCCCCCTGCCGATC[G/T]AGGAATCCAATGGCGCAAGCGGCG
TP2657	TGCAGAACCCTGACTCCCTGTGTGCGAAGCTGCTTATGGCGC[G/T]GTAATGTCCAAATGGAGATAT
TP2671	TGCAGAACCGAGCAAAAAGCCGCATCAAATCAGGGAGCAC[A/C]TTTCCCTCTCCCTGGAGGCATTT
TP2697	TGCAGAACCGTCCTTGAAT[A/G]TTCCTCCTTCAATCCTTGCCTTGGTATTCTTGAGATTAATCTAC
TP2704	TGCAGA[A/G]CCGTGCGGCAGGCCTGCATGGTTTGCTGTTGCGGGCGTAGCAGTGCAGCGGCGCGGG
TP2708	TGCAGAACCGTTCAACCGATTCCAAGATCGATCACGACCCATTTTG[A/G]CAAAGCAGAGCAGTGGA
TP2727	TGCAGAACCTCAAC[A/G]CCTACCCGTGGATGTGGACGGTCGAGAGGCTGAACCCCCCCGACCAGGA
TP2734	TGCAGAACCT[C/G]ACGCAGTACCAGGCCGTGGAGCGCGTGAACCCCACGCTGGTGCCCACCAACCT
TP2741	TGCAG[A/C]ACCTCCCCGAGCACCTGCGGCACCTTCCCGAGAACCTGCGGCACCTCCCCGACCACCT
TP2744	TGCAGAACCTCCTCCCTGGCGCGGTCTTGCCACTCGGGGTGCATGCTCAGCAC[C/G]ACCAGTGTCC
TP2759	TGCAGAACCTCGTCGTGCAGGTCCTTGGAGCGGC[A/G]TATGTCCTCTACAAATATGTCGTCGGTGG
TP2766	TGCAGAACCTGAAGATCCTTTAAATATGCGAAATAT[A/T]GCACCACCACTAGAATTTATGGCATTT
TP2778	TGCAGAACCTGCGCCG[C/T]ATCGACGTCCGCAACAACAACTTCTGGGGCAATGCCACCGATCTGCT

Table A2 (cont.)

TP2779	TGCAGAACCTGCGCTGAAACCCTAGCGTGATTTGCGCACCCAATTAGCACCAAATC[A/G]GGGGGAA
TP2788	TGCAGAACCTGGTGCCCGACTCCCTCTGTACCAGATC[G/T]CACGAACACAACGAACAGTCAGTGGC
TP2800	TGCAGAACCTGTT[C/G]CTCTGAAAAACGTCTCTGCATCGACGGCAACATCTGTGTCCCAGGATAAG
TP2816	TGCAGAACCTTGCCAAATAAAACCCACGCACCAAAACTCCGCC[A/T]GCACGTACCACATAAAACTC
TP2842	TGCAGAACG[A/G]CATTTCCCGCTTCCTCAGTCGGATCGGATGAGTTGTGCCTTTCGTCTCATGCGT
TP2849	TGCAGAACGACGGCGTGAC[G/T]GTGGAGGACATCAACGCGCTGCACCTTATCCCCAAGGAGCTCTC
TP2851	TGCAGAACGACGTCGACGCCGCGCCAGCGTCGCACAGCCCGAACGCC[C/G]CGCACATGGCGTAGGC
TP2853	TGCAGAACGAGAAAGCGATCGAGCGAGCGCGACCGACCTGCTGGGCAGGCACCTCCAGAGC[A/G]GG
TP2871	TGCAGAACGAGGGGCG[G/T]CTGTTCGAGTGCAGCTACCCGCGCAGCATCGGCGGCATCCTGGGCAA
TP2880	TGCAGAACGAGTGTGGGGAGACCGCGCTCCATCAGGCGGTCCGCGCTGCCAGGAACAATGTGG[C/T]
TP2899	TGCAGAACGCCAACATGCTGGCGCCGAACAAGAGCGAGACGCACCCGTGGCACCTGCATGG[C/G]CA
TP2901	TGCAGAACGCCAGAACGGCCTCACCAT[G/T]AGTACGCTTTCCGTGGTCTCGGTCTCGGGCGCCCAT
TP2902	TGCAGAACGCCAGAACGGGTCCTCGTGTGTTCACAAAGGTCCTGGAGGCGGAAGACGAAGA[A/G]CT
TP2915	TGCAGAACGCCGCGTCCCCCCTGCGTCGCGCGCGGGCACGCCGCAGACGAGTCAGTCAGCAC[A/G]C
TP2921	TGCAGAACGCCGTGTCGCCCCTGCAAGCACCACGCCCACGCGGCGGCAGATCCATCCATT[C/G]ATT
TP2924	TGCAGAACGCCTCGGTTCCCTGGTCAACCAAAACATCGAAAATAAGCTCATCTCCGACACCGA[C/G]
TP2948	TGCAGAACGCTAGAGACTGTAGAAGAGCGCAGAGCGGCGGCATCTCTCC[G/T]TCCGCGCCGCGCCA
TP2950	TGCAGAACGCTGCTCGGGAAGCGGAGGAGATGACGAGGAACAACTCG[A/C]AGTTCCACCTGATGCT
TP2951	TGCAGAACGCTGGTTCCGCCCAGGCCACGTCTACTCCAGGCGAACATGTGAAGGCCCTAGGCT[C/T]
TP2966	TGCAGA[A/G]CGGAGCGGACATCCTGGCGACCATGGAGCTAGGCTGCGGTGGCCGACGCCGTGGACG
TP2972	TGCAGAACGGCAAAACGATAGGATTCTACTCTTTTCAGGAAATACAG[A/C]TGGCAAAATGCCAGGC
TP2974	TGCAGAACGGCAA[C/T]ATCTGCCATTTCCATACCACAACCTAATGCAGTAGTAATACTTATGCTAC
TP2975	TGCAGAACGGCAAGGGTGGCGGGAACGGGAACCA[G/T]CAGGGTCAGCAGGGCAAGAAGGGAGGCGG
TP2977	TGCAGAACGGCACGGGCGCCGAGGT[C/G]AACCAGGTCTGGCAGGTGGGCCCCTACTCCGAAAAAAA
TP2979	TGCAGAACGGCATG[C/G]CCCGCTTCCTCAGTCGGATGAGTTGTGCCTTTCGTCTCATCTCATGCGT
TP2982	TGCAGAACGGCCGTGCTCTTGGCGTGGACGGCGGAACGGGGACGGCCTGGTGGAGTAGGG[A/C]GCC
TP2989	TGCAGAACGGCGCGGGGGGCGACGACGGGGACGACG[A/G]GCGCGAGGAGGAGGAGGAAGTGGGCGA
TP2994	TGCAGAACGGCGTAAGAACTGCAAACCCACAAGAAACGTGCTCCATTATGTGATGTGAAGG[A/C]TC

Table A2 (cont.)

TP3003	TGCAGAACGGGAG[C/T]AGAGGGCATACCGCACACGAACGCAGGCGGCGGTAGAACGGGAGCAGAGG
TP3007	TGCAGAACGGGCAGGAGGACATGA[C/T]GGCGCTATCCCCAACGTCGACGGCGGCGGTCACGACGTG
TP3012	TGCAGAACGGGGAGGAGGCGGATG[A/G]GGGAGCCCAGAACGGGCGCGGGGAGGAGCGGGAGGCGTC
TP3016	TGCAGA[A/T]CGGGTTGAAGTAGTTCCTGCATCGATCGATCCCCATGTGGTTAATTACGTGCCTTTT
TP3041	TGCAGAACGTCGTGTCTG[C/T]GATGGAAAAATTGCAGAGAAGACCCCCGTTCACTTCATTAAATGA
TP3052	TGCAGAACGTGAGGTTCAGCGACGACCCGCACTACCGCCTCGGCGT[C/T]GGCGTCCTCCCCGTCAC
TP3059	TGCAGAACGTGGCCCTCTTCTCA[C/G]CACCAGCACCAGCACCAGCACCAATCCAAGTCGATGGCAT
TP3065	TGCAGAA[C/G]GTGTGGTTAACAATAATAACGGAGAGTAAACTACAAACTTTGGTTGCCTGCGAGAA
TP3069	TGCAGAACGTTCA[A/T]GTGTCTGTCGGTCGACAGATGGAATATCTCACGGGCACGGAAAACACACC
TP3071	TGCAGAACGTTTAGGCCACGTTGAC[A/G]GCGCCCAACGGAAGCTACGTCGATTTGCAAGGCAGTTG
TP3097	TGCAGA[A/C]CTACAGTACGGAACCCTTCTTTGTGGCCACATATCACGCCATGATGGGTTCATCTTT
TP3098	TGCAGAACTACATCAAAGGCCTTGGTATTGGCGCAAGCAACAAGAGCG[G/T]CGCCGCGCCTCTTCC
TP3102	TGCAGAACTACCA[C/T]TCGCAATGACATGGAATCTTTGATTCGACGTGGTAGCTAGAATTCCAAGA
TP3104	TGCAGAACTACCAGGCGGCGGTGCAGCAGCTGGTGAGCATCCTGGGCGACGAGGACTC[C/G]GCGGC
TP3109	TGCAGAACTACTACGCTCAGCTCTATGGTCTGACCTCGCCTACGGCGGCGGCAGCCTACCA[A/C]CA
TP3118	TGCAGAACT[A/G]GCGTTGGAGTACTGGATTGGATCACAGTGACAGTCCTGCCTGCTGACCTGCTAC
TP3156	TGCAGAACTCAGCACCCAAGCTGTCTAGACGATGCCAGATAGCTGACA[C/T]TAGACAGTGGAAGTC
TP3163	TGCAGAACTCATCAGTCCCCTTGCAGTTCCAGTTTGGAACGACTTCCATCATTTGGCCGT[C/T]GAA
TP3171	TGCAGAACTCCAAGGACATCCC[C/G]TACAGGCCGCTCAAGTGCCAGTCCTGCTGCCCAGGCTTCTT
TP3178	TGCAGAACTCCCAAGCAGC[A/C]AAACAGAGCACAACCTCCAAATCAGAGCACAGCAGGAGCACACC
TP3180	TGCAGAA[C/G]TCCCGAGTCTGTAATACTGAAGGTCTGAAGCTACAACTTAGCACAACCCAGAGCAT
TP3191	TGCAGAACTCGCATTTTCC[A/G]CTGGAGACCTCAGGTGCACCGCTGCCATACCTTAACCAGCCTCA
TP3197	TGCAGAACTCGGATGATTGTGTCCTCCTGTGCAGGCAGGCGCCAGAGACA[A/G]TGACAATGGATCA
TP3202	TGCAGAACTCGTCATGGTCGACGTCGAGGCACGGCATGGAGCGCCAGAGGTGCCGCCAGCGCG[C/T]
TP3223	TGCAGAACTGAAGGCCTCGAGGGAAAGAACCTTGAAGCCCCATGCC[G/T]TTGAGATTCAAGGACAG
TP3234	TGCAGAACTGAGCCGATGATTGGGCGCTCAAGATTTCTAG[C/T]CATTGTAAGCACATGTCGACCAT
TP3272	TGCAGAACTGGT[C/T]GTTGTTGCGGCATTCGCATATTGCCTTGCATATCTTGTAGGTGACGAAACC
TP3273	TGCAGAACTGGTGTGTT[C/T]CCCCTGTGTAAATTCAGTTTGCGTCTCATCGATCTGATGTCCTGAA

Table A2 (cont.)

TP3276	TGCAGAACTGTAGTGTTCCAAA[C/T]AAAACGAGGCATGATTCTTAGTTCTCTTCCACACGCGCGTT
TP3296	TGCAGAACTGTTGCATCTGCTCTTTTCCTTAAAGCTCACT[A/G]CTATCAGTACCAGAGAGAGCAGC
TP3314	TGCAGAACTTCCAGGACTACCAGCAGAGTCTGG[C/T]CGAGTTCGTCGGCGAGGACGCGGCGAGGCA
TP3319	TGCAGAACTT[C/G]GAGTCCATTCAGGAGAAGTAGGAATATGGCATTCGTCCATTCAGGTCTGTTGC
TP3321	TGCAGAACTTCGCCGACGCTTCCGCCGCTGGGCGGGCACTTCA[G/T]CTCGCTCGCGGATGTCTACC
TP3334	TGCAGAACTTGC[A/G]TTACATCTACAAAAGGAAGATTTCAAGAAATGACGAAGAGTTTACTGACCT
TP3382	TGCAGAAGAAAAGAAGGGAAAAAGGAAAAGATGGTACCTCAAAGCATTACGATCCTTGATGGA[A/G]
TP3384	TGCAGAA[G/T]AAAAGAGGCACCCAGCTGCACCGTGCCATCGCTCGCTTCGACGTAGAAGAGTACTA
TP3396	TGCAGAAGAAACCAAACGACTGCCTGTCTGCATCAGCCGCGCGCAACCAATCAA[C/G]AGAGATAAT
TP3407	TGCAGA[A/G]GAAACGAGACGACTGAAACAGTGTATTATGGGACGAGAGAAGACGAAATTAGTGGTT
TP3410	TGCAGAAGAAACTATGATTCGAATTAGCCCAAGTTGA[G/T]TTTTTTTGTTCAAGCATCATCACTAA
TP3425	TGCAGAAGAAAGGTG[A/G]CATGTTTAACAAGCAAGACATAGAAGCATATAAGATCCGCATGAACGA
TP3437	TGCAGAAGAACACGT[C/T]GGTGGACAAGAGTCAACTCGGCATGCAGCAGATTCAACACTCGTCGGA
TP3439	TGCAGAAGAACAGCACAGCA[G/T]AAGGTGCGGCCGCGACCCTCTCGCTTGACGTGCTGTCGCGGTG
TP3440	TGCAGAAGAACAGCTGAAAAAACTGATGGCGC[G/C]AGGGCCAAGGCCCAAGAGCTTGCCTAGAATG
TP3441	TGCAGAAGAACAGGCAGTGTCCTGTAGGGCCTCATCCTCCTCGTC[G/T]TCGTCGCACATGAGCTCA
TP3457	TGCAGAAGAACGAACGAACTACGTCAGAATGCAGTAGAGCCGCACATTGACAGTTCCACACAC[A/G]
TP3462	TGCAGAAGAACGAGAAGCAGGCAGAGGTGAAAACC[C/T]GTCACATTGTTTGACGCACGCACCAAAC
TP3469	TGCAGAAGAACTGGCACT[A/G]CGTGCGACCGATGGTCGATGGTGTGCGCGCCCGACAGCTCTGTCA
TP3498	TGCAGAAGAAGATT[A/G]TCCAGGAATTTATTTCAGAAAAAAAAAGATGATCCAGCTGAATCACACG
TP3516	TGCAGAAGAAGCGGGGAGCTCTGGATCGAAGGAAGTGGC[C/G]GAGGCGGAGCAGTAGATGTGTGCA
TP3544	TGCAGAAGAAGTCCTCGGCCTGCTGCCTGAACGGATCGAGCCTCTTGTCCC[C/T]GTTCACCAGAGC
TP3548	TGCAGAAGAAGTTTGGCAGCTCGAAA[C/G]AACTGATCGAGTCGGCGAGGAGCATCATTTCTGGGGA
TP3578	TGCAGAAGAATTGTATCCTA[A/G]GTTATAGTGCGACGATGAATTCATATAAACTCTATCATTATGA
TP3581	TGCAGAAGAATTTGCCACAGTTGATCTATCTCCTTTTT[G/T]TGCTGCATTTAAGTTATTCTTTGTA
TP3587	TGCAGAAGACA[A/G]TGGTCAGAGCTGATCTCATCGGCAGCAAATGCAAGACGGCCATATTGTCGGC
TP3604	TGCAGAAGACAGATCAAGACC[C/G]AGCATGGAGCCAACTACCAATCAAAGTCGACTCGCAAGTGCA
TP3606	TGCAGAAGACAGGGCTAGCAACATTGCAACT[C/T]TGAAATGCCCAAGGCCGTCACAGAAATATTAC

Table A2 (cont.)

TP3608	TGCAGAAGACAGTCGTTGTGCGTGACGTTAGAGCCGCTGGCCTGTTCCCCGA[A/G]CCAGCGCTAGG
TP3617	TGCAGAAGAC[C/T]AATGTCATTGAGACCTTCCAGAACCAGGCGAACGACACAAAGAACGGCATCAC
TP3619	TGCAGAAGACCACTTGTTGCAGTTAAATATGGCCAAACGGGCCGCCTGGCTCG[G/T]CACGACACTT
TP3622	TGCAGAAGACCATAATTCACATAGCTTTCAGTGACTAACTAAAAC[C/T]GTGATACTTGACATGATA
TP3625	TGCAGAAGACCCAGCGAGCTTTGTAG[A/C]GCTCGAGGGAACCGTCAACTTTGAACTTGTGCTTGAA
TP3645	TGCAGAAGACGATGCGC[C/T]TTTGTTTTCAGATAAAATCAATCAGAGGATTCAGAGGCTGGGCTGT
TP3650	TGCAG[A/G]AGACGCCGCCTCCGCCGTTGCTGCCCTCGGCAGCGCCATCGTTGCTGCTGCTGCTGCT
TP3673	TGCAGAAGACTTG[A/G]GGACGAAACGGAGCCTGCGATGCAAATGCGCAGCAATGGCAGCAAAGAAT
TP3679	TGCAGAAGAGAACACAACTGAAGAGA[A/G]AGAGCAGGCCGAGCAACACCCGAACGCAATTTGCAGG
TP3693	TGCAGAAGAGAGCTACTTCGGCAATGGTGAGTT[A/C]TGTGTGTGTTGTAGTGGCCGAGTTGACAGA
TP3698	TGCAGAAGAGAGTGGTCCAGAAAGACAACTGCGACATTTGCCAT[A/C]AGGGCTCGGAAACAGTTGA
TP3700	TGCAGAAGAGATCAAGTGAAGGTCG[A/G]CAAAGATGAGAGTCCAAAGAATAATGTCCGATCCATCA
TP3704	TGCAGAAGAGATGCGGCCCAAGTAAGCTTTCCTTGGA[C/T]TGAAGCTACTACACTATCAGTGTTTG
TP3718	TGCAGAAGAGCCTGCTCTACTTCGAGGCGCAGCGCTCGGGGCGGCTCCCGCACAGCCA[A/G]CGCGT
TP3721	TGCAGAAGAG[C/G]GACAGGATCTTGTCCTGCGCGTTGAACGCCGCCACCGTGCGGATGTTGCTCAC
TP3726	TGCAGAAGAGCGGCATCA[C/T]CTCGGTGAGGCTCTACGACGCCAACTCCACGGTGCTCAAGGCCCT
TP3762	TGCAGAAGAGGGTAAGCTGACCTATGTCGAGAAGCATCTTGGGGACGCCA[C/T]CGTTGGGGAGAGC
TP3775	TGCAG[A/G]AGAGTGGTAGGCACGAACCTGTGGCCGTACTCTTTTCTTCGTTCCATCCGAGCGCAGT
TP3788	TGCAGAAGATACAGAGTGCATACTTTTTGTTCGTCCCAAAG[C/T]TCGACAGTAACATTCTGAAACA
TP3789	TGCAGAAGATACAGCTATACGGCAGACGCGGGGTTGCAACGAGAAGGCAGGCG[A/G]TTTGGGGAGC
TP3795	TGCAG[A/G]AGATAGCGACACACAGCTCATCAGCCATGAAGCTCGTGCTGTGCTTCTGCATCTGCGT
TP3797	TGCAGAAGATAGCGTTCAGATCC[A/C]AGACAGAAGCAAGTGTTCTGAACGCGAGGGTCTAACGCTG
TP3812	TGCAGAAGATCAGAGGAACCGACGCCGTCGACCAAGAGTTGGATGACATCGTCGCTGCCAA[C/T]GC
TP3826	TGCAGAAGATCGATCGCGACCGAGCTTGGAGC[G/C]AGCTACCGATCAAAACAGCGCCTGAGGTGCA
TP3830	TGCAGAAGATCGCTGATGCTTGCCGCTGCCTCCATGAAGCAT[C/T]TGGCATTTCGTTCTTTCCAAA
TP3843	TGCAGAAGATGACACAAAAGGGCAACTTGTTCCCAATTTCCTAGCGACTGTATA[C/G]CTAACCTGA
TP3848	TGCAGAAGATGATCGCGCAGCACCAAGCGG[C/G]AGGCCAGCTGAAGACGCTCAAGGAGCGGGCGCG
TP3851	TGCAGAAGATGCAGGCATTACGT[C/T]ATATATTATCCATATATATAATCTAGGCGCGGCAGCAATA

Table A2 (cont.)

TP3854	TGCAGAAGATGCCACCGCTGCGGCTTCAGTGAAGTTT[G/T]CATCGAAATTTGAGAAGAGCAGAAAG
TP3870	TGCAGAAGATGGCCTTGCTAGTGCACAGCAGTCA[A/G]CAGATTTCTTGCTGCCCGATTTGGTGGCC
TP3922	TGCAGAAGCAAAAGAGGGTGA[A/G]CCAGCTAGACAGTTTCAGCTCGTCTGTAGTCAGCAGTCAGCA
TP3944	TGCAGAAG[C/T]AACAAATCCACCATGAGAATCACAAGGAAGCAAGCAGAGGCGATGCTCCGAAAAA
TP3954	TGCAGAAGCA[A/G]CTGGAGGCCATGGTGAAGGAGGCGTCCGTGGACGACGTGATGAAGGTGCTGAT
TP3959	TGCAGAAGCAAGACTCCATGCGTCGCAGC[A/G]CCGTGGATTCTCCCAAGGTGGCGCGCGAGAAGAT
TP3976	TGCAGAAGCACAAGTCAGATCTGTAAGCATCAGTGTTCAACATCTGCCAAAAGAACAAA[C/T]GCAA
TP3988	TGCAG[A/C]AGCACAGCCTAGCACCGTAGCAGTATGGCAAGGCAGCACCGCTGTGCAGTCTGCACTT
TP3989	TGCAGAAGCACAGCTGGTGCCCGCCGCCTGGAACGCGCTCCAGC[A/T]GGGCCGATACAGGGACCCC
TP3995	TGCAGAAGCACCAACATCCAACAAAATCAACACCATCTGGACAGCAAGGAAATT[A/C]GCACCTGCG
TP4031	TGCAGAAGCAGAACAGATTAGACGAG[C/G]CCGCCTCTGCATGGGCAGTGCGTCAGTGCCGTGCGTG
TP4042	TGCAGAAGCAGACGAAT[C/G]AGCGGATTACCTGACAGGGCTGATAGGACTTGGAGGGACGGCCCAA
TP4069	TGCAGAAGCAGCAGTTGCTTCTCC[A/T]GACAAAAGTGCGAGGCACCAACTGAATTCTCGTTGTGTG
TP4070	TGCAGAAGCAGCATCTCAAATCCCATAGAAAGCAAGAGAGACACTGCTGCGCAATCGGCCTC[A/G]A
TP4093	TGCAGAAGCAGGCAGAGCGAGCTTGGCATGCATCAGCCATTATTCGCTAAGACTAGCCACAAT[G/T]
TP4109	TGCAGAAGCAGTCGAGTCAGCTGACGGTACTTGCCTG[C/T]GGCAGCTATGCTCGGCTGCGCTGCCG
TP4111	TGCAGAAGCAGTCTGCAAACCTTACCTTGCTT[T/C]CAGACTTTATATGACAACAGAATAGCAGAGG
TP4114	TGCAGAAGCAGTGGGGCAAATGATGATGGGTACACGACCGAATGATGGCAAGGCATG[A/G]CAGCAT
TP4148	TGCAGAAGCATGTCTGTCAGTCTGTCACTGTCAGTCACTCA[A/G]TTGTTGGTGAGTAGAGATGGAT
TP4188	TGCAGAAGC[C/T]AGCCGATTATTACTCCAGTAAGCCAAGATTAATACGCAGCCTGTCGCCACCGAT
TP4207	TGCAGAAGCCC[A/G]CAGTGGCTGCTGCACGACGTCAGTGTCTGGGGCAAGCTCCACCTCGGGTACC
TP4223	TGCAGAAGCCCGCGCGGTGCGACCACGCGGGCTCAACCGC[C/T]GTCGTCGCGGTTGTCAGCCCCAC
TP4235	TGCAGAAGCCGACGACCTGCCGCCGCACAGGCCAGAGGCCTGCG[A/C]CACCCACTATTGCCCGCTA
TP4259	TGCAGAAGCCTCCCATGCATTATCT[A/G]CTCCACTTGCTCCCTCCTGACGATGTTTTGCTTAAGCT
TP4260	TGCAGAAGCCTC[C/T]TGCCAGTCTCGCCGAGCAGCAAGGGCGAGATGGTGGTGGTTCTGGGCGAGC
TP4287	TGCAGAAGCGAGCACAGAGAAGTGCCTATACAACACAA[A/T]CTGGAAGCACTGCGTGGTGCGTGCA
TP4294	TGCAGAAGCGCCGACGGTAGCGCCGCAAGCGTCAGA[G/T]ACCATTGCTGCTGCCAGCCTGCCTGCC
TP4298	TGCAGAAGCGCCGCAAC[C/G]GACGGTAGCGCCGCAAGCGTCAGAGACCGTGGCTGCTGCCAGCCTG

Table A2 (cont.)

TP4306	TGCAG[A/G]AGCGCGCGACAGATCTCGTTGAGGCAGTCGGCGAGCACCTTCTCGTCCACCACGGTGG
TP4310	TGCAGAAGCGCGGCATTCGGGCCTTCATTGCAGTCGTGCTGGCTGCTGCCATCA[A/G]CATCGTCAT
TP4318	TGCAGAAGCGGAACCACTGCGATCGATCGATAACCTCAGAAGCCTCGGAAGAAT[G/T]CCGAGTGGC
TP4373	TGCAGAAGCTAAGATCATGTCGTCCGCCATCTCGGGCGCTGCTCGGCGACCCG[A/C]CGCAGCATGC
TP4384	TGCAGAAGCTACCCGTTATCATACCTTGGTGTTTGGTTCAGTTCTGTGTGCAGG[C/T]GCAGTTTCC
TP4392	TGCAGAAGCTAGAAGCTGAGAGGACGGAACGACACGGACTTGCTGAAA[C/T]GGAACGACAGAAGAT
TP4404	TGCAGAAGCTATGCTCTCTCAGGCCGTGTCGCTCTCGTC[G/T]CAACCAAGCCTTCCTTCCCTGCCA
TP4418	TGCAGAAGCTCACT[A/G]CTTTGCTGGTCCAAGATCAGTACAGGTCTCGTCTTGGAGCTGGGATCCG
TP4438	TGCAGAAGCTCCTGCACGCGGCCTACAAGCGCGGGGAGACCTCCGTCGAGGT[C/G]CGCGTGCGCCG
TP4442	TGCAGAAGCTCGCATAGGAAAAAAATATCATTGAAGCCGCTAGCATTGGC[C/T]ATGGCCACGGGGG
TP4443	TGCAGAAGCTCGCATAGGAAAAAATATCATTGAAGCCGCTAGCATTGGC[C/T]ATGGCCACGGGGGC
TP4445	TGCAGAAGCTCGCCGTCCTCTTCCTCCTCTTCCTCGCCTCCCGCCTTTC[C/G]TCTTCTCACTTCCT
TP4460	TGCAGAAGCTCTTCTAGATGAGCAGATGGCATCTGACCTCTTG[G/T]TGTTGGCTGAGAAGTATGAA
TP4464	TGCAGAAGCTGAA[A/G]CCCAACAACACCATGACGACGAGATAAGCAATCGGCAATGTCGGGAGCAT
TP4473	TGCAGAAGCTGAGGTTTATGCGCTCCTACCACTGTCAGAAAAC[A/G]GGGAGCTTTGTTCATCTTCA
TP4486	TGCAGAAGCTGCGCTTGAACAAGGTTTGG[C/T]TTTCTGATGATTTCAAAGAAGAGATGCGGCTCGA
TP4488	TGCAGAAGCTGCGGCACCCGCGCGCTGACAACG[A/G]CCACCAGCTGGTGAAGCTGTACGGCCCGCG
TP4500	TGCAGAAGCTGGA[A/C]GACGCGGCGGTGCAGCGCTTCTGCCAGGAGGTGGGCGTGAAGCGGCGCGT
TP4504	TGCAGAAGCTGGACCTCAGCTACAACC[A/G]CCTGTGCGGGCCGCTCCCCAAGGGCCACGGCGTGAT
TP4551	TGCAGAAGCTTGTTCAGGGCAGGGTGGATCTGACCCTGCCC[A/T]TCCTTTTGATGGCTCACCACGT
TP4563	TGCAGAAGGAAACACAGAGCCCATTAGCATC[A/C]AAAAAAAAAAACTCTTCCGCGAGCTGGATTCG
TP4565	TGCAGAAGGAAACACAGAGCCCATTAGCATC[A/C]AAAAAAAAAACTCTTCCGCGAGCTGGATTCGG
TP4584	TGCAGAAGGAAGAAGCAACAGAGCGGCACATCGATGGTTGT[A/G]ACGTCAGCGCCCGATTTATTCG
TP4585	TGCAGAAGGAAGAAGGAACAGAGCGGCACGTCGAT[G/T]GTTGTGACGTCAGCGCCCGATTTATTCG
TP4601	TGCAGAAGGAATAGAGCT[A/G]TACCTGTGCCCTTCTCATGGGAAAACCGTGGAAATCCTCTCACGG
TP4610	TGCAGAAGGACCAGACGCCGTGCTCGTACCGCGGCGCGTCCTACTACAACTGCC[A/G]CCCCGAAAA
TP4626	TGCAGAAGGACTCGGTGGACGCCTCCGACGCGCACGA[C/G]ACGCTGAGCGAAGACGACGGGTGCAC
TP4630	TGCAGAAGGAGAAGTCGGCGCTCGAGATCGAGGCGCGACAGCAGCG[C/T]CGCACCGCTGACGAGCG

Table A2 (cont.)

TP4636	TGCAGAAGGAGCCGATGCGGCGCGCCACGGTGGC[A/C]CAGCTGCTCTCGCACCCGCTCGTTGCGCG
TP4643	TGCAGAAGGAGGAGCCCTT[C/T]GCCTTCCCCAAGAAGGCGCAAGAGCCGTTCTCCGTCTCCTAGGA
TP4644	TGCAGAAGGAGGAGCGCAGAAGGATTTTA[A/C]TCATATCGCAGTACAGGCGTACAGCACGGAGACC
TP4689	TGCAGAAGGCAAAGATAGCCAGCTCCTGCGCATTGACCCTCC[C/G]AAAGCGATTTGTCATCGGACG
TP4713	TGCAGAAGGCATCGCTGCGACAAGGTTTGCCACACTGGTTCTTGCGGGGATTG[C/T]GCCGTTCTCA
TP4721	TGCAGAAGGCCACGTCGTGGGTCCGCATCACCTCCCTGGCGGCCTCGGCGGAGGACGCC[A/G]CCAG
TP4732	TGCAGAAGGCCCTGCGGCGGCCTAGGCAGCTGGCCAGCTGGGCGTGGGCCGTGGGTGCCTG[A/G]GC
TP4739	TGCAGAAGGCCGCTCAGATGGGCGCGACAA[C/T]GAGCAGCGGCAACGTGAACTCTCTGCTCAGGGG
TP4740	TGCAGAAGGCCGTCATGCTGCTCGCGCTCACG[G/T]CCTGGGCCTTCTGGTCCCACTTCCGCGCCGC
TP4741	TGCAGAAGGCCGTGTCCAGCATCGCTTACCTGCTGGCCGTCACCATGGTGCTCAACAGCGTC[C/T]A
TP4753	TGCAGAAGGCCTTACGGT[A/G]GCAAGGGTAATGAGTACAAATGGGAAGGTGTAGGCAATAGCAGGG
TP4765	TGCAGAAGGCGAGGCGCGCCGTGGAGAGGTAGAGC[A/G]TGCCGATGACGGGGCCCGAGGAGGTGGA
TP4766	TGCAGAAGGCGAGGGGCAAGCGGCGCGAGGCGGGT[C/T]CGTCCCATCGGTACGCACGGAGCATTAC
TP4773	TGCAGAAGGCGCTCG[C/T]GGACGCGGACGAGCTGGAGCGCTCGGAGCTCGAGAGGATGGCTAGGAT
TP4779	TGCAGAAGGCGGCCGAGGTCGACGCGCAGACGAAGGTCTTCAGGGT[A/G]CGACAGGAGGCCATCGG
TP4785	TGCAGAAGGCGGTGGCAAACCAGCCTGTTAGCGTCGCCATTGATGCTGGCGGTCTTGC[A/G]TTCCA
TP4790	TGCAGAAGGCGTCGAGCCAGTCCCTGAAGCAGCTCATCACGCTCACCGCCAAGGAGGAGG[A/G]CGC
TP4800	TGCAGAAGGCTGAAGAGATGG[A/G]GCTACTGGTTTATTACGTACGTACTAGCTAGTGTGTCATGTG
TP4816	TGCAGAAGGGAAGCTGAGAGGGCAGACAGGTGCGCAGGGAAGCGGAATGGGAGTTGTGGC[G/T]GCG
TP4821	TGCAGAAGGGACTGAGCTAGCCGTTAGTTAGCGCATCTGAGTTGAATC[A/G]GGTTAGCAGCTAAAT
TP4834	TGCAGAAGGGATGTGAAAGGCTACGAAGAAACTGACTAGAGTGTCGGTGATGGGCGAGCGCC[C/G]A
TP4835	TGCAGAAGGGATGTGACAGGCTAC[A/G]AAGAAACTGACTAGAGTGTCAGTGATGGGCGAGCGCCCA
TP4846	TGCAGAAGGGCCAAACCACGGA[A/G]AAACTGAGGGCAAGCAAGCTGCCATTCCTTGCGGGACCCTT
TP4847	TGCAGAAGGGCCAGGAGCCCCTCTTCGGCCGCGGCGTCCTCAAGGCCAACGGCG[A/C]CGAGTGGCA
TP4849	TGCAGAAGGGCCCAGCCGATCCAAGAAAAGGTA[C/T]GACTAAATCTTGACTCTGGTAACTTTTTTA
TP4872	TGCAGAAGGGGAGGGAGTAGTAGG[A/T]GTAGGGCAGCTGCGTCCTGATGGAGCTCAGCTGGTTCAC
TP4907	TGCAGAAGGTAAAGAGCAATGGAAAGCAGGGAGGGAGGGGGCTGGAAAGGCAGCAGGAAAG[A/G]AA
TP4936	TGCAGAAGGTCCTGT[C/T]CAAGTATGAAAAGCTCAAGGAGCCTGTTTGTGTTGAGCTAGAGCCCGA

Table A2 (cont.)

TP4939	TGCAGAAGGTCG[C/G]CGTCCTGGCGCTCCTCGCCCTCGCCTCCCGCGTTTTTCCTCGTCTCGCTT
TP4952	TGCAGAAGGTGATGCCGTTGCAGACCACCTTCTG[C/T]TCCACCTCCTTGGAGGCCGTGGACGCCTT
TP4957	TGCAGAAGGTGCACTTGTACGGCTGCCTTGTTCCCTCGTCGTCATCGTCGTCGTCGTCG[C/T]CGCC
TP4966	TGCAGAAGGTGGCGGCGTCAAAGCCAGCTCGAGCTCGGAGGATGAGAGCCTCGCT[C/T]AGAGGTAT
TP4974	TGCAGAAGGTGTGGC[C/T]TGATACGGTGGCTGTCGTATCCCAGTGTCCTTGCTCCCGCGCCAAGGA
TP4984	TGCAGAAGGTTCTGGTACGCGCTGAACGTCTCGAGG[A/G]AAGGAAGATCCGCGAGGCCAGGGGGCA
TP4987	TGCAGAAGGTTGCCGCTGGACCAGGAGACGTAG[A/G]TGCGGAAGATGGGCGGCGCCACGCCGTGGC
TP5029	TGCAGAAGTACGCATCAACTGACTCCACCTCGAGGAACACATTGGACCATGA[C/G]GACTTCCTAGG
TP5050	TGCAG[A/T]AGTAGAGTAGATCAAGAATAGGCAAGGGGATGTACATGCAGAAGCAGAGTAGACAGCT
TP5069	TGCAGAAGTAGTCTGTGTGGTACGGTACAAGGCACAGCC[A/G]AAGGGTGCCTATACTTGTACGTAT
TP5071	TGCAGAAGTATAA[C/G]AGGACAGTAGTTGTAAAGTTCACAGTTCCGTCACCGTCAGTAATCGGGTC
TP5095	TGCAGAAGTCAGCAGGTGCAACTCAACCAACCG[C/T]CCCATCAACCAACTTTCCAGGCACAGCTAA
TP5123	TGCAGAAGTCCTCGATCGTAGGACCACCACTCCTCGTCCAGGAAGAGG[C/T]CGTTGGGGCACTTGG
TP5125	TGCAGAAGTCCTCGTCGGACCACCACTCCTCGTCCAGGAAGAC[A/G]CCGTTGGGGCACTTGGGGTT
TP5127	TGCAGAAGTC[C/T]TCGTCGGACCACCACTCCTCGTCCAGGTCGACGCCGTTGGGGCACTTGGGGTT
TP5141	TGCAGAAGTCGGCGGTGGTGTAGTCGGCGTCGGG[G/T]CTCACCCCACCGATAAGGTGGTGTGGCAC
TP5146	TGCAGAAGTCTCCATTCTTGTCGTTGACTCAT[T/C]GACACAATGCTTTGCTTGGTTTGCAGAATGG
TP5185	TGCAGAAGTGCAGAGTAGCACC[A/G]AGACAATCATTTGACGTTTGAACGCGTCCGCCAGCTCCCAG
TP5201	TGCAGAAGTGCCCCA[A/G]CGTTGCCTTCAGGAAGGACATTGACATTGACACACGCCAACAATGCTG
TP5226	TGCAGAAGTGGAAGAACTTGTCGAAGGAGAAGGGTCGGAGACTGTGGTGAAGTCGTGACT[A/G]TTA
TP5229	TGCAGAAGTGGACAAACAAAGCGAGGAGTGACATG[C/G]AGCACGAACGACGAACCCACAGTGTGCA
TP5247	TGCAGAAGTGGGCGACGCGGCGGAGGAGAAGGCGGAGAAG[C/T]AAAGGCGGCGGCTGGTGAGGAGC
TP5248	TGCAGA[A/G]GTGGGCGGCGCGGCGGAGGAGGCGGAGAAGCGGAGGCGGCGGCTAGTGAGGAACTGG
TP5251	TGCAGAAGTGGTCGTTGAGGTGGTGGTAGTAG[G/C]GATGATGGACGGGGGTGCCGCCACCGCGGCG
TP5254	TGCAGAAGTGGTGCCTGTCTTCAGTGTT[C/G]GATGAGTACCTGCACTTCGCGGCGGCGAAGGCGAG
TP5273	TGCAGAAGTTC[A/G]CCGAGTCCTTGTGCCCGCGCTGCGCGCCGCTGCACCAGTCCTACTGGATCTG
TP5283	TGCAGAAGTTCATCA[C/T]GGATTCACGGCTAGCGACCCCATGAGCGGCGGCCGACACACAGCTTGC
TP5308	TGCAGAAGTTGAACT[C/G]TTGAAGAGCATCATTACAAACAAGGACACTAAAAAAGAGAAAAGAAAA

Table A2 (cont.)

TP5317	TGCAGAAGTTGCTCATCTCTCTACGACTAACAACTCTTTTTCTGAATGTTATCT[G/T]TTCTCAGCT
TP5320	TGCAGAAGTTGGAAACAGTCAAACACTC[A/G]AAGTCTAAAACCAATCCAGCTACCAAAACACCGCG
TP5329	TGCAGAAGTTGTCGCTGGGTACACA[A/G]CCCAAGGTGGCGGCAGATGCAACAGAGCCTGCTGCTGC
TP5333	TGCAGAAGTTTAGAT[C/G]GTACTTAAAGAGTCAGACAAGACGCCACACTATGGTAGCTTAGACCGT
TP5347	TGCAGAAGTTTGGCCGACGTCAACGTGAACGTGAAAGTGAAACAGAGAGACAGTTGAA[A/T]GTTGA
TP5353	TGCAGAAGTTTTACACTCCTTCATCTGGTGCAACCATGTTCCTCCACAC[C/T]CCACAGGTTAAATT
TP5379	TGCAGA[A/T]TAACCAGTTGATAGATAAGGTGGAGGTGCTCTACAGTGAGATGTGTGAGAGTGGTGT
TP5402	TGCAGAATAAGTGAGAGATGTTGGCCCCCACGAACAAAGCAATACTTTGCTCC[A/T]TTGCCAGCGA
TP5425	TGCAGAATACAATATGCTTTGATGTAAGTG[A/C]TAGCTGATGGTGCACCATATATATTAGCATAAC
TP5427	TGCAGAATACACATGGCATTATCATCACTAGCCCAA[C/T]GCCCCCAAACGATTCAGGTCTCGTCTC
TP5441	TGCAGAATACC[A/C]CATCTCATTTTACACCATCACTTGTTGAGTCAATGAGCATATAATCATGATT
TP5484	TGCAGAATAGATAGAGGAGG[A/T]GGAGGAGCTCGAGCTAGGGTCCACATTCCAAGGCGAGGCTTGA
TP5489	TGCAGAAT[A/C]GCAACAAACAACAAGAGCAAAAGCACAGTCAGCACCAAAATCCACCAAACGTATC
TP5493	TGCAGAATAG[C/G]AGGGTGTTCCTCGTTGCCACTTGCCAACAAGACGCGGGTTAGGTGGAGTTGTT
TP5549	TGCAGAATATCCACCACCTCCGCAGCAACCTTACCAACCCCCACCCG[C/T]TGGATACCCTCCATCC
TP5562	TGCAGAATATGAAAACCTGTGCTGGAAATTCACCAGCAATCAATTTTATTT[G/T]AACAAAAGACTC
TP5566	TGCAGAATATGATATGTGGAGCC[C/T]GCTTGTCAGTGCGGCGACTCGACTCCCAGAGTCCCACTGC
TP5599	TGCAGAATCAAA[C/G]ATTTCACTTGTCTATTCGGCTCCCACATCGGCCTGTGCATCATCCCACGAT
TP5618	TGCAGAATCACAAAAAGTTTCCTGACGTTTTCTTC[A/C]TAGAAAGAACAGAACAGTGCGCGGTTGT
TP5626	TGCAGAATCACCAAA[G/T]CTGAGCTGTCCTGGGGATGCATGTGCCGAGTTGAGTGGGTTCACTGGT
TP5631	TGCAGAAT[C/T]ACCTTTACCCTCTTTGCTATGTTCGCAAAATTCCCAGCCTAACGCATCATTTGCC
TP5636	TGCAGAATCA[C/T]GATCATCAGTGTGTGCAGGGCCGTTGACGAGATGAGCAGTAACCGTATCTTCC
TP5664	TGCAGAATCAGTTGAGGTG[C/T]CTTACATCGATTGCTTGTCCTGTCGTCTGTGATTGCAGTGGATC
TP5674	TGCAGAATCATATCACACACAGCAAAGCCTCAAAACGTGATCAGAGCAAAGAAAAAGAAA[A/G]GTG
TP5675	TGCAGAATCATATCAGTGCATCAATTTCGTTTCATCAGACCGTTTCCCACGTACTACTAC[A/G]AAA
TP5684	TGCAGAAT[C/T]ATCCATGAGAGCCTGGTTTCCGCGGTGGAGGACACCCGCGAAACCGTTATTCATC
TP5685	TGCAGAATCATC[C/G]TCGCCCTGCACCTCCCAGTCCCATTCCTCCCATTCACACAAGCCCGCTAGG
TP5687	TGCAGAATCATGCCTCGCACT[A/C]GCACACGGCTCGGTCATGGATGCAGCTTGTTGGTCCCCTTGT

Table A2 (cont.)

TP5704	TGCAGAATCCAATGCCTCCTGCTACCAGCGTACTGCCACCGCTC[A/C]GCTTTCCCGTCATCTCCCT
TP5776	TGCAGAATCGACTAGAAAGTAGAAACAGAAA[G/T]ATTTCAGCTGTAACAGAACCAGGGGAAGTTTC
TP5790	TGCAGAATCGGCCAAATAAGAG[A/C]GGCCACTTGATGGCGTAAGTGGTAGCTGTAGCTGTCATAAG
TP5800	TGCAGAATCGTCAATCCGATGAATTAGAGCCTGTTTGGCACGGCTCCTCCTGAGCGGCTCCTC[C/T]
TP5805	TGCAGAATCGTGGCATCCGCTCGCGCCT[C/T]GTGCCCACGGATTGACGGTTGGTGCATCTGTTTGA
TP5818	TGCAGAATCT[A/G]GCAGACATGGACATCACCTACAAGGCTCTTCAGGTCAAACTTGCTTTTAGCTT
TP5834	TGCAGAATCTCGATCGAAAGTCACCCTG[A/G]TTGGAGCCCAATTGCTTATGATTCGAACTCCTAGA
TP5847	TGCAGAATCTGAGGTGCATGAGTGTTACCTCTTGCCCTGGAGTCACTGATCTTGCGCTCG[A/C]TTC
TP5882	TGCAGAATCTTATCTCTATCTTTTTTTTT[C/T]CCAACCACAAGTGCCAATTTTATTCCTCGTCTGA
TP5918	TGCAGAATGAACGCGTCGGTCACCCCAACCCCGCCACC[C/T]CTTCCGCTGCCGCGCCGCCGAAAAA
TP5931	TGCAGAATGAATCCACTATCCAAGAGTATAATCTGGGATCCA[A/T]ACAGAACTGATTATCACTATT
TP5942	TGCAGAATGACGTGGGGAATGATCGCCA[A/G]GGGCAACAGGGCCATCCAGAAGTCGAAAAGTTTGA
TP5950	TGCAGAATGAGCAAGAACCGACC[A/C]CGCAGGTGAGATGACGGACTGTTTGGTTTGATCAGTGCAG
TP5971	TGCAGAATGATTCATTA[A/G]CCAATCCAAAACAATGGGTTTAAGCTATTATTAGATTGTCTCGCCT
TP6022	TGCAGAATGCGGCGACGAGCGTGTTGTAAGTCACGGCATTGGGGTCGCAGCCCGC[A/G]CCGCGCAT
TP6038	TGCAGAATGCTGTAGCATTTACCCGAGCCCAAAATATC[C/T]GAGTGAATGCGGCCCGTCACCCGTG
TP6048	TGCAGAATGGAAACAATGTGGGATTGAAGTCAGCGTATGAGGAAGCATCAGCCCT[C/G]TCACACCC
TP6050	TGCAGAATGGAACAAGGCCGAAAA[C/T]GCTTCGGGATAGGGAAGGGAAAGAGCCCATCGGTGCGGT
TP6064	TGCAGAATGGAGATAGAGGCTGACCACATTGGGCTCCTGCTGCTCGCTGCTGCTGGCTA[C/T]GATC
TP6074	TGCAG[A/G]ATGGCAAGCCTCGCGGTCTCGAAGGCACAGTAACCGAGCGCGGCAAAGCACGCGTTGT
TP6085	TGCAGAATGGCGGCCTGTGTCTGGCGCATCATCTGCTGCTGCTTGCGGTCCTCCACC[A/C]GCTGCT
TP6090	TGCAGAATGGGCCATGTGGCCCATGAGTGTAACGG[C/T]CTATTGGGCCCTTGGATCTGCGTCCTGA
TP6091	TGCAGAATGGGCCGCAAGCCTGTTTAACCCATTGGAATTCCTACGGTGG[C/T]CCCTTTCTGGTCCA
TP6135	TGCAGAATGTAGTTGAACTGATACGAACCGTGATCCGACTTTTAATTAAAATATTGTGCCA[C/G]TG
TP6153	TGCAGAATGTGACATGCATGCCCTTGTGA[A/C]AGCAGAAAGGTTCCAAGTTTTGCTAAAAAAAAGA
TP6171	TGCAGAATGTGTGACTGACTCTGTCCTGCTATGAGAGGAAGCAAT[C/T]TCTTGTGTGCTCTTCCCT
TP6188	TGCAGAATGTTGTTGCGCGTAAGATGATTCCCAAAGCCGCGG[A/C]GAGGCTGCCGCCATACATCGT
TP6197	TGCAGAATTAACGGAACGCCAGCTCTGAATCGACTCGACTGACGAGATGTTCAGGATAAACT[A/T]G

Table A2 (cont.)

TP6227	TGCAGAATTACCTTTACC[C/T]TCTTTGCTATGTTCGCAAAATTCTCAGCCTAACAGTAACACATCA
TP6278	TGCAGAATT[C/G]AGAAACAAGCGGAAAAGTGTCGGTCGGTCAGTCGGTGGGTCATGTAACCACCAC
TP6305	TGCAGAATTCGGCAGGGCATCAG[A/G]CACATACATGCATGTTGCAGACATGAGCCATGGCCGCCAA
TP6321	TGCAGAATTCTCTTGTTAGTTCGGCACAGTCTTCGCATGCACCGTACATAACC[A/G]CGGCTCGACC
TP6325	TGCAGAATTCTGCTTTGTTGCGGGATGGCACAAG[C/G]GTTTTCGTTATCCGTGTAAAATTGTTTAG
TP6353	TGCAGAATTGAGGGAGGCAGGGAAGCGAGGACAAGAACCAGACCACCGTTCGGCTGCGTGCAG[C/T]
TP6373	TGCAGAATTGCAGATAAAGATAAACAAGACCATGCT[A/G]CCGTGGCACGGATAAGCAATCGGACCA
TP6399	TGCAGAATTGGCAGTCAA[C/T]CAGATGGCAATTTCTGTGGAAAGCGAGAGAGATCGTCGATCCACA
TP6400	TGCAGAATTGGCGTTGGAGTACTGGACTGGATGACAGTGA[C/G]GGTACTGCCTGCTGACCTGCTAC
TP6420	TGCAGAATTGTTAAGCTTTTGGCATGTTACATGACTGTACGTGGAGCTTATTG[C/T]GTTATGGGCT
TP6461	TGCAGAATTTCGCCACTCTTCCGTAGAAGC[A/G]AGAACGAAACCAACGGTACCTAAAACTCTGCAC
TP6504	TGCAGAATTTTAGTG[A/G]TACTTCTTTTTGTTCTATGAATTGAATGCAGCAATGGTTACGCGTTGA
TP6536	TGCAGACAAAAAGGAAACTGATTG[C/T]GCAACCCGAACAATCCAAGCTACGAGAACTTTAGACAGG
TP6551	TGCAGACA[A/C]AAGCTGTGGCAGCATCCCCGTCCATCGCGCTGGCTGCTGAGGTCGCCTGGTCCAA
TP6572	TGCAGACAAAGACCGAAGATATTGGT[A/G]TCGTGCGGTGCTAGCTCTAGCTTGCTAGGTGATCGAC
TP6576	TGCAGACAAAGCATAGAGACTGGAGAGGC[A/G]CCTTTGCAACTGCAAGACAAACTCCCATACACCA
TP6577	TGCAGACAAAGCATAGCGACTGGAGAGGCACCTTTGCAATTGCAAGAC[A/G]AACTCCCATACACCA
TP6582	TGCAGACAAAGGAGAAATTTCAAATTTTC[A/G]GTTTCTCATGATTCCTGTGTTGACATCTGAGCCC
TP6608	TGCAGACAAATGATGCGCAGAGGCAGAGATTTGGTGTTCAACC[A/T]GCGATGACAAGTGCAGTAAG
TP6613	TGCAGACAAATGTGAGATTGCCTTTTATTTTTTT[G/T]ACAATAACAGTTACAGGATCTGCCGAGGA
TP6624	TGCAGACAACAAAGTTCTTGGTGAATTTGATCTCGTGGGCATTCCGCCTGC[C/T]CCAAGAGGCTTG
TP6632	TGCAGACAACAC[A/C]AGTGGGCACTCCGTGAAGACTGAAGCGAGCAGCAGCGCTCTGCACTCTCGC
TP6635	TGCAGACAACACCAGGTTTGATGCTAGGGCGTGACA[A/T]TGACATTCAGAAATCAATAAGGGTTCT
TP6654	TGCAGACAACATTCACGCACT[A/G]GCAAGCAAGGTACAAGCATGGATTACCTGCGAGGCGAATTCT
TP6673	TGCAGACAACGACTCGGCTTCTTTGATTCTTCTTGGATTGACAACAATTTGCTACTAGCCC[A/G]CA
TP6676	TGCAGACAACGCCGCGG[C/T]CAACGAAACTAGCGGACAACGCCTCCCAGAACAACGAATTAGATGG
TP6692	TGCAGACAACTCTATCGCTTCCTGATTGTAGACGGAATCCTCTCCCCAGTCAAACCTC[C/T]GCTGC
TP6704	TGCAGACAAGAACAACGAT[A/C]GGCTAGACCGTCGGGCCATGCGAAGGTTTCGTTCGTTCATCAGT

Table A2 (cont.)

TP6712	TGCAGACAAGAGAGAAATGAGTGAACGAAGAACTAGCAGTTGGTAGCTCTTTATT[C/T]GAGGGGAG
TP6717	TGCAGACAAGATATAGAATAGCAATTAAAAACTATAAATGTTTTCAAGACACGTGCAGGCCG[C/T]G
TP6722	TGCAGACAAGCACATCCTCAAGGATCGTTTCACGTCAAGCTGTGATTCGCAGT[C/T]CGTGAGCGGT
TP6735	TGCAGACAAGCGTTTTTAAGAACTAGA[C/T]TAGAGAAGAAGGTTAAAAGAACATTTCGCGGCCGCT
TP6744	TGCAGACA[A/G]GGCAACGCTGGAGGAGGAGGAGGCAGCAGCTAGCATCGACCAGTTGGAGACAGAG
TP6746	TGCAGACAAGGCACTGCTGCGGTGGCCAACAGCGCCAGGGCGTGGGGG[C/G]CTGGGCGGCCCGAAA
TP6751	TGCAGACAAGGTTTTGTTTCTCAACAAGTACATTATTATTCATTATTGAAAATTTAAACTG[A/T]TT
TP6757	TGCAGACAAGTACGTACTACCAACCA[A/G]CACGATGCGATGCACAGGCGCTAGCGACGCGAACAGT
TP6758	TGCAGACAAGTAGAGAGTAGGGG[A/G]ACCGATCGCGCAGGCATGGCCACATGAATCCAGTCCAGGG
TP6764	TGCAGA[C/G]AAGTCAGTGATCGATTTGTTGCACTCATACCTTGAACCATTCTTCAAAACTACTACC
TP6767	TGCAG[A/G]CAAGTGAAACAAGAATTTCAGGCTTCAGCTAATCAGGTGCGTAAAGTACTAGGCTAAG
TP6778	TGCAGACAAGTTAAACCAAGTAACCTCGCTTCTGCTGGTCTGGTTTG[A/G]TTTGGGTGCCGTTTAG
TP6782	TGCAGACAAGTTCCTATGCCACGCCTCTT[A/G]CTGATCGAGGTAACGGAGAGCATTAATTTAATTG
TP6797	TGCAGACAATC[A/G]GCGAGCAAATCCTTGGACGCAAAGCGCAAACGCCATGCAAGAAATGGGACTT
TP6798	TGCAGACAATCAGTTTTTA[C/G]GATAAATAGAACGTCTTTGTAGCTAGAAAGGGACATTTCACAAA
TP6803	TGCAGACAATCGGAGTAGATAATCAGAGGACTCAG[A/G]TTATTCAATCTAAACGAATCTGCTCAAG
TP6828	TGCAGACAATTAT[G/T]AATTGTCCTTCTCCAAGATCAAGTCATGATGGATGCACAGACAAATACAA
TP6831	TGCAGACAATTGACTCATATATTGCAGATGAGAGAGTAGGACTTGTAA[A/C]GCCTGCCGAAGGGGT
TP6833	TGCAGACAATTGATGCGTGTGCCTG[C/G]CCGCAGTCGCCGCCGCATGCATGGTGGCCCTATATCCA
TP6876	TGCAGACACACATGAGTGCCTGCCACTGCCACCCACACCCTCTCTTCTCCCTCCTGCTTCT[A/G]CT
TP6879	TGCAG[A/G]CACACCCAGTCCACGAGGGAGCCCACGTCCTTGGCGAAGTCAGGCAGGTACCAGTGCA
TP6896	TGCAGACACAGAA[C/G]TCACGCGTCGGCGTCGTGACGCCATCGCGCGCTCGCGTCGCGCTCCCGCG
TP6902	TGCAGA[C/T]ACAGCCCAGCACTAGATAAATAGGGGGGAGAACACCCTTCAAACCTACTCACCCAAG
TP6907	TGCAGACACAGGCTGTGGCAGCGTCCCCGACCATCGCGCTGGTTGCTGAGGTCGC[C/T]TGGTCCAA
TP6917	TGCAGACACATGACAACACTCGAGTCATTGGAGATGAAG[C/T]CCTCCCGAGCTGTACTCCATGGCC
TP6934	TGCAGACACCAAATTAAAGCAG[A/C]AATCATGCCAGCCATTGCAATTCCTCTCTCATTTTCTGACG
TP6961	TGCAGACACCAGAGCATGGGAGCAGAAGAACAGCAA[C/T]GAGAAGCAGAAAATTGTCATCGCTTCC
TP6963	TGCAGACACCAGCATCAGAAACCATTCGCATCTATATTATTCGCATCAGAAA[C/G]CATATATACTG

Table A2 (cont.)

TP6969	TGCAGACACCAGGAACCCTAGGAGGCGAATTGTCCTCCATCTATCAGCTGCC[C/G]ATCTGTTGAGG
TP6983	TGCAGACACCCACCGAAGCTGGCCAGGCGATTCTGCGTCGGTTTTGCTCCAGCGA[A/G]TCGGTAGG
TP6984	TGCAGACACCCACCTGACCAAGTTGGCGATCGGAATG[C/G]GACGGACGGAGAGAAGGTGATTTGCG
TP7002	TGCAGACACCGACATTGCCAGCACCACCACCAAAAGTACATCA[A/G]ATGTTGCCTCAAACTCATCC
TP7014	TGCAGACACCGTCGTGCTGGAGTTCAATCAGTACACGCCAGGCTCAAGATGGAG[A/G]CAAGCGCTG
TP7027	TGCAGACACCTCTCTCGCGGAACCAGCGAACCACGCCGCTGCCTCCTCTCCCT[C/G]TTCCCCATCG
TP7038	TGCAGACACCTTTGTTAGCACCTTCGCC[A/G]CCCTATGATCGCGCCTCGATGAGGACGCCTCTGTC
TP7055	TGCAGACACGCACAGTGCGACGTGACGGCGG[C/T]CACGGCGTCTCGCGCGCAGGAAATTCCACGGG
TP7063	TGCAGACACGCCCTGATCACAATGTTCCAGGATGTGGCGTCCTTCTGG[A/G]CCATCGCCCCGAACG
TP7068	TGCAGACACGCTCAAAGGATGC[A/T]CCTAAGTGTTTGACGAAATGCACGTTCGGAGCGCTGTCATT
TP7071	TGCAGACACGCTTGAACTGTACAATGGATCTAGGAGGGAGACGGAGCAGGATCTCCCTAGT[C/T]GC
TP7078	TGCAGACACGGCACGCCCAGATCGGTAACGGAATCACAA[C/T]AGCAACAGCAACGGAAGATAAGAG
TP7081	TGCAGACACGGCGCCGCTCGGAGGGGTAGCAAGCCCGTGTCCGTGAGCTGAGCTGCTG[C/G]TAGCC
TP7087	TGCAGACACGGCTCCATCATCGCGGGCATGGTT[C/G]TGTCAAGAAGCTCCTGATCAAGTGGTCCAA
TP7088	TGCAGACACGGGCGAAGGGG[A/T]GCGGAGCGACTATTTGGGCACACCACGATAACAAGCCGTAGCG
TP7109	TGCAGACACTAGCCGTTAGAG[C/T]TGGACTCAGACATCACTTTTTTCTTTTCTTTTTCTTTCGATG
TP7134	TGCAGACACTGAACCTGTC[A/G]GGCAACCAACTCTCTGGCGCGATCCCCAAGAGCGTTGCTAGCCT
TP7135	TGCAGACACTGAACCTGTCGGGCAACCAACTCTGTGGCGCGATCCCC[A/C]AGAGTGTTGCTAGCCT
TP7140	TGCAGACACTGCAACACGTCTCGACTCTCGAACCTCGACGACGCCATC[A/C]CGCTCCAGACGCTTC
TP7159	TGCAGACACTTATGTGCATCCACAGAATA[A/G]CCAAGAAAGGAAGCCAAAAAATTCCCCGAGGAGA
TP7185	TGCAGACAGACACATCTACCTGAATAACGCAAGCCATGCACATTTTTCCATTCCACCAC[C/G]CCCA
TP7193	TGCAGACAGACATTCAATCCAACGCCATGAGCTCATGATCGGTTGATCGACCTTCATTGTTT[A/G]A
TP7201	TGCAG[A/G]CAGACTAGAAATTGACAGCATGTGCTGCCATTTAGTTTAGTTACCCTATAGACGGGCC
TP7203	TGCAGACAGACTGCGGCTGTGCCGCCGCC[A/G]CCGCCAGTGGTGGCTGAGCTTGGTGGTCGACGAT
TP7220	TGCAGACAGAGCGCCGCGGCGGCGGCGTC[C/T]AAGGGGCAGCAGCGGCGTCAGAACGCGCCGCCGC
TP7221	TGCAGACAGAGCGCCGCGGCGGCGGGCAAGGGGCAGCAGCAGCGCCAGAACGCGCCGCC[A/G]CCGC
TP7240	TGCAGACAGATAATGTGTGGCCGTGCTTGCTGGATCAGCAGTTTAACTGCCTCTCTTCTTGCT[G/T]
TP7244	TGCAGACAGATAGGAATCGTTTTTGTC[C/T]CCTCCTTGCTTTCATCACGAGACCCATCACTGAAGC

Table A2 (cont.)

TP7257	TGCAGA[C/G]AGATTTCACATCAAAATGGACACGGCTGAACTAATATGATAAAAAGTGGGAAACGGT
TP7275	TGCAGACAGCAATTCCATCCTGGATGCGCTCCCATGTGCTCTTGCCTACTCCTCCA[A/G]CTCTTAG
TP7281	TGCAGAC[A/C]GCACCAAATTTTCCTCCCGTTCCTCCCGTGCGCGCTGCGCGGTCTGGGGCTCTGGG
TP7282	TGCAGACAGC[A/G]CCAGGCCCACCGCAGCCAAGTGGGCGTGCCATTGTGGTCCTACTTTTGATTAA
TP7295	TGCAGACAGCAGCACCTCCATTGCCAGTGGCCAATGTCCCTCACTCCCTCCAGT[C/T]CTAGGCTCC
TP7296	TGCAGACAGCAGCCAACGGTGTTGCCATAGGCATGGACAGCCCACCACCTT[C/G]GGTCATGTCAAT
TP7321	TGCAGACAGCCCATTGACATC[A/G]GTGCTGAATCGAATCAGCGCCTACGTCACCGCAGCAGCTTGC
TP7327	TGCAGACAGCCTCGCAGGGAAG[C/G]GACGAACTCCTTCAATGGCACGGGCCTGAACGCCATGACGG
TP7344	TGCAG[A/G]CAGCGGATTCTGAGCTCTTACTCCATGGCACCCTCGTCTGCGGAGGCTGACTCGGCGA
TP7366	TGCAGACAGCTCGGCTGATGATACTGTTGGTG[G/T]TGCGGCTGCTGCTGCTTCCGTTTCTGTACTC
TP7384	TGCAGACAGGACACGCGCGACGACACCATAGGACTGCGCCATT[A/G]ATGGCACGCAACCGTCACCA
TP7394	TGCAGACAGGAGTCAAGGATCAAGTCAGGTCTCTCGAGCTGGAGCTCGAGAGCGCCCACGCTG[C/T]
TP7396	TGCAGACAGGATAGCCGCAATACGCACATGCATGGAGGGC[A/G]TGTTGCTCTTATCTATCGGCAAG
TP7399	TGCAGACAGGATGGACCTGCCAACAACATC[A/G]TTGAATCGACAATCTCTGCGCGCTTGTTTCCTA
TP7400	TGCAGACAGGATGGTGAGCACGCAGCTGCGGAACGTACAGATGGTCGGCGACAAGTGACATC[A/G]C
TP7406	TGCAGACAGGCAGGGGGCAGAAGTGGAAGAAC[G/A]CGTCTTCTTTTTTTTCCATGAATTAAAACTC
TP7436	TGCAGACAGGGACTGGAC[A/G]GCCTGCTTTGAGGTTAGCGGCCAGCATTTGCCGTGATCATCGTCT
TP7454	TGCAGACAGGTCCAAGCGACAACA[C/G]TGAGAGACTGACACTGACTGGAATCAGAGGCTGCTGCTG
TP7480	TGCAGACAGTCAACG[C/T]TGGCACTGCGAGGCTGCTGTCGCACAAATGCCAATGTCGCCAGGCCGA
TP7492	TGCAGACAGTCTACACCATGTTCAGCTACTTCCAGAGTAGCTGACA[A/G]CGTCCAAATTAGGGTGC
TP7530	TGCAGACATACA[C/T]ATTACGAACAGCCCGCCGCCGTCGACGCCGTTATTAGCCGTGCTCTATCTA
TP7560	TGCAGACATATTGCTTCTCGTTTGAACATAGGTACCGTGTCAGGAA[C/T]AAACATATCCGTACACG
TP7574	TGCAGACAT[C/G]AATGTGAATGGATGAACACAAGCAGAGTCGTCGATGGACATACATGTGCATGCA
TP7577	TGCAGACATCACAGAAGAGTTCATCCAGG[C/T]CATCAGGAATAATGGAACACAATGCTTTTACAAC
TP7624	TGCAGACATCTCTGCAAGAAGCTAGGAGGTGAGTCAAGCCATACATAATTTTGCCT[G/T]GTAACCG
TP7654	TGCAGACATGAGTG[A/G]GGTCTAGCTAAAGCTTATGTTCTTCCGAGCAGTTATGTTACGATTTTTA
TP7664	TGCAGACATGCAAGAC[A/G]TGCAAGCTAATTATGCAAGTCATGCAAAGCTTAGTTTGCATGTACTC
TP7714	TGCAGACATGCTCCACGGCGGCGTCGGGATCCCCACCGCGTGCGACCGAGTACG[C/T]GATCGTCAT

Table A2 (cont.)

TP7717	TGCAGACATGCTGT[C/G]AACTTCACAGGGACCGATGGGAAGTAGTTCATGAGGACCAGCGATTTAG
TP7726	TGCAGACATGGCATCAGCGCAGCAAATCT[A/C]TTAGACAGACAATTCAGGGAAAAATCACAGGAAC
TP7736	TGCAGACATGGCTGATCATCATCATCATCATGGTTTTCATTT[A/G]TTTCACCTGGGCTTGAGGCGG
TP7743	TGCAGACATGGTGA[C/T]TGTTTGGGATGGTATAGATGAATGCAATCCAGTTCTTTGTACCTTGTAA
TP7776	TGCAGACATTCCGATCTGGAGTTGAGCATGAGCCCCATGCCGCGAACTGTTCGGCT[C/G]GGCATTC
TP7780	TGCAGACATTCCTTGTTATGATTATGAATGCCAAACAAGTTA[A/T]GGAAAAGCCCGTGATCAGTTC
TP7790	TGCAGACATTGAGGATCAACAATCCGA[C/T]GGCTGTGCGGTGAGATCGGGCCGATCAAAAGGGCGA
TP7827	TGCAGACCAAAATTCAACACATCATGAACTTTCCGTGGTGAAA[A/G]AATACACTCGGCGCTGGTCG
TP7828	TGCAGACCAA[A/G]ATTTCACGGAGCTTGTGCAAAAAGTCCCCAGTGGCTGTCTCTTTACCATAGTT
TP7847	TGCAGACCAACAGGCA[C/T]GCTCCCCGTGCACGTGTTGGCTCCTGCATCGCCACTTCAGACCAACA
TP7851	TGCAGACCAACCATTCGACA[C/G]ACACGTACGGTTATCCTTGCCGTCGTCAGATCATGCAGTGATT
TP7872	TGCAGACCAAGCTCTCCTAGACTACAACGCCCATGGAGGATCCATCAA[C/T]GCCCAGTGGAATTTT
TP7880	TGCAGACCAAGGAAAAAAGTATCATTCAG[C/T]AGAACTGAGAGAAATTTTTGTATGGAAGGAAACA
TP7883	TGCAG[A/G]CCAAGGACTTGATCGGAACTGCTAGCTCCAGGCGGGTTGCTGGAGCCACGGCTGCTGC
TP7888	TGCAGACCAAGGCGTGCTGCGAGG[C/G]GTGCGCCAACCTCAAGGCCGCCTTCCTGGTGTCGGTGGT
TP7938	TGCAGA[C/T]CACATCGTATCTGGCTGCAACTTTGTGCGCACCTTCTGGAATCGGATCGGATGGGCG
TP7957	TGCAGACCACCCATCCTT[C/G]CTCCTGAACCACCCACGATTCGTTCGTGCACGGGCAAGCAGAAGC
TP7963	TGCAGACC[A/G]CCGTCGACCTCTCCGACGTGGTGCTGGGCACGGCGTACGTCGGGTTCGCGTCGGC
TP7964	TGCAGACCACCGTCGACCTCTCTGGCGTGGTGCAGGACGCGGCGTACGTTGGGTTTACCTC[C/G]GC
TP7979	TGCAGACCACGACCTGCACGGGAGGCCAACCGACC[C/G]ACGCCCACCGACGTGTGGGGTCAGGATG
TP7996	TGCAGACCACTAGTAGTCACTAGACCAGGCTGGCTGGTTGCGCGCACACTGCC[C/T]GTTCGGCTGT
TP8009	TGCAGACCAGACCCTCACCCTGTTTGGTAGTGTCAGATACTACAGGTT[A/G]GGTTTGTGCTAGGCT
TP8028	TGCAGACCAGCAGCAGCATCCTCTGCCTCGCCTTCGCGGCCAACAGTGACGACAGCTC[C/T]CTCGG
TP8047	TGCAGACCA[G/T]CGTCACAGGAGCAAACAGCATATAAAGGGCTTTGAAAACAAGACAATGGCAAGA
TP8049	TGCAGACCAGCGTGCAGGTCGGGCAGGAAG[A/G]ACTGGCCCTGGCACATGCTACAGGCTGTTCACA
TP8052	TGCAGACCAGCTCGGCGTGCTCCC[A/G]TTCACGGTCCATCTAAAACTCTTAAGGCTCGTTCGATAG
TP8070	TGCAGACCAGGTAGGTGCATGCGTTGCAGGCAGGCCATGTGCCCAG[A/C]GCGTCAATTATGAGGTC
TP8080	TGCAGA[C/T]CAGTTCACAGCTGAGCTCCCCGATCCGACCCTCCGCTCGTCTTGCGCAATGGCCACT

Table A2 (cont.)

TP8085	TGCAGACCAGTTTTGCA[A/T]AGCGGACTAACGAGAAATGATTCAGCCCGCGTACAGCCCACGAAAA
TP8103	TGCAGACCATCACCACGATGCCGATCCTCGTCAAGGGAGTGCTCACCGCT[A/G]AAGACAGTAAGCT
TP8104	TGCAGACCATCAC[C/T]ACGATGCCGATCCTCGTCAAGGGTGTGATCACTGCTGAAGACAGTAAGAG
TP8135	TGCAGACCATGACGAGGCACGT[C/T]TTCGAGAGCTGCCTGACGGCCTTGAGCACCTTCAGCTTCCT
TP8143	TGCAGACCATGCCTTTTACGACGTTCGGCAGTCCAAAGCC[A/T]ACCATGAAGGGCCAACCAGAAGA
TP8152	TGCAGACCATGGAACTTGCCCTTGGTTATATGCTGTTT[C/G]ACGTTGATTGATGTGTTGTAACTGG
TP8155	TGCAGAC[C/G]ATGGCGGCCAGCCCCGCCGCGGCGCGCCAGTGGGTGGCGACGAACGTGCAGCCCTA
TP8164	TGCAGACCATTAGACGGCCTGTATCCAGGGTTGTATCTATAGAAGTC[A/C]TTGTTATGTTGGACAT
TP8181	TGCAGACCATTTAACATTGCAACAGCACTGTTAACATGCAGAAAA[C/T]TTTTTAGTACCTTGGCAA
TP8184	TGCAGACCATTTCTCAAAA[A/C]AAGAAAAAAAAATTCTCATCTCATGTGTTGGTTGCCAGGTGTAC
TP8200	TGCAGACCCAAGTCAACATGGCCTCCGTTTCATTCATCACAACTCAGTCATCATCAGT[A/C]GTCAG
TP8208	TGCAGACCCAC[C/T]GCCGTGCCGCGTGTGGGGCGCGCGGGGCGGCAAAGCACAAAGGCACTGCAAA
TP8219	TGCAGA[C/T]CCAGATTGACGCCGCAACCGCAATCAACAGAGCAGAGCTGCATGCAGATGCAGTTAA
TP8222	TGCAGACCCAGCACGGC[A/G]AAGCGAGTCCACAGGCGCCCGTCGCCTCCGTGGCAGCACGCCGCGG
TP8227	TGCAGACCCAGCGCTGCCACAGTCAGC[A/G]CGGACGGAGCGCCAGCCTGTGGTTGCAGGTGACTGC
TP8229	TGCAGACCCAGGTGAAGGCCACGCCGCCGTCGACGCCTAGGGGCAAGAA[A/G]CGCGCCACCACCGA
TP8255	TGCAGACCCCACAGGCACCTACATGCATGCACC[G/T]CAACTTGCCTTGCCTGCAAAGAGCAGAGAC
TP8261	TGCAGACCCCAGACCAGCCACAGCGG[A/C]CCCGAGAAGCTGGACCCGCGCGTCCAATTCAGGAACG
TP8274	TGCAG[A/G]CCCCGCCGCCCCACGACGGCGCCTTCGTCCTTGTCGTGCGTGGAGCATCAGGACCAGG
TP8301	TGCAGACCCGTACTAACCCCCCTTGTGGGTGTCTCGTGTGTGCAGCAAGGC[A/G]CGAGCAGCAACA
TP8306	TGCAGACCCGTTGGACTCAACAAGAATTCGCTGTCGTGGCGGTTAACTGCCGTCTG[C/T]TAGAGCT
TP8308	TGCAGACCCTAAAGGC[A/C]TCAAATCAAAACCACTGCACCAACAGTTCCTGGCCGTTTTGATGGGT
TP8329	TGCAGACCCTCTATACCTAGCTACATGTATAACAACGACGATGCTGATAATGGAACTTAATTA[C/G]
TP8354	TGCAGACCCTGGTGGGCAGCGAG[A/C]GGGCTCGTGTTTTTTCTTTCCCCACGTCGGTTCTCACTAT
TP8361	TGCAGACCCTTCCAGTGC[A/T]GAGGTTATCTAGGGGCGGTTGCTTCTCCCTTGGACAGTAGATTTG
TP8373	TGCAGAC[C/T]GAACCTGCTAGGTGCGTGCGCTCAGAACCCACGCAGGAGCATGCTGGATGCGTGGC
TP8376	TGCAGACCGAAGCAAGAA[G/T]CAGCAGATCGTGGTCGTGGGGTCGCCGTTTTGTCACGGTGGATAT
TP8378	TGCAGACCGAAGCTCAGCAATGGTGAAGTCGGAGACAAACCATCCA[G/T]TCTTGTGCACACCGTCG

Table A2 (cont.)

TP8383	TGCAGACCGACATCGACCTCGCCAGGCGCGCCCTCCGCGAAGCCCTCTCC[G/T]TCGACGCCGCCGC
TP8385	TGCAGACCGACATGGCACTTGGCCATTGGCTCACGCGGCGTGGCC[A/G]CTCGGTCACGGGGCCATT
TP8395	TGCAGAC[C/T]GACGGACTTCGGCGGTGTCGGCGTCGTCGATTTGCGCTACTTCGGGTACGCACTTC
TP8400	TGCAGACCGACTCAGTTCGGCGGCCTGGGGGTCAGCGACCTCAAGTTG[A/C]AAGGCTACGCCCTGC
TP8401	TGCAGAC[C/T]GACTGCACTCGGAGGACGGCGCGGTCACAGAGAGGCGGCTAACTGCGGCATGCAGG
TP8414	TGCAGACCGAGCGAGCGGCTGGCTCTCACTGCCCACGGCCCCAAGCTAACAAG[A/G]AGTCCGTGGT
TP8438	TGCAGACCGCACAGCAG[G/T]AAGAGGCGTGGGCGGGGGTCCGCGGGCGAAGGAGGGTCTCACTTTT
TP8482	TGCAGACCGCGGAGGCCGAGCTGGACGCGGCCAAGAAAGAGCTGGAGAGCA[A/T]CAAGGTCGGGAG
TP8483	TGCAGACCGCGGAGGCCGAGCTGGACGCGGCCAAGAA[A/G]GAGCTGGAGAGCATCAAGGCCGAAAA
TP8494	TGCAGACCGCTGACGATGGTGG[C/T]CAACGAGCGCACGATCTCTGGGTCCTCGCTGTAGCTTTCGT
TP8508	TGCAGACCGTCAGTCGCGTTC[C/T]GTCAGACCTCGCTCCGATCAGTCACATGTGTTCTGCGCACAT
TP8526	TGCAGACCGTCTCGCTCATCGTAGGCTACAACATCCATCTAGTTGCTTGTTTTGTGATCAGGC[C/T]
TP8536	TGCAGACCGTGCTTGCTCCCCTTCCCCAA[A/C]TGACCAGCCAAAGATGGCAGCAATAGCAGAGACG
TP8557	TGCAGACCTACAGTTGCTAGC[A/T]AGTTGGGGTGATGGATTTGAAGCCATGTTCAAATGGTTAGTG
TP8569	TGCAGACCTACTGCTTCGGGAAGATGAGCGAG[G/C]TGGCGGACCGCGCCTGCCTCATCGACGGGCA
TP8572	TGCAGACCTACTTGCTCTGAACTTCGTAGAAGCAGTGAATCACTAGAATATCA[C/G]GAGAACTCTA
TP8576	TGCAGACCTAGATGGAGTCGAGGAGCTCCGC[G/T]CCATCGCGCAGCAGATGGTCCACGACGGCTAC
TP8594	TGCAGACCTATTTGACCAATTGAAAACCCTTGTAGGGTTAGAAAAGACCCATTCCACTC[C/T]GTCT
TP8609	TGCAGACCTC[A/G]TCAAGTTCGGTGCTGTCTACTACGCGCTCGTCGCGCCGCAGCCGCCTCCCTAC
TP8614	TGCAGACCTCCAGAGAGGCAGAGCCAAATCCGATCGGAAT[A/G]GCAGCAACAGCGAGCGACGCGAG
TP8618	TGCAGACCTCC[C/T]CTCTCCCCCTCCCTCTCCCTTCTTCCTTAGCTTCGGCTGCCAGTGAGTGTCC
TP8635	TGCAGACCTCGATCTCGTCGTTGTCCGACGACTCGTCGTCCATGTCGGATCCCGAGGC[A/G]GCGCT
TP8641	TGCAGACCTCGCCTCAGCCTCAAAGGCTGGGCCGCCGCGCGAGCCACCAGGGGTGGCAA[C/T]CGCT
TP8658	TGCAGACCTCTAAACACACTA[A/C]AACAGACCTCCCATCGCACAAAATCGCATGAAACTATCTTCT
TP8663	TGCAGACCTCTGCTAAAGGCCTGGTTGAACA[A/G]CATCCTGGTCTGGAATTCGGACACGAACGGGA
TP8719	TGCAGACCTGCTGGCTAACAAGTCCGATCCCACGCCCGCCGTCCGTTTTCGTTTC[A/C]TGAGAAAC
TP8724	TGCAGACCTGGAAGAAGACGGCCTCGCCGTGGCCGCAGGCGGCGCAGCGGACGGACTTG[G/T]TGCG
TP8740	TGCAGACCTGGTTCCGATCCGCAGCAATCAGGAGGC[A/G]AGTGTCCTGCGCGCCCTAGCTAAGCTC

Table A2 (cont.)

TP8747	TGCAGACCTGTCGACAGAGAGACCAGCTTCGGACAGCAGCTCATCTCCAGAGATTC[A/T]AGCGCTA
TP8765	TGCAGACCTTC[C/T]CACCCCATTACCTGATTGCCGAGGGCCGAGGCGGCAGAGAGAGGAGCGGCGC
TP8767	TGCAGACCTTCCTTAGGAGGACTCAACTCATGGTTAAGCCTTTTACATCT[C/T]GGCTTAGTTTTGT
TP8778	TGCAGACCTTCTCCTTGGCGCAGCACGCCCACTGTCCTACGTACTACTGATG[C/G]TATCAGTACTA
TP8780	TGCAGACCTTCTGCTCCACCTACCCGTGCCAAAGCACCTGGTTCGGACACATACT[A/G]CCGTCGTC
TP8798	TGCAGACCTTGCTTGCTCCCCATCCCCAACTGACCAGC[C/G]AAAGATGGCAGCAATAGCAGAGACG
TP8837	TGCAGACGAACAC[C/T]GCTCCTCACTGTCTTATTACAGTTATTACAGCAGCCAGCATCTGCATGGC
TP8850	TGCAGACGAACGTGTACGTCCGCGGCAGCGGCGACGGCCGCATCGTGGGGCG[C/G]GAGATGCGGTT
TP8876	TGCAGACGAAGTAGGAGTATCCAAGCAGCAA[C/G]GGACGTCCTCCGACGCCCTCCATTAAAACCGA
TP8877	TGCAGACGAAGTGAGTAGACC[A/T]CTGTTTCCCATGTCGTGACTCTGATCAGATACATTTCTATCG
TP8904	TGCAG[A/C]CGACAGGATGCGCCGCCGTAGCCGACAGATGCGTGGAGGCAGCAAGATTGGAAACCCC
TP8914	TGCAGACGACCCA[C/T]GTCGGCGCCGTGCCTTCCCCGTCTCACTCGCGTGGGAGCAGGGGCTCCAC
TP8930	TGCAGACGACGACGG[C/T]GTCGAATGCCTCCTCCACCACCTCGCCGTCCTCCCCGCGCCACGCCAC
TP8947	TGCAGACGACGGAGGAGACG[A/C]GCACGCGCTCAGCCGCCGAATCCGTAGAGGGTGCGGCCCTGGC
TP8948	TGCAGACGACGGCAAGCGGCGATGAGATCGTCGCTGCGGTCGACGACTGGGACG[A/G]CGGGGGCGG
TP8952	TGCAGACGACGGCGGCAAAAGCACCACCACCGCCAGC[A/G]CCAGGAGCAGCAGCAGGACCTGGCAG
TP8963	TGCAGACGACGTCGGGCCCGTGACGTGCGCCGCGACGCAGAGCGCGCTGAGCACGTGGTGGG[C/G]G
TP8976	TGCAGACGACTCCGCCGCGATGTTACTATTCAAGAA[A/G]AAGCAGGAGCAGGGGCGTCGCCGAGGG
TP8982	TGCAGACGACTG[A/G]CCACGGAGGCGACCGACGTCCGACAAGACGGACCTGGACCTGCCGCGCGCG
TP8985	TGCAGACGACTGGAGGTCGAGGTCGAGCACGTACGCACG[C/T]CGCTCGGGGTCTGAACGGGAGCGC
TP8989	TGCAGACGACTTGAATGCTCAATTTGGGAAACCGAAACGG[A/G]ACAGCAAATGGAAGGGGGTTGCC
TP8992	TGCAGACGAGAAGTTCAGTTCAG[C/T]GACGATATATAGATTGAGCAGCTAAGGTAACTGACGCTAG
TP8998	TGCAGACGAGACCAGTGACTCACCCTAGCGGCGGCGCCTACGTTGGGCAGCCT[A/G]GCGGCGAGGT
TP9000	TGCAG[A/G]CGAGACGCCCATCTTCGTCGCCACCGACACCGATTCCAGATTACTGAACGGGGCCGAG
TP9005	TGCAGACGAGAGAGACAGGAGCGTCATCGTGATCAAAATGTTCTGTGCAACCTT[G/T]CATCTGCTG
TP9012	TGCAGA[C/T]GAGATTCCACAGATCAAACGCAACTTCGCGGCAACACACACATACCCCCGCGCGCGC
TP9015	TGCAGACGAGCACATGGAGGGAGGAGGAGGGGAAGGGAG[A/G]GGAGGAGGAGGAGGGAGCGTGCAG
TP9018	TGCAGACGAGCACC[G/T]TGTCGCCGTCCTTGTAATCCTCCGCTGGCGTCGTCACCTTGACAGGCCC

Table A2 (cont.)

TP9023	TGCAGACGAGCCAACGCAACTGGCAGAGAGGTGACAGATCAGATACACACA[C/G]ACACAGAGACAT
TP9026	TGCAGACGAGCCTGAGCAGCCCCCCACCACCCTGGGGGCGCAACCCTCCGCCGTGCTTGG[C/T]GCC
TP9034	TGCAGACGAGCGCGGCGCGGACGAGCCCCGCGGGGTTCTCTGGCGGGAAGCGGAGGAGCA[C/T]CTC
TP9042	TGCAGACGAGCTGAGTCCACGGTCGTCGTCGCCGCCGCGGAGATGGGGATGGAG[A/G]TGGACAACG
TP9048	TGCAGACGAGGAGTCTGATGAGAGCAGCGGCAAATCCGTCCAGGG[A/T]TAGGGTGGGCGGTGCCTG
TP9068	TGCAGACGAGTGAGTGATCGATTCGGTCGTGTGTGATGACTGCTGAGTT[C/G]AGAGCACGAGCAGT
TP9078	TGCAGACGATACTCGAGAAAGCCCAGAGCAACCT[A/G]TCGTACGACGCAACTGGAGGCGCGAACCT
TP9079	TGCAGACGATACTCGAGAAAGCCCAGAGCAACCTTTCGTACGACGCAGCTGGA[A/G]GCGCGAACCT
TP9084	TGCAGACGATCATGATGCATTCATGCGTAGTACTGGTAGCCGCCCC[A/G]CCCCGCCCCTTTTCTGG
TP9087	TGCAGACGATCCGTAGCGACGGGGAGGTGAATCGCGAGAGGCGATTAGAGT[A/G]GACGCTCGACAT
TP9092	TGCAGACGATCGAGTCACATGGAAAGTTTTCAAGACTGGAAG[C/G]AGAAAACAAATGGGCGCCCTG
TP9093	TGCAGACGATCGATATATGACTGATGAGCATGACGAGC[A/C]ACGCACGCATGCATTTGATTAGTAA
TP9113	TGCAGACGATGATGGCGATGATGCAGCGGGTGACGACCACGCCGTGGCTGATCCTGTTCCTG[A/T]C
TP9115	TGCAGACGATGCCATGAAATGGATGGAAGCATGTTTAAGCCTGTCGCAGTCATGC[C/T]GATCGGCT
TP9117	TGCAGA[C/T]GATGCTCTTATCGCTTCCCACACGCGATGCTTGCAGCTGCCCATGAAGGCACCACGT
TP9129	TGCAGACGATTGGGAAGAAGATACTGTACCA[A/G]CTTGGAGCAGACGTTGAAGTAGCAGAGGATGG
TP9132	TGCAGACGATTTGACCGACCCTGCTCCTGCCACAACATTTGC[A/G]CATTTGGACGCTACTACCGTA
TP9166	TGCAGACGC[A/C]GAGCCCATCGAGGAGAAGATGCTGGAGAGGCGGCAGGGAGGCCACGGCCCACGG
TP9171	TGCAGACGCAGAGCCTGATCTACCCGCTGCTGCTGTCGTCCGTGG[C/T]GATGGCGGCGATCCACGT
TP9175	TGCAGACGCAGCCACACCCGCGGCCGCAGCCTTACCACTCGACGAAGCCGCAGCGGGGCG[A/C]CGC
TP9180	TGCAGACGCAGCGGGGCCCTCGCCG[C/T]CCGCTTCCGCCACCGCCATAGAACTCTCGTCGTCTACG
TP9183	TGCAGACGCAGCTGCTCATGGCGAACGC[G/T]TCGTCGGCGGTGCAGCACCAGGGGCTGTCGCTTAG
TP9192	TGCAGACGCAGTCCGTCGTCGCGCCGCTCGTCGTGTGCATCGCGGCGC[C/T]GTTCGCGCTCCACGT
TP9202	TGCAGA[C/T]GCATCACCACGAGTAGGCTCCAGATCTAGCCTTCCTCAGGCTCATCGAGGTGGGCCG
TP9205	TGCAGACGCATCCAAGCTGAATCTCGATCGGCTGAAGCA[C/T]CAGAGGAACATCAATCACACAAAC
TP9210	TGCAGACGCATTACGCACCGCAAACGCAG[A/T]GTATGACGCCCGAAACAGGATAAAAATCGCACAT
TP9217	TGCAGAC[G/T]CCACCTGCCGCGCCGATGGCACGCTGAACCGTGGTGTGCTCTGGCTGCTTGACCCG
TP9223	TGCAGACGCCAGCTGTGGATCTAGCCACAGGCGG[A/C]GGATCCGTAGTCGCTGGCCGTGCATCCAC

Table A2 (cont.)

TP9238	TGCAGACGCCCACGTACGTGGTGCGCGCCCGCCTCGGCACGCCGCCGCAGTTGCTCCTAG[C/T]CGT
TP9248	TGCAGACGCCCGTCGAGCTGGCCACGGCCGCGCACCGCGAGCTCTGCTACCGCCAGCTG[C/T]GCGC
TP9279	TGCAGACGCCGAAGGCGATGTTCGGCGCGACCGCGAGGCAGGACGCGCACC[C/T]GCTGCCGTTGAC
TP9282	TGCAGACGCCGAGAGACGG[A/T]CGCGGCTGCCGCTGGCGTCTGGCGAGAGCGGTAGGAAAGAGAAA
TP9302	TGCAGACGCCGTAGGCGCCGCAGGCGC[G/T]GTAGCCGTCGCACTCGTCGAGCGGGTAGGACCAGAA
TP9341	TGCAGACGC[G/T]AGTTGATTATAAGATTTACTATTAACAATTGACAAATGACAACGATTTGAATAC
TP9342	TGCAGACGCGCAAGGCGACGG[A/G]TTCATCGCCATCGCGCTGGGGTTCCGCAACACGGCCGAAAAA
TP9360	TGCAGACGCGCGCTCCGCGTCCGTAACCGTAAGCGTTTTTTAAGGATTCA[A/T]TCAGTTCCAGCTA
TP9382	TGCAGACGCGGGTCTGCGGCGCCGAGGCTCTTCCC[C/T]TTGGCCGCCGCGGCCGCCTCGTCCACCG
TP9386	TGCAGACGCGGTCCGTGCC[A/G]CCGCTCCCCGTGCCCATGTCCAAGCCCGTGTTCATGTGGCCTGT
TP9387	TGCAGA[C/G]GCGGTGGGGGCAGCAGTACTTGGCGAGTGGGGGCAGCGCGTTGTCATCTCATATCAG
TP9411	TGCAGACGCGTTTGCCATTTGAAGTGCGGCCCT[A/G]TTCGCTCGAGCTTATCAACTATAATCAACT
TP9423	TGCAGACGCTCAAGAAGAAGAACCAGAAGCCGCTCTTCGAGGCGCTG[A/C]TCAAGGTCAAAGAAGG
TP9425	TGCAGACGCTCACGGTCAGCGACGCCTGGGGGCTGGACGACCTCA[C/T]CGTCCACTCTGATTCCCT
TP9426	TGCAGACGCTCACGGTCAGCGACGCTTGGGGGCTGGACGACCT[A/C]ACCGTCCGCTCTGACTCCCT
TP9442	TGCAGACGCTCTACAG[A/C]TACGGCGCGCGCAAGGTGGTCATGATCGGCGTGGGGCAGGTCGGGTG
TP9457	TGCAGACGCTGCGGTGGGCGGACAAGGACAAGGCCGA[G/T]GCGGCCATCGTGGAGGTGCTCGTCGC
TP9459	TGCAGACGCTGCTCCCCAGCGCGCGCCGCCGTGTCGGCAG[A/C]GAGGTACGTACGCGTGCACATTC
TP9465	TGCAGACGCTGGAGGACGCCGTCGGGAAGCACAACGTCACCATCTTCGCGCCGCG[A/G]AACGAGGC
TP9495	TGCAGACGCTTTTATATCT[A/G]CCCCAGCGCCGCGGTCAAAGATGGCAAATCGCTTCGCTTGCACT
TP9499	TGCAGACGGAAA[G/T]GCTCAAGTCGAACTCGAGTCGGACGGCTGGCTGTTTCTGTCATCTAATCAA
TP9501	TGCAGACGGAACAAAACTTACATGAGTGAAGCTCAAAGGAGTGCCCTGAATGCTCTCCT[A/C]TTCC
TP9509	TGCAGACGGACATCCACAC[A/C]GCACGCCATGCTCTCCAGGAGGCGCTGTCCTTCGACACTGCGCC
TP9512	TGCAGACGGACATTTCACCAACCCAACAGTCCATTCACTTCTCGGTTCACGCCACAAAGTCA[C/G]A
TP9516	TGCAGACGGACGGCGACCCCGAGAACTGCTTCGCCGTCCTCGTGCCATGCTACCGCCACGG[C/T]CG
TP9525	TGCAGACGGAGACGATCGACGGGTGGAGGCGG[A/C]AATGGAATGGAATGGATCGAAGAAAGTCGCA
TP9535	TGCAGACGGAGCTCCAGCCTCTGCTCCCGCTCCAGCAGCGACAGCCACAGCTCCCTCAGCCG[A/C]T
TP9539	TGCAGACGGAGGCCACCACGCTGTCCGCGCAGCTCACTCTGCTACAGGTAT[C/G]ATTATGAACGCG

Table A2 (cont.)

TP9540	TGCAGACGGAGGCGCAGAGCTTCGACATCCCCAGCGCCGACATGGTCTACAGCCTCGC[C/T]TACCT
TP9543	TGCAG[A/G]CGGAGTCCGACTCCGATAGCGGGCTGAATTTGATGCCCAATTCCGATGCTTTGAAATT
TP9545	TGCAGACGGAGT[C/T]GCATCCATGGCTGCGACGCTCACCAGACCAGGGAGAGAGGTCGGGAGCAGA
TP9557	TGCAGACGGATGGTGCATCATCCAGCGTGGCGCCGCCATCGAC[A/G]AAGCAGAGGAGGCCCTGCGA
TP9561	TGCAG[A/G]CGGATTGCGTTCACGGACAGCGCCTTCTGCTGCTGTTCCTTGTGTTGCTGGTGCTGTT
TP9585	TGCAGA[C/T]GGCATAAAGAAAACGATGCAGCTATTGGCGTCGTCAGTGCTACTGGCTCTGCAATTT
TP9591	TGCAGACGGCATGGCATGCATTGGCTGGCGCCG[C/T]ATTGATGCTGAGCACGCGAGGCGAGAGGCG
TP9594	TGCAGACGGCCAGGGCGCTGCGC[A/G]CGCTCCACGACGCCGACCCGCCCGTCATCCACCGCGACGT
TP9605	TGCAGACGGCCCGCACGCCGCCGCTCTGGCCGCAACCCTGCTTAGC[A/T]GGATTAGCAGGCGTCCA
TP9636	TGCAGACGGCGATCGACCGCGAGGCGGT[A/G]TTCGCGTACGCGGACGACCCGTGCAGCCCCAACTA
TP9640	TGCAGACGGCGCGCGCTCGAGTACCTGCACGAC[A/C]GCTGCGAGCCGCAGGTGGTGCACGGCGA
TP9646	TGCAGACGGCGGC[A/G]GCAGGTATGTATGTGATGAACACGAACGAACTGCTGCCTGAAATGAAACC
TP9653	TGCAGACG[G/T]CGGCTCGGCAACGTGCAACAACAGAGCGCGGTCGGCTGACCGAGCAAGGCCTGCC
TP9701	TGCAGACGGGCGCTTCATGATGCGTCTGAAGCTGCCCAACGGCGTGACGACGAGCGAGCAGAC[G/T]
TP9705	TGCAGACGGGCGGGGG[A/G]CCGAACGTCTCCGACGCCTACACCTTCAACGGCCTGCCAGGCCCAAC
TP9723	TGCAGACGGGGCTGTTCGA[A/G]CGCATCCACGTCAGGTTCTACGGCGATGACAAGTGCTCCTACAA
TP9758	TGCAGA[C/T]GGTGAGGACGGCGAGGACGAGGACGAGCAGCCCCACGGCGGTTAGGAGGCGCTCCTT
TP9765	TGCAGACGGTGCGGGTGAGCATCCCCCTGGCGCCCCGC[A/G]TGTCGTCGTCCATCATGTCCGTGTG
TP9788	TGCAGACGGTTAGCTGAGCACAGCCTTCGCATGCACCGTACCTAACCACCACGTTGGGTCGAC[C/G]
TP9802	TGCAGACGTAACAGCGCGCAGACGTGAATCGTGATCGACCCCCCAGCAACTGGGGCAT[C/G]CTCAA
TP9807	TGCAGACGTACAGCAATTCCATCCTGGATGCGCTCCCATGTGCTCTTGCCT[A/G]CTTCTACTGGGT
TP9819	TGCAG[A/G]CGTACTGCGGGGGGCAGAGCGTGACCGAACGTTAGCTGACACGAATGTATGTCTGGAG
TP9824	TGCAGACGTAGCTGTAG[C/G]TCGGAGGAACCCGAACGCCGAAGTAGCAGCAGCAGCAGCAGGCTTT
TP9856	TGCAGACGTCAGATGACGGGCTGACGGCCAGTCGGCCACTCACG[A/C]GTCACAGCGGATACGGGTG
TP9865	TGCAGACGTCCACGCGGCGACACA[A/G]CACAAACTAATAATCCATCATCCATTCATCCGACGACGA
TP9891	TGCAGACGT[C/G]GATGGATGGTCAGATTCCGTGCCCCCAGTCAAACACGATTGCACGATGCTTCGC
TP9897	TGCAGACGTCGTACGTACTAGGCAGTATTTTCTTCGACGCCTA[G/T]CGAACAAGGCACACAGCAAT
TP9902	TGCAGACGTCGTGGA[C/T]GAGGTGGCGGTCGTCGAGGTCCTCGCCCTCGAGCACGAGCCGCTGCTC

Table A2 (cont.)

TP9909	TGCAGACGTCTCTCTCCCTGGGTGGCGCTGCCTCGTCGGAGCAGGTCGGCTCACCTCCAGAC[A/C]C
TP9911	TGCAGACGT[C/G]TGCAAGAACGTGAATGCGGCCGAGGAGATCCTACGGAGCAGCAACCAGAACATG
TP9927	TGCAGACGTGATGCGTGATCTATGGCTGCAATGGCATCAGACTACACAC[A/G]TCGATGCAAGTGTT
TP9929	TGCAGACGTGCAAGTGGAGACGATATTTTTTTGCTACTCATCTCTCAT[C/G]CTAGGAGGGTCTGTG
TP9949	TGCAGACGTGCTGCTGC[A/G]CCGAGGGGCATGGAGAGGATCATCCACTCCATCATCAGGAAGAGAC
TP9952	TGCAGACGTGCTGGACGAGGCGACGAAGATGCGCCTGCTGCTGCCGCTGACGGAGGA[C/T]GGCGGC
TP9957	TGCAGACGTGGAAGCGGCAGGCCATCTTCTCCGACCCCTACAA[C/T]CTCACCGCCGACTGGGTCGG
TP9988	TGCAGACGTGTCACCTCTGAATGTTCCATGCAGTATGCACACTCGACGGACACAAAACAAAAG[G/T]
TP9998	TGCAGACGTTCAAGCTGGCTCCATTGT[C/G]TCTTTGTCCAACTCATACAAGAACATACAGCAAGAT
TP10020	TGCAGACGTTGCTCTTGAAATCAGCAATAGTTGATTCACGGTCAGTCTGATCTTTGCC[A/G]CCATG
TP10024	TGCAGACGTTGTGTATGGTGTCACGGCGTTGCTTGAATCGCTGAA[C/T]GCCGAGTCCAATGTCACA
TP10025	TGCAGACGTTGTGTATGGTGTCACGG[C/T]GTTGCTTGAATCGCTGAATGCCGAGTCCAAGGGCTCA
TP10035	TGCAGACTAAAAGTTGAAGCAA[C/T]CACTCGCCTGATCACCGACGAAATCCAGAAGCCTCCCAGAT
TP10044	TGCAGACTAACGTGGA[C/T]TATCTGTAATTCCAGAGTTGGTGTCAGCATACTCAAGTTCTTCATCG
TP10070	TGCAGACTACACCAGGTTTGATGCTAGGGCGTGACATTGACATTCTGAAATCAATAA[A/G]GGTTCT
TP10095	TGCAGACTACGACTAGCGCACCCAGCAGGCCAGCACCCCTCCAAGCTGTTGTT[A/G]GCATTGCACA
TP10105	TGCAGACTACGGTCCAGCAACCCAGCCCACCGTCCAGCAATGAATGAAAACGGAAAGCCCAGC[C/T]
TP10170	TGCAGACTATGAAGGAGATTATGCAGAAGAGGATTCACAGATGATG[A/C]GGCAGAAGCGCTCACTT
TP10187	TGCAGACTCAACCAAGCCATGTCCACGGACCACGGTGCATGCCCGCCCAGCTGCC[A/C]TCTGTAGC
TP10190	TGCAGACTCAAGCAGGTAAACAACATTCCTATGGAACTCATGATGGTCA[A/G]CTGAGAATCTTTGG
TP10221	TGCAGACTCAGTCTCTTCCCCTTGGCTCCTACCACG[C/T]GGAGTGGACAACCTTGCATGCGAGTTG
TP10235	TGCAGACTCATGTCCAC[G/T]TCCACTTGTCCAGTGTGCGCGCCTGGACGTTTAGACCCGAAACGGC
TP10249	TGCAG[A/T]CTCCACAAAAATCATGCCGAGGCGACAAGCGGGGCCCAGCGGAACAACCCAACAGACT
TP10259	TGCAGACTCCAGAA[C/T]GACGGAGGAGTTGTAAGTCGACGTGTGCTGTGTGCATACTCCAGAAAGA
TP10261	TGCAGACTCCAGACGGAGATAGTAGTGGAAGAACTCAA[A/T]TGGAAATTTGCCATTTCTTGCGTGC
TP10262	TGCAGACTCCAG[A/G]CTCATTAACATCCCACAGTTACACAAATGACGCACTTACATCTCCATCACG
TP10267	TGCAGACTCCAGCGCACCCCATGTCGCCATCCTCCACCTAGATTTCA[C/G]CTGTCGAGCACCACGC
TP10282	TGCAG[A/G]CTCCCCTTCCCCTTCTCTGCCCATATATACCACTCTCTTCTCAGCCTGCTCGGCACGC

Table A2 (cont.)

TP10286	TGCAGACTCCCTGTTCTTGATCATCCTCCTCTGCCGCCGCTCCACGACCTTCTCCACACC[A/C]GCA
TP10294	TGCAGACTCCGTGCCAGGATCAGCCTCGTCCGCCGTGTAAAGCG[A/C]TGGCGGCTTAGTCAGCACG
TP10296	TGCAGACTCCTCA[A/G]TTGTATTCCTCTCCAGCAGCAGGCGAGATTACCTCTCTCGCTAGTCGCTA
TP10326	TGCAGACTCGCCGTGGGC[C/T]GCGTGGCGCGTCGTGGGCCGTGCCTGCACATGCAGCACTCGCACT
TP10339	TGCAG[A/G]CTCGGTGCTTGGAACGACATCGTCTCAGCATCCTACGCATATATATAGTCCATGGATA
TP10347	TGCAGACTCGTCGCGGCATGGCCATTAACCTGCTTG[A/T]CACTGGAGACGTGATGATCCGCCTGAT
TP10354	TGCAGACTCGTGGCAGCAGGTGGGGCTGCTGATGGTGATCGG[C/T]TTCAACTGCGCCTACGTGCTC
TP10358	TGCAGACTCGTTACAAGGAAAGGTATAGAAGAAGAAAAAAAGA[A/T]GCTCTTCCCCTTCCCCTTCC
TP10392	TGCAGACTCTGAT[A/G]CTCTGTCCCCGTGTGCTAGCGTTTTTGACTTCTGACCTCGCGGATTCCTG
TP10421	TGCAGACTCTTGTCAATTTTCCTTTTTCAAGTAGGATACCCTGCTTTTATAGAAAG[C/T]GAATAAG
TP10437	TGCAGACTGAAGCT[C/T]AGCATTTCAGCAATGGTGAAGTCGGAGACAAACCAACCAGTCTTGTGCA
TP10442	TGCAGACTGAATTGGACCTTCTTTTGCACTGGATACC[A/T]CGACTGATGATTGATGAAAGCAAAAG
TP10470	TGCAGACTG[A/G]GGGAAGAACCTCTCGACCAGATCGAGAGACGCGCGACAGCGGCTCGCTACAGTG
TP10488	TGCAGACTGATGGAACTCGGAGAGATGCTTGCTGCTTGGATGC[C/T]TCCCTCTTCACCAACTTAAG
TP10496	TGCAGACTGCAAAGGCGATATGGTCAGACGGAGGCGGGGGG[A/C]GCAGTAATGGTGGTGGAAGAAA
TP10537	TGCAGACTGCACTACTAGTCTGAGTAGTAGTCTAGTACAACTC[G/T]CCAAGCCCATCGGGGGTGGT
TP10541	TGCAGACTGCACTGAGATACACATACTTCACATATTCTCTTC[A/G]GACAATCTCTCGCCCAGCTCA
TP10567	TGCAGACTGCCGATGCTGCACCGTTGTGGCGTTGCAGTTGTAGCCAGACATGCA[C/T]GCGTCACAC
TP10570	TGCAGACTGCCGCTGTCGCCGTG[C/T]GCACGCCGTGCGCAGGCGCCCATCAGCCAGGACACTGTTG
TP10592	TGCAGACTGCGGTGCAGGCACACGCCTGA[C/T]GCCTCAGTAGTACAGACGTGTTGGCGCCGTATTG
TP10593	TGCAGACTGCGGTGTCACCA[A/T]TGATCACTATTTTAGTATCTAATTCAGCGAGGAGAGGAAATGC
TP10594	TGCAGACTGCGGTTGAGCAGAAGTTGAATGGAAATGAGGCCGTGCTCTG[C/T]CATTGCTCATTTGC
TP10597	TGCAGACTGCGTGCGTCTCGGCTAGCAGCCGTCCTAT[G/T]GGCGACCGCAAGTCATCACCAACTTG
TP10617	TGCAGACTGCTGGCGAGGTAAGCGCGCACGCTTTCCTTCCTTGTTCCTCCAACCCAC[A/C]CGCGCG
TP10629	TGCAGACTGGAAGGCCCTCTGTTTGCGAGTGCAAGAGAGAGAGGGGAGGAGGGGGAGGGA[A/G]GAG
TP10643	TGCAGACTGGCCCCCAAGGTGGTGACCATGGTGGAGCAGGACCTGAGCCACTCGGG[C/G]TCCTTCC
TP10652	TGCAGACTGGGC[A/G]GAGGCAATCATGTCGGCCAAGCACCACGCATGCATGCGCAGCTGTTGGACG
TP10657	TGCAGACTGGGGGAAGAACCTCTGGACCAGATGGAGAGACGCGCGACAGC[G/T]GCTCGATACAGTG

Table A2 (cont.)

TP10668	TGCAGACTGGTCGACCGTCGTCAGTCCT[A/G]CCACGTACGTAACGTACTCCTCGACCTCGTCCTCG
TP10679	TGCAGACTGTAGCAGTAGTTCTGTGCTACTCTTCCCCAACTGCGCAAG[C/T]ACAACGTCCGACGTT
TP10717	TGCAGACTGTTAGAACTTGGTAGTTGTACACAAGAAGAAGAGCAAGGAACTGTAG[A/G]CCTCTCTC
TP10721	TGCAGACTGTTCCGTCACTGGCGCACTTGCCTCACGTGCGCCACACCA[C/T]CATGTGCCTCACTCG
TP10733	TGCAGACTGTTTCACCTTGCACTGAGCCCAGTCATGATGTCTACCCTGAAGAATGGA[A/G]AAATTG
TP10760	TGCAGACTTATACATGGCTTGGGGAGCTGGTCCCATCGACAAGAAAGCAGATCATATGGGC[C/G]CA
TP10765	TGCAGACTTATGCTGCCC[A/G]TTATTTTGTTTTTAGTTCGGGACGTATGGGATGAGTTGATCGGCG
TP10791	TGCAGACTTCCAGCATGTATAGTGCAGTAGTTACA[G/T]AGATTTCCGATGCTGCATGCCGAGGGAC
TP10806	TGCAGACTTCCTGTAACCAGGCAACGTGACATATGAGTTACTGTGAGAT[C/T]AGGTCATCAAAAAC
TP10815	TGCAGACTTCGCGTCGTCGTCCCCTGGGTGGCTGGGT[C/G]TGCCACGGCCATTGCACCCTTGGTCC
TP10838	TGCAGACTTCTTGAACACCTCTGGCGCAGATAAGTTCACGGCAGATTCGAAC[A/G]CCGATGCTGAA
TP10840	TGCAGACTTCTTGGTGCTACTGATGAAGCAGAGGCATC[G/T]AAACAGAGGAGGTAGAACAGAGGGT
TP10850	TGCAGACTTGAAGTCGTGGCAAGGAAGCGTGACGAGCTCGCTGGCCGACAGCCCCCC[A/G]CCGTGG
TP10858	TGCAGACTTGAGCTCCCGCGCAGGCCCAGCCGCCGACGAGA[G/T]CGTCGCGTGCCGAAAAAAAAAA
TP10873	TGCAGACTTGCAGCGTCGTGAAGGTGAATGGAGCCCAGCAGGCCCAAACCCAA[C/T]CTGCGCGCGA
TP10889	TGCAGACTTGCTCGCTTTTGGCTTCC[A/T]TCGCGTTGCTATCCGCTTCTACCCGTCCCTCCCTCAA
TP10903	TGCAGACTTGTAGTCGCTAGTTTCTCACACTTG[A/C]CACTCCCCAAGCTCCCACATACTCCGATCC
TP10929	TGCAGACTTTATTC[A/T]AGTCTCACGTGTGTGGGTGTAGTCACGTACAGACATCACAATCAGAAAA
TP10933	TGCAGACTTTCAGTGCAGAGATAGTGCGCGTGTTTTTTGTCCTCCATGCACGAGTACG[A/G]CGTCG
TP10972	TGCAG[A/T]CTTTTTCATGAGCCTGGACTAATTTTTCAGTCGGCTTAGGCTTTACGTTACATGGTAA
TP10980	TGCAGAGAAAAAA[A/G]CTGGCAAAATATCTGCCCCAGCTCGCCTCCGTCACACTGGGGCCTTGCTG
TP11012	TGCAGAGAAACACAAGAACCAA[A/G]CAAGAATCAGACACCATTGAATCAGCAGGAAACGTATATAT
TP11016	TGCAGAGAAACAGAGGATCAAAGCGAGGCAAACCTT[A/G]CGAGAGACGACAAGAATAAGCAGAGAC
TP11025	TGCAGAGAAACCACCAGCCAACTCTGTCGACGGCTCATGCTGGTGCCCCATGTACACGA[C/T]GTAC
TP11051	TGCAGAGAAAGCAAAC[A/G]ATGACGGCCTCCAGGAGAAGCTAACCATGTCTGTCGCAGTACCATTG
TP11094	TGCAGAGAACAACGAAGTGTTCAGTGTTCTAATCCGTG[C/T]TGCTGTCCGTAGGAGTGCTGAAATC
TP11134	TGCAGAGAACGA[C/T]GGAGTTCCCAGAGACGGAAGGCATCCCCTTGGCGGAGACCGCCAGGCTCTG
TP11138	TGCAGAGAACGCACCATC[A/G]ACATTGCACTTGTGCCATCCCTCCATCGTCTTCTTCCAACGATGG

Table A2 (cont.)

TP11162	TGCAGAGAAGAACAGGGCTGTACAGTATACATTTCTG[A/C]TTTCTCGATTTGCAAACATCCAATTA
TP11196	TGCAGAGAAGAGAGGAGGGCGTA[A/C]AAATCAGGCAAGGCAGCGAAGATTGGATCGGATCAATGGG
TP11199	TGCAGAGAAGAGC[A/T]GAGCGTTCGGCCCCCACGCCACGACGGATCTCATCTCGTCTCCGTCTCCG
TP11200	TGCAGAGAAGAGCTGAAACCTC[A/G]GCAAGTGATAGTGTAGGTAGCAGAAGAGGCGAGGAGAAGGC
TP11249	TGCAGAGAAGGAGTTTGATTATCTTGATGAAAGAGAGGATGAGGAGGATGA[A/G]CGGAGGGAGCGT
TP11250	TGCAGAGAAGGCAACAT[A/T]CTCTTAGAAATGACAAGCAATTCAGTTAGACTGCCATTGAAAGCTA
TP11254	TGCAGAGAAGGCCTATGACATCCC[A/G]AGAGTAGATGATAAGGTGAACAGGGCTGTTGCAGCAGCT
TP11258	TGCAGAGAAGGCTTGTCTAACGAAATTACCTAGCGATTAAAACCGCAACACTGCATGCTCTG[C/T]A
TP11281	TGCAGAGA[A/T]GTCTGTTGCACAGAAGAGGAGCTGTTGGTGCTTTCGTGTACTCCTATTTTTGTAC
TP11284	TGCAGA[G/T]AAGTGAGCATGGTTGCGCTCTCTGTAGTCTCTAGTCTGTATAAATCATGGGAGAGAG
TP11306	TGCAGAGAATATAATCATCACCTGGGCGCTCGCTCAACTC[A/G]ACGAAAGGCGCAGACTTTCCGAC
TP11308	TGCAGAGAATATATCCCGATCTGGATCCTCTGGGCCTAATACTAACTCCAACAGAGCTATC[C/T]AA
TP11324	TGCAGAGAATCTGGATTGCCCCCTGACCCCC[C/T]CTCTGCAACTCTGCCTGGAGCCCTGGACCTGG
TP11334	TGCAGAGAATGATGGAGTTCC[C/G]AGCGATGGAAGGCAACCCCTTGGAGGACACCGCGAAGCTTCG
TP11347	TGCAGAGAATTAAGCGGAGGGAGGA[A/G]AGCGTCGTCAGATTCTCGATCAGCATCGTCACAAGACA
TP11353	TGCAGAGAATTCAGAATTGA[A/C]AGCGCCGCCGCCCGCCGTGTAGTCGGCATCCGCATCGCTATCC
TP11365	TGCAGAGA[A/G]TTGGCGGAGGCAGCGGCAAGAGGACAAGAAAACGGACTCATGACGTGCAACTGTG
TP11373	TGCAGAGACAAACAGAAACA[G/T]CAATGCACCTTTCAGCATCCCAAGTCGCGCACCTTGTGCGTGT
TP11385	TGCAGAGACAAGACAGCGCAGCCAGATCAGGACTCGAT[A/T]CACAGATCCATCAGCACTCAAGTAG
TP11388	TGCAGAGACAAGCACGTCAACAAG[A/C]AAACTGGTCCCTTTGGGTAAGCAGGATGAAGCACAATCA
TP11393	TGCAGAGACAAGTCAATTAGAGTGACTGCGGAG[A/G]ATCTCGTTCCTTCCCGTAGCCGTCTCCTTC
TP11403	TGCAGAGACAAGTCGTTTTTGCCAACTTCAGAGGATCTGATTCCAGT[A/G]GGGGAGGGGGCAGCGG
TP11424	TGCAGAGACACATTGCATATCTACAGGCACAGTA[A/G]GTGTGCTGTTTGCAAGAACTATCTATCTG
TP11425	TGCAGAGACACATTGCATATCTACAGGCACAGTAGTGTGCTGTTTGCAAGAACTATC[G/T]ATCTGC
TP11432	TGCAGAGACACGC[G/T]CACAAACAGGTTAGGTAGGATCGGACACACGGAACGAAGCAGGAAGGAAC
TP11456	TGCAGAGACAGGAAGACGT[C/T]CAAGCGCACCGCAACGGCAGGGGATGGAGACGGATTCCGTCCCC
TP11459	TGCAGAG[A/C]CAGGATCCAACTCTGCATCTCCCGCGGGACCAAGTTCCTCTGCCCAGACGCACCAA
TP11483	TGCAGAGACATTGAGCAGCGCCGTGACGACGGCGTTGAACT[A/G]GTGCTCGGCGGACAGGCACGAG

Table A2 (cont.)

TP11488	TGCAGAGACCAACT[A/C]ATCGGCCATGACGTCGAAGCCGAGCATGCAGAGCGGGGCTGCGGTGGCG
TP11491	TGCAGAGACCACAGAGCACCACCGATCGCGCGGCCTCCACTC[A/C]CCGCACCGCGGCCTGCCACCC
TP11494	TGCAGAGACCACGGC[A/G]TGGTCAGCCTGGCAGGCTGATGATGTCCCGCTGACACCAGCATGACAT
TP11497	TGCAGAG[A/G]CCACTGACTGCCACAAGCAGTTTCAGTTCTGCATCCCCATTTTCGGAATCAAGCCA
TP11503	TGCAGAGACCAG[C/G]AAGCCAACGTGCAGCAAGCAGTTCAGAGCCAGTTCAGGGTGCGTCAGTCAG
TP11509	TGCAGAGACCAGTCGTTTTTGC[C/G]GACTTCAGAGCATCTGATTCCCCGACACCGACGTCGTCAAC
TP11533	TGCAGAGACCGCGGCGGCCGCGGATGCTCAAGTTCAACCGAGGATGATGCTAGCGTGGGCAG[A/G]C
TP11536	TGCAGAGACCGTGGG[C/T]CGTCGGAAGTTGAAGGATAGCCCGTCGTAAATACTACTAAGTACAAAC
TP11551	TGCAGAGACGA[A/T]CGAGAAAACAAGAAGAACCGTGCGCGTCAGGCTCGTCCGCGAAATATATGTG
TP11553	TGCAGAGACGAAGCAGCTGCAAAGCAGGAGGAC[A/C]TCTGGGCATCATCCAAGCGCCCCCACACCA
TP11556	TGCAGAGACGAATCCCCAAGCTGTCAGCAGGGCC[A/G]TAGGAACAGATCAGGTGGATCAGGGGCGT
TP11569	TGCAGAGACGAGCAAGGGCGGAGATGAGGCAGAGCACGACCTGAGGGACAGAGGGCTCTGCTT[A/G]
TP11573	TGCAGAGACGATCGAACCGAACCGCGATGGCTGCAA[C/T]AATCCACAGCTCGGCCTCGTGTTTTGT
TP11580	TGCAGAGA[C/T]GCAGCTAGCAGCGTCCAATGCCATGCGACGCACGGCGAAGTTGCTACGAAACTCG
TP11586	TGCAG[A/C]GACGCCCAGACGCCAATGAGGAAGGAGGTCTCGGCGCAGAGAAGCAGTGCAAGGACGG
TP11603	TGCAGAGACGGAGG[A/G]GAGGAGGCGCTGCTGGATGAGTGGGCAGCGGTGGCAGCGTTCTTCGTCG
TP11608	TGCAG[A/G]GACGGCATGGCGGCGCCGCCGCGAGATGGCCACCCCGAGATGGCGAGATCTCACCTCA
TP11611	TGCAGAGACGGGACGAAGACGAACCAATCAGCCACGCGACG[C/T]CGCGACAGGATCACGAGAGGAG
TP11621	TGCAGAGACGGTGGTGGCAGGTGAAG[C/G]ACTGATGGCAATGCTGTTGTTTGAATTCCAAAGGACA
TP11656	TGCAGAGACTATGAGCAGGCTTGGTTCCCTCGCC[A/G]ATCAACAAGCCTCATCTCGCAAGCTTTGA
TP11665	TGCAGAGACTCCGACGCCTGCCCCCTCGGGGGGCGGTAGCGGCGGATC[C/T]TTCCGCTGGTTCGGG
TP11670	TGCAGAGACTCTCTATTCTCA[C/G]CTAGGAAATCATTGGAACAGGAGACGGAAGCCGCAGCGGCGT
TP11678	TGCAGAGACTGGAAGCACAGGTTCTCCTCC[C/G]CGAACATGAAATCGATGACCTCGCCCTGCACCG
TP11706	TGCAGAGAGAACGCA[A/C]GCACGCGTCGTGAGCAAACGGAAGGAAGGAATGGCGGCGACGGGGCGG
TP11725	TGCAGAG[A/G]GACACAGGGGGGTTTCGCCATTTACCTCTCTCTCGGCGCTCACCGCCGTGCGGCGG
TP11729	TGCAGAGAGACACTTCCTGTGTGCCAGTGCATTCTTCGTGGGCGCAGTG[C/T]GTATGAGCAGCTCT
TP11753	TGCAGAGAGAGAAGGC[C/T]AGGTATAAATAAACCATGTAATAATGCAGGCGGCGACGGTAGCCCGT
TP11782	TGCAGAGAGAGAGGGCGGCGGGATGCAGGCCGAGGGGGTCAGCATCG[A/G]GGTCCAAACCCCGACA

Table A2 (cont.)

TP11799	TGCAGAGAGAGG[A/G]ACCTGGATAGTATGGTTCTCGAGGAGAGGATCATCAAATGCAGGTTGTTTG
TP11802	TGCAGAGAGAGGAAGAAGAGGTGAGCACGGAGA[C/G]GATCCGTGCGGCTAGCGGAGGGACAACTCT
TP11809	TGCAGAGAGAGGGAGGGGCAGAAGCGTCAGCAACAGAACAG[C/G]GGAAGGAACCCAAGCCGCAGGG
TP11836	TGCAGAGAGATCGC[A/C]ATCCATCAATCGCTGGACGGAGCGACGGACGGACGGATTGATTCTGCAC
TP11858	TGCAGAGAGCAAAG[C/T]TGGCGCGTGCCTCCGATCCGATCCGATCCGCTTGCTCCTCCTCGCCCTT
TP11861	TGCAGAGAGCAAGCTTTAGCTC[A/G]TTCGGCTGGCTGATATGGGCTGATTCGAGCACTGTAGCAGT
TP11885	TGCAGAGAGCAGGCACGCAG[A/C]CAGAGATAGGACGCATCCTACCGCTGGTCCGCTGCCCGCCCTC
TP11886	TGCAGAGAGCAGGGGGATAGGATGCACACCCTCCCT[A/G]GTCCCTCCTACTGCCCGTACGCTACCG
TP11910	TGCAGAGAGCCGAAGAGATGGACGAAGTAGCATTGG[A/G]CAAGCCCACTGGTTCTAGGTATGGGGC
TP11921	TGCAGAGAGCGAGAGGGACGGCACACGGCAGCATGAGGTTCGTTGG[C/T]CTCGTGAGCTTGGTCGC
TP11924	TGCAGAGAGCGCACGA[G/T]GGTTCACCGCCTCTGGGGCTAGCAAATAAATTAGGGTGACCCTCGGC
TP11925	TGCAGAGAGCGCAGAGGTGGCGGAGGGAGCGGAGG[A/G]GGCGATGGGAAACGAAGTTTCTGGAGGA
TP11926	TGCAGAGAGCGCGAAGCTGGCATGCACGGCGTACGAGGGTGTCGAGCAGGA[C/T]TCCACCTTGGAA
TP11932	TGCAGAGAG[C/T]GGTAACGATGAAGATGTGGACTCTGGTTCCGTGCTTGAGTTCTTATCTGGCTAT
TP11944	TGCAGAGAGCTAGAAC[A/G]ATGGCATTGTAGGAGGCGGCCACGGGCGGCGCCGCAGCCAGCACCTC
TP11946	TGCAGA[G/T]AGCTAGCACAGTCAGCTGGAGAGAGAGCACCCAGCGATGCAAAGCGCGCGTCGTCGA
TP11948	TGCAGAGAGCTAGCTAGCTAGAGCGCGTGTTGTGCCACCCAGCAACAAG[C/T]CAAACCAAACAAAA
TP11954	TGCAGAGAGCTATATATATATAGGAGTACATACATATCTT[C/G]GCAGCTGCATGCCGTCAGCATTA
TP11982	TGCAGAGAGGACAGGGCACGAGTCCGTTCTCGTTGCACGCGGAGCACGGCA[A/C]GCGGCTGGCAGC
TP11992	TGCAGAGAGGAGGATCAACTCACTTGGGAATTGTCATCGCCCAACGATTGCA[C/T]CAGATGCCGCT
TP12002	TGCAGAGAGGATGATGGAGGCAGAGCCATGG[A/G]GTTCAGGAGCACATGTGGCGATGGCAAACCTC
TP12009	TGCAGAGAGG[C/T]AATCACAGCAACAGCAACGAGCAGCAGCAGCAGCAAAGACGTCGATCGATCTA
TP12019	TGCAGAGAGGCCATTGCCCTCACTTCCTAACACTAAGCACA[C/G]AGACTCATTCAACAGTGAATCA
TP12022	TGCAGAGAGGCGAAGCCAAAGGATTCTCGAGTCGGTGAGGCGGA[A/G]CCTGCACGTCGACGATGGG
TP12026	TGCAGAG[A/G]GGCGTTCTGAAGCTGCACGGTGACGAGATGACCGTTCGTACATCTTTGGGTGGTCA
TP12029	TGCAGAGAGGCTCCCCATGGGCATGAAGTCGTAAACAAGTAGCTTTTCATCTTTG[C/T]TGTAGTAG
TP12045	TGCAGAGAGGGGAACGGGACGGACCAATCAGCCACGCGACGCC[G/T]CGACGGGATCACGAGAGGGG
TP12051	TGCAGAGAGGGGCAGCTCGCCGCCGTAAGCTTCCTTTCCCAAGCCTG[A/T]GCCACACGCGGTCGCC

Table A2 (cont.)

TP12062	TGCAGAGAGGGTGGAGGAGGGGCCTCTTCTCCCTGAAGCCATCACAATGCGC[A/G]GTTGGGTCCAG
TP12063	TGCAGAGAGGGTGGGC[G/T]AGCCTACAGAGCGTGGGTGAGAGGGGGTTCGAATCGAACAGAGCAAC
TP12065	TGCAGAGAGGGTTGTTGTCGACTT[G/T]TTCCGCGCCACGTTGGCGACTGCCCGCATACTCTCTGTC
TP12067	TGCAGAGAGGTACTGCTTACCTCCGTGGCTCCGCGCACTCGTCT[G/T]GCTTTAGGGGAAGGTGTTC
TP12072	TGCAGAGAGGTCGCGGTCCATCGGTTTGGCTGTAGCTTTGCTGGACTGGACA[A/G]CCGTGTCCCTG
TP12081	TGCAGAGAGGTTCACTGTCAGGCGGCCCAACCTGAAACACGAGTTTTTTATT[C/T]GCCTCAACCTT
TP12091	TGCAGAGAGTAGTAA[A/G]CATCATCTTCATCAATCTTAGTTGCGTAGTTAACTGGTCAAGAAATCC
TP12099	TGCAGAGAGTCCCCGTCCCCGTGGTGATGAACCACATCGCGCGGTTCGGCGTGCTGGA[C/G]ATGGT
TP12107	TGCAGAGAGTCTGTGCCACGCAGCAC[C/T]ACTGATTGGACTCTGCACAACTTGTAAACTTCTGTAC
TP12118	TGCAGAGAGTGTGAGCCCGC[A/G]CTGCATGAGCTAGCAGAAAGGGAAATCCAGAGATGCCGTTGTT
TP12131	TGCAGAGATAAA[A/G]GACAGAAAGAAAGGCAACCCAGCGGTCACAACTCCGATCAGCAGTTACAAG
TP12132	TGCAGAGATA[A/G]ACCCTAAACCCTTGTAGTCGGGGAGCACCAACTGAACCCAATGGAAATACAAG
TP12197	TGCAGAGATATGATCATA[A/G]TTTATCATCAGTAAGACTCATCATCACGAGACACATGATGGTTGC
TP12203	TGCAGAGATATTCAGTAGTATATCATCGTCAGGATACTCTCGATACAATCGAGGAAC[A/C]AAAAAT
TP12227	TGCAGAGATCACGAAAAG[A/C]AGGCCACGACGGTGTGCTGCGGCCGCGCACCAAATGGGCGTACCA
TP12231	TGCAGAGATC[A/G]GATCACTACTAGTATACACGGTAGTAGTAGGCAAAGTGAAGTTACCCACCCTC
TP12233	TGCAGAGATCAGCTGAAAGGGACAAGTG[C/T]TGTGGCTGGGCTACCCTGCCCACGCTCGCTCCAAT
TP12252	TGCAGAGATCCCCAGCCTTTCACAGGGCGCAAGCCATCGAGCTAGTTC[A/G]TCCTTCCTCCGCCCA
TP12255	TGCAGAGATCCGCAACG[C/T]GGCTCTGGAGCTAGGCGACGGCTCGATGCTGGGTGGCTGCGCGACG
TP12266	TGCAGAGAT[C/T]GATGTTTACTTATGGATAGCGGCATCCATCCATGTCACGTCATGGATACATCTC
TP12282	TGCAGAGATCGTTTCGTTACCCTCTCCGCGATGCTGTGGGGATCCGTCGCCTGCCCACGCCG[C/T]G
TP12294	TGCAGAGATCTCTGATCGGTTCCTTCGTCTATTCTTCCACAGCAAGG[A/C]CAGTTCTTGCGAATCA
TP12300	TGCAGAGATCTTCCACCAGTTCCAGCGACTTCTTG[C/G]AGACGGCGCACGACGATCCTTCCACCCT
TP12302	TGCAGAGATCTTGCACAAAAT[C/T]CAATCGCTCACTCGTTAGTTTGCAGGCCAGCTAAGTTTCCCT
TP12305	TGCAGAGATGAAAAAGGTAAGTACTGATTAGCTACAGTTTATAC[C/T]CTCATCGAAATGAAGACAA
TP12330	TGCAGAGATGAGCAGCGAATAGTAGTTGGTCTCGCCGAGCCCGAACGC[A/G]GCGGCCTCCCTTGGC
TP12335	TGCAGAGATGAGGGAGGTCTTGGGTCAGAGAGACAAGCTTATAGAATGAAAAAAGAGTAG[C/T]ACT
TP12366	TGCAGAGATGCGATCATACCTCGCAGAGATGCCCTCAGCG[A/G]TGGTGAGGAGGTCGCCCATGGCT

Table A2 (cont.)

TP12377	TGCAGAGATGGAAATCACGCCAAGGGAGGGTTAGCAATCGAAGTGCTTGATGCATGGTAA[A/G]CAG
TP12381	TGCAGAG[A/G]TGGACTGGAAGACTGCATCAGCTCCAGTCGGTGGCGCGGACGTGGAGAGTCCCCAC
TP12396	TGCAGAGATGGCATGGC[A/G]ATGATATCCGCTTCGGCTTCTTCCTCCCACTCCCATTCCTCCCATT
TP12410	TGCAGAGATGGTGTCAGCAGCCATACACGCACTGGTGGCAC[G/T]GCACGGAGTTGGAAAAAGGAAG
TP12412	TGCAGAGATGTAAATATCTGGTTTTTCATGATGTA[A/G]TCTGTGTGCCACTAGCTCATCTAGTCAC
TP12458	TGCAGAGATTATCAGGCGCCGCGGTCCGTGCAGGGAGCAGCCACTTGAGAA[A/T]GCGTGTGCCAAT
TP12476	TGCAGAGATTCGCGGCGCGACATTGGGCGCAGGTTCCTCT[A/G]AAGCTTGACATCTGCGCGGCACT
TP12481	TGCAGAGATTCTCGAGGGGAATT[C/T]CGCTGGTGCCCTCGCGGCTTTTTTGCGAGGCGAGTGGCGT
TP12482	TGCAGAGATTCTGTGAGCACAAACGG[C/T]GGCTGCTTGTTCTTCTTCTCCTCAAGGAACTGAGGCG
TP12535	TGCAGAGCAAAAGCAACAACACAGATTCTGTCAATTGGTG[A/G]CTCACTCGACGGGGACAGGTTGC
TP12537	TGCAG[A/C]GCAAAAGCGAGCAGGAAAAGAGAAAACATTTAGCAGTCCAGACTCTATGGTTATCAAT
TP12573	TGCAGAG[C/T]AACAATCGCCCTTGCGTTTGCTGATGAGTGGCCACAGAATTCCCCAGGAGAGGACC
TP12577	TGCAGAGCAACACATGATCCGACTGGGAG[C/G]AACTACCGAAAGAATATACCACTGATCGCGATCC
TP12583	TGCAGAGCAACATTCTACCACTTAATTTACAACACTTCCAAAG[A/T]TTTATCCTCTAAATAAAACT
TP12594	TGCAGAGCAACCTGGGCCTGCGCAACGCCGA[C/T]CTGGAGGCCTCCCGCGCCGCGCTGCACCGCTT
TP12602	TGCAGAGCAACGGGTTTGACTCGTACGCCATGTTGTATCCGACGTCCTCGGCAGC[A/G]TCCGACGC
TP12615	TGCAGAGCAAGAAGACGGCAGCACATCACAGAGGTGAGTTAGGGCTCGTGCTGC[A/G]AGCAGCATG
TP12644	TGCAGAGCAAGGCAGGCAGGCAG[G/T]CATGGGGCTTCCTCTGCTGGCCCTGGTGTGCTGCGCCCTG
TP12656	TGCAG[A/G]GCAAGGTCCAGCGCGTCGTGCACGGCCCTGGCTTTGGCCGACAGGTACCGCTCGAAAT
TP12662	TGCAGAGCA[A/T]GTCGGCGCAGATCAACTTCAGCCTCTCCATTGCATACCGATCTGCCGCGACAAG
TP12676	TGCAGAGCAATCTTATGCATAGATCTGCTCGAGGCACCACAATTCT[C/T]TGGAAGAATGCGCAAGA
TP12689	TGCAGAGCAATTTTCATC[C/G]ACCACTCCTCGACCCCGAGTAAAAATACTTCCTTTTGATTTCTTA
TP12698	TGCAGAGCAC[A/G]ATGCCGACGCGAGCCATGGATGGAACGTACCGAAAACGTTCGCGATCAGCAGG
TP12699	TGCAGAGCACAATGGTTCGCGGGCGCTCATGCACCGTGCTGCGCAAATGAACA[A/C]GCACGGCGAT
TP12704	TGCAGAGCACACAGGATTAGCAGC[A/C]GAGCACACGGGTTTTCTTCATTTGTACGCGTGGACGGAA
TP12706	TGCAGAGCACACCCGCTGCGCCGT[A/G]GGACCAGGAGTTACTGTGTCCCACCTGTCAAAGGTGAGT
TP12710	TGCAGAGCACAGACGAAGGTGTGGTCGAGGTGAGAG[A/C]GCTTGCGGATGGATCGACCCGAATTTA
TP12734	TGCAGAGCACCAGGTCCAGGTGCGACCGCCTCGTCCCGCTCGTGA[A/G]CCGCTTCGTCGGCGGCAT

Table A2 (cont.)

TP12740	TGCAGAGCACCCAGTCCTCCTGCACGCACGCACAGGAACG[C/T]GCGCACCAAGATCGAGTCAGCAA
TP12750	TGCAGAGCACCGCGGTGCC[A/G]ATGCCATGAAGTCAGAACCCGCACCAGACCCTCCCGCTGGCGAA
TP12751	TGCAGAGCACCGCGTTGGCC[C/T]TTTCCCTTTCCGTCCGACCGCCTCAGGTCAGGGTCCGTCGCCT
TP12763	TGCAGAGCACGCACGGGCACGG[C/T]GTAGCGCATTCTAGAGGTGATGGAGATGGAGGCCGCGCGAG
TP12768	TGCAGAGCACGCTCCGCCTCACGCGCGACAACATCAAGGCCATCATCATGGTACGTA[C/T]ACACGT
TP12777	TGCAGAGCACGGGGGC[C/G]CCGCTGCTCTGCAACGTGTACCCGTACTTCTCCTACACGGGCAACGA
TP12793	TGCAGAGCACTCTCCCACTTCCATAGTTGCTTTACTCTTCTCTCCTGTC[A/T]TAGTCTCTCCCTTC
TP12796	TGCAGAGCACTGACAC[A/G]CCTGTGGTCATAATCCATCTCTTGAGCAGCAATCTCACAGGCAGCCC
TP12801	TGCAGAGCACTGGCAGTAGTTTGAAGAGGCTCCGCTGTCCGTCGAAAAGCGAAGATG[C/G]CGAAGC
TP12810	TGCAGAGCACTTTAACGACCTACAGTCACTAAGACTTGC[C/G]TAATCTCAGCTGCAAAAGATGCTA
TP12815	TGCAGAGCAGAAC[G/T]CAGGTGGCGCCTAGGCTGTTCGTCGCTGTTGTTGCAAGTAAACAGTGCCG
TP12816	TGCAGAGCAGAACGCAGGTGGCGCCTGGTTGTTCATCGCTGTTGTTGCAAGTAACA[G/T]TGCCGTG
TP12828	TGCAGAGCAGAC[C/T]GTTGCTCTGGGTCGCTTCGTTCTCCTATGCTATGATGTACTCATGGTGTCT
TP12837	TGCAGAGCAGAGATGCTCCTCGACGAGGCGACGGCCCGTACAGGGAGGCGTAAAAAGGC[A/G]GTGT
TP12848	TGCAGAGCAGAGGAACTCCCCTCACGGCCTCTCCACCGCTT[C/T]ACTGTTCACTCTGCTAGCTGCC
TP12853	TGCAGAGCAGAGGCGATAAGGATGGGACTCACTCGATGAC[C/T]CGCGTTATGATGATGGGGGAGTC
TP12871	TGCAGAGCAGATGGCTCAGATG[G/T]CGACGAGCACGATCGGACAGTGGCTGCACTGACCTCTTCAG
TP12882	TGCAGAGCAGCACGTCAGAGGTCCCTGCCACAC[C/G]CGCCCCTACCCATTGTCAGAGGACATCTTC
TP12893	TGCAGAGCAGCATCTCTACGGCTCCATCGGGCTCAACTCCAACAAGCGGCTCCTCGGCGA[C/T]GTC
TP12901	TGCAGAGCAGCCCGCTGTTCCTGGTCGCCGAGTCCTACGGCGGCAAGTACGCCGCCACGCT[C/G]GG
TP12906	TGCAGAGCAGCCGTACTGTCCTGCTATTAAACAAGCCCAGAGCTTTGC[C/T]GCTCCTCCCCTTCAC
TP12907	TGCAGAGCAGCCTCGACGATGACGACGACCAGGGACCAGCAGC[A/G]CCATAACGAGAAAGCTGCTA
TP12926	TGCAGAGCAGCGTCGGCGTGTCGGGGATGCACATGCAGCTCCTGCACAACGA[C/T]CGCCTGATCCT
TP12935	TGCAGAGCAGCTTTACAGTGGGAACGAGTGG[C/T]ATCGGGAGAAGAGCAATTCGCTGAACACGACG
TP13015	TGCAGAGC[A/T]TATGACTGACCACGACGGTGATGCCTCTGAAGACATCCAGCGAGGCCAGGCGCTG
TP13019	TGCAGAGCATATTGTCGTCTTAGAGCTCCCACTCCATCA[A/G]TCTGTTCGCTTGGTCGCAAACGAT
TP13023	TGCAGAGCATCACACACA[G/T]ATTTTATCACAGGGTTCTGGAGATATACTACCAACTGATGGCACG
TP13034	TGCAGAGCATCCAGCAGGCGCCCGCCTCCACCATGGGACGCGGCGCCGCTGGCTTTTGC[A/G]GGCT

Table A2 (cont.)

TP13035	TGCAGAGCATCCCGCAGCGCAAAGTGGTGAGCTGCACGATACCCCTCCGTCCCATCCA[C/T]CAAGA
TP13038	TGCAGAGCATCCGCGAGATCGACCTCTTCCCCGCGGACGCAATC[G/T]CCGACCTCCACGCCATCGC
TP13045	TGCAGAGCATCG[C/G]TAGAGGTGGCGACCTGACCGACCACCCAAAGCAAGGTACCCCACAGCCTGC
TP13046	TGCAGAGCATCGCTCGAGGTGGTGACCTGACCGACCACCCAAAGCAAAGGTACCCCACAGCC[C/T]G
TP13047	TGCAGAGCATCGGGAGAGAAGCCGATCTCATCGTGCAGCACTTGGTAATG[C/T]GCTGGCCTTGTTG
TP13067	TGCAGAGCATG[A/G]TGGCGGCATTTCCTGTCCTGCGTGCGCCGTCGGTCGTGGCGCATGGCAGCCG
TP13071	TGCAGAGC[A/T]TGCAGACCAGCCGTTCCGTTATGGTTTCTGTCTGCAAAGCTTACGCGAACATGAT
TP13111	TGCAGAGCATGTTGAGGAA[A/G]GACTGCGTCTGCACGAAGGTGAGCGCCAGCGAGATGGCCTCGCT
TP13120	TGCAGAGCATTCAACTGAATGGCTTCAGGGC[A/G]ATGATGGTCGCGAGACCACTTTTCACCACATC
TP13147	TGCAGAGCCAATCGTGACAGGGTACAGC[G/T]CATTGCGATTGGAATCGATCTGAAGATGAAAAGCA
TP13149	TGCAGAG[C/T]CAATGCGTCGTGGACGCGTCAGACCACTACAGCGGCCCGTTCCAGGCGACGACGCA
TP13153	TGCAGAGCCACA[A/G]GAAACCCCACGGCGGCGGGCAACGAACCGTCCCTCCTTGGATGGAACGCAC
TP13172	TGCAGAGCCACCCATCCTCCTCACCTCCCCCTGCATCCAAATATCCACGAGGCAGCACGCG[C/T]TG
TP13180	TGCAGAGCCACG[C/T]GTACCAGTCCATTCGCTCGTTCGCGCTCGGCGGAGCGGAGCGGCGAGTGGC
TP13181	TGCAGAGCCACGGCAAGGAGGA[C/G]GAGGAGAGGTTCTTGGACTTCCTCAGGGCAGCTCCTTCCAA
TP13190	TGCAGAGCCACTGTGGCCAAAAATTGATTCATTTCTCTTTTGTTTCTTCTGTAGATTC[A/C]TGCTC
TP13199	TGCAGAGCCAGCAGCCAATTAAGTGGATCCCAAAAGACAGGTCTCGATCTGGTTAGTT[A/G]TCGGC
TP13202	TGCAGAGCCAGCCAGCTTCTTTACA[A/G]CTCACACCCGCCTCTGTTTGTTCGTTCGGGCAGGATGA
TP13205	TGCAGAGCCAGCCGCCGTTCAGCGAGGCCAGGTACGGCGCGG[C/T]GACCAAGGTGTACGTGGTCTG
TP13213	TGCAGAGCCAGGCCAACCGCTGGCTCGAGTGCCTGCACAGCTGC[G/T]CCGAGCTGGAGAGGAAGGA
TP13218	TGCAGAGCCAGTACATGGGCCTGGCCAACGCGGCCGACAACGGCAA[C/T]GCCACCAACCACTTCCT
TP13234	TGCAGAGCCATCCTCAAGAACAATGGAAAC[C/T]TTGTCATAGAATCATTAGAAAACTCCTCCAATA
TP13236	TGCAGAGCCAT[C/T]GCCGCGTTCGCTCGCGCCGCGGTTCATGCTCCAGGAGTCGGAGGCGGCTACC
TP13255	TGCAGAGCCCAAGAAAATTTGGCCCAAACGCCCTCCTTTCAGTTTCACCCCGTCACTCT[C/G]GTCT
TP13266	TGCAGAGCCCAGA[G/T]TCCTCGACGCACGAACCGCTCCGACGCCATGACGCGCCGCAGCACGTCGA
TP13269	TGCAGAGCCCAGCTTCCTAGTGTCTCTAGCGGCTGGCATGTG[C/T]GATCACTTGCTAATATCGCTC
TP13280	TGCAGAGCCCCAGAGCACGGCCAGACCCCAGAGCCAGCGCGCTAGCCGATGCCGCTGCTG[C/G]TGG
TP13284	TGCAGAGC[C/G]CCCAGCTTCCGCTCCCCGCCTGCGACGTCATTGGCGTTGCTCGACGCCGAAGCCC

Table A2 (cont.)

TP13294	TGCAGAG[C/T]CCCTCAGGTAAGAAGTACGATGGTGTCGTCCACTGCACTGTCGGGATCAGCTGGTC
TP13301	TGCAGAGCCCCTCCTCGTCGTC[C/G]TCCTCCTCCTCTTCTCCGACAGCAGTAGTGGAAGCAGCAGG
TP13305	TGCAGAGCCCGAGGCCTGCCTGGGCTGGGTCCTGGGCGACTGCCGAGTG[A/G]TTGTTCTGGCCTGC
TP13310	TGCAGAGCCCGTGACAAGTCTGTAGGGCCACTGGAGATACGGCTGGTTGAAGCTGG[C/T]ACCTTTG
TP13325	TGCAGAGCCCTGCACCAGGCACAGCTAGCTG[C/G]TAGCCACAGCAGCACAGAAATGGTAACAGCCG
TP13342	TGCAGAGCC[G/T]AGTCGGACAACACAACCGCGACCACGAGGCGTCGTCGCGGAGCAGTCGGAGCCA
TP13349	TGCAGAGCCGC[A/G]CCGCATCGTGCCTACGTGGTGGTACCGCGCTAGAGCTCATGGACAGGCAGAG
TP13357	TGCAGAGCCGCCGC[C/T]GTCACCAACCGACTCCGCCGCCCGCAGCCGCCGCAGTCCGCACTACAAG
TP13362	TGCAGAGCCGCCTCCACCCGCTC[C/T]GCCCTCCGACGCTCCCCAAGAACGGCCCCATGGTCCATCG
TP13368	TGCAGAGCCGCGAGCTCGGCACGTACCTCTACGCCGAC[A/G]AGGACGGGGTCGGCGTCTCCCTGAG
TP13373	TGCAGAGCCGCGCCGCCGCCGCCGACCAGGGACACGACCACGACCACCC[A/G]TCGTCGGAGCCGAA
TP13377	TGCAGAGCCGCGGGAACCGCAACAAGTACGTCCACGCCGA[C/T]GGGGACTGGTTTGGGGTCTCCCT
TP13380	TGCAGAGCCGCTCATTAGTCCCATCGATCTACGTGTTTGGTGATTC[C/G]ATAGTCGATGTCGGAAA
TP13382	TGCAGAGCCGCTGCTGAAATTGGCTCTCCTCTC[G/T]CGGACCAGCGAGTTGAACTGCATGCACGCA
TP13385	TGCAGAGCCGTCGCTGAAGGCGCAA[C/G]TCGCATCGCAGCTAGAGAAGGCTGAGCGGAGCTTGTCC
TP13406	TGCAGAGCCTCACTA[A/T]TATTTTGCTCGATTTGCTGAATTGAACAAGAATCGAAATTTGCTGAAG
TP13428	TGCAGAGCCTCGGGGTCGTTCCAGTACCTGAACCATCAAACACGCATTCGATCATTCGT[C/T]CACC
TP13440	TGCAGAGCCTGAAGCAGAGCCACAACCTGCTGCTGGGCCTCTGGAAGAA[C/G]CAGTGGAACCTCAG
TP13446	TGCAGAGCCTGACGGTGCACGCCACCGCCTG[A/C]GCCCAGTACTTGAGCCTCGCCTTCACCTCGTC
TP13449	TGCAGAGCCTGAGCAGAGGGAAGGCGACGATGGACTGGGAAACAGCTCAACA[A/G]GTCTGGGAGAG
TP13452	TGCAGAGCCTGAGCTTCGG[C/T]TCCTCCTCGGACCGCTCGCGCTCCCGCTCCGCCTCCACGGTCTC
TP13457	TGCAGAGCCTGCGAAGGGCGATTTGACTTGGCTCATGTGAG[C/G]GCAAACGCTACTGGAAGGCGTA
TP13461	TGCAGAGCCTGCTGAGCTCCGAATGAAGAGCCATTCTCACAGTCAGCACC[C/T]GTTCCCCTACTCC
TP13470	TGCAGAGCCTGGGATCGGCCATCAAATGACA[A/G]TAGACATGGTGAAGGCAGCAAGCGAATGGTTC
TP13473	TGCAGAGCCTGGGTACGCACGGCGGCGATGAAGGCAAG[A/G]TCGCCGAAGGGGGCGAGGCCGTCGA
TP13505	TGCAGAGCGAATACCCTTCAGACGCTGAGAGCTTTTC[A/T]GTAAACCTCGCATTCCTCCACTTGGG
TP13522	TGCAGAGCGACGGTGACAGCGACAGTGTGTTGTCCGACGACTTGGTGGCGGCCGCGCT[A/C]GCGTC
TP13525	TGCAGAGCGA[C/T]GTGCTGGCCGTGACGCGGGCCATGCTGGCGTTCCCGAAAAAAAAAAAAAAAAA

Table A2 (cont.)

TP13549	TGCAGAGCGAGCTCGCCGATGACGTACGGGCTCTG[A/T]GCTGAGAGTACTGGCAGTAGTATCTAGC
TP13550	TGCAGAGCGAGCTCGGCGAGAACAATGTCCTGATGACGGCGA[A/G]GCGGCGGCACAGCAAGGGGGA
TP13563	TGCAGAGCGA[G/T]GTGAAGAGGGTGGTGTTCGGGTCGCTCAAGGCCATGATCATGAGCGTTCCCGA
TP13564	TGCAGAGCGAGTGACAAGTGCATGAAGGAGAGGCGAAAGACCATCAACGG[C/T]GACGACATCATCT
TP13568	TGCAGAGCGATCTCAATTGGTTCAAGTTCATTGAGAATTCCC[A/T]ACTTGCGGCACATGTTACGTT
TP13573	TGCAGAGCGATGAACACCTTGAACCCT[C/T]CCCGCCGCCGCTCATCCCCCGCGCCGTAGGGCAGCA
TP13577	TGCAGAGCGCAAAAGTGCATATGTTATGGTGGGCCAGGTGTATCAATGCCATAAGCGGAGCC[A/G]C
TP13584	TGCAGAGCGC[A/G]CGGTTTAGGCAACCGAAACTCATGTGCGATTCCCATGTAATCGGGCCGACGAG
TP13591	TGCAGAG[C/T]GCAGAGTGCGGACTATTGCCTGTCGCCTGTCGGCAGCCAGCCTACAGCGCAGACGA
TP13612	TGCAGAGCGCCAAGGAG[A/G]GTTCAGAAGGTTTGGTTCTTGATGCCTGGGTCCTCGCCCAAGAGCT
TP13640	TGCAGAGCGCGAAGCTCGTGAGAGGCCA[C/T]GCGCTGGAGGCGGCCTTGATCCTGGACTTCTTTGG
TP13644	TGCAG[A/G]GCGCGAGGAGGTGGAGTAGACGTAGAGGAGGAGGAGGAGGGAGAGGAAGGGGAGCGCG
TP13645	TGCAGAGCGCGATAAACGAGGCGTCAGTTAGACAGACATGGCACGGGGTTGAGGC[A/G]GCACGCGA
TP13651	TGCAGAG[C/T]GCGCGCCAATTCCTTGTCCACGTGCTTGTGTATCGTTTGTTCGATTTTTACCTGAA
TP13657	TGCAGAGCGCGGCCGT[A/T]GTGGTGAGGGTGAGGGAACGCCAGGTTGAGGTCGTGCGAGCCCTCGT
TP13669	TGCAGAGC[G/T]CGTGCCAGACGGCGGCGGTGCGGGCGCTGTGGGGCCGCGCAGTGCGCGACCCGAA
TP13685	TGCAGAGCGCTTCGGTCGACTT[C/G]AGAGGATCTGGTTCCGCCACTTCCTCCTCACTGCACTCTCC
TP13687	TGCAGAGCGCTTG[A/G]CCCTGGATGAATCACTGAAAGCGTAAGTTTCTTTCCTGTCATTGCAATGC
TP13707	TGCAGAGCGGCAGGCAGGCAGCACGCACGTACGCGTAGGTACGCACGCCCGACGCGACGCGA[A/C]G
TP13711	TGCAGAGCGGCATTCCATCGAACGGTTCATGGGAATGTGAGGGGTGC[C/T]ACACCCGTGTTCCCCG
TP13712	TGCAGAGCGG[C/T]CACTGTCCGTGTAGGCGCAAAGCTCCAAGCGGGAGCAGCTAATACCTCCAAGC
TP13737	TGCAGAGCGGGAAGGCTTGGTGCCCACGCACGTAACTTGGGTGGAGTGTGAAA[C/T]CTGAAATGGC
TP13745	TGCAGAGCGGGCACGTCACGTGCATCTGTAGCCGACGTGGAACA[C/T]GTGCCAGCACTCGGGCAGG
TP13746	TGCAGAGCGGGCAGGAGCCGTGCTTGATGAGCCAGCCGTCGATGCA[C/T]GGCACGTGGAACACGTG
TP13756	TGCAGAGCGGGTGCAAGCAGGCGAGCGCGCGCC[A/G]TTTGCGCCGCGGCGGCGCACTGGATCCGAA
TP13758	TGCAGAGCGGGTGCATGTGGGCTGCACTGCGGGTGCAAAGGCC[A/G]CTGCACAGCGGGTGCTGTCC
TP13763	TGCAGAGCGGGTTGTGCATCTGCATCACTCGCACTAAAATTCTCATTCTCAAACTTCA[A/C]AGCTA
TP13767	TGCAGAGCGGTGAGACAGCTGATGAGCTGAGACAACCACACGAAAGCAC[G/T]TGCACCACGCCACA

Table A2 (cont.)

TP13783	TGCAGAGCGTCAAGGTGC[A/T]GGCTGGAGTGCTGGACTCTTTTTGGAGGGAGACATCGTAGTCTGC
TP13792	TGCAGAGCGTCGTCGCCCTTCTCTCCATCGGCTGAAGAAGCAG[C/T]GAAAGAGACAGCAGGCTTTG
TP13795	TGCAGAGCGTGACGCTGAGCCCGC[A/C]GCTCTGCTGGCCCTGTGCTTGTGATCCCTCGGCCAGATT
TP13802	TGCAGAGCGTGCACCTCCTCGTCTCCTAACACCGCGTGATCCATGTGTTGGTG[C/T]TCATAGCAGG
TP13817	TGCAGAGCGTGTAGGTAACAGGTAAAAATTACATGGTACACTGCCAAGGAACAAAAGGT[C/T]AACT
TP13848	TGCAGAGCTACAGCGACCTGGAGG[A/G]CGACGACGGATCCTCCTCCAGCGGGGAGCTGCTGCGCGG
TP13849	TGCAGAG[C/T]TACAGCGACCTGGAGGACGACGACGGATTCTCCTCCAGCGGGGAACTACTGCGCGG
TP13865	TGCAGAGCTACCGACCGCCGCACCTTTTCCGCGCGTGCATTTTCTCCTTTGCGC[C/G]GCCCCTCGC
TP13875	TGCAGAGCTACTCATACGTGCCCT[C/G]TCATCTCGTAGTAGCTAGCTTAGTAGCTTATTAGGTGAT
TP13890	TGCAGAGCTAGCAGAGGTTAGGAGGGGG[A/G]AAAACTACTGCTAGAAGCCTAGAAGCCTACTGTAG
TP13908	TGCAGAGCTATGCCAAACGCTT[C/G]TTTTGGAAAGGGCTCCGCATGGGGAGCCGAAAAAAAAAAAA
TP13927	TGCAGAGCTCAAC[A/T]GCCTTAGGCAAAGAACAGTACAACACGACGAACGAAAACAAAGCAGAGGA
TP13965	TGCAGAGCT[C/G]CCAGAGGGTGGTGAAGCTTCAGCAGTAGTTTCAGAGCTTGCAGAAGCGGCAGTC
TP13972	TGCAGAGCTCCGCATCGCCAGCAAGCCCCACTTTGCCGCCGAGATTCG[C/T]GCCCGAACGCTCCGT
TP13979	TGCAGAGCTCCTCGGTGGTGTTGCC[G/T]CCGAAGCCGCAGATGTCGGCGCCAACCATGGGGATGCC
TP13982	TGCAGAGCTCCTGTCCCGACGATGGCCCCTTCTCGATTCAGAG[A/C]GCTCCCGTTCCCGCTCCTTG
TP13989	TGCAGAGCTCGCACAGCCTCACCCGCGGAGCTC[A/G]CGAGGCTTGCCGCGGAGCTCGGGCTGGCCG
TP13993	TGCAGAGCTCGC[A/G]GTCGGAGAGGCTGACACGTACGTGCTGAGCCACACTTCGCTTCTTCCTCCC
TP14013	TGCAGAGCTCGTGGTGCCCTGTGGTCTGCGGCTGAAGGGC[A/G]AAGGCCCACGCACATAGAAGCCC
TP14026	TGCAGAGCTCTCATCGTCTTCTTGGGAGCAGCCATGGCTTGGTGCTTGCTTCTATGC[G/T]CGTGGA
TP14034	TGCAGAGCTCTCTCTCCATATTTG[C/T]TCATTGCGAACAAGGAGAGGTGGACAAAGGGAGGAAAAA
TP14036	TGCAGAGCTCTCTGAGACGTGCGGACCGCGGACCGCG[C/G]ACAGCGATGCCGTATATTCCGTAGGA
TP14043	TGCAGAGCTCTTACGCTCGATGACTTGAGGGATGGGGAA[C/G]TTGACGGGCGTCTCCTTGACCATC
TP14044	TGCAGAGCTCTTCACTGTGGAGAAACAACTGCTGAACTCCCACAATGCGAAGCTGAACTTTCA[A/G]
TP14051	TGCAGAGCTGAAACAAGCCACATGGCATCTTTGCCTGCTG[C/T]TGCTAGTGCTAGGAGAGGGCCAA
TP14083	TGCAGAGCTGCGGGTGGGGCGGCGGGGACTACGCGTACCAGGTGG[C/T]CCACGACGCCCGAAAAAA
TP14085	TGCAGAGCTGCTAGCTAGTAGCTGCTTTCGTTGCAATGTATGTATACGTATAGGACCATA[C/T]CAG
TP14097	TGCAGAGCTGCTGCTCCGCGTTTTCCATTGTAGTTCGTGGAGTTGCCGATGCCC[A/G]ATGGCCGTG

Table A2 (cont.)

TP14124	TGCAGAGCTGGGACCCCACGCTCGTCAACCCCTGCACCTGGTTCCACGTCACCTGC[A/G]ACCGCGA
TP14126	TGCAGAGCTGGGATCCCACGCTCGTCAACCCCTGCACCTGGTTCCACGTCACCTGC[A/G]ACCAGGC
TP14135	TGCAGAGCTGGTAATGTTG[C/T]CACAGCCTTTCTTCTCAGTTTCAACCAGAGAACCTGTCTGCATG
TP14137	TGCAGAGCTGGTCGACGTC[A/G]CGGTTGCGCGCCGTGAGGACGTTGCGGTGGTCCGAAAAAAAAAA
TP14141	TGCAGAG[C/T]TGGTGGTGGCGTTGTGGGCGAAGGGGATAGGAATGGATTGGAATGCGGCGGCAGAG
TP14162	TGCAGAGCTGTGGGTATGTTCCTGAAAGGAACACCATATGGGTGCTTGAAGGCATCAT[C/T]TATTA
TP14163	TGCAGAGCTGTGTCAGGCTGACCAGAGTAAACTACCTCGAGGATCCAACCGATGTAC[C/T]TGACGT
TP14169	TGCAGAGCTGTTTAGCTTTTGAGAGATACGGAGTAGAGCGCATCCGTTCCCAGTGC[G/T]CACCGAC
TP14193	TGCAGAGCTTCCACCTAAATCGCCTGACGAGGT[A/G]ATGCATCGTCACCAGCGTCTCGATCCTGGC
TP14195	TGCAGAGCTTCCAGCGCCTCT[A/T]CCATAGGTCCTGCGAAAATGTCTGCGCTGCTGGTGAAGGCTC
TP14197	TGCAGAGCTTCCAGGGCCTTTTCCTTCGCCACCATTGCTCGCGGA[C/G]GGAGTGCACGTCCGTCCT
TP14199	TGCAGAGCTTCCCTTCCATCAACCAATCACCCATCCATCAGCACTCTTCA[A/G]TCATTAGTGTGTA
TP14203	TGCAG[A/C]GCTTCCTCCCGCCCTCCCCGCACGCGGCGCCGTCGTCGTCGTCGTCCCGAAAAAAAAA
TP14209	TGCAGAGCTTCGAGCACCC[A/G]CTGCACGAGGTCAAGGCGGTGCCACGCGTGGACAGCCAAGGCCA
TP14227	TGCAGAGCTTGAAGGTGGCGACTGGGATCCCATCATGTGGCAAGAAGCTCCTATGTGGGCA[C/G]GA
TP14253	TGCAGAGCTTGGCAATCTGACTATGTTAATAAGTAGCCTGGACTTCTCGGTCTGCAACCT[A/G]ACG
TP14256	TGCAGAGCTTGG[G/T]GAGGGAGATGGCGAGCGTGCGGTTGATGGGGAGGCTGAAGGGCACGTTGCC
TP14276	TGCAGAGCTTTCGCATCCAAAGCCATGGCTTAGGCGCTTGTGGGGCTCCGCTGTGCA[C/G]TGGCGC
TP14280	TGCAGAGCTTTCTCCTCGCCCCCAGCAACATTCTCTTCC[C/T]CGTTCTCCTGCTCCTCATCTGGCT
TP14281	TGCAGAGCTTTCTTTTAATCATTTTGCTGCTGTAA[C/T]AAAGCTTGCCGCCGCTTGCCGAACGGGT
TP14297	TGCAGAGGAAAAGAATCTGCACAGACCAAGAAATTCACGCCACTTCACGGGTCCAAGCACATG[A/C]
TP14298	TGCAGAGGAAAAGCAATATTTTATTTATTATTATTTTTATAAGCGGCCC[A/T]GGATTCGATTGGAG
TP14319	TGCAGAGGAAAGAGCTTAACGAGAGGAGCAAGCTTA[A/G]GAGATTGGGTACTGTGGAGGACATGGC
TP14322	TGCAGAGGAAAGGAATCCATC[C/T]GCACATACGAAATTCAGGCTCCAGTTCACGCGTCCATGCACC
TP14326	TGCAGAGGAAAGTCGATGTGAAGCG[G/T]GGCACCTCTTCCCTGGGCATTGTGGAGCGGATCGAGTA
TP14337	TGCAGAGGAACAACATGCT[A/C]CAGGACCTGGATTGGTCGACCTCAAGGTACCAGTACGACGCCGT
TP14358	TGCAGAGGAACGGTCATAGT[C/G]CGTGGACTTCACCGCCTGCGCCACCATGGAAGCGTCCGTTTCC
TP14359	TGCAGAGGAACGTCCGTCCCTCAT[C/T]AGCCATGGCTTCCGACCGAGTTCATGGTACTATGCAACT

Table A2 (cont.)

TP14382	TGCAGAGGAAGCAATGGTTCCATCGGGCGTCGCTCCACGCAAGCAGAGC[A/G]CTTTTTGGTGTGGG
TP14393	TGCAGAGGAAGCTCAAAGCAACATGTCTCGGCAGCGGACAAAAGGCTCCAGCTCGATTCATCC[A/C]
TP14416	TGCAGAGGAAGTGGAAGGAGTTCAAGCAGTCCGATGAGTCCTGGAAAGAAGCCCCGAGGAAC[C/T]T
TP14424	TGCAGAGGAATCAGTGACTCGCACTCCTTAAGCTGCGCTGCCTCGTC[C/G]ACGACGACTACATCGA
TP14426	TGCAGAGGAATCGGACGATAACCAGGACATGTAGAGTAGAATCAGAGAA[C/G]AACAGAGAACAACA
TP14440	TGCAGAGGAATTGGCCCAGTGGACAACTGTCTCAAAGAAAAAG[G/T]CATCTTCTCCGACGACGGTA
TP14446	TGCAGAGGACAAACAGGTCACCAGGACGATCGCT[C/T]CAGTGATGCAACACCACAACATACTGAAC
TP14452	TGCAGAGGACAAGAAAACAAACCAAAGCTTTTTAT[C/G]AACCAGTGTTCTAAAACTACTAGGTGAG
TP14474	TGCAGAGGACATCCTCTTG[C/T]TGTCTTTCACCTCCTCTTTCTCTCTCTCCAGTCTCGCAAGAAGA
TP14476	TGCAGAGGACATCTTGCTGGAGGGCAGCCAT[A/G]GCGACATCGCCATGTGGCCCTCCAATCGCGGC
TP14477	TGCAGAGGACATCTTGCTGGAGGGTAGCC[A/G]TGGCGACATCGCCATGTGGCCGTCCAATCGCGGC
TP14487	TGCAGAGGACCAGAAATGTAATG[A/G]TATTTTCATCGAGACGTTGGCTCAACCTTGTCCGTCTCTG
TP14491	TGCAGAGGACCCGCCCATGGCGGCAGTCGAGCGTCCACATGCGGTTGTAATCGAACGG[A/C]GGCGG
TP14492	TGCAGAGGACCGC[A/G]CGGGAGTCGCCGCAGTTGGCGACGACGAGGTGGCGTGGCCCCACCACGGC
TP14502	TGCAGAGGACG[A/G]GGACGGGTGGCGCCGCCATGGTCGCGGACTCGCGGCCAAGCGGGAGGCGCTG
TP14518	TGCAGAGGACGTAGGCGCAGCCGATGCTGGTGGTGCCGCGCCACACCACCTGCGTGTACGAG[C/T]C
TP14519	TGCAGAGG[A/G]CGTCAAGGGTCCCTTGGCCTTGGGTTTGGAAGGACGAGGCGAAGCGCTCGGCCAC
TP14536	TGCAGAGGAGAAAAAGGT[C/G]GGGCAGGCGCTGGAAGGCGAGCTGGACGCGGGGTTTGCAGGCTGG
TP14543	TGCAGAGGAGAAGCGCGCGGCTGCC[C/G]TAGCGCGGCGCGGCGAGGAGGTCATCGCCGCGGAGGAG
TP14547	TGCAGAGGAGAATAATGCATGGTGACGTACTCTTGAACTCTGCCATATCGCGGTTGGC[C/G]GAGTA
TP14551	TGCAGAGGAGACAGCGAAGAAGCTGCTCTCCCA[A/G]CTTGTTGAGCTGAGCATTATCCAGCCGCTA
TP14561	TGCAGAGGAGACGCGTC[A/G]TGGACCGAGTTCGCGGAAGGCGGAGGCGACTCACCTCCTGGCTGCG
TP14569	TGCAGAGGAGAGCCAACTTCCCCTC[A/C]ACATAGGCTGCTGCTAGTACCCAAATTCCTCTAATCTC
TP14575	TGCAGAGGAGAGGAGACAATCATAC[A/G]TGCATATCATATGCGATCAGCAGCTAGCCAACATCTCA
TP14576	TGCAGAGGAGAGGAGAGGAGAACTCTACCGTGCAGGACGATGAAGGGCAGGG[A/G]GGAGGTCTGCA
TP14617	TGCAGAGGAGCCCTTGCCATGGAATCCGATTACTTAACCAAGTCTATTTACTGTCCTCG[A/T]TGAA
TP14664	TGCAGAGGAGGCCACGTGGGCGGGGC[A/G]CAGGGAACAAGGTCCGTCAGATGGGACAGCATACCGT
TP14665	TGCAGAGGAGGCCCTTGGGGACACCGAGCTGCTGCCATTAGGGGTGTGAGC[A/G]CTCGTTGATGCG

Table A2 (cont.)

TP14679	TGCAGAGGAGGGGGCACTGGCTGGACAGCGGCGCACGGGGCAGCCAG[C/G]GCCCTGTCTGGACGGG
TP14685	TGCAGAGGAGGTGCCAGAATCC[A/G]TCGTCACCAACCCTGTGATGGCCCGACAGATCAGAGGCCTC
TP14701	TGCAGAGG[A/T]GTGACCTGCTGGCGTGCCAGCTCGCGCGACCGTCTTCCACCTCGCGCGCCAACGC
TP14706	TGCAGAGGAGTGCCTCCATCCTCATGATAGAATATTGAAATCTCAAACATG[A/T]TCAAATTTGTAA
TP14736	TGCAGAGGATCACGGTCTCGGAGGAGCAGGAG[T/C]AGGAGCAGTCGCACATGGCGGCGGGCTCCTT
TP14749	TGCAGAGGATCCCCTCCAGGATGTCACATTTGGTAGA[C/G]CCCTCTCGCAGGACATCCTCGCATAG
TP14759	TGCAGAGGATCGATCGAGATCT[A/G]GGCCTGCTTCGAGATGCAACGACGAGAGATGACGCAGTGGA
TP14777	TGCAGAGGATCTTGATGCGCCCTCCACCTCCG[T/C]CACCGCCAGCTCCGCCCGCGCCGCCGCAGAT
TP14787	TGCAGAGGATGAGGAGGCCGTCAGGTGAGGCCTGT[C/G]CGCACCCACGAGGGCCACGTGTGACCCC
TP14790	TGCAGAGGATGATGCCGTGGTGCGGTGCTGACTGTCAAGGGCCGCCATGA[C/G]CACGAAAACGAAC
TP14819	TGCAGAGGATGGTCTGCTCCGACAAGGACCC[A/G]CCTCCCAACATCGGCATCCCCGTCGTCATGGT
TP14905	TGCAGAGGCACCGAGGAAGGAGAAGGTCTGACCTATTGGGGTCTTCAGCAAGCCACC[A/G]ACTGTG
TP14927	TGCAGAGGCACTGAGGAAGGAGA[A/C]GGTCTGACCTATTAGGGTCTTCAGCAAGCCACCAACAGTG
TP14952	TGCAGAGGCAGCTGAAGAG[C/T]CCGCACGCTAGGCACTTGCAGGGGCAGCACAGGCACGAGACGGC
TP14973	TGCAGAGGCAGTTCGGGCTCAGCAGCAGCCAGGTCACGGCACAGCAGTATCCTGCCGC[A/G]GCGCA
TP15001	TGCAGAGGCCAAAATCCGTGGCGACTAAGGATCTCTGTGAATGAT[C/G]TGACATGTCTTGTTCTGC
TP15025	TGCAGAGGCCAGGCACCGTCAGGCTCACAAAAAGATGAGAG[A/G]TCCCCATCCAACAGTGGCAGCT
TP15042	TGCAGAGGCCCGACGCCATGGGGAGGTT[C/T]GGGAAGTTCGGCGGGAAGTACGTCCCCGAGACGCT
TP15052	TGCAGAGGCCGACCGCCACCGCCTCGCCACC[C/T]CCTCTCTTGCGAGTGCCAACTGCTGAGCAGAC
TP15057	TGCAGAGGCCGCCCGCCGCCGTGCTACTTTTGTGCCGCCGCCGATCC[A/C]GAAGAGACCGAGAAGC
TP15061	TGCAGAGGCCGCTGGAGCACGGCA[G/T]CTTGGAGAAAGACGACGACTTGTTTGGGTAGTAGGAAGG
TP15069	TGCAGAGGCCTCACGCCCACACTTGCATTTGAGAAAAAATTGGGTGG[C/G]CGATGGGTCCACCCAA
TP15074	TGCAGAGGCCTGGCCCAATGTTTGAAGGGACTGATGGAGGGTTATGGAG[A/G]GAATGCAAATCGAG
TP15087	TGCAGAGGCGACCAGACTGTCAGCTGCAAATCAAA[C/T]GATATAATAAAGCAGGGAGCTTTAGCCT
TP15111	TGCAGAGGCGAGCGAAGAGCTTAGCACACAGCAC[A/G]CACGCGCTCGTGTTTGGTAGGTGCAAGTG
TP15116	TGCAGAGGCGATAGATAAAGCTCGAGGAAGACGACCTTTGAACC[A/C]GAGGCGTACATAGCTGCAC
TP15118	TGCAGAGGCGATGGGTGATCACGAGGCTCGCGGTGACGACTTCGAGAAGAAGGCGGA[G/T]AAGAAG
TP15133	TGCAGAGGCGCCGACGCCGCCTTGCCGT[C/T]CCCGTCGCCGTCGTCTCGCGGCTTCAGCGCGGCGA

Table A2 (cont.)

TP15134	TGCAGAGGCGCCTCCACCCGCTTCGCCCTCCAACGTTCCCCAA[A/G]AACGGCCCCATGGTCCATCG
TP15141	TGCAGAGGCGCGGCGGAGGCGGAATCAGCAGCAGGGGAGAGGGCAAAGAGAAACGGGAGA[A/C]GGG
TP15164	TGCAGAGGCGGACCCGAACATGCCAAACTTACCAGAGGTCACA[A/G]CAGAAAAGGATAAACAGGAG
TP15172	TGCAGAGGCGGATGGATGGGTGGGGAGGCAGACTGGCAGTGGCATGCGTGCCCCGACGCCGA[C/G]A
TP15182	TGCAGAGGCGGCGGCGAGCT[C/G]GCGCCGTCGCGCACCACCACCCCACGGGGAGCTCTCTGCGTCC
TP15188	TGCAGAGG[C/T]GGCGGCGGCACGCGCGCAAACTTGAGCAGCCTGGAGGCAACGGTGGCGCACACGC
TP15201	TGCAGAGGCGGCTGTACG[G/T]ACGTGCGGTGCGCCCCCAGATCGCGCACCGATCACGCGCGGACGG
TP15219	TGCAGAGGCGTACCGCGA[C/T]GACGAAGCCCCAGTTGGCGACAGGGCCCCAGAAGTGGGTGGTCTT
TP15235	TGCAGAGGCGTTAAGGTGAGAAGC[A/C]TATGGTATTTCCTCCACTGGCTCCTCGGAATCGCAATCT
TP15236	TGCAGAGGCGTTAAGGTGAGGAGCTTATGGTATTTC[A/T]TCCACTGGCTCTTCGGAATCTCAATCT
TP15240	TGCAGAGGCTAAAATCCGTGGCGACTAAGGATCTGTGTGAATGATCATCTGATATGT[C/G]TTGGTT
TP15256	TGCAGAGGCTCAGCTCAGATCAGTCCAGTGCCAGTAGGTGATCAGCTCTTCTGAT[A/C]ATAGTTTT
TP15275	TGCAGAGGCTCTTCATTGGTCGACGAACAAATATACAGTTGTTATCTGTTTCGTGTTTTTTTT[G/T]
TP15288	TGCAGAGGCTGCCCAAGTGCAGCATCACCTTCTCCTTTTACAGC[C/T]CCGCCGCGGTTCTGTGCGC
TP15300	TGCAG[A/G]GGCTGGCAGCTCGATGAGGACGATCGATAGTCAGGCTGCCCAGGCTACTACTTATACA
TP15309	TGCAGAGGCTGGGAAGAAGAAGCGAACCCCACGGATTTGG[A/C]GGCCTTGACGCCCCCGTCTGCGC
TP15350	TGCAGAGGCTTTTGCGGATGCGGTCACAGGGCTTC[A/C]AATACTTTTGCAGAGAAGCTCATCGGGG
TP15394	TGCAGAGGGAGACGATTTGGAGTTTTAAAACCAGCTCGTCCTATACGTTACG[G/T]ACGCGGGCGCT
TP15397	TGCAGAGGGAGAGGAAATGGCGCCGCCGCTCGTCAGCA[A/G]CTCAGCCGTACTCCGACGACTACGG
TP15398	TGCAGAGGGAGAGG[A/G]ACTGAACCGAGCGAGAGCCGCCCCAGGCCCTCCTCAGCAGAGAAATCAC
TP15424	TGCAGAGGGAGGGATGCCGCGACCGCGATCGGATT[C/T]GGAAGGCCATCGAGGAGAGCCTGCGGAT
TP15427	TGCAGAGGGAGGGCCCACACCCACCGCCA[C/T]CTGGTGCTGGTAGGGCGTGGCAGCCCATGCGCCC
TP15493	TGCAGAGGGCATGCATATGCT[A/G]CTGCTGGCAGTGGCACTCGGAGTCCAGCACGATAATGGCACG
TP15497	TGCAGAGGGCATTCCACAAGTACCTGGAGCTGCGTGGCATTTCACC[A/C]ATGACCACAAACTTCTT
TP15511	TGCAGAGGGCCTGCACGGCTCTCGGAGACCACGG[A/G]GAGGAGAGCGCCCTCCCGACGCTCTGGGA
TP15537	TGCAGAGGGCGGCGCTGCCCGACGAGCGCATCCA[A/T]CCGCTGGACATGGAGCTGCTGGGCATCGC
TP15539	TGCAGAGGG[C/T]GGGCAAGGATCACGCGTCGATGAACTTCTTGAGCGTTGGGCTCGCCATGAACTT
TP15547	TGCAGAGGGCGTTCCTGCGACCCCGCGAAGCCGATGGCTAGGAGCGACACATCTGA[C/G]TATCTGA

Table A2 (cont.)

TP15558	TGCAGAGGGCTCGGCTCATCAA[A/G]CAATCGCCTTGGCGTCGGAGTGTCAGACGGCGTCATCAGGA
TP15570	TGCAGAGG[G/T]GAACTGGGGAAGTGAAGGACCTGGAGAGGATTTGGGCATCGAGATCCTTGCGGAT
TP15602	TGCAGAGGGGCTGGTAGGAATGGCCGATGCACAAGGGCTCAACGATGTGCTCTGCGTTGCAGT[G/T]
TP15604	TGCAGAGGGGGAAGCCCGCCACCGTGGC[G/T]CGCACCGCCATGAACGTGGGGCCGTCGAACGCGAC
TP15610	TGCAG[A/G]GGGGGATCCGCGGATGCCGCCGCTGGCGGCGGCGCCTGCTGCTGCGCCACGACGAGGG
TP15654	TGCAGAGGGGTGCACATAATGTAGGCGGCCTATTTGTTGAAACATAAC[C/T]TGTTGCGTTGCATAT
TP15681	TGCAGAGGGTGAGCACGTCGGTGGCCATCCGCGC[A/G]CAGACGGCAGCGGTGTCCTCCCCATCAGT
TP15689	TGCAGAGGGTGCAGCGGGCATGGGGCTTCGTGAGTGGTGGGCAGTACGGGATC[C/G]ACCACCCTTT
TP15695	TGCAGAGGGTGGTGGGGAAGGGCTCGTTCGCCGAGGTGC[A/G]CCGCGCCGCGCACCGCCGCACCGA
TP15700	TGCAGAGGGTTC[C/G]GCTCATCAAGCAATCGCCTAGGCGTCGGACGGCGTCATGAAGACACGAGCA
TP15714	TGCAGAGGTAAAGCAGCAATGCACGCTCCTAGGTGGAGTGGCTCCTTTGACTGTACA[A/G]GCAATG
TP15716	TGCAGAGGTAAAGGGAGATGGAGATCCT[A/C]AGAAACTTGAGCTGCATTGAGCAAAGTTTGAAGAA
TP15723	TGCAGAGGTAACAGAGGCCA[C/G]AGCCGTCGCGCGCGCGAAAGCAGAGGAGGAACGGCAATGGC
TP15724	TGCAGAGGTAACCAGTCACCACAACAACATCCACTCGAGAGCTAGCTAAGCAATCG[C/T]TCCACAG
TP15735	TGCAGAGGTACCAGATGGCGAGGTAGAGGAGGAAC[A/G]TGAGGATGCCGATGGCGAAGGAGAGGCC
TP15759	TGCAGAGGTAGGTAGGTAGCTAGCTAGCTAGGTAGATCGAGCAGTAT[A/T]ATCCAGCAAGAGGCAA
TP15765	TGCAGAGGTATAGGCACTGGCCGACAACACAGGCGCCTGACCGAG[A/C]TGCTCGATCAGTGTAAGT
TP15772	TGCAGAGGTCAACAGCATGCGAGGTGCGTGCTGTTTGCGAACATTTTAGAGA[A/G]AAGGAATGACT
TP15790	TGCAGAGGTCCAGAGCTTGACGCCGCTGGTG[A/G]CCTGCATCCTTCGAAGGCTCGGCGCTGACATC
TP15791	TGCAGAGGTCCAGCAGCTTCTTCCTG[C/G]CCTCCACCACCTCGTCGAACAGGTCGTCAATGAGCGC
TP15821	TGCAGAGGTCGTCG[A/G]TGTCGTTCCGCCGTCAGGGCTCGTCGGGGCGCATCTGGGACGACCCGCT
TP15824	TGCAGAGGTCGTGGCAGCACTTGAGCGAGCGGGGAAGCTTGCATGGG[G/T]ACGTCGAGTAGGCTGG
TP15827	TGCAGAGGTCTAGTATATCCTTGATACAGCGCTC[A/C]GCCAGGATATTGTGAAATGTGAAGGGACT
TP15837	TGCAGAGGTGAAAATGCTTGTCCTTGGTGGTGAGGGAATCTCACATTGCCTTGATGTGATTA[C/T]C
TP15838	TGCAGAGGTGAAATTTGTGATTC[C/G]AATTGAAAGCCAGTGAAATCGATGGCGGCGAGCGGAGGAG
TP15839	TGCAGAGGTGAACGCACACAAGATGTCAGTCATCAGACA[G/T]TGCCCTTAGTAGGCAGGCACTGAT
TP15843	TGCAGAGGTGACC[A/C]ACATTAATGGACAACTGAGTGAGAAAGAAGATGGTAGAGATGGGACGAGT
TP15851	TGCAGAGGTGAGAGGACCCGTACGAATACCAACCCAACAAACCAGCCGC[A/G]GGGCTGGCGAGGAG

Table A2 (cont.)

TP15887	TGCAGAG[G/T]TGGAGGTGGAGGAGGTGGCATGGCATGAGCATCATGATGAGGTGCTTGAGCACCGT
TP15892	TGCAGAGGTGGCCATCACGATCAT[C/T]GCTGTCGCGACATAGGCCAAGAAGCGCGGTCCCCAGGCT
TP15893	TGCAG[A/C]GGTGGCCGCGGCGTGAGCAGTAGTGTTGGGATGGTGCAGGTACACGTCGGTGTGCGCG
TP15894	TGCAGAGGTGGCGAACAAC[C/G]ACTCAAGGACTCGGCCACTACGCAATCGCCAGATCGCCGATCCT
TP15903	TGCAGAGGTGGTAAAGCAAAATCCCCATGGGTGCTGCTACTAATGATC[A/G]AGAAGCTGAAAGTAG
TP15916	TGCAGAGGTGTACCACATTATCCACACAATGACGAGGCCACCGCCCACATGA[C/T]CCATCGATGCA
TP15917	TGCAGAGGTGTAGATATATATTGCAGATTGAATTGA[A/G]GGCGAGGTGTGTGTTCGGATGATACTC
TP15929	TGCAGAGGTTAAGGAGCCA[A/C]AGCATCCATCCTGAATTGGGGAAGCAAGTACTAGTGCTATAGTG
TP16017	TGCAGAGTA[A/G]AAATCATCGTATTGCATTACAAACTAAATTGCTGGGTTGAAACCAATATTTTCG
TP16023	TGCAGAGTAAACAGAGATCTGTATCTCGTGCATT[A/G]TTTGCCGCAAGGACACACACAGCATCAGA
TP16027	TGCAGAGTAAACAGTTTTACAGTAACCGTATGGGTTGATGCCGTTCATGCAAATTGCA[G/T]CTGCC
TP16038	TGCAGAGTAACCACTAACCACCGTTCCACCAAAATCCACTCGTAGTCGCAT[A/G]TCTTGAGTTTGT
TP16041	TGCAGAGTAACTGGCCACGTGTCGCCGCATGGTGATCGTTGCGCGCTT[C/G]TTTATCAGTGTCACA
TP16045	TGCAGAGTAAGGGGGAGCTTGAACACGCGGCGCCCGTTCCCGA[A/C]GGCGGCCGAAGGGTTGTACA
TP16053	TGCAGAGTAATCCAAGA[C/T]CTGGAGAACCAGCTCATGGACACCGCCGTCGAGCTTGAGGTGCTGC
TP16077	TGCAGAGTACCTGAACCGTTCCACTTCCACCAAGATGTGACGGTTCCAGTTCA[C/T]GGGCCCCTCC
TP16098	TGCAGAGTACTCATCGGAGGACTCGCTGGAGATGCACGAACTCGTCGTCGACGTCG[C/G]AACGCCG
TP16138	TGCAGAGTAGC[A/G]TCCTCGCGGCGTAGTCGCAGCAGAGCAGATCGATCGGCAAAGAAGCTTTGTA
TP16172	TGCAGAGTAGTAGATAAACGAGTTTGAGCTGATAGTCGTTTTTCACTCCTGACGCTTTTTTT[G/T]G
TP16176	TGCAGAGTAGTAGGAGTACAC[A/T]TTCACCGCGCTCTCCGTGTTTTTTCTTGCTCCAACTGCCAGT
TP16204	TGCAGAGTATCTATGGGTTTATTGTAGTGGATTACA[A/G]CTTCCAAAGTCTGATGTTATATAGGAG
TP16216	TGCAGAGTATGGGTACATGAT[A/G]AAGATCACGGAGAAGAGCGACGTGTACAGCTATGGTGTGGTG
TP16218	TGCAGAGTATGTTCGGGTTGCCCTCCTATGCCGCCAC[C/T]AGTGAAGTTGTTCCGTGGTAGGTCCA
TP16222	TGCAGAGTATTCGATTTTTTATTAATTTCGCAATTCTTGAGTACGCCTGTGGATACGTATCT[A/G]T
TP16237	TGCAGAGTCAAGGTAGGGCAAGCGCCCTACCTTGCCCTACTGGGTCCTC[C/T]GCCACTGTGTGTTC
TP16259	TGCAGAGTCAGGAGACGCACACACAAGCAGTGT[C/G]AGTTTGAGCCGAAATTAGGAGCAGAACAGA
TP16269	TGCAGAGTCATGGGGGCACCATCTCAGACAAAGGATGGGCCAGCCCCCACAAGAGGAAACCT[G/T]G
TP16284	TGCAGAGTCCAGCGCAAGCTCGGCCAGGCG[A/G]CCCCACCACGTGGTGGCGTGCGCCATGAGGGAG

Table A2 (cont.)

TP16297	TGCAGAGTCCCGCGGTTACCCAATTCGACCCAGTAAGGCCCAGGTTCGG[C/T]GCTATACAGGCCCG
TP16320	TGCAGAGTCCTGGCCTGTTTGACATCAGTATAACTGCTGATGAAGTGTCACTGTGTCAGAC[C/T]TG
TP16334	TGCAGAGTCGCGCGACGACGGGCG[A/C]GAAAGAGGCCGCGTGCGGCCGTGGGAGTGGGACTGTGAA
TP16335	TGCAGAGTCGCTGGTAACGCCGTGCTTGAATGCCAGCAGGGCGT[C/T]CCTCTCGTGGGGTATGCAG
TP16360	TGCAGAGTCGTTTGGCAGTGGTTCTTCGGCTGC[A/C]TCAAAACAATCTCGGAGCTCGATGCCTAGA
TP16368	TGCAGAGTCTCCTCCGATGGGATTCCCAGCGACGCAAAACGTTT[C/T]TGCGGAATCGTGTTCTGTC
TP16369	TGCAGAGTCTCGTTGGCTCCCTTCCTGGGTGTCCCCCACTCTTGAGGACATCGCC[A/G]AGGATTGT
TP16393	TGCAGAGTCTGGGTTCGGTTTCATT[C/G]TAGCCTGCCACGTCTGGGCTCAGGTCCCCAAGAGTCGA
TP16422	TGCAGAGTG[A/G]AGAGACGCTCTGCTCTGCTCGCGGTTTATCGACGCGAGTAAGATGCAGGAGGTG
TP16423	TGCAGAGTGAAGAGCCTGTCCTCGAACTGCAC[T/C]TCCTTGGTGAGGAAATCCGCGCCAATCGTAG
TP16429	TGCAGAGTGAATTATACGCATTCACGCACAGCTTAAACTTCTCCTCAG[C/T]CATGGCCTGCGCACG
TP16432	TGCAGAGTGACAGAACAGGGTGCACGGCTGCACGCACGCACGTAGCGCGAAGCTGCGAAGTGC[C/G]
TP16433	TGCAGAGTGACAGCACGCACGTA[A/G]CCGCGAAGGGTGTGCAAAATATGCAAACGCGCACTCCCGA
TP16434	TGCAGAGTGACCAATCCAACGAAAA[C/T]GAAAGAACTGAATAAGGAAACACTAATCCACAACGAGA
TP16445	TGCAGAGTGACTTACTCCAATAAACAACTATGATGACCTTCCGATCCGAGTCAACATA[A/G]TAGTG
TP16460	TGCAGAGTGATCGGGACGTTGTTTGAGTAGCTAATAATGGCACGGCG[A/G]CAGTGTAGCAGCAGCG
TP16466	TGCAGAGTGATGGGAGGAGCG[A/C]CGACTAGAGGAGTGAAATATGAGTGTGCTTTATTAGCTCTGA
TP16477	TGCAGAGTGCAAATAGAGAGCTTAACCTGAAGGAATCGCCCTGTTCGCTTGGCTTATAAGCC[A/G]T
TP16481	TGCAGAGTGCAAGGTTGGATAGCAGCGTACGCGTACATG[A/G]TGCTGCTGAAACAGCGGCTTCTAA
TP16484	TGCAGAGTG[C/T]ACAGTGCATCGGCTCAAACACGAGGAATTCAGACAAGCAAAAGATAGCCAAGAA
TP16487	TGCAGAGTGCACGAGGCTTGCCCTAAAATTTTGTGTCCACC[G/T]AGCACAGCAGCTCGTCGATGGT
TP16502	TGCAGAGTGCAGACATGTACTGCAA[C/T]TGTACTTGCCACATGTCCTGACGAGTGACGACTTAAGA
TP16508	TGCAGAGTGCAGACGCGCCCA[C/T]TCTCCCCACTACTCCCTGTTGCATTTCTCTCCTATGGCCGCA
TP16519	TGCAGAGTGCAGACTTCGCCCACCAAATC[G/T]CATGTCCTGTTGGTTACCGCAACAGTGCATGAGT
TP16542	TGCAGAGTGCAGAGGCAGGCAGGTGGTACCACACGGCCACGCGTCGCAGAGGATCGGAGGG[C/G]GG
TP16545	TGCAGAGTGCAGAGTCCAAGCAAGCAAGTCGATCCATACGCGCGCGCACGGGGGG[G/T]CGTGACTA
TP16579	TGCAGAGTGCATCGCAAACACGAGGGCGAGA[A/C]GAAGACGAATTCAGACATTCAGTGGACATGCA
TP16605	TGCAGAGTGCCTGCTGTTGAACTCAGCCCTGGACTCTATGAGGTCCTTCTCATGGTA[C/T]GGTGTG

Table A2 (cont.)

TP16623	TGCAGAGTGCTCATTGAACCCTCTCGTGAGAGTCAAATAGCTTGTTCAGAGGGTGACCGTGCT[G/T]
TP16639	TGCAGAGTGCTTGGGTTATCAAAGCGTTTG[C/G]CGCCGATGTTCGTTCCAAGGGTTCGTCGTGCTG
TP16644	TGCAGAGTGGAACCGCCAGAAGGAAGCTGAACTTAATCAAATGTTATTGA[A/T]AATGATGGAAGTC
TP16656	TGCAGAGTGGAGATTCTCGGTGAAGGCTCG[C/G]ATGGCGGCGTTGGGGAGTACCTTGTTGAGGTCG
TP16659	TGCAGAGTGGAGGCACGCGAGGG[C/T]GACTGGGCGAGGTCGGCTCGGTCAATGCAGCCTCGCAGCG
TP16660	TGCAGAGT[G/T]GAGTGCGATGTCAGAACTCAGAACGCCTGCAAGAGATGTACGTGGCTGGGATGAG
TP16664	TGCAGAGTGGATATGAATGACCATGACAGTATCTGGTGCTGCTCGC[C/T]ACCACCGCCAGTCGCTG
TP16677	TGCAGAGTGGCCCCGC[A/C]ACCCGTCCCAGGCTGGACACGACGGCGGCGAGCAAGGTGAACACCAG
TP16708	TGCAGAGTGGTGACACTGGAA[C/G]GAAGGAAGCTGCGAGGAAACTGGGGTGGGGAGAGTGACGGCA
TP16711	TGCAGAGTGGTGGGCAAATTCTGTGGAGAGAGTCTCTGGACAGGACAAGGGCTAAATTC[A/G]ATTG
TP16716	TGCAGAGTGGTGTATGAATGTTCCAGCCATCCAGGA[C/G]GGCTACCTTTGTTCTTGCAGAGTATGA
TP16722	TGCAGAGTGTAAGGCATGTATGTTCCGAGGATCTTGTCCCACA[C/T]GACAAAGAAGGGCTGAGAGA
TP16742	TGCAGAGTGTCAGTTTCGATAAGAAGGAGAGTTTTTCAGAGGTGATGCAT[G/T]CAGTCAGTGGTTC
TP16747	TGCAG[A/C]GTGTCGGCGGCGATGAGCCGCTCGTTCATGTGGTAGGGGTCGTTGGTGGAGACCATGT
TP16753	TGCAGAGTGTGCAGTTGCAGGGCTTCAGGGCACTTGTGGTCCCTGGACCACTTTTTGCCAC[A/C]GC
TP16760	TGCAGAGTGTGGGTCAATGCAAATGCCATCATCAGTTCAAGGGGTTTTTTTCCTAACTG[A/G]TGC
TP16779	TGCAGAGTTAACATATATGAAATTAGTTGAATTTTACTGTT[C/T]GTACTCACAGTCACAACACATT
TP16824	TGCAGAGTTCAACTCCTACTAGAGCCATTCAGTTCAATGGGTTGGTGGAGCGC[G/T]GCCCTGTGCG
TP16882	TGCAGAGTTCTAGTTCGAGGGGGTGGGTCACCAGAAGGGCGGCAGAGGCAGCAG[G/T]GGGCAGTGG
TP16883	TGCAGAGTTCTAGTTCTAGGGGGTGGGTGGGTCAC[A/C]AGAAGGGCGGCAGAGGCAGCAGTGGAAG
TP16893	TGCAGAGTTCTTCACAATCAGAGTCGACGTCCAGGGGAAGCATGGATCATGCTTCGAGCCA[A/C]GA
TP16898	TGCAGAGTTCTTGTCCATATATAACCTGTTCAGTGTCAAC[A/G]TTTGTCAATTTTAGGGGAACTTT
TP16910	TGCAGAGTTGAGAGGAGCA[C/T]GCGTCGTATGGGAAAAACTGAATCGGCGCACGCGTCGGATGGGG
TP16918	TGCAGAGTTGCACGACTGTCATGGGCATCATGATGCTGGGTTCT[C/T]TGTTTGTGTCGCGGTTCGT
TP16922	TGCAGAGTTGCAGGCTGTTACTCTGGCACGCAGTCTCATTTGCAGGCACAAGGCTGGTAT[A/G]TAT
TP16946	TGCAGAGTTGCTGAGCAATCTCCCTGAGCAGAACAACCTG[C/T]GCCTTCTCATCTCCCATGGACAT
TP16947	TGCAGAGTTGCTGAGCGATCTCCCTGAGCAGAACAACCTGCGCCTTCTCATCTCCCATGGA[C/T]AA
TP16960	TGCAGAGTTGGTTTCATCTCAT[A/G]TATACAACAATGGTTGAAACATTCAGAAGACTTTACAGTGA

Table A2 (cont.)

TP16984	TGCAGAGTTTAGCTTTTGCAAAGATAG[C/G]GTGGGGAGCAGAATTCTTGTGCGCGTGAACTTGCAC
TP16986	TGCAGAGTTTATATATCTTTG[C/T]CTTGTAACTATTTCACCAGGAGCTGCACAACAAATACCAGCG
TP16994	TGCAGAGTTTCAAAAAGCTGCTCCCAATCATCTGCGGCAGAGGCCAAACTTGGCACGC[A/G]GCAGT
TP17015	TGCAGAGTTTCTTTACATCACTTCTATATCATTTCTTTATTTTGTAGTAGTATGTAAAATGG[A/T]G
TP17017	TGCAGAGTTTGACAGCTC[C/G]AAGTCAAGGGTGTTCGCGCTGGAATCCTGTGTGCCTGGAAGACCG
TP17035	TGCAGAGTTTGTTGGCGTGCAGAG[C/T]TTGGCACCAGGGGTGGGGAGGGAAGCCGTGAGGTTCATC
TP17061	TGCAGATAAAAAACAAAAAATAATGCAGAACAGAGCACGCTACGGCAATATTTCAAGCATGC[A/G]C
TP17064	TGCAGAT[A/C]AAAAAGCAGCGCAGCAGACAATCTGAGCCTTTCTGTGATTAGTTTGCTTGCTTGAT
TP17069	TGCAGATAAAAATGGGGAGCTAATGACAGTGGTCTCA[C/T]GTAGGCTCCAACCACCAGAGCACATG
TP17077	TGCAGATAAAACTGCGGTCACGTCAGGTCATCATTTG[C/G]CCGTGGAAAAGTCCTGGCGAATGGCG
TP17098	TGCAGATA[A/C]ACATTGCTCCATCCATCCTTGAATTCTATTTATTCTACACTCTATCTTTAAAGAT
TP17102	TGCAGATAAACGA[A/G]GTGTATATGTACGGTACGTGTGTGTCTACGGACGAGCCACGCGGTCGCTG
TP17103	TGCAGAT[A/G]AACGACAACCGAACGTTTTGAGAAAACCAGAGTATAATTATGTCTAGAGCCAGATT
TP17119	TGCAGATAAAGCCATCGTCGAGGGTGGCACTAAGCTGAAGCGGTTCGTGCTGGCAAACCTGGC[C/G]
TP17131	TGCAGATAAATATAGA[C/T]GACACCATGTATAGTGGCCGCCTGTTTGGTGGGCTCTCTTTCTTAAA
TP17167	TGCAGATAACCTTATTCGACATTCCAGCCAGCCAAAGGTTTTCCATGATTCCATCTCTCTCAA[C/T]
TP17183	TGCAGATAACTTCTCCAATGATC[A/G]ACTGCCATTATGATCGCCATGTATTCCTTTTCATATGCCG
TP17189	TGCAGATAAGAAGCAGACTGAGGCTGCTGGTGTGGTACATAATGGGCGAC[C/T]TGAGGCTGCTGCT
TP17190	TGCAGATA[A/G]GAAGCGAATCGCTTGCTCTCTACTGCTGCCGCCCGCCGCTTGCTTCGGCTTTGGA
TP17203	TGCAGATAAGCACAGCCAAGCAAGCACG[A/G]ATAGATCGAATGAACACGTCGCTTTTGTTTTTAAA
TP17213	TGCAGATAAGCCGCACCCAGTATATATGTGTGAGTGTGC[A/G]GCTCTGGAAGTTGCCATGGAAATG
TP17219	TGCAGATAAGGAGAACGCTGCTCCTTCTACTTGGGACGCCACCGCCTCGGCTGCTGCTG[C/T]GGCG
TP17220	TGCAGATAAGGAGAACGCTGCTCCTT[C/T]TGCGGCGTCTCGGCGGCACGGCTACGCTGTCAAGAGC
TP17241	TGCAGATAAGTTAAACCAAGTAACCTCGTTTCTGCTGGTCTGGTTT[C/G]GTTTGGGTGCCGTTTAG
TP17261	TGCAGATAATATTCTGCATATGATACATATGAAAACATAAAGAAAAAAACAAATA[A/C]GAGAAAGG
TP17262	TGCAGATAATATTTTTCTTCTCTTCATGCATGTTAAATTGG[A/G]AACGGAAAATCAGCGTACGTAG
TP17307	TGCAGATACAAATCCCGTTCGGTCGTTGTCGCTGTCCGCGCCGCGACGTCG[A/C]CCAGCTGACGGT
TP17317	TGCAGATACAAGAATGGTCTTGTGCAAGGTCAACGGCTTCTTC[C/T]GTGAGTACATCATATCAAGG

Table A2 (cont.)

TP17320	TGCAGATACAAGACATACCTTGGTCTGGAACCCAAGCGTGAACCCGA[A/G]GAGGATGGCGAGGGGC
TP17335	TGCAGATACACCATGTATATTGCCTCGGTCAGCAATAAAACGG[C/T]CGTAACGACGGCGACGTGCT
TP17357	TGCAG[A/G]TACAGCAAAAACCAGCCGAAAACACATCACAACCCCGACACATGGGCAACCACACACA
TP17387	TGCAGATACATTTGCTTCTGAAAAGAAAATTCTGAAGGGTGGAATGGATGGAGGTGGA[C/T]ACTGA
TP17388	TGCAGATACATTTGTCTTCTCAGGCAGGCATGGCGTGCAGCCTGGACACGCTGTGCGGGCA[G/T]GC
TP17397	TGCAGATACCA[C/T]CAATCTCCTTCCTGGCCCAAGGGGGCAGATTTTCGGCCACCATTGCCTAGAT
TP17398	TGCAGATACCACCTGCAAATATATTGTTGGGGGAATTCCCCATCCG[A/T]CGCCCAAAAATGGTCCT
TP17402	TGCAG[A/C]TACCACTTTATACTTGGTGCGTACGGAGTACACGCGCCGAGCTACGGTGTACGGGCAT
TP17421	TGCAGATACCGCAGCGTGCA[C/T]GCTGAGCTCAGTGCTCACGGTCCGCACCCTGCTCGCGAAGCAA
TP17423	TGCAGAT[A/C]CCGCTCTATGTCTTGATGTTTTGGACTCTATGTGTTTCCTCTATGCTCATAGGCTC
TP17426	TGCAGATACCGTT[G/T]GTATAAAGGTCTGCGCAGCATTTGCAAGCATCCTGTGCTCTTCTCAGCTG
TP17442	TGCAGATACGAATGGAT[A/G]GCAAGTGGCTAAGCGAAAACGCCCTTGATGGTGCTTTTATACTAAA
TP17446	TGCAGATACGACGACCAACGGCTCACGG[C/G]GTTCACCTCGTCGTTGTACATCGCAGCGATGCTCT
TP17483	TGCAGATACTACGTGATCTTGGTGTGAGGACCATGCGGCTG[A/G]TGACTAACAACCCTGCGAAGTA
TP17504	TGCAGATACTGCGCGTGCAGTCGTCGTCG[C/T]CGCCGCCGCCATCGCCGTCGCGCGACGAGGGGCC
TP17530	TGCAGATACTTTTT[G/T]ATATGGATTAAGGAAACTTACCTAGCCTTCTATCACCATCGTGGTTTGC
TP17557	TGCAGATAGACATGTATTTGGAACCACCCATCTCCTTTCAAGCTCTTCAAATACCG[A/T]GCAGCCA
TP17574	TGCAGATAGAGGCGAATCTATAAAGCTACGAGAA[C/T]GCCGCGCGAGACATGGAATCGTCGAGTCC
TP17582	TGCAGATAGAGTGACGTCGCCGACGGTGGACGGAGGCCTGCGGCTGTTC[C/G]TGCGTGCACCATGC
TP17583	TGCAGATAGATACTCCGTGCAGACTGCTCTGGCGCGTCCCCTTTCCTTGCTCGATCGGAAGA[A/G]G
TP17587	TGCAGATAGAT[A/C]GTTGCTTGCGCCAATGCTGCTAGCTACCATCGAGGAAGCCGACTGTCGAGGT
TP17593	TGCAGATAGATCCGTCCATCCATCGCCATCGCCGTCGTGCGCG[C/T]ATGGTCATGTCAGTGACAGT
TP17598	TGCAGATAGATGAAGTGCGGAGCCCGAGGAAGTGCATGAGGGAGGCGG[C/T]GATGGACCAGGGACG
TP17626	TGCAGATAGCACTTCCTCTGCTTCGAGCAGGTGCGCCAAGGTTATCCTTATCTGTAATG[G/T]AAAC
TP17629	TGCAGATAGCAGATTAGTACAAGTACTAGTACTACTCAACGGAAGGACGCA[A/G]GAGATGAGATGA
TP17631	TGCAGAT[A/C]GCAGCAGGCGCAGCCACGACTGCTGGCGCTGCAATTCTACGGAAGCAACAAAGCAA
TP17634	TGCAGATAGCAGCGAATAAATCCAT[C/G]GCCACTATAAAAGGAGGCGTTGATGGATCAGCCTTCAC
TP17652	TGCAGATAGCCTTGCAGTTGCAGCTTGCGGCAAAAGGGCGCAACTGCGCAAGTCAGCTAGC[A/G]TG

Table A2 (cont.)

TP17656	TGCAG[A/G]TAGCGGTACCCCACTGTCCGAGCTGCCAGCAGGGACTCTTGGCTACCTTGATCCTGAG
TP17657	TGCAGATAGCGGTAGCTGTTTTTCAGTCCTTGTGGGTGGGATTGGGAAGGAGCATCTT[C/T]ACACA
TP17675	TGCAGATAGCTGCTCAGTCACAGATTTGCCGCCACGGCTGTGAATGGCTGGTGGTAGGGCTTT[A/T]
TP17701	TGCAGATAGGCCATTACACGGTAATATGTGATCCAAGAAGACG[C/T]CGCGCTAGCAGGAGGCCAAC
TP17708	TGCAGATAGGCGTGATAAAGGCAGTGAGGAACTCTGTGGCTGCTGATGGGGAGGTTGC[C/T]GCGTT
TP17716	TGCAGATAGGGCAAGTGGTCTTGCCCTGGCGGAGCCACTCGGCGATGCACCC[C/T]CTGTGGAACGC
TP17723	TGCAGATAGGGTTTACTGAAAATCGATGGCGTAAATCGAC[C/T]TGGCGTTGCTGATTACTACGACG
TP17726	TGCAGATAGGTACCCATGGATCAGACAGGTATATGTCTGGATATTTGG[C/T]TTAACACCTTTATCA
TP17735	TGCAGATAGGTCGAGTGTGCCAAGGCTGGCAAGTGTATAAACGCCGAC[A/G]GTTTGGTGTAACTAG
TP17736	TGCAGATAGGTCGTCACACGCGGACATGCATG[G/C]CATGGTCGGCGGCGTGCTCCACTGCGTAGTA
TP17737	TGCAG[A/G]TAGGTGAGGAGTGCCGTGGTGGTGGCGCTGTAGGTGGCGTTGGCGAGGCTCTGGTACA
TP17745	TGCAGATAGTACTAGTTATTACTGGCTTGTTATCTCTATGATAGTTTTATCTTAGA[C/T]AGTTAAA
TP17767	TGCAGATAGTGAGGCTAAAACGTAAAAATTGTC[A/G]ATGGAACGTTACTCTTTTTTCATGTGACTG
TP17794	TGCAGATAGTTTGATTCCTCAAAAAAT[A/T]AAAATCGCAATGTTCTGTGAAGGAGAGAGTATTAAT
TP17803	TGCAGATATAAGATCATCAACATAAATTTAGTAGATTATGTTATGTACTAACTAGTTTAAAG[A/G]T
TP17821	TGCAGATATAGATAGATATACTTGTTAATTGCTTG[C/T]CTCTATCTTGATTTCACTTCTCGAAGAT
TP17851	TGCAGATATATATACCTAGGCGATCAAAGATGTGGATGTAGGACGACTTGAAGGAGAAG[A/G]TTGT
TP17857	TGCAGATATATCAAGGAGGGCAGCACTGTGAGTGTGATGGGTGTTGT[C/T]CAAAGGAATGAGAACG
TP17886	TGCAGATATCACGAAGAATGAGGCTGACAGCTGATTTCTGTG[C/T]ATGTAGAGTGTTCCACAGATT
TP17900	TGCAGAT[A/C]TCCAAGACAATCCAGCGGCTGTTCTTCTTCGACGGCCCCGACCTCCCGCCGTTCCC
TP17923	TGCAGATATCGATCGTCCAATGGCT[C/T]TAATCAGCTTCCTCGCTCCTCCTCTATGTCATCATCAT
TP17972	TGCAGATATGAGCATATGTATATGGTTAGTCAC[A/T]AGAAACTGAAGTATACCTTTGCTCCAAGAT
TP17995	TGCAGATATGCCTAAGAAGAACATTTACTGTTTAACTGGGATTATATATTGGATTATT[C/G]TTTAT
TP18080	TGCAGATATTGACGATGTTAATGAATACTGACC[A/G]TGCAAATCTAGGCTCTGAGGGGCATAACAC
TP18081	TGCAGATATTGCGCGATCTTGGTGTCAGGACCATGCGGTTGATGACTAACAACCCT[A/G]CGAAGTA
TP18107	TGCAGATATTTCTGCGATCTTGTCTCGAGATTGCGATTGATGGCGAGGTGCAA[C/T]AAGAGAACCT
TP18112	TGCAGATATTTGGAAC[C/T]CTCAAATGCAGAGATGTTTGGGCTGTGGCGGATGGGGAGTTGGTCTT
TP18146	TGCAGATCAAA[C/G]CATGTAGCATGAGCACTACAAGTAATTTCCTTATACAAGTCCCAACTCCCTC

Table A2 (cont.)

TP18154	TGCAGATCAAATCCAGATCATGTTT[A/C]TGAAGAAACTCGGCAACTATGTCAGCTCCAAAGGTGTA
TP18171	TGCAGATCAACGGCTAGCATCTTGGTCACGTTGTCGTAGCTGATCATGGCCGCCT[C/T]GGTGAAGG
TP18172	TGCAGATCAACGTGTGTGGTCTTGTCTTGGGTCCAGTACGTCCAGACGACAAC[A/G]GACGCTTGTC
TP18187	TGCAGATCAAGAACGATGGGGATCAAATTTTTGATGTTCTGGACAGTAG[C/T]AGCCTGGCTGTGCA
TP18194	TGCAGATCAAGAGCAAGA[G/T]CAAGATGGCAAGAGGTGCTCGGCCATCTGCGCGGCTCCTGCTCCT
TP18201	TGCAGATCAAGATCCTCGAGC[A/G]ACTCCAAGCGGACGGCGAGCGGCCCGTCCGTGCTCCAGCTGT
TP18208	TGCAGATCAAGCTCGGGGTGCCGA[A/G]GTCGACGCAGCACTTGCTGGATGCTGAGAGAGTCAAGGC
TP18218	TGCAGATC[A/G]AGGTACCGAGTAGCAGCTTCCTGCGCAGGGGCCAGGGGCTGTGGCGACTGTGTGG
TP18220	TGCAGATCAAGTACAACGCCATAGGGGTCTACCTCCAC[C/T]ACACCGACGGCGCGCTGCTGTCCCA
TP18221	TGCAGATCAAGTACTCCGCCGCGCGGCAAATGAACTGAATCCGCGACG[A/T]GCTGGAGTGCCCGTA
TP18225	TGCAGATCAAGTTCTCCGACGACTTCCTCCTCGCGGGCGGCGACGGCAAGGGCGTCG[A/T]CGACGA
TP18235	TGCAGATCAATGGAAGGACTACTCTGGACACATC[C/T]AGTTAATTTACACTAACAAATATATAATA
TP18236	TGCAGATCAATGGACAAAGCGCGTTAGGCCAACAGCACAGCACATGCAATGC[A/G]TGACGATACAC
TP18241	TGCAGATCAATGGCTTGGTGGGCCTATGAGGGGG[C/T]CAGCTCCCAAGAAGGCCTCGGCGGTCAAG
TP18261	TGCAGATCACACGCCAAAACACCGCAGGGGGTGCACTGCTCGGGAGGCA[C/T]ACGTATACTGCGAG
TP18276	TGCAGATCACAGTTCTCCTAGCTCTA[G/T]CTGTTTGCGTCCCCTTTGGACGGAACGGCAGCCAAAA
TP18284	TGCAGATCACC[A/G]ACGACCTTGTCCCGCTGTGCGTGCGCACGGCAGAGCTGCCGTCCTCGTCCGT
TP18298	TGCAGATCACC[C/G]CCGACACGGGCAACAGCGCCACGAGCTTCCTAGTCAACCAGTCAGGTCACGT
TP18303	TGCAGATCACCGACGA[C/G]TTCTCCGACAAGAGCCTGGAGCTCCGCGCCGAGTCCTTCCTCCGCGA
TP18309	TGCAGATCACCGTCCAGTGACCAGGGACCCACGGGCTCGCGATGGCGATC[C/T]TATCCACGCCACG
TP18315	TGCAGATCACG[A/C]AATGGAAACAGCACCTACTGCTGGTACCACAACCTGAGAAAAATACAGCTCA
TP18320	TGCAGATCACGATCACATGCCAAGATTATCCGAGC[A/G]CATTGCGCAAGCAACCGTTCGATGAATG
TP18328	TGCAGATCACGCCGCTCGACGAGGAAGACGATGACGGTGGCCCCGACGCCGACGAC[A/G]CTGGTGG
TP18364	TGCAG[A/T]TCACTCTAACTCACTGCGAGGCTGCTATACAAACCGACGTGGAGGCCGAGTGCTTATG
TP18394	TGCAGATCAGATCAACCGAGACCGTACCAACAAGAAGACCACATGGCTCGCCCTG[A/C]CAAGCAGC
TP18402	TGCAGATCAGATGAACATTGGACGGAACTGTTTATTCA[C/T]CGCTTCGATTTAATACTATATATGT
TP18412	TGCAGATCAGCAGATGGATGGGATGCCCGCAG[T/C]AGTGCAGGTGTTGCAGTCAGAGGATCGGAGG
TP18444	TGCAGATCAGCTGGCCCAACAAA[C/T]CTCGCGTCGGCCCCCTTCCGTTGCTACTGCCGTCTACCTC

Table A2 (cont.)

TP18456	TGCAGATCAGGCGGTGGTGTAACGGA[A/T]CCATCAAAGTCAGTGGTTCAAGACGGAAAGGGTGGTA
TP18457	TGCAGATCAGGCTCGCGAGAGTTCTGCTCC[A/T]CGCGTGAGCTTCGGCTTCGCACGGCCCACAGGA
TP18468	TGCAGATCAGGTGATGAATG[A/C]GAGTGCCCAGCCCAGCGGCCTGTGTACACTGAACATGCATGCA
TP18484	TGCAGATCAGTGAGGCAGGAGCACCAGAACAT[G/A]CACATCTCTCTAAGAGTATATACAAGAGCCT
TP18517	TGCAGATCATATGCGCCGCCGCCAACGATCTTTTTTACCTCGG[A/C]AAGCTGCTTGTCGTTCATGA
TP18523	TGCAGATCATCACGCTGAGCGCGTCGGCGAACAAGCT[A/G]TCGAAGATCACGGAGCAAGCGGAGGA
TP18525	TGCAGATCATCAGTAGCAATGGAAGGTAAGAAGAAGACCTCGTCGTCATGGACGACCTTAAC[A/C]G
TP18526	TGCAGATCATCAGTAGCGATGGACGGGAAGAAGAAGATCAAGTCATCATCATGGG[A/C]GACGGTAA
TP18540	TGCAGATCATCGTGCACGGCCGCTCCACACCATTGGCGTCGGCGCACTCGGCCGCGATGTC[A/G]AA
TP18541	TGCAG[A/T]TCATCGTTCGGCTCGGATGAGCTCGCTTGAGAGTGGACGGTGTCTACGACGATTCTAC
TP18554	TGCAGATCATGATG[C/T]CCCTGTCACTCCAGATGAGGTGTCTCATGCTTTTAATATATTTCCTCTT
TP18584	TGCAGATCATTAACTGGATGCAGAATCGCTTCAATGG[C/T]AAACATGAGAAGAGGCGACCCGAGGC
TP18588	TGCAGATCATTCGTGTACGTCATCTCAGCTCGATCGGCATATATACACAGTCACT[A/C]GCCATCGC
TP18590	TGCAGATCATTGCAAATTGGCAGAACACACAGCTGATCAGTGTTGCTG[A/C]ACTACACTCGCAAGC
TP18592	TGCAGATCATTGGCAGCATCGGCGCCGTGTCGTCGGGACTGGA[C/T]CTCGGCAAGGAGGGCCCGCT
TP18595	TGCAGATCATTTCCCAAGTGCTTCTGAATTGTTCAGAGGT[A/G]GTGATCAAGGATTGGAGATGAAG
TP18607	TGCAGATCCAAATGGT[A/C]CTCTGTCACAGCAGTACGTGGGGGCATCGATCATGTCTGCCTGTGAA
TP18618	TGCAGATCCAACGGCTGGGCTGCCGCATGACTCGGTTCTCCCTTCCCCTACGGCCCTA[C/T]CGATA
TP18624	TGCAGATCCAAGGACGGTCAATTCATTGGTTCCTGTTCACTTCATCCGCTGCGGCAGAGAGC[C/T]C
TP18658	TGCAGATCCACCACCGCTCCCTCTTCTATGCCCCTGTTGTCGC[C/T]ATAGATCCAGGCCAGCCCCT
TP18667	TGCAGATCCACCTCCCACCAGGCTCCGACGTC[A/C]GATCGACCAAATCTGGATGGTGCGTGGAAGA
TP18674	TGCAGATCCACGGACGCTGAAGCCAGAGTTAGAAGCTGAAACCAGAGTTAGAAGCCGAAGC[A/G]GG
TP18683	TGCAGATCCACTGCAAGGACGTGGTGCTGGACGAGCACGACGTGGCCAA[A/G]TCCATCATCGAGTT
TP18727	TGCAGATCCAGTTGCCAAAACGCTCTACGGGCGCTGGCAACACCGTGCATCGATCGGCAC[A/G]GTC
TP18734	TGCAGATCCATCATCCATAGTTCCATTTCCAAACTGACAGGATACTAGCTAGTCGAACA[A/G]ACAA
TP18751	TGCAGATC[C/G]ATGATCTGTACGTGATACACACGTACGATTGAAAGTATGCATTCCCATGACCAGC
TP18760	TGCAGATCCATGGCCGACGAG[A/G]AACACCAGCAGCACACCAGCCACCACCACGGCCACCATTTCC
TP18771	TGCAGATCCCAACCATCGGCATCGGGGCTGGACCCTTGTGCAGTGGCCAGGTGAGGTCAAC[C/G]TA

Table A2 (cont.)

TP18783	TGCAG[A/G]TCCCAGAAAGAATCGCCGATGCCCCCTAAAAACAGCATTCTAATCCATATACCAAAAC
TP18785	TGCAGATCCCAGCATGCAGGAAAATGCTGTAACAGTACTCCTGAATTTGTCGTTAGATGA[C/T]AAC
TP18795	TGCAGATCCCCCTGA[C/T]CCTGCTGCTGCTCATACAGCACACAGATCTGGGGATGCATCGGCGGCC
TP18799	TGCAGATCCCCGTCGCCG[C/T]CTACCTCCTCTGCAAGAGCAAGCGGATGACGCCCAGCTCCCTCAT
TP18802	TGCAGATCCCCTGCCTGCGCGGGCACGGCTCACTGCTGCTGTGGAGGCTGTTGCGC[A/G]CGGCGGT
TP18803	TGCAGATCCCCTGCCT[G/T]CGCGGGCACGGCTCACTGCTGCTTTGGAGACTGTTGCGCGCGGCGGT
TP18813	TGCAGATCCCGCGTCTCCCTCCGCGATTCGAGGTCAGTTTCCTCCGATTGGTGTTGCGC[A/G]TGGC
TP18820	TGCAGATCCCGTGCGCCGTCGTCCGCG[A/G]TCGCTCGATGCCGCCCGTGAAGCTCGCGTGCCGCGG
TP18821	TGCAGATCCCGTTGCTGCTCAGTTCTTGTTCCGCGCACGCCATC[A/G]TCGTCGTCGACCCTGCGGC
TP18849	TGCAGATCCGAATGCGATCTCGCCAC[A/G]CCGTGCCCGTGCACCTCGCTCCTGTGTCAGGGGCCGT
TP18906	TGCAGATCCGCCGCAGCGCGCAGGACGCTAGTCA[A/C]AGTGTCGGCAGGGCAGATTGAGATTGCTA
TP18930	TGCAGATCCGTCGCCACTCGGGG[C/T]TTGGGATACAAGCAACTCTCGGTAAGCAAAGCAATCCCTA
TP18932	TGCAGATCCGTCTTGGCACGCA[C/G]CTCTGTGTCCTCGCTCTTCGCACGTACGCACGGTGTAACAA
TP18940	TGCAGATCCGTTGTCAGTATATCGTTATATTGTTCAAGAGCCAAACCTTCTTTGG[C/G]CAGGCCTC
TP18941	TGCAGATCCGTTGTCAGTGTAT[C/T]GTTATATTGTTCATGAGCCAAACCTTCTTTGGCCAGGCTTC
TP18947	TGCAGATCCTAACCTCCAAGGCTCCGCCCCCTCAAATGCC[A/G]CTGGCGATGGACGGCGGCGGCGG
TP18953	TGCAGATCCTACACTAGCACTTGCACTAGCAC[T/C]GCTCATATTTGGAGACGCCATCTACTCTCTA
TP19022	TGCAGATCCTGCTGCAAGCAGACTTTGTCCATCTCTG[G/T]TCTACAATTCGACCACTGTACCTCGC
TP19029	TGCAGATCCTGGCCCTGGACATCTACGTCCCTCGTGACGAACGCTTTGGGCATCT[C/G]AAGAAGGA
TP19030	TGCAGATCCTGGGCCTATTCCAGG[C/T]GCTCCCCCGCCTCGTCGTCTTCGACCTCGACTATACCCT
TP19042	TGCAGATCCTGTCCTGCTACACACTAGGTAATCTCCTCTGAAACTGAAATG[C/T]CATCTGATTGAC
TP19046	TGCAGATCCTGTGCGCA[G/T]CCGCTCCAGGGAGTAGTAGCCCTTGCTCGGCTTCCTTCCTCCCCCA
TP19054	TGCAGATCCTTCACCACCGCC[G/T]CCGTCATGGAGCCTCGACACGTTCGACATACTTGATGTCACT
TP19074	TGCAG[A/G]TCGAAACAGTGGCGAACTCGAGTACCATTGCCCGTGACAGGGGCACGCGAACCCGCAC
TP19078	TGCAGATCGAACTAGA[C/T]GGGCCATCGAGGTGCAGCGACGCTGCTGCTGCTCGTGGGCGCGGCGG
TP19084	TGCAGATCGAAGAGCGAATGGGACGAGCTGGAGAAATGGAACGAGGAAT[A/T]TGGTTCAGCTGACG
TP19091	TGCAGATCGAAGTCCAGGCT[A/G]AGCAGCCCCCACGAGAGGTCGAACCAGATGACCGTGCTGTCGA
TP19106	TGCAGATCGACCGATGT[C/G]AAGGCATGCAGTAGAACAGGGCGTCATTGCATGCGTATACGTGTAT

Table A2 (cont.)

TP19121	TGCAGATCGACGGCGTAGCTGTTCGCCTGCACCTTGCCTCCC[A/G]AGGCAGTAGTGAGGGTCCCAA
TP19128	TGCAGATCGAGAAAACACAAATTCAGAGACGGATTGAGAATGGATGGTCACCTGAAG[G/T]ACGGCG
TP19133	TGCAGATCGAGAGATG[A/T]CGTCTCTAGATCAACTCATATAAGTGGCCTGGTAATTAAACTTCAGG
TP19145	TGCAGATCGAGCACAGTATGTGTATTATTTGATCGCCCCTTTTT[G/T]ATGTAAATTTGGGATGTGC
TP19146	TGCAGATCGAGCAGAGCAATGGCAGGTGGTGGA[C/G]GCCTGTTGCACCTGTGGAACGAATGGGGGA
TP19148	TGCAGATCGAGCAGAGCTCCCGCGTCACGTCGCATGCGATTTTG[C/T]GTGCTGTACGCCGCTGTCT
TP19165	TGCAGATCGAGGCGCTAGCTAGT[C/G]TGCGCCCGCGCTGCATGTGACGTCGCCCTGCGCGGATCTC
TP19171	TGCAGATCG[A/T]GGTCGGCCAGCGAAATCTTGCCACGCCGTGCAAGAACAGAGAGGAGGCTTTGAT
TP19173	TGCAGATCGAGTACGGGCAGTGCCCGCCAGGCTTGATGACCTGCCCTGTTCCGAGCC[A/T]ACGCTC
TP19185	TGCAGATCGATAGCAAGTC[A/G]CAGCAGATATCCGCGAGTGAGTTCTCTTGGTGAACGATCTCTCA
TP19188	TGCAGATCGATATACATGTATAATCCAACATTCACACATTCATGC[A/G]TACGCATGTCCGCCAATG
TP19199	TGCAGATCGATCCAAGAGCGAA[C/T]GGGACGAGCTGGAGAAATGGAACGAGGAATTCGATCCGAGC
TP19206	TGCAGATCGATCGATGATGGATCCATCATATATACGCTCACCAGGA[A/G]CCGACACTTGCCGCCCG
TP19212	TGCAGATCGATCGGCCGCAGCTCCGCGGCCGAAGATGTTGGCGCTGTCTGATATGACCTG[A/C]ATG
TP19233	TGCAGATCGATGTACCCATAGTGCCCTAGGACATGCTTGCCATGATCTGCGTCTG[A/T]CAGTTGAT
TP19259	TGCAGATCGCACACCGCGCAGTAGAACCTCGAC[A/G]GCTCCGCGCGCCTGGCCTGTGCCTTCTCCC
TP19261	TGCAGATCGCACGGCGTCGCCTCG[C/T]CCGCAGCGTGGGCGAGGAACGGCAGGAGGCTCTTCTCCA
TP19262	TGCAGATCGCAGACCGTGCCGCGACGGGGAAAACAGAACAGAGATTCTA[C/G]CTGCCTAACAAATA
TP19266	TGCAGATCGCAGCGCGCTGGGCGCTGGCGCTGCGGCCGCGACAGGGGATTCACGTGCCAGTGC[A/G]
TP19267	TGCAGATCGCAGTGTGC[C/T]CTTGTACACAGCTCCGAACCCGCCTTTGCCCAGCTTCCTCGCCTCG
TP19286	TGCAGATCGCCCGCCCTTCCGCTGCCGCTGGGATTATTCCTCCGCTCCTTGC[A/G]CCCGCATCTTC
TP19307	TGCAGATCGCGAGCACCAGCGGGGTTCGGAGGCGGGGCCTGGAGGCGAGCAGCTTCGGTCGC[C/G]G
TP19314	TGCAGATCGCGCGCGGCATGGAGTACCTGCACTCGAGGAAGATCTACCACGGCGACCTGAACC[A/C]
TP19315	TGCAGATCGCGCGCGGGATGGAGTACCTGCACGCCAACAAGATCTACCACGGCGAGCTCA[A/G]CCC
TP19322	TGCAGATCGCGGGGCGGCGAAACCCTAGGCGCGGATCAGGGGAGTCGATTGG[A/G]GGAGGGAGGAA
TP19340	TGCAGATCGCTCCTTGCCAGAAGCCGTGAA[A/G]GATCGGACGACGACGACAAGGCAAGGAAAGCCG
TP19341	TGCAGATCGCTCCTTGCCAGAAGCCGTGAAGGATCGGACGACG[A/C]CGACAAGGCAAGGCGGCAGG
TP19354	TGCAGATCGGACGAGGTAGTACGTGTACAC[A/G]GGCAGTACTCGCTGCGGATCGGACGAGGACGAG

Table A2 (cont.)

TP19376	TGCAGATCGGCCTGGACCA[C/T]GGACCAAGCGCGAGCACGACGGTGTCGGCATCCACCACGCCGTC
TP19399	TGCAGATCGGGGAGGGGTGCGGTGTCATCTCTCCTGAGCAAGCGGCGC[A/G]GCGATGGCCGAAAAA
TP19420	TGCAGATCGGTGCTCGTGCTCTGTCGCCTGGCC[C/T]CTGTCCGTACGACCATGCGAGCGCGGCCGC
TP19424	TGCAGATCGGTTATAAATTCTCCTGCATCGACCCAGCTATTGCTACACACAGC[A/G]CGAAGCTCGA
TP19426	TGCAGATCGGTTATATAGACGGCTAAGGCGGGTTC[A/G]GGGTGGTAAACAAAACTGGGATCCAAGC
TP19427	TGCAGATCGGTTCGCTTAATTTA[C/T]TGATGAGTTCGCTGGGTTCGCTTAATTCCTTGCAGTAGAT
TP19431	TGCAGATCGTACGTTCTAAGTGTTGGTGGATATGCACCGAGGAATCGAGA[A/G]GACGACGTACGGG
TP19463	TGCAGATCGTGACGGC[C/G]CGCCCGCCCATGGGGCTGACGCACCACGTCGGGCGCGCCCTGGAGCG
TP19468	TGCAGATCGTGCAGTTCCTCTTCAGCTTCGC[C/G]GCCTCCGTGGTGATGCTGTGGCTCCACTTCAC
TP19473	TGCAGATCGTGGCGCACTGCCTGCTGGGCC[A/C]CACGGGATCGGACGAGCTGAAGGCGCAGGCCGC
TP19474	TGCAGATCGTGGCTAATTGAAGTCCCCATATGTCTAAAATGCATGCA[C/G]ATGCATCTCTACACCT
TP19480	TGCAGATCGTTCGGCATGGGCGGTTCCTGTTCTTCGTCCATTGCTTGCATGCGC[A/G]GCGCCTTGA
TP19483	TGCAGAT[C/T]GTTCGTGCTCTGGAAGGGGACGCGTCGCTGGACGACCTGAACGAGGGGGTGAAGCC
TP19495	TGCAGATCGTTTGTAGCTAGTC[A/G]ACAACACAATGATGCAGCTTAGCGCAGACTTAGTGGCCTTG
TP19500	TGCAGATCTAAATCGAGGTGAATCTGGAAGCTGTGTG[C/T]CGAGATGCTGCCCACAGTGCAGAAGG
TP19510	TGCAGATCTAAGCTTAAACGTTTT[G/T]AGCGCCTCGGAGCGGATGGCAAGCTGGGCCAATCCTTTG
TP19519	TGCAGATCTAATGATCTATGTATGGA[C/T]GAGAGATACATACAGTATATATAAAACGGGCCCATGA
TP19527	TGCAGATCTACAGTGGCAAGGGGGCGCGACGCTTACGTTGGGGCAGTGCTT[G/T]GCGATGGCAGTG
TP19536	TGCAGATCTACGCGTGGAGATCTTCGGA[C/G]GATAATAAGGCCACGAGAGTTTGCAGCTACTGGGT
TP19549	TGCAGATCTAGATCGGGCATGCATCGCCGTGGTGAGCTCCTTCCCCCG[A/T]TGGTTTTGTGCCTAT
TP19558	TGCAGATCTAGCCA[C/T]GTGATTCATGAATCCAGATCCATTTCCTCGTTGTTTCCTAACTTCCGAT
TP19562	TGCAGATCTAGCTAGCAAGAAACCGAGCC[A/G]AGCGGCAGGAGGAATCCGTGGGTTAATTAATTAC
TP19579	TGCAGATCTATCGTGAACTGTCCAAC[C/T]CCAACATGCGCAGGGCTCGACGAGACGACGACCACCT
TP19597	TGCAGATCTCAGAGATTTCGCTCGCTTTACCGTGCAGCGTGTTCCCTCCCCGCCATGCATGC[A/G]C
TP19634	TGCAGATCTCGCGAGGGCAATG[G/T]TGGCCGTGGACGCGGACCATCCGAACGGGACCGAGGGCCGC
TP19654	TGCAGATCTCGTGGAACTACAACTACGGGCCCGCGGGGCAGAGCATCGG[C/T]TTCGACGGGCTGGG
TP19682	TGCAGATCTGAACATCATG[A/C]ATCCCATTCTGGTTCTTGCAGGTGTGCAGAGGCACGGCTGTCAT
TP19702	TGCAGATCTGAGTGCCGTGCTTCGCGCCTTCGCCTTCGCGCGCTTCCGATCCATCGG[C/G]AGTAGT

Table A2 (cont.)

TP19729	TGCAGATCTGCGAGGACAACGCCGTCTACCGCACCATGGTCGCCCGCGAGGGCGCCAT[C/T]CCGCC
TP19730	TGCAGATCTGCGCGCATCGCGCAC[A/G]AAACGCAGCAGGCTAGGGGAGCCAGCAGTAGCCCGTGGC
TP19732	TGCAGATCTGCGTCGAGAGCGGTGACAAGGCGGTGCAGACGGAGCA[A/G]GGCGCGCACATGGTGTA
TP19734	TGCAGATCTGCGTCGGCCACCGCTGCCTCGTCTTTCAGATCCTCCACGCCGACTA[C/T]CTTCCTGA
TP19748	TGCAGATCTGCTTAAG[C/T]AACGCAAACACTAAGCACACAAATGCTTCACCTCATCCTCAGAAGAG
TP19761	TGCAGATCTGGCTGCAA[C/G]CACGCAGCGGTGTGCATGTAGCTTCTCTCCGCTGACCTCGAATACG
TP19787	TGCAGATCTGTATTCTTATTGCATCTTTGCTGACGAAACACGAAAGGAACTTAG[A/C]AGTGAAAAA
TP19795	TGCAGATCTGTGCGCTGATGAGCGGC[A/G]CGGAGCTGTTCGTGCGCGACGACCTGGGGCTCACCGA
TP19797	TGCAGATCTGTGTCGTCAGGCCGACGCACACCTCCAGGACCTGGTCC[C/G]TGTTCGTCATGGTGAC
TP19823	TGCAGATCTTCCA[C/T]GACTCCAAGGGGTTATTAGAGTGAGCACTAGGGCTACCTGGGGTGGGCGT
TP19830	TGCAGATCTTCCTCTGGAACGGGACGCGCCCGCTGATGCGCGACGGGCCCTGGACGGGCT[A/T]CTC
TP19844	TGCAGATCTTCTAACTG[C/G]GTCGCCCCACTATGCATAATGCATTATTGTTGACACATTGACTGAC
TP19846	TGCAGATCTTCTACGGCCTCATGGGCAGCTGGAC[A/C]GCCTACCTCATCAGCGTCCTCTACGTCGA
TP19858	TGCAGATCTTGATCAACGTGCCGTTCTG[A/G]TACTACGCGTTCAGCGCCCTGTTCTACCCGTTCCT
TP19931	TGCAGATGAAATGCAG[A/G]TCCGCCAGCTGAGCTATGATAGACTTGGTCTTGAGCTTCGACAGCGG
TP19960	TGCAGATGAACGCAGGCGCAAGCAGGCCGTGCAGCAGCAGGCTTTAGCTTC[A/T]CGGATAGCGACG
TP19979	TGCAGATGAAGAAGGCTTCCAGCCACAGCGCCAGCGCGGACGCCATCAAACCATCCACAGACT[A/C]
TP19988	TGCAGATGAAGATGGCCCTGACACAACTGACCATCAACAAGACTATGGA[A/G]CAGATGTTGCTGCC
TP19989	TGCAGATGAAGATGGTTGGGCCAAGGTCCTGCCGAGTCACTGGTGG[C/T]GCCGCCCAGAGTACAAG
TP20005	TGCAGATGAAGGCGTCCAAACGTAGATG[A/G]CACCTTGCCGCAGCCGCCTCGTGTAGATGCAGAAA
TP20046	TGCAGATGAATTCATACCATTGGGATGCGACGTTAACG[A/G]TGAGAAGAACCTTCCCCTTGTAGGT
TP20061	TGCAGATGACACGGCGGTGAGTTGCTCCCAACTCTGTGAG[C/T]GGCGCATAAGCTCACCTTGGGAG
TP20078	TGCAGATGACATCAAGAT[C/T]GACGACGAAGCACCGTCAAAGGCAGCACCACCGTCCACGTCTGTT
TP20079	TGCAGATGACATCCTCCGTCTCACTCAGATGAACAC[A/G]GATCTATTTGGAGGTATTGATGCTGTA
TP20089	TGCAGATGACCATGTTCTCCCTAGGAGTTGCCTGAATTTTCACGTGGAGATTGGTGAGGGAGG[A/C]
TP20105	TGCAGATGA[C/T]GAAGAGAGAAAAAAGAGGGAAGAGAGGAATAGAAAACACCTGCAAATGAATGCA
TP20129	TGCAGATGACGTTCGTCGCGAGGTACGCGGAGAGGACGGTGTTCGAGCGGCCGCTGA[C/T]GAGCGG
TP20137	TGCAGATGACTCATCGAGCATGCATGC[C/T]CTGTCAGCACAAGGGAAAGCGAGCACTGCACTTACG

Table A2 (cont.)

TP20160	TGCAGATGAG[A/T]CGAATTTATGATCACCAGATAATTCCTCGTGTTCCGCAAGTTGCAAATGACAA
TP20166	TGCAGATGAGAGCGGCAAGGCAATGG[A/C]AAGCACGGTTAGGATAAACCGCACCACAGGGCCAGGA
TP20170	TGCAGATGAGAGGCGGCGTGCGTCG[C/T]TGCGGTGGAAGACGAGGCTGGACATCATCCTCGGCATC
TP20190	TGCAGATGAGCAGCACGTCCAGCTGCT[C/G]CTCGCACAGGGCGTCGACGCTTCTGAAGAAACCAAT
TP20195	TGCAGATGAGCATCGCAGCAACGCACGGAGCCGATCGA[A/G]CGCACATTGCAGAAGCTAGCAAGCC
TP20198	TGCAGATGAGCATG[C/T]GAATGGGTGTGGTCTTCAACCCGTAGGCGCTGGAGCTGTTCGTGATGAA
TP20212	TGCAGATGAGCGCCACCACAAAGAACTTGAAATGGGAAATCTGGCGCCACCACAAAGAACTTG[A/C]
TP20255	TGCAGATGAGGTCATGCGCGCGTTACTCCTCG[A/C]TGTGGTCGGCGTCGGCGTCAGCGTTGCGGGG
TP20258	TGCAGATGAGGTCCCACCGTCCCAGGCACCCATGCATGCGC[C/G]GCTGCGCTCTGCTGTGCACGCA
TP20261	TGCAGATGAGGTTCGTGCTGGCGTTACGGGTCTGCCGC[A/G]GCAGACATGGATATCAGCAAATTGG
TP20286	TGCAG[A/G]TGATAAACCGCACCACAGGGCAATGGCAAGCACGGGAAGGATAAACCGCGCCACAGGG
TP20288	TGCAGATGATAAAGAGCTAAACTATCCCGCAGCTTT[A/G]GCAGCTACGAGCCTACAACCCGTTGGA
TP20316	TGCAGATGATCACAGTGTCACAGTGTCATG[C/T]TGGGAGTATTTCTTCCGTTTTTGCTTCAGGTGA
TP20321	TGCAGATGATCCGACAGCCCTAGCCCGAGCCCCGAGGGCGATCTGCGATGGGCCGAGG[A/G]CATCG
TP20329	TGCAGATGATCGTCGCTGCG[A/C]TCGCCGCGCTCGCCGAGGAGAACGGCTCCAGCCAGGCCGCCAT
TP20336	TGCAGATGATCTTAG[A/G]TCGACTGATTGTTTCCACGGCGAGATAGATTTGTGCTACGGCGAATTG
TP20351	TGCAGATGATGCAGTCGTTCCTG[A/C]TGACAGCCGACGAGGAGCGAAGCCAGAGCAAGGTGCTCAC
TP20363	TGCAGATGATGCTGAGCGTCTTGCCAGTGCCTGCGGGG[C/G]GCATCGAAAAGGGCGCGAGACCAGT
TP20373	TGCAGATGATGGCCGATTGAAGGATGCAACTGAG[C/T]TTGGGTTTCCCCTGCCTCTTCCAGCAGCA
TP20376	TGCAGATGATGGCGGACACGTTCATGATCAGCAGTGTCCCGCGGTGGATGTAGATATA[C/T]ATTGA
TP20409	TGCAG[A/G]TGATTTTGAGTACTTAACTCTCACATGCCACTGCCCGTTTGTAATGCAACGCCGTGTG
TP20410	TGCAGATGCAAAAGCTGGACCAGAGGCACTGTAGCT[A/G]GGGCGATTTCGGGCACGAATAGAGATA
TP20414	TGCAGATGCAAAATGTGTTTTTTATGAATACATTGTCCTTTT[G/T]TGAACATATACATGTAGTACA
TP20424	TGCAGATGCAAATGTGTACTTTTCTGAATACGTTGTCCTTTTTTGAACTTAA[C/T]ACATGCAGTAC
TP20436	TGCAGATGCAAGTGACGCGCTTCACGGTTGCCCGCCGCGGCGTCAC[A/T]GCCGTACGTGCTTGTTA
TP20438	TGCAGATGCAAGTGGAGAATGCAAGGAGAGGAAGTTACATAACTG[C/G]TGGTGGTGGTGCTGCCGT
TP20454	TGCAGATGCACAGCACCCAACTCTGCGCC[A/G]ACCTGTAACGTGACCCTTGGGCAGCAGGACGGAG
TP20497	TGCAGATGCAGAACATAGTTTGAAACTAGGA[A/G]ACGATAAATTGGTAATTATTCCGTAAAAATTG

Table A2 (cont.)

TP20502	TGCAGATGCAGAAGGTGAGTTTTCAGTTTTCACTGTTTTCCGTACTCTG[C/G]ATTCTGCTTCTGCA
TP20557	TGCAGATGCAGGACATAACTGAAATGGGGAAACGATAACTTGGTAGCTACTCCGTATAAAT[C/T]GT
TP20572	TGCAGATGCAGGGGAACGATTGGCG[C/G]GAAAGGATTGGGGCTGCGGTGCGCTGAGGTTGATGCTG
TP20574	TGCAGATGCAGGTCAGCGCCATGCGCGCGCTC[G/A]CCGACGCGCTGGCGGCCGCGCAGCTGTCGTC
TP20609	TGCAGATGCATCAAATC[A/G]TATCAGAGGCCCATGCACTTCTTCCAGCACCGCGGCTCCTCATGGC
TP20624	TGCAGATGCATGCATCTACACGCAGAC[A/G]CAGTCTGATGAAACAGGGGCAGAGGCAGAGCAGTGT
TP20629	TGCAGATGCATGCGCCTGCCTCCAATGTGCGGTCCCCACGCTGCATGCAGAGCAAAATGGC[A/T]CG
TP20635	TGCAGATGCATGGGAACACCGTCTCGTCAGAACCGATGCGTCAGGTGATTTGGACACACCACC[A/G]
TP20637	TGCAG[A/G]TGCATGTCCCACGTGCCGCCGTATTGTCTTCGCATCTGGTGGTCAGACGGCAGCGGCA
TP20640	TGCAGATGCATTAACTCAGGATGCAGTGCAACGAAGATTTTGCAGCC[C/G]AACGACAATGATCCCA
TP20645	TGCAGATGCATTCAGGTGGGTCTCCTGTGCGTGCAGGA[A/G]TTACCAGCTGAGAGGCCAACCATGT
TP20657	TGCAGATGCCAACAGGCAACAGCTAGCACG[A/G]AACTTGCACAAACATATGGCACGGGTGTCCAGG
TP20661	TGCAGATGCCAATGGCACGCCCACACCGCCGCACACGCACATAGTTTTCAC[A/T]AAGATCTGATCG
TP20664	TGCAGATGCCACATCCTAGAACTTTGATGTCACCTCGCTCTACCTGGGCGA[C/G]AAACCATGGGAT
TP20665	TGCAGATGCCACCACTACTGTTACAGCAGGTAAAGCAA[A/G]AGCCCGTTGTCGTTGCTCCTTGCCT
TP20672	TGCAGATGCCAGACTTCGATTTGCGCAAGCAGCGACCTTGCCAAGGT[C/T]GCCACACTGCAACAGG
TP20693	TGCAGATGCCATTACCATCGAAAGTTCATCACGAGATCATCAGTGATCATCGCCATCCAG[C/G]AAA
TP20721	TGCAGATGCCCTCGTGCTCGGCCCCCG[C/T]CCCTTTCCGCGTGGGTGCAGGCACGGGCTACGCTAG
TP20742	TGCAGATGCCGATGCTGTGGCCGCC[A/G]CCCAGCATCGCGGTCATCTCCTCGATGTTGAAGCCCTG
TP20767	TGCAGATGCCTCGCTTTTTACCCTTTTAAAACGTACTACT[A/G]GTACTCTACTAGAAGGCTAGAAG
TP20769	TGCAG[A/C]TGCCTCTCTGTCTCCTCCCTCCCTTATCCTCCTCTTCTACCTCCACCTGGCAAGTGGC
TP20777	TGCAGATGCCTTCAGATCCCCTCAAAAT[A/T]GCCCCATGAAACTATTCCCCAAAGTCCTTGCTAAC
TP20795	TGCAGATGCGAGTGTCCACCACGGCGCTGAATCA[A/T]AGCCATGGCTGCTTTCGAAACGAACAAAG
TP20833	TGCAGATGCGGCCTGTGTGTGCTCTCTGCAATCGTGTCCGTACGGCAGTGTATAT[A/G]CGCGCAGC
TP20838	TGCAGATGCGGCTGCGTCGGCAAGACGGGCGCCTTGTGGTCGAGCTC[A/G]CTGCTGCCTCCATGTC
TP20856	TGCAGATGCGTGGTTCAGAACAAAATGACTGATCGAGT[A/G]GCAAAGGGCAAAGGCATGTGCGCCG
TP20886	TGCAGATGCTCAAGCGCGGGATGCGCCTCGT[A/C]GTCGCCTCCCTCGGCCCCGCCGACCGCCTCTC
TP20893	TGCAGATGCTCACGGGGCTGCTGGACCTCAACATCGC[A/G]GAGCAGGCGCGCGAGGCCGTGAAGAT

Table A2 (cont.)

TP20899	TGCAGATGCTCATCTCCAGACGTCGAGGGTACTCC[A/T]GTTCCACTGTTCCAGTACCATTAATCAT
TP20919	TGCAGATGCTCGTAGG[C/T]TCATGGCCCTAGGCGACTAGGGGATTCGGTTGATTGCTGTGGTTAGG
TP20928	TGCAGATGCTCTGGATAGCGCTCTTAC[A/G]ATAGCCTGATCTTCTGCGGCGGTGCTTCCTACTCCG
TP20936	TGCAGATGCTGAAAGAAATCAAGAATCGCTTTCCTGTTGTTTTTCTCTCTCT[C/T]ACAAATAAAAT
TP20942	TGCAGATGCTGAGGGACGA[A/G]CTGGAGCTCACCATGGCGCTCAGCGGCTGCACGTCGCTGAGGGA
TP20960	TGCAGATGCTGCTGCTG[C/G]TCTGCTTGTGCAGACGGCTCAAGGCGAAGGGACGACGAGGTGACGC
TP20977	TGCAGATG[C/T]TGTCGCGACGAAACGTTTATGACCTGCGGGCTGCGGCGGCGCTGCCTTTGCCAAC
TP20978	TGCAGATGCTGTGAGAGTGAAAAGGTGTGGGGAAAGGCATGGG[A/C]TTGAGAGATGGCAATGGACA
TP21022	TGCAGATGGAAACCATGG[C/T]TGGTTATAATTAGGTCCTGTACGGGATCGATCGATCAGGCATCCC
TP21023	TGCAGATGGAAACTAATCTGCACCTGGTTTCTAGCCATTTGTACAATAAACTGAACTGGTGAA[G/T]
TP21030	TGCAGATGGAACAGCGAGCGACGTGAATCCCGCCGCGACCCAGTCTTCTGCCTCCCGC[A/G]CGACG
TP21034	TGCAGATGGAACTCGACGCTGGAGGGCATCGT[G/T]GCGGGGCTGCCGCTCCTGTGCTGGCCCATGT
TP21054	TGCAGATGGAAGTTCGTGAGTTTCTACCTTCGTATGCATGCTTCCAAGGCATGGAGA[G/T]GAAACA
TP21058	TGCAGATGGAATGAAGAGCGGCGCCCGCGGGCGGCAAACTGCGCGCCAG[A/T]CGCGGGGGCGGCCA
TP21064	TGCAGATGGACAAGGCCACCTTGCTTGCCAGAGTGGTAGAGCAAGTGAAGCTCCTGAAGAGG[A/G]A
TP21069	TGCAGATGGACAGCAGCGGCGGC[G/T]CATACGACATGACCTTCTCCATGGGCACGCCGCCGCAGAA
TP21088	TGCAGATGG[A/G]CGCTACATAGCTGGTCACCGAAGCGAAGATGGGCGGTAGCTATAGATGAATTTG
TP21100	TGCAGATGGACTTCATCT[A/G]CTGAACGCCGACGCATGTTCCTTTCAGTGGTACGGCGATGAAATC
TP21137	TGCAGATGGAGGAGGAGCTGGTTTACATCGGACGACGCCTGCTGTCGGG[C/T]GGCCTGGGGTCGCG
TP21139	TGCAGATGGAGGATGAACTGGTACAAGGGGTC[T/A]GGCTGGATGAGGCCCAGCTGGACTGCTCCCT
TP21145	TGCAGATGGAGGCCAACTTTTGCCTTGGAGACTGGTGGGCCATCTAACAC[C/T]GATGGCCAAGACT
TP21167	TGCAGATGGAGTTTGGGGATTTTAGCGGCCATCATTGG[C/T]TGAGGGGACGGACGGACGGACGGTT
TP21177	TGCAGATGGATAGGTGGAATGGAAC[A/C]TAGCTTAGCTAGCTAAAACACTTGTTAAAGATTACTGA
TP21185	TGCAGATGGATCTCCTCTCCGCTGC[A/G]TACGGCGCTACCTCTGATGACGAGGATGCTACTGGCCC
TP21240	TGCAGATGGCATCTATTTCTTTGCGCGCCCAAGTTGGGAGGTCTTCGG[C/T]CATCATTGCATAAAT
TP21255	TGCAGATGGCCCGACCGCTCGGCACATCACCTCCATGATGCACAC[G/T]TGTACAGTAGGAGTAGCA
TP21257	TGCAGATGGCCCGTCTGCCGACGACTCATCCGATGA[C/T]GCTGCGGACAAGGCCGCCGCTGCGCCG
TP21309	TGCAG[A/C]TGGCTATAATCTCTCATGGTCTCCTCCCTTGGTAGGCAAGTAGTGGTGTACATACGCA

Table A2 (cont.)

TP21315	TGCAGATGGCTCCTTC[A/G]CCTGCTACAGCAGCGGCAGCAGAACACAAACCAACAGTGGCAATGTG
TP21325	TGCAGATGGCTGCATGCCAAGCGTTGCCCCTCCATGCTTCTCAAAGTTGATCTGG[A/C]AAAGGCGT
TP21327	TGCAGATGGCTGGACACTGTCAGGCAGAGGAAGGTTGCTCAGCTGGAGCAGAGGCAGAG[C/G]ACAG
TP21338	TGCAGATGGGAAAAGGAAGATGAGGAGCAGCG[G/C]CAGGAGCTAGGCAGCAGAGGGGTCAGGCCGT
TP21344	TGCAGATGGGAAGGCCTGGCATGCAGCGGCGGCGGCCAGGTGGTGTC[A/G]CTGAGCCTGCCCTCCT
TP21356	TGCAGATGGGAGACA[A/C]GGATCCACCGTACGTGTCGGCCCAGCACCGTACCGTGTCGCCGAGAAC
TP21374	TGCAGATGGGCCGA[A/T]CGATTGATGCGTTCCATCCGTGCATGCATGCAAATAAATGAATGATCAG
TP21380	TGCAGATGGGCGCTGATCAGGGATGACGAGGTGGCCCAGAGGGCGTTAGACTACCTGTC[A/G]AACA
TP21477	TGCAGATGGTCGTAACATTTGGTATGTCTCAAATTGGTCCATGGTC[C/T]CTGATGGAGGGTGGAGC
TP21498	TGCAGATGGTGGTTTCCTTTTGTGGCTGCACAA[A/G]CATAATTAGTACACTTGATCTGTCAGCGTC
TP21501	TGCAGATGGTGTCTTCACTGCTTACTGCGAAGACAACGGCAGCGTCGACAA[C/T]GAGCAATGTCAG
TP21534	TGCAGATGTAACAGATCCGTA[A/T]TAAGTTTTGCATACCTCCTCTTGGACCCTATTCTCAAGGTAA
TP21565	TGCAGATGTACATGTGCATTGCATGCATCGCTCTCCTCTCCTCTCCTCTCTGCCG[C/T]CGTCCGTG
TP21570	TGCAGATGTACCTCCAGGCGCAGAGCAAGAACATGATCATCACCTACCTCGC[C/T]GTGCTCAACCT
TP21580	TGCAGATGTACGTGGACCCGCTGGCGCAGATG[G/A]CCAAGATCCGCGGCTACGGCTTCCAACAGGG
TP21584	TGCAGATGTACTGATTGATGTTGATCTGGTTAACCCTTT[G/T]TTGCAGTGGATCTTCTGGGTGGGC
TP21600	TGCAGATGTAGCGCCCGATGCCCCGATGCCGAAG[A/G]AGGCCCGACGAGCCCGCGAGGGACGTGGG
TP21607	TGCAGATGTAGGGGACGTGACCAAGTTTTTCGCATC[A/C]CCTAAACCTGCATTTCCATTTGATGAA
TP21642	TGCAGATGTC[A/G]CGGTGGGAGAGCAGCCGCGGCACGATCGTCAAGGGGGAAGGGTACCTCGACTT
TP21649	TGCAGATGTCATAGATGGCCTCATTGTCGAGCAGGATGGAGACATC[A/T]GTGTGCTCCAGCAAGGA
TP21653	TGCAGATGTCATCATCTAGCACATGTTTTTGGAGGAGAT[G/T]GGCGCACGAACTCAGCCTGTCTTT
TP21684	TGCAG[A/G]TGTCGCGGGAACAGCCGCCGCGCTGCCACAGCGCGCACAGCTTCGTCTTGTACGCCGA
TP21686	TGCAGATGTCGGCGGAGCACGCGCAGTGCGCAGCAAGCGCGCGAGGCTGGATGTC[A/G]CCAGAGCG
TP21690	TGCAGATGTCGTGGAGGGGTTCAGCGTTTTCAAGGGATTGGCGAATAATAATGCGG[A/G]GCTGCGT
TP21704	TGCAGATGTCTGACTGACAGGATTTTT[G/T]AAGGTTCTATCAACCTTGCAATGACTGAGTTCACTC
TP21707	TGCAGATGTCTGTGCAGGTTCAGGTTCTTGGAGGCCAGCTA[C/G]CTAGCTTACCGTGCGTCGTCTC
TP21720	TGCAGATGTGATGGAAAGCCGCGGTCACTTGCTGGCTCTCTCCGCTCTTGCTCG[C/G]TTGCTCTGA
TP21723	TGCAGATGTGCAACTTCGTCTGGCTCTTCCGCGTGCTCTGGCGGATCCTCAG[A/C]GTCGCCTTCTG

Table A2 (cont.)

TP21747	TGCAGATGTGCTCCGATTCCCCGCATAACCGTGCGCTTCTTGTACGCGAGGG[C/T]GCCATCCCGCC
TP21842	TGCAGATGTTGGCGCATCCATCGGCTGCACAG[G/A]CCCTCCTGTCGATTCAACCACTTTTCACAAT
TP21848	TGCAGATGTTGTCGA[A/T]CGCGAAGCGCTCGAACACGTCCTGCACGTCCAGAGTGCGCCAGTCCCG
TP21851	TGCAGATGTTGTGGCCC[A/G]CATGCTGTTCATGCCAAGCTCACCGCACCACGCGTGCTTGCCGCCC
TP21854	TGCAGATGTTGTGTATGGTGTCAC[A/G]GCGTTGCTTGAATCACTGGATGCTGAGTCCAAGGATGCA
TP21866	TGCAGATGTTTCACCTGGGACCTGTTCGTGGCCCTTCTCTCTCG[C/G]CGTGACGGATCGCGATCGC
TP21872	TGCAGATGTTTCTGTTTTTATGCATAAACAGCTACACATACCTCAA[C/T]ATCTATGCTATCTGGC
TP21882	TGCAGATGTTTGGTGGTTTGGTTTGGAAAGAAAAGAAATGTGCAACGGGGAGCCA[A/G]CTGGTGTG
TP21901	TGCAGATTAAACTAGTAACTTATTCATTGTATAACCAGACTATCTGGGGTCTTCT[C/T]GTGAGACC
TP21907	TGCAGATTAAATTATCAGAAATGCTATACAACACACG[G/T]GTGTTTTAGCACCAAAAAACACATGG
TP21920	TGCAGATTAAGCAATAGTAATAAGCAAACTAACTAAGAAAACCAGC[C/T]ACGCCGTGACATTGTGC
TP21935	TGCAGATTAATTATT[C/G]GTGGATTAGGATGAGATAGATATGTGCTGTGCTGTGCTGTGATTGCAA
TP21982	TGCAGATTACTTGGGTGCTGGAGCTATCCGAACGCCGACGTCCA[C/G]CTGCTCGGCGAGGTACGTT
TP21990	TGCAGATTAGACACACCACCAGAACCAGATCGCGACACCACGCCTTGCT[C/T]ACTTTCCACAATCC
TP22014	TGCAGATTAGGA[A/G]TTGGAGCTGGTCAGCTCGGCCTGTCCACTCTCTACTGCTGTAGCTAGTAAG
TP22027	TGCAGATTAGTCGGGACGGTGAT[A/G]TTCAGAAACGAACGCGCAACAACGTCATCGGAGACGGAGA
TP22032	TGCAGATTAGTTGGGACGGTGATATTCAGAGACGAACGCGCAACAACG[C/T]CGTCGGAGACGGAGA
TP22055	TGCAGATTATCAGC[A/G]AGCAGCTAAGCATGCAGAATCTGGCTGCTTGAAGGTGTAAGATCGCTGA
TP22070	TGCAGATTATCTGACCCCATCTGATTGCCCAAATTGACCTGTGA[C/G]GAAGACGGGAACGACAGAG
TP22086	TGCAGATTATGTGGGCTCAAATTTGATCTTCTGCCAGATCTTGGCCGCCACCATAAAG[C/T]CGCAC
TP22095	TGCAGATTATTACCCAACCCGCCCCCATTCGCGCACGAGCAGAGCGGCCGCCGCTGTCGTGC[A/T]C
TP22112	TGCAGATTATTGTTGGTGGCGTTCTGACTGATGTCATTTGACGACGGCAG[C/T]CCTCCGAGGACGA
TP22163	TGCAGATTCACTCTTGCAGAACAAC[G/T]AAGCCCAGCCCCAATCATCAGACGAGATCTCCACACCA
TP22176	TGCAG[A/G]TTCAGATCAGTATTCCCAGTCGGCGCATCAATTCCACAGTGCAGAGTCCAGACTGTGC
TP22227	TGCAGATTCATGACAGCTGCACCCGCACGGCCGCACGCTTGCACCAC[C/T]GACCTGCATGTGCGTT
TP22232	TGCAGATTCATGGGCCTCTACGGCGAGTGGTTTCCCTGGGTCTTCCGC[G/T]AGCTCTGCGGGAGCG
TP22239	TGCAGATTCATTCTCTATGCATGCCTCTGATTCATGTGTCTGCACTTGTACAGT[A/G]TTGTACGAG
TP22247	TGCAGATTCCAATCCTTCCTCCTGATACAGAGTGAG[A/C]GAGGGACACGATTTCCAGGAAGCCTGC

Table A2 (cont.)

TP22248	TGCAGATTCCAATCTCCAAACACTGAGCCGTGCCACAACAGCCGTCTAAGCT[A/G]ACTGACGAGCT
TP22265	TGCAGATTCCATCCTCCTCGCCCCCTTCTCCGATC[C/G]GATCGATCGCGGATCGCTGCGTTTCGTG
TP22267	TGCAGATTCCATGGCCC[A/G]CCGCAAGCCGCAATCAACTCCGACACTCGTCCATGACCACGCTCCA
TP22308	TGCAGATT[C/T]CTGCTGCGTTGGGCTGATCCGTGGGCTAAAGAAAGAGAGAGTGCATAGCCTAATG
TP22333	TGCAGATTCGCAGGCCAAAGGAGAATCCAAGACTTCATTTTGTATGCGTGCATTGC[A/G]CGGCTGC
TP22358	TGCAGATTCGGTGCTGGTAGCGCGTGGCTTGGGGAAG[A/C]AGCAGCGTCGGACGCGGGAGCGGATC
TP22362	TGCAGATTCGTAGTTGGATTCAGCATATGC[A/T]TTTTTGATGCTGACATAGGATGTGCTCCACCAT
TP22371	TGCAGATTCGTTGCCCTTCACGCGGCCTTAACTTGGATTTAGGGTTCAGGCATACAACGGAT[A/G]G
TP22374	TGCAGATTCT[A/G]AATCTCAAAATCAGAGCCGCTAGCTCCTACTTCTATCTAGCTAATTGATCGAT
TP22375	TGCAGATTCTAATCGACA[A/G]GCAGATGGGAGAGGAATTCGTCGACTTATGGGCGGACCAAAAGAC
TP22387	TGCAGATTCTAGTCGGCTCGCCCGCCGTGAGCAAAGTTTTTAGCTGGTCTTGCGGCCTGTTTG[A/G]
TP22389	TGCAGATTCTATCAAGGCCGACAGCCCACTAGGTT[C/T]TCACAAAGGACTGGCTTGTCGGTGTTGG
TP22418	TGCAGATTCTGATGAGTTATAAAGATGTAATCATGTCTAAACA[G/T]ACAAGAATTGAGACAACGGC
TP22426	TGCAGATTCTGCCTGCCTTTGCCTTGCCTG[C/T]GTGGCAGCCAATGGCTCAAGTCTGCGTTAGGGT
TP22441	TGCAGATTCTGTGCC[C/T]GCGTCATCGTCTTGGATCGCGGCAATCACCACTGTCATATTTCTGACA
TP22465	TGCAGATTCTTTCTTTCTGTTCCTGATTT[A/G]TCCTGCGTCGTGTGTTTGTCACAAACATAGCAGC
TP22482	TGCAGATTGAAG[C/T]CGTCGGCGAGCGCGGGTACGTGGTATGTGCTCGTGCAAATGGCTGATGCTG
TP22507	TGCAG[A/G]TTGACGTAATCATTGCATATGACCTTGAACCATTCTCCGTTCAGGCCAACAGCATCTC
TP22515	TGCAGATTGAGAGCACACTTTCCCCTAGAAATCCCATCCAAAA[A/G]ATTCTCTTGATTCTTGAAGA
TP22521	TGCAGATTGAGCATTAGCTCGTAGTTCTTGTGCCCTCT[A/G]GCAATGGTCATCCCCTGCCTCTTGG
TP22523	TGCAGATTGAGCTATTGATGACGTTTGTTTGCGTGCGT[A/G]CGTGCAGCTGGTGGAGCCCTGGTTC
TP22527	TGCAGATTGAGTCAGTGAGGCGCGGGCCAGGTGCTGGGA[C/T]GGAGCGGGCGACTGATCGAGCGCT
TP22532	TGCAGATTGAGTGCCGCTTGCCGAGACAAGATGACGACCAAAGTTAACGGTCTG[A/T]TGGATAAAC
TP22542	TGCAGATTGATCTCGTTCTTTGCACACCGAGATGTTTTGTTTTGC[C/T]AATTCTCTCGCTCTTGAA
TP22562	TGCAGATTGCAAATATATATGTTTTATTT[A/T]GCATGCATTATTACTAGGCATTATCGCAGGAATA
TP22570	TGCAGATTGCA[C/G]CAAAGTGAGAGCCGCTGGACCCAGATTCCCACGTGGCCTGCCCCCCCTACGG
TP22573	TGCAGATTGCACGTCGTACCATGAGACAGAGAAA[A/G]TAGATAACTATCCAGGAACATGGCAATGA
TP22614	TGCAGATTGCGAGCGGCGGCGGCGCC[A/G]TTTCGTTCCTTTCTTTCTTCTTCCACGGGATAGAATC

Table A2 (cont.)

TP22617	TGCAGATTGCGATTGCGATTGCATGCCCAAGCAGTTGA[C/G]TTTGAAGCAGCAGTCATCGATGGAT
TP22618	TGCAGATTGCGC[A/G]CGGGATGGAGTACCTGCACTCCAAGAAGATCTACCACGGCGACCTCAACCC
TP22620	TGCAGATTGCGGAAGTGCTGCTGCCAGCATAGGCTCTGTCCTACACTCG[C/G]TCAGCAGCCCGAGC
TP22627	TGCAGATTGCGTACAGGGAGGAAGATGTTCTTCTTGCTCCCTTCCGCTTGGTCGGGAATGTC[A/C]C
TP22631	TGCAGATTGCGTTCAGGGAGGAAGATGCTCTTCTTGCTCCCTTCCGCTTGGTCGGGAATG[C/T]GCC
TP22636	TGCAGATTGCTATACAACTGCTTTTGCTTGACCTGGCACAACAATTTGCACACATTTATAGT[A/G]T
TP22642	TGCAGATTGCTCGGGGCAAATGGCAGCGGCAGTTGGGAAGCTTGGCA[C/T]TCTAGAAAGCTTCCTA
TP22652	TGCAGATTGCTGTGCCAACAAGAAC[G/T]GACCAGATCCCAATCATCAGTACTACTACTTTCTACCT
TP22654	TGCAGATTGCTTACATTTACTTTACCTTTATTGCATCTT[G/T]TTTGATAGATCTTACATGTCACTT
TP22656	TGCAGATTGCTTCACGCCCTTGACTTTGCATTTCTTCTC[A/G]TTGTCAGCATCGACAGGAGCCAAG
TP22689	TGCAGATTGGCACTGATCTTGGATCGAGATTGAGACACCAGGAGGAGAGGGAGCGAGACCCA[A/C]C
TP22738	TGCAGATTGTAATGC[A/G]CCTTAATGAGTTTCAATAAGTGGCTCACGCTTGCATGTTCCACCAACA
TP22759	TGCAGATTGTCCACATAGCTCGCAGACGTCATTGTCGAGGACATGTTTTTT[G/T]TGCAAGCTCACT
TP22772	TGCAGATTGTGATCGATTGGTCATTGCATTGTGGTGTTAGGCCGCCAT[A/G]GCTTTTTGGGTGTGT
TP22794	TGCAGATTGTTCATCTGGTTGAAGCGGAGACCAGACATCAGAGTCCTCTGCTTCC[A/G]TCGTGCGG
TP22834	TGCAGATTTACAGTATGC[A/G]TAGAGGGAGAAGTTACCATGGTCACCATGCGCAGGTTTCACATGG
TP22880	TGCAGATTTATTTTGAATGAACCACGATGGCTGGTGGATGGATAGCAG[C/T]AGCAGGGGGCATTGT
TP22888	TGCAGATTTCAAGTAC[A/G]ACAAGAACGACTCGGTGCTGGTGGTGACCCGCGACGCGTACCAGCTC
TP22912	TGCAGATTTCATCAG[A/G]TATAAACACAAAAGGAAGGGACGGGCATCTTTTACGGGTGATCCGATT
TP22913	TGCAGATTTCATCTCAGTGTACCTTCAGCTCTTGAGCAAGGACGCCAAGGTGCGGGCGTC[C/G]TGC
TP22919	TGCAGATTTCCACAACGCAAGTCCACTGACGCTATGGT[G/T]ATTCTTTGCGGCACTCCTTCTCTGT
TP22945	TGCAGATTTCCTTCCTCCCCACTCGATGGCCCAACAAGGCC[C/G]AGCGGCCTGTGGCCCAACTTCT
TP22976	TGCAGATTTCTCCGTGTTCCATCCAATCTCCAGG[C/G]TAGGGGATTCTCACTCAGCTCGGATAAAG
TP22986	TGCAGATTTCTGGCCATGGAAGGCCTCATCCC[G/A]TTCATCTACAGGGCCATCGTGCAGTACAAGA
TP23041	TGCAGATTTGATCCGTAATCTCAGGTCTGAGCATGCGAT[C/T]GTCACTGGTGCCATTTTCTCGCTC
TP23043	TGCAGATTTGATCCTAGTCTCCACCCAAACCAGTTCATCCTAGCCATATGGTT[C/T]AACTTTAATG
TP23050	TGCAG[A/G]TTTGCAATCATTTGAATACTGGCGTGATATGCTCTCTGTTTTCGGAACAAATCAGCCG
TP23061	TGCAGATTTGCATCCGC[A/G]GGAAACGTGGCATGACAGCAGGCATTGGTACCTCTTGGCGTGTGAG

Table A2 (cont.)

TP23121	TGCAGATTTGTTATCTGAAATCTCACTGCAAAATGACTTGAACTGC[C/T]GCCACTCAAAGTACATC
TP23141	TGCAGATTTTACACAGACCGCTGCTGCTGCCGTCTCT[C/G]AACGGTGTCTTCGACGGTGTGAAGTG
TP23142	TGCAGATTTTACACATACTTTACGGGTCTGTTGCTGCTGCTGCCGTCTCT[C/G]AACGGTGTCTTCC
TP23144	TGCAGATTTTACATCAATATGAATGGCACTTACGTTGGTGTGGGGATGATCAGCCCTTA[C/T]CTGA
TP23175	TGCAGATTTTCCTTTTCTTTTTATTTTTA[A/G]AATAGAAGATGCGCAGAGCATGCCATCTTTGTTA
TP23178	TGCAGATTTTCGGGCATACGATCCGTAAAATGACAAGAAAAATCTGCTA[C/T]ATTACTGAAACCAA
TP23199	TGCAGATTTTGCTGGCAGCTTGGCAATAATGGTCGTTGGGCAGTGTGG[C/T]AAATTTTTAAGAGAG
TP23211	TGCAGATTTTGGAGAAGCAAGTGCTGTCGGCCGCGAAGGCGGTGGAGGACAAGCTCGATGAG[C/G]A
TP23222	TGCAGATTTTGTCTAGAGCCAGGGACGTGTGTTTTACCTGTGCC[A/G]TGATGGTGATGTTGAGTGA
TP23240	TGCAGATTTTT[A/G]TAGCCAGCCAGGAGAAATTCCATGCCAACGCAGGCAAGCTGTACTGGAAATC
TP23249	TGCAGATTTTTGCTAAATAAAAGTGGTATGTTCTT[C/G]CTCTGTGGTTTGGTCCAAGCTCAGTTCT
TP23253	TGCAGATTTTTGTTCTAGGTATG[A/C]TAGGATTTGTTTCTTGGTACGATGCGCGCACGGAGCGGGT
TP23254	TGCAGATTTTTGTTCTAGGTGAGCTAGGATTTGTTTCTTGGTA[C/T]GATGCGCGCACGGAGCGGGT
TP23272	TGCAGATTTTTTTAGTGAACAAGTCGACGGCATAGCTGCCAGGTGCTGCTCGAGTT[A/G]GTAGTCA
TP23294	TGCAGCAAAAAAAAGCACCGCGTCGAGGCTCTGGAAAGG[C/T]GAGCCCGCCTAAGGGTGATCAGAC
TP23328	TGCAGCAA[A/G]AACTCCATGACTCTCTCCTTCTCCATGTGGCGGCCAAACATGCACCTGTCTATAT
TP23340	TGCAGCAAAAATAAACAAGCTGCATGCAGCAACGTGCCAAGCTGTGCATGGACT[A/T]GCTGCTGTG
TP23382	TGCAGCAAAACCTC[A/G]TCACGGAAGACTCCGCAACAGTGCGATGTTCTTTCCAGTCTGACAAAGG
TP23386	TGCAGCAAAACGGTTTGGATTGAGTGCTATAAAAAGGGCGTACC[C/T]AGTGCAGAGAGCTCCCGCT
TP23405	TGCAGCAAAAGATCAG[A/G]AGCAATCAGCAGATTATCTTACAAATAAGACATATAGTTAATTAGTT
TP23409	TGCAGCAAAAGATTGTGCTCAAGTT[A/G]CCCCTGGATGACGAGAGGAAGAGGAGGAAGGCCTTCAA
TP23438	TGCAGCAAAAGCTGCTCAT[C/G]ACGGGCTGCTCAACCAGGTCCTCGATGATGGCAGGTCAGGCGAT
TP23454	TGCAGCAAAAGGCGGCCGCCCACCAGCACAAT[T/A]TCCGTCCATCGCAGCGACGGGCACCAGCGTC
TP23483	TGCAGCAAAATATTTAAT[G/T]TGGACTCTTTCATGTTTAAACTGTATTGACTGATCCAAGCAAGAT
TP23493	TGCAGCAAAATCTAAACAAATGCTCGTC[C/T]CTCTCGCGTGACCAACCTTTCCATCTCACCACTGC
TP23512	TGCAGCAAA[A/G]TTGTTGAGCGCCTCACGGAACCTTGACACAAAGAAAGCCCCCCTGTATGATCCA
TP23554	TGCAGCAAACACTCCAACATGGCC[G/T]TGCGGAGGCGAGCCATGAAGCGTCTGCTGGCATTGGAGC
TP23572	TGCAGCAAACATCCTTTCACGGGTTGATATAGCAGATCTAGCACTTGATGCATCTCTAAGC[C/T]AC

Table A2 (cont.)

TP23590	TGCAGCAAACCACGCGCAC[G/T]ATTACCTTGGACGAGCCTGAAGGACGCCAATGCAAGTGCGGGCG
TP23612	TGCAGCAAACCTTGGGGCGAATGCAACTGTCTCTCCAGGAATGGGACCGATCT[A/G]TGTTCGGCTC
TP23614	TGCAGCAAACGAAGTAGAATGAAGTATAGCTTGATAAGGCGA[C/T]GATATTTAATTTGGGTTGTGA
TP23616	TGCAGCAAACGACATTCGGCCACGGCCCTACCAACGACCTTTACAGG[C/T]TAGCAAACATATATAC
TP23631	TGCAGCAAACGCAATCTCCAAGAGTTGCATTGTACTAGAACACACAGATG[C/T]CAAATCCCCTCTC
TP23653	TGCAGCAAACTACAGGGTTTATGAGTAAACCTGCTACCGTGAT[C/T]CAGACCATAACCAAACCAAA
TP23664	TGCAGCAAACTGCAAAGAGAGCGC[G/T]AGCTTGTTGGTAGAAGAAAGTAGTATATGCCCCCATGAC
TP23678	TGCAGCAAACTTTGTAAAGACCGCAACCGCAAATCGATCTGCAAGCTAGGATA[A/G]TCATATCAGA
TP23684	TGCAGCAAAGAAGCCAGAGGCCGCGGCAGGCA[T/C]GGACACCTCACGCAGGCCGCGCACTAGCGCC
TP23724	TGCAGCAAAGATTTGCAGTACGGCGTGATTTTCGCCGCGCGCGTC[A/C]GTGGAAAAGGTGGATTCA
TP23726	TGCAGCAAAGCAAACA[A/G]ACAGATTCAGAGCAGGACCCAACGACAGTGACACAACAAACACATGC
TP23729	TGCAGCAAAGCAAAGC[A/C]AAGCCAAGCCAAGCCAAGCAGGGGAAGGCCGTCAGCATCATCGTCGC
TP23749	TGCAGC[A/G]AAGCCACGCGCAGCCCTGACCCCTGAGCCACCCTATGCACATAGCACCTTATTGACA
TP23755	TGCAGCAAAGCCGCATGGAGCC[C/T]CGCCCCGCATGCTCGGCGACCTCGACAGTCGACACCCTGCG
TP23756	TGCAGCA[A/T]AGCCGCATGGAGCCCCGCCCCGCCTGCTCGGCGACCTCGGCAGTCGGCACCCTGCG
TP23762	TGCAGCAAAGCCTCATGGAGCCCTGCCCCGCCTGCTCGGCGA[C/T]CCTCGGCAATCGGCACCCTAG
TP23764	TGCAGCAAAGCGAATGCATGGGCTGGCAAAGAGGCT[A/C]TTGGCCCAAGTCAACTGAAAGGGGCCA
TP23774	TGCAGCA[A/G]AGCTAGCTTTGCGTCGCGCATTAATCAAGAGGTATGTACTGTATGTTGCAATAACA
TP23794	TGCAGCAAAGGAGGA[A/G]GAACAGTCACGTGAGAATTCGTCACCGAATAGCAGATGGGAGAACTGG
TP23809	TGCAGCAAAGGCGCATCACGGATCAGTTAAAAGCGAGCG[A/C]GCAGATCTGATGCGTCGCCAGTAC
TP23860	TGCAGCAAAGTGGAACGATGTGCTCAAGGCATCCTTCAGTTACGTTGCTCG[C/T]GGAAGCCGAGTC
TP23879	TGCAGCAAATAAGCACGCAGCAAGCACTATTCATCCAGAAGAGACT[A/C]ATCCAATATGGAGCACA
TP23893	TGCAGCAAATAGCAGCCTGCACGTTCAACCACTCGGGCTCGCCTATA[C/T]GTCCTGCGGCTCCAGC
TP23912	TGCAGCAAATCAGATTTGAAAATTGCTAAGATCTCTAAATTC[A/C]AAAAGGCTACGGTTCAGTAGA
TP23920	TGCAGCAAATCCAAATCCAGCACGTTCAGAAACCCTAGGTTTAGGTTTTAG[G/T]CCCCGAGCCGTG
TP23921	TGCAGCAAATCCAAATCCAGCACGTTCAGAAACCCTAGGTTTTAGGCCCCGTGC[A/C]GTGCCGTGC
TP23927	TGCAGCAAATCCATATTGGCCCACTGTT[C/T]CTTTCTGGTTTTCCTGTCTCTTCCCGCTGCCTTTG
TP23934	TGCAGCAAATCGATCTACCGCAACATCTGAACGCATAAGCGGG[A/C]GACAGAGGAACGGTTCCGTT

Table A2 (cont.)

TP23941	TGCAGCAAATCTCTCTCGAC[A/C]ACGCTTCTAATCTAAGGTTTAATTAACGCCATTGGTTTGGTTG
TP23951	TGCAGCAAATG[A/G]AAGGCACTGCATGCGCCTGTACGTGGCGCCGCGGCGTCTGCTTTCAGTTCAG
TP23953	TGCAGCAAATGAACTGAGGGGTTAGGAGACGAGCTCGCTGTAATCCTCGCCCTGTCGTCTCGG[G/T]
TP23969	TGCAGCAAATGATTG[C/T]TGTTGCACATATGAATGAACCACTCTTGCGCCCTCATCGATGATAATC
TP23971	TGCAGCAAATGCAACTTGAATTTTATTTTAGGGTTTGTTGAGGACTAAAGCTGGAGCCGCC[A/G]AT
TP23988	TGCAGCAAATGGTCTACTTCAACGTTTGATCTGCTATACACGAGGC[A/G]CTGCGGTGGTTGTGGTG
TP24004	TGCAGCAAATGTTCCTTGTTTTGTTATGTTACTGTGGAGCTGATTAAC[A/T]TTAAACTCATTCTGA
TP24017	TGCAGCAAATTAGGAAGGCAAAAATCAATTCCCATAACAATC[A/G]TGATCAATTCCGCGATCTTGC
TP24021	TGCAGCAAATTCACGTTACCA[C/G]CTCTGAACACTGACACAGTGGACCTCTCCGATAGACCATGAC
TP24036	TGCAGCAAATTGATCAGGCGATCAATTTCGTCGCCTGGGTCCAGATTGCTGCCTGGCCGC[A/T]GCT
TP24042	TGCAGCAAATTTATTATTGAAGCATGTGCCTGT[A/C]CCTACAGCCTCATAGTTATCCACTGTGAAT
TP24047	TGCAGCAAATTTTATC[A/G]GATCCGATCTTAAAACTCGTGACGAGATCGGAATCTGTCCCGCATGC
TP24053	TGCAGCAACAAAAGCGCGCGGCACGGCACGGCAG[A/C]CTGACGCGGAAGCTAAATACAGGCAGCAG
TP24060	TGCAGCAACAA[A/C]CAAAAACACCAATCGCAACTCTCAGTACCCACCATCCCAGCGCAACGCACCA
TP24062	TGCAGCAACAAACAC[A/G]CGCGCCACGGCACGGCAGCCTGACGCGGACGCTAAACACAGGCAGCAG
TP24108	TGCAGCAACAA[C/G]CTGGGTATTATTTATGATTCTATCCATCCTGCTGATGGATTGCAACTGGAAT
TP24115	TGCAGCAACAACTAATGACGAATCGAGACGAGAAAATAA[C/T]CCCAGCTAATTTCGGACGCTGATA
TP24139	TGCAGCAACAAGGGGGCACA[G/T]ATTTTTAGCTCGAATCCAGCAGCCTTCAACAGGCCAAAGAAAT
TP24146	TGCAGCAACAATCAAACGTGGAGACGCTCCACGAAGCCA[A/G]CGCAGCAGCGCACGTCGCAGAACG
TP24151	TGCAGCAACAATCATGACCACTTA[C/T]TAAAAATTAAATAGACTGACAAGTGACAACAACATAAAG
TP24173	TGCAGCAACACAAGCCGACCACCATTCTT[C/T]CTCTCCACCGTGCCCGAGCGCTGCCGCCCGCCTT
TP24191	TGCAGCAACACATTGGGTGAGCATGGTGCACGTGTGGCTCCCAATCT[C/T]GTTGTGCAGGAGCGGC
TP24213	TGCAGCAACACCGACGAGGCCCTGCGCGTGACCCCGCCGCCACTGCGTGGC[C/G]ACGCCGTTGGAC
TP24220	TGCAGCAACACGAGCAAGCAGGGACGCTGCGAGCTCTGCC[A/G]TTTTAATGTCGCTGGTCGTGGGG
TP24223	TGCAGCAACACGCAGAGAGCGAGGGAATCAGCGAAGCCCATAAAGAAGGATGGGTTTCCT[C/T]CAT
TP24224	TGCAGCAACACGCCGTCGTCGGCGTCAGGCGGGGGCGCCCT[C/T]GGCCTCCTCGGCGCAGCCGCCA
TP24227	TGCAGCAACACGGGCGCTTTCCAAAATCCTAATCCACGGCTAGCTTACG[C/G]TTACGGAAAGATCA
TP24242	TGCAGCAACACTCGTGCACGGGAAAAAATCAGCACGAAACTTGTAAAAAA[A/T]AATCGCGAAAAGC

Table A2 (cont.)

TP24267	TGCAGCAACAGAGAAGAATTGACAACTAGCTCAGTCTGATTGTCGTTTGGAGC[A/G]GGAGGAGCAG
TP24280	TGCAGCAACAGCAACAGCAACAGCAGCAGCA[A/G]CAAATCAGCATCGCCAGGCCACACGACACGAG
TP24285	TGCAGCAACAGCACCGTGGACTCGAGCGGTGGCGGCAGCGGC[G/T]GTGGCGTCCAGGCGCCTATGC
TP24294	TGCAGCAACAGCAGCCACGCCGA[A/C]AGTTACAGGCCACAACAACGCCTCCACTAATCAACCAGCA
TP24299	TGCAGCA[A/G]CAGCAGTTGAGCAGCAATCAAACGCTAGGCGCAGAGAGGGAGCTATGTCACCCAGC
TP24304	TGCAGCAACAGCCACAGCAATAG[C/T]CGCTTATAAGGGCTTCCGAGCTTTTGCCAGTACAACCATT
TP24311	TGCAGCA[A/G]CAGCCCTTCCCCAACTCCTGATGGATGGATAGATGGATGGATAGACCATGCATAGA
TP24323	TGCAGCAACAGCGCTGG[G/T]GATGTTGCTCACCGTCTCTATCTCTGTCTCGTCGAAACGACATGGC
TP24324	TGCAGCA[A/G]CAGCGGCTGCGCTCCGTGCGGAGGCGGACGCGGGCGAGCAGGACTATGGCGCCCAG
TP24329	TGCAGCAACAGCTACCTTGGGAGGGGGTGGC[C/T]TAAACACACTGCCGCCTCCCGCTGCCCGTTTC
TP24332	TGCAGCA[A/G]CAGGCCACGAGCATACAGCTGCCCCGCCGCAGCCACATCCGCCTCCTGCCCGATGA
TP24333	TGCAGCAACAGGCCGCAGGC[A/G]GGCACACACTGGCCCATGGCCCATCCAACTATCCAAGTCCATC
TP24352	TGCAGCAACAGTTACAGATCCTATCTTGTTCGTTTGCAGAGAGGCGAGTAGTTACCAC[C/T]CATCC
TP24400	TGCAGC[A/G]ACATTAGTCCTTGCAACCAGCCCATGCTTGCTTTGATCCACCCTCCGCCGCTGCATT
TP24403	TGCAGCAACATTGGTGTCACCAAGAAAGTCCATGAG[C/G]AGGTGCACTACAGACCCAGCCACCTCT
TP24410	TGCAGCAACCAAAGCACCCG[C/T]TTTATCTCTCGCCGCCATGGCGACAATGGCGACTCTCCTGCGG
TP24413	TGCAGCAACCAACCACAACTGCCTCTGGGCTTCTTCCAGCTACTCCCC[A/G]CCGTCCTACGGCGTG
TP24459	TGCAGCAACCAGCAGACCACGGGCAAGCGGCAAACCACAGTAGGCAAGTGCAGTAGC[A/G]TGGGTA
TP24466	TGCAGCAACCAGGTTATATATACACATATCCATCAAACAAAGAAA[A/G]AAGAAGAAGAAGAAGAAG
TP24469	TGCAGCAACCAGTGCTTCGTCAGGT[C/T]GTGCTTCGGTTAGGAATTCCAGAGAGCTAGCACTTAGC
TP24473	TGCAGCAACCATCA[A/G]CATACTGCGCCAGAACAAAAACGACACACCCCTGATCATCAGCATTTGC
TP24514	TGCAGCAACCCCACTCAGGAGC[A/G]TTGCAGCTGCTAGAGACATGTTAAAGAAGCAACAGCCGCAG
TP24517	TGCAGCAACCCCAGCTTCGTGGTGTCCTCGTGCGCCACCTCCCTTGC[C/T]ACTGTGTTGGTCGCCG
TP24530	TGCAGCA[A/G]CCCTACTGCATGACTCTGAGGATGAACATCGACTGCAACGGGTGCTACCAGAGGAT
TP24535	TGCAGCAACCCTGCTGCCCCCGCTCCTGCT[A/G]CATCTCTCGTCAGCAGCAGCGGAAACCTTGTCC
TP24539	TGCAGCAACCGAGTGACCTCTGTTGGGCGGGGGCGA[C/T]GGAGGCCTTGAGGGGGACCCTGCCACT
TP24598	TGCAGCAACCGTGCTGTGTGC[C/T]CACAACATTTGTCATCGTCGAAGGACGGAGGCTAGAAGGGGG
TP24614	TGCAGCAACCTCAAGAGCTTTGTTATCAACAGTCATATACGTT[A/G]CTTTGATTGGCTCGGCAAAT

Table A2 (cont.)

TP24621	TGCAGCAACCTCCTCCTGCTGTCGTTTCACAAATCAGAATCCACATACAAATATCC[A/T]CCTCATC
TP24657	TGCAGCAACGAACC[A/G]TTCTACTCGGGTGACATGCACAAACTAAAAGAATGTGGGAGTTGGAAAG
TP24659	TGCAGCAACGAACGATCGAGCCCGCACGACATGGCCGTCGGCACACAATGAC[A/C]CAGCGCGCCAA
TP24666	TGCAGCAACGAAGCAAG[C/G]TGAGGAGCTGAGGATCCTCTGCATCGACGGTGGTGGCATCCGCGGC
TP24678	TGCAGCAACGACAGGAAAGGGTGATTTCGCCACGTCC[A/G]ATGACGGAGAAATCTTGCTTGAATTT
TP24688	TGCAGCAACGAGAGCAGATC[A/C]TCGGCTGTGCTGTATCTCTCGTGACTGGTAAGAGCATAGCACA
TP24692	TGCAGCAACGAGCACTGCACT[C/T]TGCACTTCCTACTAAAGATCTCATGGCAGCAACTTAGAGCAC
TP24695	TGCAGCAACGAGGAGTGGGCGGGCGAGT[A/G]GTTGTTGGTAAGTGGGGTACCACGGCTCAGAGCGC
TP24698	TGCAGCAACGATATCATTGACAAGTTCTGGCGTTTTCCATTATCTTGGATTATTTCGATG[A/C]TTC
TP24713	TGCAGCAACGCAAGCAAGAATCCG[C/T]GGCGAGGGCGAGGATGGAGGCACCACCCGCCACGGCCAC
TP24741	TGCAGCA[A/G]CGCCGTCGTGACGTAGTGGTCGGCAGGGAACAGCGCGTTCCTGACGAGCAGCGCGT
TP24747	TGCAGCAACGCGCAACACCGCGGCC[A/G]CGCGCCTACAAATACCCGCGCGAGCGAGGTGACCACCT
TP24770	TGCAGC[A/G]ACGCTCGTGCGGAGACCGCGCGGAGGCGGAGGCAGCGCGCGGCGGAGAGGACATGGC
TP24781	TGCAGCAACGGAGGAAGAGTGCTTGAGCGGAT[A/C]TGAGGCCGCCGCACCGCCTGAACCAGAGCGG
TP24798	TGCAGCAACGGCATGAAGATCCGCGTCTAC[A/G]TCGTCGCAGGGGGCGCCACGCCAGGCCCAGCCC
TP24839	TGCAG[C/G]AACGTCATGGACATAGTAGATTCGAGTTCCGCTGCTGATGCCATTATTATTTTCTCTA
TP24846	TGCAGCAACGTCGACAACACCTTGTCGTCAGCTAGTACA[C/T]CTTCCCTACCAGGCTAACCCTACC
TP24853	TGCAGCAACGTGAGAATAAGGTAATGAAAGCACTAACCTCTTAGCTGGCTCATGTGC[C/G]CCAAAT
TP24863	TGCAGCAACGTGTGTT[A/C]TCGCTTTCCTTATATATCTGGGGATTAGGGAGATGAAGAAACGAAAG
TP24864	TGCAGCAACGTGTTATTGAGTACACTCT[A/C]TGACTTGTGGGCCATTATGGTCAGTGAGTGTAATA
TP24866	TGCAGCAACGTTGTAGGAGTCGGATCATGCACGCATAGCAGAAGACAAGTCACAAGAACGTA[A/C]C
TP24887	TGCAGCAACTAGCAAGAAGACGCGACTTCCCA[G/A]CCAAACGCCAGATGCCAATCGCAGCGAGTTC
TP24899	TGCAGCAACTATGGCATCC[A/G]AAGGTTCCATGGCGACAAATGCAGCAATAAGAGCAGTCACAGCG
TP24909	TGCAGCA[A/G]CTCAAGAGCCTGCTCGGCATCGTCCACTTCACCTCCCACATGGGCTTCGTCGACGT
TP24914	TGCAGCAACTCACTCTAATATAATTA[A/G]AAAAAGGAGACATACATGGAGGAGTCCCATGACATCG
TP24928	TGCAGCAACTCCACGGGCCATGTCACC[A/G]CCCTCGACCTCAGTGGAATTGGATTGAACAGTAATG
TP24929	TGCAGC[A/C]ACTCCAGCACATCAAAGATGGACACCATGTATGGCCTATCCCGCGGCTGTTGCGCCA
TP24953	TGCAGCAACTCGTTGCGAATTCGGCTCTCCTCACCCGAAACTCGTCACGCATCGCGCGCTG[G/T]CG

Table A2 (cont.)

TP24955	TGCAGCAACTCT[A/G]TCACCTCCTCTTGCTCACGCCAGATGGCATTGCTTTCATTCCTACTTTCAA
TP24964	TGCAGCAACTGACCTACCAATACGCGTTGAAGCGGGCCTCTCTAGCC[A/C]TCGTCGCTAGAAGGGA
TP25010	TGCAGCAACTGTGAGTGAGAAGAGGATCGATCGATGCACGCACGGAGCGG[C/T]TGATCATTCCTTG
TP25021	TGCAGCAACTTCAAGCATGCTCGT[A/G]ATATTTTAGAACTCACTTCCAAAATATACCAAAACAGTT
TP25056	TGCAGCAACTTGTCTCCTCCCCAGACCCAGAGGCCCAGATCAAG[A/G]AATTCAGACCAAACAAAAC
TP25060	TGCAGCAACTTGTTGATGTAAGGATCGACGTGTACCTTTCTGTGACCGTA[C/G]GATCGGGTAAGCA
TP25070	TGCAGCAAGAAAA[G/T]CTCTTCTTCGCTTAATACCTGTGTGGTCTTTCCTCAGAGGGCTGAGTTTT
TP25108	TGCAGCAAGAAGCCAAGATTTGGGTCTTCGGCGTCTGCCTGCCAACGCGG[A/C]GTCTGCCAGCACG
TP25114	TGCAGCAAGAAGTACCCCGACCTGGAGGAGAAGAGCACCGC[C/G]GCGCAGGCCACCGTCGTCCTGG
TP25134	TGCAGCAAG[A/C]CAACCAACACAAAAGGCTCAATCCCGAGGCCAACGAATGAAACAATCGGAAGAG
TP25151	TGCAGCAAGACGAAATAAAAACATGCATGGCCAGCTCAA[A/T]GGAGCATGGCGAAATGGGAAGCTA
TP25156	TGCAGCAAGACGTGCGGGACGGAGACGGGCTGGAGGGC[G/T]CCGCCGTCGCGCCATAGGTGGCTGC
TP25158	TGCAG[C/T]AAGACGTTCGTCAAGTCGCAGGCGCTCGGGGGGCACCAGAACGCGCACAAGAAAGAGC
TP25161	TGCAGCAAGACTGGGCGATC[A/G]ATGGGCAGATGAAGAGTTGGAGCAGAGGAGGTACCTGGAGCGC
TP25166	TGCAGCA[A/G]GAGAATTCGTGGTGGTCAGAATTGCAAATTTTCGTCACAGCATGGATGGAAGGACA
TP25174	TGCAGCAAGAGAGGGATGAGCTGGACAAGCGGCCCTGGCGA[C/T]AGAGACAACCTCGGCGCAGGAG
TP25185	TGCAGCAAGAGCCCGATCTGAATCTAGGTGAGCCACCCTAACAGCGAAGGAAAATGAT[C/T]CATGA
TP25208	TGCAGCAAGAGTAGATTCA[C/T]TGTCAGCCTCCGTAGAGAATGTCCGCAGCAGCTGCGGAACTGAG
TP25211	TGCAGCAAGATCACTGGGTGCCGCGGCTGATCGATGCGATGCACGCATATAT[A/G]TGTGTGTGCAG
TP25233	TGCAGCAAGATGTACATATCTCTCTCGTTCTATCT[A/G]GTGTTTTAACTGTGAGGCCATTGCATTT
TP25235	TGCAGCAAGATGTATTGATCTCTGTCGTTCTACCTGGCGTTTTAACTGTGAGGCCAAGCCA[A/T]TG
TP25236	TGCAGCAAGATGTGCTTGAATTCTATATGCCTAGCTCAATTTGTCGG[A/G]TTCAGTTGCTTCCCGT
TP25237	TGCAGCAAGATGTGCTTGAATTCTATGCCTAGCTCAAT[A/T]TGTCGGATTAAGTCGCTTCCTGTAG
TP25268	TGCAGCAAGCAAGCCATTACTCATTTACT[C/T]GCTTCTTGAATTGCACGATTAGATTTCCATTTCC
TP25269	TGCAGCAAGCAAGCCTTCTGCATGCATCGATCGGCCAGTCAGCATCCAAGTGGA[C/T]GCCCCTGGA
TP25271	TGCAGCAAGCAAGCG[C/T]AGCAGATTACGTGTGCCACGGTCTGCACGCAGCTGCACAGGAGACGAT
TP25292	TGCAGCAAGCACCATCTGC[A/G]CGTTCCTCATCTCAGACTCAAGGTTCTCCACGTCTTCGGCGAGC
TP25295	TGCAGCAAGCACGAAGCACCTCAACATGGTGCTGAGTAGTTTGTTC[A/T]GACCAGCTGCGAGGTGG

Table A2 (cont.)

TP25297	TGCAGCAAGCACGACCAGCTGCGCCGTCCTCCT[A/G]CCGCTACCACCGAAAAAAAAAAAAAAAAAA
TP25303	TGCAGCAAGCAGAAAGGAGCTCCTAACA[G/T]GAACCTCAACTCTGCTTTTGCACATCCACATGGA
TP25322	TGCAGCAAGCAGGCATCATCATGATCAGGAAGCAGCAGGAGATGCGCGCCACTGCCA[C/G]GATCGG
TP25381	TGCAGCAAGCCAGCAATCAAACAACCTGGGAGGGAGGGGAGGAACGGAGGAGCG[C/T]GTGGAAGAG
TP25391	TGCAGCAAGCCATGGCCAAGCTGAAGCAATCCGC[C/G]GCCAAGCCGTGGCAAGCCACAGCTGGCCG
TP25423	TGCAGCAAGCCTGCAAGCGAAGCTTCCATGT[C/T]CATGCACCGATGCACGCACGCGGCGAAAAAGA
TP25427	TGCAGCAAGCCTTCTTCGCCACGCCGCAGCCAAGAAACGAAGCGCCGCCCCAGCAGCCGCCGA[A/C]
TP25428	TGCAGCAAGCCTTCTTCTACCTTCCTC[A/T]CTCCAGTTGTTCCGCACTCCCCACCACAGCCTAGGA
TP25432	TGCAGCAAGCGAAAGAAAAACGCACTCGCACGCAGACACAGTGACACAGCACGCA[A/G]ACACAAGC
TP25440	TGCAGCAAGCGATATAATTGGAAACAAACAAACGCTCTGTAAATAAACTAACGTTACATCC[A/C]CC
TP25447	TGCAGCAAGCGCCTACAGAACGAAT[A/G]CGGATGGAATCAAATTGAAAGCACAGCCCTCCAAACTA
TP25457	TGCAGCAAGCGCTAG[C/T]GGTAGTGGACGCACGCGCCGCTCCCAACCGAGACGACGAGCCGCCCAA
TP25458	TGCAGCAAGCGCTAGTGGCAGTGGACGCACGCGCCGCTCCCAA[C/T]CAAGACGACGAGCCGCCCAA
TP25462	TGCAGCAAGCGGCCCTAGCATCTACGGCTAGCGACCCCA[C/G]CATCAGCGGTCGGTGGCCTCCTCC
TP25481	TGCAGCAAGCGTGCGTGCGTGACCGTCACGGTAGAACAGGGGGGGTCTGCACCTGCGA[C/T]TGGCA
TP25499	TGCAGCAAGCTCACAGCGTGGCCAGCACCCAGCATGGATGGCGCCGCGACCCCGAAGGC[A/G]GGCA
TP25512	TGCAGCAAGCTCGAAGCAGCAGTCAGCGAGAGCCAATTCCCC[A/G]AATCGCCCCTCCCAAATGCGA
TP25523	TGCAGCAAGCTGAGGTCG[A/G]TGCCGTTCGCTCGCAGCCTCGCAGGCAAGGGCGTCCATATGCCTG
TP25550	TGCAGCAAGCTTTTACCACGCGGC[C/G]AAAGCACAGTGCAATATGCAGCAGGGGGCAGATTTGTTC
TP25564	TGCAGCA[A/G]GGAATAGGGATGAGACGATCAGTCATGGCGACGGCAAGAGATCTCGCGCCTGCTCC
TP25580	TGCAGCAAGGA[C/T]CGACGACCCGCACACCTTTGGTTTGGGGTTTCTCAGCTCAGGTGTACTAGAG
TP25589	TGCAGCAAGGAGCGCCCCGCGCAT[A/T]TGGGTTCAGCATCCTGCCAGTTCGTGCAGCTGGACTGCT
TP25601	TGCAGCAAGGATCGAATCGATGACCCGCACACCTTTGGTTT[A/G]GGGTTTCTCAGCTCAGGTGTAC
TP25604	TGCAGCAAGG[A/G]TTGCTTTGCTGACACTACACTGCCAGCCTTGGGACAAGCAGGAGCTTCTCCTT
TP25610	TGCAGCAAGGCAACTCGG[C/T]AAGCGCCGCCGTGCGGCCACGAGCGAGCGCACGGAACGCAGCCGC
TP25613	TGCAGCAAGGCAAGAACAGCAT[C/G]AGCATCACGCAGACGATGGCGTTCGGGCCCTTCTTGGGGGT
TP25617	TGCAGCAAGGCAATTTCTTACGTCCACTTTAGAGCGACAGTAGCGTCCTGCAAGGGTCAGTCC[A/G]
TP25624	TGCAGCAAGGCAGAGAAGCCCTCCGCACACAACAGAAATAGGTATGGTGATAAC[A/G]GGTCTCCTT

Table A2 (cont.)

TP25639	TGCAGCAAGGCCACCAGCTTGAATAAGACCACTACTGATCCTGATTAATTTGTTGTTAAACA[A/C]C
TP25642	TGCAGCAAGGCCAGTGTCGGCCTGGGTTTGG[C/T]CAGTGCTGGCTAGGAGGCTCGGGCAGTCTAGG
TP25649	TGCAGCAAGGCCCTTTCAGGCGC[C/T]TGTCGTGAGTACGTGCGCCATGTGGTGACCCACGACGAGG
TP25651	TGCAGC[A/C]AGGCCGTTGACGCGCTCTCTCGGCCGAGGACAAAGAAGGCGAGGAGCGGCAGCGTCA
TP25653	TGCAGCAAGGCCTGAAGAATCATGTAACTTGGCTATGCATCTGGTGGTTCTATTTAATGAA[A/G]GG
TP25659	TGCAGCA[A/G]GGCGACTGCACGCCGACTCGCTGAGTCGCCAGCCATGCGAGTATAGGTATACTCGT
TP25667	TGCAGCAAGGCGGGTGTCTTCTT[C/T]CCCGCCCACGGTGATGGCCCCCGCGGCCACCATCTTGCCG
TP25671	TGCAGCAAGGCGTGCGAGGAGATGGACCCATGGGCCT[C/T]GCCTCGCAACGGTACACAGCTTTTGC
TP25673	TGCAGCAAGGCTCACAGCTAGCGTGGCCAGCACCCAGCAGCA[C/T]GGATGGCGCCCCGACCCCGAA
TP25682	TGCAGCAAGGCTTTGAAGAATCTTATACACATTATTCAGATTTCTGCAACATACAACGA[A/G]CAGA
TP25690	TGCAGCAAGGGATCACAGTGGTGGGGGCAAATTATCAATGGAAGTTTCATT[A/G]AGAGTTAAATGC
TP25696	TGCAGC[A/G]AGGGCCACGACAGCCAGCCAGCGCGCGAGCGCTTTGCGTTGCGTGCTTGCCTGGAAC
TP25766	TGCAGCAAGTAATGCCTCGCGGCAGC[C/T]GCAATCAATGAGCTGATTGTCCAAACCACCCGCAGCT
TP25776	TGCAGCAAGTAGGTGGAAATGAACCGTGC[A/C]AGTAGCTTAATCGAAACAGTCAGTAAACGAGAAT
TP25785	TGCAGCAAGTATGTTTGCTGGA[C/G]AATGGTGCACTATCATAGAAACTATTTTCAGTGACGCCCTA
TP25793	TGCAGCAAGTCAGTCAGTGGCTGTACGCCATCTAGACGGTCGGATCCGAA[A/T]CAGACGGCTCAGG
TP25794	TGCAGCAAGTCATCGCCGCCACCACCTTCTCTCTCCTCCAACGT[C/T]TTGGCCAGCGCGAGGAGAC
TP25804	TGCAGCAAGTCTAACAACCCTTCAGAA[C/T]TTCACCGTCAATCACCCGCTGATCTCTAAATTTCAC
TP25807	TGCAGCAAGTCTGAATCTTTCGTCTC[A/T]GGGGATCCATCTCACTCTGCATTCTAAGCTGGAAACT
TP25808	TGCAGCAAGTCTGCCCTCATGGCCTTGACGCTGTGGGCGTCCAC[C/G]TCCCTCCTCACCGCCTGGA
TP25823	TGCAGCAAGTGCAACAGCGACCTAAACCA[A/G]TATCGTACAAACTGCAAAGACATTTGGTTGGAAG
TP25864	TGCAGCAAGTGTAGTCTTTGGACACGGCTCCACTTCGGGACAGGGGTTGGGCGG[C/T]GCCCAACTC
TP25868	TGCAGCAAGTGTCCGCCCGCGCGCGAGCACGGTCCGTGACCGTGCCGCCGAAGCCCT[C/G]GCCCCC
TP25899	TGCAGCAAGTTCGGCTACTGCGGCACGACCGAC[C/G]CCTACTGTGGTGACGGGTGCCAGTCGGGCC
TP25901	TGCAGCAAGTTCGGTTACTGCGGCACGACCGACGACTACTGTGGCGACGGGTGCCAGTCGGG[C/G]C
TP25918	TGCAGCAAGTTGTCAGGGTCGGGTCGAGTGTGCGTC[C/T]GTGCCTGGGTAAAGAGCGTGAGAAGAC
TP25931	TGCAGCAAT[A/G]AAAGCCATCATGGGAAAGCGGTCCTCATCTGCCATCAGCTCTCCTCGGCAGCAA
TP26028	TGCAGCAATAGTTGAGGAGCTAGAAATAAGCTGAAT[A/G]AACTCCACTGTATGAATATATTCATGC

Table A2 (cont.)

TP26039	TGCAGCAATATTGAATTGCCTCCATTTGACCATTTGTTC[C/T]TGTCACGTTTAAATTGATGAAGGT
TP26058	TGCAGCAATCAAGGCACACAAAGCGCGTCCAATTCAATGTCGCAAAATTGCTCGTTCTTTT[A/T]TT
TP26072	TGCAGCAATCACTAACTAGACGGCAATCAGCAGAGGCAACAACGCAGCTGCACC[A/C]AGTATCACA
TP26094	TGCAGCAATCCAGGCTTACGGTTTCTGGTTGCAGACTGGGAGAGGCTGCCTGGATT[C/G]GGTATTG
TP26100	TGCAGCAATCCCGAGTTGCTCCAGAACACGCCATCCATTGACATGGACACC[A/G]ATGGAGCCGCCA
TP26112	TGCAGCAATCCTTTATTCGCGGTCT[C/G]AAACCAGCAAATTACTAGTTAATTAAGCTGCGCAGGTA
TP26125	TGCAGCAATCGCCTAATTGCTTTAGACACCGCAATTACCATCCTGGACTGA[A/G]TCACCGATCGCT
TP26126	TGCAGCAATCGC[C/T]TTGGCACGCTGGCGAGACATCCGTTCACTTCAACAGTGCAAGATTATCATG
TP26162	TGCAGCAATCTGCACTTGGTCGAGTGGG[A/C]ACTGTCCCTTGCTATCGGAATCGGCGAGCTCCAAA
TP26168	TGCAGCAATCTGTAAAACAAACAAGTAGTACTTCAGATGGGTCCGATCT[A/G]CGCTGATTGCAACA
TP26204	TGCAGCAATGAGCGGCGCGCATCACGA[A/G]GAGCAGATGATGGCTGCCTCTCCTTGGCCCCCTCAC
TP26210	TGCAGCAATGATAATCACAATGTCTACAGTGCGACTGTGGTGGGAGTGTGTGTT[A/G]CATTTGAAT
TP26229	TGCAGCAATGCAATGCAACTTTGCATTCGGTATATCGTCATCAAGTGCTATCCAG[C/G]CAGAATGG
TP26238	TGCAGCAATGCACTGCCCACTGGGGATGTTCATGTCCTGAAGCAAAGCTATAG[C/G]TTAGCTAGGA
TP26259	TGCAGCAATGCGATGCGCCTGGCTGCCTACCGCA[C/T]CTATCGTACTATCTGGGATTCTGGCCCTG
TP26345	TGCAGCAATGGACGTTGGAGTTGGACGCAGCACCGTCCAGGTCACAGG[C/T]ACCTCCTCACGCACT
TP26360	TGCAGCAATGGATGGGGCTTTTTGTTCGTGAGCTTTGACCACATGGG[A/G]AAGAAGTAAAAAGCGG
TP26370	TGCAGCAATGGCCGTAGGTGTTCGCT[A/G]GTGGCCATGGCCACGTGGTGAATGCTGCTCTGCCGCT
TP26397	TGCAGCAATGGGCTTAATGCCTGGTTCCCCATCATC[A/G]GTTTCAGCGGTAATGTCCCCATTTACC
TP26409	TGCAGCAATGGTGAGCAT[A/G]CAAGTGACGGCAGGGATTGTTGCCAGGGACGATTCTGCTCCAAGA
TP26411	TGCAGCAATGGTGGACCTAGTGGGGTGGTG[A/G]GCTGGTGGCCTTCTCACAGCGCCATGATTGGAG
TP26430	TGCAGCAATGTGCGCAGAGATCTTTCTAATGTTGGTGAAGGGTGGGAAGATCGATCCCTTG[A/T]CA
TP26451	TGCAGCAATTAAGCAACCCTATCAAAA[A/T]GGTAAGAGTTGTTGAACCAAGGTCCAAGGCCAAATA
TP26454	TGCAGCAATTACAGCAAATTAACTTCGCCAG[C/T]TCTAATGACCTGCTTCGGTTAAATGTATGAAG
TP26475	TGCAGCAATTCCAGTCAGAGTGGGCGGAGACAGACGGAC[A/G]AAGACAGATGGCCCCCGCGGGGCC
TP26502	TGCAGCAATTGAGAAAATCCATCCCCTATATGTACATGAGACCCACATGTCATGGCAACTCTC[C/T]
TP26510	TGCAGCAATTGCTGCCTCCCTGCCTGTAGCGGCAGCCGCGGAGGCGAGC[A/G]CCTCTCCCACCGTG
TP26512	TGCAGCAATTGGAAAATCATATCA[A/G]AAACACGGATTGGAATCTAACTCCAGCAAGATTTGGTGC

Table A2 (cont.)

TP26514	TGCAGCAATTG[G/T]GAGTTTGGGGGCACAGCAAATCAACCACAGATACACACGTACATCACGAACA
TP26541	TGCAGCAATTTGCATGCCTAAATCGCTGTCAGTGCCTTGTCTGAAACCCGTGCAGGT[A/G]GGCACA
TP26555	TGCAGCAATTTTTCCCCTGTCCGAGCAGAGCCTCAAGAGCTGCGCTTCCAG[A/G]GGTGCATCCACG
TP26565	TGCAGCACAAAAGGATTTAAGCGTTCAAACAGCAA[A/G]GCGTAAACTAAGGACAATGGAAGATGAC
TP26567	TGCAG[C/G]ACAAAAGTACTGCAACTGTTTCCAGTGGCACAGAAAGAAGAATGAAGGATCCACGGAA
TP26571	TGCAGCACA[A/G]ACAGGACAGGTCCAGAAATTGGGTTGCATCCCACTTCACTTCCCTTCGACGAAG
TP26593	TGCAGCACAAATCTCTTTCGTGTTCTTGTTCGTTCACCTCCTGCTTGCATTCAG[C/T]ACGCTGCTG
TP26623	TGCAGCACA[A/G]CCCTGACACTCGGACTTGCGCCATTAAAAGCTGTAATTGTTCTGATGTTTCCAG
TP26641	TGCAGC[A/G]CAACGGAATAGCACCGCTGCCCATATAACCAGCGTCAGAGAGCAATAACTCGATCGG
TP26654	TGCAGCACA[A/G]CTCTCATATCACATAGCCTCTCAACTAGTGCCCTGCACGGAGCAGAAGCAGATT
TP26658	TGCAGCACAACTGCACTGGCTAGGTA[A/G]ACAGGCATCGGGGGACGGGGAGCATCCGAGAGCATGT
TP26659	TGCAGCACAACTGCCAGTCGCCCGCCCTCTAGTCTTCT[C/T]GCCGTCTCTGTCCCTCTCGGCCTCG
TP26664	TGCAGCACAACTTCCTGACGGG[A/C]ATCGAGATATCGCCGTCGTCGTCGCTCCCCTCCACCGTCTC
TP26681	TGCAGCACAAGATTTCTGCCGCCGCCCTGC[A/G]CGCCACCGCCAGCCAGGCATCCACGACGGCAAT
TP26688	TGCAGCACAAGCAGGGAAT[C/G]TGCCATCTTTTCCAAGATGTTGTACGGGCGTACGGAACATGTAG
TP26698	TGCAGCACAAGCGGGCGGCCCGACACGA[C/T]GAGCACGACGCACTTGACGAGCCCGCACACGTCCT
TP26699	TGCAGC[A/G]CAAGCGTGTGTCAAAGCTGATGAACGTGATGCTGCCGCCACCAAACTCAAGCGCAAG
TP26703	TGCAG[C/G]ACAAGCTTCCCGCCGCCGCCCCTGCGCACCAGCACGAGGGCCACCACGACGGCGACGG
TP26704	TGCAGCAC[A/G]AGGAACATGTCCAGGAACACCTTCGTCATGCCCAGGAGAAGGGACGACATCGTGC
TP26719	TGCAGCA[C/T]AATAACAACCACAACAACCTAGGAGTATACGACAGCTTCGACTTCGCTGCCGCGGG
TP26723	TGCAGCACAATA[G/T]ATATAGAAACTATATACACACGCATATCAAATTACAAATTACAGATATCAT
TP26730	TGCAGCA[C/G]AATCTGTTCACTAAGGTAGGTCAACTCCCTGCCTACACATTCATTGATTCATATAT
TP26743	TGCAGCACAATGTGTGTCAGTCA[A/G]TTACGGATGCTGCACTAGGTTAGGTCCCTTAATTTATTAT
TP26754	TGCAGCACACA[A/G]ACGTAAAGTAAAAACGAAGAAGAGACACGAATACGAGACGAGAGAGGCCGCG
TP26766	TGCAGCAC[A/G]CAAGCGCTAGCGAGGGGCCCTACTGTTGTTCATTCACACAATCATAGCATAGACA
TP26770	TGCAGCACACAATGGACTATGGTCCACAGACCACA[G/T]CATTTTGGAGCACGATCAAAGCCCGCAG
TP26772	TGCAGCACACAATGGACTATGGTCCACAGCATTTTGGAGCACGATCAAAGCCCG[C/T]AGGTTCCCA
TP26776	TGCAGCACACACAGAAAGGGTAGAGAGGAAAGTATGGCTTCCCTGACAT[C/T]GGTGCTGTACGGAC

Table A2 (cont.)

TP26780	TGCAGCACACACATCGCAAACAACCCCCAATC[T/A]GAGAACTACTGCGCCCGAATTGTCGCGCTAA
TP26781	TGCAGCACACA[C/T]CACCTCACAATCCCCAAATCCACCAATGCTCCGTTTCTTTTGAGAACCAACA
TP26782	TGCAGCACACACCATCGTCAGAAACCCGTCGTCAGGTCGAGCCAGCAGAGATCGATTATAC[C/T]CC
TP26787	TGCAGCACACAGATACTCGAGCTCGGACTCGGAGCAAAGA[A/G]AGCAGCTAGTTAGTCACTTATTC
TP26792	TGCAGCACACAGCATTTTCCGCAG[C/G]ATCACCCACGGTCGGACAAACTCAACCTCACGGCAGCAC
TP26811	TGCAGCACACCAACCTGGTGCGCCTCGTCGGCTGCTGCGTC[C/G]AGGACGAGGAGAAGATGCTCGT
TP26812	TGCAGCACACCAACCT[G/T]GTGCGCCTCGTCGGCTGCTGCGTGCAGGCCGACGAGAAGATGCTCGT
TP26813	TGCAGCACACCAACCTGGTGCGCCTGCTGGGGTGCTGCGTGCAGGCCGACGAGAAGA[C/T]GCTCGT
TP26831	TGCAGCACACCCAAACCGTCGCGTGGGCGAGCGAAACAGCGCCCCCTACGGC[A/C]CCAAACGGCAC
TP26838	TGCAGCACACCGAGAAGAAACAGTACCCAGCAACATGAGTCC[C/G]ACGCCGTGCTGTACCTGAGTC
TP26845	TGCAGCACACCGTATGCGGCA[A/G]CCACTAATCTCGCTGGGTGCTGACCTCGACATCGCCTACGAG
TP26862	TGCAGCACACGACGCAAGCAATTCCGACATCAGAAAAGGTGTAAGCATGCAC[C/G]TCGCCGATCGT
TP26865	TGCAGCACACGACTGAGGCGAGC[A/G]GCAAGGCACGACGGGGTGACCCACCAGCATTCAAGCTCAG
TP26876	TGCAGCAC[A/G]CGCTATCAGTGCAGAGCCTCTGCGCTGCCGCACCACATCCTGAAGCTGCCATGCT
TP26877	TGCAGCACACGCTCCGCCTCGCCGTCGCCAGGTGCGC[A/T]GGGGCAAAAGGGTCTGGGCCCACATG
TP26886	TGCAGCAC[A/G]CGGCCGATAGGCACGTGTTGCCATTCTTCACACAGGACATGATCGGAGACGATGA
TP26887	TGCAGCACACGGCGTGCCCCGAGAGCGTGGCGTTCCACTTCCTCA[A/C]CGCCGACGCCGACGACCA
TP26917	TGCAGCACACTGGCACTGCCTGTTGGTGCTTGGCCCTTC[C/T]GCATGTGATGAACAACAGAACAAA
TP26926	TGCAGCACACTTGTTTGTTCTAGCCAGATTCCAGAAATCCAGTGACAAGTATCCATTAAGG[A/T]CA
TP26929	TGCAGCACAGAAGAGA[A/G]TTGGCGGTCATGATCTTACTCGGCGCATCATTGTGTCCCCTGGGTCT
TP26936	TGCAGCACAGACACGACAGGTCCAAAAATTGGGTTGCATCGCACTTCACTTCCCTT[A/C]GACGAAG
TP26939	TGCAGCACAGACAGGACAGGTCCAAAAATTGGGTTGCATCCCACTTCACT[A/T]CCCTTTGACGAAG
TP26948	TGCAGCACAGAGAGCGCCGCACGGCGAGGCGCCACAGCCCAC[A/G]CACAGGCTGGAACCAACGCCT
TP26960	TGCAGC[A/G]CAGATTTTTCTTTTATTTTTAACATTTTTTTAAACTAATTTTAAATCTAACACTGTT
TP26964	TGCAGCACAGCAACGTCGGTAGCCCCCGCGGCCTCCTACTCCGTCCCC[G/T]CCCGTCCCGTACCCG
TP26969	TGCAGCACAGCACAGAACCAAAGCTCGGTCGGTCGT[A/T]CCACTGTTGTTGCTTCGCCAATTGTAC
TP26973	TGCAGCACAGCACGCACAGTGCATAGCTCGCCGTGGCT[A/C]TCCACAACGCATACAGTAGGGCTGT
TP27005	TGCAGCACAGCATTGTAGGGGTCGCTGGCCCTTGACC[A/G]TCTGCGGCTGGCCGCCTGGCTCCGCC

Table A2 (cont.)

TP27008	TGCAGCACAGCCACCACCACCACCAATTTCGTTCTTCCAAAGTCTCATCACGACGTAAC[G/T]GAAG
TP27014	TGCAGC[A/G]CAGCCCGCACGCGTGCCTATCGGCGGCCTTCCTCCAGCAGGCGGCGGCGCTGCTACG
TP27020	TGCAGCACAGCCGC[A/G]AGGTGCGCGCTCGTGCCGCCGATCAGCCAGAACTGCTCGTTCCGCCACC
TP27036	TGCAGCACAGCGTGGCGTACTGGCTCA[C/T]GCTGGACATCCTGTCCTCCGCGCTGCCGCCCGAAAA
TP27039	TGCAGCACAGCTGAGCACGGAAAAGAGAG[C/G]TCTCGGCCCCTCCCAGCCTCTCTTGGTGTCGTCT
TP27043	TGCAGCACAGCTTGGTCGCTGTCCGTACGATGTCCCGCCGCTCCCGACGGCTCGGCACGGT[C/G]AG
TP27078	TGCAGCA[C/G]AGGGTGCGGACGGCGTCGGTCTCGTCGGGGCAGCATGCGGTCACGACGCACTCCGC
TP27081	TGCAGCACAGGTGTATGCCATGAGCTGACGACTATGATGATATAGAATTGAAAG[A/G]TGGAGAAGC
TP27087	TGCAGCACAGTAAGCTGGGAGAGATTGGCAAGAACAG[A/T]TGGAACAGGGCCAACCAAGTAGTTTG
TP27097	TGCAGCACAGTA[C/T]TTATTTTTTTGGTTAGTAAAAGAACATAGTTTAAGACATGACATGAGCAGG
TP27112	TGCAGCACAGTGCCAAAGACAGCAGGCCAGCACCCAGCCATACACGCCCGTACCTACCTCT[A/T]CC
TP27129	TGCAGCACATACAGAATCAACAGATTGCCTTTGAGGAAGGAAGGCCAACAAATACG[A/C]AGCAACG
TP27149	TGCAGCACATATGGCCAACTCCAAGCTGCCA[A/G]AGCATCGTGTCCCACGAGGACGCTGCTGAAGA
TP27167	TGCAGCACATCATAT[A/G]ACACAACTGAAACAGCAGAACTTTGTTTTCTCACAATGGGGAACACTT
TP27176	TGCAGCACATCCGTTGCCCATGTACTTGGATGA[A/T]AATTTGGAATCGTCACCCCCTCAACCTTTT
TP27190	TGCAGC[A/G]CATCGGAGTTGGAGCCGACGGCAACTATGGCGACGGGTACTTCTACGGCCGCGGGGA
TP27225	TGCAGCACATGCCGATGAACCCAAAACGGG[A/G]AAAACATGGGATCAGACGATATACGTATATCCT
TP27257	TGCAGCACATGTTGGCCCTGTTCGTTTCGCTGAAATGCTGTGAGAA[A/T]AAACACTGTTGATTCGC
TP27273	TGCAGCACATTGACAATAGGCTAGGCTGGGAGAGGAGTGCGCGGGCGGGTCAGGGG[C/T]AGGTCCC
TP27277	TGCAGCACATTGCGGCCGCCCCTTGGTGACCTC[G/T]TCGTGCAGTACTTGCTCGCGTAGCTCAAGG
TP27288	TGCAGCACATTTCACAACACACTGACTAACACTAGCAGCCATTCGATCCAGGACCGTGAGG[C/G]GG
TP27302	TGCAGCACCAAAAAA[A/C]CCCCACACTAGCGAACCCACCTTGTCGGAGAAGCCGAACATGACGGAG
TP27310	TGCAGCACCAAACAACCATAAAAATCAGAAATGAGCAGGCCAGACTTCTTCCCA[A/G]TCGTTTTGG
TP27313	TGCAGCACCAAAGGCGCGCACGCGGCCTGCCGCCTCGGAACGGATCGGAGGGCATGCAG[C/T]ACCA
TP27318	TGCAGCACCAAATC[A/T]TGCGGCTAACACTGCTCTTCAGTACTCTCCAGGCACTTATACATAATTA
TP27323	TGCAGCACCAACACCGTA[C/G]CAAATTAGCAAATTGATACTGCCTTCATTCAGCACTGAACTGAAA
TP27325	TGCAGCACCAACACCGTTACACCAACGGCAGCATCCCTTGCAAACGCACCAACAACATCAGCA[C/T]
TP27330	TGCAGCACCAACATGTTCTA[G/T]CTGCATCTGTGGTCACACACACTATATGCCTTATTGCCGCGAG

Table A2 (cont.)

TP27334	TGCAGCAC[C/G]AACCCCTTGACCCTCCCTCAAGGCATCCTCGCTTGGTCTGATCGCCACCAGTGTC
TP27354	TGCAGCACCAAGTGTGTCGATCTCACAACCT[C/G]TTCTGTACGTACGTGCTCCCAAACAACTACAC
TP27368	TGCAGCACCACAACACCACACTGCTGCCATCATCAACTATGGGTTACACCGTTAGC[C/T]GTCCCAA
TP27377	TGCAGCACCACACCAGCGGACCCTTGGGC[A/G]CGCAGGCGCAGCAGCGTCCTGACGAGATGGGAGC
TP27382	TGCAGCACCACACTTCGTACCGTCTGCATGTCGCGCTCCTTCGCTAG[A/G]TGGACCGAGACCGAGA
TP27408	TGCAGCACCACCACTACCAAGT[A/C]CAACAAGGCAAAGACGAGGAGCTCAAGAGTGTAGAGAGGCT
TP27462	TGCAGCACCACGACCCGTCCACGGAGCTGCGCCTCGTG[A/G]TGGGGCTGCACGGCCCGCAGGACGT
TP27468	TGCAGCACCACGATCTGCACCATGAGGTTGCCCGAGAAGTCGCCGTACATGGC[A/G]CGGAGCAGCG
TP27469	TGCAGCACCACGCATGCTAGATAACCATCAAGAAACGATGGAATGACGGAACAGATC[G/T]AGAGCA
TP27480	TGCAGCACCACTCGCGCAGCTACCCGCAGGTGCATCCGTCCTGCCGCCGCGCCGTC[C/G]AGAGCCT
TP27491	TGCAGCACCAGAACCATCCGCCGCCGC[A/C]GCAGCAGCAGCCCTACGCGTACCAACCGCCACCCCC
TP27515	TGCAGCACCAGCAGCAGCAGCATCCGCTGCACTAGCAGCA[G/T]CATCATCATCGGCACCAGCACCA
TP27517	TGCAGCACCAGCAGGCACAGTCGCCCTGGCCTGTAGACTAGCAGGCTT[A/G]CGGAAAGAATTGAAC
TP27518	TGCAGCA[C/G]CAGCAGGCGCCGCTATCCCCGTCCTCCCACGTCAAGATGGAGCGCTCCGCGCCGTC
TP27523	TGCAGCACC[A/C]GCATTACGCCGCGTACGGGTACGACTACGCGACGCAGCCCGCGTACACGTACCC
TP27548	TGCAGCACCAGCGTTGTCCCCACGCTCAATGTCCCAGAGGATAGCAGCAAGCTCT[G/T]CCTCCCCA
TP27550	TGCAGCACCAGCTCCACGGAGGAGTTGTACGCGAGCTTGCTCAGCCTCGTGCCCAGAGACG[C/T]GG
TP27556	TGCAGCACCAGCTGGGGACGGTGCAGGAAAGCGTGAGCGGCATGAAGGACGCGATGCTGGC[A/T]CT
TP27577	TGCAGCACCAGGGCACAA[A/T]AGGAACCAAAAGAACCATGGTGAGCTCCTTGTCAGAAGTTTCTCG
TP27579	TGCAGCACCAGGGTCTTGTCCTTGTTGCTGAACTCGGGGTACTGCG[A/C]TGAAATGGCGTAGAACC
TP27588	TGCAGCACCAGTGCGCGCGCGCGTGTGCCTGAGAGCTGAGAAGACTTGTAGTGAA[C/G]GCTTAGTG
TP27592	TGCAGCACCAGTGCTCCTGTCCCTCACCACCTTCCTCG[C/T]CATCACCTTTTTCCCTGTGCTCACC
TP27598	TGCAGC[A/G]CCATAACTTGCTGGATGCGGGCCTCCTCTTGACCAATCAACCCATGTGACGGTCCTG
TP27617	TGCAGCACCATCCACCTCTGGGCGG[C/T]GGGGTCGTCGCAGGGGAGGTATCGCATCCCATTCCCAT
TP27629	TGCAGCACCATCTCCGCCCCTTGGCCGCGCCTCCCAGCGCCCCGACCCCG[C/T]GCCCCCACCTCAC
TP27635	TGCAGCACCATCTTAACACAGCGAAG[A/G]CCAACAAGTCATCTCGCTGAGTGGCCAGTGGCCGAGT
TP27659	TGCAGCACCATGTTTGCACTAACTTGGCAAAGAAAG[A/G]ATAATGACAGAGAAATGATTCAACAAA
TP27666	TGCAGCACCATTGGT[A/G]CGCGGCGGCACCATTGCATGTTCGCAATTTCTGTTTATCTCTGGACGA

Table A2 (cont.)

TP27670	TGCAGCACCCAAAAACA[C/T]GACGAGGTCTTCAGCTCTTACCTGCATACATAAATGAAAAGGTGCG
TP27680	TGCAGCACC[C/T]AACCAGCAGCCCGTTCCCCCCTTGCCTTATCTTCTCCCGTTCACCCCGCGTGCG
TP27682	TGCAGCACCCAATACGTTT[C/T]TCCGCACGTTCTGCGCGTCGCCCAATCTGCTCGGCCTCTTAATT
TP27687	TGCAGCACCCACATCACACCCACCGTTCGATGAGCGCATCCACCCTTGGTGGC[C/T]GTCCGATGCG
TP27703	TGCAGCACCCACTGATG[C/T]CTGATGTTACAGTGGAATACCAGGCACTATTTCCACTTCTTGGGAA
TP27719	TGCAG[C/T]ACCCAGCCAGCCAGCTACTACGCAGCAGTGGACGACGAAATTGGAGCGACGTGCATGC
TP27744	TGCAGCACCCCACGGCGCCCGACCTCCTCCCGCTGCTCCCCTACGCGCCGCTCCGCTGCG[C/T]CTC
TP27749	TGCAGCACC[C/G]CCAACCACGCCGACAGCAATCTTCCACGCGTCTGAGCTCCCCTTCTTACCACCT
TP27759	TGCAGCACCCCCG[C/T]CCTGCTGTCACTTCCCCGCCGCGCTGATGACAACGACCTGTAGCTTGCCG
TP27767	TGCAGCACCCCGATTCGTCAGCCCCTAGTGCCCCTTTCTATCAGCCCCCCTGG[C/T]TAGGGGCGGA
TP27791	TGCAGCACCCGACAGAACATCCAGCAACAGGCA[C/T]GGCCAGTCAGTAGCCGAATTGGCCAAGGAG
TP27815	TGCAGCACCCGCAAAG[C/T]AAGTTACAACAGCCGTGATATACCACAGTTACAACAGCAGTAATATA
TP27817	TGCAGCACCCGCAATGCCGAGAACGGACATTAG[C/T]GCCTGCATGAGCGTTGCTGCGACCCCAGCG
TP27822	TGCAGCAC[C/G]CGCAGGCGCTGCTCGCGGAGGCCACGGGTACCCCCGCGCGCTGTCAGGCCGCGTT
TP27844	TGCAGCACCCGCTTTTGCTTCTGAC[A/G]TCAACGGTTCGATGGCTGTAGTGTTGACGGTTCGGTTG
TP27847	TGCAGCACCC[G/T]TCCCAAGACGCGGCGTAAACGGCAACCGAGGAGGAGGCAACGCTGCCGCCTTG
TP27849	TGCAGCACCCGTCCCGAGGCGCGG[C/T]GTAGACGGCACCCGAGGAGGAGGCAATGCTGCCGCCTTG
TP27860	TGCAGCACCCTACGACAGTCCACCGCAGACGCAGCCCGCCCCCGCCTG[C/T]GGCGGCGTCTGGGAC
TP27867	TGCAGCACCCTC[A/G]TCACCTGGAACCGCGGCACGAGCCGCCCCTCCAGGTCGTACCTCAGCAGCG
TP27874	TGCAGC[A/T]CCCTCGCGACAACTGTTCCCGTCCAGGCGGTTCTGTTCGACATCGACGGGACGCTGT
TP27877	TGCAGCACCCTCGGCCGCGTCCACAGCTTCTACCACTGCGCGCCAGACGACATCTCCTA[C/T]CCCA
TP27881	TGCAGCACCCTCTGGCCCACGTGAAAGAACGACGCGCGAAC[C/G]GTGCTACGTGCGCATGCGCACC
TP27904	TGCAGCACCGACGACAAGGAGGCGAGCGTCGGCAACAAAGAGGCCGAAGAGGCGGC[A/T]GCGGCCA
TP27910	TGCAGCACCGACGCCCGCCAGCTGTTCGACGCAATGCCTCCGAGGAAAAGGGG[C/T]GGAAAGGTCA
TP27912	TGCAGCACCGACGCCCGCCATCT[A/G]TTCGACGCAATGCCTCCGAGGGAGAGGGGCGGAAAGGTCA
TP27921	TGCAGCAC[C/T]GACTCTATCATTTAACAGTAAACTGCACACGCTTTCATCCTCCTCTTATATACAG
TP27931	TGCAGCACCGAGCTCACTGCGGCCCAGT[C/T]CCACTGGACACCGCGCAGCGAGAGGTGATCCAGAT
TP27941	TGCAGCACCGAGTCGACGCCCTTCTCGTGCGTGAACACTGCGAGCCAGGAGGAAGGA[A/G]CACGTA

Table A2 (cont.)

TP27942	TGCAGCACCGAGTGGGTCGCC[A/G]TTCTCCACCGAATGCGCCTCGTGGAGGTGTGGATCGACCTCA
TP27956	TGCAGCACCGCACACGTCCACCTCGACACTGCCCCGCACGCCCGCCCACCACT[C/T]AACGTGCCCA
TP27965	TGCAGCA[C/T]CGCATCGGTGACGGTGCGCGTTCACCACGTCTTGTGAGGGTGTCGACACGCTCGGC
TP27969	TGCAGCACCGCCACACGGGAACACCAGCTGCTGCCGCTCGCATTG[C/G]GCATCTACCGAGACTGGC
TP27994	TGCAGCACCGCCGCGGCACCACCGCTGC[A/G]CCGCCGCTTGGGTTGCAGACCTCGCCTGCGCCACC
TP27999	TGCAGCACCGCCGTCTTGCTCCGCCGCGGTCCCGACCACCAC[C/G]GTCTGGATGATGTAACCCACC
TP28007	TGCAGCACCGCCTCCACCTGAAAAAGAGA[A/G]AGCATGCCAGGAATTTCGGATCAGAAACAGCCAA
TP28029	TGCAGCACCGCGGCGAGGCAGGACCGTGCCTGGGCGACGGCCTCCTGTCTCGACGACGGCGG[G/T]G
TP28032	TGCAGCACCGCGGGGAGGAGGGCGCGGGCATCGTTGC[G/T]TCGGACGCCGACGGCAAGCTCAATTC
TP28034	TGCAGCACCGCGGGGGTCGCGGAGTGCCTGGCCACCGCGTGCAGCGCGCGCACCGC[G/T]CTCTCGG
TP28035	TGCAGCACCGCGTACGAGCCC[A/C]CCGCCGCCGAGGGTACCACGGCCACGGCCACGGCGGCAGCCG
TP28036	TGCAGCACCGCGTACGAGC[C/T]CCCCGCCGAGGGTACCACGGCCACGGCGGCAGCCGAGACGACGG
TP28038	TGCAGCACCGCGTCCACGGCAACCTCCATGG[A/G]CACACCTCCGTCCCGAGTCCCGACCGCCATGG
TP28040	TGCAGCACCGCGTCGTCGCCCGCGTCCATGGCGAGACGGACG[A/C]GCGCGCGCCCCTGGGTAGGAT
TP28066	TGCAGCACCGTAAGTGGTCGCGTGATGCAGTACA[A/G]TCTGAGTGATGGCTCCTCGTCGTTGGCGG
TP28068	TGCAGCACCGTACCCCGCCGCACTTTCTCGTACGCGCCCCGTCCTCCCTCG[G/T]TCCGCCGTTGGG
TP28083	TGCAGCACCGTCGCCACCACCCACGCTGATGAGCTGCTTCTTGCTGTGGTGCATG[C/T]TCCAGTGG
TP28095	TGCAGCACCGTGCTGG[G/T]GATCGGAGACGCTCTCCTGCTCGCCGCGAATGTGCGATGCGACGCGA
TP28097	TGCAGCACCGT[G/T]GTGGACCTGCTCGCCAAGCACGGTCGCCTGGGCGACGCGCTGCGGGCGTTCG
TP28103	TGCAGCACCGTTCCTTCTCTCTCTGCCATTCGT[G/T]CGGTGCGGGCCTCGTGCATGTTCGTGTTCC
TP28107	TGCAGCAC[C/T]GTTGCTGCTCAGTCGGGCGCGCAAGACCTGGAGGATAAGACGTGAACTGGGCCTC
TP28318	TGCAGCACCTCATCCGCCGCCACCCCCTGCTCCTACGCCTGGGCTTCAAGAC[A/G]AAGACAAAGAG
TP28324	TGCAGC[A/G]CCTCCACGTTTGTGGTGGCGGCGGCCAAGGGGAGGGGGCTCAAAAAGGCTTCCTTCC
TP28327	TGCAGCACCTCCAGCAGGCCCAGCTCCAGCGCGTTCTTCAGCGTCATGGGCAGGAT[C/G]GACGACG
TP28354	TGCAGCACCTCCGTCTTCACCACGCGCGCCGCGGCGTCGAACGCCACCAC[A/G]CGGCTCTTGAGCG
TP28355	TGCAGCACCTCCTACCACCGTCGCTGCCGCCATTGCCGAAGCTCGGCCCAAA[A/C]TCCCGATCTCC
TP28367	TGCAGCACCTCGAGGCTGGGCAGGTCGCCGACGAAGTCGGGGATGTCGCCGCG[C/T]AGCTTGTTCC
TP28376	TGCAGCACCTCGCGACGCTGGCATAATCGTCTCGTCTGTGCACTCCCGTCAAACGT[C/G]TTCACTG

Table A2 (cont.)

TP28390	TGCAGCACCTCGTCCCCGACCTGGTCCCC[A/T]CCCTCGACCAATCCCTCCGCCTCATCGCCGCCTT
TP28392	TGCAGCACCTCGTCGTCGAGGTACTCGAACTCGATCACGTCCCTGCCGCCAGAG[C/T]CCTGCTGGG
TP28395	TGCAGCACCTCTAATTTTGCCATACATCGAGGAGAAC[C/G]AAAAAATGCGATCTTTTCCAATAACG
TP28405	TGCAGCACCTCTGGCGCCGTGTACCCCAGCGTGCCCGTC[G/T]GCCCTATTACCTCACTGCTCTGCG
TP28407	TGCAGCACCTCTGTTCTGGCCAACCTTCATCGTAGCAATC[C/T]TCGCTGCCATCATTGCAAGCCAA
TP28408	TGCAGCACCTCTTGCTCTTCGAGGGCGACCAGCTGC[C/T]AGCCTTCGACACCGCCGTCCAGTCCCT
TP28410	TGCAGCACCTCTTGCTCTTCTCGGGCGACCAGCTGCCA[A/G]CCTTCGACACCGCCGTCCAGTCCCT
TP28420	TGCAGCACCTGACCTCGTCCATGTCGAACATCCCCTCGCCGAACGT[A/G]TACCCGACGGGCACGAA
TP28459	TGCAGC[A/G]CCTGCCTTGCCGACGCCAGTCGCCAGATGCCAAGCTGTGAGAGCGGAGTCAACACTC
TP28462	TGCAGCACCTGCGCCTGCGGCGGCGGCGGCGCAGGATGCGGGCGACTGTAAGAA[C/G]GACTGCGAC
TP28463	TGCAGCACCTGCGCTGCTTGGCTTGGCCTTTCCTCCTCGCCTGGCGAAAGGG[A/G]ATGGATGACGA
TP28470	TGCAGCACCTGCTCAGAACGGCCAGCCTTGACATG[C/T]GCCCGCATGATAGCATTGAACGTCGCTG
TP28471	TGCAGCACCTGCTCCGATTTCCAAGAAAGCATGCGTAATATCATTAGATCGAAG[A/G]GCAACCAAC
TP28479	TGCAGCACCTGCTGGTTATACCCCTGGGC[C/G]GACGCCATTTGGTGCAGAGGACCTTGCCACACCA
TP28484	TGCAGCACCTG[G/T]AGCGGCGTCACCGTCACGCACGGCGGGCCGAAGTAGTTGCCGAGCAGCCTGG
TP28514	TGCAGCACCTGTGCACCAACAGCAGACTT[C/G]GTACGTAAAACTAAAACCTCGTAGCAGTACCAGG
TP28602	TGCAGCACCTTAGACACGAACGACATCTTCAATGAT[C/T]GGATTCACCTAATCGCACAAGACATGA
TP28603	TGCAGCACCTTAGACACGAACGACATCTTC[A/G]ATGATTGGATACTGAATCGCACAAGACATGATC
TP28611	TGCAGCACCTT[C/T]ACGGGCACCTGACACGCCTGTAAGTCAGAAACCATGAGAGGTGAAATTTGTT
TP28642	TGCAGCACCTTGGACATGTCCGCCGCGGCCTGCTTGGCGTTCTT[C/G]GCCACCAGCGCCGTGTACC
TP28643	TGCAGCACCTTGGACTTCTTGAACCTGTTATCGAATT[C/T]GGCGTACTTCTTCTGGTTCTCCGCTT
TP28651	TGCAGCACCTTGGGGCTCCGCCTCCGCCGAGGTACGCAGATGCGGG[A/G]GGGGATGAGGTCGGAGT
TP28656	TGCAGCACCTTGTCCATGGC[C/T]TCCTTGAGCTCGGGCTTCTCGAATCCGTCGGCGCAGGTGTAGA
TP28661	TGCAGCACCTTTCTACGAGCAGTATG[A/C]CATGCTTTGGTTGCTCACGCAGGGTAGAGGGTACTCG
TP28678	TGCAGCACGAACACAACCACGGCCGTC[C/G]AGGAGGCCGTGAGGCGTGCCTACCTAAGGACCGACG
TP28706	TGCAGCACGAATAATGATTGGCAGGAAG[A/G]ATTTCGATTCATCAGGTCTGCTGTACGACGAGTGT
TP28710	TGCAGCACGACAACTTC[A/G]TCCGCCTGCTCGGGTACACCATCAGTGGCGACCTCCGCGTGCTGGT
TP28726	TGCAGCACGACCAACAGGCTACAGCACAAAAAAAGACATAAGATG[C/T]TTGACTTACAAACTAGAT

Table A2 (cont.)

TP28732	TGCAGCACGACCACGTGGTGCCTTATGGGCTGGGGCCACGTGTGCTGCC[C/T]CGCGGGCCCCACGC
TP28741	TGCAGCACGACGATGTGGTTTTGAGGGAGATGCCCAGGCGCACCAG[A/G]ACAGAAGCAGAAGAGGC
TP28751	TGCAGCA[C/G]GACGGGCAATGGTTCACGGCTGAGGAGGCTAAATCGGACCTGGTGTATGAATACTA
TP28752	TGCAGCACGACGGGGACAATGCCGTCCGCCTGCTCCACCCGTTCACCCG[C/T]GACGTCGCCGAGTT
TP28760	TGCAGCACGAGAGATCTCATGCATGCATCTGGCTGACGCTCAAGGGCGCC[A/G]CCTCTCCTCTTAT
TP28776	TGCAGCACGAGCGGGCGCCCCGACACGACGAGCACGACGCACTTGACGAGGCC[A/G]CACACGTCCT
TP28777	TGCAGCACGAGCGGTGGCGCCGCGGCGCGCGGC[G/T]CGCTGGGCCCCTTCGGCCTGCTCGTCCTCG
TP28780	TGCAGCACGAGCTAGTGCTGGATCGCCGCCTGCACGCAGCCCGCCT[A/C]CACATGCTGCGCAAGAG
TP28789	TGCAGCACGAGGAGCACCTCGCG[A/G]AGGCACAGCGACGCGGACCGCGGCATGTCCCCCCCGAAAA
TP28795	TGCAGCACGAGGCAACGACGGCGAGGTACAAGGGCACAACT[C/G]AAAGCACTGTAATAATGTAACA
TP28811	TGCAGCACGAGGTCGGGGAGGCAG[C/G]ACAGGATGTAGGCGTACGCCGTGGCCGCGATGTGAGGGT
TP28817	TGCAGCACGATACGGTCGTATGAAACCA[A/T]AGTATGTTCCTCACTGGTTTAAGTATTTAACGTAC
TP28821	TGCAG[C/G]ACGATCCAGAGGGACCACGTCGTGTTGGACAGCAGCATCAAGAACGTGCCCTTGATCC
TP28824	TGCAGCACGATCTGTCATAAAGAAGGGGATGGAAAATAAAAACTGTAGGCGTCACTA[A/T]TGCGGC
TP28837	TGCAGCACGATTTCTAGTCGAATCAGCTCAC[C/T]GTGCTTGGCGAACTCGGTTCCCCACTTCTAAA
TP28838	TGCAGCACGATTTGGCCATGCTTGCCGTCCATCTGTTAGGAA[A/C]GTAGGATGAGGCCTGGCTACT
TP28858	TGCAGCACGCACCAACTTACAGTAAATTAATTAACGGTGA[A/G]TGTGTGTGTTAACGGCTGAATAT
TP28874	TGCAGCACGCACTCGATCGGTCGTCGGAGCCGCGGCCTGCCGACAGATTGGGCCGCCGCC[A/T]CCT
TP28877	TGCAGCACGCA[C/T]TCGGACTCGGCGTCCAGCGCGCTGGTCGCCTCGTCCAGCAGCAGCACGGCGG
TP28880	TGCAGCACGCAGAGA[C/T]ATCAGAGTGTCCACCCACTCTATGCTACAACTGCATTAACCATGATGC
TP28891	TGCAGCACGCAGGCCGCCCAGGAAGCCGTCGCGGCGACAACGTGGGCACGGCGAGACGCT[A/C]CAC
TP28903	TGCAGCACGCATCATGTGCCACCACTCTGGCCGTCGACTTCCGTC[A/G]ATCCAACGATGGTAGCGG
TP28908	TGCAGCACGCATTCTGGCACTTGGAGGTTGTCGTCGACGTCTGGGAGAGGAGGG[G/T]TAGCCGCGA
TP28918	TGCAGCACGCCACGCCAATGGTCCAGGGGTTCAGGCACCTGCCAGACGGACCAGCGGTC[A/C]AGCG
TP28951	TGCAGCACG[C/T]CCTCGTCGTCGATCATGTAGAGGCCCGTGATGTCCCCGAGCTCCGCCGACGAGT
TP28957	TGCAGCACGCCCTTGGTGGTGAAGTCGAACGCGGCGGCGGGACCGC[C/T]CACGGAGTTCGCCCAGT
TP28960	TGCAGCACGCCCTTGGTGGTGAAGTCGAACGCCGCGGCGGGGCCGCCCAC[C/G]GCCTGCGCCCAGT
TP28963	TGCAGCACGCCGACCTCGTT[C/G]AGCACGAGGCGGGAGAAGGGCGCGTCGGTCCTGGCGTTGAAGA

Table A2 (cont.)

TP28978	TGCAGCACGCCGCTCTCCATGACGGCGTT[A/G]GATCCCCACATCGAGCCGAACGCGCCCAGCGGTG
TP28986	TGCAGCACGCCGTTCCTCTTCCTCCTCACCTGCTGCTG[A/C]TGCTGATGCTCCATCGGCGCGCTAG
TP28988	TGCAGCACGCCTCGGTGCTGTACTGCTGTCTGTCGCTGCATCTCTGTT[C/T]TATGTTTTCTTTCTT
TP28993	TGCAGCACGCGACAAGGACCAGCGCGAAGAACCCTCTTGAGAGAGCCATGATCGTTCTG[C/T]GATC
TP29004	TGCAGCACGCGATGGAGGCCCACCACCCGCTCAACTCCACGCGCGTGGCGCG[C/T]CTCGGCCTCCG
TP29014	TGCAGCACG[C/T]GCAGGAGCAGCATGCGCATCAAGGAGGCCATGGGGGAGGCCGACGTCGTGTTCC
TP29022	TGCAGCACGCGCAGGCGCTCGCTCACGCGCTCCCGCCGCAGCCGCGC[C/G]GCCACCGTCTGCGGGT
TP29024	TGCAGCACGCGCCACGTCTACAACGCACG[C/T]GCTCTACACCTTACTACGGTCTCTCGAGAGGCGG
TP29030	TGCAGCACGCGCGGGCGCGGTCAGTA[C/T]GTATTATTCTCAGGCACGATTCTTCAAAAGAAAAAAG
TP29044	TGCAGCACGCGGAGCGAAAGCAAATTCTCTAGCGAG[C/T]AGGAGTAGGAGTACTCCTGGTTTGTTT
TP29049	TGCAGCACGCGGCCAGCGCGAGCTGCTCCTTGC[C/T]GCTTCCGCATCCGTATGCCGCCACCGCCGT
TP29075	TGCAGCACGCGTCAGAAACCCGCGGAGAAGGATGGATGTCTGTCCCCCGCGGC[A/G]CGGGGGAAGT
TP29076	TGCAGCACGCGTCAGAAACCCGCGGAGAAGGATGGATGTCTGTCCCCCGCGGCGC[G/T]GAGGGAAG
TP29104	TGCAGCA[C/T]GCTGCCGAGGCTCCAGTGCCTCCAAACCTGTCCGTGCGGCCGTGCCCGCGCGCCCC
TP29118	TGCAGCACGGAAATAGGCAAGCGATCGACCGC[G/T]CGCTGCTCTCACTATATAAACATCTCCCAGC
TP29119	TGCAGC[A/G]CGGAACCGAGCTTGGCCGAGACCGCGTCGACCAGGGAGGCGAGCGGAGGGGACCGAA
TP29125	TGCAGCACGGAAGGTATCTTCAGGGAAACT[A/C]TCTCTCTGCAATCCTTGAGGTCCAAGCGCTCCA
TP29127	TGCAGCACGGAAGTGAAGCTGCTCGAGCT[C/T]TGCTGGTACACCAGCTCGCTTGGCATCATCACCG
TP29138	TGCAGCACGGAGAGAAACATCCCATCTGCGGCACGG[G/T]GAGAAATAGCCCATCTGCGACAAGCTT
TP29153	TGCAGCACGGCAGCAACAGCAACTGTCT[A/G]CCACTGCTCGTCAGTCGCCACTGCGCTTCTGTTTG
TP29159	TGCAGCACGGCATATGCCGCCGC[A/T]GACCCTGATCTCTCAGTCCTGGTCCTGGACCTCTATAAGA
TP29170	TGCAGCACGGCCACGGAGGCCTAACCTA[A/G]CGGCGAAGCGAACCAAAGGAGCGAGCGAGGGACGA
TP29180	TGCAGCACGGC[C/G]GCCAGGTGCGCCGACGTGCCGCCGATCACCCAGAACTGCTCGTTGCGCCACC
TP29182	TGCAGCACGGCCGCCGTCAAGGACGCGGGCGGCGAACTGGCG[C/T]TCACGCTTCAGCTGCTGCCGC
TP29196	TGCAGCACGGCGAGCTTCTCCTCGAGGACGACCCTGAGGTTCTCCT[C/G]GTGCGGGAAGGCCAGCA
TP29204	TGCAGCACGGCGCCGAGGGGTTGG[C/G]CGCATGGGCCATGGCCGCGTGCCTGCCGAAAAAAAAAAA
TP29206	TGCAGCAC[G/T]GCGCCGCCGCCGCCGTCGAGCTCCTCGACGAGCTCGCGCAGCGCGACGAACGGGT
TP29211	TGCAGCACGGCGCGCGT[C/T]AGCGTCACGCACGCGCACGAAACGGCAACAACAATTGACGAGCAGC

Table A2 (cont.)

TP29216	TGCAGCACGGCGGCCAT[A/T]GCGGGGCGCTGCGCGGGCGCCTCGGCGGTGCACAGCAGCGCGACGC
TP29217	TGCAGCACGGCGGCCATGGCGGGGCGCTGCGC[G/A]GGCGCCTCGGCAGTGCACAGCAGGGCGACGC
TP29225	TGCAGCACGGCGTCGGCGTCGGGAACGAGGGGCAGGC[A/G]GCGCGGGTAGGAGCGGAAGCCGTCGC
TP29226	TGCAGCACGGCGTCGTCGGCGGTGGCCTTGGGAGGGTAGACGACGGCGAAGGCGATGAC[A/G]AGGA
TP29227	TGCAGCACGGCGTGGACGAGTCCTACACGCTGGAGATCCTCCCCACGGGCGCGGC[C/G]ACGGTCAC
TP29241	TGCAGC[A/G]CGGCTGCGGGGCAGCAGGGACAGCGAGCACAAAAAGGACGATATCTCTTTCATCTTA
TP29242	TGCAGCACGGCTGGCGTCGCAGCGTGGCGCG[C/T]CACGGAGCGCAGCACGCGCACCGCCCGCTCGC
TP29267	TGCAGCA[C/T]GGGCGAGACGGCAAAACTGTATTTGGCTTGCAGGCAAGTCAAGGGAGCTGGGAGGA
TP29273	TGCAGCACGGGCGTTG[A/C]GGACTTTTGCTTTGAATTTTCTCTTCGACCACTATTCGTTGGCCAAT
TP29278	TGCAG[C/T]ACGGGGAAGCACCAGTTTTCTTTCGCTTTCAACCAACGAGTAGTGCTCCTGTATCTAA
TP29297	TGCAGCACGGTCCCTG[A/C]GGCGTGAGGCCCTATTCTCTATTTGGAACGGGGGAACATATATATTC
TP29303	TGCAGCACGGTGACCACCTCGTGCAGCTTGAAGGGTCGCTCCACG[A/C]TGCTGATCAGCACCACGT
TP29309	TGCAGCACG[G/T]TGGGCAGTGGTTCTCAGCTGAGGAGGCTAAATCAGATCTGATTTATGAATACTA
TP29310	TGCAGCACGGTGTAGGGCGCCACCGTGCTGAGCTTGGTCCCGCCCACGCCG[C/T]CCTTCCTGTCGA
TP29320	TGCAGCACGTAACGAGTGCAGCAAGAGTGGGCACCAAAGATCCCGAGC[A/T]GCCCTGCGCGCGGGA
TP29337	TGCAGCACGT[A/T]GTGTTCGGCATCGCGGCGTCGGCGCGCCTGTGGGAGAAGCGTAAGGAGTACAT
TP29340	TGCAGCACGTATCAGCAGCGCATCATTGGCACCGCAT[A/G]TCCAACAACACAAATAATTACCGATC
TP29345	TGCAGCACGTATTGGAC[C/T]TTGGTTAACAATAATAATGGAGAGTAGACTACAAGCTACTACAGTT
TP29362	TGCAGCACGTCCATTTCACATTC[A/T]GACGAGACCCTTCTCAGTTCACCTGTCTCCATGGACTCAA
TP29388	TGCAGCACGTCGGCCAGGC[C/T]ACCATGCATTTGCCTTGCACTGACTGATCTGAACCAGCCCAGAA
TP29391	TGCAGCACGTCGGCGCATCTCTTTTGTATT[A/G]TTTTAAATGTCTCTGTTTAGATTAGAGGATGAC
TP29397	TGCAGCACGTCGTAG[C/G]CGAACGTCAGGTCCGCCTTCCGCCGTGTCTGGTACCGCGTGCTGTTGG
TP29402	TGCAGCACGTCGTAGTCGACGCGGTCCCCGTGCCGCGCCACGA[C/T]CCGCCGCTGCTCCTGGACGG
TP29411	TGCAGCACGTCTGGCGTTACTTGGAGGAGTAGAGGAGGTGGAGGAAGGCGAGGAC[C/G]GTGATGGT
TP29415	TGCAGCACGTGAACCTGGTCAGGCTCCTGGGCTGCTGCGTCCA[C/T]GGAGAGGAGAGGATGCTGGT
TP29417	TGCAGCACGTGACGCTAGCATAGCATGGTTATCGAATTCAGACTGAATTCACATT[A/T]AAAAAAAA
TP29424	TGCAGCACGTGCACCACCTAGTTGACCCTTGACCGCA[A/T]CCTGTTTCTCTCTCTCCATCCGAGCA
TP29448	TGCAGCACGTGGCGCCGTCA[A/C]CGTCGTCAGTGCAGCCGCAGCGGACCAGCACCGCGGCGCGCCC

Table A2 (cont.)

TP29456	TGCAGCACGTGGTGTTCGGCATCGCGGCGTCGTCGCGGTTCTGGGACAAGCGTAA[A/G]GAGTACAT
TP29504	TGCAGCACTAATTTCGTAGAAGCAACGAGGGTTTAGGAGGAGGGC[A/G]GGATGTACGAACAAGGTC
TP29509	TGCAGCACTACAGCACCGTACTCCTCCATCGAAGATC[C/G]TCGCCATCCACCAGAATCCTTCTCCA
TP29513	TGCAGCACTACATCATCTGCTACTACATAGAAAT[C/T]GGATATACAACCAGTTCTATGTGCTGTAA
TP29527	TGCAGCACTAC[C/T]GCGTGCTTGCCCACCATCCATGGCGATCCTTCAAGTGCCTTCTTCTTGTCAA
TP29538	TGCAGCACTACTACACGATCC[A/G]TCGTTCATGCACATCTATTCTACTTGTCTGTCTCTGCGTTGC
TP29561	TGCAGCACTAGAGCGGTAGAACCTAAACGGAAACAGAGAA[G/T]TGCACACCGAAAATGAAACGATC
TP29588	TGCAGCACTAGGACGGTAGAACCTACAGGGAAACAGAGAAGTGCACACCGAAAAT[G/T]AAACGATC
TP29594	TGCAGCACTAGTAGAGGAGG[A/G]GTTGCTGCTCTTGCCTCCCCAACTACATGAGCTGTGGATTTAC
TP29614	TGCAGCACTATCAAAGGTCTGGAAGACCAGAACCTGCATTGCCGTCCCCC[A/C]AAAAAACTATGAC
TP29619	TGCAGCACTATCTTAACCACGCTGCGCACAACAACAAAAAAGCATCGCGCTCA[A/G]ATCCTTTGTC
TP29625	TGCAGCA[C/G]TATGTTGTCAAGGGCTTCCAGTTCAAAGGATGCGACATTGGAGAGCCTGGGAGCTA
TP29650	TGCAGCACTCAGCTCGTAGATTTTGTGCTTGCTTGCGACCGCGACACACTTCATACGGGCATC[A/G]
TP29657	TGCAGCACTC[A/C]TGCTGCCGTCACGGCGGCGCCCGAGTTCTGATCGCCTGTGCGAGAAGACGAAT
TP29673	TGCAGCACTCCCCGCAGC[C/T]TGCCAAAGCTACGATGCTGCTACAGTGTGAGTCACTGTGCTCCAC
TP29682	TGCAGCACTCCGCGCCACCACGGGCCGC[A/G]CGCTCCGACCCCGCCTCTCGATCCCTCCGTTCGCG
TP29686	TGCAGCACTCCTATACTGTTCAGGAACGAGCAATCATGCACTCGCCCGCGTAACGC[A/C]AAGCGTC
TP29689	TGCAGCA[C/G]TCCTCATCATTGCAGCTACCACTATTAGTTGCAGTGGCAGCAACATTCGAGTCATC
TP29718	TGCAGCACTCGCCTCGGGACCGTACGTGCCTATGCTAAGCACCGTTGAAT[A/C]CTTGCATTGAATC
TP29723	TGCAGCACTCGCT[C/G]GGTAAAGCTCTTGAGGTGTCGCACACGGATGTGTCGCTGACCACAGTCAA
TP29764	TGCAGCACTCGTCGGCTTCCTTTGCTGCCGCC[G/A]CCCAGGTGAGGCGCTTCCTCCCTTGTGCAGC
TP29775	TGCAGCACTCTCCAGCTTGGCAACCTCTGGCAGCACCATGGAGTTCATGAA[C/G]GCATCGAGCGGA
TP29782	TGCAGCACTCTGCTGCGCCTGCCGTGCCGC[C/G]CAGCCCAATGGAGAGGGCCGCCTCATTCCTCTC
TP29783	TGCAGCACTCTGTACTTCTCCAGCACCGCCCTGACCCTGGACACGGGCCGCTCGCC[A/C]CGACGCC
TP29788	TGCAGCACTCTTCCCCTTCCCCTTGTTCTTGGCAGCCTCTTTAGC[A/G]GCCTTTGACAGCGCCTGA
TP29792	TGCAGCACTCTTTTAACAATGACGAATA[A/C]TATTTTCATATCACACCAAATCGCGTAAGCCAAAT
TP29805	TGCAGCACTGAATGCGATCTGGCCGACCCGTTTCCTGTGTGTTT[A/G]CTTCACGCAGCACGCCGCG
TP29810	TGCAGCACTGACCTGAAAATCT[G/T]TGGGCGACTCGACGAAATCTGAGATCAATACGACTGGTCGG

Table A2 (cont.)

TP29815	TGCAGCACTGACTCTACCCGCGGACCTCTCCTTCACCATCCACCATCACGGC[A/T]CCTCCCCTGAA
TP29818	TGCAGCACTGAGATGTTGTA[C/T]GGGCGGGAAGCGACGGACTTCACCATATGGGAGGTCATCTGCG
TP29835	TGCAGCA[C/T]TGCAAGAATAGCACGACCGCCACCGCGATCCTCAGCATCACTGACGCCATTGGTAC
TP29843	TGCAGCACTGCACAGGGACTTGAGGAGGGACTGGCAGTTGGACCCGCGGGAGACGTCGGCC[G/T]AG
TP29858	TGCAGCACTGCCACGAGCA[C/T]GGCATCCTGCACCTGGACATCAAGCACGGCAACCTGATGATCGA
TP29890	TGCAGCACTG[C/T]TCCTCTCATCATCCTGGCAAAAGGGTGGCGATGCCGACGAGCGGCCTACCCCG
TP29900	TGCAGCACTGCTGTTACTCTG[A/T]TGTTCAGAGCCGTCGCATGCGTCGCATTATCAGGTCGCCCCG
TP29933	TGCAGCACTGGGCGCGGCAGCAGCAGAACGAG[G/A]GCGCAGATGGAAGTCTGCACGAGCGCGGCAT
TP29937	TGCAGCACTGGGGGACGCGCCGCGTGGCCTTCCTGTTCGCGCCCGTCGTCGTCCT[C/G]TGGCTGCT
TP29945	TGCAGCACTGGTGACTGGACATGG[G/T]GTCCCGCTGACAATGCTGCGTGAGGGTCATGCGGTCCTT
TP29981	TGCAGCACTGTAGCTTGCACAGCAATTGCACATTCA[C/T]GCATGCATGGGTTGCAGTTGCATGCAT
TP29994	TGCAGCACTGTCCACCTCGGCACATACCGCA[G/T]GGCGCGGGAAGGAGAGGCCCTGGGCTACGCGG
TP30013	TGCAGCACTT[A/G]CTACCAATTGCCTTTTTGCATCGCATACCCGCGCGCGCCCGCTGGCCATGGGG
TP30025	TGCAGCACTTCACCGTCGGCGGCGCCACGCTGCGGGGCTTCACCGT[G/T]TGGGCGTTGCTCCTGGA
TP30027	TGCAGCACTTCAGCCATGCTGGGACGATCCAACGGG[G/T]TAGGGTCGGTGCACGCCAGTCCAAGAA
TP30032	TGCAGCACTTCATCTTCCTTGCGTGATCTGCTAGCCGAATCAAACC[A/G]TAGCTAGTCGCCCTGAC
TP30039	TGCAGCACTTCCCTTCCA[A/G]CTAAAATGGCGCACCATGTATGACTGGCATGGTTCCTTCTTGTTG
TP30046	TGCAGCACTTC[C/T]TTTTGGCTCCACAACTGGCTCGGTTCCCAACCCCTCGCCGCTGCCTTTCCCG
TP30051	TGCAGCACTTCGATGAAGTTGGACACCGTCCCGTCGCGGCGGCCCGA[G/T]GGCATGTCGAAGCTGG
TP30093	TGCAGCACTTGCAC[A/G]CAAGGTGTTCGACGCCTTGCTCAACCAGACTTGCAGCCTTGATCCGAGG
TP30101	TGCAGCACTTG[C/T]CGAAGAGACCCAAGAATGCTGCCAGCAGAGTCACGACGGCTGTCACCGCACT
TP30109	TGCAGCACTTGCTCTGCGGCGTCGGCGTCTGCTCATTGCTCGAACGCGAACGGTACCGCATA[A/G]T
TP30150	TGCAGCAGAAAAA[A/T]TGGATTTAGTTTGTTAACGGAGGCAAGAATGGAGAGGCTGAACTCCATTG
TP30164	TGCAGCAGAAACAGAAAGTATAACTGAATGAACTAGCCAA[C/T]TGCCTGTTCAATTTCGACGGCGT
TP30167	TGCAGCAGA[A/G]ACCAGGTTATCTGCTGTTGTGAAAGAAGCAGAAGCATCCGTAGCATCAGAGAGG
TP30172	TGCAG[C/T]AGAAACTGTCGCGAACCTGCTGCGAACCTCTCGAAGAAGGCGCGAAAGTTTTCCAAAA
TP30188	TGCAGCAGAAATT[A/C]ACCAAAAATAAACTAGTGTAAAAAAGGGAGAATTTTTCGAGTTTTGGAAA
TP30194	TGCAGCAGAACAACAGCTCATCGAGCTGTACGTATGCATGG[A/C]ATGAGTGAAGGTGACTCACGAA

Table A2 (cont.)

TP30205	TGCAGCAGA[A/G]CACCTTCATGACGCACGCGCGGTTCTCCTCGCGGACGCTGGTGATGAGCCAGGA
TP30235	TGCAGCAGAACTACCTAGACGGCGCGCTGCC[C/T]GACGAGATCTTCGGGCTGCGGCAGCTCACTAT
TP30239	TGCAGCAGAAGAAAGGAGGACTTCGCGCGGGAGGCAACAAGGCAG[C/T]GATGTTTCCAGCGCGGAC
TP30254	TGCAGCAGAAGAGGAGCTCTGCCCAGCTCTCGGCTGCCAAGAGAGGAGGAGGTAGTTGTGGTG[A/G]
TP30257	TGCAGCAGAAGATGAGCGCCAAGGAGACGGA[A/G]ACGTGGTCCAAGATCCTGCGCCAGGAGGAGAC
TP30265	TGCAGCAGAAGCACAACA[C/T]AACACGGGACCTGCTTTCTCTGATCGAGCTTCGGAGAGAACCGTA
TP30274	TGCAGCAGAAGCAGTAGCCGAGCGCATCACGGAACTG[G/T]GTTGATAGCGCACCGTGCAGATCGTT
TP30287	TGCAGCAGAAGCTCCGACGGTTGCGCCACCGACGCTCTCAGTCCCGCTGTATCGCGGCA[A/G]CGGC
TP30292	TGCAGCAGAAGCTGGTATGC[C/T]CAAAGGGGGCAGCAGCTCAGGCGCTTCACCAGTGACACCAGCT
TP30294	TGCAGCAGAAGCTTCAGGAATGCAGGGGCTGAT[A/C]GCCGATGGAGCAACGCCACTGTGCGTCACC
TP30300	TGCAGCAG[A/G]AGGAGGCCGTTGATGGAGTCGAGGATGCAGTGGTCCCTGAAGAGCGGGAGGTGGA
TP30301	TGCAGCAG[A/C]AGGAGTGCAGATGCTCCCTCGGCGGTTGTTTAGCTTCGTCATCCACCCACCACCA
TP30307	TGCAGCAGAAGGCGGTAGCCTCGTGGCGTTCAAGTACAACGACAT[C/G]AGGAGGGCGACCAAGAAC
TP30314	TGCAGCAGAAGGTGGTAGCCTCGTGGCGTTCAAGTACAGCGAGCTGAGGAG[G/T]GCGACCAAGAAC
TP30320	TGCAGCAGAAGTACACGCAGAGCGGAGG[G/T]GTGCGCCCCTTCGGCCTCTCCACGCTCATCGTCGG
TP30321	TGCAGCAGAAGTATACACAGAGTGGTGGAGTCCGCCC[C/T]TTCGGCCTCTCCACCCTCATTGTCGG
TP30341	TGCAG[C/T]AGAATCACTCCCTCCGCCTCCGCAGCAACTTCCACCGCCCTCTTCCCCGCGACGAGCG
TP30368	TGCAGCAGACAACCAGACTGCTCTTGTGAAGATGTTGCTGAC[A/T]TTGAGTATGACAGCAGCCGCA
TP30377	TGCAGCAGACACCACCGCTTCTCGCCGCCCAGCAACCAAGAACAGTCCCCTCAGGTTGTCTT[A/G]T
TP30393	TGCAGCAGAC[A/C]GCGCAGGCTCCGCGCCTCACGGCCTTGCCCCGCTCCAGACTGGCGGCCCCTGC
TP30404	TGCAGCAGACAGTAGAGAAGGTCTCAGCCCGCTGCTGGCA[A/G]CGTTCCGACGGATGTCCTGTGAG
TP30411	TGCAGCAGACCAACCCGCCAAT[C/G]GTGTGACGCCACCACCACCGCCCCCTGCACGGGGAAGCACA
TP30417	TGCAGCAGACCA[C/G]TAGTCACTAGTGTCACTAGACCAGGCTGGCTGGTTGCGCGCACACTGCCTG
TP30419	TGCAGCAGACCCAAAAATATAATAGTTTTGACGAAGACATGCAGA[A/G]GACGATCAAGCAGCAGAA
TP30420	TGCAGCAGACCCAGCGCAAACGCAAATCCAAGGGGGC[A/T]GGACCGACAACACAGACACCAGACCT
TP30425	TGCAGCAGACCCGCGTCCGCGGG[A/C]TCGCTCCGCAGGACGCCGTCCCAGTCGTCCACGTCCTCGT
TP30452	TGCAGCAGACGAAGAGTATCCGAAGGCGGATCCGACAGTTCCCTGGCGTTGCCCTGCCGTCA[A/G]C
TP30453	TGCAGCAGACGACACCCCAC[A/G]ACGACGTCATCATGCCCGTCGCCGCGGCCTTGGACCGAACCGA

Table A2 (cont.)

TP30467	TGCAGCAGACGCACCC[A/G]CACGGCCACACCCGCCCCCATCGTCGACCCTTCATCTTCGACAGCAA
TP30470	TGCAGCAG[A/C]CGCCACCAATCCAAGAAACTAAAGAAATTGAAACAGCAAGCAAGAAATAATCATC
TP30485	TGCAGCAGACGGGGGTGAT[G/T]GAGGCTAGCCCTGCGATGAGCGGCGCCCTGGAGGATTTGGAGGA
TP30503	TGCAGCA[G/T]ACTGGCGGACAGCTCTGAAGTGGTTGTCGTGCTGTGTGCATGTCTACCCTGCTCTT
TP30514	TGCAGCAGAGAATCTACCAAACCCACGA[G/T]CCACGACGTTGGGAGATGACACTGCAAAGGTGCAC
TP30518	TGCAGCAGAGACCAGACATGGTTGTCTCCAATCAGTAAACCAGCTGAAC[C/T]GAGCAATCTTTCAT
TP30524	TGCAGCAGAGAGACCGTGTCCTCGATGGGGATGCTGGTGTCGACGCGGTGCAGGTAG[C/T]AGAGGT
TP30534	TGCAGCAGAGAGCAGGCGAG[C/T]GGCGAGGCTTGGGTTGCAGCAGCAGCTGCACGGACAAGCAGCA
TP30572	TGCAGCAGAGCAAGTGGTGACC[A/G]TGTCTGCGTCGATGTGCAGAGTAAGTGGTTTGCAGTAGATA
TP30576	TGCAGCAGAGCACCAATACGTCAAC[C/G]CTAATATACACTTACATATGGGGCCTGTCTGACAGTAT
TP30600	TGCAGCAGAGCCATACAGCTTCTTGATTGCCCCAGAATCAGAAGGGGTGGACACCCCTGT[C/T]GGT
TP30615	TGCAGCAGAGCCGTAACGCGCACACAACCCTGTTGCTCTAGGC[C/T]CTAGCTTCTCGTCCTCCCGT
TP30625	TGCAGCAG[A/G]GCGACTCCGATCGGCAATGCTCTTCGTATTGGTGATCGATCCGCAAGAAGGCACT
TP30637	TGCAGCAGAGCTCTTG[A/G]GCTGCCTTGCCGTCGCGGCGTGGCGTTGCCGAATGCCGATGCCCACG
TP30645	TGCAGCAGAGCTGCGG[A/G]GCAGTTCAGGCCTAGGCGGTGGAGGGGGCCTGTAAACAGGCAGCTTG
TP30671	TGCAGCAGAGGCAACTGTCACGTCAGCTGCATA[C/T]GCCGATGGCTTCTCACGCTCTCCTCCCTCT
TP30674	TGCAGCAGAGGCACCTTCGCCTC[C/T]TCCGCCGCCTCTCCGCCACTAGCGCCTTGGCCAGTGCTCT
TP30685	TGCAGCAGAGGCCCCGCCTCCATGACGGA[G/T]GCCAGCAGGCGTCCTTTGTGTGGCAGGGGCCTCT
TP30730	TGCAGCAGAGTGCGGTTGCTGGTTGGCCGTTGGCTTGGC[C/T]CCCCTCATCCGCGATGCAGGTGGA
TP30755	TGCAGCAGATAGCCGCAGGTAAGCAAGAGCACCAAATTGATTCTGATTCCTCA[C/T]TCTCTCTCTC
TP30759	TGCAGCAGATAGTAAGCAACTGT[C/T]ACGTCAGCTAAACGAGGAAGACAAGGCAGAAGCTGCTGCT
TP30773	TGCAGCAG[A/G]TCAAACGCCTCGCCCCACATACCAGCCAACGCGTACCCAGACACCATGGCGTTCC
TP30778	TGCAGCAGATCACAAGATGTACAACAAGGTCA[T/C]TTTGACCATGTCTTATACTGAAAAACTAAAC
TP30789	TGCAGCAGATCAGATCGATCGAAGTGAGCTTCTTGCGATGCATTTATGGCGATGGCGTGGCGG[C/T]
TP30790	TGCAGCAGATCAGATCGATCGAAGTGCATCCATA[A/G]CGATGGCGTGGCGGCATGCATGCAAACGA
TP30798	TGCAGCAGATCCATGCATCATCGTCACCAATCCATCATGGCGGATAGGC[A/G]GTGCGTGCGACCGT
TP30806	TGCAGCAGATCC[C/G]TTCCGTGTTCCACTCGTGCGCGACTCCATAGCTGTAAGTTCTTAATTTATT
TP30808	TGCAGCAGATCCGCGCAGCGCGC[A/G]CACTCCACCGAGTTCGTCTCCCGTGACGCTTATCGACCCC

Table A2 (cont.)

TP30824	TGCAGCAGATCGCCAAGGTGCTCGCGTCGCTGGGGTACAACGAGATGGCTTCGTCGGCCAC[A/G]CT
TP30825	TGCAGCAGATCGCGTCGCTCAATGGCAACAGCAT[A/C]ACGTCCAGCTTCTCCATGCTGCACGCGTG
TP30828	TGCAGCAGATCGGGCCACTCCGCGACGCGGTCGGCGTTGCTGAA[A/G]AGGTAGGCGACGGCGCGGT
TP30833	TGCAGCAGATCGTGCGCTCGGCTGGTATTTTGTTCCGTTGTGGTTTTGT[A/T]GAAGTGGCGATGTT
TP30834	TGCAGCAG[A/C]TCGTGGCATCCCGCACCAATGCCTGTGGCTGGTTGGAGCTCCTGCCGTGAGAGGG
TP30844	TGCAGCAGATCTGTTTTGTGCAAAACGCCTATATTGCCGTGTGCTCCCTC[A/G]CCAGTCGCTATGG
TP30850	TGCAGCAGATGAAGACAGCACGAGCCTGACCCTGACGAGAGACTGCC[A/G]TCGTCCATTCGTTCAG
TP30886	TGCAGCAG[A/G]TGCCAGCGTCGTTCACCACGGCGGACACCCCGCTGTCGTCCCCCCAGACTGTGTT
TP30899	TGCAGCAGATGCTCCACGACGGCGAGTTCGAGGGGCA[C/T]CGCGACACCTCGGAGCGCTGGGTGCT
TP30900	TGCAGCAGATGCTCCACGACGGGGAGTTCGAGGGGCACGGTGACACCTC[A/G]GAGCGCTGGGTGCT
TP30905	TGCAGCAGATGGAGCCGCGGATGCAGC[A/G]GGCCTTCGCCGCCATGCGGGAGCTCGAGAAGGGCGC
TP30912	TGCAGCAGATGGCAAGGCGG[C/T]ACACTGGGAGGTGAACACGGGTGCAGGCTCGCTTGCTGTCGGA
TP30925	TGCAGCAGATGGCGTCCACCTCGTGCCCGTCGAG[C/T]GTCAGCGTGTGCGGCGGCGGCGGCGATGG
TP30940	TGCAGCAGATGTACCTCCCC[A/G]CGGCCGCCGCCTCCTCGGCGACGAACAGCTCCGCGCGGCAGAG
TP30944	TGCAGCAGATGTA[C/G]CTCCCGTCAGCCGCGTCCGCCTCTGCCAGGAACTGCCTCGGCGCGGCAGA
TP30962	TGCAGCAG[A/C]TTCGGATAAGATGAGATGAGGTGAAACGACTGATTTTCCACAGTGGAAAACACAC
TP30976	TGCAGCAGATTTCATTT[G/T]ATGAGAATTTCATGTAATTATGCAGAGAGCTTGTTACATACATTAT
TP30978	TGCAGCAGATTTCTGAA[A/T]CTCTGTGGGTGTTTGATGAAAATCCTATGGGCTGGAGGATCCACTC
TP30990	TGCAGCAGCAA[A/C]AGCGCAAAGCTTCGATGTCACCGCTATCCACCTACCCTCCACCCGTCCACCG
TP30996	TGCAGCAGCAAACAATCTCGCGAACGA[A/G]CGGCTGACCGACCTTACGTATATGCTTGTTGTGGCC
TP30999	TGCAGCAGCAAACGCCGCACAACAGCATCCGCTCGCTCTGGTGGTTGTC[A/T]ACACCTCTGCCACC
TP31003	TGCAGCAGCAAAG[C/T]GCAGTGGTCCGATGCATCAGATCCCAGCCCGCGTAGGTGTGCATTGGGAA
TP31005	TGCAGCAGCAAAGGGCAGTGGTCC[A/G]ACGCGTCGGATCCCAGGGCCTGAAGGTGACAGTTCGGAA
TP31013	TGCAGCAGCAACAA[A/G]CTGTGCCTACTAGTACCTGCTGTGCGCCCGCACGCGCGCGCGCGTCGTA
TP31015	TGCAGCAGCAACAAATCGAAGGCGATACGATTACGGAAGGAACAAAAA[A/G]CGTAACTAATCGTAT
TP31037	TGCAGCAGCA[A/G]CAGCAGAAGCAGAAAAGAAGAAGAATGTTGAGGCATGGTTCAATTGAGTATAA
TP31092	TGCAGCAGCA[A/G]GAACGCCGAGCGTACCAAGAAAGCCAGCACGCGTCGTGCGGTCCCTCGCGTTC
TP31094	TGCAGCAGCAAGAAGCCCTCACATTGGGCCACGGAGGAAAAA[C/G]TCGACCAGCAGGTCGAGTGCA

Table A2 (cont.)

TP31095	TGCAGCAGCAAGAAGCGGAAGAGCAGCAGCTTCG[G/T]GAGGAGATCCAACTGCGAGGAAAGGCAAG
TP31098	TGCAGCAGCAAGACGATCTCCAGTCGTCGGAGAA[G/T]GGGGCCACCCCCACGCTTTGCCGCGACCG
TP31101	TGCAGCAGCAAG[A/C]TCCAGAAGATCCTCTGCTGCATCCAACAAGGCACGTACTCCTACCATCTTT
TP31103	TGCAGCAGCAAGCAGCAAGTG[C/T]CTGCGTCTTCTCCATTTCTCCATGGGCTTGGAGCTCAAGCTC
TP31104	TGCAGCAGC[A/T]AGCAGTCGGGCGGGCGGTCGAGCGCGCAGTTATGCCGAAAAGCAACGGGTAACC
TP31105	TGCAGCAGCAAGCCAAACCTCCCCACCAACAGA[A/T]CTTTGACCTCCAGAACCACCTCACTCACCA
TP31114	TGCAGCAGCAAGGAGATGTGTGATGTGA[A/G]CAAACAGTGTCCGTGTATCTATCAGCCATGGATGA
TP31129	TGCAGCAGCAAGGTGATGTTTGAGGCATACAGAGACCCTG[A/C]AATGAAGAAGCCACAACTCTCCG
TP31132	TGCAGCAGCAAGTCCCGCCTAACGCAACG[A/G]ATTTCGTTGGGCCCTCTGCGTCAGACAGACAGAC
TP31155	TGCAGCAGCAATGGACAC[C/T]GCCCCTGCTGTAGGTGCAGATGACAAGAATGGTAAGAGCTCAAAG
TP31175	TGCAGCAGCACAAAAGTGAGCACATTGGACACA[A/G]CTATGGGATGGTGGTGTTGGGAGAGGGAGG
TP31179	TGCAGCAGCACAACCTCAGCGAATCCTCCAACGC[C/T]GCATGGTAAAGAAAGGTAACAATGCTGTA
TP31185	TGCAGCAGCACACACTC[A/G]CACAACGGACTGCTGTACGCGGTGAACGAGGCGGCGTGGCGATCGC
TP31197	TGCAGCAGCAC[A/T]GAGATGCGGAGGATAGTGGGCGGTGGCGGCGCAAAGGGAGGCGAGGCGAGCC
TP31201	TGCAGCAGCACAGCCGCA[C/G]GCCCGCAGCAAGGTTCACCCAGCCCTCGACTCCGCCATATTGACA
TP31210	TGCAGCAGCACATCAAGCCAAGCCTGGCGACATCATCATC[A/T]GTGTTTTAGTGTCAGGCACACCA
TP31228	TGCAGCAGCAC[A/G]TTGTGCATCTGGGCGACAGGTTCAGCGCCGCCAGGCAGCCGTTGGCGTCGTA
TP31253	TGCAGCAGCACCATGCC[C/T]GTCGACGGAAGCACCGCCGCGTTCTTCGCCCACAGCTGCATCGAAC
TP31255	TGCAGCAGCACCCCATCGTCGGCGCTCGCGAAGATGGAGTCCACGGGGAGGCCCGAC[A/G]GGACGT
TP31256	TGCAGCAGCACCCCGCTCTAGCGCCGCCGCGACAGCCGTCATCCA[C/T]CGAGCGCCGCGCCGCCGT
TP31264	TGCAGCAGCAC[C/G]GACGACGGTGAGAGTGAGATCATTGTCGTTGCTGATGGAGCACCGTCACCGA
TP31285	TGCAGCAGCACGAAGCCCTCCTTAGCCACCTTGTACGCCCCAGACTACAATAACTCGCACAC[A/G]C
TP31296	TGCAGCAGCACGCAGGTTGGCGGAGCCAATGGCGGACGCACACGGCACTGCGGCGCTGCT[C/T]CGA
TP31305	TGCAGCAGCACGCGCGGGAGCAGCATCTCCGAGT[A/G]CCCCACGGGGAAGCCCATCGTGGCGTCAA
TP31308	TGCAGCAGCACGCGGACGACCCGCACGGCT[A/G]CGTGAACATCGCGTTCGCCGCCGCTCCGTCGGC
TP31312	TGCAGCAGCACGCTGAAGTCGGTGGCGTCCTCGCCGCCGTC[C/G]GCGGGCTGCCCGACGTCGCCCT
TP31328	TGCAGCAGCACGTGGAGTGGA[C/G]AAGTGGAGTTGAGGGACGGCTTGTTCCCATTCGTCCGCGCGG
TP31334	TGCAGCAGCACTAGACAGTAGACAGGACCCC[A/C]AAAAATGCAAGCATAATACAGAAGCATTCGAT

Table A2 (cont.)

TP31338	TGCAGCAGCACTGA[C/G]AAAGATAAGAGTAGCAGTAGCTAAACAGACCACACACCCAAACTGATCA
TP31358	TGCAGCAGCAGAAATGG[C/T]CACTGTTACTGCCACCTCCCCTGCTCTCCTCCTCCTCCTGCTGCTC
TP31359	TGCAGCAGCAGAACCTTAGCGTGGGCCGCGTGGTCCTCACCGCTT[C/T]CATGTGGCGGATGGCGCA
TP31383	TGCAGCAGCAGAGCC[A/G]CGGTTTCAGTCCAAGCTCTAGTCAGACTGTCAGATCGCCACGCAGCAA
TP31388	TGCAGCAGCAGAGGGTAAGGGCACGAAAGTAG[G/A]AGCTAAAGTTTAGCTCGTACTTTTAGCGCTC
TP31389	TGCAGCAGCAGAGTCTTTTTTCTGTAGCCGATCACAG[C/T]ATCCTTCCAACGGGGCACGCAACCTG
TP31396	TGCAGCAGCAGAT[C/T]ATAGCAGGTGGTGTGGTGGAACGGGGTCAGTCCAGGTTGACTTGCTGGCG
TP31403	TGCAGCAGCAGATGCAACGTCTGTCAGGCGTCTCGGCGAGCTCACATTGGTGGTTCTCGGCAG[C/G]
TP31406	TGCAGCAGCAGATGGATCATAGATTTGGGCCGC[C/T]GTGGCATGATCATGCTTAGCGTGCACCTTT
TP31408	TGCAGCAGCAG[A/C]TTGCCGAGCTCGTTGCAGCCACATGACGAAGGAGCTGGAAAAAGGAGAAGGG
TP31433	TGCAGCAGCAGCAAGAAGATGAGCGGTAGTACGGTGTCGCTGGTAA[A/G]GAAGCTTTCTTCTTCGC
TP31450	TGCAGCAGCAGCACCAAAGGATCCGCTTGCCAATGAGTGATATTGGTTATAGT[A/C]CCAGTGTACT
TP31463	TGCAGCAGCAGCACGGTGGCGTCGTCGCCGAAGGCCACGTTCTGCTGCTCGAA[C/G]TTCCGCTCGG
TP31484	TGCAGCAGCAGCAGCAACCTCCCCGAAGCGTCGTCCACGCGGTGAT[C/G]GCGGACGGGCCCTCCGC
TP31494	TGCAGCAGCAGCAGCA[C/G]GACGAGAAGGACGTGTCCGAGCTGCACCGCCTGGCGATCGAGATACT
TP31535	TGCAGCAGCAGCAGCAGGAACCGCACCTTGGCACCGC[A/G]AGAGCTGACCGACCCTCGGCCATGTC
TP31559	TGCAGCAGCAGCAGCCGATGCACGTGCTTCAGTTTGTGGGTGGCGGCGG[A/G]GGGAGGGACTCCAG
TP31564	TGCAGCAGCAGCAGCCGTGCCGCACCCGACCCACTCGGG[A/C]CCTGCCACATGTCGGCTGTGCATG
TP31566	TGCAGCAGCAGCAGCGAGTACCAGACAAGGCAGAGACCGATCCTTC[A/T]GCCTTCACCTGTAGCTG
TP31571	TGCAGCAGCAGCAGCGTCCATCAGTCGTCGATCAAAATCGAAGCACCAGCGACA[C/G]ATCCTGATC
TP31579	TGCAGCAGCAGCAGCTCATTTGCTCGCTACCAACACACAGCCCACT[A/G]TTACTGCACTGCGCGCC
TP31606	TGCAGCAGCA[G/T]CAGTCAGGCAGAGCAGCAATGGCACCATCCACCGTCTCCTTCCTCGCCATGGT
TP31631	TGCAGCAGCAGCCACCGCCAGCACCAGCACAGCCACCACCAGCACCAGAGCATGGCGGC[C/G]GATT
TP31640	TGCAGCAGCAGCCAGTCGTTGTCAGCACACAGCCACAGAGTCGTCGTGTTAGGACGCGGCGG[A/C]G
TP31641	TGCAGCAGCAGCCATAGCAGCC[A/G]TCACTTGCGAGCAGAGCCTCAACCGCACGCGCTTGGTCCAT
TP31666	TGCAGCAGCAGCCGCCACACTCTCGCCGCCACGGCCCCTCGCCGA[C/T]GTCGAGAGTATAGACCAC
TP31683	TGCAGCAGCAGCCGTCAAGGCCACCAAGGGCGGCGGCAGAGGGGCGTTCCTGCCCCACTTCTT[C/T]
TP31694	TGCAGCAGCAGCCTCCCTCCACTCGCTCATCTCACACTCCTCACTCAACCAC[C/T]ACTGCCTCCAC

Table A2 (cont.)

TP31706	TGCAGCAG[C/T]AGCGACTAGTGCCCTCTCATTTCAACTAAAGATCAGTGTTCCACTTCCACAGAAC
TP31709	TGCAGCAGCA[G/T]CGAGGTACGGCAAATTTTCTCAATTCCATTCCGAGTCGTAGGAACTTATTCGT
TP31721	TGCAGCAGCAGCGCCGCCGCAACGGGTAACCGTGTATCCGACAGCTGCTGCTGCTCCACCAG[A/T]C
TP31760	TGCAGCAGCAGCTAGAGCCTAGAGCTAGGTAGCATCGTCCGCGG[C/G]CCCCCCTGGGCCTAGGGAT
TP31768	TGCAGCAGCAGCTCATTTGCTCGCTACCAACACACAGCCCA[A/C]TGTTACTGCACTGCGCGCCAGC
TP31775	TGCAGCAGCAGCTCGCCTCCAGGGCGGCCGACCTCGACGAC[G/T]CGCGGATCGCCGCGGCCACGGG
TP31804	TGCAGCAGC[A/T]GCTGCTGGGAAGAGCCCGCCATCATCGCCTTCCTCTAGACAACCAGCAATGCCT
TP31809	TGCAGCAGCAGCTGGTCCCGC[A/G]CTGCCGCCGCGCTCCATCCCGCTCACCTTCTTCGACGTCAAG
TP31810	TGCAGCAGCAGCTGGTCCCGCACTGGCGCTGCGCTCCA[C/T]CCCGCTCACCTTCTTCGACGTCAAG
TP31817	TGCAGCAGCAGCTTCGTCCTCGGG[C/T]TTGGGCTCGTTGAGGCGCTTCATGAGCAGCTCGGGCACC
TP31825	TGCAGCAGCAGGACA[C/T]GTTTGCGCTGCGGAGGCAAGGCGGCTGGATGGGGCGTCGTCGTGAGGC
TP31826	TGCAGCAGCAGGACATGTTTGCGCCGCGGAGGCAAGGCGGCTGGATGGGG[A/C]GTCGTCGTGAGAC
TP31833	TGCAGCAGCAGGACTTTGGCGCCGACCGCCGACGGCTCCTGTACGGCG[C/G]CAGGACGCGATGTGC
TP31840	TGCAGCAGCAGGAGCAGCACAGCCCGCTCTGCTGCTTCCAGGAGA[G/T]AGAAGAAGAGGCAGGAAG
TP31842	TGCAGCAGCAGGAG[C/T]CGCCCTTCCCGCCCAGACAGCGCCAAGCTGGCGGCGACGCGGGAAAGGA
TP31853	TGCAGCAGCAGGAGTGCTCGC[C/T]GACGACGACCGTCCAGTGGCAACAGCAAACGCGCCGCGCGCC
TP31855	TGCAGCAGCAGGCACGACTTCCCCACGCCT[A/G]CAACACAAACAACCAATCAACCAACCGATCAAT
TP31874	TGCAGCAGCAGGCGACGAGCGCCGC[C/G]GCCGCGACCGCGACGAACCAGAGCGCGGCGAACGCGAA
TP31886	TGCAGCAG[C/T]AGGCGGTGGGGCTGTGTCTCTGGCTCGCCGCCGCCTCGGTGCATCGGCGCCACCA
TP31889	TGCAGCAGCAGGCGTTCCTCACGGGGAACACGATGCCGCCCGCC[A/G]ACGCCTACACCATCAACGG
TP31893	TGCAGCAGCAGGCTTCTCTGCTAGCTAGCTATATAGCTACTG[A/G]TTCGTGGTTCCACAATGGCCG
TP31896	TGCAGCAGCAGGGCCAGAGCTAC[C/T]GTCGACTCCAGGAGCGCGAATTGGTCCCCCACACATTTGC
TP31897	TGCAGCAGCAGGGCGCAGTGGTCAGTGTTAGTGTTGATCCCTCCAGCTTGGTCCAACG[A/G]CTGAG
TP31902	TGCAGCAGC[A/T]GGGTCTGAGTGTGTGGTGCGATGGAGGCTGCGGTGGTGAGCGCTGTCCTGAAAA
TP31906	TGCAGCAGCAGGTAGCTTTTTATA[A/G]GGGAGCAGAACAAGAACAAGAACGTACACGCCGCCGATG
TP31922	TGCAGCAGCAGGTGGAGGC[A/G]CTCCAGGCACAGCTGGCGCTGGCGCAGGCCGAGATGGTCAGGCT
TP31926	TGCAGCAGCAGGTTCCATAGCCAGCTACAGAAGCTTC[A/C]TGTTCCCTGGCACTGGCATGGCTTCT
TP31939	TGCAGCAGCAGTATGCCAGTATCGATCTCTCGTTCGCATCGCAGGCCACAGCACG[G/T]CGGCCATG

Table A2 (cont.)

TP31941	TGCAGCAGC[A/G]GTCATGGTCACATGGATCTGTTGGGAGCGCTTCAGGGTCATGTGTCTATTAGGG
TP31967	TGCAGCAGCAGTTGGGCATGGTGCTGTCAGAGCAGGACATTTCACCCCTAGTCGG[C/T]TGCCACTC
TP31972	TGCAGCAGCAGTTTCAGTAGTGGCAGATACAGGACCAAGCTCCTCCCAAATCAAGTC[A/C]TCGCCA
TP31980	TGCAGCAGCATAGCAATGCAAGAACGTACGGAACAGCTTAGCTCAGCTTGTCAGTTATTA[A/G]TCG
TP31983	TGCAGCAG[C/T]ATATCATCTCTTCTCTTCGTATCCACCAGCTCCTCTCCACCCCTCTGCACCAATG
TP31987	TGCAGCAGCATCA[A/G]CAGCAAGAACAATGACCCGTGAGTCGCCAGCTCGTTAGCAAGAATAATAT
TP31989	TGCAGCAGCATCACAAGCCCA[C/G]CAGGATCTCAGGTGCGTGCCCTCCTCTGCCTCCTCCTGCTCT
TP32004	TGCAGCAGCATCAGTAGTGTCTTCTATGTGCATGTAGCAGCCTCGGGATGACACACCTGGGGC[A/T]
TP32019	TGCAGCAGCATCGGAGCAAGATTCCT[C/G]TGTGTCATTTGATGCTCCTGGCAAGCATACGAATGTC
TP32024	TGCAGCAGCATCGTCTTGGCACGAGCGAGGGTGCAGCAGTCTCTGGCAGC[A/G]GTGTCGCACTCGC
TP32036	TGCAGCAGCATCTGATGAGCCTTGCAAACGGC[G/A]CCAGCGAGCATCCAAGCGCAATGGACAAGGG
TP32039	TGCAGCAGCATCTGCGACGGTGGCGCGAGCAAGCAAGGAGA[A/T]GGTGGAGATGGCCGAGCAGGGG
TP32041	TGCAGCAGCATCTT[C/G]ACGCGCTCGATCGGCGCCGCCACGGTCTTGGACACCGACGACGACACCC
TP32047	TGCAGCAGCATG[A/G]ACGCATGCACACTCATTCGGCACTGTGGCACGAAAGCTCGGTTGGGTCGGA
TP32058	TGCAG[C/T]AGCATGCCAGGGACAGCAGCATCAGCCACCGCGCCACATCCAGCACCCCGCCACCGCT
TP32060	TGCAGCAGCATGCCTTTCTACCTGAGGGGAGAGACA[A/G]CTGATCGTCGTCGTGTAGCCGTGGTGT
TP32068	TGCAGCAGCATGGCGGCAGCGACGACGCTAGCAC[A/T]ACTCGTGACGCTGGCGGCGCTGCACGGTG
TP32071	TGCAGCAGCATGGCTAGTACTGCAAGGATCGCCCAGGAGGATGTACAGGCCAATCGATGGAAA[A/C]
TP32072	TGCAGC[A/G]GCATGGGGATGGGGATGGCCAAGATGTTGTTTTGATTCTGATCAATCTCAGCGCCAG
TP32097	TGCAGCAGCATTGTACCTGAACCACA[C/T]ACATACTGACATACCAAGTAGTGGCAGTAGTCGTCTT
TP32148	TGCAGCAGCCACACGCGCTGCGCGAGCACAGGTTAGCA[A/G]CTCACGTTGCTCTCTCTCTTGCTCT
TP32174	TGCAGCAG[C/G]CACGCGCGCGCGCGCCAACAACAACAATGACAAAGACGCATGCATTCATGCTCAT
TP32193	TGCAG[C/T]AGCCACTCGATGGTCTCGCCGTCCGACTTGTGGCCGAGCTCGCGGGTGAGCTGGAACA
TP32195	TGCAGCAGCCACTCGATGGTCTCGCCGTCCGTCTTGTG[G/T]CCCAGCTCCCGCGTGAGCTGGAACA
TP32197	TGCAGCAGCCACTCGCTCCACAAGTACGCGCCGCTGGACTGGTCCGCCTACTTC[A/G]ACGAGGAGC
TP32213	TGCAGCAGCCAGAGCCAGGTCCCGCCGCGACACCACGC[G/T]CCCGCGGAGCTGGAAGCACCAGCCA
TP32216	TGCAGCAGCCAGAGCGCGCCGACGACGCCCAGCCCGACGGCAAG[C/G]CCGAAAAAAAAAAAAAAAA
TP32234	TGCAGCAGCCAGCAGGGGCCGCGGCGCCTCAACACTACGGGGCGGCAGTG[C/T]CAATGCTCAGGAC

Table A2 (cont.)

TP32243	TGCAGCAGCCAGCCGCCGAGTGATCCAAGGCGCCCGCCTCTGCCTGACTGCCTCTGCTGCC[A/G]TT
TP32246	TGCAGCAGCCAGCGCAGCGTCTGT[C/T]CGTCCCCGCTCGGCCGCCGTCATCACAGGTTGTGCAGCA
TP32251	TGCAGCAGCCAGCGGAGAGG[A/G]GTCAGACGCGTTCAGTTGCAAAGGGTGGGTGAAAGGGTGCAGA
TP32254	TGCAGCAGCCAGCGT[C/G]AGGTCCACGACGGAACGCCGCCGTGCTGGCGTGCTAGCTCAGTGCAGT
TP32260	TGCAGCAGCCAGGGCAGGTGCAGGGGTCAGTCAATTCGGCAGATCGGC[A/G]CAGATCTGGCGGAAA
TP32273	TGCAG[C/T]AGCCAGTGGTACTGACCTTCCACGCCCATGTGGTCCGCCGAGTGGAGGTGGAAGATGA
TP32288	TGCAGC[A/G]GCCATGGCAGATGGCATTGGCTGTTCCCACTCCCTGTCTAGCGTCCACTGTCCACCC
TP32298	TGCAGC[A/T]GCCCAAGAGCTGGAGGAGCATCAAGACGGAGAGGCAGCAGCGGAAGACTATGACTAT
TP32301	TGCAGCAGCCCACCCACCTACCAAAAAACAA[C/G]AAGAAGAAAATTGCCCAAAACCCCACACGACG
TP32324	TGCAGCAGCCCATCCCTTTCTCCTTGGAAAAGGCTGTGGACTTTTGGCTGGGTCGTCGT[C/T]GGCG
TP32325	TGCAGCAGCCCAT[C/G]TTTATTTGGCTGGACGCGATTTAGGCCTGGGCAGCGCGGTGCTTAAAGCA
TP32326	TGCAGCAGCCCATGCATGCAATGCAAATTATGCAATGATTTCATTCATTCTCAACTAA[A/T]TAACA
TP32330	TGCAGCAGCCCCAA[C/T]TGTTGCAAAATCAGGGTCCAAACTTGTCGAGCGAAGACACAGCCCACTA
TP32342	TGCAGCAGCCCCCGCCGAGAAGTAGACCAGCAAGCACTGGAACAAACAGGAACCGCAC[C/T]AAAGT
TP32344	TGCAGCAGCCCCCGTCAGGCCTCGACCACTGCTGGTGTATTCACGGCGCCAGGCAG[C/T]CGCTCCT
TP32348	TGCAGCAGCCCCGATTGGAGCCCGCCT[A/G]GAGCCGTTGGGGCCTGGTGCGGGTGCCGTGTGGCCG
TP32359	TGCAGCAGCCCCTTGGTAGTGAAGTCGAACGCCATCGCGGGCCCTCCAACAGCCTGCACCCAG[A/T]
TP32378	TGCAGCAGCCCGTGCATTGCCCACTCTAT[A/C]TATCGCCATGTATGCAAGTGCCATGGGCGCGGTC
TP32383	TGCAGCAGCCCTAGTTGCCCGAGCAAGCGAGCTGCGTGGAAGAGGACACGAGAGCGCCC[C/T]GACG
TP32389	TGCAGCAGCCCTCTGACGAGTCCATGT[C/T]GGGGCGGATCCGTGCTAGCTCCGCGCCGCGGACGGA
TP32404	TGCAGCAGCCCTTCTTCAA[C/G]ACGGAGACGGTGTCGCAGCTGGTGCGGGAGTGCGAGGCCATGAT
TP32412	TGCAGCAGCCGACGCGGCCATGACGTGGGAGCGCATGTGGCCGCCCAGCGCGCG[G/T]CCATTGTGG
TP32428	TGCAGC[A/T]GCCGCACCGCTGTTTGGCGAGAGCTGCTGCTTCCTCCGCCAGCTCCAGCTGCGAGCG
TP32438	TGCAGC[A/G]GCCGCAGGTCCACATCGTACCGCCAGCTGCCACTGCTCACCCTATCCACGCTCCACA
TP32441	TGCAGCAGCCGCATCATCTCCTCCTCCACGCGCTCCTCGATTGCGATGCTGGC[A/G]TCGAACACCT
TP32442	TGCAGCAGCCGCATCGCCTCC[C/T]TCCTGCTCTCCCTCAGGGGATGAGGAGCGGCGGAACCTCCAG
TP32449	TGCAGCAGCCGCCCCGCC[C/T]CCTCTTCGGCCGAGGGGGCCACCGCCGACGCTGTGAGGCTGCTGC
TP32450	TGCAGCAG[C/T]CGCCCCGCTTCCACCGTCGGTGCGGGCGTCGGCGCCGCCCCCAACTTCTCCGACC

Table A2 (cont.)

TP32470	TGCAGCAGCCGCG[A/C]CACGTCTCAGCGGTCCCTGCCCTGCTGCACCAGACTGCGGCTTCTCAGGG
TP32488	TGCAGCAGCCGCGGCCGCAGTGGGCCGATGAGATCACGACGGTG[A/T]CCGAGGGCCGAAAAAAAAA
TP32499	TGCAGCAGCCGCTGCTCCAGCTCCTGGTAGATATGTTC[C/T]TAAGTTTAAACTCAGCGGCGATAGG
TP32500	TGCAGCAGCCGCTGGTACTGTGGATACAACTATACGCTCG[G/T]ACAGTCCCACGGCACGAACCTGG
TP32506	TGCAGCAGCCGCTTGTCACCACCTGGCGGCCAGGATTTGCTGA[A/T]GACGTAGATGGCCACGGTGA
TP32507	TGCAGCAGCCGTAG[A/T]ACACAAGCACACCACCACCTCGACTCCACCTCCCCTGTTCTCAGCGTGC
TP32518	TGCAGCAGCCGTCGTCCATGGACCCGACGACGGTGGCCGCCGTGCT[C/T]GACTCCCTCGCGGCCGT
TP32527	TGCAGCAGCCGTGTGGAGAAAGCTAGCTAGCATCATT[A/G]GCAAGCCGCGTCGGTCGCGTCCGTCG
TP32552	TGCAGCAGCCTCATGGCAGCCAGGCGTACCTCGATCTCCTGGCGGCGCTCCTC[A/G]GGGGTCTTGG
TP32589	TGCAGCAGCCTGCAATGTAACATGGTCACCCCACTCTCCGCTCCTGGTT[C/T]GATTGTTTAAGCAA
TP32591	TGCAGCAGCCTGCACCTGGGGTAGTGGTTGTATTAGGTAGCTACCAGGT[A/T]GCTTCCCTCTCTGG
TP32592	TGCAGCAGCCTGCATCCTTC[A/G]TATAACTAGTTATGATTGAATCCTATACTACAATAATCCATAC
TP32624	TGCAGCAGCCTTCCCGAACGGGACAGGGTGTCTTACGTTGTGGATGAGCCCGACTT[A/G]TCGGCAC
TP32628	TGCAGCAGCCTTGAGCCGCCCGTGCAGCAATATCC[A/G]AACGCTGAGGCCCGTGCACAACCCGAAG
TP32630	TGCAGCAGCCTTGCAGAGCGCAGCGGCGGCGGCGGCGGCATGTGATGTGCGGCGGCGGTG[C/T]GGA
TP32635	TGCAGCAGCCTTTCTTATCATCCACGTCCATAAGATA[C/T]GGTTTGGACGAGCAGAGAGAAGAGAG
TP32678	TGCAGCAGCGACCTGCCCGCTTGCATACGCATGGGTGTGGAGTGGGTG[C/G]CACGGTGCACGCGCA
TP32685	TGCAGCAGCGACGCAAAAAGGCTCTTGTCGTGACGCCGAGACGGGCCCGCACGGCAGCGGC[C/T]AG
TP32687	TGCAGCAGCGACGCCGATCGACGCTGCTATAGGGTATACTGCTGGTATACGCA[A/G]ACAGCAGCAC
TP32689	TGCAGCAGCGACGCTGGCAGCAACGGTGGACCCGCCTGAACG[A/C]CGTGGCGTTGGAGCCTGCACC
TP32699	TGCAGCAGCGACGGTGACGACGCACGTTGCGGTGCATTGCATGCAAACGCACTGTAGTGTC[C/T]AA
TP32700	TGCAGCAGCGACGTGTGCTCGTACTGGTTCGACTTGGAGCGCTTGTAGCCCAAGATCATGCCC[C/G]
TP32715	TGCAGCAGCGACTTCTGCTTCTGCACCGCGGCCGCGGCCGCCGCGGCCGTCGGGCCC[A/G]TGGCCG
TP32744	TGCAGCAGCGAGCTCGCGCTCTTCTACGA[A/G]AACGGCCCCTTCAACATAGCAGACAACTTGTCGC
TP32751	TGCAGCAGCGAGCTGTG[G/T]CCGAGGGGCAGCTTCTCCTTGGCGTGGATGCGGAGGCCGCCGCCAC
TP32764	TGCAGCAGCGAGTACAGGGTGCAGTTGAAC[A/G]AGTCCTGGAGACGAAACAGCGTCGCCCTGTCAC
TP32772	TGCAGCAGCGAGTGGTGGCGAGGGCGCGAGGCAGCAGGGAGTGGTGGCGAGGGCGCG[A/T]GGCCGC
TP32794	TGCAGCAGCGATCATCAGGCAC[C/T]ACACCAGCAAACTCGATCGATCGACATGGGCCGTTGGTTGA

Table A2 (cont.)

TP32826	TGCAGCAGCGCAAGGACGCCAGCCACGAGTTCAGCACGC[A/G]CTCGCTGAGGAGTTTCATCGCCGA
TP32853	TGCAGCAGCGCAGGGGTGGTGGTGTGGTGGC[A/G]GTCATCGTCCGCTTTTGGAGCTCTGCAACAGT
TP32856	TGCAGC[A/C]GCGCAGTGCACAGACATCGCGGAGGAGGTATGCACAGACATAAACAGGGGCAGCA
TP32867	TGCAGCAGCGCCAAAGACGCACACACTGATCGGTG[A/G]TCACAAGTCTTCAGCTCGAAGGCAGGAA
TP32870	TGCAGCAGCGCCACCACGGCGAACTCCTT[C/T]TCCTTGGCAGGGCCGTCCTCGATGGCCTCAACCA
TP32877	TGCAGCAGCGCCACGGCGATCATGGGCGCCGCCAGCGC[A/C]GCCAGCCGCCCGAAAAAAAAAAAAA
TP32905	TGCAGCAGCGCCGCAGCATCTGCATCAATACGTGCATAAAAAT[A/C]AAAAGGTCACATGTACGTCG
TP32915	TGCAGCAGCGCC[G/T]CCGTCTGGCTCGCGTCCTGTTCCGCTCGTACCCTCTGCATGTCGATCCTCG
TP32918	TGCAGCAGCGCCGCT[A/G]GGGTAGCTGGCCCTGGACATGAACTGGAGCGGTGCCTGCACGGTGCCC
TP32923	TGCAGCAGCGCCGTCGT[C/G]GGGAGCACGAAGGAGACGTTGTTCACGGACGCCGCGAACCGAAAAA
TP32929	TGCAGCAGCGCCGTGTGCATCCACGTCCACGCACACTTTGCTCGAGCGAGCC[A/T]GCCTGCCGCCT
TP32948	TGCAGCAGCGCGACCATCTCCTCCTCGGCGCTGGC[A/G]CCCAGCCGCACCAGCTCGACGTCGAACA
TP32950	TGCAGCAGCGCGA[C/T]GCGAGGTTCGGCGCGCCGCCGTCGCGCTCGTGCCGAAAAAAAAAAAAAAA
TP32968	TGCAGCAGCGCGC[A/C]TTGGGGACGATGCGTTTAAAGGCGAGGCGCGGATTCGCGTGATGCGTAGT
TP32974	TGCAGCAGCGCGCGCGGCTCACCTGGGTTCTGGAAGGCGGCGGCGCGGCCTCCC[C/G]AGCCGCTGC
TP32976	TGCAGCAGCGCGCGGACGCGGTCGTTCGTTGGACGCGAACGCTTCAGAGTCC[A/G]AACAAACGCCA
TP32982	TGCAGCAGCGCGGCGACACGGCGG[C/G]GGAACGCGACGCGGCGCAACCGCCACCAGGCCGTGATGA
TP32985	TGCAGCAGCGCGG[C/T]GGCACAGTCGTCGCTGGAGGCTGGGGCCAGCTGCCGCCGCCGCCTCCACC
TP32989	TGCAGCAGCGCGGCGGCGAGGCGGACGGGGCGGATCTG[G/T]CCGTTGTGGAAGAGCTCGTCGGCGG
TP33000	TGCAGCAGCGCGTATACCCTGTCTGTCGGCATTCAGCAGCAC[A/G]ACATGAAGGTAACCAACTAAC
TP33003	TGCAGCAGCGCGTCCTCGAGCTCGGCTACAACTTCCTCTTCACGGTACGCGTC[A/G]GCACCAATCA
TP33004	TGCAGCAGCGCGTCGAACTCCGCCTGGTTGAGCTGCTTGTT[A/G]ATCTCGGCGTTGAAGAGGCGCT
TP33039	TGCAGCAGCGCTCGTCGCACGAACCGCCGTGATCACCTCCCGATTTGTTCACCAACGCC[A/G]AGCT
TP33045	TGCAGCAGCGCTGCGTGCGTGCCATCTGGACGAC[A/G]CAATCTTAAACAAGGTCATGTTCGTTTAT
TP33046	TGCAGCAGCGCTGCTGCGTCAGCAGCTCTCCGCTGTCGCTGGGGAAGGCAGCGTCGCCAC[C/T]ACA
TP33050	TGCAGCAGCGCTGTGTGCAGGGC[A/G]CTAGGCAATGGGGGAGACAGCAGCAGAGCGAAAGAGGTTG
TP33055	TGCAGCAGCGGAACCAGAACCCACAGCACCGCCATGGCGTTGAGCTTGATGCTAGGCTCGGAC[A/G]
TP33058	TGCAGCAGCGGAATCACGACCCACTGCGCCTCCATGGCG[C/T]TGAGCTTGATGATAGGCTCGGGCG

Table A2 (cont.)

TP33061	TGCAGCAGCGGACCACCACCACGCCGCCAACCCTAGGGTCTACGAGGAAGG[A/G]GGAGGAGGGAGC
TP33069	TGCAGCAGCGGAGAGAGCACGCGAGGGCAGAGGAGAGAAACGAGGGAGAGAAGACG[A/T]CGCTGCA
TP33073	TGCAGCAGCGGAGG[C/T]GCAGCCGAACGTCCAGGCGGAGCTACTGACGGAGCGCGCGGCGCAGAAC
TP33076	TGCAGCAGCGGAGTGGTCGAGTGGAGTTTGTGGTGGAGCCTTTT[A/C]AGATCAGATTCAGATAAGA
TP33081	TGCAGCAGCGGCAACACGGTGGCGTGCCAGCCCCCCGAGGCCCACATCACGGA[C/G]GTCTACGCCG
TP33091	TGCAGCAGCGGCACGAGCGGCTCAAGAACGTCCA[G/T]TTCGTGCCCCTCTCGGCCGCGTCCTTCCA
TP33098	TGCAGCAGCGGCAGCCATCCCAAACGTACGTTACGTGTTTATCCCGCAGCTTGCACACGG[C/T]GTA
TP33099	TGCAGCAGCGGCAGCCATGAACTCACCACGA[A/G]TCATGATGGGCGGGAGTAAATAGTCACAGGGC
TP33107	TGCAGCAGCGGCAGGTGCAGGTCGATGCCCAGGTAGTCCTCG[G/T]CCTCGTCCTTCACGGGCCTCC
TP33109	TGCAGC[A/G]GCGGCAGTACATGGCAGGCGGCTGTTTGGGCACGTGCCAGCCAACCATCACCCAGCC
TP33115	TGCAGCAGCGGCATGAAGCTGTCCGTCACCGTTGCCGAGAGCGGCCCCG[C/T]GCCATCGGGCGCTA
TP33125	TGCAGCAGCGGCCTCGGAGTCGCAGGGCAG[A/T]TGTCGACGGCGAAAAGACGTGCCTCTGCCTCCC
TP33126	TGCAGCAGCGGCGACACCCACAACACAAAATCTCCGCCAGAAACCC[A/G]ACTGAATCTCTGCTTCC
TP33133	TGCAGCAGCGGCGCCGACAGCGGCACCAGCGCCGTGGGGGCAGCAGCAGTAGTAGA[A/G]ACAGCGG
TP33134	TGCAGCAGCGGCGCCGTGGTCTGCTCCACGTACAGCG[G/T]CGGGATCTCGAGCCTCACGCGGTCCT
TP33137	TGCAGCAGCGGCGCCTCCTTGTCCCTGTGCCCGCG[C/G]GCCGCCGCCGCGTGCGCGTGCTCGTGCT
TP33141	TGCAGCAGCGGCGGCAGTCATGACGCGCGAGAC[C/T]GAGCAGGCGTTGGGCGTGTGGACCGAAAAA
TP33143	TGCAGCAGCGGCGGCCACTGCACGCCGTGCGCGGCGTCGAGGTC[C/G]ACGATGTGCAACCGCCGCG
TP33161	TGCAGCAGCGGCGTCGTCACTCG[G/T]CAGTAGTTCACCACACAAAACAGAAGCTTAAATTGGCTTT
TP33175	TGCAGCAGCGGCTTCTTCGGCCTG[C/G]CCAAGCCCAGAGGGGCCATGGTCACCGTGACCTGAGTTG
TP33185	TGCAGCAGCGGGCAGCACTGCTCGTCCTCGGGCA[A/C]GCCGATGTTAAGCCTCAGCAGGTTCAGCA
TP33186	TGCAGCAGCGGGC[C/T]GAGGACCAGCGACGGGTTCACCACGACCAGGTCCACCTGGCGCTGCCTGG
TP33197	TGCAGCAGCGGTAGGCA[C/T]GACAGCAGAGGCTGGGGTCGGCAGCGAGCAGCGGAGGCCTGGGTCA
TP33239	TGCAGCAGCGTCATGGGCGGTGGCCATCTCGATGCT[C/G]TCTTTCGCCATTACCTGCTGCTCCTCT
TP33241	TGCAGCAGCGTC[A/G]TGTGGGAGTGCGTCAAGCCGACGGCGGACACCGACAGCGGACCCTGGGCTG
TP33245	TGCAGCAGCGTCCGCTTCCACTGCTCGACGTCGCGCAGGTTGTAGGCGGAGAGGGAGTCGGCG[C/G]
TP33246	TGCAGCAGCGTC[C/T]TGATGGTGGCGTTGACCAGCGCGCTGAGCGGGGACGGCCTGAACCCGAAAA
TP33252	TGCAGCAGCGTCGAGTTAACTGACAGCAAAACATCCTTGTAACGCAGG[A/G]GGATCATACGCTTGT

Table A2 (cont.)

TP33254	TGCAGCAGCGTCGTGCTCTGCCTCGCCGCTCCTCCTCCCCTCAGGTATCCTGGC[G/T]CACCCCCCA
TP33260	TGCAGCAGCGTGAGCGGTCGCTGAACCGCTTCGTGCGAGCTGTTGCCTTCT[G/T]GGAATGGGCGGG
TP33263	TGCAGCAGCGTGCCCAGGGCGGCTTCCAGGGACGCCCTCCACCCGCTCACGACGGC[C/G]CGCGCGA
TP33279	TGCAGCAGCGTGGTGACCACGGAGCCTTGGCCCACGC[A/G]CCCGCGCTTCAGCGCGCCCAGCCTGG
TP33282	TGCAGCAGCGTGTAAGCGCACCCGACGACGGCGACGGCCAGGA[C/T]GTACCTGTAGGCGTAGACGT
TP33293	TGCAGCAGCGTGTTTATCCCCGTCACGAA[C/G]AGCAGCGTCTGCACCACCCTGACCCTGTCTCCCT
TP33318	TGCAGCAGCTAACTTCGTCGTCGTCGTCTCTGACGAGGTTTCTTGGGTAGG[C/T]TGAGCTTGAGCA
TP33344	TGCAGCAGCT[A/G]CCTATACAGGAGAGATTCGGACGCCCCCATGAGATGGAGCCCTAGCGCGGTCG
TP33354	TGCAGCAGCTACGCCTCCAGATCGCTGGCGTGCTCCCCGTCCCCCGTGC[A/C]AGTGGCCGTCTTCT
TP33358	TGCAGCAGCTACTACCAGCTAGTAGTACTACTGGAGCGAGCACCA[C/G]TGAATCACAAATGCCCCA
TP33360	TGCAGCAGCTACTACTCCCACTC[C/T]ACTAGGCACTCGTCGCCTTCCAGGAATCTTCTTGCGCAGT
TP33362	TGCAGCAGCTACTGCGGCAGCCTACCTAGAAAACTGACGCGCAC[A/T]GGCTGGAAAAAGGGCCAGT
TP33385	TGCAGCAGCTAGCTAGCG[G/T]CGCACTGCAATATTTAAGCACTCCAACTCGATCACAGTCACAGCA
TP33396	TGCAGCAGCTAGTACAAAGTTTCCAGACTCGAGCATGCTGGC[A/G]TGGGCCGCCGCACCAGCAAAT
TP33399	TGCAGCAGCTAGTGCAGGCGGCCGTATCTGCCGTCGTGTTCATGGTACGTAC[A/G]TTAGTGCACTC
TP33411	TGCAGCAGCTATATATATGTCAGCACGTACGCACGCAATTAGACACGTGAATGAAGCA[A/T]AAAAC
TP33418	TGCAGCAGCTATCTTAATTAACCCCCCACCATACCAGTGATTATTTCCTTTCAATAGCTAGC[A/G]T
TP33423	TGCAGCAGCTATTTCTGTCTACCCTCCCCACCTCAATCAAATCAT[A/C]AAAAATTCTATCTAAAAA
TP33434	TGCAGCAGCTCACCGATGCCGTCGATGATGGCAGTGGCACGCAGAAGCAGCTCCTCGTC[C/G]TCGG
TP33436	TGCAGC[A/T]GCTCACGCCGAGAGGGCTTGAGGGAGTAGATCGACCTTGGGGCTCCTCCTTGGCTTG
TP33437	TGCAGCAGCTCACGCCTCAGCAGAACGCGACCCTGTCTGAATGGTGGCAGCAG[A/G]CTAGACAGGC
TP33441	TGCAGC[A/G]GCTCAGCCCGACTCACGCATGAGCGGCTGGGCCGAGGCCCACGACGAACGGGCCAGG
TP33447	TGCAGCAGCTCAGCTGAAGCCTGGGCA[G/T]TTAGTCGTCGCTGAAGTAGGTTGCGGATCCCCGTAG
TP33460	TGCAGCAGCTCATGGACGCCGTGTACGAAGCCCAAGACGTCCTCGACGACTTCGAC[G/T]ACTCGGT
TP33468	TGCAGCAGCTCCACCAAGAACACACGGATCG[C/T]CATCAGTACAGGAACAAATAAATTTTCGAGTT
TP33474	TGCAGCAGCTC[C/T]ACTGCAAACAAACACCACCCGTGCCTCCGCCAGTCGCCACCTGTGCAGCGCT
TP33486	TGCAGCAGCTCCATGCCCACTCCTCTCGTCAGGGT[G/T]GTGAAGTGCTCGATGACACCCCTCAGCC
TP33489	TGCAGCAGCTCCCAAAAAAGTCTCCGTCCTCTCTGCCTCTCTC[C/T]CTGTCTCTGATACCGTGATG

Table A2 (cont.)

TP33536	TGCAGCAGCTCCTGCCTCCACCTTCTGCGGCATATCTCCACAATGGGCACAGATCAGCTGGCT[A/G]
TP33554	TGCAGCAG[C/T]TCGATCGGCGGTTTGCCTGTGCAATGCACTCGCCACTCGCTAGCAGTAGCAAAAA
TP33565	TGCAGCAGCTC[G/T]CGGTTCTGCTCGGCCAGCCTGTCACGCATCGCCTGCGACTCCTCGAGCAGCG
TP33587	TGCAGCAGCTCGGCGTTTCATCGCTTCCTCTGTTTTTGTTTTCTGTTTCCCTAGGTGCCC[C/G]TGG
TP33612	TGCAGCAGCTCTAAGCCTCTGCTCCTCGAGATCTGT[G/T]CTAGTCCAGTCAAGACACACTGAGAGC
TP33619	TGCAGCAGCTCTCAGCTCCTCGCCCCGCTGCGCTGCGTCCTAATTGGTGGCGGGGAACG[A/G]ACGG
TP33630	TGCAGCAGCTCTGGGGATCGATCGGTTTAGGGATATGTAATATACTATATATACTTGTTGGTA[C/T]
TP33643	TGCAGCAGCTGAAAAATAATGTAGCAGCTGTTTTTTTA[A/G]AGAAAAATATTATTTCGGCTAAAAA
TP33664	TGCAGCAGCTGAGGGTCGGTCGGGGTCGGGCAAGACGGCTGGTGCTCACTC[A/G]CTGGTGCCTATA
TP33668	TGCAGCAGCTGATCGACGAGGCGGA[C/T]GCCAACCCCAACGACGCCGCCAAGCAGAGCGCGCTCCT
TP33671	TGCAG[C/T]AGCTGATGGCACAGTGGAGGCACCAGTTGCAGACACGGAAGCTAAAGTTGGTGTAGAA
TP33677	TGCAGCAGCTGATTTGCTCTCCCTGGAGCTAGAGGACCAGGACGAATCTGAACTGCTGCT[C/G]GCG
TP33681	TGCAGCAGCTGCAACAC[A/T]CCCCGCCGCGGGACGCCGCGGGGAGGCGCCCTAAGAAGCGCCGCCG
TP33684	TGCAGCAGCTGCACAATCACGATGTGTTCTTGGTTTAGTTGGGCCTAAAGCCGAGCCTCC[C/T]CTG
TP33687	TGCAGCAGCTGCACCATCCTGC[C/T]GAGGCTGCCCTGGATCTTGTCGTAGCAGGCCACCTGGAACG
TP33688	TGCAGCAGCTGCACCATCCTGC[C/T]GAGGCTGCCCTGGATCTTGTCGTAGCAGGCCGCTGGGAAGG
TP33709	TGCAGC[A/T]GCTGCCATGTTTCGGGCAACTTGCTGGCCCGCTGCCCAGAGTTATCACCTTCCTGCA
TP33710	TGCAGCAGCTGCCCCACTGCTCGTCGC[G/T]GCATAGAAGGCGGCGTCGACGTTGATCTTGGTCCAC
TP33715	TGCAGCAGCTGCCCTCGTCTCGATCGTGCCCAGC[C/T]GCTGCCGCTCTCGCTCTCGCCGCCCGTCC
TP33716	TGCAGCAGCTGCCGAGGTGAGGCCCAATCTTTGATTAACAAGCGTGCGTTGGCAATCTTT[A/G]ATT
TP33734	TGCAGCAGCTGCGCCTGGG[A/T]TCCAACCAGCTCGACGCGGTCCAGGAGGCTCCCGACGGCGGATC
TP33745	TGCAGCAGCTGCGCGCTGAACTCCAGCAGGCCCTCCAGGGCCTCGG[A/C]GCGCTGCTGGTACGACG
TP33751	TGCAGCAGCTGCGGGACGAGAAAGAGGCGGCGAGGAAAGAGGAGGA[A/G]CTGACCGAGCTTGAGCA
TP33762	TGCAGCAGCTGCTCTCCTGATCTCCTCCTCCTCTACAGACTAC[A/G]GAGGATGAGGATGGAGGGG
TP33766	TGCAGCAGCTGCTGCACCTTGGGGATGCGGGTGGAGCCACCGACAAG[A/C]ACGACGTCGTGCACGC
TP33801	TGCAGCAGCTGGACCCGTGCTCTCGCTCAGATCACGGAGGCCATCCGTCTGGT[C/T]GCATCGCTCT
TP33807	TGCAGCAGCTGGAGCGCGACTGCAACTTGGCAATGAAGGAGCTGGCGC[G/T]CGCGGGGGACGTCGA
TP33819	TGCAGCAGCTGGCCTACAGCGCCG[A/C]CGACGTGCTCGACGAGCTCGAGTACTTCCGCATCCAGGA

Table A2 (cont.)

TP33821	TGCAGCAGCTGGCCTACGATGCCGACGACGTGCTTGATGAGCT[C/T]GAGTACTTCCGCATCCAAGA
TP33825	TGCAGCAGCTGGCGCGTCGTGGCAGATCTCGCTCGCCCGCTCGCCGCCGCAA[C/T]GCCTCCAAGAG
TP33840	TGCAGCAGCTGGTGCAACGGAAGACGTAGACCTCAACTCCCAGGCCCCCGACCTCGATTTCGG[C/T]
TP33844	TGCAGCAGCTGGTGCAGTTCCCGTCGGCCGCGGCCGTGGGCGGGGGAGGCTACGCCATCGAC[A/C]T
TP33852	TGCAGCAGCTGGTTGTGC[C/T]TCTTGGAGAAGTCGTTGAACCAGACGAGGCAGCCGTACTGGTCGT
TP33854	TGCAGCAGCTGGTTTC[C/T]CCGTTCGGAAAGGTAAAAAAGGCAGACGCTTCAGGCTTTTGGCGATA
TP33857	TGCAGCAGCTGTAGCCA[A/G]CAAGATCCTCAATAGGCAATGGATGTTTAAAAAATCAGCATCATTT
TP33867	TGCAGCAGCTGTGT[A/G]GATGTGTCGCCATGGACGACCAAGAGCTGCTGGTAGTGCGCTGCTGCTG
TP33871	TGCAGCAGCTGTTCGATAATGCACCCATACGCCATCTCGTGCTGCTTCCCGTC[A/G]CGTACCATGC
TP33883	TGCAGCAGCTTACAATTTCTATGGCCATGG[A/C]CATGGTGGTGAGGAGATCCAGACATCGGGGATC
TP33898	TGCAGCAGCTTCAATGCTTCACTCTCTCCACTCTCCAGCAGGTGCGGTGCAGCTC[A/G]CTTTGGTC
TP33899	TGCAGCAGCTTCACCTTGGTGGCCATGGCGTTCGCTACCTGAGGGAGGGGCACATG[C/T]ACATGCA
TP33900	TGCAGCAGCTTCAGGCAGGCACTGTGCTGTGC[G/T]CCTCTCACCCTTCCAACTTCCAAGGCCTTGG
TP33917	TGCAGCAG[C/T]TTCCTGTACGCGTAGAAGCCAGAGGAGTCGGAGGAAATTAGGCTTCTTGAGGACA
TP33918	TGCAGCAG[C/T]TTCCTGTACGCGTAGAAGCCAGAGGAGTCGGAGGACATGAGGCTTCTTGAGGACA
TP33952	TGCAGCAGCTTGCTACTGTCTTGGTCCCCCGTCCCCGTGGCGGTGACCACGCTCTCG[A/G]GCGTCG
TP33960	TGCAGCAGCTTGGCGATCCTC[C/T]GCCCGAACGTCTCGACGACGAGCGCGTCCACCTTGCGCGTGT
TP33999	TGCAGCAGCTTTGGAACAA[C/G]TGTTGCAGGTGTGGTCATTGTTGTAGGTGACGTGGAACATGGGC
TP34018	TGCAGCAGGAAAAGGTCAGATCACCCTAAT[G/T]AAAGAAACTGATCGGTCCTGATCGACTCCTGAC
TP34021	TGCAGCAGGAAACACCATCAACTGGCCTTCA[C/T]TCATCGCAACAGCGACGGCACGACCCGATATG
TP34049	TGCAGCAGGAACGACG[A/G]CTTCTTGTGGTTGAATTCCCTGGCGCTGCCGCCGCGCGAGTCGTCGT
TP34050	TGCAGCAGGAACGCACTCGCTTACGCGTGGG[C/G]CCCCGCCCTCCCACCGCGCGGGCCACGTGGGC
TP34061	TGCAGCAGGAAG[C/G]AGCTCCTGCACGCTGGAGCCGCCCTCCTGGCTGCTGCGTCAACGTAATGCA
TP34072	TGCAGCAGGAAGTTACCTCTGTAGT[C/T]GGTGAACTACCACCTCTAGTTGTATATACACCAGGGAA
TP34104	TGCAGCAGGACCGAGGGTGCCTGGACTGGCT[G/T]GACGAGCAGGGCCCTGCGTCCGTTCTTTACGT
TP34133	TGCAGC[A/T]GGAGAAAGTCGTCGACGAGATCACGCGCGTCGTGCAGATCGGGCTGCTGTGCACACA
TP34137	TGCAGCAGGAGACCATCACAGCCCCGAATCCAC[C/G]GCGCTCCCGCGCCTTCGGCTCCCCGTCGCT
TP34146	TGCAGCAGG[A/T]GAGCCCCGCGAGCTCGTCCAGGTTCCTGCTCAACTCCTCCAGGCTCATGATGCA

Table A2 (cont.)

TP34149	TGCAGCAGGAGAGGAGGCAGTCCTGTACTCCTGCTCCTGCTAGGAAGGAACACACACGAA[A/T]GCC
TP34150	TGCAGCAGGAGAGGGTGCCGCTGTCGG[C/T]GCAGGTAACCATGGACAGGTTCACCACCGACTCCTT
TP34154	TGCAGCAGGAGCAAGAGCAGCACTGCG[A/T]CCGCGGTCGCTTCGCTGGCGTTGACCCCTCATCACC
TP34158	TGCAGCAGGAGCACAGCCGCGGCTGCTTCGTGAAGCGCAACATCATGA[C/T]AGGCTGTCGAGGGCA
TP34161	TGCAGCAGGAG[C/G]AGCAGTAGGAACAAACAATTCTGTGTTGATCATGAAACCCTCAGCCATGTTG
TP34162	TGCAGCAGG[A/T]GCAGCCGCAGCTGGTGCCGCACTTGCAGGTGTTGCAGTCGCAGCCGCCACCCTC
TP34174	TGCAGCAGGAGCCTGTACCATGGG[A/G]CGTGCTGGCGCGGCTGGCAGCATGGGAGGCAGGCAACCT
TP34189	TGCAGCAGGAGCTGGAAAAAGCTCACAATCAGGTATGCTACCATACCAGAACAAGCC[A/G]TCAGGA
TP34196	TGCAGCAGGAGGAACCAACTCCAACTGCTGGGTCA[A/G]GAGAGTGGCGATTCAGCAGGGACAACGT
TP34211	TGCAGCAGGAGGCAAAGTTACTGATGAGAGAGAGGCACATGTAGTACTCGTACTAGGTG[A/T]GCTG
TP34214	TGCAGCAGGAGGCCACCTGCGCC[C/G]TCTGCGATCAGCAAGACGAAACCACAGACCACCTGTTGGC
TP34217	TGCAGCAGGAGGCCGTGCAGCTGGTGGAGGACATCCGCGCCAAGGTGCACGCGG[C/T]GTGCGGGCC
TP34254	TGCAGCAGGAGTGTGGGGGCGATCTAG[A/C]GGTCGGAGCGCACGGGCGCATCATGCATCCAGCTTC
TP34265	TGCAGCAGGATC[A/G]AGAGGCCAGCAGAGACGGTGGACGATGAAGCTGGTGTGGTGCCCCGACACG
TP34270	TGCAGCAGGATCCCTACTAGAACACCTAAATTTGGGTGGCCACCTAGATTCTCCCTCCGACTC[C/T]
TP34275	TGCAGCAGGATGAAGCGGATCTG[C/T]ACCGCCCCAAGCCAAGAAGACGGAAATGTTAGTCGGATCC
TP34282	TGCAGCAGGATGCATCTTGTGTGCTGTGCGCG[T/C]AGGAGGATGAAACCTCGGACCACCTCTTGTG
TP34316	TGCAGCAGGCAACCCT[A/G]TCTCAGTCCTCCCTGTCCCTGGCGCCAGCGTTGACAACATCTGTCGC
TP34322	TGCAGCAGGC[A/T]ACTGTCTTGGTCCCCCGTCCCCGTGGCGGTGACCACGCTCTCGAGCGTCGCCA
TP34323	TGCAGCAGGCAAGAGAA[A/G]CCAGAAAAACAGCACCATTCGTGCTACACCAAGTCGAGTGTTTTTC
TP34324	TGCAGCAGGCAAGATGGCCCTTTGTACATAGGTGACGGTTCCGCGTGCGCGCGGGAGCGT[C/T]GTC
TP34346	TGCAGCAGGCACATTACATTTGAGTTCCCTC[C/T]CCCAATACCAGCAAGTCCATCAACTGCTCCTC
TP34352	TGCAGCAGGCACG[A/C]TAGCTCTAGCCATGGCCGCCTTCCTTCTAGATCCCTGACTCGACGTTGCA
TP34362	TGCAGCAGGCAGAAGGTGCACATCCATCAACCATTCCTAGCTGCTGAG[C/G]TCTCGGTCTCGCCCG
TP34364	TGCAGCAGGC[A/G]GAGAGGATCGGAGAAGACAAGCGGAAGCAACGCGCGCGAGAACGAAACGGCGC
TP34380	TGCAGCAGGCAGCTAGCTCTAGTTAAACTTATCT[A/C]TCTCTCGCAAAAGAAGGCATGCAGCAAGC
TP34382	TGCAGCAGGCAGCTATAGTAGGTAGCAACTGTCTCACCATAA[C/G]TGCATCAGGCAACGCCAATCT
TP34399	TGCAGCAGGCATCATCTCC[C/T]CTGTGAACCGCACATGCCGCAGCTGACGATGATGCATGGGTGTG

Table A2 (cont.)

TP34422	TGCAGCAGGCCACCTTTTTTCATTTAGGGGTTAAACAAGGGGGTTAGGTGAGTGGTGTAA[C/G]CCT
TP34429	TGCAGCAGGCCAGCAGTTCACACTAGAAGATTCAGGAAGGGAGG[C/T]GACCGTCAAATATCTTAAG
TP34430	TGCAGCAGGCCAGCGGTCCATGTGGTGGGCGTTCTCG[C/G]CCGAATTTCAATAGGCTTTGTTCAGA
TP34432	TGCAGCAGGCCAGGCCCCACGGCACTGTCCTGCA[C/T]GCAGACAGCAGAGCTGGTGCTCACTGAGT
TP34451	TGCAGCAGGCCATTTC[C/G]TCGACCGCATCGCCGCCCGCGCGCTCCGCCTCCATGGCCACCTCCGC
TP34458	TGCAGCAGGCCCAGGTGCTCCACGAAGCAGTGCCC[A/C]TGTCTACCTCTCGCTGTGCCAGACCACG
TP34495	TGCAGCAGGCCGACGCCACGCCCGACA[A/G]CCGCGCGCGCCGCCGCGGCTAGCTGCCGAGCTGGCC
TP34505	TGCAGCAGGCCGCCAGGCTCACGGAATAAAGTCTGAGATTCCAAAAGAAAT[G/T]AGACCGTCCGCA
TP34519	TGCAGCAGGCCGTCGACTACTGCGTCAAGGAGCGCCTCGACGAGGG[A/G]TTCGCGGGGCTCATCGC
TP34543	TGCAGC[A/T]GGCCTGGAGTTGTTTGCGGCCGTCAGCACCCCGACAGGGTCATCGCCCTACGCTTGG
TP34554	TGCAGCAGGCGAACAGGAGCCTCGAGGC[C/T]GCGGCCGCGGTCGCCCGAGGGCGCGGCGTCGGCGT
TP34560	TGCAGCAGGCGACGGGACATGGAGGTGAGGAGGAAGATGGAGGTGCTGAGGCGCCTCGTG[C/T]CGA
TP34563	TGCAGCAGGCGAGGAGACTGTACAAGATCGC[G/T]GCGCGGCGCGTGTATGACGTGTGGGCCCGTAT
TP34574	TGCAGCAGG[C/G]GATTGCCGACTGTCCGATCGAGAGCTGACGACGAGAGCCATATGATATGCATGC
TP34575	TGCAGCAGG[C/T]GCACAGGATGCATGGTTCACTGACCAGGTTGACGCCGTCGCGCGCGGCGAGGGC
TP34580	TGCAGCAGGCGCAGGAGGTGGCCTCGGGGGCAGGAAAGCTGTGGAAG[C/G]CATTCGGCGAGATACA
TP34583	TGCAGCAGGCGCCAGGAGG[A/T]GCCGCAGCTTGCACGAGCGGGCGCGGCCGCGCGCGTATTTATGC
TP34584	TGCAGCAGGCGCCATA[A/G]CCATGGAAGGGCGGGGGCGGGGGCGCTCGAAAATTGAAATTCGGCGT
TP34612	TGCAGCAGGCGCTCGACGCCCAGCAGGCGCGCTTGTGCGGCGGCGCCA[C/G]TGGCGCTGGCACCGA
TP34623	TGCAGC[A/G]GGCGCTCTCCACCGCCCCCTCCGACGCCGCCGACCTCGAGGCCGCGCGCGTCGCCAC
TP34632	TGCAGCAGGCGGCAAACCATTCCGC[A/G]GAGAATCCCGCGCCGTTCCCCACGCGTCACCGAGGTGC
TP34636	TGCAGCAGGCGGCCAG[A/C]GACCCCGCGCGGCACCGAGCCCACGCACCGCGGTGGCCTCCTGCGAC
TP34644	TGCAGCAGGCGGCGACCGCGGCGCAGGCGAGGGGCAAGGCCGCCGAGGAAGAGGA[C/T]AACGCGGG
TP34662	TGCAGCAGGCGGGTGCAGCGCGTGAGGATGAAGAGGATCCGCGTGTG[A/C]GCCTGCTTGGGGAGCC
TP34713	TGCAGCAGGCTGCGGCGCTCTTCGGCTCG[A/C]GGGCTCGCTTCCTTGGATCACTCGCTAGCTGCGT
TP34721	TGCAGCAGGCTGGCCACCGCTACCTCGACGTCAGGTAGTATAAACACGGTCACGCCACGCT[A/G]CT
TP34752	TGCAGCAGGGAATCCCTGAATCCA[C/T]GAGCACTTCAGGGGACATCACCGTCGTCTTATCACCCAA
TP34760	TGCAGCAGGGACCTGTGCAGTCCTGTGTGCACGCAGACAAAAAGAG[A/G]GAGGCTTTCACTCTCCC

Table A2 (cont.)

TP34765	TGCAGCAGGGACGGCGCGAGGAC[C/G]GCGACCACCTCGCGGAGCGCGTCAGCGGTGTCGCTGTAGC
TP34771	TGCAGCAGGGAGCAGAGGAACCCACGGAGTTGGTCGTTGTAGCGTTT[C/T]ACGATCTCGAAGTACC
TP34785	TGCAGCAGGGAGGGG[C/G]AATATCGCGCCAACACAAGGCAAAGAGCCGATCGTAGAAAAGGGCCGA
TP34811	TGCAGCAG[G/T]GCACTAGCGCAGAACGAGGATGCTGGCCATCTTCCAGAAGCAGGTGGCGCACGCG
TP34821	TGCAGCAGGGCATCCGAGAGCTGCGCCGATCCTACA[A/C]GTCCGCGACCATCTCCTACGCCGACTA
TP34835	TGCAGCAGGGCCGACGCTAAAACGTCACATTGCTTTG[C/T]TTTTCATTCTGCTGGGGCTGGTACTG
TP34836	TGCAGCAGGGCCGACGCTAAACGTCAC[A/G]TTGCTTTGCTTCTCATTCTGCTGGGGCTGGTAGTAC
TP34838	TGCAGCAGGGCCGTCGCGTCCTCGTC[A/C]TCTTCCAAATCCATCCCATCTTCTCTGCCGCGCCGTA
TP34839	TGCAGCAGGGCCTCGGAGGCGCCAAGCGGCGACGATGGAGATCGAGC[A/G]GCACCCGAGCCGTAGG
TP34854	TGCAGCAGGGCGG[A/G]CACGGGGCGATGCAATTATTAGGAGCGCGGCAGCGGCAGGGGAGGAAGCC
TP34873	TGCAGCAGGGCTTGTAAAGTTCGCTTTGGAGGGGTGAAATGGCG[A/G]ACGGGGTTAAAGGGGGCGC
TP34892	TGCAGC[A/T]GGGGCAGCACGGCCTCGTGACCAAGGCGTGGGTGGACCAGGAGGCCCTGCTGAAGCA
TP34896	TGCAGCAGGGGCAGGCGCGGTGCACGGCGAGCCATGG[A/G]AGCACGCAGCCGAAAAAAAAAAAAAA
TP34899	TGCAGCAGGGGCCGCGATCTCCTATCTTGTGAACAAGGCGCTGGGCC[G/T]CCTTTCGGCGGAGGAG
TP34910	TGCAGCAGGGGG[A/G]CCATCAAGCATCCTAAACCCACCACACAGCCAACAGAGAGGCTGAGAGGGA
TP34919	TGCAGC[A/T]GGGGGCCGAACACCAACCCTGGATTGATAGTCACCACGTCGAGCCCAGTTTGCCGCC
TP34922	TGCAGCAGGGGGCGGACCTGGTCGTTGGCAAGCATGTTGAGCTTGAC[G/T]GCGTCCATGGCGGTGA
TP34932	TGCAGCAGGGGTAAAGGGGACACGAACGGAGCA[G/T]AACGCCATGGACACGATGCGGGGCGCGCTG
TP34939	TGCAGCAGGGGTGTAAAATCATGCGTGTTTGTGGCTAATTTGCAGCGCTTTTTCCCCCTAAC[C/T]G
TP34951	TGCAGCAGGGTCATGTAATTGGATGGAGGTCGC[C/T]GTCTCCATAATTATCGCATGGCGAGTGGAT
TP34960	TGCAGCAGGGTGCAACAAGGCACAGGCAGGCAGGCTCGCTCTGTGCAGGCCCAGAGTTGC[G/T]CTA
TP34964	TGCAGCAGGGTGCTGCGGTTTCGGCGCGGTTCGTGGGTT[A/G]CCGCGGCGTGCTCCGAAAAAAAAA
TP34967	TGCAGCAGGGTGGATCGGATCCGATTCG[A/T]TCGATTCCGTAATAACATCGAAGAAGAGATCGATG
TP34970	TGCAGCAGGGTGTTGA[C/T]GCGGACGAGCATCGCGGCGCGCGTGGCCGCCGCCGAAAAAAAAAAAA
TP34974	TGCAGCAGGGTTACCCACGGCGCCCATCAAGGTCGGTTGTCACGGGCCCCCAAAGATTT[A/T]TTTT
TP34992	TGCAGCAGGTACCCCCTGAT[C/G]GGGAACTCGAAGCTCCACTGCACGCCGTGGATCCCGTGCCGCG
TP34998	TGCAGCA[G/T]GTACGGGGAGGAGGGAAGGCGGAGGCGGCGATGGGGATGGCTCCTGCACTGGCGGC
TP35003	TGCAGCAGGTACGTCGGCGACCGCACCAAGGTCGTCGTCGCCGTCGTCGCGCTC[A/T]GCCGTGCAC

Table A2 (cont.)

TP35007	TGCAGCAGGT[A/G]CTGGAGTCGCTGGAGGCCAGGAAGAAGCGGCGCAGCAGCGGCGGCGGACA
TP35020	TGCAGCAGGTAGCGAAAGAGGCGGCTGGAGCGAGCCGAGCCCTGGGCGTGACAG[A/G]AGCGAGCCG
TP35024	TGCAGCAGGTAGGAGACTGGCACCATCCT[A/C]GGTGTATACTACTAATTTTAAAATGTTAAATAAA
TP35030	TGCAGCAGGTATGATACGGTACGGGCTACCACAGATTTGCATTGC[A/G]TGCAGACGAAAAATCTCA
TP35032	TGCAGCAGGTCAAACGCCTC[A/G]CCCCACAAACCAGCCGACGCGTACCCAGACACCATGGCGTTCC
TP35041	TGCAGCAGGTCAATGTTGAACATTGCA[C/T]ATTCAGGGGTGGCGTCAATGGACTGGAGCAGACACA
TP35057	TGCAGCAGGTCCCCAGGCGGCGACGAGCAGCAGCAAGAGGAGCGTGAG[A/G]CAGAAAGGCGCTTTG
TP35063	TGCAGCAGGTCCGC[A/G]GCCCCCACCTTCTTGCGCAGCGCACATGCAGGTGAGCTTCACGGGATCG
TP35067	TGCAGCAGGTCCGCTCGGCGCTCGCAACGCTGAACCGTGCGTTA[A/C]ATGGGCCCTTCCGTGCACC
TP35070	TGCAGCAGGTCCTCC[C/T]CACCACTAGAGCGAGTCAGCGGCAGGTAACTGCCATGCCAGCGAATCG
TP35080	TGCAGCAGGTCGAGCTCATCGAGGAGGCGGCCCATGA[C/G]GTCCATGTCCTCGGTGGCGCCCTCGA
TP35092	TGCAGCAGGTCGGCGCAGGCTAGCACGAGGTCCCGCGCGGACGGCACCGCCGCCGCGAGGAC[G/T]C
TP35102	TGCAGC[A/T]GGTCTCCGTGCCAATTACTCCCATTTGGGGGTTGGGGGGCGCTAAACACTTGTTTTA
TP35122	TGCAGCAGGTGAGAGATCGATGCACGTGATATTAGTCATTATTAAC[C/T]TCTCCATCGTTAATACT
TP35154	TGCAGCAGGTGCGAGTCCTC[C/G]AGCTGCACCAGCAGGCCCGTGCGCTGGCTGAAGTAGCCCCACA
TP35157	TGCAGCAGGTGCGCGGGCCCCACCTTCTTGCGCAG[C/T]GCGCTGGTGAGCTTGACGGAGTCGACGC
TP35163	TGCAGCAGGTGCTTCTGCGTAGTACATACTGATACACA[C/T]ACGTACAGCAGTGTGCCGTACATAC
TP35172	TGCAGCAGGTGGCCAGCGACCCCGCGCGGCACCGAGCCCACGCACCGCGGTGGCCTCTTG[C/T]GAC
TP35199	TGCAGCAGGTGTCCGAGATGGTCGCCCAAGTC[T/A]GTGGGAGGCACAGGCACACGGTCGTTGCTCT
TP35204	TGCAGCAGGTGTGTTCCTTGTGAAAGCTGGCGACGCCGAAGGCCGAACAG[C/T]GGAAACTTCCTTC
TP35206	TGCAGCAGGTGTTCGTGGACATGTTCCAGGACGACCTGGACGCGGG[A/G]TTCTTCGGCGGGCTTCC
TP35208	TGCAGCAGGTTAAAGTCTCCAGATGCATGGCTGTGCTCGATCGG[A/G]CTCTCGAAAGCAAGCCAAG
TP35213	TGCAGCA[G/T]GTTAGTTGCTTGCGAGAAGAAGGGCGCGCAGCGTGATATGATCACTTGCCGATGCA
TP35216	TGCAGCAGGTTATTTTTAATTTGTCTAGAGCAAAGGACTTTAGTTTCTATATAGTTGGATT[A/G]CG
TP35222	TGCAGCAGGTTCCCAGGCTCCCAG[C/T]CTCGACCAGGGGATCGGTACCACCCAGATGGACAGGTAC
TP35225	TGCAGCAGGTTCGCCTTCGTCAGAGGTCGCCTTCCTGA[C/T]GGCCTGGCTCAACACCACGGCCGCG
TP35231	TGCAGCAGGTTCTGGTTCAGCCGTTTCCACCGTGCCCTCATGGCCTCATGTCAGTGATG[A/T]CCAC
TP35232	TGCAGCAGGTTCTGGTTCAGCCGTTTTCACTGTGCCCCAGGCCCTGTT[C/G]TGCCCTCATGTCAGT

Table A2 (cont.)

TP35235	TGCAGCAGGTTCTTGTACACCCCCGTCTCATCCTA[C/T]ACAATGCACGCACGGTTTCACTTCCACG
TP35240	TGCAGCAGGTTGCCAGCCAAAAACATGCCCTCCTCGTGCGTTCGCTTCCATG[A/G]CCTCTGCAACT
TP35243	TGCAGCAGGTTGCCGAGGTCGTGCAGCTTTGCGCCCAGGCCAAC[A/G]CAGCAGTTGGCGTGCATGG
TP35260	TGCAGCAGGTTTGGGATGCGTGGTGAAGGCTATCGCCGTGCTGATGGTAGCGGT[A/G]GTGATTGGA
TP35261	TGCAGCAGGTTTTGGCCTAGGCCCTCAGAGCATGACTTCAGGAACCAGACCT[C/T]ACTGTCACTGA
TP35262	TGCAGCAGGTTTTTAAATGATTTTAACTGCTGCAAAACATTGTAGCGCGACTGGAAAAG[C/T]GGCA
TP35280	TGCAGCAGTAAGAACTGAACTA[C/G]TGCAAGAACCAAGAAGGCAGGCAGAGGACCAGGACCAGCTT
TP35307	TGCAGCAGTACATGTAACTGCGTAGC[C/T]TGCTCCAGTGCTCCTTACTGGCGCATAGATGTGCTGT
TP35330	TGCAGCAGTACGTAGATGAGACGAGGACGAGCCTTTTTTTTTTTACCCGCTCTGTCAGAACT[A/G]C
TP35347	TGCAGCAGTACTCGGGCGTGCCGAACGCCTCGCACGCACT[A/G]CGGCAGGCCTGCGCCTGCCCGCC
TP35348	TGCAGCAGTACTCGGGCGTGCCGAACGCCTCGCACGCGCTGCGGCAGGCCTGC[A/G]CCTGCTCGCC
TP35355	TGCAGCAGTACTGCGGCGTCCCGAACGCC[C/T]CACACGCGCTACGGCACGCCACGGCCCCGCCGAA
TP35371	TGCAGCAGTAG[C/T]ACCTGTCAGCTGCTGTGACCACCCCACGCCATGTTCCTGAGGGAGGGCAATT
TP35372	TGCAGCAGTAG[C/T]AGCAGTACAAGGAGCACTGACCGCACTGCACAATTGGTAGTAGTGGCGGTGG
TP35385	TGCAGCAGTAGCCGCAGAGCCAGG[C/G]ATCACAGTTTTTAGATTCCGCCACCCCACCTGTCAATGA
TP35386	TGCAGCAGTAGCCGCCACGGCCCCTC[A/G]CCGACGTCGAGAGTACAGACCACGTCCTCCCCTCTTC
TP35426	TGCAGCAGTATATGCTTCTAGGACACTGGCAGAGGCCTTCCTAACCGC[C/T]TTCATTTGTATGGAA
TP35472	TGCAGCAGTCACTCCACTTCAGTACCTCACCCCGTGCCTGCCTGCCTATCACTC[C/T]GTCGCTCGC
TP35482	TGCAGCAGTCA[G/T]TCTCGAAGTTCTCCAACAACGGAAAGACCCCCTGTGGTGAGAGCGGAAGCTC
TP35519	TGCAGCAGTCCTCCTCCCAACTCAGCTCCCCACCCTGTGAAAAAATGCAG[C/G]AAGCAGCAGGAAA
TP35521	TGCAGCAGTCCTGCACCTTTGAGTGTGAGGCGGCGAGGC[C/T]CCGAGAGTCCAGTTTTCTCGAGGT
TP35530	TGCAGCAGTCCTTGGAGCAGTGGGCTGGTGGTCTG[C/T]TGTGTGACCGCGGCGATGAAGCTGGACG
TP35533	TGCAG[C/G]AGTCGAAGGCCGACCCATCGACCCCTCCCTTCCCTCTCAGGCCTGCTCGCGGCTCTCA
TP35539	TGCAGCAGTCGATCGAGGCGATGGTGGTGAGAAGAATGGTGCTGGCGGCGGCGCT[A/G]GTGGTGGC
TP35558	TGCAGCAGTCGGACCAAGATCGGGCTTGGAGTCAGTGAC[A/C]AATCAAAACCACTCCACAAGTCCA
TP35560	TGCAGCAGTCGGAC[C/T]AGGATCGGGCTTGGAGTCAGTTACCAATCCAAACCACTCCACAAGTCCA
TP35570	TGCAGCAGTCGGCGTCGCGCGCCTTCATCACCTCCCGCGC[A/G]GCGTCCGCCGACGTCACCACCAG
TP35577	TGCAGCAGTCGGTGGAGGCCATGGAGC[C/G]CCTCGGGAAGGAGGAGCCGAGCGTCAGCGGCGGGCA

Table A2 (cont.)

TP35580	TGCAGCAGTCGTCGGAGCAGGCCGAGGAGGCGCTCGCCCAGGGCCTG[A/C]ATCAGCTGCACCAGTC
TP35622	TGCAGCAGTGAAAAACTGCTGATGAGCTAGGTTGCCCATGACACTTG[A/G]CTTTTCTCATTTATCG
TP35628	TGCAGCAGTGAAATATGATATTCTATGTTTGTTGAGAAAATTGGATGCTTCATATATATATA[A/T]A
TP35662	TGCAGCAGTGACTGACTTTAGTTAGCCTCGTTTTTTTTAATTAACTCT[C/G]CTTTGCCCGTGCAGG
TP35664	TGCAGCAGTGACTGGCCCTGATTCCTGTTG[C/G]TATTGGGCTGTTCCTGTTCCTCTTCTTCCTAGG
TP35668	TGCAGCAGTGAGCAGTGTGAGCCAGCGGAGGTCTTGTCAGAATCTTCTCTTCGGA[A/C]AATATCCC
TP35699	TGCAGCAGTGCAACAGCGTG[G/T]CGGCCAAGATCAAGGAGCAGCTGGACAAGCGGCAGTTCGCGGA
TP35721	TGCAGCAGTG[C/G]AGCGGCAGGAGAACAATCAGAGGAGGGAGAGCATAGAACAAGCAGGGGATTCC
TP35725	TGCAGCAGTGCAGG[C/T]GTTCTCCTTTCGATCAGTGGCAATGCGCGGCGGTGGCGCGACACGGACC
TP35732	TGCAGCAGTGCAGTC[C/T]CCTTTTGCTGCTGCTATCTGTGCTTGCGGTCGATCAGTGGATGCAATG
TP35733	TGCAGCAGTGCAGTGCACTACGAGCG[C/T]CGCCGCCGCCAACATGCTCACGTGGGAACCCGTATGT
TP35744	TGCAGCAGTGCCAACATCATCTCTTCCATGTACTCCACCACCTGTATTGTCATGATCACCGTC[A/T]
TP35762	TGCAGCAGTGCGCCGCGGGGCGGGACGTCTCCGCGCTCGCCCGCAC[C/T]GCGGCCACCGAGATCCT
TP35783	TGCAGCAGTGCTGCTGTTCAGGTGCGTCAAGATCAAGACTGCATTAGTGTCACCAGCTAAAC[A/T]C
TP35831	TGCAGCAGTGGCGCTCATGTTGACCTCTTGTCACCAGCGCCACGTGC[C/T]TGCTCGTCATCGACCC
TP35844	TGCAGCAGTGGCTGGCACAGCGTGGCCCAGAGCGCCTG[A/G]TACCATGTCCGAGCCAGCGTCACCT
TP35846	TGCAGCAGTGGGAGAAGCAC[C/T]GTCAATTCGGTCAACAGTTTATTTGGGCCACAGTGCAGGGAAT
TP35897	TGCAGCAGTGTAATGCGATGCGTCGTCCGCCGTGAGCGACGACGGCCGCAGCA[C/G]GCTGAAGGCG
TP35899	TGCAGCAGTGTACGTGATTTGTTATC[A/C]TGCTTTGTGCTTTATACCATGATAGTACTAGTATCAT
TP35916	TGCAGCAGTGTCCATAAGGAGGTAGACA[C/T]TTGGAAGCCGAACACGCTGACGTGTAATCGGTGCA
TP35924	TGCAGCAGTGTGCAGGCTGACAGGGGTTGC[A/C]TGCCTTGTTCTTTTATCTCCCTGTGATCACGCG
TP35943	TGCAGCAGTGTTGCAGTTGCTGCACACCACTCCAACCCCCAGCTCCAG[C/T]TCCAGCTCCATGGAC
TP35947	TGCAGCAGTGTTGCAGTTGCTGCACACCGCTCCAACCCCCAGCTCCAGCTCCATGGACGACGG[G/T]
TP35973	TGCAGCAGTTCAATGCCACTAGCGGGATAGGGGGACTGCGCCACT[A/G]GCGGATGTAGACTTGGAT
TP35982	TGCAGCAGTTCAGGTAAATTACCTTGTCTATATTTGAAACTTGCCACGTC[A/G]CCATTTTTCGATC
TP35993	TGCAG[C/T]AGTTCATGGAAATGGAACCCTTGATTGCTGCGGTTCACAAAGCTTAAGCTAACACTAG
TP36000	TGCAGCAGTTCC[C/T]CTAAATCACTAGCTAACCGAAAGCCACAGCCGCTCTTCCAGCGGCCAGGTT
TP36012	TGCAGCAGTT[C/T]GGCATCATCTTCCACTACGCCTTCTCTACCCTCGTCTTCGCGCACAGTAAGCT

Table A2 (cont.)

TP36030	TGCAGCAGTTCTTCGCGCGCAACTTCAACCGTCG[C/G]GCGCGGCGGCTCCCCGCGGTGGTCGACCC
TP36039	TGCAGCAGTTGACACCTCTCCTCATAGTGGTCATCCACCTCAACA[C/T]ATCCCTTGGTCTCCAGCT
TP36065	TGCAGC[A/G]GTTGCCTCGCTGATGCCGTCGTCGTCGTAGCAGCGCACGAGGCTGTCCTCGAGGACG
TP36095	TGCAGCAGTTGGT[A/G]GGTGCCGCTTAGGAGTAGCTAGCTAGGTGCCGTTGCTTTCTGCGCTAGCA
TP36123	TGCAGCAGTTTCCTGGCTT[C/T]CCGTGCACTCAAGAAGCTCGAAATCAGATCGCTACCTACATCGC
TP36131	TGCAGCAGTTTGTCT[A/T]TGATGCCCAGGATGCTGTTGACCAGTACAAATATGAGCTGCTGCGGCG
TP36138	TGCAGCAGTTTTGGCCCTTTAACCATTTCAGAACCTGTGGCATTTGCGTTCCAGCA[A/T]CGCCTTC
TP36193	TGCAGCATAAT[A/C]CATGCGTACGGGACGATGGCACGCACACGCATCAAAATGGCACACGGCTGGC
TP36204	TGCAGCATAATTAACACAGGCCTATTAGCTTACTAG[A/C]CCTTCAAGCGGTGCCTACCCTAGCTAG
TP36216	TGCAGCATACAACACTACAAGATATACA[C/T]ACGTTACAACCCCCAACCCCACCAAGTAACGCCTC
TP36242	TGCAGCATACATCAACCAAATCAAGAACACAACCATGGTATATAG[C/T]TGCAAATGGCGTGGCCAG
TP36254	TGCAGCATACATTCACCTGACAGCTGACACTTGCAATTCTAAAAATTCT[C/T]GAGTCCAGTGGACA
TP36257	TGCAGCATACATTGGTTTT[C/T]GAAATTGGCTAGCCAAATAGAAGGATTAGGAGTTCCCCTGTGAA
TP36261	TGCAGCATACCA[C/T]TTTACTCATTGACATAGCCCATTCAGTTTTTTGGGTCTGTAATTTCGACAA
TP36262	TGCAGCATA[C/T]CAGGGATCACCTCCAGCAGGTACGTGAGCAATCCACCTAGCAGGAAGAGAAACA
TP36340	TGCAGCATAGACGCA[C/T]ACTAGCCATTGCCACAAGTTGGACTTCCGTGTGGCTTCCACGACTTTT
TP36353	TGCAGCATAGATCACTGTTTTAACTCTTTAACTGATACAAGGTGTCCCCTCAAG[C/G]TAATTATCA
TP36362	TGCAGCATAGCAATGGCCACCAGCCCATTTAGGCATTCAC[A/G]TAGTAGGCAGGAAGAGGGACGGA
TP36363	TGCAGCATAGCACAGACGACGATCGACGACATGGCGGCGGCAACCTTCTTCGCGCGTG[G/T]CGGCG
TP36391	TGCAGCATA[G/T]CTTTGAACGTATGCATGGATCGATCGATGGATCGCGTGTCGTGTCTCACCAGCA
TP36393	TGCAGCATAG[C/T]TTTGAACGTTCTATATATGCATGGATGGATCGATCGATCGCGTGTCGTGTCAC
TP36421	TGCAGCATAGTGTATTGC[A/G]AATGCATCATCCAAGGTCACCGTCGACTCCTTCAACAGCAGGCCA
TP36427	TGCAGCATAGTTGCGGCGGCGGAACGTACAGGGAAGTCGGCTAGGTCGTAGTCA[C/T]GGAGCTGCG
TP36473	TGCAGCATATCCT[C/G]TTGCCTTCGGCCCGCTTTCGCTCCTCACTCCTCTTGCCTGTCCTTCCAAA
TP36475	TGCAGCATATCGGATTCCCGCGGCG[A/T]TGGACTAACTGGATTTCTATCCTACTGTCCACTGCAAG
TP36482	TGCAGCATATCTGAATGTGTTCAACTCCATCTACTCTGTGCTGTCAGACCTCAAGAA[A/G]GACGGC
TP36551	TGCAGCATCAACATACA[A/C]CTAACGAGATCAGATAGTGGGTGGGCATGCGGTATGCAGACACAAT
TP36565	TGCAGCATCAAGGCAGCACGCTTGTAGAACTTGTCTTATGGAGAGAGTCTCATTTC[C/G]GAAGATG

Table A2 (cont.)

TP36567	TGCAGCATCAAGGCCAGGCTTTCTTTGGCCCTCCACCCATCC[G/T]CCATCCCATGGCGAATGGGTT
TP36574	TGCAGCAT[C/G]AATATCAAACGCAGTACAGCTAAAGTCTGCCCCAAGTTGCCAACAACACGCACAA
TP36616	TGCAGCATCACCCGATTTGTTTGCACCACTGCTTGCCCCTCGATTTG[G/T]CCGAGCTAGCGCTAGG
TP36631	TGCAGCATCACGAAGAGGGGCGCTAGGGTCGTGCTCATGGGGAGGCACACGCACGCTTA[C/T]AGGG
TP36633	TGCAGCATCACGACACC[A/G]AAGCTGTAGACGTCGCCCTTGGGCGTCCACGCCGCGGCGCCGCCGC
TP36634	TGCAGCATCACG[A/G]CGCCGAAGCTGTAGACGTCGCCCTTGGGCGTCCACGCCGCGCCGCCGCCGC
TP36639	TGCAGCATCACGCCGATGCGTGCCGCTTC[A/C]GCTGAATTTAAAACCCCTCCTGCTCCATCCAATC
TP36666	TGCAG[C/T]ATCAGACTATCAGCATGGGTGCGATCGAGACTGATTCTGTCTGTCTGATGTGCCGCTG
TP36674	TGCAGCATCAGCAAGATCAATGACCT[A/G]GTGGATCTGAGGGGTTTAATTATCTTGAAGGAGGGTG
TP36705	TGCAGCATCAGGTGCCGTCGATG[C/G]TGGCGGCGCCCAGCAAGTGCCGTCCGTCGGCGGCAGCGCT
TP36709	TGCAGCATCAGTAGTTGCAGTATCCGCTGTTGTGTTT[G/T]AGGACAGCGGCTGCCAGCCTGAAGAA
TP36710	TGCAGCATCAGT[A/G]TCGGTCGGCCAGTGGTTGAGCGCGTGATCCGAGGCACTTGCGCAAATCGCT
TP36711	TGCAGCATCAGTATTTTCGCCGTGTCGAAGGCTCAAACGCAAG[A/G]GCAAAACCGATAACAATTTG
TP36743	TGCAGCATCATCTGATGCACCTTTCCGCCGTGAAGCGATGGGC[C/G]CGAGCTCGTCCAGTAGTTTC
TP36746	TGCAGCATCATCTGCTGCTGCTGTTGCTGCTGCTGCATCAGGGCCATGTACTGCTGCTGCTG[C/T]T
TP36762	TGCAGCATCATGTCGGA[C/G]AGCTGCTGCGCGTCGACGGCCATGTAGTTGACGATCATGCCGAGGC
TP36780	TGCAGCATCCACACGACGCAGGCGGCAGAGAGACGTCGGCTCTGACACGAGCCGTCGC[C/T]GCGGC
TP36792	TGCAGCATCCACTCCCCACCCACGGGACAGAGAAGCATAAACCGAGGAGCCT[C/G]GCATCCATCCC
TP36794	TGCAGCATCCAGAGCGGCACATAGACATCTAGACGGCCACACACCCCACTGTCCACAG[C/T]GGAAG
TP36796	TGCAGCATCCAGCATCAAATTGTCAATGCCATTGC[C/T]GCCATTGCCACCCAGATGCAGCAAGGAA
TP36801	TGCAGCATCCAGGAGAA[G/T]CAACGAACTCTCCATCTCTGTCGTCAGGTTCGTTGGTGATGACACA
TP36844	TGCAGCATC[C/T]CCTTTGATGACCGTGGGAGTGAGGAACACCATCCTGGGGTTCTCCATGCCTCCA
TP36850	TGCAGCATCCCGTCGCCGCCCCTTCTTCTTGCCGACGATCTCCTTCCGCAACTCCG[C/T]TGAGCAG
TP36859	TGCAGCATC[C/T]GAGGGCCGAGGTGGGCGCGATAGTGTGCTCCGAGGGCGGCGCGACTGTGAGGAG
TP36880	TGCAGCATCCGCACGACGCAGGCGGCGGAGAGACGTCGGCTCTGAC[A/G]CGAGCCGTCGCCGCGGC
TP36888	TGCAGCATCC[G/T]CGCGTAGCACCCGTCGGGATGGTGCTTGAGCAGGTGCGAGTGTGACCCTTGCT
TP36901	TGCAGCATCCTAACACCGACCCTACTACATGCACCCCTGTAATTAAATTGAGGTGTCATTTG[A/G]T
TP36907	TGCAGCAT[C/G]CTCAAGCAAATTGCCAGAGAGGAATGGACAATGGAGTGCTGTCCACCGCTCACAG

Table A2 (cont.)

TP36911	TGCAGCATCCTCCGTCCTCCCTCGTCGTCTCCGAGGACCAACCCCCATGTGATGT[C/G]AGCGAGGC
TP36933	TGCAGCATCCTGGCGAGCGGGACGTTGAGCACG[A/C]CGCAGACTGCGACGGGGACCAGGCCCGAAA
TP36934	TGCAGCATCCTGGCGCTCACCTTCTCCTGCTTCTTCATCATTCCCAGCACCTCTCCA[C/T]GCACAT
TP36935	TGCAGCATCCTGTCGATAGCGTCCTGCACCAGCCTCTCCGACACGGTGTC[C/G]AGCGCGCTCGTCG
TP36939	TGCAGCATCCTTCCATGATCCTTTGCATGCATGCAGGTAAAT[C/G]CTGCGCGCGATGCAATTTGAG
TP36984	TGCAGCATCGACGGC[A/G]CGAAGATGAGCGCGGCAGCGGCGGCGAGCGAGACGGCCACCCACGGCG
TP37009	TGCAGCATCGATCCTGGCTGGCTGTGCGGCCTCACACAGGCTTGAACGACG[A/G]CGACGGACCAAC
TP37015	TGCAGCAT[C/G]GCAAATTCATATATGGATGTTGGAGAAGAACACAATAACTAGAGAGACGTGACGG
TP37029	TGCAGCATCGCATTGCTCCACGGGAACGCGTT[G/C]CCGCCGCCGTCAGCACGGAGCCTGCCGCCAT
TP37033	TGCAGC[A/G]TCGCCAGCTGCGGCGGCCAGTGGCCTCGCCGCGGTGCTCCTTTACAACGGCGACCTC
TP37036	TGCAGCATCGCCCCATAACCT[C/T]GGGTCGCGGCCGATTGCCCAGGCGTTGACAAACACGGTGGTG
TP37044	TGCAGCATCGCCGT[A/C]GCGGTTTCCACTTGCGGTTCATCTTCTCTGGTGCGGTTACTGTTACTGC
TP37058	TGCAGCATCGCGCTGGACGTGGCGGAGGAGCTCCGTGTGCCCGC[C/T]TACTTCTTCTTCACCTCGG
TP37070	TGCAGCAT[C/T]GCTGGATCTATCAGTACCATCCATCACCTTGCTGGAACGCTCGCCGTGGTGGCTG
TP37079	TGCAGCATCGGATCCAAC[C/T]AGTGAAGCTGCCAAGGCAATTCCTGATACGAATGTCTCTGGACTT
TP37083	TGCAGCATCGGCACCACATCCATCGCATCGCCACCATTTCCTTCC[A/T]GCCGTCTTGCTTTGCATG
TP37099	TGCAGCATCGGCGTCGTGGTTTCCACTTGCGGTTCATCTTCTCTGGTGCG[A/G]TTACTGTTACTGG
TP37115	TGCAGCATCGGTTCAGCAGGCACCGTGGAAGATTCTTCCTATCCTA[A/G]AAACGAACTGTGGATGG
TP37123	TGCAGCATCGTATGGTAT[C/G]CGTTCTTGTCTGGCTGAACCATCCTCGGCGGACCCTGGGCCATCT
TP37127	TGCAGCATCGTCATGCTGCTCGCCTACGTCGCCTACCTCTT[C/T]TTCCAGCTCAAGACGCACGCCC
TP37172	TGCAGC[A/G]TCTACAGGGAATATCCGTTCGTGCAGCCGTGCGCAGTGCTGTTCACGTGTGAAGACT
TP37173	TGCAGCATCTACCAACAATGCAGCTTTGGATGAGGAGGAGCATAGGCAAAGTTCATC[A/G]TCAGAG
TP37174	TGCAGCATCTACCATGAATGAGAGCTTAGCCAGTCT[C/T]CTCCTCCTCACGTTGATTCATCTGCTT
TP37211	TGCAGCATCTCAAGAAATGTCTCTTCAGCAAGCTTGATCTTCCCAACCCT[A/G]CCATACAGCCGCA
TP37246	TGCAGCATCTCACTCTGCAAAAAG[C/T]CAAGCAAGACCAGCAAATGAGGAAGAAAATTAACCAACC
TP37250	TGCAGCATCTCAGATCTCCCCTC[C/G]TGATCATTCAGGTTGAAACGTTCATCAGTTCAATAGCCAC
TP37299	TGCAGCATCTCTCCCAAAAGGTCCAGCAACGG[G/C]CGCACAGCTGCCCGCGACGAGACGACGCGGA
TP37306	TGCAGCATCTCTGCTCTCAGTTGCGGCCGCCGCAACTTCGTTTC[A/G]GTTTGGGGGAGGGGACCTG

Table A2 (cont.)

TP37358	TGCAGCATCTGGAGCAGCTCGGTGGAGAGCACAGACCTCAACCCA[C/T]CCAGCAGCTTCAGCTTCT
TP37382	TGCAGCATCTGTGGTAGATGAAGCCTCTGC[C/T]AGAACATAGTCGCAATGGGGCAGCCGTTGATGA
TP37387	TGCAGCATCTGTTCCAGCTGCACGGCAAGCAGGTGGC[A/C]GACGAGGACACCGCCGCCGTCGTCCC
TP37423	TGCAGCATCTTCACGCCTGTTGGGGTTTAGT[C/T]CCACATCGTGTAGCGATGGTGGGGGAGCACAA
TP37436	TGCAGCATCTTCTTC[A/G]GAGAAAAATATCTATAATCTGATGGACAGGAGTTTGTACGCATGCGAA
TP37444	TGCAGCATCTTGCCTCTACCTTCGTGCCTCATGCTCGTCGCT[C/T]GACATCAACGCCAGGTACACG
TP37449	TGCAGCATCTTGCTGACA[A/T]TGCTGGCGCCGAAGACCTTGTGGACGATGGCGAACTTGTGAGGGT
TP37452	TGCAGC[A/G]TCTTGTACACGCAGGCTACCTTGCTGTTTGTGCCTCCCTGCCCATCACGCATGGCGA
TP37464	TGCAGCATCTTTGC[A/C]AACCAGCTGCTGTTTTTGCTTGGCCTCAGCTACACCAACCCCACCTACG
TP37493	TGCAGCATGAAGG[A/G]CAGGAAGCAGAAGGTAACAAGCACACACGTTACCTTCATCAGCTTCGTCA
TP37508	TGCAGCATGACACGAG[G/T]CTTGCACTCGAACCATGCGTCCACCTGGCCCAACAACTCGTCAGCAG
TP37515	TGCAGCATGACCAACCTTTGGCATGACAACCTTCGGCTCTAACCAAACA[C/T]GCCTTTGTGTCTTG
TP37541	TGCAGCATGAGATAATCGGAGCATCTCTACCTGCGTTATAAATGGGCAAAAAAG[A/C]CATTAGTGA
TP37555	TGCAGCATGAGCTTGAGATGATTGCTAGAACTATTGATGACCAGATCTCCAGG[A/G]GAGAGCATCT
TP37563	TGCAGCATGAGGCGCGGCACTAGTCTA[G/T]GCCAGCATCCACGACTGCTACAAGGTCTGACGGTCA
TP37564	TGCAGCATGAGGCTGAGGCTGATGACTTGATGAGGC[G/T]CCCTTTTGATCCTCCTAGGAATCTCCC
TP37565	TGCAGCATGAGGG[A/G]CGTGATTGAGAGGAGACAGGAGACAACTCAGAGGGGCGCGATTGAGAGGA
TP37571	TGCAGCATGATATCCTCCTTTGGGGCGAAGTACTCAGTCTGCATCTCCGTCACCT[A/G]CATGCATG
TP37576	TGCAGCATG[A/G]TCATTGTGTTATACATTTCCATGTCTGGCACGAGTCCTCCACGCCCAACAAACT
TP37584	TGCAGCATGATCTCCTG[C/T]GCCTCCACCGTGCGGACCCCGCACCCTGTCCCTGGCCCGTGGACCT
TP37595	TGCAGCATGATGCCGACACTGCCGCCGACGTCGCCACTGCTC[A/G]GCGCCGTCCGCCTCCTGGCGG
TP37607	TGCAGCATGATTTGGGGATCATGCGTTTAAAAGGGCGCTCTGCCACCGATTAACAGTGG[C/T]GGCC
TP37611	TGCAGCATGATTTTCGCGGTGCTCGTGTC[C/T]TTGAACGTGATGGCCCGCTGCGCCGCACCGATGG
TP37622	TGCAGCATGCAAGAGAAATCAACAGCGCAAAATT[C/G]AAATCAGCACGACAGCTTCTTCAGATCAG
TP37626	TGCAGCATGCAAGCCGAGCCTGGGAG[A/G]AACGAAGGTGAGTTTTGATTCTTGGGATGCGGCTTTT
TP37631	TGCAGCATGCAAGTACGTACCACTCGAATGCCATGGACGGGAAGGCCACTGACCAGCCG[C/T]CGCG
TP37641	TGCAGCATGCAC[C/G]GCCACGGGCTCGCATCGCATGGCGTACTCGTCCAGCCTGCCTGCCTCCACC
TP37660	TGCAGCATGCAGATTTGCAAATGATCAGGACGGGGCGAGGGAGGCTAGA[C/T]AGGCAGATAGCTAC

Table A2 (cont.)

TP37662	TGCAGCATGCAGCATGCTCTACCGATCACATAC[A/G]GAGTACATGATCCATGATGCGTTCATCACT
TP37676	TGCAGCATGCAGTCGATGCAC[G/T]TGCCTGACGGGCGGTGGTCTTATCGTCGGAGATCTCCTCCCC
TP37677	TGCAGCATGCAGTGCAGTGGGCA[G/T]CTAAGCTAGCTTAGCAGTGGGTGCTTATCTCACCTCTCAA
TP37681	TGCAGCATGCATACGTACGCAGAGAC[A/G]ACGCGCGCCTACATCTGCGCATATTATGGCTGTGGTC
TP37699	TGCAGCATGCATGATTAGTGCATGCATGCAAGCCGTAATCACTCCTCCTCTCATCGC[A/G]CCGATC
TP37724	TGCAGCATGCCACCCATCGAGGTAACTGG[C/G]GCTTATTGGCTAGGTTGAGATGTAGCGCCATTGA
TP37729	TGCAGCATGCCAGTTTTCAGATGTTTGATTAGAGACGTGGCAACATGTATG[C/T]ATCATTCAGAAG
TP37737	TGCAGCATGCCATTTTTTGGTTCTCCAAGAGGCATGTGGTATCAACCTCTTCCTC[A/G]AATTCCTC
TP37739	TGCAGCATGCCCAGCTGCTGCCGCGGCAGCGCGGCGGCCAGCAC[A/G]TGGCTGGACACGAACGTCA
TP37753	TGCAGCATGCCGATCCGAGC[C/T]AACCTTCCCCGTATCGCCATCGTTGTCGTCATCCCTCGCCGAT
TP37782	TGCAGCATGCGCGCGCGCTCCTCGCACATGATGACGAGCCC[C/T]TCCTCCATTTTTTGCAGCGCCG
TP37801	TGCAGCATG[C/G]GGAGTTTTAGCCGTTAACTGCACCTTCGAAGAAGCGGCTGCTGAAATTTCAATC
TP37806	TGCAGC[A/G]TGCGGGAAAAGCCAAGAGTGCACCCAAATGTCGAGCGCGGCGACGCCAGTGGAGCTC
TP37811	TGCAGCATGCGGTCGGTGAAGGATGAATTAGCTCTCAACACAAATGAGT[C/G]TTCGTACATACAGT
TP37835	TGCAGCATGCTCCTACGCCGTGTGCCAGCTCG[T/C]GGCCAGCGCGCCCTCGCCACGCCGCCGTTGC
TP37849	TGCAGCATG[C/G]TGCTCGGCTGCCGCAGCCGCCGCCGCCCAGAAACCCCGTACACGAGCCCATCAC
TP37853	TGCAGCATGCTGTCGAGGGAGCCGAAGCCA[C/T]CCGCGAACTCGTCCTCCTCCACCGACCCGCCTC
TP37855	TGCAGCATGCTGTGTAGTCTCCGTCGTC[G/T]TCCGAGGTCCGTCCGTCCCCATAAACTTTCCAGAA
TP37887	TGCAGCATGGACGGAGACACTAGAATACTAGTAGTGCTGATGGTATAGTAC[G/T]GCTGCCACTTTA
TP37892	TGCAG[C/T]ATGGAGAAGGTAGGAAAAGGAAATTAAAAAAGAAAAGAAAGGGGAAAGACTAAGAAAG
TP37895	TGCAGCATGGAGACGCAGAAAGACACCAGCATTCCCCTGCA[C/T]TCTTGCAGATTTTTGGCACCCT
TP37912	TGCAGCATGG[A/G]GGCGACCACGTCGGGCAGCTGGCGGCGCAGGAACCGCGGCTCTGCACCGAAAA
TP37924	TGCAG[C/G]ATGGATGAGGAGTACGACGTGATCGTGTTGGGGACGGGGCTCAAGGAGTGCATCATCA
TP37947	TGCAGCATGGCAGTGCTTAA[C/T]TAGGGGGAGTACCTCACAGCGGCACTGAACCCGTACGTGATCA
TP37950	TGCAGCATGGCATGACTGGCGG[C/G]CGAGACCCAAAGTTGCGCTCCCTAATGATGCTGAGCAGATA
TP37957	TGCAGCATGGCCGATTTCATCAATCTGGACAGTAAGT[A/C]AAATAAAAATCATATAAATAGAAAAA
TP37958	TGCAGCATGGCCGTGCTCTGGAACACGATGTCCACCACGTCGCCGTGCCTGAACCGCCGCACC[A/G]
TP37963	TGCAGCATGGCCTGGCCTGCCTT[A/G]GAACGGAACACGCGCGAAGCGTCCACCCTGACGATTCGGT

Table A2 (cont.)

TP37996	TGCAGCATGGGCATCCTTCGGGGGGGCACTCGCCCAGTGCAGTCGCCGCCGCGTGTGGCA[A/G]AGC
TP37997	TGCAGCATGGGCCAGCTTAACGCCCAGCAG[A/T]CGCATGCTCCACTGCGCTGTCCATTCCAATTGT
TP37998	TGCAGCATGGGCCCGCCCGAGAGGATGGACATGGGCTTGCCGAG[A/G]AACTTGGTGGCGAGGGCAT
TP38012	TGCAGC[A/G]TGGGGCCGACGGGCCGTAACGCGAAGTTGACGTCGCCGTGCGTCTTCAAGATCTCGC
TP38016	TGCAGC[A/G]TGGGGCGGATGCAGTCCCCGATCGACCTCTCCCACGAGCGTGCCAAGCTGGTGCAAT
TP38021	TGCAGCATGGG[G/T]TTGCTGTCGTAGAACGCATACGCCTCGTACCTGAAATAACACCGTATGACAT
TP38035	TGCAGCATGGTCAGCACTGAATCGCTGAATGCAGAGAA[C/G]CATGACCGATGTCCTTGGAACATAA
TP38046	TGCAGCATGGTGAGGCGCTCCGCCGCGCCGTCGAGC[C/G]CCCACAGGTGCGCGTTCTTGGGGTCAT
TP38051	TGCAGCATGGTGATCCCCGTCGGCCGCCCCGTGTAGCGCCGCGCCAGGGG[C/G]ACGAAGAGCCGAA
TP38062	TGCAGCATGGTTAGGCAACAAGACTG[C/T]TATCCCTAAGCAGGTATTGTTATCGCAGGATAACTGC
TP38077	TGCAGCATGGTTTGATTAAAAGGGTTGTCGACGGAGAATCCACTGATATTTGGGGCGATCG[G/T]TG
TP38085	TGCAGCATGTAAAGCATTTTGCCCATT[C/T]GGTCCAGCATACGAAAGGCTGCCATGACTCATGTCA
TP38089	TGCAGCATGTA[A/G]CCGTCGATGAGCTGCACGTTGCGGCCGAGCGCGAAGGAGCCCGTCGCCCTCT
TP38093	TGCAGCATGTACAACAGCTGGTACGAGAGCCTCCTGTCGCACGTCGCGTCCCACGGGTTC[A/G]TCG
TP38119	TGCAGCATGTATGCACGCAGTGGATTGATCGAAAACAATCGGTGCA[G/T]GTGTTTCTCTTCGACTA
TP38127	TGCAGCATGTCAAGCGGCC[A/T]CCCATTTGCATTATCGACTATAGACGGATCAAATGCAAAAGGCT
TP38151	TGCAGCATGTCGAGAATCGCCAGTTCATGGTCCGTGCGGTGGCCAGCTCAA[A/G]ACCATTGCCGAG
TP38153	TGCAGCATGTCGCGGTGTCCCTGTTCGTACAAGGGGTCGTCTGCTTGGGC[A/G]GATCTATCCCTTA
TP38156	TGCAGCATGTCGGTGTGGTGGCCCCGCGAGCTGATGGCTTGGACGTACCAGCTCGGC[A/G]GTCTGC
TP38157	TGCAGCATGTCGTATGTATTGTTGGCTTCCATTCCATGGGACGTACTGGACGTGGATG[A/G]GGCTG
TP38160	TGCAGCATGTCGTCGTCGGCTTGGCTGTCGTCGTCGGTGCGGCTCTTGCGGG[A/G]CCTGACGATCT
TP38166	TGCAGCATGTCTGAGAGGGCGATCACGAGGTCGCCAGACTG[A/G]ATCATGCCCCTGGCCTTGAGCA
TP38171	TGCAGCATGTCTTCCTCAGACTG[C/T]CCAGAGGCCTTGCGGGACTTGATGATGGTGGCAAAGATTT
TP38177	TGCAGCATGTGCAACTGACATCTCTGCTAATAAGGTGACTGGATGCCTG[A/C]AAAGTTGCACCATA
TP38195	TGCAGCATGTG[G/T]CCCCTGGCACGGACGAGCTCGGCGAGGTCGTCGTCCGTGACGACCATGCGTC
TP38204	TGCAGCATGTGTCCTTACCTTCTTCT[C/T]CTCGCGCGCGGTAACGTACGATTCCATGTGCTATATG
TP38222	TGCAGCATGTTCAATCCCTAACAATTTCCCCGAAGGACTGCCGTGCTTGCATCGTGGA[A/G]AAACG
TP38231	TGCAGCATGTTCGGCAGGCCGTAAACTATCGTGGATTATAAGCTG[G/T]AACAATATTTTTCTCTCA

Table A2 (cont.)

TP38270	TGCAGCATTAACTCATA[A/G]AGTCTTAGTATTCTTGCGGCCGATACATATCAGCGTTAACTCATAC
TP38296	TGCAGCATT[A/G]CCGTCCTTCAGTCGCTTCACAGCCACAAGAGTTCCATCAGGGAGCTGCCCTCTG
TP38300	TGCAGCATTACGACGAACATCTCAGGCCGTCGGAAATCAGGTTCGACC[A/G]TATGGACATCTGGGT
TP38301	TGCAGC[A/G]TTACGCCATTACCAAAGCCCCCAAAAGAACAAGAGAAATTTGATTACTCGCACCTAA
TP38314	TGCAGCATTAGCATGTGGTGTGGAAGGTGCTCACATGAAGGGGAA[A/G]GGTATATAATCGACGGAC
TP38325	TGCAGCATTAT[A/T]AGTCCGCAAGGAGGATGGTGTACCTTACTACCTTGTACGCTGCAAGGCCCGC
TP38334	TGCAGCATTATCTCCATCTCCATCTGCTCCTTGGTCTTGAATACGAACAA[C/T]ACAGAAAAAGAAG
TP38343	TGCAGCATTATTGACTAGGCGAAGACTATAAATTTCACGAAAATGTTCGT[C/T]CATGGTAACATTC
TP38344	TGCAGCATTATTGACTCTCTAAATCCTACTGACAAAGCCTCAAGGCGAAGAC[A/T]ATAAATTTCAC
TP38360	TGCAGCATTCAGCCAAGCAGATCCAGCCAACCA[C/G]CAGCAGCAGCAGCAGCATGAGGTGTGTAGC
TP38365	TGCAGCATTCAGTAGCAAGCC[C/T]GAATCAGTAACAAGCCACTGACCTTGGCTCTGAACTTGTCAT
TP38379	TGCAGCATTCCAGAGCAAG[C/T]GATCGATGTCTTCTAGTAGGTCGATCGTGTCGCAAGTCCTAACT
TP38386	TGCAGCATTCCCCCAATG[C/T]CGATCGCAGGTCATCTCGCCGTCGATCATCGACGTCAGTCCCCCA
TP38392	TGCAGCATTCCTATCA[A/C]ACCAAGCAGCAGAAGTAGAGAACTGAAGCAGCAACCTGGGCATCGGT
TP38397	TGCAGCATTCCTTGT[G/T]TCCTACGGTCGCCACAGAACACCAAGAAGGATGGAGGGCCAGAGTTTG
TP38403	TGCAGC[A/G]TTCGATTCGAGACGGGATGCTTACTGGATTGCTTGATGAGTCCTCGACACCTCGTTC
TP38410	TGCAGCATTCGTCCATTCGGCGAAGCT[A/G]TGATCCGATCGCGTAGGGCTCCATCGATCCGCTGCA
TP38414	TGCAGCATTCTACATTTCCGTGAAATATACCCATGCAGAAGTAGGT[A/T]ACATTCGACATCAGACC
TP38418	TGCAGCATTCTCCCCGCCACAAGCTTACTAGCGTGTGGGACCAAGGAAAAAGGAAATAACAAA[A/G]
TP38422	TGCAGCATTCTCGGC[C/G]AGCTGCTCGATCCCGATGCTATGGCGATGGCGATGGGTCGGTCAGGAC
TP38436	TGCAGCATTCTTGTCAAGTACTGAAG[C/T]GAAATGCCTTGTATTGTACATCAAGGGCCTATGCTTG
TP38488	TGCAGCATTGCCCTGATCAAAT[C/G]ATCAGTTACAGCAACTGAATTCTCTGATCCCTGGCTGATAA
TP38503	TGCAGCATTGCTGACCAAAACTGAAAGGCTATGCGCGTACGGCGTACCTCTATGGTGC[A/T]CTCGT
TP38510	TGCAGCATTGGAAGGCGGAGGCATGGAAT[C/T]CAGCTGGGAGAAGAAATCAAAACCCATGGCATTG
TP38519	TGCAGCATTGGATGGATGAAGCCATGAAGGGCC[A/T]CGATCGGCAGGCAGGCACCTGAACGACGTC
TP38540	TGCAGCATTGTAAAGTTTGGTG[G/T]GCGGCCCAAGACCTCCGCTGCACGACAGCACGAGTGGGGCG
TP38543	TGCAGCATTGTACGTATTGCTGCTTGCTGTTCAGCTATATATTT[C/T]CAGTGACACTACTTATTGC
TP38555	TGCAGCATTGTCGACATTTGCAGTGCGCAAA[A/G]GACACAACGTGTCGTGGACACTCATCGTTCTC

Table A2 (cont.)

TP38577	TGCAGCATTGTTTGGAGACAACTACACCAATGAAGCACT[C/T]AATCTTGGAACCAACAAAGTGGAG
TP38608	TGCAGCATTTCAGGGCCA[C/T]AACAAATGCAGCGTCAGAGTACACGCATCTGAGTGCCACCGCCTG
TP38626	TGCAGCATTTGAACAACATATC[A/C]ACAGATCCAATCTGTTCAGGCCACTGAATCATCACTGACTA
TP38645	TGCAGCATTTGGAGCTGCTGGAACTGATCGTCAAG[C/G]AAACCCTAGCACCAAAACAGAGCGCAAT
TP38657	TGCAGCATTTGTTGAGAATTATTATAATTTA[A/T]AGTTGTAAATTTCGTTTGACTAAATCCTGAAT
TP38714	TGCAGCCA[A/G]AAAGCATGGGATCAGAGGTACGGTAACTACCAGCAGAAGTTCAAGCAGCACGGAT
TP38738	TGCAGCCAAAATCCCAAAACATTCAAAATCGCACACTACACAC[A/G]AGGGAGCTAACCAAACCCTA
TP38740	TGCAGCCAAAATCGGAAAAGCACCGCAAGCAACAGCAGGGA[A/G]GCATTGCACTAGAGACGGGGAT
TP38766	TGCAGCCAAACCACACGGTTCACGCAGCAGGCTG[C/T]GCCTGCGCAGAGGCGGGCGAGCGGGACCT
TP38830	TGCAG[C/T]CAAATACCTCGCCGCAGCACGGCGCCCGTATCTTGCATTTCCTCCTGTAGTGCGCGCA
TP38832	TGCAGCCAAATAGAAACAGGACCAGACGGATCTGAGGTG[A/C]AGTTAAACTCGACCAAAGAAATTT
TP38836	TGCAGCCAAATCAACTAGTACCTGTGAAAACTGAAA[A/G]CCCAGGCACACCAAGGCCACGCGAACG
TP38847	TGCAGCCAAATCCTGTCCACTCCATCAGCTCTGCAATCC[G/T]ACAAGAGATTTGCCAATTATTAAT
TP38848	TGCAGCCAAATCT[G/T]GGGCAGTCCCAGCGAGAGATGACTGAATCGATCAGCGCGCCGCGCGCGGA
TP38853	TGCAGCCAAATGATGCGTCCACGTTGCAGCCATCACTACACCAGTGCTGGTACGACCATGGT[C/G]C
TP38856	TGCAGCC[A/G]AATGTGGTAGGCTGGTAATACATCAGCATCAATCTAGCATGGCATGTGTTCGTGAC
TP38863	TGCAGCCAAATTTGAC[A/C]GAGAGCGAGAGAGAGAGCCGCTGCTGCCCTGTATGTCGAGCAATCCA
TP38871	TGCAGCCA[A/T]CAACGCGCGCGGCAGCGCCCGCGCCAGCCCATCCCAGCTGCACCCGCCCCTGCCC
TP38875	TGCAGCCAACAATCAGAA[C/G]AAAAATAATGTTCTACAAGCTATATACGTTCGAGAGGACAAGAAC
TP38935	TGCAGCCA[A/G]CCCCCTGAGACCGAGACGCGCGCCGTCCATGTCGATCCATCGGCAATAATAATGG
TP38949	TGCAGCCAACCTTCAAATACCA[C/T]ATCTTACGAGCTTCTTTGAGGCATCACCATGGTCCTGGTCC
TP38954	TGCAGCCAACGCCACGTTCAGTCTGGTCCATAAGTCGGAGCATGAGCCTGCCA[A/G]CGGAGACTTC
TP38957	TGCAGCCAACGCCATTAAAAAACGCGCGACGTCACAACCAACCAACCGCATCGACGCGTCG[C/T]GC
TP38983	TGCAGCCAACTCTT[C/T]CGAGCGCCTTAAATGGCTAAATCTGCAAATGATATTTATATATATAAGA
TP39013	TGCAGCCAAG[A/C]CAAAACATCCTGCTCCGTCGAAATTGGACGCACGCACGGACGGGCACATCGGC
TP39023	TGCAGCCAAGAGCTGCGACGG[A/T]GCAGCTGCCCCAGGTGTACAGAGCAGAGGTTGTTGTGCAGAC
TP39045	TGCAGCCAAGCAATCACGAGGGGAGAGGAGCCGCCGCGGGTCCGACGCCTC[G/T]GCCTCCACCTAC
TP39050	TGCAGCCAAGCATGCATGACGTGATCACGAG[G/T]GGCCATTGCAAGGACGTGACGTGACTCGCTCT

Table A2 (cont.)

TP39064	TGCAGCC[A/G]AGCGCACAGCGAACGTGGGCGCCATCGTGGGCTGACGCGCGGGAAAAATGCCTC
TP39120	TGCAGCCAAGGCTGC[C/T]GTTTTGGTGCAGTGAGTTGGTGCCTGGAAACAAAGCGCCCAGACGGGC
TP39137	TGCAGCC[A/G]AGTAACCACCCGAAGACAATGATCGAAGATCGCTTGTCGCCGAGTGCTTGAATGCT
TP39151	TGCAGCCAAGTGAGTAGTAGTCTGACTCTGACAGCACCTACGTGTTCAGAAGAACAG[A/T]CTCTCG
TP39166	TGCAGCCAATAAGGTGGAGAGCAGATAGATCCTTGCAGCCAACAACCACTGGGAGAAGCCC[A/C]GA
TP39211	TGCAGCCAATGCG[C/T]CACCGCAGTCCACATGCGTGGAGGTGCACATCCTACGCCAGTCTCGCGTG
TP39224	TGCAGCCAATGGGCATCATGGGCACCATCAGTACCAGCAGCAGCTTCTTGATTTTGACAT[C/G]GAC
TP39243	TGCAGCCAATTCGTCCGTGTTGTCCATTATAGTTGCTTTGCGCGCG[C/T]GCAGACAGAGCGAACTA
TP39268	TGCAGCCACAACAACAAGAAGCAACACTGTTCCACAAATGGCAACCAGATCATCG[C/T]TGGTGCCA
TP39295	TGCAGCCACAACCTGAAGGAGGCCTCCGAGTTCGTCAG[G/T]TCCTCCTTCCCCATGGCCACCCTCG
TP39310	TGCAGCCACAAGAAACTTCGCAATAGATGGCTTCGAGGAAGATGCGAGCAGCGCGGCAG[C/G]TTCA
TP39318	TGCAGCCACAAGCGCAGCGCTCGACAGCCTCACCAGCCGCCATCACTCGCGGC[A/G]GTACCCGAAA
TP39319	TGCAGCCACAAGGGCCCCCGAGTAAATTCACCTCCAGAGTGCAG[C/G]GCAGCCAAGTGCAGACGCG
TP39330	TGCAGCCACA[A/T]TCCGCACAAGCACATCAGTCAGCGAACCTCGAATTCCGAGAACCCCACTAACG
TP39348	TGCAGCCACACAC[A/G]GGTAGCTTTTAAAACCCGTGGTAACCCTTTCCTCCCTCCAACCGACTCCC
TP39374	TGCAGCCACACCAAGCCGT[A/T]AGCCGTCTCCTCCCTCATCTCCTCTCGTCCGACGCAGGTGGTCC
TP39390	TGCAGCCACACCGCCACCGTCCA[C/T]GGCAACCACCTGCTCGTCCATGTTGGCCGCGGCGCTCGTC
TP39402	TGCAGCCACACGAGGAACACGCCTATGGCTTCCTTCTCCAGCTCGTCGTGCTTCATT[C/T]GTTCCA
TP39414	TGCAGCCACACT[C/G]GGCGCGGTGAGCAGAGCAGCGGCGTTAACGTTATTGTCACTGCCAGCAACG
TP39415	TGCAGCCACACTGCCACAGACAAACAAGCTGGAGTATCTAGGAGAGAGAGGCAGGGGAG[A/G]AGCA
TP39417	TGCAGCCACACTTTACCAACCAGGGAAACGGACAA[A/G]GCATGTTTGGAAATACGGAGACAAACAT
TP39427	TGCAGCCACAGCAAACACGAGCAGGAACAAGGAAACAGCATTATTACACCCCTCAC[A/T]CACCCTC
TP39429	TGCAGCCACAGCACACGGCAGGCGCAGGGCGAAC[A/T]ACGGCACAAGTACAGCTGCACAGGCTTTG
TP39432	TGCAGCCACAGCACC[A/T]TGCTGAAGCCCAGCGCCGCAAATGGGTGCCGTTGGGTGATGATTACCT
TP39437	TGCAGCC[A/G]CAGCAGTGACGCCCGTCGCCGCCTGCGCAACTATCTCATGGAACTTGTGAGGAAGC
TP39442	TGCAGCC[A/T]CAGCCATCAGTCATGCAACATGTCTGAATCTTGTTTCATTCCCATTTGAACTCGGT
TP39445	TGCAGCCAC[A/G]GCCCCTTTTGGTTTCGGAATCGTGCCCCATTACCACACACTAGCAGATGACGAT
TP39450	TGCAGCCACAGCCGTCTCCCTCGAGCAGGCCTGGCAAGGGCAGCGGGCCCAG[A/C]GAGGACGACGC

Table A2 (cont.)

TP39455	TGCAGCC[A/G]CAGCGGCTGATTCAAACGCTCCCTAAAATCTCAAGCAAAAAACCAGTTGCTCAGAC
TP39456	TGCAGCCACAGCGTGACTG[G/T]TGGCTGTTCCATGCTTGCACGCGTGCAGAGTGCAGTGTGCAGCC
TP39458	TGCAGCCACAG[C/G]TACCATTCATTCCATTTGCTCGCAACAAAGCCAGCCAGGCACCAAAGAAAGC
TP39479	TGCAGCCACAGGGGTAGGCATTGAAG[C/T]TGGTGCTGGCGGTGGCGTAAAGCTGGAAGGTTTAGCA
TP39501	TGCAGCCACAT[A/G]AGTGACAGTCCACGATGGAAGGAAAGCCTTCTTCTCGTTCTCTAGCTGGATT
TP39527	TGCAGCCACATGCA[C/G]GCTGCGGGTGGCAACGCGCGTGGTCGAGAGTAATGGGCAGCGCCCAAGA
TP39555	TGCAGCCACCAAAAGCAGCACGCCTCCCGCGCTCAGAGAGAGAAAGGACA[A/G]AGAGGGGGCGGGT
TP39562	TGCAGCCACCAA[C/T]CGTGCCATCACCTCAGCCTTGCATGGACTTTGCTTCAGTCACAGCTGACAC
TP39598	TGCAGCCACCACGGTGGCGGGCCGTGTGTACGGGTAGCAACTTTGGATTCTCTGA[G/T]CAATGTGG
TP39600	TGCAGCCACCA[C/T]TGCCCATCCCGCTGCCTATTCCCGCTCGCCGCCGCCGCCAATGGCGAGCCTC
TP39617	TGCAGCCACCAGCTGGTCGTGGTGGTCCTAGTCATCCTGGCGCTAACGC[A/C]CGCCGAGGCGAGCA
TP39621	TGCAGCCAC[C/G]AGGAGGTGCTGAGACAAAACGTCTTCATCGTCGTCGTCTATGCCTCCCTCTTCC
TP39633	TGCAGCCACCAGTTCCCACTCACCCATGCAGCGGC[A/C]GCCGTCGTCGCCCTCGTGCACAGCGGCC
TP39639	TGCAGCC[A/C]CCATCGACCTTTCCATGTGCAGTCTGGAGTGACGTTCCCTTTCTCGAGCAGCTCCA
TP39655	TGCAGCC[A/G]CCATGAGGCGCGGCTCGAAGAAATCGTCGTCGTCTGCCGCGACCGCCAGCGCTGGT
TP39658	TGCAGCCACCATGCCCATCTGGTGG[C/T]ACAAGTTTATCTGCGGCGGCATGACTATCGGAAGGCCG
TP39660	TGCAGCCACCATGCTCCACCCCAAGCTGTGGAATAATG[A/C]TGTGAAGCGAGGAGCTGAGGTACCT
TP39662	TGCAGCCACCATTGCCGCTCAAGCTCACAGGAGCAAATTCGAGCAGCCTGAGCA[C/T]TCATCCATG
TP39670	TGCAGCCA[C/T]CCACAGAGGCGCTCCACCTCCACTACTATCTCCAACATTAACAATGGGGTCGTTG
TP39691	TGCAGCCACCC[C/T]GCTTCCATCCCAAGGTGCACCTCTGTCTCCTTCCCGCAGAGGTCCATGCCAC
TP39698	TGCAGCCACC[C/T]GATCTGCGTGAGCGTCGGGAGCCCTCCGCCCCTCCACGGCGAGAACACGGCGC
TP39741	TGCAGC[C/G]ACCGCAGCGCGTTCGTGTTCTGGGACGCCTACCACACCTCGGACGCCGCCAACAAGG
TP39747	TGCAGCCACCGCCAGCGGCGTCGAGGAGCGGCAGC[A/C]CATCGACGCCCAGCTCCGAAAAAAAAAA
TP39760	TGCAGC[C/T]ACCGCCGTACGTGTTCCCCGTCAACAGCGGCTACTGATGGCGGTCGGGGCGGCAATC
TP39763	TGCAGCCACCGCCTCCTCTGCTCGGGGTCGTCCAGGTCCACGGGCGCCGC[A/G]GAGGAGGGGAGGG
TP39767	TGCAGCCACCGCGCCACCGC[A/G]TGCCGCCGCGGGCGCTGGCCCAGCACGAGCAGCGACGCGCCGT
TP39772	TGCAGCCACCGCGCCTACTTGCGCGCGCGCGCGC[A/G]CACACACACACACCGTCGCCACTCGCCAG
TP39776	TGCAGCCACCGCGCTCACCTCCCACCGCACCAAGTC[C/T]AAGTGGTCCCACCTCTCTTCGGTCCCC

Table A2 (cont.)

TP39785	TGCAGCCACCGCGTTTGCCCTGCCACAG[C/G]CCAGCCGCCGTGCGGCGCCTGCACTGTGCGTGCAT
TP39788	TGCAGCCAC[C/T]GCTGGGACACGCGGCCTCAGGTCCCTCGATAGAGTTCTGGACCGTGGGGACTGG
TP39789	TGCAGCCACCGCTTGCCTTTTCATGCCCATCTC[A/G]AGGTCCACGCTCATCTTGGGCGGACTTAGA
TP39793	TGCAGCCACCGTAGAGAAAAGGCAGC[C/T]GAGTGTGTCAGCTTGGACGCATGAATCGAATGGAAAC
TP39795	TGCAGCCACCGTCACCGCGACG[C/T]CTCCCCCGCGGACGCGACGCGACGCGAGGAAAGCAACGCGT
TP39803	TGCAGCC[A/G]CCGTGCCAGCACCAGCACCACCTGCCCCCGCGCATCGCGGTGCCGACGTCGCGCCA
TP39811	TGCAGCCACCTACTCTGCTCTT[C/G]TTGGCATGAACGATGAACACTTGGTTTCCCAAATTCATCCT
TP39839	TGCAGC[C/G]ACCTGCGGGAGTCACGGGTACGGCGCACGGCGGGCACCTGCATGGCTGTGGCTGCAT
TP39848	TGCAGCCACCTTGCTTCGAGCCTCCGACTCACC[A/G]CTGTGTGGATGGCCGCAGCTGCGTATTTGT
TP39851	TGCAGCCACCTTTGGCTGGCCCTAGC[C/T]AGCTACGGCTAGCCACGGCTGGCTGAAAAAAAAAAAA
TP39873	TGCAGCCACGACCTGTCTTGCCCTCTCCTTCAGCCTACTCGCGTTC[A/G]CCCTCACCTGCACCGCT
TP39886	TGCAGCCACGAGCTTCCCGTCCTATGCAATAATGCAAATGCAGCACATGAC[A/C]AAACAATCAAGC
TP39889	TGCAGCCACGAGGCCGACGAGCTCAACTACCGCATCCTTCTCCTCCGCGTG[C/T]TCGCCGCCTTGG
TP39914	TGCAGCCACGCATCTTGCCGAGGAAAATGGAGCTCCGCCTGTCTGC[A/G]CCGTCAGCATGCGCATC
TP39935	TGCAGCCACGCCGCGAGTGC[A/G]GCGGACGAATCGTCCGCCACACATTTGGCAAGCTGAGGCATCA
TP39937	TGCAGCCACGCCGCGCGCGCGCCGTCAACACCCCGATTTCGCAAGAACTTGGGAGGACAGCA[A/G]A
TP39948	TGCAGCC[A/G]CGCCTCGCGCTGGCAGTTCCTGCCTGTAACATGTACAAGTACTGAGAGATCAACAC
TP39960	TGCAGCCACGCGGACGCGGAGACGTCGCTG[A/G]CCGTCGTCGTCGTCGTCGAAACTACTCTAGCAG
TP39972	TGCAGCCACGCGTCCCCGACGGACGCGTTCGCCACGCACCAG[C/T]TCGCCAGCGCGCCGCCCTGGA
TP39976	TGCAGCCACGCTCGCGCGTCGCGCGGGCATCGCGTGGGCTTGTGGCAGCGC[A/G]GGGAGCCGCAAA
TP39982	TGCAGCCACGCTGGG[A/C]GCGGCGAGCAGAGCAGCGGCGTTAACGTTATCGTCACTGCCAGCAACG
TP39988	TGCAGCCACGGACACCGCCACCGTCAAAGACGACGGAAGCACGGCCGCATTG[C/T]AGGCTCCGCTG
TP39997	TGCAGCCACGGATGGATGAGTTCCCAGCCACCACGGACGAACGAACGTACGAGCTCCACG[A/G]ACG
TP39999	TGCAGCCACGGCAACGGGGGTCAGTG[A/C]GGCCGTGCTGGCCGTGGAGCCGCAGAACGCAGCGGCC
TP40004	TGCAGCCACGGCAGC[A/T]GCCACAGCCGCTACGGACACTGCTGCGTGGACCTGTGCGTTGTGCGCC
TP40012	TGCAGCCACGGCCGCCGCCGCCGACGACGCGCAGCCTCGCTGCTGTCGTTGTCTC[G/T]TGCCGCTT
TP40030	TGCAGCCACGGCGCCGCCGCGCCGCCTTCCTCGTGT[A/T]CTTCGACCTCGCCATCCAATCTCCCAC
TP40037	TGCAGCCACGGCGGCGGCGTCG[A/G]TGTCGGAGGATTGCGCGATTTGCTTGGGCCAGTTTGAGGAC

Table A2 (cont.)

TP40069	TGCAGCCACGGTTAGATCCAGGAACGAGGCAGCGGCAACCAGGACGAGGAGCAGG[A/G]GAGCCACA
TP40083	TGCAGCCACGTCATCCGTTTCCCCTGG[C/G]CGCACCATGCCGCGCCTCCGCAATCCATCGCGTGCC
TP40085	TGCAGCCACGTCCACTGCGGCGTGTACTTGCCGTAGGCCGAGTAGGAGGCGAGCACGA[C/T]GACGT
TP40092	TGCAGCCACGTGATGGACGTGCCTGAGTCGATGATGACCCCGCC[C/T]GTGCCGTCGTCGTTGATGG
TP40109	TGCAGCCACGTTGTACACATGAACAAAGTCGGCAGGCTCCGAGAACACCAGGAACCGACC[A/G]TCG
TP40119	TGCAGCCACTACTCTCCGCACCGCCGCGTGCTCATGTGACACGGG[C/T]GGAGAAGGCGCGGGCGGC
TP40139	TGCAGCCACTCACTCAGGCTCTGATCGAT[C/T]GGGACGAAACGGAAAAGGAGGAAGGGAGCAGAGA
TP40151	TGCAGCCACTCCAGTCTCGGAGCAACGATGTTGAGCCTATTTTTGA[C/T]GTTGACAACACGCAGCG
TP40195	TGCAGCCACTCGAGGCTCCCGCACCGCCGCCACAACCATACAA[A/G]CCCGTGGTCGCTGGAGCGGA
TP40197	TGCAGCCACTCGATCGCGCTTCACTTGCCAAGCTTGGCTGAGATTTCCCGTGGGCGCC[A/G]CCGAG
TP40204	TGCAGCCACTCGCGCGCGGATCT[A/G]GGGAAACGGAGGTAGACGGTCGGCCGCACCAGTGCCCCCT
TP40208	TGCAGCCACTCGGCCCACTCCGCCACTCTACTCTTCAGCGATCC[A/G]CCCCCTGTGCAGGGGAGCC
TP40210	TGCAGCCACTCGGGAAGAAAGAAAGGCAACCGAGCACAGAA[A/C]GCTAGCCTCTCCTACATGGACC
TP40237	TGCAGCCACTGATGGCGGCGTGGAAGGCAGCGTGCGGATCAGCTGGCGCGGTGACG[A/C]TGGTCGT
TP40257	TGCAGCCACTGCTCCACGGTGGCGTCGCAGGCCACCTCCACGATGCGCACGCCGCAGTC[A/G]TTGC
TP40269	TGCAGCCACTGGATCACAAGGCGTCGAGCAAAAATCCTGGCTGTTTCCTGTCCAAACC[G/T]ACCTG
TP40293	TGCAGCCACTGGTCGATGCAATGGCGGTGGAACACGTGCAGGCACAGCGGCAGCCGCTTCGCC[G/T]
TP40307	TGCAGCCACTGTGGCAGATTTGAACAGCTCCT[A/C]GCTCCGCCAGAGCCATCGACGCTTCCACTTC
TP40311	TGCAGCCACTGTGGGGAAATCACAG[C/T]GGAGCACAGCTCATACTCGTATAATGAGAAGTTGCTGC
TP40318	TGCAGCCACTTAACATCCTGCACATTCACAACACCAACACCGCTCTCAAGATCAC[A/G]CAGGATGC
TP40322	TGCAGCCACTTATTTGCTGAACAGACGCCCCTCCTCCTCCATCC[A/G]CAAAGAAGTCCCCTACGCC
TP40323	TGCAGCCACTTCAACACCTGCAATGTGAGAAGAGAAAAGCACACCACACGTTACTTCGA[A/G]CAGG
TP40332	TGCAGCCACTTCTACTAGC[C/T]TGTGCACGTCAACTTATTGAGCACATAAGGTTTGCTTCCTACAC
TP40349	TGCAGCCACTTGACATCCTGCACATTCACAGCACCAACACAGCTCTCAAGATCACGCAG[C/G]ATGT
TP40386	TGCAGCCAGAAAGCATCGGATCAGAGGTACGGTAACTAACAGCAGAAGCTGAAGCAGCAC[A/G]GAT
TP40389	TGCAG[C/T]CAGAACACGAGCGCCTACATCATCGGCTTCGGCGTGGTGCAGGTCATCTTCAGCCAGC
TP40390	TGCAGCCAGAACACGATGAAGCATCC[A/C]AATAGCTTTGGCAACAAAAATCTGTCGCGATTAGCTT
TP40393	TGCAGCCAGAACGA[A/G]CGGCTGGGCACCTAGTGCTGCTGTCCAACATGTATGCTGGCGTTGGACA

Table A2 (cont.)

TP40395	TGCAGCCAGAACGGCATGGCTGA[C/T]CATTTGTTCGCTCGATCGTTCTCCCGTGCAGAAGCAGAAG
TP40401	TGCAGCCAGA[A/C]GAAGGTGAGGAGCTCCCCTCCTCTGGCCAGCTGCGCCGCGTGCTGCTCAGGCC
TP40406	TGCAGCCAG[A/C]AGCAGGGGCGGCGGCGCCCACGGCCACTGGTCGGCCTCCATATATGCCACAACC
TP40419	TGCAGCCAG[A/G]CATATAGATGGAGTGGATCAGTGGAAGCACGGCAGGAAGATGCAGAAGCCACGG
TP40420	TGCAGCCAGACATGAGAAGGCAGTG[A/C]CATCCGCTTCTTGACCTCGTCGGCGTTGTACAGGTCGC
TP40431	TGCAGCCAGACGGCAGTTAGGCAGGGAGACGCCTCTTTTCCCTCCTTT[A/T]AAACACCCAGCGGTG
TP40455	TGCAGCCAGAGCGA[A/G]GCGATTCCTGGAGAGGAGTCGGAGGAAGGCGAACACGGCGGTGGCGAGG
TP40456	TGCAGCCAGAGCGCCAGTTTGGACTTTGCGAACG[C/T]GCCGTGCATGCTGGGTAACACTGTAGCGG
TP40460	TGCAGCCAG[A/C]GCGGCCACTGCTCCGCGTACGCCGCCGTCGCGGCCTCCTCCTCCGAAAAAAAAA
TP40467	TGCAGCCAGAGCTTCTGGGTCTTGTGCTCAGGCGCCTTCCCTCCCT[A/G]GCCGACCGTGTTCGATT
TP40480	TGCAGCCAGAGGGGATTGAAGGCA[C/G]AAGCAATACCACACGTCAATCGAACAACAGCGTAAATAA
TP40500	TGCAG[C/T]CAGATCCCCAGAGGCCTTAGCAGCAGAGGCAGCTCTAATTTACTAGTGACCCTAGCAT
TP40510	TGCAGCCAGATGCTCCCGACGAGGCTCAGCCAGTGGGCCGAGGAAGG[G/T]GAAGGCATGGTGAGAG
TP40530	TGCAGC[C/T]AGCAAGCCGCTGCCCCCGACACCTGCATCGTGGCCACTCTAATCCACTGACTAGGTT
TP40534	TGCAGCCAG[C/G]AAGTGAGGAAGAAGGGAGGGGCGAGTCAGAGACAAGTACAACAACATCGAGACC
TP40548	TGCAGCCAGC[A/G]CCTGCGCTGCGCCACCAATTTAAATTTGCTTACACTGGGCAGCAGTTTCCCAG
TP40549	TGCAGCCAGCACGCAC[A/G]CACGCGAACAGCCGAACACGCTCAATCAGAGAAACCAAATCAAAACC
TP40563	TGCAGCCAGCAGCAGCAGGGCCGAGGGGCGGCGG[C/T]GCGGTGCGGTAGGAGTCGGGCCAGCGGCC
TP40568	TGCAGCCAGCAGCAGCCTGGCCA[C/T]GGCAGCAGGTGGCATCGGCGGCGATGAACTGCGGTGGCGG
TP40595	TGCAGCCAGCAGGATTGGTTACGAGCTGTC[A/G]CGGAGGGGAGAGAACTGGGGTTTTGGGGGAGGA
TP40617	TGCAGCCAG[C/G]ATTCCTCCTGCCAATCCTTTCATCCATTAACATTCTAATCCTTGCGACATCCTC
TP40632	TGCAGCCAGCCA[C/T]GCCGCCGCCCGCAGAAGCAACCGCGGCCGCGCCCGCAGGATTCGCCCGCCG
TP40657	TGCAGCCAGCCCAGCTATA[C/T]CAGTACTGTGCGCTGCTAACGACGCGCACCGAGCATAGCATATC
TP40663	TGCAGCCAGCCCCGTG[C/T]GCCGCCACCCGACAGGGCCCCACCCCGCTCCCTGGCTCTGCTCGCTG
TP40690	TGCAGCCAGCCTCTCTTCCCTCTGCCTG[C/T]AATGCCCCGTGCATTCATGGTGTGGTGTGGTGTTC
TP40691	TGCAGCCAGCCTGACGTGGAGACGAAGCACAGGCAGGAGA[A/G]CCAGAAGGCCAACAGAACCTGCT
TP40692	TGCAGCCAGCCTGAGTCAAGAGCAGTTTACAGTTGCCCCTGCCCTGCGCTTCTCTGT[C/T]GATGTG
TP40719	TGCAGCCAGCGAT[G/T]CCAGCTTCACGCGATGGCAAGAAAACACGGAGCGGCATAGGTAGTTGCGC

Table A2 (cont.)

TP40722	TGCAGCCAGCGCCAGTCGCCAGACCACGACC[A/G]TCGGTCCGTCGCCCACTGGCGCCCGCCGCGTG
TP40732	TGCAGCCAGCGCGCCATGACGGCGTCGCCCGAGTCGCCGCCCATCGCGGCCTGCGC[A/G]CCGAAAA
TP40743	TGCAGCC[A/T]GCGGCCATCGCATGGATGCATGATGCGACCTGTTTGGTGATGTAAGATGGATGGAT
TP40745	TGCAGC[C/T]AGCGGCCTCAACGATCGGTCCCAATCAGAGGAAATAGAAGCGCATGCGAGCGTGAAA
TP40756	TGCAGCCAGCGGGCCGTGCGGGCGCACGACCGTTCGTCCCCGCGCCCACGGGGATGC[A/T]AGCTGC
TP40793	TGCAGCCAGCTCACGGGTCACAGCCAAGGAAAGGAAGGCCA[C/G]CAGCGTCAGTCAACGGCGGTAC
TP40805	TGCAGCCAGCTGACAGCCGCTGGGG[C/G]CCCATTCCCTTCGCGTTCCGCGAGGACCACGTGGTAAC
TP40808	TGCAG[C/T]CAGCTGATGACGGGCGGTTGTAAGGCGGCTGCGACGACGAGGGGGAGCGGCGGCGAGC
TP40812	TGCAGCCAGCTGCCAGCGGCCAACGCTCTCT[C/G]TCTCAGTCTCTCTCGGGGCACACGCCTCGCCT
TP40819	TGCAGCCAGCTGCTTGCGTTGCTTGACTTGCTCAGTGC[C/T]TATCCACCCCCAATCCCACTCTGAT
TP40830	TGCAGCCAGCTTCACACAGATTGGTTGCTCATTTGATGAGTGTCTCAATCACGTTGTACTCAA[A/C]
TP40835	TGCAGCCAGCTTGC[C/T]GAGCTTGATCTTTCAAATTGCATGGTCAGTGACTATGGTGTTGCGGTCT
TP40854	TGCAGCCAGGACCAGGCGGGCACCGCGGCCAG[G/C]GGCGGACTGGCGCCACCGCATCAGCCATCAC
TP40869	TGCAGCCAGGAGTCTTCTCGACCCCATGTCGCGCCATTTTCCTCCTAATTTGCTCTGC[A/C]TGCTC
TP40871	TGCAGCCAGGATGCGACCGAACCGTTTCCGATCCGCGGCCGCACGG[A/G]GGGGACGAACGGGCGAT
TP40880	TGCAGCCAGGCACACACACAGACACGTCACGTCACGCCACGCAGCCCAAGGATC[G/T]ACGCGATGC
TP40888	TGCAGC[C/T]AGGCACTGACGAACGAGAACAGGATGGAGAGCAGGGACGGCCGCCGCAGGAGATGCC
TP40896	TGCAGCCAGGCAGGCGGGCAGTACATCATC[A/G]ACTGATCTGATCCCTGACTCTGAGCTATATTAC
TP40897	TGCAGCCAGGCAGGTGCTCTGGCTGGCTGCGTTCTTTGCGGGCCTCGC[A/T]GCCTGCGCAGTCGGC
TP40902	TGCAGCCAGGCCACCCACGGGAGCGAGAGTTACCAGGTG[C/T]ATGCATGCATGCACCCACGGTAAA
TP40913	TGCAGCCAGGCCTAGAGGCATGTAAAGAACGGCTGTTGGCGTGGTGACGTGCAGGGTGCTCC[A/T]C
TP40917	TGCAGCCAGGCCTTGCCATCCTATA[A/C]GCTGTGCTGCTCTTGATGGATGCTAGCAGCAGGGTGGC
TP40929	TGCAGCCAGGCGTAGGTGATCTGGGGGCCCGCCCCTGAACACAACGTCGTGCCGATGTTTCCA[C/T]
TP40941	TGCAGCCAG[G/T]GAGACAGATGAGGAGGAAGTGGCGGTGACGTAAGCACTGATGCATGCATGGCGT
TP40958	TGCAGCCAGGGCGAACTAGTGGCGAGGACGCGCCCGCCCGCCGCTGCGACGGCCATCG[C/T]CGCGC
TP40961	TGCAGCCAGGGCGGACCACCCGATGATTT[A/T]TGTAAAAAGTTCAAAGTAAGCAAGCATAAAATAG
TP40989	TGCAGCCAGGTCGGGCCGTTCGTGTCCAG[C/G]CCCCCTGCCACAAGCAGAGCTTTGGAGGACATGG
TP41020	TGCAGCCAGGTGTTCCTTACCACCGTCACCGTC[A/G]CTGTCCGTGAGAACCTTGGCATCCCCCTTC

Table A2 (cont.)

TP41043	TGCAGCCAGTAGAACAGCCGCCCGACGTGGCC[T/C]GACAGGAAGCTCCAGCTCCAGCTCATCCAGG
TP41046	TGCAGCCAGTAGGAGCAGCGGCAGGAGCGACG[T/C]CCAGAGCACCGCCACGCCCACCGCGCGCCGA
TP41049	TGCAGCCAGTAGTAATGCTTGCGCAGCTCCACGAAGCGGGTGCCG[C/T]GGCGGTACAGATTGACCC
TP41064	TGCAGCCAGTCCTATAAACA[A/G]CAGCGCGTCCACCTCACGTATCATCTGTAGCTAGCCCGTGCTG
TP41098	TGCAGCCAGTGGAGAAAACGTGTCAC[A/G]GGTCGGTGCCAATTGGGCTGTCCAAAAGCCACCCACG
TP41105	TGCAGCCAGTGGGGCTGGTGCGGCTCCACCTCCGACTACTGCGGCGACGGC[A/T]GCCAGGGCCAGT
TP41115	TGCAGCCAGTGTTCTCACGGAGCCCTCGACCACCAATC[C/T]TGTTCTTGAGCTTCTTGACAGCCTC
TP41126	TGCAGCCAGTTCTTGGATTGAAAGTAGTAGAGGACAAAAA[A/T]TTCGACCTTAATTGAGCTTTTCC
TP41130	TGCAGCCAGTTGCCAATGCAAATGCGTGCGCAGCG[C/T]AGTGCTGGTGAGGTGAGCGCGCATGCAT
TP41142	TGCAGCCATAAACCCCACCCCCACTATCAGCCGATGCGTTTGCTTCACCTTCACAGCCAGC[A/C]GT
TP41144	TGCAGCCATAAAGGCTTCTCTGATTCGTG[G/T]GCACGACACGCACAAGGACGACGACGCCTGTGTC
TP41159	TGCAGCCATAATCAAGCGAACTGCACTCAGTGGGGTTGCTAAATAAAATATCTATATTAG[C/G]CAA
TP41165	TGCAGCCATACACACGACGCCGACTTGGACCTCTGTTTGGGG[C/G]AATGAGCGACGGACCATCGCC
TP41207	TGCAGCCATAGGAAACGAGCAGGCTGCTTGGTGCGGAGCTCGGC[A/G]GCGGTGCCCCGCTCCCCCC
TP41218	TGCAGCCATAGTACTACAAA[C/T]GTGATGCATCTGATGCGTTGCGAGTTGCCACGCATGCGATACA
TP41227	TGCAGCCATATAACCACCACCACCCCGCAGCCAT[A/G]GAATCACTCACTCATACTGATCCAGCAAG
TP41259	TGCAGCCATATTCTTCAGCGGGTTCTTCCT[A/C]GGCTCCCTACGCTTCACCTCCTTGTTGATGGGC
TP41260	TGCAGCCATATTGACAAGGTGGATACAGGTTTTGGTGGTTTGTTTGAAGCAGAACGAGATGT[A/C]C
TP41268	TGCAGCCATCAAAGAACAAGGGGGTCAGTCCCAATCTC[C/T]CCAACCCAACAGGGGCGAAAGCAAG
TP41286	TGCAGCCATC[A/G]CCCAGCACGTACAACAGAGGTGACCGTCTGAAGCACGGAAGTTCCTCATGAAT
TP41299	TGCAGCCATCAGCCACCGCTAGATTTTGAAGCGCGACGGTGG[A/T]ATGATTCAATCAATTTTTAAA
TP41313	TGCAGCCATCATGCGTACAACGGCAAGGTCCC[A/C]ATGGGAGGATGTGTGGGCTTGGGAACCAAAG
TP41323	TGCAG[C/G]CATCCACTCCATTGGTGACATCAAGAACTAAAGGACATGCATGGACGGCACGTCGTGC
TP41324	TGCAGCCATCCAGATGGGATGG[A/G]ATCCAACCCAAAACTTTCAGCTGCTGCTGACCACCGCGACC
TP41334	TGCAGCCAT[C/G]CCAAAACGTGCAGCCGAGCAGGCTCAGTGTATTCATCTGTCATGTAATGTCTCT
TP41342	TGCAGCCATCCG[A/T]GGTGGTGCCCCAGTGCCCAACGCCCGCGGCGCACGACTCTGCCCCGTGCCA
TP41344	TGCAGCCATCCGCC[A/G]TTCCCGAGCGTCCAGAAGCTCGCCTGGCAATGGCGAGGCTTCTCGTGCT
TP41350	TGCAGCCATCCTATTCCTACGCCGACGACGGATTCTTGTAACTGCCACGGCGGCG[A/C]AGCCGAGA

Table A2 (cont.)

TP41361	TGCAGCCATCGAACCTCCAGCTAGGTACCA[C/T]GCCACAGGATCTGCAAGGGGAGGGGGCGCCACC
TP41362	TGCAGCCATCGAACTTTACTTGT[A/C]AGAGCTGCTAAAATCGGCTGTTGCAGACGCTAGCTGGCCC
TP41374	TGCAGCCATCGATAGCAGGCTCTAGTTCTCCTCCAAAGCCGAAGCGTGCGGCGTGAGATTCCA[A/C]
TP41404	TGCAGC[C/T]ATCGGGATCCACATTAACTTTGGGAAGTCCACCTTCATCCCCATGAACTTGGACGCC
TP41418	TGCAGCCATCTCACACCGCCCAGCGTGGTGGCCTCCTGCGCCTGGCAAC[A/G]CGAACAGCACGGGG
TP41422	TGCAGCCATCTCATCGCCAAGTGCCTTCATCTTC[C/G]CGAAGTACTCAGCAGCGGTGGAATTTCCC
TP41425	TGCAGCCATCTCATTGCATCATCACTCATCAGGTGACTTTCCTCAAGTGTGGA[A/G]GAGTGGTGTT
TP41429	TGCAGCCATCTCCATAGCAGCTGTTGCTGAAGCCCTTGGGGATGGCAC[C/T]GCTGATCCAGTGGAG
TP41462	TGCAGCCATCTTTACCGAGCAGGCCAATCTATGTTTTGGATGGACAGGATGTCCAGGGCG[C/T]GTG
TP41508	TGCAGCCATGACTGCGGGTTGAAGCCATATCC[G/A]TGGATGTGCTGCTCGTCGCACGGCGACTCTG
TP41510	TGCAGCCATGAGCCACCTTCCATTTTCAGAATGG[A/G]GCACGCGCTCCTTGCCGTCGCCGTGGCTA
TP41519	TGCAGCCATGATATACCCATGCTGCAAACAACACTCCAAGTCCAAGGC[A/T]CTGCTCACACATGCT
TP41521	TGCAGCCATGATCAACAGCACC[A/G]CAGCCCCTTGTCTCCCAGATGAAGCTTCTTCCCTCCTCCAG
TP41543	TGCAGCCATGCAC[A/G]CTTGCTCCTCTTTTTTATCTGCAAGACTGGCTTTGCCCCAGTGTGTGCTA
TP41567	TGCAGCCATGCATGAACGCCCTGACATATATACTACGTA[C/T]ACGTTTAATTACCTGCTTAGGAAC
TP41580	TGCAGCCATGCCATG[A/C]CATGCCCATCTGGTGTATGTGGTAGCATCAAAGTCTCGTGATCCCACC
TP41616	TGCAGCCATGCTCACCATG[A/T]CCACGTCCAAAATTTCCTGGTTTTTAATTTCCCATGCAGCATGA
TP41620	TGCAGCCATGCTCCTCCACCTGCTTCCGCTCTCCTGCCCCGCGC[C/T]GCCGTTCCACCTGCGCGGG
TP41635	TGCAGCCATGGAATCACACACTCCAGATCACTTCTACATACTGATCCAGCA[A/C]GTGACTGCTGCT
TP41636	TGCAGCCATGGAATCA[C/T]TTCTACTGATCCAGCAAGTGACTTCTGCTCGCTTGCTAATAACCATG
TP41647	TGCAGCCATGGATAAATAAAC[A/C]TCATTCGCCCGCGAATGCTACTTCCAAACAGATGAAAACAAA
TP41654	TGCAGCCATGGCAATCGATCAGGCCCAATATATCCAT[C/G]GACCTAGATGTGTTATCTAGGACGTG
TP41656	TGCAGCCATGGCACCACCTCAGGAACTCGTCCTCCACGACGACGACGCG[C/G]TCGTCGAATATGTG
TP41673	TGCAGCCATGGCCCACCAGCTCCCCATGCCGTCGGAGTGGGACCCCGTCCTGGACC[C/T]CGAGGTC
TP41674	TGCAGCCATGGCCCATGCTGTTCTGGCAGCTTCAATTCCCACGCCTGATGCAG[C/T]CGTGCGCGCA
TP41683	TGCAGCCATGGCCGCCGCCGCAAGCTCATCTTCGCCTCATCCGCTCCTCCGCCGTCTTCTTC[G/T]G
TP41685	TGCAGCCATGGCCGCCTGTCACAGACACGCTGGAGTTT[C/T]AGTCTAACCATAAGATCGGCGCAGT
TP41687	TGCAGCCATGGCCGCTGATCTCCT[C/T]GCAGCTCTTGCCCTCGCCCTCACCCTCTTGACCCTGAGT

Table A2 (cont.)

TP41704	TGCAGCCATGGCGGCCATCGTCGTCGGCAGC[C/G]ACGCCCAACTGCGACTTCGCCCAGCTGACGGC
TP41713	TGCAGCCATGGCTGCCAGGACCTGG[A/G]ACAGTTTCTTGTTGCCCAGCTGAGTGGCCGCCCTGATC
TP41720	TGCAGCCATGGCTTGGAGCTCGCGCAGATGTTCTGGTATCAGCGTGCCCAGCTGAGG[A/G]TTCTGC
TP41763	TGCAGCCATGTC[C/G]AAGGCCTTCGCCAAGTCCCTCTCCCAGCTCAACAAGGCCCTCATCAGGAGG
TP41774	TGCAGCCATGTGAAAGGCACACCTGGGGATCAGTT[A/C]GGGTTCGGTGCTCGGTTTCGCACAGCAG
TP41779	TGCAGCCATGTGCTTCGATGGAACACGGATTCGT[G/T]TGTTCTGACTGGCATCTGACACAAAGCAA
TP41802	TGCAGCCATTCA[A/C]CCATCCAATGTCAGTGTCATCAATGTCAGCGAGTTCAAACTGGGCGACAGA
TP41807	TGCAGCCATTCAGCCATTCAGGCAAGCAAGCTGCCCAAGCACGGAGGCAGCACCCGATACCTG[C/G]
TP41824	TGCAGCCATTCCTGGATGGCAGAACGAAG[A/C]GCGCGATTGGGAATGAGCTCGTCGTGTTCTAGTC
TP41836	TGCAGCCATTCGGGTCTAGTATCTAATGGA[C/T]GCCTCATTCTCGAATCAATGGAGGACCATGGTA
TP41854	TGCAGCCATTGATGTCAAAATCGCTAAAA[C/T]TATGCATGGCTCAACGGACTCAACTGTGCATTCA
TP41859	TGCAGCCATTGCCAGAATGCGAGGGCAG[A/C]GAGGAGGACTCCAAGGCGCAGCAGCCGCACGAGTG
TP41867	TGCAGCCATTGCTCACCGATTCTGCATCGTCCAAAGCCAATCAGCCT[A/T]TGCCACCATCGTTTAC
TP41974	TGCAGCCCAACAGATCTCGG[C/T]GCTGGTTCGTCAGCATGCAGAATATGTGTGGAAGGAGTACATT
TP42025	TGCAGCCCAAGAGTTGAAAGTTGAAACGAATGGCTTAGCCGCTCCCGCC[C/G]AAGAGTGCCTTGAG
TP42027	TGCAGCCCAAGCAGCTC[C/T]AGGAAGTAGAAGCGACCAGGGCCCAATCACTCCTGGGCCCTAGCCC
TP42038	TGCAGCCCAAGCGGGCGGCCGCACATGCTCTCCGT[C/G]TCCTCGGACGGCACCACGGACGCCGTGC
TP42042	TGCAGCCCAAGCTTTGG[C/T]TGTGTAGCAACTCCAGTGGCCGCCATCCCTTCCTCTGAGCTGGAGC
TP42068	TGCAG[C/T]CCAATAAACTAAGGAGTATAACCCATCTAACACCGCGCTGCGCTCGATCGATCAAAAA
TP42077	TGCAGCCCAATCGAACCAGCTCATCACACGCACCAACAAAAGGAAC[C/T]CGTAAACCCTACGAAGC
TP42085	TGCAGCCCAATGTTATGTCTGAATCAAGAAGTCA[A/T]GAAGCATAAACCGTTGACGAAGAACAGCG
TP42103	TGCAGCCCACAAGAATCCGCCGCGCCGCAGACATGCGCC[A/C]GCTTATCCGAACCGCTCGCTGCTG
TP42141	TGCAGCCCAC[A/G]TGGATCTGGCGAGCTGCGGTGGCGGTGCATTGAGGGGCTCACCATTTTTTATT
TP42150	TGCAGCCCACCACCCTACCATCCGCGGCGA[A/C]CTCCGTCTTCTCCTTCCCCCTCTCACCGCCATA
TP42151	TGCAGCCCACCACCGCGGTCGGAGAGGCCTCTGCCGCAACGAGGGTGCGCT[G/T]CTGGGAGTGTGC
TP42155	TGCAGCCCACCATACACCTCCATGGCTCCACCATGCC[C/T]ACATGGATGTCGATGCAATCACTAAT
TP42160	TGCAGCCCACCCACTGGT[A/G]TATATACCCCACCACTCCCTCCCCCACAGTCCACAGAGCACACAA
TP42162	TGCAGCCCACCCAGCCTCGCGCAATCACCATCTTATTCTAAA[C/G]GATCGTAAATTTCCAGCTAGA

Table A2 (cont.)

TP42184	TGCAGC[C/T]CACCTTCTCCTGAAAGCTCCCTGATTTCGCCAGGATCTTGGACGACACACACCCCAT
TP42185	TGCAGCCCACCTTGCCTTCACCGCGCATGCTTTGGCGCCTTGCGCTGTGTTCGATC[C/T]GAACGTC
TP42251	TGCAGCCCACGTCCTACACGCGGAGGGGGCTTAGAACGCCACTTTAA[C/T]GGGCCTCTAGTGGGCT
TP42288	TGCAGCCCACTTCCACAGTTCCTCGTGAAAGTCATTAATGCTTTAA[A/C]CCCTCTAGAACCCGTCT
TP42306	TGCAG[C/G]CCACTTGGCTCCACGAACTGCTCTGCGCTTGCGAACCACAAGACTGCACGAAAACGAA
TP42317	TGCAGCCCAGAACGTGATTTGCTTTGCTTGTGTCGCCGT[G/T]GGGGCATTTGCTTGAACACCTCAT
TP42321	TGCAGCCCAGAAGTCCCT[A/G]AACACAACAAGGCCGACACTGACGTTGTCCCAACTGGCGGCATGC
TP42326	TGCAGCCC[A/T]GACCTGATGACGCGCGCCGTGGCGTGGCGTGGCGCGGTTGGGTTTCGGTTCGGCC
TP42328	TGCAGCCCAGACTCCATCATCTTTTTCTTGACCTTGCATGC[C/T]GAGGTCATGTCCCCTCTCTTGC
TP42330	TGCAGCCCAGAGCGTGTACGTGTACCGCGGCCCCGCCTTGG[C/G]GCTGGCCCTGACGCACGCCAGC
TP42342	TGCAGCCCAGCACAGGCACAGGGGCAGCCGCACAT[A/T]GCACAGGGAGTGGGGACAGGCACCAGTA
TP42346	TGCAGCCCAGCACGGCAGCAGCAGGCCCCAACGTGC[C/G]CCGTCGCATGCACTGCATCCATCCACT
TP42352	TGCAGCCCAGCAGCCCTGCGCTCTACGAGGTCGAGAGCACGTCGT[C/T]GCAGGCAGCAGCGAGGAC
TP42371	TGCAGCCCAGCCACCTGCTCAGGGGGGCAAGCGGTCCAGCCGCTCCAGGC[C/T]CCACGAGCCACTG
TP42374	TGCAGCCCAGCCACTACGACGCCGACGAGGTGATGTTCGTCAAGGAAGGCGAGGGC[A/G]TCGTCGT
TP42379	TGCAGCCCAGCCATCATGACCAACTTTTGCAGTCACAAACTGCAAACCCTTGAG[C/T]GCTACAGCA
TP42401	TGCAGCCCAGCCTTGGAGGACCGCGACACCGACTTGGTCG[C/T]TGGCTTCGCCTTCCCGCGGCCGC
TP42409	TGCAGCCCAGCGCGAGAGGCGACGTCGCCTATGGTGACGCGACCGCCGAAGTGGTC[C/G]ACCGCCT
TP42435	TGCAGCCCAGCTTGGAAGCCCATCCATCGGCCCTGTACATGACACTCCTCTCCGCGCGTTC[A/G]GT
TP42444	TGCAGCCCAGGCACTGGGGCT[G/T]CCTCTCCTTCCGCCGTCACTGTCGAAGAATCAAAGCTTCAAG
TP42448	TGCAGCCCAGGCCCTAG[C/T]CGTCGGCCTAGTAACGCTACATACGCCATGTAGTTTTCAGCCCAAC
TP42455	TGCAGCCCAGGGACGG[C/T]GCTGACCTGGAGCAGCAGCGTGAGCCCCGTGGCGTCCGAGTGCGGCG
TP42457	TGCAGCCCAGGGAGCAA[G/T]TCGCCGATGGTGATCGGCGCCTGCACGCGGTGCATGATGTACTGCA
TP42460	TGCAGCC[C/T]AGGGCACGCACGGCGCTTTTGCTCAAACGTGCTAGTGCCAAACTTTTCCCCCATCC
TP42462	TGCAGCCCAGGGCGAGGCCCAAAAACTCTGGGAATAAGTTTCTTAAAAAC[C/G]TTGTAATAAGGCC
TP42475	TGCAGCCCAGGTGAAGATGACCAGGGGCGCAGGATGCTCGGACGCAGCTGGACTTGAC[C/G]CCGCA
TP42476	TGCAGCCCAGGTTCCTCCTCCCTCGCTTTTGCCCGCACGGGGAAAGC[A/T]AAGCTGCGCGCAAGAT
TP42478	TGCAGCCCAGGTTTAGCCATTGTAGTTCCTGCTACCTATATTCAGGACGTGTTTGGTTGCCA[C/T]C

Table A2 (cont.)

TP42502	TGCAGCCCAGTCGACCACGCATGTC[C/T]GCCTCGCCGCCGAGGCCTCCGCATCACGCGCCAACGAG
TP42511	TGCAGCCCAGTGCAGTTGTCTGCAAGTTTGCACACGCGGTCCAGGCATAGATCGACAAT[C/T]TCCT
TP42517	TGCAGCCCAGTGGACCAGTGCC[A/G]ATTGGTCTGTCCACCACCAAGCTTCGAAATGGAAGACGGTT
TP42562	TGCAGCCC[A/G]TCGACCCAGGCACGTGCTCGGCTCGACCAAGCACCATGTCGCTGGCCGTGTCGCT
TP42570	TGCAGCCCATCTAGCGCCCCCTAATCGGG[C/G]CGCCCGCAGGCGACACGATGAAGCCCACCTCGCC
TP42575	TGCAGCCCATCTCCTGCTACTCT[C/T]GCAGGAGTTGCTCCTTCCTGTGCTATGCCGTGCGTGCTTC
TP42577	TGCAGCCCATCTGAGTCTCACGAGTCGACATGCTCCGTCAGGAAACAACACCGCGC[C/T]GCCCCTG
TP42584	TGCAGCCCATGAAGACC[A/C]GCGACGGCCGCGGCACCACCGACGCGTACTGCGTCGCCAAGTACGG
TP42585	TGCAGCCCATGAAGCCCAACAAAATAGAC[A/C]GTTCGGCTCCAACAGAGCAAGCCCATCTGGCATC
TP42617	TGCAGCCCATGGATCGGAGGTCGGCCGCACACCC[A/G]CGCGTGTATATATAACTATATATACGCGC
TP42624	TGCAGCCCATGGCGGCGTCTTCTGTGCGCCGTCCAGCAGCGTCCATGCATGA[C/T]GAGCCAGAAGA
TP42631	TGCAGCCCATGGT[A/G]TTAGACTACTGTTAGCATTGACAGGCCAGCTAATTACTCCTACTTGAGAG
TP42635	TGCAGCCCATGTCGACATTGCATAGAGTATGCGTCCCTTCCACCCTCCCAGGAGCCACTGA[A/T]GA
TP42643	TGCAG[C/G]CCATGTCGCTTTCTCCTGGCCGAGGTCCAGAGCCTACGGTGCAGTGCAAGCCAGAAGA
TP42646	TGCAGCCCATGTGA[G/T]TTCCCATATCGATAACTGTTGCCAATTAGTTGATGGCGAATCGATCATG
TP42656	TGCAGCCCATTAAGCCCAACAAAATAACCCGTCAGGCTCCAACAGAGCAAGCCCATCTGG[A/C]ATC
TP42678	TGCAG[C/G]CCATTTAATAATGTTTTTATTTAATGGGCCACCATAGGATATTTTTCCTAATTCATTA
TP42687	TGCAGCCCCAAACGAACCATGCCCACCTCGTCCCTGGCGCCGACATCTGCTCTCGTCCTCGA[C/T]G
TP42705	TGCAGCCCCAACCTCTTTTGTTGGAACACGGTGATCTCAGGGCTCGGAATGAATGGCCGCGG[C/T]G
TP42747	TGCAGCCCCAC[A/G]GCGGACAGGTTGGCGGCGTCATAGACCAGCAGGCCGAGCACCGAAAAAAAAA
TP42754	TGCAGCCCCACCAGCGTCGCCGCCGCCAGCTGCCATGCGTTGTC[A/G]CCCTTGTCAAGCCACTCCG
TP42755	TGCAGCCCCACCCACGCAAAAACAGAGTGATAATAGCTAAACTTTCACCATATTCACACC[A/C]TCA
TP42765	TGCAGCCCCACGAGTTGATCGCCGCAGCGCTAGCTCAAGGG[A/G]GAGCACGACGAGTCGGCCGAGC
TP42766	TGCAGCCCCACGCA[C/T]TGATGGCACCGCACGGAGTGGGAAAAAGGAAGCAGGCCAAGCTGCTGGT
TP42769	TGCAGCCCCACG[C/T]GCCGCCGTGGTCTGCTGCCGCCTGCACCATGCTGCCTCACGTGTTGGCGCA
TP42774	TGCAGCCCCACTCCCCATTACCTCACGCACACGCCAA[G/T]AACTTCATCTCCGCCTCCAACTCCCG
TP42777	TGCAGCCCCACTGCGGAATTCATCAGTAGACTGTCCAAGAAGCCTGAT[G/T]GACTGATTCCAATCC
TP42782	TGCAGCCCCAGAACAAACCGTAATTTCTACACACATAGAAGAAACTATTTAGAGTACCCAT[A/C]AA

Table A2 (cont.)

TP42783	TGCAGCCCCAGAAGAGTGGAGTGGCGTGGCCAACAGAACACGTAACGTA[A/G]CATGGCGCGCGATA
TP42785	TGCAGCCCCAGAGGTGGCCATGGAAGGCCGCCGCACCTCCCCTGCACCTCGTGCTCGACCG[C/T]CG
TP42787	TGCAGCCCCAGATCCCCTTCCGTCTCTACTCTTTCGCACGCCGCCGTCATCCGCAG[A/G]GGCCCAC
TP42819	TGCAGCCCCAGTCTGCGCGCCACG[C/G]CATCGAGCACCTAACCTTGGCGTGGTTGCTGATGAGCCG
TP42839	TGCAGCCC[C/G]ATGAGGCGCCACTGCACGCTCCAGCACGCCCATGATGACGCGTGGCCATCCCGAC
TP42846	TGCAGCCCCAT[G/T]GCCGCGGCCGCGCCAGGGTTCAGCCGACCTCCTCCCAAATCGTGCCGAAAAA
TP42848	TGCAGCCCCATGGCGCGCAGCACAGCGACCGACATCGCG[C/G]AGCTGCGTGCTTGGGTTGGAGGGG
TP42854	TGCAGCCCCCAAGCAGCCGTGCTAGGAAGC[C/T]GTTGACGCCGACGCACGAGCCGAGCCAAGATGC
TP42869	TGCAGCCCCCACCAGAGGCAGAAGAGGATCTTGGCCGTCAGGTTCTCCGTGGAGTA[A/G]ACCCCTG
TP42873	TGCAGCCCCCACGCTGGGCCCACGGCTGGGCTGCATGCATGATGCAGCTGC[C/T]ACGCTAGATGGA
TP42880	TGCAGCCCCCAGCCTTGCCGCGTGCCCATGCCGCATTGGTCGCCGT[A/T]GCCCGCATGCCGCCGCA
TP42891	TGCAGC[C/T]CCCATGCAGCGCGTGCTTCGACCCCTTGCAGCCCATCCACGTACGTACGTGCACTGT
TP42892	TGCAGCCCCCATGCAGCGCGTGCTTCGACCCCTTGCAGCCCATCCTCGGCGGCGGGGAATG[A/C]AG
TP42899	TGCAG[C/T]CCCCCACGGACACCACAACCTGCTTCAATCGTTGCTGAGCGGTATCGAAAACATTAAG
TP42992	TGCAGCCCCCCTGCCGCGTTTGCCAATCCGAATCAGCCGC[C/G]CATTCACTGGACCTTGCCGACCG
TP43056	TGCAGCCC[C/G]CGCCCTCCGCTCAGCCCACGGCCGCCCCTGCCGCCACTCAAGTCCACGCCGCCTA
TP43121	TGCAGCCCCGA[A/G]CAATAGTTCGATTCCATGGCACTCTGCCTCACTTGCCTCCTTCGCCTTCGCC
TP43122	TGCAGCCCCGAAGAGGAAAGCAAGCTAAGGTTTCGCTGAAACCCACGC[A/G]CGGATCAGCCTCTCG
TP43129	TGCAGCC[C/T]CGACCGCAGCGCCTCGTACACCTCCTTGACGAACCGCTGGCCTTCGGCCACGTCAT
TP43130	TGCAGCCCCGACGAGGTGGTCTTCGC[C/G]GCCGCGGACATCGCGCAGTCGCTCTACTGCCACCTGC
TP43132	TGCAGCCCCGACGCTGTTCCCCCTCCTCCTCCCCACGCAGCA[C/T]CCGCAGGTCCACGTCCACGAC
TP43154	TGCAGCCCCGCACTCTCATGGTTGGGACTCTAGTGAAGC[A/G]TCGGCGGCGCGCAATCACCAAATC
TP43156	TGCAGCCCCGCAGCTGGGCCTGCGCAAGGTGAACACAAGA[G/T]TTAGGCGACGGCTCCATTGAAGC
TP43165	TGCAGCCCCGCCAGGTGGCCATCTGGTTCCAGAACCGCCGCGCCAGGTGGAAGAC[C/G]AAGCAGCT
TP43175	TGCAGCCCCGCCG[C/T]GGCTGCGACGACCCCAACTTCCCCTACTACCTCAAGGTCCGTGTCCCCAT
TP43183	TGCAGCCCCGCCTGTTCGGCAAGATCGTCCCC[G/A]ACAAGTGCAGGTTCGCCGTGCTCTCTACCAA
TP43187	TGCAGCCCCGCGACCGCCGCGCCGTTCCCCATCTCCACCGC[A/C]GCGGTGGCGGGGGACGCCGCCT
TP43219	TGCAGCCCCGCTCCTGCACCCACCAAACTGCATGCCTCTTG[C/T]CCCATGCCCGCATCCGCGCCAC

Table A2 (cont.)

TP43225	TGCAGCCCCGCTTCCCCTGTTACACGAGGTGCGTGCCGTGGTCACTGG[C/G]CGCTGTTCGCGAGCG
TP43234	TGCAGCCCCGTCCGAATCCCGCGCCCCCTCTGCTTCCTGCTCTTGCATGCGTGCGGGG[A/C]CGTGC
TP43240	TGCAGCCCCGTCGCCATCGCCTGGCAAAGCGGAAGCAAAAGAACAGAGC[G/T]TGTCGTCAAAGATG
TP43241	TGCAGCCCCGTCGGGCGC[A/G]CAGGCCATCCCTGGCGGCGCGCAGCTCATCCCCGCCGAAAAAAAA
TP43252	TGCAGCCCCGTGAGGTTGAAGCAGGTGTCCAAGA[A/C]CGAGAAGCTGGGGGCCTTGCTGTACCCGA
TP43254	TGCAGCCCCGTGCAG[C/T]GCTGGTGCATGCGCGCGGCACCCCGTGAGCATTGCCAGGCGCGGTGCT
TP43257	TGCAGCC[C/T]CGTGGCGGAAGACGGCAGTGGCGCTATGCCACGGTCGAACACTGGGCGCGCCGCGT
TP43265	TGCAGCCCCGTTGCACTGGCAAATTGATCAAGGATC[A/G]TTCTCAGGCTTTGGACATCTGTGAGCT
TP43275	TGCAGCCCCTACGGCAGCTGCGG[A/C]GCCTACGGCTACTGCGACAACACGCTGCCCGTGGCGACGT
TP43285	TGCAGCCCCTATCAATGTCCAGCCTGAATGAATCCAGCAGTGCGATGTTGCA[A/G]CGGAGCATGAG
TP43313	TGCAGCCCCTCCCTCCCAGCGGATGGCGCTCACCTACCTTCCCTTCAACGCCGCGGC[A/G]TCGCCA
TP43315	TGCAGCCCCTCCGATTTGTTGGGATTTTTGTGGGGAT[A/C]CCCGAGTGGAGGACTGGAGAAGTGGA
TP43316	TGCAGCCCCTCCGCCGCC[A/G]CCCATCAACTGCTCAATGAAATTCCAGTGAAGACTTCTATAGTGG
TP43327	TGCAGCCCCTCGACGACTGCCGCACCACTAATGTTATTGCTGGCAAGCAGGGCGTC[G/T]ATCTTGG
TP43329	TGCAGCC[C/T]CTCGAGACGGAGGGCAAGAAGGGCGCCACCAAGGAGAGCATCAGGGGGCAGATCAC
TP43335	TGCAGCCCCTCGCAGCCGCAATTCGCA[C/G]CGTTGCGCGCTCTGCTCTTCGCCCCGTTTGCGCCGC
TP43341	TGCAGCCCCTCGCTTCCCGTTCCTCCATGGCCACAGGAGGCAAA[A/C]GTTGCAGTTGCCATCTCCC
TP43343	TGCAGCCCCTCGGC[A/G]ACTACGGCTTCGGCAAGCGCAGCGTCTGGGAGGGCGGCGTCGGCCTCTT
TP43381	TGCAG[C/T]CCCTGCCGCAGAAATCAATCCTCTCCAGAAAAATAATCACACCCCACCATCAGTCCTA
TP43394	TGCAGCCCCTGCTGCCTCCCTCGACCTCC[C/T]TCTGTCTTCCCTCCCCTCTCGTAGCGTGCTCCTC
TP43400	TGCAGCCC[C/T]TGGAGCTCGAGCTTGAGCTCGAGCGTGGAGCGGTAGGAGGTGGCGCGCCAAGCAA
TP43422	TGCAGCCCCTTAGTGTTGCGCCTCCTTCATTGCCAGCCACCCGCTC[C/T]CTCTTCGCCACTTCCAC
TP43429	TGCAGCCCCTTCCTTGGTTCAGTAT[A/C]AGCACAAATTGCATCATTCATTTATGATATGCTTGAAT
TP43440	TGCAGCCCCTTGCTGGCCT[G/T]TGTCGATATGATTTCCGTTGGCAAATTGGCCCCCTTGAATTTTC
TP43464	TGCAG[C/G]CCGAACTCGCCCTCCAGGTCGTCGACGCCGTCCTCCTCCTCGTCGCCCGCCACGCGCG
TP43470	TGCAGCC[C/T]GAAGGGATGCAGTGGCAAGGCCTATGCTTCCCCCCGCAAGACTGCTAGGGTCGTGT
TP43489	TGCAGCCCGACCCACTCGCGCGG[C/T]ATCGGCAACGCCATCCTCTCCCTTCCCTTGCCCTGCCACA
TP43514	TGCAGCCCGACGTCGGAGAG[C/T]GCCAGGTTGTCGAGCACGGCGCTGAGCGGCGCCAGCGCGCGGA

Table A2 (cont.)

TP43516	TGCAGCCCGACTATGCCTCGAACGGGCACATCGGCATCTGT[C/T]ATCAGCTTTTGATGGGTCCAGT
TP43537	TGCAGCCCGAGCCTCAGTGGCCACGTGGCCTCGGTAGGCGCGGCTGCTCGCGCTCAA[A/G]CCTAAT
TP43541	TGCAGCCCGAG[C/T]GCGGCCGTAGCGGCGACGGGCGTCTTCTTCCGCCAGGAGAACGTGGCCCTCG
TP43547	TGCAGCCCGAGCGTGAGCGACACGCCGCCAGAACCA[C/T]CGCCACCGAACCCGCCAGCTGGCCCGC
TP43549	TGCAGCCCGAGCGTGGTGGTGGCCGTGGCGAGCAGAGGGGG[C/G]AGGAACGAGTCGGAGCATTTGG
TP43551	TGCAG[C/G]CCGAGCTCGTCCTCCACGTCGTCCGACGCCGCGATGAGCAGCAGCTGGCACCCCTCGT
TP43552	TGCAGCCCGAGCTGAGGTGAGCTGATTCGGCGGGCTCTGCTCCACATCCACCCGCCTTC[G/T]CCCA
TP43573	TGCAGCCCGAGTACTGAAAGACTGATATGCATACTGTATGCGGCGG[C/T]GGCGTACAGAAGAAAAA
TP43578	TGCAGCCCGATCACGATGGCCGCCCCGCCCATGAACCC[C/T]ACGATGGCAGCGTGCGACAGGAAAT
TP43587	TGCAGCCCGATT[A/C]GCTAATCGCGACCCCTCGAGAAGCCTCGTCGTACTGGTTTGGGGATTTTGG
TP43593	TGCAGCCCGCACAGCCCAAATAGCAGAAGCGG[G/T]CCTTCCTCTCTCCCGACTGTTCGGTTCGGCC
TP43600	TGCAGCC[C/T]GCACGCGGCTGCCGCCTCGAGTAGAGAAGAAAAACTCAACTGCGCTGAGGGGGACG
TP43603	TGCAGCCCGCACTCGTCCGCCGAGCAAGAAGCGCCGAAGTACCACGAAGACAG[C/T]AGGAACACCT
TP43604	TGCAGCCCGCACTCGTCCGCCGAGCGAGAAGCACC[A/G]AAGTACCACGAAGACAGCAGGAACACCC
TP43615	TGCAGCCCGCAGCTAGGCAAAAGG[C/T]GCTGGGGCAGAAAGGTAGGGTGCGTCCTTGCGGACGCAG
TP43620	TGCAGCCCGCAGGCCATAAGCCAAAGCCAACGTCTCCT[A/G]CTCGTACTACCAGTCGTCGCAACTG
TP43631	TGCAGCCCGCATTCCGCGAGGTCGAGGGTGGTGACG[C/T]GGCCGTCAGCGGTAGCGCAGGCGACGC
TP43635	TGCAGCCCGCC[A/G]CGGACGCCGTTTCATCACGTGCTCTGGCCCCACGTGTAAGTGGCGTATTAGT
TP43639	TGCAGCCCGCCAGGAAGACGCGGGACAGGTCGGCGTGCTCCAGCAGCCACGG[A/G]TCCTCGCCGTC
TP43660	TGCAGC[C/G]CGCCGCTGCCGCTGCCGCGCAGCGAGGGTAGGCATAGGTATCACGCGGGGTCGGTGG
TP43661	TGCAGCCCGCCGCTGCTCAGTTGCACTTCTCCATCCACTACGGGAGAC[A/G]CGCTCTTTGCCGAGT
TP43662	TGCAGC[C/G]CGCCGTCGTGGTCGCTGCCGCTCTCGGACGCCATGTTGCTCGCCATGGCGCCCGCGC
TP43667	TGCAGCCCGCCT[C/G]AGCACTCTGCTTCGGCGCTGCCCGCCAGCCCAGCGCCACCGCGCTGGCCCA
TP43694	TGCAGCCCGCGCCGCGCCGCTCTCCTCGGCGGCCGCCGCCTTCCGCC[G/T]CACCAGCCCGCTCCTC
TP43712	TGCAGCCCG[C/T]GGAGCCAGAGGTGTTCGACGACGACGACGAGGTGGAGCTGCCCTCTGGCGAAGA
TP43717	TGCAG[C/T]CCGCGGTCGATCGGCAGCAGCGAGTTCCTCAACCCCATCGCGCACGAGGTCGTGCTCA
TP43721	TGCAGCCCGCGTAGCTGACGAGGGGCGGATGGGATCAGCGGACCTGCCAATCTAGGAAGCAGG[C/T]
TP43727	TGCAGCCCGCGTCGCCGAGTCGTGAGGAGTAGCCTCGCCGCAATCATCC[C/T]GACGAGCTGCACGG

Table A2 (cont.)

TP43740	TGCAGCC[C/T]GCTCGTCGCTTGAGCGACGTTCCAAATCGTTACGGCCACCATGCTCGCGTAGTTCG
TP43755	TGCAGCC[C/T]GCTGGTGGTAGCAGGGGCATTGAATCCCTGCCTGATGGAGTCCTTGAACACATCCT
TP43826	TGCAGCCCGTCTGGCG[G/T]CCGCGATCACGTATCGCACGAACTGTCGTGCCTTGAGCAGTTGTTGA
TP43853	TGCAGCCCGTGGAGTGG[C/T]GTGGGGCGGCGCAGCAGGCAGCACTGAAGAAAGCTTGAATACCAAC
TP43872	TGCAGCCCGTGGCTCTGCGGCCTCTGCTG[C/T]GGCTCCCCCCGCTCGCCCTCCGACGATAGGCACG
TP43885	TGCAGCCCGTGGGGCGGATGGTGCTCAACCGCA[A/T]CATCGACAACTTCTTCGCCGAGAACGAGCA
TP43889	TGCAGCC[C/T]GTGGTGTTGAGTACATCCACTCAACGAGCTCAACGGCTTCCCACGGTAACATCAAG
TP43892	TGCAGCCCGTGTGCAACCTACCTCAACTTCAAGTGTGGTAATGCCAGGACCAAGTCCCAAC[C/T]CT
TP43895	TGCAGCCCGTTGCTGTCACTCGATAAAATGGAATGACCGTCACTTCGCTCACTTGGCACGCTT[A/G]
TP43931	TGCAGCCCTA[C/T]CTTTCGCCGCCGCCGCACCATCGCCCGAAACCCCAGCCCCCTTCGGCGCCACC
TP43988	TGCAGCCCTAGAGTTCACGTAGCGCTACAGTAAC[A/G]CGGGTACTGTTCACACGAGGGAGAGGGCA
TP44003	TGCAGCCCTAGAGTTCCGT[A/G]GCGCTACAGTAACGCTGGTACTGTTCACGCGAGGGAGAGGGCAG
TP44016	TGCAGCCCTAGCGCAACGAGCTTCTTCGACGCTACCTCC[C/G]CTTCTGCTCTCACAAGCCCAGGCT
TP44017	TGCAGCCCTAGCGCGACGAGCTTCTTCGACGC[T/C]ACCTCCGCTTCCGCTCTCACCAGCCCAGGCT
TP44018	TGCAGCCCTAGCGGCCAGCCGAGTGGAATCTTCTCTCTC[C/T]GTCCCTCGTCCAGCACTCCATCGC
TP44021	TGCAGCCCTAGCTCCACAGATAAAACCCCACCTCCTCCCGTCGCCCACGCCTC[C/T]CTTCCCTTCT
TP44040	TGCAGC[C/T]CTATCCAAAAACGACGGGCAACTTCCTCCTCCCGCTCCCGCTTGGCTTCTTCACCAT
TP44074	TGCAGCCCTCAACGTGATCTCCTCCCGCAA[A/T]CCCGTAGCCCTCCACGTATAAGTGGATCTCCAC
TP44100	TGCAGCCCTCATCCCCCGTGGCCCGTC[A/G]AAGCATGAACCATGAAGCCGCCGTCGCTGACGCAAA
TP44113	TGCAGCCCTCCAGAAATAGG[G/T]CCAGAGCAGAAAATATCCCTTCCCTGCCCAGCTGAGTAGTGCG
TP44126	TGCAGCCCTCCCAGCCCAGCGC[A/G]CAGGTCCGCCCCTGAGGACGATAGGGAACAAGAATAGGACA
TP44127	TGCAGCCCTCCCCAGACCGTCTTTTTTCACCGAATAATTTTTTACCCACCTGC[A/G]TACACACAAC
TP44131	TGCAGCCCTCCCCCACCCACGTGTGGGCGACTG[C/G]CGAAGGACTTACCGTGTTCCGAAGCCGAGA
TP44176	TGCAGCCCTC[G/T]CCAGCGTGATACGCTTACGAGATCTGGCCTCTCTTTCTCCTTCCCGTACAAGC
TP44178	TGCAGCCCTCGCCCCAG[C/T]AGATTGGACGCACGTCACGCACGCAACGCATCTGCCTCATCTGAAC
TP44179	TGCAGCCCTCGCCGTGGTGTTTGCTGA[A/T]TTTGAAATGCGCGGAGGAAAGCGGGCGGACTGGTTG
TP44190	TGCAGCCCTCGGTCTCCATGCCT[A/G]CGCCAAAATCCTACTGCCCCTTGACCTCCAACCTTACCGC
TP44195	TGCAGCCCTCGTCGCCTC[G/T]CTTTGCTGTGGTGTTGGCTGATTTTGAAATGCGCGGAGGAAAGCG

Table A2 (cont.)

TP44199	TGCAGCCCTCT[A/G]ACGAGTCCATGTCGGGGCGGATCCGTGCTAGCTCCGCGCCGCGGACGGGGAG
TP44221	TGCAGCCCTCTTCCTGC[A/C]CCCTGCTCTCAGCTGCAAAACAAGAGAGATAACGACATGCGTGTCA
TP44230	TGCAGCCCTGAAGCCCACATC[A/G]TTCGCTAGCCTCAAGAATCTAAAGAAAAATAAGACCACACAT
TP44242	TGCAGCCCTGACGCTC[C/T]GCGCCGTGCCTCTGTTTCCTCTTTCGCACCTCCCTTTTCCTCCTCCG
TP44244	TGCAGCCCTG[A/T]CGTAGGAGAGCGCGGCCAGCGACGCGGCGGTGACCGCGTCGTAGCCCTGCGGG
TP44250	TGCAGCCCTGATCGAAGCCCACATCGTTCGCTAGCCT[A/C]AAAAAACTAAAGAAAAAATAAGATCA
TP44252	TGCAGCCCTG[A/G]TCTCCACGTAGGAGACACCGCTTGCCTCTCTGCTTCCTCCCTCGGCCTCGAAG
TP44274	TGCAGCCCTGCACTGCACCCTGCTGGGCTGCTGCCTGCCATTGGCCATGGACGACGTCGGTA[C/T]G
TP44324	TGCAGCCCTGCTCCT[C/T]GCCGCCCTGGCACTCATGCTCGCGGCTTCTGCGCCGCAGGCCCAAGCA
TP44331	TGCAGCCCTGCTCTCCTCCTCCACCTC[A/G]ACAACGACGCCACCGCGGGCTCATCTCATCAGCTTG
TP44375	TGCAGCCCTGGTCCCTGGAA[G/T]GCCAGCAGCGCGGGGAGTAGGCGCCGCTGGAGCACACCACACC
TP44378	TGCAGCCCTGGTCGTG[C/G]GCCGAATTAGAAGGGAACAGGTCTTCAACACCCAGCCCAAATCGAGC
TP44388	TGCAGCCCTGTATGGAACTCCTGAGAGTGCCCTTGGGTAGCCCTTTGTTCGTT[G/T]CTGCATTTCG
TP44391	TGCAGCCCTGTCATC[C/T]CGTCCACGAAACGTACGAACTACGGACATCGACCCCATCGCCAGCGGC
TP44432	TGCAG[C/T]CCTGTTACTCCAGTTGGACGGATCGGTTCCCCATAGTGCTTGCCTTTGCTCGGGGACG
TP44443	TGCAGCCCTTAGAGTTAGCACTATTTTTATTTT[A/T]TTTTGTTTTATTTATTTATCGATATATAAT
TP44459	TGCAGCCCTTCCTCGACGTCGTCCTCTCCGAGGA[C/T]GCCGACGTTGCCGTCACCTCCGCCTCGCT
TP44467	TGCAGCCCTTCGATGTTGCTCGGACGGTGGATGTGGCATCCTG[A/G]CAGGGAAAGTCACGGCGTAA
TP44483	TGCAGCCCTTGCATGTAGGCTCTCAATCTCCTGCTCCCT[G/T]GCCCGTGCCACCGAGTTAAGTTCA
TP44511	TGCAGCCCTTT[C/G]ATCATCAGCAGCAGTAGCATAGGCACCTAGCTAGGTAGCGACCGCGACAATG
TP44548	TGCAGCCGAAATTCTCTCACAGTTGAATGTACAAGAAGCAAAG[C/T]AGCTTAAGCGAACGGGCCTT
TP44553	TGCAGCCGAACACA[A/G]TGGCAAAATCATTGCGTTCCGTGGGACGGGACGCCCTGGGCTGGGCGGT
TP44558	TGCAGCCGAA[C/G]ACCCCCGCAGCAATTTTAAAGGAGCACTGCTTTCGTACTAGTAGTTGCAATGC
TP44560	TGCAGCCGAA[C/G]ACCGCCGTTGTTCACTCGGGTCAAGAGGTTGCATAGTTCCCCGCCTTGCAAAA
TP44591	TGCAGCCGAACGCTACCAAAAGCACT[A/C]CCAAATCCAGGCAGCAGCATGCGCTCGTTCCGCGCAA
TP44603	TGCAGCCGAACTGGAATCGGGCTC[G/T]GCTCAAGGGAAATTGCACTGCCTGTAACGATCGTATCCA
TP44614	TGCAGCCGAAGCCAATCATTTGAACTCCTTTCGCTGGCC[A/G]TATCCAAAATTCCAAACACCATGG
TP44618	TGCAGCCGAAGCCCCCA[C/T]CTTCATCTCCTTGCCCTCGGCGCACTCTTCAACAGCTGCCCCAGCC

Table A2 (cont.)

TP44623	TGCAGCCGAAGGCTTGGCTGAAGA[C/T]GGCGGGGAATTGGAGAAAGGCACCAGCTTGGGCCACGGT
TP44649	TGCAGCCGAATCGATCAGAGTCAGTCATGGCTAGCTGTGCACACGTCAA[A/G]CACTGTAGAACCTG
TP44659	TGCAGCCGACAATCGAGCGGACAGA[G/T]AATCGGTCAGATGTGCCGAGCCCAAATGACGAACGCGC
TP44683	TGCAGCCGACCACAAGTTTTCTCTAGGGCGTACTAGTAGTAGTAGGCTGCCATGT[C/T]GGCGAAGA
TP44690	TGCAGCCGACCAGCAGCTGTTTACCAGCACGTTCAAGTGTCTTCAGCCACCCTCCT[C/T]CATGGCA
TP44705	TGCAGCCGACCTGCAAGAGCAGGAGCAGCTTCTGGAACGCCCCAACCCGCA[A/G]CGCCTCGACAAG
TP44713	TGCAGCCGACGA[A/T]GCAACCGTAGGCAGGCATGCTGCAAGCAGCAGCAGCCGTCGCCCGTCGGCG
TP44744	TGCAGCCGACGGTACCATCCCCGAAGAGGTGA[G/A]CTACCAGCTCACATCGGCGCCGATCGAATCT
TP44750	TGCAGCCGACGGTTCCTGACCTTGGCGCTCTC[T/C]GTGCGCGCGCCGCGCCTCGCCGTCGCCTCGA
TP44805	TGCAGCCGAGCCACTGCGGCTCGACCACGGCGCCCTCAGATAC[C/T]ACGCCGCAACGATGCGGTAC
TP44820	TGCAGCCGAGCGACACGTTCCCGCGGCGGCACAACTCGGCC[A/C]CGCCCGCCGAGCAGGCGGCCAT
TP44824	TGCAGCCGAGCGCACCAA[C/T]AACAATTGCTCGGCAACCCCGCAGGGCTGGGTACGTACTTGTCCG
TP44831	TGCAGCCGAGCG[C/G]GTGAAAGCGCCTGGAGGCGGATGCACCAGATGTTATCTGTTGTCCACGTGG
TP44836	TGCAGCCGAGCGGCGCCGTGCCCGTGTCCGTCTCCAGGA[A/T]GGCCCGCTCGTCGTCCGTCAGCGG
TP44839	TGCAGCCGAGCTAGA[C/T]GGCGACTCATGGGATCGTCGAGCGCAGCATCTTGCAGATGCAGGCGCA
TP44854	TGCAGCCGAGCTGAGCTGCATGTGTGGGCGTAGCCG[C/T]GTCCCGTCTCCCGTCTCTGCTCTCTCG
TP44866	TGCAGCCGAGGAGGCGGTGGATAAGCAGAAGCCGCCGT[C/T]GCTGAAGCTGCACATGAACCGCCGC
TP44871	TGCAGCCGAGGATGATGATGCA[A/G]CAACCCTCGCCCTATCTTGACCTCCATATGCATGTAGACGC
TP44877	TGCAGCCGAGGCGCCCACACCCCGCTCCTCCAATC[A/G]CAGGTACCCAAAACCCACGGTCATCTGC
TP44880	TGCAGCCGAGGGCAAGGGCGCAGGGTCAGCCACGGTACA[G/T]ATCGGAGCCGCTGCCGCAAGTGGG
TP44882	TGCAGCCGAGGGCT[A/G]CCGCAAGGCCTTCATGATAGAAAGTTGTGGACAGGCCAGCCGTGGGGTC
TP44906	TGCAGCCGAGTGAGTCACAGATTCACAACACACGACAGATTCATGGACAGTTGTACA[A/T]GCCTGC
TP44908	TGCAGCCG[A/T]GTGCTGAACCGCCCAGCGCCTGCGTGAGCACCATCACGAGCATCAACAACAGCTG
TP44913	TGCAGCCGATACAAAATGTGGCTCCACATGAGGAGGTCATCCAA[G/T]CACCTGCTAACTTTGAGGC
TP44916	TGCAGCCGATACTACCTCGGTCTTGGTCTCT[C/T]GTTCAGCTCCCTCGGCCTCGTTGGGAGTGGGC
TP44923	TGCAGCCGATATACACGCAGGATGCAAGCAGTGCCCCTTGTGCAAAA[C/T]CTAAGGGCACATGAAT
TP44930	TGCAGCCGATCATCTTCTCCACGTACGAGGCCAAGAGCGACGCCCTCAAGAACGCGCACCT[C/T]TC
TP44934	TGCAGCCGATCCATGACCAATGTTGCGCCCTGCTGCACCACTGCACGCACGAACCCGATG[A/G]CAT

Table A2 (cont.)

TP44966	TGCAGCCGATGCCATCACCGCGTCTGCTGTCTTATGGTCGCGCACA[A/G]CCTCCTTGTCATCGCAG
TP44970	TGCAGCCGATGCCTCCTGCGATTCAGTTGCATCG[C/T]GTATCTCTTCGATGCATGGCGCACTTGGA
TP44971	TGCAGCCGATGCGATCGCAGATTAATTACTCGGGGAAATCGCCGATCATGCG[G/T]GGGCTACCTCG
TP44999	TGCAGCCGATTGCAAGCGATCTTGCTCAGCGCCTGCACAGG[A/C]GAAAAGGGATCGATCGAATTGT
TP45006	TGCAGCCGATTTGTTATCGATCAAATCGGACGGACGGGCAGGCGGGCTTCC[A/G]AAAACAAAACAT
TP45025	TGCAGCCGCAACCTGCGCGCTAGCTCACGACCAGACGCGAGTACGCGACATTATTATCCGCCA[A/C]
TP45026	TGCAGCCGCAACCTGCGCGCTAGCTCACGATCAGACGCGAGTACGCGAC[A/G]TTATCCGCCAAGGC
TP45030	TGCAGCCGCAACGCGCTGCCTAGTGTCT[C/T]CAGCTACTGATGAGATCGCCATTGTTTCTTTGTGT
TP45036	TGCAGCCGCAACTCTCGCGCGCGGGTGGAGTAGTACGGGGTAC[C/T]GTCTCCTGTCGGTGGGGTGG
TP45046	TGCAGCCGCAAGCAGATGCTGCGCGATGATGGTGCCATCCTCCTGC[C/T]GCTCAAGCTCGGGCACC
TP45052	TGCAGCCGCAATGGTAGGAGAAACGTCGCAGA[G/A]GAGAGAAAACATCGTCGCCACGCGTAACTCG
TP45066	TGCAGCCGCACAGCACCGTGGA[C/G]TCGACCTCCATGAGGACGCACCTCCCGTCCCTCCCCCGCAG
TP45078	TGCAGCCGCACCAG[A/G]CCCTTGAGCGCCCGCAGCGCCCGCCGAGCCTGCGTTTTCCGAAAAAAAA
TP45080	TGCAGCCGCACCAGCCCCTTGAGCGCCCGCAGCGCCCGCCGAGCCTTTACCAACGACGAACAC[A/G]
TP45082	TGCAGCCGCACCAGCTCGGCGACCTCCGC[C/G]GCGGCCGCGGCCGACGGCGACGCCGCGCGGGGCC
TP45104	TGCAGCCGCACCTACCTCCTTGACGTTGATCCATGCGTGCACGTCAATGCTGGCCCATGCCCC[C/T]
TP45119	TGCAGCCGCACGCGCAGGGGCTTTTCTCCCAG[G/A]GCAATGCGGTCGCGCCGCAGACCATGCAGCT
TP45120	TGCAGCCGCACGCTGGCCTGCGAAGCCGC[A/G]CGCCGCGCGTGGGTCCACAGGCTCTGCTTTTTTT
TP45122	TGCAGCCGCACGGCGAGGCGCTCACCTTCGAGGACGGCAACGTCACCCTCGTCGGTACGTACA[A/C]
TP45124	TGCAGCCGCACGTCGGCGTCGGCCTGGACGAAG[A/G]CCACGCCTTCCGCGGTGCAGTCCACGACGA
TP45145	TGCAGCCGCAGCAACAGGACGGCCTCGGCCTC[G/A]GCCTCCTCCTGCCGCAGCTTGGCGTCGAGCA
TP45155	TGCAGCCGCAGCA[C/G]CGCCGCGCCATTATTGGTCGCCCGCCGCGGAGCTCTTCCCGCCACCACCA
TP45158	TGCAGCCGCAGCACGTCAAGTTCG[A/T]CCAGCCTTCCAAGTGCTTTTACCTAGGGTCACTAGCACT
TP45175	TGCAGCCGCAGCCACAAAAATCACAGCCGAGCACAC[C/T]CATTGACTAATTGAGGTGTGTTGAGTA
TP45180	TGCAGCCGCAGCC[A/G]CCGTTCGCAGGGAGGAGAATGATCTCCCCCGAACAGGAGCACCAAGTCAT
TP45184	TGCAGCCGCAGCCATCAGCCATGCAACATGTCTGAATCTTGTTTCATTCCCATTTGAACTCG[C/G]T
TP45191	TGCAGCCGCAGCCGCAGCCAACGCCGTCGGTGCTCCAAGGAGATGGTCCGAGCGCTGCTAC[A/G]CC
TP45204	TGCAGCCGCAGCCGCTGCCCCTCCTCGTCCTTGGCGGCGGAGCAACAAGCGACA[G/T]CACCGATGT

Table A2 (cont.)

TP45210	TGCAGCCGCAG[C/G]GGTTAGGCAACAGTCCCTTGCGCGTTCACAACAGCGGGAGAAGGGGAAGCAC
TP45221	TGCAGCCG[C/T]AGGAGATGAGGTGAAGTGTCTGCAACTACTGGTACGAGGTGAAGATGCTCTCATA
TP45224	TGCAGCCGCAGGCAATACGA[C/T]AGAGAGCCCAACCTCCACGGCCAATTCCACTTCGAGCCCGACC
TP45230	TGCAGCCGCAGGCTCTGGTGCGT[G/T]CGCCGACCGCATGCAGATGCAGAGGTGGCAGTGACGGTAC
TP45241	TGCAGCCGCAGGGCGGCC[C/T]ACCTTCCTCGGCTCCCTCGGCTGCGCGCGAGGATTTGGTCGCCCA
TP45243	TGCAGCCGCAGGGTCTTGAGGTTCCCACAGAATGCTAGGGC[A/G]GCAAGCCACCCGCCGTCCATCC
TP45249	TGCAGCCGCAGTGCAGCTAGC[C/G]CAACCAGACAGGCTAGACATTGTTGACATATCTGATTTGATA
TP45261	TGCAGCCGCATATGCCGTCGCCGACATGCA[A/G]CGTGCGCCCTTGTTGGCTTGTCGAGAGTACGTA
TP45262	TGCAGCCGCATATGGAGCTGGTTTCTTCGGTCCCGCGTTGAATTTTGCAGCTGTGCCCCA[A/G]CAG
TP45267	TGCAGCCGC[A/G]TCCAGAAGTTGCCCCTCTTCGCCTTCCTCTCATCCTCCCCCTCCCGCTCCTGCT
TP45271	TGCAGCCGCATCCTGCTCCCATTCTCGTTTAAGGCGAGTGAGGTAGTGCTCTTT[G/T]GCCTTCTCC
TP45298	TGCAGCCGCCAAGCTTGAATCGATGGG[C/T]GTGGCCATCGGAACTGGACCCCGAGGTCCAGCGTCG
TP45299	TGCAGCCGCCAAGTAG[A/G]TCCTTCACCAGATCTGCGGTGCTGCCTCCTGAGCCTGCTGACCGCCG
TP45343	TGCAGCCGCCACTCTGTCTGGCTGACCACCTTCGTCGCTGTTCTCTTCGCCGACCCCAGCCCA[C/G]
TP45371	TGCAGCCGCCATCAAGAACCGTCTGCGCGATCA[A/G]GCCCATGAGCCCGACGCTGCCGCCGCCGTA
TP45374	TGCAGCCGCCATCGGGTCCGAACGCCGCCGCCGACGCCGACGCGGCCCATTCCAACTCTC[G/T]CTC
TP45391	TGCAGCCGCCATGTGGAGGGGCGGC[A/G]CCACCGCCACCTCCACCGCGAGGGCTCTCCGCTCGCGC
TP45393	TGCAGCCGCCATGTGGAGGGGCGGCGCCACCGCCGCCTCCGCCGTGAGGGCTCTCCGCTCG[C/T]GC
TP45423	TGCAGCCGCCCCGTTAGGCCAGGCACAAGCCGCACAACAACCAGTTGAGGCGCGCCGCGCGA[A/G]G
TP45424	TGCAGCCG[C/T]CCCTACAAATATGTTCATTGTAGTAGTGGAGGCCAGCTGGGCGAACTCCTGCTCC
TP45444	TGCAG[C/G]CGCCCGTCGCTGCCGCCCCTACCGACCCGCGGCCGCCGCTCCGTCGCCCGCTGCGCGC
TP45465	TGCAGCCGCCGAAGCAGCCATGGAGGTACAGCAGCGTGC[A/G]CTGCACGGTTGGGCGCAGGCCGAG
TP45470	TGCAGCC[G/T]CCGAATCCAATGCCAAGAAAGTTCTCTCGAACCGTGCCGAGTGGCGAGTGTGGCAA
TP45497	TGCAGCCGCCGCAGCGGCGGC[A/G]GCGGCCGCTGCGGCAGCGGAACCAGCTCTCAACCTCCCCTTC
TP45504	TGCAGCCGCCGCC[A/G]AGACGAAGATGCCTGGCCACCGCCGAGTCGTGTGCGACGAACTCGGTTCG
TP45519	TGCAGCCGCCGCCGATCCTG[A/C]ATTTGTTTGGTTTGAGAAACGTCTCTGTTTCTTAGATAGTTCC
TP45536	TGCAGCCGCCGCCGCCGCCGCCATCTATACGCATGCCAG[C/T]GCACCTCGACACATCTTATCCGTA
TP45542	TGCAGCCGCCGCCGCCGCCGC[C/G]GCGGCGTCACGGTGGCTTCCGTGGATGAGGATGAGCTCCTTC

Table A2 (cont.)

TP45554	TGCAGCCGCCGCCGCCTCAAAAGTCAAGCCCCACCGCGT[A/C]TATAAAAACGACCGCCTGCCGCCG
TP45555	TGCAGCCGCCGCCGCCTCAAAAGT[C/G]AAGCCCCACCGCGTATATAAAAATAGAAACGACCACCTG
TP45556	TGCAGCCGCCGCC[G/T]CCTCCTGCCGCTGCCCCTCCACTCCCCAGCCCCCCCGCTCTTCCCACTTC
TP45563	TGCAGCCGCCGCCGCGGCGG[C/T]CGTCACGTCATCCTCGGCGGCGTCGACGCTGTCCCTCCCGCAG
TP45569	TGCAGCCGCCGC[C/T]GTCGCAGGTCCAGGTCCGCCGCGTCCCCTGCCTGCCTGCCTGCTGCATTAG
TP45572	TGCAGCCGCCGCCGT[C/T]GCTGCCGTGGTGGACCGAGCCTACGGACCACTGGGCCTAGGGCGGGCC
TP45575	TGCAGCCGCCGCCGTGGTGACCGCCGCCCCCACCCCCGCCGTGCCA[A/G]TCGTTCACGCCGAAAAA
TP45582	TGCAGCCGCCGCGCACGCCCGAGCCCCGTCCACGGGGCCCAACCGTATCTCCT[A/T]AACCTCCTGC
TP45605	TGCAGCCGCCGCTCTCTCCTGTCGCCTCG[C/G]CCGCAGTCCGCGAGCGCGCGCGTCGCCACCCGTC
TP45607	TGCAGCCGCCGCTGAGGCTTTTCGTGGTGGCGAGGATGTTCCAGAGGCGCTCAC[A/G]GAGTTTCCT
TP45612	TGCAGCCGCCGCTTC[G/T]GTCCTCTTCCAGATGCGCGTGCCCTCGCGCTGCCTCGGTTCCCCGCCG
TP45636	TGCAGCCGCCGTCTCTCCTCTTCTGCTTCCTGCACTCGATGAACAT[C/T]CGCCGCTTCACATCCAT
TP45641	TGCAGCCGCCGTGGAGAGGGAGGTAGCCGCCGCGCAGGAGAAAAACCCT[C/T]GACTCGCGAGTCGC
TP45646	TGCAGCCGCCGTTGGTGTCTGCGCAGCGCCTCCTGCCGCTCCCGTCGGT[A/G]CCCATCTGCCCGTG
TP45649	TGCAGCCGCCTACGTCCATCAGTGCGAAGGTCCTGTGCAA[C/T]GCCGCCGCGGATGAAGTCCTTCT
TP45650	TGCAGCCGCCTACTACTACTCGGCT[C/T]GGCTCCCCGCACGAGGCCGCGACGGGCACGTGTCCCGA
TP45656	TGCAGCCGCCTCAGGAGCTGCTGGTTGGCGGCACGGAGCTTCTTG[A/G]CCTCCTCTTCCAAGCAGG
TP45665	TGCAGCCGCCTCCGCAGCAGCCTTGGCCCGCTCTTCCTCGGCGC[A/G]CCGATTCACCCTCTCCGCC
TP45674	TGCAGCCGCCTCGCCGTCATTGCCCTTGTCGG[T/C]AGGGAAGTACCGCGGGTAGTGCTGTGAGAGG
TP45687	TGCAGCCGCCTGCATGTC[A/G]CGGGCACTAGGCTGGAAGCCGCGTCCATCTAAGGCGCTGCTGCTG
TP45689	TGCAGCCGCCTGCGACCCCGCGATGCTT[G/T]CGAGCTCGCCGTTGGTAACGCCGACCATGACCTGG
TP45690	TGCAGCCGCCTGCGCCTGCGGTCTGCCACACACGTCCGCACGGTGCCACACTACCGCCTGCCG[A/T]
TP45697	TGCAGCCGCCTGCTTGATCAGCATCAGCAGTTCAGCACAAA[A/G]TCATTTCTGACAGCGGCAGCTC
TP45702	TGCAGCCGCCTGTAG[A/G]CCAAAGGCCATAGCCGCCATCAGAATTCAGAAAGGGTTCCTGACCAGG
TP45706	TGCAGCCGCCTGTTCTGGTCGGCTTGTCTCCCTGGCCGCCGTCGTTGGAGATAGCGG[C/T]CACCAG
TP45713	TGCAGCCGCCTTGC[A/T]TGCCGCCGCGGCCCGCTCATCCTCTTCCGACGGCGGCGCGAAGACGAGG
TP45717	TGCAGCCGCGAAAGAACCATATCACGACCAAATCACG[C/T]GAACCATATCATGACCAAATCACGCG
TP45740	TGCAGC[C/T]GCGACGCGCCAGTGCTGCTTGCTGGCGGGGCACTGTGCGGCAGATCTCGTGAGGTCA

Table A2 (cont.)

TP45743	TGCAGCCGCGACGGCAATGGCAGAGGCGCAAACCCTAGCAACGTCA[C/T]AGGGCCCAGAGGTGGAG
TP45745	TGCAGCCGCGACGGCGGCGAGGAGCACGACTTGTTCCGCGCGGTGCAGCTCAGCGACCTGGA[C/G]G
TP45746	TGCAGCCGCGACGGT[C/T]TGCTCGAGGACGGGCTGCGGTGCTTCGACCGCATGCGGCTGGAGCACA
TP45748	TGCAGCCGCGAGCACGGGCCAAGCGCGCCGCGCGCTGCCGCCCTGCCT[A/T]GCCCGAAAAAAAAAA
TP45753	TGCAGCCGCGAGCGAGCGCGCAGATATCAGCCCCGCCCTTGGGCGCCCCCGC[G/T]CCGTCGTCGCT
TP45771	TGCAGCCGCGATTCATTCACCTGTCCCTTCACAGTATACTATAGTACGA[C/T]TCGGGCCATGGCAA
TP45779	TGCAGCCGCGC[A/G]CGGGGACACTGGTCGTCGGGCGCGAGCGCGTGCCCGTCGTGCGTTTGCAGCC
TP45795	TGCAGCCGCGCCATCGCCTGCATGCAGTGGATGGCCACC[A/T]CCGCCTGCCGCCGCACGAACGCGC
TP45803	TGCAGCCGCGCCCGCACCGTGTGCGACGACAGCTCCGTCGGGATGTTCGTGCACTCCTTCG[C/T]CC
TP45805	TGCAGCCGCGCCCGCGCGCGTTAC[C/G]TGCGGTGCGGTGTGGGCGTGCGGCTGCGGCCTAGAGATA
TP45813	TGCAGCCGCGCCGCCTGGTCCCGCACCCACGACTCCA[C/T]GCGGCTCGCCAGGGCGGCCGCCATTG
TP45826	TGCAGCCGCGCGACGCTGCGCTCGGCGCAC[G/T]CGCCGACGCATGCGGGGCGGCAGGGCCGAAAAA
TP45830	TGCAGCCG[C/T]GCGCCCACCATCCTGGCGCGGTCGTACCGCGCCCGCACCACCTCAGGCGGCCTTG
TP45831	TGCAGCCGCGCGCCCGTCCGCTCGTCCAGGGACAGCTCCACGGTCCGCCCGCCGTCGCGGAAC[C/T]
TP45834	TGCAGCCGCGCGCGCGAGGGGGGTTCGCCGTTTCCT[A/C]TGCCACCGCCGCCGCCGCCGCGAGATT
TP45839	TGCAGCCGCGCGGCGTCCCGCAG[G/T]TGTCCCCCAAGGATGGCCATCAGTCGCGCGTCCGAAAAAA
TP45845	TGCAGCCGCGCGGGGTCCTCGCAGATGAGGTCCCACACGGGGTAACCCCT[G/T]CGCGGCATCATGA
TP45846	TGCAGCCGCGCGGGTAAGAT[C/T]AATGTAGTAATGCGGTGCACTCTTCTTCGCGGATAATCAATTT
TP45847	TGCAGCCGCGCGGTCTGCTCGAGGATGGGCTGCGGTGCTTCAACCGCATGCGGCT[A/G]GAGCACAA
TP45868	TGCAGCCGCGGAGCAAGACGCCTCGCGAGGCACTTTGCAAATAACTTACTGAAACTATGCAT[A/G]A
TP45874	TGCAGCCGCGGCAAAATCGCATCGGCCTCCCTCTCTCTCGACCAGCCGTCGT[C/G]GTCGACGTCGA
TP45889	TGCAGCCGCGGCCGCCGCGGAGGCGGCAGAGGAGGCGACCAT[A/G]GAGGAGATGGAACCGCTCTCC
TP45901	TGCAGCCG[C/T]GGCGCTGCGTGCTGAGATGGAGCTAGAGCTGGAGCCAGCGGGAGGAGGATCATGC
TP45904	TGCAGCCGCGGCGGCACGCGTCCTTGCCACAGTGGTCCAGTAGCAATGTCAC[A/G]GGCCACAGCAG
TP45905	TGCAGCCGCGGCGGCAGGTGGAGCGGCAGCA[A/G]GTTGCCCTTGTAGAACAGCTCGTCCGCCGAAA
TP45913	TGCAGCCGCGGCTACTGCTGGAATGGCATGAAGGTCTCCGTGCTCGTCCAG[C/G]CGCCGCCCGCGT
TP45917	TGCAGCCGCGGCTGCTCCGCCATCACGCAGTGCCGCAGCTGAGCCAG[A/C]GCTGCGAGCGAGACTG
TP45920	TGCAGCCGCGGGACGACACGGCCATAGCGTACCACAGCGATGGCGACTCCTTCCAAGTCATCG[C/G]

Table A2 (cont.)

TP45926	TGCAGCCGCGGGGCAGTCCACGGGACGCGTAGC[A/G]TGGTGAGGCTCCTACATGACGGCCACGTAA
TP45937	TGCAGCCGCGGTCGTCTCCTCAGATCGCAGGTTTTCGAGTGGCTCCCGTCTCGAAAAAAA[A/T]TCT
TP45940	TGCAGCCGCGGTGGAGCCGCAGCGCC[C/G]CTCCTGCGATCTCTTCCGCCACGGTCAGCCTGGACTC
TP45944	TGCAGCCGCGGTTTTGCGTTAAAACAAGGATTAAGTCCCCTCAACTA[C/T]CACGATGGTCTAATTT
TP45946	TGCAGCCGCGTACGCTGCCTCTACCCATCCCCGCTCCCTGCGGCCGCACACGCC[A/G]CCGCTCCCC
TP45950	TGCAGCCGCGTATCGTCGTCGTCCGTCGTCTCGGATCCCTCTCTCTCTCTTGGCGTTTACTGC[A/G]
TP45973	TGCAGCCGCGTCGTTTGGTACTTTGGGTGATGGTGGCGGTGCTGGCGGTGGTGTCATGGCG[A/G]AC
TP45974	TGCAGCCGCGTCTCCCCGACGCCCAGGCCCGC[A/C]GACATCGCCGTCATCAGACGCCCGCACAGCG
TP45977	TGCAGCCGCGTCTTCACGGTGTCCAGCGGCATGGTCACCAGCGCCG[A/C]GGCGGCCCCGAAAAAAA
TP45998	TGCAGCCGCGTGCTTGCTGGTGCTTGGCACCATTGATGGCG[A/G]CACTTTCCTGGACGGCGGTTGC
TP46009	TGCAGCCGCGTGTGC[A/C]CGCGGGGGAACGGGCGGAGGCCTAGTTATAGTAGGCGGCGGCGGGCTA
TP46017	TGCAGCCGCGTGTTGATCTCCCGCTCCAGCAGCTCGCCGAAGCTGCT[G/T]GGGCTGGACCGCGCGA
TP46019	TGCAGCCGCGTTG[C/T]GTTGTTCAGAGTTTGAGTTCTTCAGCGAGGTACTGCATGCCCAAGTGCAA
TP46021	TGCAGCCGCGTTTCAC[A/G]GCAGAGCCCAGCCGCCCAGCATGCGCCGCTCTTCCTCCCCTTCTCCC
TP46031	TGCAGCCGCTAGACCTGCCTACATGCATGTGGATGTGGAGGGGGCACGAGCCGTAGGCAC[A/G]GGA
TP46060	TGCAGCCGCTCCAGCACGTTGCCCGTGTCGATGTCCTC[A/C]AGCAGGCTCTCGTGGCAGGCCTCCC
TP46064	TGCAGCCGCTCCAGCGCATGGACGATGGCCACCATGCGTGGCCTGTCCCGCAGCTGCTGCGCC[C/G]
TP46066	TGCAGCCGCTCCCAATCCGCTGCCGCCACTCCCGTCTCCTTCTCCTCTCGC[C/T]GCCCGTCTGCGC
TP46071	TGCAGCCGCTCCGTGTCGAAGCGCTCGGGGCTCATGTACGCGGGCGTGCCCTCGTAGGC[A/G]GCGC
TP46116	TGCAGCCGCT[C/G]CTATAGTGGCCACGCCAGGGTCCCACGTGTGGAGCCTCTTCTACAAATGGAAC
TP46119	TGCAGCCGCTCCTCCGC[A/G]ACGCGCATGCCACGCCCTGCGCCGCCGCCGCCGCCGCAGGCCTCGG
TP46214	TGCAGCCGCTCGACGGCGTTGGCGGG[C/T]TAGCAGTAGCAGGCGGAGGAGAGGCCGCGTCGGCGGC
TP46231	TGCAGCCGCTCGCTCGCTCGATCTCCCAATGG[A/C]GCGGGGACAAAGCTCGTCGGAGACGCAGAGG
TP46234	TGCAGCCGCTCGCTGGCGTTCGTCCTGTCCAAT[C/G]GGGATCGCTGGCGTGAAAGGATAGCTACCT
TP46238	TGCAGCC[G/T]CTCGGTGATCCACTCGTCCGCAGCTCCGTTGCCGCCCTCAGCCCTGTACCACGCTT
TP46239	TGCAGCCGCTCGGTGGCGCCCCGCTTCGTTCGAACAACCGCCGATCGAGGC[C/T]ATCAAGGCGGAG
TP46250	TGCAGCCGCTCTCCCCCGTGCGCCTCCGCCTCG[G/T]CGGCGGCGGCAACTCCTCGTCCGTGTCGGC
TP46288	TGCAGCCGCTGCACTCGC[A/C]TCTGCTGTGTGCAGACCACCCTGTCGCCTCATACCCATGTGCAGC

Table A2 (cont.)

TP46296	TGCAGCCGCTGCCGCAGGGACAAGAAGGCGGCCAAGGAGCACGC[A/G]CGTGAGATCTCCGCTAGGC
TP46298	TGCAGCCGCTGCCGCGCTGACCAGCGAGCGCCGTGGGCAGGGCGCA[G/T]GGCACCGAAAAAAAAAA
TP46303	TGCAGCCGCTGCCTGTGCCTAAGGCTTCATGGGAAATCATTTCGATGGACTTCGTTGAGGG[C/T]CT
TP46307	TGCAGCCGCTGCGGCAGCACAAGGTGGAG[A/G]AGCTGGTGCGCTACGTCTCCGAGCGTGCGGCACT
TP46309	TGCAGCCGCTGCGGCAGCACAAGGTGGAGGAGCTGGTG[C/T]GCTACGTCTCGGAGCGGGCGGCGCT
TP46313	TGCAGCCGCTGCTACGCCGTCATATGGCGACCTCCACGACGCGGCCGCACGG[C/T]GGGGGCGTCGA
TP46327	TGCAGCCGCTGGAGC[A/G]ACGGGCCGCTGGTGTGAGCTTGGTAGATGAAATAGTCGAAGTCGTAGC
TP46333	TGCAGCCGCTGGATCCAGGTACAAAGCTTTGTATCCACTCCAAGCTAAGGCAG[A/C]CTATCTCTAC
TP46338	TGCAGCCGCTGGCGTCGGAGACACTGTCGCTGGTCTCCGCCT[C/T]GCTCTTGACCGACGGCGCGTG
TP46355	TGCAGCCGCTGTCCATGGACGCCCACGGGGAGGGATGGGAGGTGATG[C/G]TGGAGCTATAAAATGC
TP46361	TGCAGCCGCTGTGCACGCTGTTGCCCAAACTCGCTGGACTTCTCCAACAACAACCTGTCGG[C/T]GG
TP46365	TGCAGCCGCTGTGCATGGACACGTCAAACGCCCTCCGTC[A/G]TGCAGAAAGGCAGCGAGAAGAAGA
TP46368	TGCAGCCGCTGTTCGCCGCCGTGGAGGCCGACGTGGCAGCGCGGTGGCC[C/G]TGCGCCACGCAGGA
TP46375	TGCAGCCGCTTCACGATCTC[A/G]TACTTGTGCTCGGGGAAGACCCCCGCGAAGCCGTCGGCCTTCT
TP46377	TGCAGCCGCTTCAGAGGTGAAAGGGGGAGAGGGATTGTTTCAGGT[A/G]GGCAGGACGTACCCTTCT
TP46383	TGCAGCCGCTTCCCTCCCTCCCCCACGCGTCGGC[A/G]GCACCGTATCACGCCGCACACTGGTCACC
TP46385	TGCAG[C/T]CGCTTCCTCTGCCCCATGGAGAGCATCCTGGCCTTCTCGTTCATGAGCCTGCCGAGGC
TP46427	TGCAGCCGCTTCTTGCTGAACGC[A/G]CCTGGCGCCGTCGCCTGCTTGGATGTCGTCCCAGAGCACG
TP46430	TGCAGCCGCTTGAGGGGATCGCGGTGGAGAG[A/G]GCCGTAGACGAGGTGAGGGGATGCGCGTTTGA
TP46442	TGCAGCCGCTTGCTGTGCAGGCGCTTGAACTGGTTGGCCACGTACTTGAGGTCCTC[C/G]GCGCGGA
TP46449	TGCAGCCGCTTTAAGTATGGATCACGTATTGTTCTAGCACTGGATATG[A/C]GAGGGGGAGGCGTGT
TP46494	TGCAGCCGTAGCGGC[C/G]GATACGTACCACCCAAGATTTTTTTTAATTTTAACACTTTTGATAAC
TP46510	TGCAGCCGTAGTTGTCGACGCGGAACGCCACGCCGCCGTCCGCGCCGTACACCGT[A/G]CAGCCGTT
TP46517	TGCAGCCGTATTCATACGTACGTGAAGGTTCGGACATTTGTGGTAGCT[C/G]ACCACATCACTGTCA
TP46538	TGCAGCCGTCATTCTTGGTCCGCACGAGCCTGTGGATCTAGGGGTGGGGTCCAACCCTTG[C/T]GTG
TP46545	TGCAGCCGTCCACCATGGCCGCCGCGAGCTCCTCGCAGTGGCCAGCCGTCTTGGGTTGTT[A/C]TCT
TP46550	TGCAGCCGTCCAGCCAGGCTGCC[A/G]CCCCCTCCCTGCCAGCCGCTGCCGCCAGGGAGCTGCCGCT
TP46557	TGCAGCCGTCC[A/G]TTTTGCATCGTGCCGCTGCCGCTGCCAAATTCTCATACAGATGTTGTCTGAT

Table A2 (cont.)

TP46583	TGCAGCCGTCCTCCTGCT[A/C]GCCGCGGCCGCCTCCGCCCCGCCCCCGCGCCCCGCCCGCGCCGAG
TP46596	TGCAGCCGTCGACGGGGCACCCGTACGGCGCGTGGCGGCAGCTCTCCT[C/T]GTGCGTCCGCTTCTG
TP46613	TGCAGCCGTCGCCGTGCTTTGCTCTGCTTCTTCCCCGCCGCGCGCTGCTC[A/G]TCTCCGCCAGAGC
TP46619	TGCAGCCGTCGCTACAAAAGACAGCG[C/T]AGCCGCTGGTCCATCCTTCCGCCATGCCGCAGCCGCT
TP46621	TGCAGCCGTCGCTACTGCCGTCTTTGCTGGCCTCAAACTCTGGCTGCCGCGG[A/G]CAGTACAAGGT
TP46624	TGCAGC[C/T]GTCGCTCGATAGAATTTCCGTTTCGGCTGCCTCGACTTTCGCGTGCGTCGATGGCAA
TP46631	TGCAGCCGTCGGAGAG[G/T]CCCGCCAGGGGAGAGGGAGCGGGTGCGGTCGTCGTGGTGGCTGTGCG
TP46632	TGCAG[C/T]CGTCGGAGCCCCCGAAATGTCCCTAGCCCAGCGGTGGTCGTGGCGCAGAAATGCAGAT
TP46635	TGCAGCCGTCGGCAACCAGAGAGGGTGGTCTC[T/C]CTGCTCATGGGCTCCTTCAACCTTTCAGGGC
TP46639	TGCAGCCGTCGGCGCGTGCGATGCTCTCCGACGGTCGGCGCATGCAAGGCTATGTGA[G/T]ACGGCA
TP46644	TGCAGCCGTCGGTGAACGCCAGCCTCACGCACGTGCTCAAGTACCTCAACGGCTCCGTCA[A/C]GAC
TP46659	TGCAGC[C/G]GTCGTTGACGTGCAGCTAGCTTGCACGTCTGGTTCGTCTATTCGTACGCGTCGGTTC
TP46664	TGCAGCCGTCTCCATGGCGA[C/T]GGCGTAGCGCAACAGCGGAAGTGGAAGCTAGGGTTCTGGGTTT
TP46700	TGCAGCCGTGAGTCCCCAACGGCCGCGTTCGCCACGCACCAGCTCGCCTTCGCGCCGCC[A/G]CCGC
TP46712	TGCAGCCGTGCAACTG[A/G]CACGGAGGCTACACCTGCGTGTGGGGCCCACGCGGCCGTTCCACTCC
TP46719	TGCAGCCGTGCACGCGACTGGAACGCCTGGC[A/G]CGCAACGGCTCAAGCCAAGCGGCTGGCCGTGG
TP46729	TGCAGCCGTGCAGGCGAGAGGCGAGAATGTTTGGGAAGCAGAGCAAG[A/G]AGCGGTCAGCTACCAA
TP46745	TGCAGCCGTGCCTCGGCCATCGACAGCGCCATGGTAGCCTTCTGGAC[A/G]GCATCCTTGGCGTCTG
TP46751	TGCAGCCGTGCGCCCAGTTGCTGATCTCTTTGGTTCAGAGTGCCTATAG[C/G]CGAATGCTACGGTG
TP46769	TGCAGCCGTGCTTGCTGGGATGATCGCCTTCCACGGCTACCCTTCCTCGATCGTGGAGGA[C/G]GAG
TP46771	TGCAGCCGTGGAACAACGGCGCCGAGAACACCAAGCCAG[C/T]AGCAGGCGTCGTCATGCGGGGCCA
TP46774	TGCAGCCGTGG[A/G]CCGTGGTCCCAGAGGTTTGGAATTGGAATTCGCCTGATGCGAGATCCGACGG
TP46793	TGCAGCCGTGGCTGAGGTCGCTGCGATCCGACGCCGTCGGGCTC[C/T]CCGAAAAAAAAAAAAAAAA
TP46807	TGCAGC[C/T]GTGGTAAGCATCACAGACAAATTGAACAAGCGCCTCAAATGGTTGCGAGCCATCGAC
TP46813	TGCAGCCGTGGTCGCTTCCAGACA[A/T]CCGAGGTTGCGCCATGGATGTTCCTCGATGCCGCCGCCG
TP46816	TGCAGCCGTGGTGGGTGCCGT[A/G]GTGCATACCTTGGATTGCCAGGCAGTGACGTCGCTGCGGCAG
TP46818	TGCAGCCGTGGTTGAGTAAACTGAGGTGTACTATGTACTATGTG[A/G]AGATGCTTTTTTGACTGAA
TP46844	TGCAGCCGTTCCAGGCCGAGTGCCGCACTCGGTCAGACCGAGTTCGCTGGGCAGGAGGCCC[C/T]AC

Table A2 (cont.)

TP46847	TGCAGCCGTTCGACGATTGCAACTACGGCTGGCGCGTCCTCGAC[A/T]GCCGCCATGGTCGTGTCCT
TP46848	TGCAGCCGTTCGCGACGGCGAGCATGGACTGGAAGGAGACGCCGACGGC[A/G]CACGTGTTCATGGC
TP46863	TGCAGCCGTTGCACATTG[A/G]CGCCAAGTTTTTGACTTTGCATCTGAAGGGACACGTGTCGGGACA
TP46867	TGCAGCCGTTGCCCTCCCACATTTTGCATACATGTCAATAAG[A/C]GCATTGCATATAATGGTGTCA
TP46876	TGCAGCCGTTGGGGAAGGCGCAGAA[C/G]ACGCCGTCGCCGCGCGGGTGGACGGCCATTCTGTACGG
TP46898	TGCAGCCGTTTCTCT[C/T]CCGCAGGCAGAAAAACGCGGAACGGGAGAAACGTGTTGCCCCGCTCGC
TP46904	TGCAGCCGTTTGTAGCGCCGCTCAAGACGCTGGAGCTCTCTGGCACGAACCTCACCC[G/T]CGCTAT
TP46921	TGCAGCCTAACCTTATATAGAAGTAGAACCG[A/C]GACGAGACCGCAGGAGAAGATGAATATGGAGT
TP46982	TGCAGCCTA[C/T]AGGGGCACTGCTCATCCGCTTGGTGGTTGGGTGCCTGGCGCTTGACGCTCTGGC
TP47038	TGCAGCCTACGGTGGCCGACGAGGCGACGACGAGGAGAGACAAGACCGACGGTCAA[A/G]GCAGGCA
TP47054	TGCAGCCTACTCACCAGATTCCTCTTCCAGGGGAAGTA[C/T]TCCATGTCGACCTTGGGCTTGGGCA
TP47091	TGCAGCCTACTGCCCCATCCGCCCTCGGC[A/C]TCGGGAGGCTCAGTCGCGTCTCGGTCTCGCGGGG
TP47125	TGCAGCCTAGAGGAAGTGTACTTACCTTGTCGGC[C/G]TCCACGGACTTGATGGTGACTTGTGTTTG
TP47132	TGCAGCCTAGATCCGACCACGATGACCCAGAT[T/C]GACACGAGCTGGCGGCGTACTTCGGGAGCGC
TP47170	TGCAGCCTAGCTAGTTCGGACCCATCCAATCT[G/C]GGACTAATCATAGTCGGCGACCGTCGACGGA
TP47178	TGCAGCCTAGCTTC[A/G]GCCATATCCTTCTGCGCCTTCCTTCGCCGATAGAAAATCGGACAATCCC
TP47233	TGCAGCCTAGTGTCCAATTTCCTATTGCATTTTAACTAACCAGCAGTTT[A/T]GCATTTCCATCCAA
TP47252	TGCAGCCTATATGACGATCGAGCCGCCCGTGTAGTTACATAGCTAACCATCGTCAC[A/C]CATGCGG
TP47253	TGCAGCCTATATGCAGACGACGTCA[G/T]AATGTTCGTCCATCCAGAGGCTACGGAAGCTGTGGCGG
TP47259	TGCAGCCTATCATCTTCTCCACCTACGACGTACGTACGTCGTCGT[C/T]ACGAACAATTCAGCTGTA
TP47268	TGCAGCCTATCGCCTTGGGCAATACAGGCGATCGACAAGAGGAGACGCGCCTTCCTTTGG[G/T]CAG
TP47315	TGCAGCCTATTCTCTGGTCACCACAGTTGCAGCTCCCAAGGGAGCAATCC[A/G]TCCGTGCCTGTCT
TP47332	TGCAGCCTCA[A/G]AGTGGATGCGACCACCAGGGAGAGGACGGCGAAGCAGGAGGGGATCAGGCCCG
TP47348	TGCAGCCTCAAGAATGGCGGACACGAAGAGCAGCGCG[A/G]GGAGAGGCACCATGAACACAAGCTTC
TP47349	TGCAGCCTCAAGACCTCCTAGCTAGCGCTGCGGCCGCGGCAC[G/T]TGTGGTGGCTGCCTCCTAACG
TP47351	TGCAGCCTCAAGAGGACACCCAGAAGGTCCTCG[C/T]CTCGCTCTGGCGTCGGCATGGCTTCACGCT
TP47353	TGCAGCCTCAAGATCCTTTCAAAAGTTCTAACCAGAAG[A/G]CTACAAGATGACATTCCAAACCTTA
TP47374	TGCAGCCTCACATATAGCACA[A/C]GTGGTCAGATCGAAAGATGGATCTAAAATATGCACACAAATT

Table A2 (cont.)

TP47404	TGCAGCCTCACCTGTCAGTGCTCCC[C/T]CGACGTCTTGGGTTCTTGATTCAGGAGCTTCCTTCCAT
TP47413	TGCAGCCTCACGTGACCCCGCTCCTAAACACCCGCGGCG[A/C]GGTCGCCGTGGAACTTGGAACAGC
TP47417	TGCAGCCTC[A/C]CTACTCTAATAGGTTGGTACTTGGTACCTGCAACGAAGCCGCGCTCGTCTCATC
TP47442	TGCAGCCTCAGCCATGATGACTGAGTGAGCGCC[C/T]GACATGATCGCCCTGATGTTGATTGTTTGC
TP47450	TGCAGCCTCAGCGCCGCCGCCTCGTGCTTGGGGCTGTCCGCGGCC[A/G]CCGAAAAAAAAAAAAAAA
TP47479	TGCAGCCTCATCGCTCGGT[A/C]CCCGAAGTGGCGAGGACCCCAGCGGCCAGCGCCCCCTCCCGCTC
TP47488	TGCAGCCTCATCTCCTCGTAGAACCGCTGGATGAAGCGCTC[C/G]GCGCGGCCGTCCACCTCCTCGT
TP47527	TGCAGCCTCATGCTGGCGGTGTCGGCGTCGGCGTCGG[A/G]CGGCGGCGTGGCCGACGACGGCGTCG
TP47555	TGCAGCCTCCAATGATAGGCAGCACGGTTATTGCCGCCCCAGTAGGCCTAGACGGGTCATC[A/C]TC
TP47566	TGCAGC[C/G]TCCACCCTAGCGCTTACCTCGACAACTCGTCCCAGTGCGGCCGCGGCGCCGCGGACT
TP47576	TGCAGCCTCCACTAGGTGATCGATGCATGCATATGGTCATCTTTAGTTTATACTGCTAGCTC[C/T]G
TP47599	TGCAGCCTCCAGTTCTAGGTCTGGTTCTCCTGGTTG[A/C]TTACGGCTGTTCAAACCCTGGTTCGAG
TP47611	TGCAGCCTCCATTCTGTCGCCCCTCCGCGACACGGGCTC[A/C]TCGAAGCCGCGGCCCTCGTCATCA
TP47619	TGCAGCCTCCCAAGATCGCGAGGCACGAAGCCGCTGAATCCGTTC[C/G]TTGACAGCTCGAGTTCTC
TP47627	TGCAGCCTCCCATCACCATGGCGCCGTTCGCGCCACT[G/T]CCGCACAACACCTGCAAGCACGACGT
TP47629	TGCAGCCTCCCATCCAGAGGCAGCCC[A/C]AACTCCTTCCTGCCGCGGAGCTGCTCGTCGATCACGG
TP47638	TGCAGCCTCCCCATCATCGACGTCCTTGGGCTCCA[C/T]TCCGCGGGGCAGTTTCCAGTCGAAGTGG
TP47639	TGCAGCCTCCCCATCGAGCTGCCACGCTTGGAACCACAGCAGTCGTTGGCACCTT[A/T]ACTCTTCA
TP47640	TGCAGCCTCCCCATCGTCGACGTCATTGGGCTCCATTCCG[A/C]TGGGCAGCTTCCAGTCGAAGTGG
TP47649	TGCAGCCTCCCCGCGCCACGCGACCGCAGGACGAGGAAGCAGCTGCCTA[G/T]CAGGCTAGCTCCGC
TP47660	TGCAGCCTCCCGACCCCAAACCCGTCGACCATTTCATCCACCGCCTTCTGCTCCCCGATGGTG[G/T]
TP47676	TGCAGCCTCCCTCTCTCTTCCCGC[A/C]CCATCTGGCCAGGCCATCTCCCTCCCCAGGCCTTCAAAT
TP47706	TGCAGCCTCCGCCTCGTCCTTCCACTTGGCCGCGCTCTTCCGCATCTCCTCACTTGCCATCG[C/T]C
TP47723	TGCAGCCTCCGTG[A/C]ATCCGCCCATGATGGCAGCTAGTCATTGCCCCCGCCAAACATGGCTGGCC
TP47726	TGCAGCCTCCGTGGCAC[A/G]TACGTGTCCGTAGTCCACCCACGCATGAGTCGCATTACTTACAAAT
TP47737	TGCAGCCTCCTCATCGATGGCGCAGTGGGGGCTGACATCATCCT[A/C]GGCTTCTTCTTCAGAGTCT
TP47752	TGCAGCCTCCTC[C/G]TCGTCGTTGTCGCCACCGCCGTCGTCTCCGTCGTCTGCACTTTCGCCCCCT
TP47769	TGCAGCCTCCTCTCAGCAGCAGGGCTCCGTGCTCCGTGCTGGACACAGGAAAACTCTGCGTGC[G/T]

Table A2 (cont.)

TP47771	TGCAGCCTCCTCTCCCACGAGCTCGTCCTACGAGACAGCGACCG[C/T]GGCCGCGGACCCGACCTCA
TP47772	TGCAGCCTCCTCTCCCCGTCTGGCCGTCTCGCTCTCGTCCTC[C/G]TCGATCTCCGCTCTCGCCTCG
TP47777	TGCAGCCTCCTCTCGGCGAGCGCGTGCTCCAGTTCCGTCACCCTGGCG[A/G]CCATGCCATCCTCCG
TP47783	TGCAGCCTCCTCTTCCATCCGAGAGCATGGACGGCGGCGCCATGTCCCTTGCTGCGGCGGCC[G/T]C
TP47792	TGCAGCCTCCTGGCATCCAGCCAAGCGGCGGCGTCGGAGAGCCCAACAGAGACAACCAAA[A/G]GGA
TP47794	TGCAGCCTCCTGGTCAACTCTACTTGGTTGGGCTCC[A/G]TCGTGTGGAGACCTGAGATCAGTGGTC
TP47825	TGCAGCCTCGACCGCAAGGACTC[C/T]ATCCTCGCCGCCGTTCACCTCCTCCGCCGCTCTATGGCCT
TP47836	TGCAGC[C/G]TCGAGCCCGAGCCTGTCGATATGGCGGCGGAAGAAGGAGATGGGCAAGGAGGGCCTC
TP47840	TGCAGCCTCGAGGAGCCGCCGTGCCGCCCTCCCCTCCGACGCGCGGGCTAGATTTGGGTG[A/G]CTA
TP47849	TGCAGCCTCGCAAGCGACGCATCCATGCCCAGT[A/G]GCATGTTGACCCACCGCAGTGCGGGTACAG
TP47851	TGCAGCCTCGCA[C/T]ATGGCCTTCACCATGGTCAGCTTGGTCTCCAGTTCGCTCAATAACTCCTTG
TP47871	TGCAGCCTCGCCAGATTGCTCGGCAGCCAGCGATG[C/T]TGGAACGGTGGGCTCCGCTACCGACGAG
TP47894	TGCAGCCTCGCCTCACGGAGTCCCAGGGAATGGAAGCACTGTGATCC[A/G]CTCACCACCACCCCGC
TP47895	TGCAGCCTCGCCTCGGCCATCGACAGCGCCATGGTCGCCTTCTGGA[C/T]GGCCTCCTTGGCGTCCG
TP47908	TGCAGCCTCGCGTACACACTC[A/C]TGAATCTGCCGAGAAAATTTTGGAAAGATACAACGGAGATTT
TP47910	TGCAGCCTCGCGTGTTCTAGTGCTGCTATTTGCAAGTGCAAGCTCAC[A/G]GTAATGCTCATCCTCA
TP47948	TGCAGCCTCGGCGCACGCACTACGTTTATCGA[T/C]GGGCCCCAGTTGATGTCGTGCGCCAGCAGCC
TP47980	TGCAGCCTCGTAGCTCGATCTCTAGCTTCAACTTC[A/C]CAGCTGTGTTAAGCGATCCATAAGCCAT
TP47986	TGCAGCCTCGTCCAATCCTATGTGCTGCAACGACCAT[C/T]TTTCATGGGGCTCGCAGAACCAGATG
TP47999	TGCAGCCTCGTGGACCCGACGGT[C/G]ATGCCCTTCAGCGACAGGTAGTAGAAAGATGGAATTTTGG
TP48026	TGCAGCCTCT[A/C]GTCTCTGCCTCTGTCTCCTCCCTCCCTTATCCTCCTCTTCTACCTCCACCTGG
TP48032	TGCAGCCTCTCAACGGCCGCCATTGCCGCCGATCCATGGAGAGGAGACG[A/G]CGGAGGGACCAGGG
TP48047	TGCAGCCTCTCCAT[A/G]GTGTCAGGGTGCAGTGCGACGACGGAGTTATCGTCGTTGGTGGCCTCGT
TP48056	TGCAGCCTCTCCGCCAGTGTCTCCATGCCAAGGAAGGACATGAGCATCCAGACGTAG[C/G]AGAGGT
TP48062	TGCAGCCTCTCCGTCCGTCGTCGATGGACCACC[A/G]ATCCCCGCCGCGGGAGCTGCTGCCGCCGTG
TP48070	TGCAGCCTCTCCTCTTGATGTTTGACCTCTCCGCTCACTCTTTCCTACCTTGGC[A/G]CAAGCAGCG
TP48073	TGCAGC[C/T]TCTCCTTGAGATTGGCGCCTTGCAGTTTGTGCAGCTGGTGCGTCTCGTCGAAGGTGA
TP48080	TGCAGC[C/G]TCTCGAGACGGAGGGCAAGAAGGGCGCCACCAAGGAGGACATCAGGGGCCAGATCAC

Table A2 (cont.)

TP48081	TGCAGCCTCTCGCAAGTCGAAACTCGCCAGAAAGGG[A/T]AACCGCATCTGCTCCCCTCTCCCGTCT
TP48095	TGCAGCCTCTCGTGTTGTTGACCGA[A/C]GAATTATATAAGCACATGCTGCGTTCCACGGTTCAAGT
TP48109	TGCAGCCTCTCTTCGTTCTCTTGCACACACC[C/G]TACTCACACACACTAAGCCGCTCAATCTCATC
TP48132	TGCAGCCTCTGCGAGTGTAAACACGAACCTGCCATGTTGGCGCACTCCA[C/T]CGTGCACCGTTGAC
TP48135	TGCAGCCTCTGCGTGCGCGCGCAGGTGGACCATCGCGTGCACCTGTTCGCGG[C/G]CAGCAGGGAGC
TP48139	TGCAGCCTCTGCTCCGCACCGCCGCACCGCGTT[C/G]CAACTTGCAAATGCTTCAAGCAAGGTACTA
TP48172	TGCAGCCTCTTCAACCCCACGCCGTCGCTGTCGGCCAT[C/G]ATCGTGAACAAGTACAAGCTCCGCG
TP48175	TGCAGCCTCTTCCTCTGCCTCTCGCTGTCCACGCTGCTGG[C/T]GCGTGCCGCAACGCGTCGCCACG
TP48196	TGCAGCCTCTTGGAGCTGACTCCCTTCTCGTCTTCCATCTGAA[C/T]AAACCTGCAAATGGTCGTCG
TP48202	TGCAGCCTCTTGTCGTCCGTAGTGCCCGTCTTGTGGACAGCCTTCTTCTTCCTATAAACCCA[A/G]A
TP48228	TGCAGCCTGAACG[A/C]TAGTTCACATGCATGCGTTTGTTTGCAGCATCTACACTGTTTTGAGGTGC
TP48234	TGCAGCCTGAAGACGGGTGACGACTGCGTCTCCATCGGCCAGGGCAACGACGACGTGG[A/G]CGTCG
TP48243	TGCAGCCTGAAGTGCAGTCGTGTACTCGTGTCTTCGCCAGGGGCAGGACAAGCGCCGC[A/C]ACGCT
TP48257	TGCAGCCTGACAGCCTCGCACGGTCGCATCC[A/G]TACGTCGGAGCCACCGCTAGGCCCACAGCCGC
TP48280	TGCAGCCTGACGGCCGCGGCCTGGTGCTTGGGGCTGTCCATTCCGACCAT[A/G]GGGTAATCATAAT
TP48287	TGCAGCCTGAGC[A/G]CAATGGCCAAGCAGCCTGGGCTCCTGATTTACCGTGCCTGAGGCTTGGAGT
TP48297	TGCAGCCTGAGGAGAGCGTAGATGAGCGCGGCGAGAGCAATGGAGCCCGCGGTGA[C/T]GAGCCAGC
TP48304	TGCAGCCTGAGTCCATGTCCCTTGAGCGCGCCCTCGAGGTCTGACTGGAGGAG[G/T]ACGCAGGCAT
TP48314	TGCAGCCTGAGTTGGGC[A/G]CCAGCAGCGATCAGTGTGTGTGTCAGGCCGAAAGCGAAAGCGGTGC
TP48321	TGCAGCCTGATCCGTCATCGACCAATGCCAATCAG[C/G]CAATGGCACCATGCAGGTCAACAGCAAC
TP48324	TGCAGCCTGATGAGCGTCGTCAGGTCCACCGCCTTGCCCAGCACCTTGTA[C/G]TGCTGCTTGTTCT
TP48330	TGCAGCCTGATTAACCCGCTCCGA[C/T]CCCTAATATCGTCTTCGTCCAGGTCTCCACGAAGAAGAA
TP48331	TGCAGCCTGATTGCTC[C/T]TGCTCTTGCTGCTGCTGTCCCAGAGCACCTGAACACTCGCGGTCGCG
TP48334	TGCAGCCTGATTTCACTTCAAATCGCGCCAGCCAATGCGATAGATAGGAAAGAA[A/G]CTATGTGAA
TP48338	TGCAGCCTGCAACAAGCATCACTGCATGCCAGCATCCACGTAGCAGCTGAGCTCATGG[C/T]TCAGA
TP48339	TGCAGCCTGCAACAAGCATCGCTGAATGCCAGCGTCCACGTAGCAGCTGAGCTCATGGTTCA[G/T]A
TP48341	TGCAGCCTGCAA[C/T]ATCAACACCAGAGATACAAGCAGCAGGACTACAGGGATGAGCTTGGGCTCC
TP48353	TGCAGCCTGCAAGCGAGGCGGCTCAAATGAAGAGAGCATGCGTGCGCACGCACCAGGGAGG[G/T]CC

Table A2 (cont.)

TP48356	TGCAGCCTGCAAGGCATTCATCAGAGCCACCTCCGATCCTATCGCATGCAGCTGTGTCAGCAG[C/T]
TP48373	TGCAGCCTGCAATG[C/G]CCTGGTGTTCGTGTACTCCTACTTCACTTTCCAGTAATCCAGCCTCTTG
TP48387	TGCAGCCTGCACCCACCGCCAGCGGCGGCGTGGCCT[A/C]CGCGGACGGCGCCGCCGCCGTGCTTCC
TP48401	TGCAGCCTGCACGAAGGCTAGGTCCCTGCTACAACCTGAGCTCCAAATCGAGCTCCTCGG[A/C]GCT
TP48408	TGCAGCCTGCACTAATGT[G/T]GAACCGCTTTCACGATCGCCGTGCGTGGGCCATGGCCATAAACTT
TP48416	TGCAGCCTGCACTGCGACGCGCACAAATAAAAAATTGGCTCTGCGAGCCTGCTGGCCTGC[G/T]AGG
TP48421	TGCAGCCTGCATACTCGCTCGTGGGCCAAGAAA[C/T]TTTAGAAACAGATCTTTAGACCCAGCCCAA
TP48423	TGCAGCCTGCATAGTTACAGAGAGAAAGAAACAAAGCAAATGGGATGGAGAGGGAGAGGGAGA[C/G]
TP48427	TGCAGCCTGCATCAC[G/T]CGTGCTGTTGTGCGCCTGCAAGTACACCCAAGTGGCTGGAATTTTTGG
TP48430	TGCAGCCTGCATCCATAGAACCACCATTCT[G/T]GTTGAGGCTCCTTATGAACTGTACAACCACCAC
TP48453	TGCAGCCTGCCAAGATGGACCTGCCAACGACGGCAC[A/G]GAAGCGCAGGCAGAGACGCAGAGTTCG
TP48456	TGCAGCCTGCCAATCTTGCACAGCCCATCCACTAC[G/T]GTGTTCAAGATGACAATATCCGCGCAGA
TP48459	TGCAGCCTGCCAGATTAGCCGCACCGCGGTGGCGTCCACGTCAAAACCGAA[A/G]CGGACGCAGTCA
TP48462	TGCAGCCTGCCATCACTAAGAGTGAA[C/G]AGACCTATCATGTCTTCCCCTGCCTCTACAATGGCCT
TP48470	TGCAGCCTGC[C/G]CCCACCACCTACGACGAGGTGTTCAAGTCGATTTTTGATTACATCGACCACCT
TP48487	TGCAGCCTGCCGCGGTGGTGGCAGGCAGGCAGGCACGGCCAGCCACAGGGTAGTGCTCTGCT[C/T]T
TP48498	TGCAGCCTGCCTCGGCCTCGGG[C/T]TCGGCCTCGTCATCAGCGGCGCGCAAGCCGCCGCGGAAGCG
TP48508	TGCAGCCTGCCTGCGCGGCGAGCTCGGTCACGAG[A/G]CTGTCTAGGGTCGGCAGGTACGTCGTCGT
TP48516	TGCAGCCTGCCTGTGTGGCGTCAAGTGCGTATCGTGTTCGCAGGTGCTCAGGT[C/T]GCGTCGCGTC
TP48535	TGCAGCCTGCGATGATCGC[G/T]GCAAACTTTTGATTCACTTGACCCATGGGCCATGGTAACGTAAC
TP48546	TGCAGCCTGCGCCGAGTACCATATGACGT[A/C]CGTGATCACGCAGCAGACGCCTCCGTCGTCAGAA
TP48555	TGCAGCCTGCGCGCCCACGCGGCTCGGGACGACGAC[A/G]CTCACGTTCGCGGCGCAGATGCCCCCG
TP48570	TGCAGCCTGCGGAGCCAGAG[A/G]TGTTCGACGACGACGACGAGGTGGAGCTGCCCTTTGGCGAAGA
TP48574	TGCAGCCTGCGGATGCCCTTCTCCATCACGCCGTCGTCCACCCTTGCAGCGTGCGGA[C/T]GCCGAC
TP48577	TGCAGCCTGCGGCGA[C/G]ACGACGAGATTAGAGACCAGATGAGACGAGACTCACAGAGGCGAGGCC
TP48586	TGCAGCCTGCGGGGGTGTCCGTCCACATCGGTTGCCGAAGAGACGTCAGCGTAG[C/T]GGAGCGCTG
TP48588	TGCAGCCTGCGGTTCTCCTCCCAGGCGACCTCCATGTC[A/G]CGCAGCGCTGCCTCATACTCCGAGT
TP48589	TGCAGCCTGCGTATGTTCGTTCCGATCGATCTGGTTAGTGACGGT[A/G]GTGATCGAGCAAGGGAAG

Table A2 (cont.)

TP48593	TGCAGCCTGCGTTGCCA[A/G]GCCGAAGTGCGGTGGTGGCGGAGGCAGAGGAAGAAGGGTCGGCGAC
TP48603	TGCAGCCTGCTAACGAGTCATGCGCGGCAACGTCTGTTTC[G/T]CACTGTGAAGCTGATGTTGAGCT
TP48606	TGCAGCCTGCT[A/G]CCCCATCCGCCCTCGGCCTCGGGAGGCTCGGTCGCGTCTCGGTCTCGCGGGG
TP48623	TGCAGCCTGCTATAGGACACG[A/G]GGGGCGACGGCGAGCCGTAGCTATTGATGGTGGCGGCGTACG
TP48644	TGCAGCCTGCTCGTGCTCGGTGGCGG[C/T]TGGCGGCGGCGTTGAGCTGCCAGAGCTACAGCTACTT
TP48660	TGCAGCCTGCTGCCGAAGCGTGGGCGAGAT[C/G]CATCCATGGCGTCCGTAGCCACCAGCACAGCCG
TP48664	TGCAGCCTGCTGCCTGCAATGCCCTGGTCTGGTGTTGGTGTACTCCTACGTGCAGT[A/C]CTACTAC
TP48670	TGCAGCCTGCTGCTGATCATTGCCGAATGCGTGCGTGCGT[G/T]CAGATTGCCACCCTTGTCGCGGT
TP48683	TGCAGCCTGCTGGCTCCCCAGTCGCCTGACGGAGCGGAAAGCCAGCAGCAGCCGCAGCCGCA[A/G]C
TP48711	TGCAGCCTGCTTCTTGCTTAGAAGGTCGAGGAGCATCGCCCTCGCGCCGCCCAG[A/C]GCCATGGTG
TP48729	TGCAGCCTGGAATCC[C/T]TGCATCTCTGGAAGTCTCAGGTCGGTAGCAAACCACAGCAGAGACCGT
TP48732	TGCAGCCTGGACAACTCACACTAGTGTCCTCACCGTAGAC[A/C]GCACATTGCAACGGTGGGCTCGC
TP48738	TGCAGCCTGGACCACCACCAGAGCCGCAGAATAATGCCGCCGCTGAGGGTCAGGGGG[A/G]GCAGCT
TP48739	TGCAGCCTGGACGACGCCACGCGGAGCACGAACCTGGTGGACGA[C/G]CTCCACGCGCATGGCGAGC
TP48745	TGCAGCCTGGAGAGGGAGGAAAGCAGAAGAAATCCCTTGTCAACTCCATC[G/T]CCATCGCCAGATG
TP48750	TGCAGCCTGGAGCTCCTGG[C/G]CAGAGTTGCTCGTGTCGTCGTCGGCTGTGTGGTCATCATCAGCC
TP48769	TGCAGCCTGGAGTGCAGGGAGCGGCACATCACGCAGGAGGAGTGGAAGGACAAGTGCGCC[A/G]TGA
TP48775	TGCAGCCTGGATGAGCGGCTCCTCCTCCCCACCGCCCTCCTCCTC[C/G]TCGTCCTGGACCAAGTCA
TP48779	TGCAGCCTGGATGTC[A/G]GTTCCTACTGGCTCCTGCCCCTACTTAACTCTAAGCCAGAAGTTTAAG
TP48791	TGCAGCCTGGCAAGTTCGTTGAAGCTTTGACGAGACGAGACCACAGTACAGCTCCTAGGAAAG[A/C]
TP48804	TGCAGCCTGGCCAGCAACCTCCCATTCCCATCCAGTCGCTACCTGCGGTATATTT[A/G]GCCATCTT
TP48814	TGCAGCCTGGCCTCCAGCTCCTGCTTCTCGGCGCGGAGCC[A/G]CGCCGCCGACTCGCGGACCTCCT
TP48828	TGCAGCCTGGCTCATCTGAGAAGCTAACCAAA[T/C]GCGCCCAAATACTCCTACATGGCAGAAGAAA
TP48856	TGCAGCCTGGGCC[A/G]CGGCCGCCTGCTCCGCAGCAGCGATGCGTGCGTCGGCATCTGCCACCGCG
TP48860	TGCAGCCTGGGCGGTCGAGCCATT[A/G]GCGCCCGTCCCGCGCGGGGATGCTGCGGGCGGCGCCAGG
TP48892	TGCAGCCTGGGTGCG[C/T]GTGCAAACCAAAACCAGGGGAGCAGGTGAACATTTTGGGCGACCGTGA
TP48893	TGCAGCCTGGGTGCGCGTGCAAACCAAAACCA[T/C]GGGAGCAGGTGAACATTTTGGGCCCGTTGCT
TP48901	TGCAGCCTGGTAGATAACTAGTACGTGCAGCACCTGTAGGCAG[A/C]GAGCAATTTTGCTGTGCAGC

Table A2 (cont.)

TP48928	TGCAGCCTGGTGGTCCATGTAT[A/C]TATCAATAACGAGGGAGATATTATTTAAGCCGCAAATGAGC
TP48931	TGCAGC[C/G]TGGTGTCCCCGTAGCATGCGGCAGGACGCACTGTGTGTGTGTGGGATTGTAATGGTT
TP48937	TGCAGCCTGGTTTAGCACACAATATCTTACAGCTTACTCCTACTGCTACTA[C/G]TTATCTATCCAG
TP48976	TGCAGCCTGTAGGTGCTAGTTCGCTCCCGTGCGCAGTCACCGCAGATTGATTTGG[A/G]GGGCATCG
TP48988	TGCAGCCTGTATTCCCTGGATGAGTTCATTAACTTTTCCATGGATCTGGAACA[C/T]CAGTACCCTA
TP48989	TGCAGCCTGTCAC[A/G]GATCTCAGCCAAGAAAACATCACGATCACGAAGCTGCCGATCCACCGCGG
TP49007	TGCAGCCTGTCTTACCGAAGGCATTCTCGGTGACTAGCTGGCGTG[A/G]ACCATCGGAGACTGCGGC
TP49013	TGCAGC[C/T]TGTGCACGTACGTAGCCGCGCGCGGCGGACATGGGGCGCGCGCCGTGCTGCGACAAG
TP49019	TGCAGCCTGTGCATTGCAGGCAGG[C/G]GAGGCGAGGTCCTTTTACTGTGCTGCGGAGTACGAAGAG
TP49025	TGCAGCCTGTGCGCTGT[A/G]CCCATTCGTTTTCCACGCGCCCGACGCGCTTTGCATTCCACCGCTG
TP49030	TGCAGCCTGTGCTGGGTCACGAGCGTAAG[C/T]TGCAAGGTCTACCACGCCAGCGGCCGCGGCGGCA
TP49053	TGCAGCCTGTGTGAGTTTGGGATGGGGACTGACACTGGTGGCGGATGCAGG[C/T]GACAACAACCGC
TP49060	TGCAGCCTGTGTTGTTTGCAACAGCGGCGGCATCAGCGGTGCGGCTGCCTAG[C/T]GGTCCAAGGAT
TP49061	TGCAGCCTGTTAAGAAAACACTACGTTTTGACCATGAAAGTGCTATGCATTCAGCATTT[C/T]AGTT
TP49085	TGCAGCCTGTTCGGGAGGCCGTATC[A/G]TATCGTGGATTATTTACTGCTGGCTGGTTTGGTGTGAG
TP49107	TGCAGCCTGTTGAGCACGCAC[C/G]AGGGCCCTCTCCGTCGCTTCTCACTCACCTATCACCTATGGG
TP49111	TGCAGCCTGTTGGG[C/T]AACATGACGAACAGAAGCCCGCTCCTTGGGCAGACGACATTCGAATAAT
TP49121	TGCAGCCTGTTTGGAAGCCGA[A/T]TTGGCTACGAACTGATCTGGTAGATTACAGTAGCAGTACCAG
TP49161	TGCAGCCTT[A/C]GGAACAACTCCACGGCCTCCTCAAACTCCCCACGCAGAGCGTAGCCCTGCACGA
TP49168	TGCAGCCTTATCAA[A/G]AAATCTACGCAAAGAAATTGCCTGCCAGGTCAGAGAAACATGGGGCCTA
TP49172	TGCAGCCTTATCTCTGGCGCCTAGCTCCCATCATCGGCATCTTCTTCTCCAC[A/G]AGCTCTCATGC
TP49174	TGCAGCCTTATCTTGATGATGAGG[C/T]GGAGGCGCGGGGGCGAGAGGGCGGAGAACCAGAGGAGAG
TP49188	TGCAGCCTTCAATCAATTGTTA[A/C]AAATTTTAGCCAAAAATCAAACTCCCGCCTTTAATTGCTGC
TP49199	TGCAGCCTTCAGCCGCTCTCGTCGGGATGGGCACTGGCGCAAAGTTGGCGAGGCAAGGGCAC[C/T]T
TP49215	TGCAGCCTTCCAAGTTATTATTGGTCCATGTTCTTGTTTATTATAATTTATATAAGCAC[A/G]AACA
TP49260	TGCAGCCTTCCTCGACCTGCCACGGCGCGGTAT[C/T]GCCGCCTCCTCTTCCTCTTCCTTTTGCTCT
TP49262	TGCAGCCTTCCTTCATGAGC[G/T]CCCGCCTGGCCTCGTCCCCAGCGAGCGGGAACAGCACCTGGAA
TP49281	TGCAGCCTTCGGAACAGCCCCGC[A/G]GCCTCCTCGAACTCCCCACGCAGAGCGTAGCCCTGCACGA

Table A2 (cont.)

TP49301	TGCAGCCTTCTCCTCCTTGTACTTC[A/T]CAGCTTCATCAATTGCTAGACCCCCGAGGGCTCCAGCC
TP49306	TGCAGCCTTCTCCTTTGCCATAGCCAGCCTCTCCCTGAGC[C/T]TCTCCCCTTCCTCGGACTCCATC
TP49307	TGCAGCCTTCTCGACGACC[G/T]CCGCGGACTCTGGCGGAGGCGGCGCTGTGGCTGTGTATGTGAAT
TP49338	TGCAGCCTTGAAAAGACGGTAGCTTGATGCTA[G/T]GGATGCATCTGGGCTATGCAGCAGAACCAGA
TP49357	TGCAGCCTTGAGGAGCGGATGCGGCAGCCCT[A/G]CTGCTGTACCTCCCGCTCCCGCCAGCTGCTAC
TP49378	TGCAGCCTTGCAGCGACAACG[A/G]CACTCGAGATGTGCCTCCGCAACTGTTCTTGCACCGCATACT
TP49382	TGCAGC[C/T]TTGCAGGTTATTCCTTTGGAACTAGCTGGGCTTATGTTTGGAGCCTTGGAGGAGCAG
TP49398	TGCAGCCTTGCCCTTGGTTTTTTGTACTTGCA[G/C]CGTCGAGGCGCCGTGCCACGCTTTGCCGCCA
TP49399	TGCAG[C/G]CTTGCCGAAGACCTCTGAAATGTCCTGTTGTTCCTCTCCTTCCAGACACCCCATGCGA
TP49401	TGCAGCCTTGCCGC[C/T]GTAGTCCACCCTTCAGTTCCTGTCCTTCAGACCTCAGGAGCTCAGAGCC
TP49405	TGCAGCCTTGCCTAGCGCTCGCTTCGACAGCAAGGAAGCGCCACCC[A/T]GCCAAATCCAAAGATCT
TP49411	TGCAGCCTTGCGCTCCTCAGGAACGTGGCTGAGCGC[A/G]GCGCGCAGCACGACGGCGAGGCTTGGC
TP49445	TGCAGCCTTGGGTGATGTCGTATTG[C/T]CGTCTGGCAGTAGTGATGCTCGTGGGATGAGGCGGGGG
TP49448	TGCAGCCTTGGGTGTCTTGGACGTGGTTGGGGTACTGCTCTTTGAAATAGGCGGGATACTGTG[C/T]
TP49457	TGCAGC[C/T]TTGTACTTTGCCCGTTCCTTCGGCTGTTCACTCAATAGTTTACCTTTACCCTCCCAG
TP49460	TGCAGCCTTGTATGGACTATACAGGCTCCACATAGTTCT[C/T]TCAATGTGTCCTTGCTGCCTTGCC
TP49462	TGCAGCCTTGTCACTGTGGTAAGGATCAAT[A/G]TGCAAACCAGACACCCCGTCCACAATGATTTCA
TP49464	TGCAGCCTTGTCATATTATGTCATGAATCTATATTTTGACTTTTTT[A/T]AAAAAATGAACTTGTTA
TP49466	TGCAGCCTTGTCCATAGCTCGGC[C/T]ACCTGATTGCTCTGCTCCTACCCAAGTGCGTGTGCTCCGT
TP49487	TGCAGCCTTGTGGG[A/C]CTCGCTGCCTTTGCCACCAAGAGCGCCAGTCTCAATGTACTTCTTTGCA
TP49495	TGCAGCCTTGTTGTTCAGGCGGCTCTGTTGTTTGGGA[A/C]GCAGCAGCTATTGTTGGTAGCTGTAG
TP49517	TGCAGCCTTTCCCAGGTTCACGACCTAGCATGCCTGCCTGTCCTTTTGAGC[G/T]GCATCCTCTAGC
TP49530	TGCAGCCTTTCGGGTCCTATGATATTATCATTAGCAGATTGATTTAGATGTTCGATGGACTT[A/G]G
TP49549	TGCAGCCTTTGCAGACACTGCTGGTGCTGGATTCGGGCAGGTGACGTGTCTGTG[C/T]ACCGCAGCT
TP49561	TGCAGCCTTTGTATATCTTCGTGAAGCCTCCAACTGA[A/G]TTTGTTCGCCTCGCTGTGTTGCACTG
TP49591	TGCAG[C/T]CTTTTGATCTGGCTTGGACGGTAGATGCGGCACAGCAAGTTACGCCGTGACTTACCCA
TP49649	TGCAGCCTTTTTGTGTTGTAGGCTTATCACCGTCAGTTCTTGGCTAGAACCGACAGTGTCCCA[A/C]
TP49684	TGCAGCGAAAACCTACGTACCACACGCACTCGGTTACGTAGCCATCAGCTAACCGCGTCGA[A/C]AA

Table A2 (cont.)

TP49685	TGCAGCGAAAACGACGGATGC[C/T]ACGCCTTCTTCACCTATCAGGATTCAGCGCTGCCCCGCGACG
TP49694	TGCAGCGAAAAGGAGTCGTTTTCAGGGTCTATCGTAGCGATTAG[A/C]GAAGGCGATGGCATTCTTT
TP49697	TGCAGCGAAAATATCTGGGACGGGGAGCACTGTTCG[A/C]CGAAGTTGGATCGCTGACGCGAGCGGG
TP49703	TGCAGCGAAACAAACAGAAGTTTC[A/T]TGCCAAAATCTGGGTTCATGCGATGTATGACAGGGAATA
TP49741	TGCAGCGAAAGCGATTGAGTCCGTCTGTCCGA[G/A]CAGGAATCTCTGAAATGCCAACCAAATCACG
TP49742	TGCAGCG[A/C]AAGCGCAAAGCAGAAGATAGGCTATCAGAATTCAGAGGCGAGAGGCGACTGGTTCG
TP49752	TGCAGCGAAAGTAACAAAAAGTCACTACCCTCTGACTCCCCTCATGGTCACGCTG[C/T]TCTCTTCT
TP49755	TGCAGC[G/T]AAATCAACTAGTCGGCCCGTACGAAGATGCGACCTCAGCCAGTGGCAAGTCTCCAGC
TP49775	TGCAGCGAACACATAATGTCAGCACAGTAGCCTCGTC[C/T]GAGTGCCTTTACCGAGCGCCACCGCC
TP49788	TGCAGCGAACACGG[C/G]CTGGTCAGGAAAGGTGGAAGGGGCGCTGCTTGGTGTGGGAAAGGCCGAC
TP49793	TGCAGCGAACAGAGTGTACCGCATCTCGGGGACGCAGAAGTTTGAGATGCCGAAGCAGGGGCT[C/G]
TP49814	TGCAGCGAACCTTGACAAGTCGGATGGCGCTGTGGTCGGCGTCACCAAGTC[A/T]TGGCACGTCCAA
TP49821	TGCAGCGAACGAGA[C/G]CCACCACGGCAGGGACGACTCTGCGTCTGTGCGGGCATGGAGATGGGCC
TP49833	TGCAGCGAACGCCGACGAGCAGCCGCGATCCG[T/C]AGCGTGAAGAATGAACCTCGAACCCAAAACC
TP49845	TGCAGCGAACGGTGGACGGCGGCGGCCACGGCGAATGGTTCAAGTTTCTAAA[C/T]GGCGCCACGTA
TP49856	TGCAGCGAACTGG[A/G]TCTCGACTCATCGAGAAAAATATGGCAGTGCAGGATCCGATACCCGTCAG
TP49882	TGCAGCGAAGATGATGCATCAGAAGGCAGTGA[T/C]ATACACTCGATTGAGCTGAACGTCGATGGCA
TP49901	TGCAGCGAAGCTA[A/C]AGGCCCTTGAGTGCGAGCTACCGCCGCTGATGGTGGGGGCCGCGATGCCG
TP49929	TGCAGCGAAGGGGAGGGGGAACCGCCGCCGCCGCGGTTCCCGCCGATG[A/G]ACCCGAAGCCGCTGT
TP49955	TGCAGCGAATAGTGATGACCTATGGGGTGCCATTGCAGCACCTCC[A/G]CCAGCAACCAAAGCCAGA
TP49957	TGCAGCGAATATCGC[A/G]GCAGGGCCGCAGGGGGGAAGTGGCCACCGCACCAGCAGTCAGTCAGCA
TP49960	TGCAGCGAATCAGCACCGCTGGC[A/G]CAGTACAACTTTGATTCTACATGTCTAATGGCGCACCGAG
TP49992	TGCAG[C/T]GAATGGTCCCCTGCCGTTAACAACCAGCCAGCCAGCCACAGCCATCCATCACCCACCC
TP50004	TGCAGCGAATTCTGCATCTCATCC[G/T]CTGCCTCTGGGGGCGCCGCCATGATGAGTCTCCAGCAGA
TP50009	TGCAGCG[A/G]ATTGTGCTGGTGATAATGAGCAAAGCCACCAGCGAGGTTCTCGAGCGATGGAACTT
TP50010	TGCAGCGAATTTAGGGCCCTTGCCCTT[A/T]GCCTTCCCCATCTCGAGCCAAACCCTAGCACCCGCA
TP50026	TGCAGCGACAACAGACGCATGCATGCAATGCATTCCC[C/T]TCCCCGACCGCTGACCTTGTTGTTCA
TP50035	TGCAGCGACAACTATCCATGGGGAAGCTGTCGA[G/T]CGCCGTGAGGGACCTCCTACGACCACTATC

Table A2 (cont.)

TP50036	TGCAGCGACAACTGTTCTTCACTACCCAATCAGTATACAACATGTTC[A/G]TTTGGTTGTAAACGAT
TP50042	TGCAG[C/G]GACAAGCTTGCAGGAGGTAGGAGAGAACTACTTTAACGAGCTCATCAATCGAAGCTTG
TP50051	TGCAGCGACACCACAGACACAGGTCAGGAGTCAGGACAGGACAGCCCATGCATTATTT[A/C]TCATC
TP50059	TGCAGCGACACGAATCCCCAAGCCCACACGCGCACACGCATCGGGCATCCGT[C/T]CCAGTCCATCT
TP50061	TGCAGCGACACGACCAGGTCAGAGCCGAAAACTA[A/G]GCCGCGAGAGGAAGTAGTGGCGAGAACAT
TP50062	TGCAGCGACACGATGACGGCGGCGCCGCCCATGAAGCCCGTCAGCGTCGGCTT[C/G]GACAGGAAGT
TP50066	TGCAGCGACACGCACC[C/T]CCAGTGTATACGGGCGCACGGCGCGGCACGTCATCACTCATCCGTGC
TP50076	TGCAGCGACACGTTGGAC[G/T]GCGCGTCCGTACAGCACAAGTCTTGTACGCATATATGGGCAGTGG
TP50084	TGCAGCG[A/C]CACTTCAAGAGGAGGCGTCGTGACACCACCATCCCACCTTTGATTCCTTGTATTTG
TP50090	TGCAGCGACAGAGT[A/C]ACAGACGGCTCTCGGTCCGTAGACTGTAGCCAGCGCGAGCTGAAAGCCA
TP50092	TGCAGCGACAGATCCG[C/T]GACTCTGAGATGGAGCTCCAGTTTGTTCGACAGCAGATCGCGATCTG
TP50099	TGCAGCGACAGCACACAAGCACAGGCGTGGCGGTATGGGCGGCCCTCTTGCGTGC[C/T]CTGTGTGC
TP50124	TGCAGCGACAGCGGCAAACCAGTCAGCACAGAACTCGGAGACGGAGGGG[C/G]AGAGAGAGAGGAAC
TP50131	TGCAGCGACAGCTT[A/G]TTCAAACTCATCTAGTCATCTGAGTCATAGTCATCTTCCATATTAATTA
TP50165	TGCAGCGACATAGTCACTGCCGCGACGGCGTCTC[A/G]CAGTTCAGGACGCCCAGCAGGTGCCACGG
TP50166	TGCAGCGACATATATCAATCAGTGAGGTGAGCCTT[C/T]AGGAAAATGGAACGGATAGTCTCGTGGC
TP50179	TGCAGCG[A/G]CATCGTGGACGTGGTCTGGCGCTGCTGGCCTCGGCTTGGCTCAGCCGCTCAGCTCG
TP50219	TGCAGCGACCACGCGC[G/T]CTCGTCCAGCGTCCCGCCCAGCCAGTCCAGCGCCGAAAAAAAAAAAA
TP50221	TGCAGCGACCACTAGAAGAGCAGCCAAATGTACTATGGCTGAAAAGCTC[A/C]AAACCGTAGAAGCC
TP50224	TGCAGCGACCACTTGGATCACCCAGCAGGCTGTAGAGCACTGGGTGGGTTCGTTC[A/G]CCCCTGAC
TP50239	TGCAGCG[A/G]CCCACACCCGCGGTAAAAGCCCCTGAGCGGGAGATTTGCCGCGCAAAAGCATATAT
TP50241	TGCAGCG[A/G]CCCAGCGGCAGCAACTCTATGGCCGCGACGAGAAACGGTGCTCCACACCCGATGAC
TP50245	TGCAGCGACCCCTCATAAAGACGTCAGGTTCGTCACCCCCGAAAAG[A/T]TTTTACCTTTCCTCCCA
TP50260	TGCAGCGAC[C/G]GAGCGAGCAGAGCGGCAGAGGAGGGAGGGGCATATTCCCTTCCCGTCAGCCACA
TP50265	TGCAGCGACCGCAAGTGAGGCCTCCACCTCGCGGACCCGCGCGGCCAGACGAG[A/C]GCATTTGCGC
TP50279	TGCAGCGACCGCGCGTGCGCGTCTGTCAGAGATTTGAG[A/G]CCGCGCGTACGAAAGGGATGCTTGC
TP50288	TGCAGCGACCTCACCTC[A/G]AGCTCTATTCACACAGATCATGAAGCGTCAAACATCGATCCGACGG
TP50291	TGCAGCGACCTCCTCACGCTCACAGTCACGGCGAGCGGCCA[C/T]GGCAACGGCACGGTCGCCATCT

Table A2 (cont.)

TP50307	TGCAGCGACCTCGTCGGCAGCAAGTTCGGCAG[T/C]GGATCCATCGGGAGATCATCTGCATGCCATG
TP50316	TGCAGCGACCTGTACCCGAGGGCGGCCGCGTACAGGCGCTGCAACTGGTGCCTGCGGGCGCCG[A/C]
TP50317	TGCAGCGACCTGTACCCGAGGGTGGCG[A/G]GGCCGTACATGAGCTGCAACTGGTGCCTCAGGCAGG
TP50323	TGCAGCGACCTTAGGTCTC[C/T]CCATGAAGGAGTTCTGTCTCGACGGCGCTTTCTTGCCGCTGGTC
TP50331	TGCAGCGACGAACCCACTGCGAACCGCAGCACAAACCTGT[C/G]GTCGACCACCGTGTGCGCGAGGT
TP50335	TGCAGCGACGACAAATTATCTTTGTT[C/G]TGGGTGTCTTGCATTGGTCGTTTTCGTCATGACGATG
TP50338	TGCAGCGACGACAAGTCCCTCGCGAATCACGTGAGTCGAGAAGGCACTGGAGACGCTAG[C/T]TTTT
TP50345	TGCAGCGACGACACGCAGTTCTCGAACGGGCGGGG[C/T]AACCGCGACACGGGCAAGGACTTCGGCC
TP50347	TGCAGCGACGACACTGACGCCCACGTTAGG[C/G]AACACTCGTAGTCGTAGTCGAAAGAGGTACGTA
TP50353	TGCAGCGACGACATACC[A/G]ATCATTATGGCTGACGACGTTGTTTGTCGTCGGCGCGGCAGTGGCG
TP50357	TGCAGCGACGACCCCACCGCGAACCGCAGCAC[G/A]AACTTGCCGCCGACCGCCGTGTGCGCCAGGT
TP50381	TGCAGCGACGAGATGACCTCGAGCGCCT[C/T]GTCGCGGACGGCGGAGGCTGTTCCTTCCGACGACT
TP50396	TGCAGCGACGAGGATGGCGGAGGCGAGGAGGACTGTAGGGATCGT[A/G]CTAGCCGCCATGGCCTGC
TP50400	TGCAG[C/T]GACGAGGTCAGCAGATTTCAACGTTCGTCAGTGATTAATTTTTAACAAGATTTAATTT
TP50404	TGCAGCGACGATAGGGTGCGCCGTCATTTC[A/G]CCATGATCCTGTACTCCTATGGGTCTCTTCTTG
TP50407	TGCAG[C/T]GACGATGCGTAGTACGTCCTCCTTCGCGACTGTTGTTTTCTCGTGGCCGTGTCATATC
TP50431	TGCAGCGACGCCCATAC[A/G]CCAATGAGGAAGGAGGTCTCAGCGCAGAGAAGCAGCGCGAGGACGG
TP50441	TGCAGCGACGCCGC[A/G]TACGCCGCCGCGCACACCTGGCTCAGCTGCGCCAGCGCGTCCCGCACGC
TP50445	TGCAGCGACGCCGTCGGCCTCACGGACGCCGCTGA[C/T]GGGGCCGCCGCCAAGCGGAGGTGCCTCA
TP50454	TGCAGCGACGCCTT[G/T]AGGATCTTCAAGCCCTGCACGGACAGTCGGACACCCATGTCGATGTGCA
TP50458	TGCAGCGACGCGAGATCCAACAGC[A/T]GACGAGGCTGGGCTGGGCTGGGCGACCGTAAAACGAAGC
TP50459	TGCAGCGACGCGATTCAC[A/G]GTCACGGTAGGGTGAAAATTGGGCCTTGCCGCCTTGGCTTGGGTC
TP50479	TGCAGCGACGCGGGCGCGGCGGTGCAGGCGCGGAGGACGTGCGGTTCCACGGTCAAAAAAAAA[A/C]
TP50483	TGCAGCGACGCGGTGGC[C/G]CTGCAAGCTGCCATCAACCCATCATTGCCTGCGCGCGGTGCCGTCG
TP50484	TGCAGCGACGCGTACACGTTGGACAGACCGTACGCCGCGCCGTCGTGGAGGTCCAGCTTC[C/G]ATA
TP50496	TGCAGCGACGCTTTCCTCCGCCATGGACAGCTCCGC[C/G]CCAGGCATCAGAGGGAGTATCTTCGCC
TP50502	TGCAGCGACGGAGCTGGACGCGGAGCGGAA[A/G]CCGATCCTGAACTCGTCCCACGCCCCGAAAAAA
TP50516	TGCAGCGACGG[C/T]AGTGCAGGTAGAGAAGATCAACTACATTGACATCACGGGCACGTCGGCGTCG

Table A2 (cont.)

TP50523	TGCAGCGACGGCCGATCTCCCGCTGCCGA[C/T]GGATCAAGAATCCTGCACAACGGAGCAATCGCAT
TP50539	TGCAGCGACGGCGGCCCTACTGCAAC[A/C]GAGAAGTTTGCTGAGACCACAAAAAGCCCAAGCAACA
TP50563	TGCAGCGACGGGCGGCGGAAAGAATCAGCGAGATCAAA[G/T]CACAATTGCTCATGGCGAGGGAGCT
TP50572	TGCAGCGACGGGTGCGCGTCC[A/T]GGGGCGCGAGGTCGGTGGAGCCGAATGAGGTGGCGAGCAGGC
TP50574	TGCAGCGACGGTCGAATCGGGTCTTCGGCGTACGGGGATGCGATGCGATTCC[A/G]TACGGGAAGAA
TP50581	TGCAGCGACGGTGGAGTCGAATCCTGGACCGACGCCGTCTCATCGTCCC[A/T]GGGCATGATGGCCT
TP50584	TGCAGCGACGGTGTGGG[C/T]GTGTGGCATGCAGGGCAGCAGGGGTCACTCCAAGATCATAGGAAAC
TP50616	TGCAGCGACGTCTTCCCGCGCGATGCAGCGAGGCCCACGC[G/T]CGGCCCACATGCGTGCATGCAAG
TP50620	TGCAGCGACGTGACGCCGAAGAGATCGTCAGGGAGAA[C/T]GCCGTCGATGCCGTTCCCGTCGAGGG
TP50646	TGCAGCGACTAAACCAATCGGCTACCGACGGCCCAACAGATGGCAAGTT[A/C]GAATCGGCAGAGGA
TP50658	TGCAGCGACTACGGCGACCCCAACGCCACGTACGTGCCGCCGCACCGCGCCGTGCG[A/C]GCATCGT
TP50687	TGCAGCGACTCGTCGGAGTAGGTCCCCTTG[C/T]GCATGAAGCGCGAGAGGAGGTCGTCGTACGGCG
TP50716	TGCAGCGACTGCGGCCTTGCGAGCTTCGTCCGCGGCGGCGATGGCGGCCGCGC[A/G]TGCTCCGTCC
TP50727	TGCAGCGACTGTGCCAAAATCATGGTCAGGATCATTCCGAGCCAGAA[C/T]ATGGTCGATCCACAAG
TP50748	TGCAGCGACTTCTCGTCGTTGCGGGGCACGTCCT[C/T]GAAGCCGTCGATGGACACGACGTGGCGGC
TP50763	TGCAGCGAGAAACGACGGGAGTTATCCTGACACTCCTCCTCC[A/G]CCTGCTGCTGCGCCTCGCTGT
TP50785	TGCAGCGAGAATTGGTCGTAGCGAGC[A/G]AGAGCAATGACCAGGGTAATCAACAACCGCCACTGAG
TP50795	TGCAGCGAGACCGCGAGAGGTAGGAG[C/T]ATATCCCAGAGACGCTGTCGTACACGTAAACACGTCT
TP50805	TGCAGCGAGACGTTGTCCACCCATATGTCCACCGTCGTCGTGTTGCTCTGCATCCAG[C/T]GGACCC
TP50808	TGCAGCGAGAGAAGCC[A/T]TCGCATAAAAGTCAAGCAACACGGACGGCAGAAGCAAAGCGCACGTT
TP50813	TGCAGCGAGAGAGA[A/G]AAAGATGGAAGGAGTAGCGCTCGAGGCACGCGAGAGCGGTAGAAAGCGG
TP50821	TGCAGCGAGAG[C/T]ACTGCTAGGCTGCCGTTAGCAAAACCGATGTCGCTGCGCCTGGTTCATCGTG
TP50822	TGCAGCGAGAGCAGTGGTGTGCA[C/T]GGTGACGGTGACTCGGTGAGCCGCGGCAGAGAAGGCACAA
TP50826	TGCAGCGAGAGCGAGCTAT[C/G]GAGGAGGTGCGGTTTTGGTCTTTTGCGTGGTTCGTGACGCGCCT
TP50829	TGCAGCGAGAGCGGCCGCGCGCTGGTGTC[C/G]CACCACTCGGTCCTGGTGTTCGAGGCCTTCTCGG
TP50831	TGCAGCGAGAGCGTTGCCCAGCCGCCCAGCACAAGCGCACAACCTACGTACCCCCA[A/G]TTGCTTT
TP50844	TGCAGCGAGAGGGACAGGAAACGGACGGC[C/T]GCGTCATCGTGCAATCCCGTCCTTGTCATCCGCT
TP50855	TGCAGCGAGAGT[A/G]GAGGCAGGGCCGCAGGGGCCATGCGGCCAGTGGCCAAGGCCCAAGGATGAG

Table A2 (cont.)

TP50873	TGCAGCGAGATCATGGCGATGTAGGGCTTCGCCTTCTCCACGAACCC[A/G]CCGCACCCCGCCATGG
TP50876	TGCAGCGAGATCCGATCCAAGCAGCTTTCGTTCTCAGACGGGGTAACGTCGCAACTGA[A/T]AACCT
TP50882	TGCAGCGAGATGAGCTCCATCCAGTCGAAGGG[G/A]TTGGTCACGTTGTACATCTTCTTGCACCCGA
TP50883	TGCAGCGAGATGCATGGGGCGGCGATCTGGACGCTGTTAGATTGATCTCCACCGAGCTC[A/G]GTCC
TP50886	TGCAGCGAGATGCGGTCCGCTGGCAGGAACACGATGGCGGGGATCCCCGCGGCCGCGCAGTA[A/G]G
TP50894	TGCAGCGAGATGTCGGAGTCCTGCCTGGGAAAGGC[A/G]GAGAGGAGGAAGCCGCGGAGGCCGATCG
TP50918	TGCAGCGAGCACACTCATGGTGTCGTGCTCGTGCGTGACG[A/C]CTATTTAGTAGTGTGCTTTTGAG
TP50929	TGCAGCGAGCACTTCGCAAGTTAAAGTGCTTTTGATGCCTCACCAAAAGCA[G/T]TATAACAGCCTT
TP50933	TGCAGCGAGCAGCGT[A/C]GATCTCCTTGCCCATCCTCTTGCCGTCAAAGACCCCGCGGGCGGCTTC
TP50940	TGCAGCGAGCAGTAAATAGCAATGCCATGCATTGGTGGATCAT[A/G]TGGCCGCTTCTTTTCTTCTT
TP50948	TGCAGCGAGCATATAAGCGAGCAAGCT[G/T]ATGAATGCCTGAATGCATGATGGTGGCTAGTATCTT
TP50952	TGCAGCGAGCATTTCT[G/T]TTTTTTAAGAGAGAAAAGCTGTCACTATCTATGTCGCGTTAGCTTGA
TP50954	TGCAG[C/T]GAGCCAATTATTAGAGTTCGCAATAAGCACTGGAGCCATCCAACGTTATCTCCATCGC
TP50961	TGCAGCGAGCCAGCCAGCTAGTACCATGCCTAGCA[C/T]GACTGGACGAGTCGTAGACGTGGTACGT
TP50996	TGCAGCGAGCCTGAAACATAGTTCTGGACTGGACATGTACGATATCTTATCAACTTCTCGAC[C/G]G
TP50998	TGCAGCGAGCCTTGCGACCTCCGCGGCGGCCTGCGCAAGCTCTGC[A/G]ACAAGATTGCGCGAGCTC
TP51003	TGCAGCGAGCGACGGCG[A/G]CGGTTCAGCGGCAGTGCGGACGCGCGGGTCCCTGTCCCTGGTGGGG
TP51019	TGCAGCGAGCGAGCTGGACCTC[A/G]GCAGCAACAGGCACCTGAGGCAACAGCAGCACCGCCGCCAC
TP51021	TGCAGCGAGCGAGGACGT[A/G]GGCATTTTTGGAATCGCTCCCTGTCTAGGGTTTTATCTGTGTGCC
TP51036	TGCAGCGAGCGCTCACCTTTACCG[A/C]CCTCCAGTGGTCGAGGCAGTCGCGGTGCACGTACTTGGA
TP51039	TGCAGCGAGCGGAAGCAGCTGCCAGCTGGGGGATTTTCGGATTCGTGAGAGACATGCCACTGC[A/G]
TP51054	TGCAGCGAGCGGCGGAGCACGAGGAGCGGGCGGCGGCGGTACACGGCCG[C/T]GATGCCGAAAAAAA
TP51064	TGCAGCGAGCGGGT[A/G]CGAACGGAAGTACGAACACGCGCCGAGCCAGATTACTGTCGCGGTCCTG
TP51070	TGCAG[C/T]GAGCTAAGCTGGAGGCGAGGCCAAAGCGCCTCATGGCGGAGCCTCGGCGGCCGCATCG
TP51090	TGCAGCGAGCTCTGCTAGCTCTGGTCAGCG[A/G]TCACCGATCTGATCGCTCACTCGTTCTTGTGTT
TP51093	TGCAGCGAGCTGCGCGTCCCGCAGATGCACAGCCTGCGGCACAGCCAGATCTCGGGGGCGCT[C/T]T
TP51106	TGCAGCGAGCTTGCGAGGCCATTAATGGCAATGCAA[C/T]TATGCAAGCACATATCCTGCGCAGGTC
TP51107	TGCAGC[G/T]AGCTTGCGAGGCCATTAATGGCAATGCAAGCACATATCCTGCGCAGGTCAACCCCGT

Table A2 (cont.)

TP51120	TGCAGCGAGGAACAACCGC[A/G]TGGGTGACGTGCTTGGTGCGCGTGGAGCGAGCACGCGGGCATAC
TP51142	TGCAGCGAGGACTGCCGCTACCAGCGGATGCACC[A/G]CGACGCGGCCTACGCGCGGCAGGCCAGCA
TP51143	TGCAGCGAGGACTGCCGCTACGAGCAGATGCACCA[C/T]GACGCGGCCTACGCGCGGCAGGCCAGCA
TP51152	TGCAGCGAGGAGCCAGTGCACCTTGAGCGCGATGCGGAGCGACTTGGC[A/G]CAGGTGTCGATGACG
TP51161	TGCAGCGAGGAGGAGGA[C/G]GAGAGGCAGACCGCCATGGAACGCCTGCGGAGGCTGGAGGATTGCG
TP51164	TGCAGCGAGGAGGAGGAGGC[C/T]GCGATGATCCTCCTGGAGCTGGCCTCCTCCAGCCGCACGTCGT
TP51167	TGCAGCGAGGAGGCACGGGTCGGTACGAGGTGGACGCGGC[G/T]GGCGGTGCCCCTGTGCCGCCTCC
TP51168	TGCAGCGAGGAGGCGGCGACGCCCATGCCGTC[G/C]TTGAGGAAGAAATTGACGCCCAGCCACGGGA
TP51204	TGCAGCGAGGCCATCGGAGGGCCGCACGCATGGCGCCGTGCCGCTCCC[A/G]CCAGACGCCGCCAAG
TP51218	TGCAGCGAGGCGCACA[A/G]GCGGCAGCGCGGGGAGTAGAACTCCAGCACGGTGGCGGGCGTCCCGA
TP51225	TGCAGCGAGGCGGCGGCGGCGGCAGCGTCCACGA[C/G]GCGTCGTTCGCGGTGATGGCGGCCTGGGT
TP51230	TGCAG[C/T]GAGGCGTCAAGCGAGTAACTCAAACTGCTAAGCGAGCCGTCCGAGCCATCAAGCGAGC
TP51261	TGCAGCGAGGGAGCGGCGGCGGCGGCTGCTGTAGCCCCAGAACCCTC[A/G]TGTAGCTACAGTAGAG
TP51285	TGCAGCGAGGGCGCGAGGCCCCGCTCCTC[C/G]ATGGAGCGCAGGGCAGAGCGGCGCGCGCGGACGC
TP51288	TGCAGCGAGGGCTCAATGATGCCACCGCGGAGCCTGAGCACGAGGTGGAGCGTGGACTCCTT[C/T]T
TP51290	TGCAGCGAGGGGAGCAG[A/T]CGACGGGGTCTTCCTCGGCGCCGACCTCGCCGAGTCAGCCTCCCGC
TP51299	TGCAGCGAGGGTGGCCGAG[C/T]GACGGTGGGCGGGCAAGGGTGGCCGAGTGCGAGCAAGAGGTTAG
TP51306	TGCAGCGAGGTCA[A/C]GGCCGACAAGTCAATCTCGCTGACCACCAGCTGCACAAACACAGAGAGGC
TP51324	TGCAGCGAGGTGGCCGAGGCCCGAGGGCCGC[G/T]GCCTCCACAGAGATCGACGCCACGCGCTCGCC
TP51327	TGCAGCGAG[G/T]TGTGGTTTGTTGTGGTTGAGACTTGAGAGAGCCCCTGTCGCCGTCTTGCCGATG
TP51343	TGCAGCGAGTAGCAGCATGAGCCACCCGTCAGGGCAGG[A/C]ACATCGCGTCAGCATGTGCTTGCTT
TP51345	TGCAGCGAGTAGGACATTCGACCTGATCCAGTCGACGATAATGTATCGGATCAACA[C/T]AGAGCCC
TP51392	TGCAGCGAGTCGGGACGAGCCGCGTGCC[A/G]CGCCCGTGTCCGCGGCCTCGTCGTCTTCCGAAGCG
TP51416	TGCAGCGAGTGGCCGTCGAGGCTCCCC[A/G]TCTCCTCGGCCGCCGCACTGCCGCTGGCCGAAAAAA
TP51418	TGCAGCGAGTGGCGACGGCTTGTGAAGCTTCTGGAACCCATCCTCGCAGTCC[A/T]AGGGCGCGTCC
TP51431	TGCAGCGAGTGGTGGTGGTGATGGTGATGGTCGTGGACTGATGAGGCTCGTACA[C/G]GCGATGCGA
TP51438	TGCAGCGAGTTCTGCACCCCACCCACG[A/G]CGCACCGCTCGTGATCAGGCACGCCGTCCTGCATCA
TP51468	TGCAGCGATAACGGTGGCGG[A/C]GGAGTCCCTGAAGAAGGTGGAGGAGAAGGCGGTGAAGCTGGGC

Table A2 (cont.)

TP51497	TGCAGCGATAGCAAACAAGAAAC[G/T]CCCCGTACAAAATACGGCAAAATATGCAAGTTCAATAACG
TP51504	TGCAGCGATATAAACATATCTCTTTTTGGACAACTGAGATTTTGCGAT[A/T]AGAAAGGGTGACAAT
TP51510	TGCAGCGATATTTGGCGAACACTAATAGTTGTTTGCCCCAATTTAAGATATCTTTTTATT[A/G]CAT
TP51511	TGCAGCGATCAA[A/G]GCTGCACGTGTCGCGCCCAGGGCATGGGCGCGGACACGGCCCCACGGCC
TP51534	TGCAGCGATCCACAACAGTGGGAGCGCACGAGACGAGAGCGAGTGGCTGGCTGCGGAG[C/T]TACGT
TP51551	TGCAG[C/T]GATCGACGCGGTGGAGGATGGGGGTGCAATGCAAGACCCTCCGCCATTGCTTATAAGG
TP51570	TGCAGCGATCTACGGCCG[A/C]CACATTCGACACCCACGCCATCGGCTATGACATTGAACATTAGGG
TP51574	TGCAGCGATCTCCCTCGCCCTCGCCACCACGTCATGCTTCCCGCCGA[C/T]GGCCGTGTGCAGCACC
TP51588	TGCAGCGATGAACGTGCCGTTGAAGGCTTGCCGAAACGGTAGAAGCC[C/T]ATGAGGGATTTGCCTG
TP51632	TGCAGCGATGATCAGGAGGAAGGTGGCTGCTGA[C/T]GCCATTGTTCCAACTTGAATGGGGGCAAAG
TP51633	TGCAGCGATGATGAAGGTTTTCGTGGAGCCTGGTTCGAGG[C/T]GACTGTCGTTAAACCTGTCGACA
TP51644	TGCAGCGATGCAACGCGAGCGCACGCGCGGTCATTTTTTCGGCTCCAAAGAAACAAGT[A/C]TGTAT
TP51729	TGCAGCGATGGAATTGGAGATAGTCCA[A/G]TCACTTGTGGCTACAATCCATCTGTCTGATCGGCAA
TP51733	TGCAGCGATGGACGCTCGATGGATGGATGGACACGTACGGGCGGACGCCGACGCGGCC[A/G]TGCTC
TP51735	TGCAGCGATGGAGCAAGCAAGCAGGTAAGTAAGCAGAAGGGAGACTAGC[A/G]CTGCTGATCAACCT
TP51736	TGCAGCGATGGAGGAGGAGTTGAAATCCATC[A/C]GCGACAACGACACTTGGTCACTCGTCGAGCTT
TP51743	TGCAGCGATG[G/T]ATCTGTGATTCGCGAAATCGCGGGCATGGTCGTCCACGCTTCGGCGCCGTGCA
TP51753	TGCAGCGATGGCTGAGATGGTGGGATGCCAGGCCCTCCATACGAATATGG[C/T]GGTTCAGAACGGC
TP51795	TGCAGCGATGTGATGAGAGCCAAATGACATGTTTAATTAGTTTTG[C/T]AGCATATGGAGCATGTAC
TP51799	TGCAGCGATGTGTTGGTGCCACTACAGCCATCTCGCCTTGGCACAGCGGCGAC[A/G]TGCAGGCCTC
TP51802	TGCAGCGATGTTCCCACTTCTTGTCGACGATTGCACATTTGT[A/G]GTTTGCCTGGTGGTGCTTGAG
TP51820	TGCAGCGATTAGAGGCCACACTGCGGTGGTGA[G/A]CCTGCTGCTGGAGCGAGTTTCTGGGTTGGTT
TP51825	TGCAGCGATTCAATAAAAATAAGCGA[A/G]AGGGGAGCACTTTATATTAGTATATTACGACGCCTAC
TP51853	TGCAGCGATTTC[A/G]GCACAATAGTTCATAACAGCAACAGCAGCAAGCAGAATGAGAATGCGGCAA
TP51856	TGCAGC[G/T]ATTTCCCCGTTTGGATGTTTCCTTCTTGAAGCGGAGGTGCCGTTTGCTCTCCGTGAG
TP51871	TGCAGCGATTTTTTTATTTTAACCTTTTTAATAATTTAATAATAATTTTAAAATTAATAC[A/G]CAT
TP51885	TGCAGCGCAAACTCGAGCATGAACTGCTCGAAGAGGT[A/C]TCTCTTCTTGCTCTGCTGCGCCAGTC
TP51889	TGCAGCGCAAAGTGGAAAAGGC[A/G]ACCGACTTTAACGTACTCCAATGCGGGCGATGACGTTGATG

Table A2 (cont.)

TP51905	TGCAGCGCAACCAGAAAATTGCCCAAAGCAGA[T/A]GACGCAGAGCACATAGCTGCTCCAGAATAAA
TP51906	TGCAGCGCAACCAGAAAATTGCCCAAATCAGATGACGCATA[C/G]CACATCGCTGCTCCCGAAGAAA
TP51911	TGCAGCGCAACGACAC[C/G]TTCACGCTCTGGAACGCCGACATCGCCGCCTCCAACGTGGACCTCAA
TP51912	TGCAGCGCAACGAGAAGCGCGTGTCCGTGAAACACTGG[C/G]CACGCATGCATATGCATGCAATGCA
TP51915	TGCAGCGCAACGCACAGGGTCGGCTTGAAGCCACCACTGATATATATATTGCTGGACACTG[A/G]CT
TP51945	TGCAGCGCAAGAACTTTGGCACAGGAGTTTTTCCCCCTTTGATAA[A/C]CTTAGCCGCATTCTTCTT
TP51948	TGCAGCGCAAGAGCGACTCACGACACTGTGTGAGCTACGACAAATTAATGTTGGCTGGTCA[C/T]CG
TP51954	TGCAGCGCAAGC[A/G]AGGCGGAGGTGGAGGAAGAGGAAGTGCCCCCTTGATGGTCGCCGTCTTGGA
TP51958	TGCAGCGCAAGCGCAAAGCAGAGAAGATAGGCTATCAGAATTCAGAGGC[A/G]AGAGGCGACTGGTT
TP51976	TGCAGCGCAAGGTCGAGGAGCTCCGCGCCAGGCACCCCGCCGTGCGCATCGTCTACGC[C/T]GACTA
TP51984	TGCAGCGCAAGTTCTCGTGCGTCTGGATGCGCGTCGCGATCGGTTGGCAC[C/T]TGGCAGTGGGCCA
TP51988	TGCAG[C/T]GCAATAGAAGAAAGCATGGTGAGCAAACCACCCCGATCTTGGTGGCGATGAAGTGGAC
TP51993	TGCAGCGC[A/G]ATCCGCGCCAGGTAGAAGGTGTCGACGGCGGTGCGCACCACGGTGGCGACGGTGG
TP51996	TGCAGCGCAATCCTCTCCTCGTCGTCCATCATCGC[A/G]GGTGGAGGCGAGCCAGTCGTGACCGTGG
TP52003	TGCAGCGCAATGC[C/T]CATCCACCTGCATGCATGCACGCACCAGTTTAGTTTGTTGACGACAACAC
TP52010	TGCAGCGCAATTTGCACAGATGACA[C/G]TATAAGGCGGCAGCCTTGATTCCCAAACCAACCGAAAT
TP52012	TGCAGCGCAATTTGCCGCCGCCAGTTGATGGTGGAGTGCCACGCATAGTGAGCTTTGTC[G/T]CCAA
TP52020	TGCAGCGCACAAGCGAAGTGACACAAGCTAAG[G/C]GAACACAGAAATGGCGAAGCGCACGTCGAGC
TP52029	TGCAGCGCACACGTCCACACCTGCGTGCCGCGTGCCGCGTGCCGCGTGCCTGATGGCTGATG[C/G]C
TP52079	TGCAGCGCACGATCCCCAGCTCACCTAAACGCAGAAATTCTAGGCACACG[G/T]CTACCAAGAATCC
TP52100	TGCAGCGCACGCTAAGCAAAGGCACCA[C/T]GTTTCCGCCCGTGACGGCACCGTTTTCCCCGCGTGG
TP52107	TGCAGCGC[A/G]CGGCCGAAGGAGAAGGACAGCGTCCAGGGCTTGAGCACCTCCAGCTTGTTCATCG
TP52124	TGCAGCGCACGTGCGGCCTACGGCGACTCTGC[T/C]GCGGAGATGGACCGAACGGGGCTCCGATCTA
TP52127	TGCAG[C/T]GCACGTTGGCGCGACGATGTGTCCGTGGCGTCGTCCCCGTCGCCGTCGCTCCACCCCT
TP52133	TGCAGCGCACTATTTGCTAGAGAAATATAAATACATCAAAAGCACCCCAGTCCCCAAAC[C/T]GATA
TP52137	TGCAGCGCACTCTGATCTCCATGCGTGCACCTATCT[A/G]TCTCTGCCGCGCCCGCCCCTCGTCTAT
TP52141	TGCAGCGCACTGCCGCCGCCTGACGCAGGCGGCCACCA[A/G]CGTGGAGACGTACGCGACGAGAAGG
TP52144	TGCAG[C/T]GCACTGCGCTCGTGCTGCTCGCATCGCATTTGCATGGGGATGGTGGGAGAAGCGACCA

Table A2 (cont.)

TP52164	TGCAGCGCAGACGAGCGGCCAACAAGA[C/G]GTTCCGCCCTCCACGGGTCTCCAACCTCGCCTGCGC
TP52171	TGCAGCGCAGAGCCGCCACCGCTGCCTCTCTCCACGGGACACGCCGCC[A/G]CCGAAAAAAAAAAAA
TP52180	TGCAGCGCAGAGGGGCCGACGTTCTTGGCGTAGTGCAGTGCGCACTCGACACGTGGCTGC[A/G]CGC
TP52198	TGCAGCGCAGCAGAGCAGCCAGCGACCTCCTCG[A/G]TCCAGCGGCCCCTTTGCTGCTCGCGCCTGT
TP52200	TGCAGCGCAGCAGAGCAGCCAGCGGCCTCCTCGGTCCAGC[A/G]GCCCCTTACTGCTCGCACCTGTG
TP52202	TGCAG[C/G]GCAGCAGCCTGTGCATGTGACTTCGCCTCTACTACAGCAAGGTGGTCGCCGATTCGGC
TP52208	TGCAGCGCAGCATCGGGGTGTCGGCGATGCACATGCAGCTGCTGCACAACGACCGC[G/T]TCATCAT
TP52239	TGCAGCGCAG[C/T]GCACTGCCCTGTATAAATATACGCGGCACAGGTGTGAGGCGCTGCTCGCCCCT
TP52240	TGCAGCGCAGCGCAGCCAATCCCAACACAACA[T/C]AGATGTTATCGCAAGAGAATTGAAGATGGTT
TP52243	TGCAGCGCAGCGCAGTT[C/G]TGGGCTTCCGTTCCGTGCCAGCAAGGAAAGCCATGCATGCCGTTCC
TP52246	TGCAGCGCAGCGCATCATCATCGTCCGCAGTTGATCGTCCGTGTTCT[C/T]CTTTGGCCCGAGCGGC
TP52248	TGCAGCGCAGCGCCCTCCGTGCATTTCTTTCACGGATTTCAGCTTACGGCCCCACGGGACC[A/G]TA
TP52252	TGCAGCGCAGCGGGGA[C/G]TGATGGAAGGAGGTGGACGCGAGGAAAAGGGACAGGTGGGGAAGCCG
TP52271	TGCAGCGCAGGAGGCCAAGAGCTGCTGGCCAGCTATCCTCCTCCGCCTGTGCTTGCGCTACT[G/T]T
TP52272	TGCAGCGCAGGAGTTCGCCGCACGCCACAGCACGGGCGTCCC[A/G]CCCGCGGCCCCTACTGCCCTC
TP52273	TGCAGCGCAGGATGAGAGGACACC[A/G]ACCAAGGTTATCTTGTCTGGACGCAGCCCAGCTTCCCTC
TP52277	TGCAGCGCAGGCGCCGCGATCCCTCTCTC[A/G]GATGACCACAAGGTACTGCGAACAGAGAGAAAAA
TP52302	TGCAGCGCAGTCACCGAAGCCTTCGAGACTTCGGTG[A/C]GTGGGTGTTTGTGTGTGTATGCACATT
TP52314	TGCAG[C/T]GCAGTTGCTGCTCGTGAGTCGTGACTGATCTGAGGCGGCAACGGAATCACTGCGGTGT
TP52331	TGCAGCGC[A/G]TCACGGAACCGTGCCATGAAGAAAGCGCTGCTGTGTGACCTGTTGACTATGGTGT
TP52335	TGCAGCGCATCAGCGAACCCCTGGGCCACGAAGCGCGGGCCGCGGCCAGCGCC[A/G]AACTCGCGCT
TP52351	TGCAGCGCATCGCTGGTGTGAAGCGTTCCACCAGGACATCACCTGGGCGTGCC[C/T]TGGCGGCGAG
TP52352	TGCAGCGCATCGCTGTGGCGCTACCGCACCTACGACCGCGTCAAGCTTCAC[C/T]TGTCCAAGGAGT
TP52355	TGCAGCGCATCGGC[G/T]CGGGCCACGTCCTCGCCATCCTCAGCCTGGCCGCGTCCGCCGCCGTTGA
TP52356	TGCAG[C/T]GCATCGGCGCGGGCCACGTGATCACCGTCGTCAGCATGGCCGCGTCCGCCGTCATCGA
TP52377	TGCAGCGCATGCATA[C/T]CCACATGATGAGAGTGCGTATTTGGTTGCATCATCACGTGACACAAAG
TP52384	TGCAGCGC[A/G]TGCGCCAGCTCCCCCGCGTCCGCCACGCCGCCGCCGTACTCGAGGATGCCCCAGG
TP52392	TGCAGCGCATGGAGGCTA[C/G]CTACTTGAGGCATCCCTCAACCTGGCACTACTCTCCTAATGCGGA

Table A2 (cont.)

TP52400	TGCAGCG[C/G]ATGGGCATCGGCCTCGTCGTCTCCATCTTCTCCATGGTGGCGGCGGGCGTGCTGGA
TP52419	TGCAGCGCATGTGTGGTAGCAGCGTGGGCATGGGGAGACCGTTAGG[A/G]CGAAGGTGGATAGCCGT
TP52426	TGCAGCGCATTGATGGATCGAGCGGCCTCCTCTCGACCTCTCCTCC[A/C]CGCCGCTCGCCCAATCG
TP52428	TGCAGCGCATTGCGCTGCCGCAGGTGTCGCGTCGCTCGAACACCACGCGTTGCGTCG[A/G]TCCATG
TP52443	TGCAGCGCCAAAAAAAAGAACAGCCGAACACG[T/C]TGAAAAAAAATATTTAGTACAGTAACAAACT
TP52446	TGCAGCGCCAAAAATCGACACAACTGTGGCAGAGTTTTGTGCTGAAAAGAGCAGTGT[A/G]GCTACC
TP52447	TGCAGCGCCAAA[C/T]ATTGGTAGGTGAAAGGAGCTTTAGAGCTACGGACAGTAGTTTAGATGTCGA
TP52458	TGCAGCGCCAACGCCATGCTTGCT[C/G]TCGCCTCCAGTCTGTCTCACTCGAGTATGGGAATGGGCT
TP52475	TGCAGCGCCAAGTCGGCGACCTGTCACACTGTGAGGCCGCTGT[C/T]GAGAGCCGCCCGTCCATGTC
TP52479	TGCAGCGCCAATGGCACGGAGGCGGCGGGCGCGCTTGGGTGGCTCAACGG[C/T]CTTTACGGGTTCA
TP52480	TGCAGCGCC[A/G]ATTCTTCAGGAACTGAGGGAGCTCCTCGGCAGAGAACTCCATTGTCGCCGTGTT
TP52482	TGCAGCGCCACAACACAACAATCCGTCAGTGAACCACGAATCCACTTCCGAA[C/T]AAGAGTGGTGG
TP52487	TGCAGCGCCACAAGCAACGCAACTGTTTTTTCAAACG[C/G]GAAGAAAAGCTCACACCACCCAGGTG
TP52505	TGCAGCGCCACC[A/C]GAGGTGGTCGCAGCGGACGCCATGATGCCCTGTGCTTGCCCACGGGCGGCC
TP52507	TGCAG[C/T]GCCACCAGCTGCTGCTCTAGTTGCTTCACGTAGTCGATCGCGCCACCCACCACTGTCG
TP52510	TGCAGCGCCACCATCAGCGGAGTCTCCAGCC[C/T]GAACATCCTCGCGTCCATCTCTCGATCGCTCT
TP52517	TGCAGCGC[C/T]ACCGACACCCGCCGAGCCCAAGGCATCGGCGCCGCCGTGGCATCGCCGTGGAGCT
TP52531	TGCAGCGCCACCGCGTCGGCCTCCGCCTCCTCGCGCCACCGCGT[C/G]GGCGCCCCGTCCTACTCCC
TP52541	TGCAGCGCCACCTGCAACAAGCGATGCCCTC[A/G]CAAGTGCCTCATCCAGTGCCCAAGCTGCAAGA
TP52560	TGCAGCGCCACGCTCCACGCTGACCAGGTCACC[A/G]CCGCCACTGCGCGCGCCCCGCCCACCGCCT
TP52589	TGCAGCGCCAGACCCCT[C/T]GTGCTCCACCTTCCCCTCCTCCCGCCGCGCTCCCCCTGCCGCTTCG
TP52624	TGCAGCGCCAGCATCGCCACGTGCAGCCGC[A/G]CGGCGCGCTCCGTCTTCGCCGCCGAAAAAAAAA
TP52627	TGCAGCGCCAGCCACGTC[G/T]AGGTGTGCACCGACGCCGTCTCCTCCATCCGAATGCCATGCCCCG
TP52628	TGCAGCGCCAGCCAGA[A/T]GTCGAGGATGGTGAAGCCGAAGTTGTCCACCAGCCAGTCGGCGGACG
TP52636	TGCAGCGCCAGCCTGCAAGCGTCCAGCAGC[A/C]GCCCTCAGGCAGCTGCAAGCGCCAGCGCCGCAG
TP52640	TGCAGCGCCAGCGCAAG[C/T]GCGCCCATTGTGGTGTTCGTGTCCAAGATGTTCGCGGTGCCGTACA
TP52643	TGCAGCGCCAGCGCAGGTGGGTGTCGTGTCGTTGCCCGCTT[C/G]CTTCCGTCCAAAACGGATGAGG
TP52653	TGCAGCGCCAGCGGGCAAGCAGCAGCATCAGGGGCGGCGGTGAGCT[C/T]GTCGCCGCGGCCGCCGA

Table A2 (cont.)

TP52675	TGCAGCGCCAGGGGACCAGGCACTTCATCGGCCGAGGGCTCCTCATG[G/T]CCAACGGCGCGCACTG
TP52684	TGCAGCGCCA[G/T]TAGCCAGTAGCCCAGTACACCCCACTATCAGCAATTCGAGATTCCTGCGTCCC
TP52685	TGCAGCGCCAGTCATCCACCTTGTGCCCTGCCTCTGCCATCCAC[A/G]CGTGCGAGAAGCAGTGGGT
TP52689	TGCAG[C/T]GCCAGTCCTTGGTGGGCACTGTTGCCCGCCTCCGAGAGACCGCGAGATCATTTGGGGC
TP52721	TGCAGCGCCATCGGAACCCTGCTCGACTCGAACACTCTA[G/T]GAACTTCTCTCGTGAACGGGGCAG
TP52723	TGCAGCGCCATCTACTTCAAGGGCAGATGGGAGGCGCACACTGTGGTGGA[C/T]AAGTTCCACCGCC
TP52729	TGCAGCGCCATCTTGAAGCTACATCGGGATCGAGTACGAGACAACACACGCA[A/G]GCCAGTGCAAG
TP52730	TGCAGCGCCATCTTTAGGAGTGTCCCTGAACCACTGCTCACACACCCGACCTCTCCACCAACA[C/T]
TP52763	TGCAGCGCCCAATCCTAATTTAGCCATGGAT[C/G]GGAGCCACACTACTCAAAAGCTTTTGTCTGCT
TP52767	TGCAGCGCC[C/T]ACAGGTTCATGTCCATGGAACCATCACGGAGGACGGCCGCCACTGTCAGAACCC
TP52778	TGCAG[C/T]GCCCACGCGAAGCTCTTAAACGAGCCGACGGCGGAGCGCGACGTCTTCCCGTAGACGA
TP52780	TGCAG[C/T]GCCCACTCGTTTGTTCCGCCGCTCGCTCCTCGTCCTCGCTTGCCCGCCACCGAGAGAC
TP52783	TGCAGCGCCCAGACCTC[A/G]ACCTCCTCCTCCTGCTCCTACACAGCAGCAGTCCTCATCATCGGAT
TP52786	TGCAGCGCCCAGAGCGCCCAGTCCAGGTCCAGGTCGGCCGCGGC[C/G]GCGGCGGCGCAGCCGTAGT
TP52807	TGCAGCGCCCATCCGAACTGGACGCCCGCGGCGACCAT[A/G]CAGGCGAGCACGAGCTTGGTCCTGT
TP52817	TGCAGCGCCCCAAATCGCCGCCGCCGCCGCCATGGCCGATTTCGGCCCAAGGTCTCAATCT[A/C]CC
TP52834	TGCAGCGCCCCCGTCAGGTTGTTGCCGTT[C/G]AGGTACAGCGCGCCGATGCTGGGCAGCTGGGCGA
TP52841	TGCAGCGCCCCGAA[A/C]ACCCTCCTCCCCCTCCTCCTGGCGTCCTCCCCAGTCACTGCCCGTCGCC
TP52845	TGCAGCGCCCCGATACATGTTCTTCTTCTTTTCTCGGGTTT[A/T]TATCAGCGGTACGTCGTTGGAA
TP52848	TGCAGCGCCCCGCGGAGTAGCGGGGGCGGCGGGGC[C/G]AGAGGCGCACCCGAAAAAAAAAAAAAAA
TP52850	TGCAGCGCCCCGCGGTGGCGGAGATGGCCGTCGACG[C/T]GCTGCTCTGCGCGGTGCCGATCTGGGC
TP52853	TGCAGCGCCCCGCTGAAC[A/G]CCCCGTACGCCGCTCTGCCGCCATCCGCAGACACCTCCAGCGAAA
TP52856	TGCAGCGCCCCGCTGTTGCGCGCACCGATCGATATCACAG[C/T]GGTCATTCACGGCCAGCTGACCA
TP52861	TGCAGCGCCCCTCAACTTTGGCAAGGGTGA[A/G]CACCGAATTGCACAGACAGAGCTCAGGCGTCTC
TP52864	TGCAGCGCCCCTCTCCTCTCCTCCCTCCTGAGCCCACCCCCTCGTGG[C/T]GTCGCCATGGATGTCC
TP52888	TGCAGCGCCCGCCACAACGGCTCGCCTCGCACTCGCGAAGTCGTCGCAGTGCATTATA[G/T]CGTCT
TP52894	TGCAGCGCCCGCCGTCCGCGGAGGCGCCCTTCTGATCTCGGTCGCAAATTAATTAAAGC[A/G]GTGG
TP52899	TGCAGCGCCC[G/T]CGCCTTGGTCTCGATGATGGCCTGCCCGCAGAACTGGTTGCCCGTGCACGCCA

Table A2 (cont.)

TP52910	TGCAGCGCCCGTACGGATTTCCCCTGGCAGC[C/G]GTGCCCGTGCACACAGACAGGCGAGCGAGCGA
TP52922	TGCAGCGCCCGTGGCGACTTGCTCATGGTTTGACACGTCTTCAGTACCTA[C/G]CTAGTGGCAAGTG
TP52954	TGCAG[C/T]GCCCTGGCCTCCATTGCCCTGTTCGCCAGTGGATTGCCCGTCACTGCACGGGCCCGTA
TP52972	TGCAGCGCCGACCGA[C/T]CGAACCCAACGGCACGGCAAGCTAAGCGAGGCTGCGAGGCGGTGGCCG
TP52975	TGCAGCGCCGACCTCATCCTTGGCCCACCG[C/T]CCTTCCTGCTCAACAAGGTACTGCCTGGACCAA
TP52985	TGCAGCGCCGACGCGATGAGGCGGCG[A/G]TGCGACTGCGCCACCGCCTTGGTTCGCCCTGTCGTGC
TP53003	TGCAGCGCCGAGCGCAGCTTGGTAGCTTCCTC[G/A]TCGCCAGAGTCGAACGCCAACAGCCGTTGGA
TP53019	TGCAGCGCCGAGT[C/T]GTGACGAACGTCACGGCACGCGGGGTCATCTCGAGCAGCTCCTCCTCAGC
TP53020	TGCAGCGCCGAGTGATATCGGTGGACTCCAACCCCGTT[A/G]AGCAAGGACTGGTGCTATGGTCTGG
TP53022	TGCAGCGCCGATCTCGTGAC[A/G]AACGTCGTGGCGCGTGGGGTCATCTCGAGCAGCTCCTCAGGCG
TP53028	TGCAGCGCCGCAACCAACGCCCA[A/G]CTCACTCCCGCCGCTTCCAGTTCCCACCCAACCGAGCTCG
TP53038	TGCAGCGCCGCACGCAGCTCCG[C/T]CGCCTGCCTGCCCTGCTCCTCCACCCAGTGCGCGTACTCCA
TP53055	TGCAGCGCCGCCACCGTC[A/G]TCGCGAACACCATGTACGCGCATCCCTGCAATGCAAACCAAGTTG
TP53056	TGCAGCGCCGCCACCGTCGTCGCGAACACCATGTACGCG[A/C]ATCCCTGCAACCAACCAGCAAACA
TP53071	TGCAGCGCCGCCCCGAGGAGCTCACCAGGGC[A/G]CCGATGGTGCAATTCTTCGGAGGGACAGCGAC
TP53075	TGCAGCGCCGCCCTCCGCAGCGGTGGTGGCGCGCACCAGG[A/C]GACGCAGCATCGAGCGCATCTCG
TP53109	TGCAGCGCCGCCTCCCCCGC[A/C]GACGGTAGCGGCAGCCCCGTACGGATCCCTACCATCTATTGAC
TP53115	TGCAG[C/T]GCCGCCTGCCGCCTGCCGCGCGCGGGGTTGGGGCGGTTGTTGTTGACTTGTTGGTGAG
TP53118	TGCAG[C/G]GCCGCCTTGGACGGGTACTGGCCCTCGAGCCGTGGGTCGACGAGGCGCGCCAGCTTCC
TP53120	TGCAGCGCCGCGAACGCGCTCCTGTCCCAGAACGACGGCAACAC[C/G]ACGGTGCCGCTGACGGCGC
TP53126	TGCAGCGCCGCGACGTCGGCAGCGGACACGCGGTAGATGCGGTTGG[A/C]GGCGGCTGTGTCTGGCA
TP53129	TGCAGCGCCGCGAGATCGGGGGCCGCCAGCTCGCCGCGCGCGGCGG[A/C]GGCCCCGCCGCCGCCGT
TP53131	TGCAGCGCCGCGAGCGGCTCAAGGCTCCCCGAGAGCTCGTTGTGCGA[C/G]AGGTCGAGGCTGCCGA
TP53150	TGCAGCGCCGCGCCGCTTGCGCATGTGAAATTTTTGTATTTTGGTCTCTTTTGAAAA[C/T]AATTTT
TP53157	TGCAGCGCCGCGCGCCCTGCAACTTCCTCGTCTTCGG[C/G]CTGGGCCACGACAGCCCGATGTGGGC
TP53164	TGCAGCGCCGCGCGTTCCGCTGCGCCCGC[A/G]ACGAGCTCGCCGCCATGCCGCACTTCCCGCGCCG
TP53182	TGCAGCGCCGCGGTTGGCCATGGGCGCGGGTGTGTCCACCCTGACAGAGGGCCACCGC[C/T]CAGCG
TP53195	TGCAGCGCCGCTCCCAGGACGTGGACCTCGACATGGTGGACG[C/T]CAAGGTGCAGAAGCTCATGCC

Table A2 (cont.)

TP53196	TGCAGCGCCGCTCCGACCGCGTCACCGCCGCCGCCGCGGCGCC[A/C]GACGCGCACGCGCCGCGCAC
TP53225	TGCAGCGCCGTCATGAGCAGCAGCCCGACGGAGGCGAT[C/G]AGCGTCAGCACCTTCCACGACCTGA
TP53228	TGCAGCGCCGTCCACCTCCCGAACAGCAAGCC[G/C]ATGCACTCCGCCATTGCCGCCGCCCCCTCAT
TP53238	TGCAGCGCCGTCGCTGACGCTGAGATCCTCGCGGCCGCAGCCGAGGCCTGCCCT[A/C]GCCTGAAGC
TP53240	TGCAGCGCCGTCGGAGGTGAAGCTCCTTCTCTTCTGC[G/T]CCGCCGATTGGGAGGCTTGGGCTGAG
TP53263	TGCAGCGCCGTGCA[C/T]CCCGCCGCTCTCGAGTGACGCCAACACGGGTCTGCACACTGGCTGCGCG
TP53265	TGCAGCGCCGTGCACCC[C/T]GCCGCTCTCTAGTGACGCCAACACGGGTCTGCACGCAGGCTGCGCG
TP53279	TGCAGCGCCGTGGAG[C/G]TGATCGACAAGCTGGTGCAGGCGCTCACGTCCACGTCGGCGGCGCTGC
TP53289	TGCAGCGCCGTTGGACTGC[C/G]GATGATCACTCGGTGGAGCAAGGCCTCATTCTGTGGACCAACTC
TP53291	TGCAGCGCCGTTTTACCAGCCAGAGACAT[A/G]GTGTAGCGGAGGCCCTCGCCTTCACCCGTGCGAA
TP53314	TGCAGCGCCTCAAATTCGAGCGCCATGGCAGCACGC[C/T]AGTGTGGATCCTTCAGAGCAGCTCTAG
TP53326	TGCAGCGCCTCATCGAGTC[A/G]CATCTCACCGTGCCCGTCCCGCTCCAGCGCCTCTCCCTCGACCC
TP53339	TGCAGCGCCTCCCAGACGAAGACCAAGAAACCACGGGACTCCGCCTCCG[C/T]GAACTTGTTGACGC
TP53340	TGCAGCGCCTCCCAGACGAAGACCAAGAAGCCACGGGGCTCTGCCTCCG[C/T]GAACTTGTTGACGC
TP53343	TGCAGCGCCTCCCCCTGTCGCGTCTCCACCCACCTCGCTCCTCCTGCCTTTC[A/G]AACCATTGCTG
TP53350	TGCAGCGCCTCCGCGAGTTGCAAGGCCATCGCCGTCGGTCGATCGCATTTCCCATCA[G/T]CTCGTC
TP53352	TGCAGCGCCTCCGCTCCTTCTCCATCTTCTCCTTCCCCTCCGCCT[C/G]CTTCAACACCACGCCGTT
TP53360	TGCAGCGCCTCCTCGACGCCCGCGAGGCAGGC[G/A]GCGCCAGCCGCCGCCGCGCCGTCGACGACGG
TP53381	TGCAGCGCCTCCTTGTTCAATGCCTTCGCC[G/T]CCACGGCCTGAAACGGACATCGTTGCACTCAGA
TP53390	TGCAGCGCCTCGACGGCCGCGACGACGGCGTCGGT[A/C]GCAAGGCGCTCGCCGAAGCACATGGTGA
TP53393	TGCAGCGCCTCGAGCTGTTGCTTCTACCGCGTGTTGACGAGG[C/T]CCAAGAAGTAGACCGATGTCC
TP53394	TGCAGCGCCTCGAGGAGCGCAGGAAGCAGGGCCTGGTCCCCGCCT[C/T]TGACGACGACGAGTTGGA
TP53403	TGCAGCGCCTCGCCTGGGTCGGCGACGACCACCAGCGCTTCCTCTCCAAGTTTAAGGACCGC[A/G]T
TP53409	TGCAGCGCCTCGGACAGCGTCACGGCGCCATTACCGCGTTGC[A/G]CATCTTCCTGCTTGATGCCGT
TP53438	TGCAGCGCCTGACGACGAAAGCCCGCCGCGGGATG[C/T]GTTGAGCTGCTCGAAAACCTCTTCCAGG
TP53448	TGCAGCGCCTGCACGAGGCCGACATGGTACGTTTTTTTCCTCGTCCTTCTCCTTCTC[C/G]TGCACG
TP53452	TGCAGCGCCTGCATC[G/T]CCCTCTTCTCCAGCCTCGACGTCCTCTCCAGCCTGCTCTCCGTCAGCA
TP53471	TGCAGCGCCTGCGTCG[C/G]GATGTCCGTAGGGTAGCCTGCCATGAGCATGAACAGCTGGTCCAGGC

Table A2 (cont.)

TP53496	TGCAGCGC[C/T]TGGCCCCGCGCATCCTCCCCGCCCGCGAGCTAGCGCGCTTCGCGTCCCGCCTCCT
TP53511	TGCAGC[G/T]CCTGTACCCTCTCCTTGGCCACAGCCATCGCCCACTTCCCCTCCTTTTCATCTTCCC
TP53514	TGCAGCGCCTGTAGACGTAGTCAAGTCACTCCTCCACAGCAATGCAGCAGCT[C/T]TCGAGGAGCTG
TP53528	TGCAGCGCCTTCATCTCCACGCAGCTCAGCCTCAACTCCC[C/G]CCTCCACCTCCTCTCCTCCGCCG
TP53547	TGCAGCGCCTTGC[A/C]GAGGAGGAGCTCGTTGGTGTGCGGGCCGTACAAGTCGGAGGTGTCGAGGA
TP53557	TGCAGCGC[C/T]TTGGCCGACCTGGGGTGCTTGATCCGCTCCTGTTTCCCGTCGCCCCCTGCTCACC
TP53562	TGCAGCGCCTTGGTGACCTCGGCGACGGTGATGAGGCGGTACGCCTGGCC[G/T]AGCACCAGCGTGT
TP53564	TGCAGCGCCTTGTCCGACGCCCCGCTCCGCGCGATGCACCACG[C/T]CGCGCCCGCCGAAAAAAAAA
TP53567	TGCAGCGCCTTTATTGCACTCACCAGCCTTG[C/T]CCTTCCCAGCTGCCCTGCCCTGCCAACGTCGT
TP53589	TGCAGCGCGAAGCCCCGCAGC[A/T]TCCGCAGCGACGACTCCATGTCCTCGCCCCGCGAACCCGAGT
TP53590	TGCAGCGCGAAGCCCCGCAGCTTCCGCAGCGATGACTTCATGTCCT[C/G]CTCGCGCCTTGCGCCCC
TP53601	TGCAGCGCGAAGTCATTGC[A/T]CTTGGCGGCCGACGAGAGCACGCAGGCGGTGTCCGCGTCCTCAA
TP53614	TGCAGCGCGA[C/T]CGCAACGGGGATCGGCGGCTATCCGAGACAACAGAACGCGATCTCAGCTTGGT
TP53619	TGCAGCGCGACGAGCCGCGCG[G/T]TAGCGGCGTGAGGCGGAAGGCGCGAGCAACGGTAGCGGCACA
TP53621	TGCAGCGCGACGCACCGCGCCCGCGCCAGCTCCAG[C/T]TCGGAGTCGGCGGCGCACACCTGCCGTG
TP53624	TGCAGCGCGACGCCGAACACGTCGAAGCGGGCCTCGCCGTAGGCGGCGACGG[C/T]GACGCCCGCGG
TP53646	TGCAGCGCGAGACGCGC[A/G]AGAGGGGTTAGATGTAGGCTCAAAGCGGCACGGGGTTACAGGAGAC
TP53665	TGCAGCGCGAGCGAGCGAGGCA[A/G]TACGTCCGTTGGTCGGCTCGCCCGCCACACACGTCGCGCAT
TP53667	TGCAGC[G/T]CGAGCGCGTCGTCGTCGGGGCACTCGCCGCTGACGTTGTACGTCATGTACTGCGCCA
TP53689	TGCAGCGC[G/T]AGGCGAGCAACGGCTGGCGCTGGGAAGGAAGGACAAGAGCAACGCGATTCGCATG
TP53692	TGCAGCGCGAGGCGGCGCTGTACTGGACCAAGG[C/T]GGCCAGGGAGAAGCGCGCCGCGTGGAGATC
TP53699	TGCAGCGCGAGGGAGAGCGAGAAGGAGTTGCCGAGGAGGCGGGGCGCCCGCGGCAGG[A/C]GCGAGC
TP53701	TGCAGCGCGAGGGCAGCCAGCGTTCCC[A/C]GCCACGGCGGCACGCGGCAGTCCACGGCGGCCCCTG
TP53704	TGCAGCGCGAGGGCGCGCGCGCGGGTGCGG[A/G]CTCCGAGCGGAGCGGAGGACACATCCATGATGG
TP53737	TGCAGCGCGATCAGCGTGCCCACCACGATCTG[G/C]GAGATGAACATCTGCGTGCCGCCCTGGAGGA
TP53755	TGCAGCGCGATTT[C/G]GTTAATTTGCTTGGGTCTTGTGTTGACGTTTTCCTCTGATTTTGTTTCGG
TP53757	TGCAGCGCGCA[A/G]CTTTCAAAGCGTTGGGAGAGATGGCAGAGGAAACGCAGCCAGAGGCCGCCGC
TP53760	TGCAGCGCGCACAAATTGGCCCGCGGGGCGCCGTCGTGTGGGGCAGCAGG[C/T]GCACGCCCTGGCC

Table A2 (cont.)

TP53765	TGCAGCGCGCAC[A/G]CTACCACCACCTCCCTGCACTCCCCATGCACGACCGTCTCGAACGCAGGCT
TP53767	TGCAGCGCGCA[C/G]AGACAGCACGAGACATTCTTTTCGTTTTCAGAAGAAGGCAGAACCGAAGAAG
TP53774	TGCAGCG[C/T]GCACGGACCAGATCTATCCCGCACCAAACGTGGCGGCGCCTTCACCCCTACCGTCG
TP53795	TGCAGCGCGCATCGCTCGCTCACTCACAGTCAGAGCACATGTTTTG[C/T]CCCCTCACGAAGCGACC
TP53804	TGCAGCGCGCCACGCCGAAGATCTTGAGGTAGAAGATGCAGGGGAGCAGCATCGCGGCCAT[A/G]AC
TP53811	TGCAGCGCGCCATGTCCGACCTGGC[C/T]CTGGAGCTGTCCAGGGACAGCAAGAAGGCCGAGGCCGC
TP53823	TGCAGCGCGCCCTCCATGCC[A/C]GACAAGACCGTCTGCGAGAAGCACTACGTCCAGGCCAAGAAGC
TP53826	TGCAGCGCG[C/G]CCTCGGTGCAGAGCGCGGCCAGGTCGGCGCCGACGTAGCCGTGCGTGTCCTTGG
TP53834	TGCAGCGCGCCGAGGTCGGC[A/G]ACGATGGCCATGTCCACCTCCTTGAGCACGAACGTGGCGTCCC
TP53839	TGCAGCGCGCCGCCGC[C/T]GAGCCGCTCCTCTGCGTGCGGCTCTACGTCTGGGCGTCGCGGTTCGG
TP53840	TGCAGCGCGCCGCCGCGCTCTACAACCCGCAG[T/C]TCGTGGACATGATCAAGGGCGTCAACGCCGA
TP53847	TGCAGCGCGCCGTCCTCCGCGTTGTTCTTGGCAACGCACCACAGCAGG[C/G]CCCCACCACTCACCC
TP53854	TGCAGCGCGCCGTGCCGTTGATGGTCCG[C/T]CCAGCACCCAGGCTGCTGCCGTCTGCCTACGCAGC
TP53887	TGCAGCGCGCGACGGGCGCGGTGTGC[A/G]CCGTCATCGGCAGCTTCAGCGGGCGGGACTCGAAGAA
TP53893	TGCAGCGCGCGATGAAACGATCCGAGACAGGCAGAGAGAGATGCTCGGC[C/G]AGTCGCCATGCTAT
TP53895	TGCAGCGCGCGATGAGACGATCCGAGACGGGCAGAGAGAGATGCTCG[A/G]CCAGTCGCCATGCTAT
TP53904	TGCAGCGC[G/T]CGCAGAGTCGCCGAGCTCGAGTCGGTGTCGGATTGCTCCAATTCGATGTGCTCGC
TP53907	TGCAGCG[C/T]GCGCAGTGCATGCCAGGCCGTGCCGTGCATGCCCGTGCGATGTGACGGCTTGCATG
TP53917	TGCAGCGCGCGCGCG[A/T]AGTAGTCGTGCGGCTCCAGGTTGGAGCAGGTGCCGTGCTTCTTCCACT
TP53930	TGCAGCGCGCGCTGGGGCTCCCGTTTTTGCGGCTGTACTTCG[G/T]CGGGCGGCGCGTCGCGGACTT
TP53945	TGCAGCGCGCGGCGCACCGCCAGGAGGCTCGCCAGCGGCCG[C/T]GCCTTTCTCTCGTCATCTTGGC
TP53969	TGCAGCGCG[C/T]GGTGGTGCCTTTAGTAAATCACACTGTCATGTCAAGGTGCGGCACCACACTGGT
TP53977	TGCAGCGCGCGTGGCGTCCTACGTGGAAGCA[A/C]TTTCGAGATCCCGTGCGGGCGAGGAGGGCCTG
TP53986	TGCAGCGCG[C/G]TACCGAGCGCGGCGCGGAGGCTGTCGATCTCGTCCCTGGGCAGCACCGCCGTGA
TP54000	TGCAGCGCGCTCTCCTTGTCGGCGACGGCGTCGTTGAGGCGCGCGTTCTCGGCCCT[C/G]GCGAGCT
TP54018	TGCAGCGCGCTGGTTGAAATCTCCCTCGATGGCAACAGGGTTTGGCGGCGCCA[A/T]GCCAGGCTCG
TP54030	TGCAGCGCGGACATGGGCGCCGCCCACTGCGC[T/C]TGCTTGGGCGGCGCGACGGGGGGGTTGCTGG
TP54034	TGCAGCGCGGACGCGGCTGAGCAGGCACCTGAGCG[C/T]GTCTAGCTTGCCGCTGACGACGGCAGCG

Table A2 (cont.)

TP54044	TGCAGCG[C/T]GGAGACGAGCGCGGAGACCAGCGCGTCGTTCGTCTCGGCGACGCGGCGCAGGCACT
TP54048	TGCAGCGCGGAGCAG[C/G]TCAATCCAGAGCTCTAATGGCGACGCTCCTCCTTCGGCTGCTGTTCTT
TP54051	TGCAGCGCGGAGGACAAACGATGAGGCGGGGGCAACCAGGACGAA[C/G]CGAAAGCTTTAGGCGAGG
TP54055	TGCAGCGCGGAGGAGGGGGTGGCCGTATGCGTGCGCCGAGCCCTTGTTTATCCCA[A/G]TATTATAC
TP54080	TGCAGCGCGG[C/T]CACGTAGTCGGCGGCCTCCTCCAGGAGCGCGGGCGCGGGGAGCTTCCGAAAAA
TP54081	TGCAGCGCGGC[C/G]AGCGTGCGCAGCAGCGCCGACGTCGGCTCCCCCGCGAACAGCCGCCCGAAAA
TP54093	TGCAGCGCGGCCTCGACCCCCGC[A/G]GCGCGCGCGAGCCCGCGGAACCTCATGCTGCCACGGCTCA
TP54102	TGCAGCGCGGCGAACTTGCCGCGGTTGGCGGTGCACTCCTTGAGCATGGCCTCGAAGGCCCGC[A/G]
TP54105	TGCAGCGCGGCGACCGAGTCGAGCTCGGA[C/T]GCCACGGCCTCGTCGGCGAGGGCCACCCTGTCCG
TP54121	TGCAGCGCGGCGAGGCCGCCGAGCTCCCTGGGGATCCCGCCACGGAAGCCGTTCTGCGAGA[C/G]GC
TP54141	TGCAGCGCGGCGCTGAACGCCCCGCACGCCCTGCCGCCGACCGCC[A/G]CGACGTCGTCCCCCGCCA
TP54144	TGCAGCGCGGCGGAGCGGCGGTTCCGCCAGGTGAGCGTGGCGTTCTTGCGGAGCAGCGCGC[A/G]GT
TP54145	TGCAGCGC[G/T]GCGGCAAGAGCTGCCGCCTGCGGTGGATCAACTACCTCCGCCCCGACCTCAAGCG
TP54155	TGCAGCGCGGCGGCGCTGGCCGCCGTGGAGGCGGCCGCGACGTAGAGGCA[A/G]TTCACCGCCGCCA
TP54157	TGCAGCGCGGCGGCTCGGAGCTAGGATTTGTTTAAGCACCGTGG[A/G]ATGGCAATGGCATGTCGTC
TP54160	TGCAGCGCGGCGGGCGGGATCCAG[C/T]CGCTGAGCACATGCATGGAGTGCACGATGTCCAGCGTGT
TP54164	TGCAGCGCGGCGGTGCGGCGGCGCA[A/G]CGGGTTGACGGCGGCGTAGAGGCGCATGGTGTCGGCGT
TP54168	TGCAG[C/G]GCGGCGTGCACGAACCCCTTCTTGAAGGGCAGCAGCCTGCCGTTCTTGGATCGTGTGC
TP54171	TGCAGCGCGGCGTTGGCAGCCAGGTTACGGCGGAGGGGGCCA[C/T]TGGGTTGTGAGAAGGATGGCA
TP54184	TGCAGCGCGGGACCCACACGCACCCCGCCCAGTTGTCCGTCGGTCCACACTGGCCTTGG[C/G]GTGG
TP54186	TGCAGCGCGGGATTTGATTGGGCGCACCAATGGATCTGCTGCTCACACGTAGTAG[C/G]CAACTACG
TP54190	TGCAGCGCGGGCACGGGCCCAGGGCTGCTAGGCTGCTAGCAGTCATA[C/T]TCCCAGAACGATAGGA
TP54196	TGCAGCGCGGGCAGGCGGCGGGTTTCCTGGTCCTGCCGCCGCACGCG[A/G]CGAAGTGCCGCATGAG
TP54205	TGCAGCG[C/T]GGGCGATACAGCCCCAATGGATCTGACCAGGCAATCTTCTACAATTCCACCAGCTA
TP54221	TGCAGCGCGGGGC[A/G]GATGCAGTCCCCGATCGACCTCTCCCACGAGCGCGTCTCGCTGGTGCGCT
TP54233	TGCAGCGCGGGTCCACCAACTGACTGGCTGGGAACAGTACTGTACAGACGTACACGCA[A/G]CATAC
TP54257	TGCAGCGCGGTGCTTCCAGTCGGTCGCCGCAGCACAGACCCAGACCATTTCCT[C/T]CGCACATCAA
TP54269	TGCAGCGCGGTGTAGATGGTCTCCACCATGAGCATG[A/G]CGAGAACAACGGCGAGGATCGCCCATG

Table A2 (cont.)

TP54278	TGCAGCGCGTAATATATAGACGTACGCCGCGCCGCCGCCGCCTGGGAGCTGGC[C/T]GACAAATGCC
TP54288	TGCAGCGCGTACGCGTACATGAGGTTGTCGAAGCCGATCAGGAT[C/T]CCGATGCCCAGGTACACGG
TP54304	TGCAGCGCGTCATCGTCTTCGGCGACATGGGAAAG[A/G]CGGAGCGAGACGGGTCGAACGAGTACGC
TP54317	TGCAGCGCGTC[C/T]GCCTCATCCTCCGCCGCGGCGGCCTGGGACGACGACGGAGACGGTTTCTGCG
TP54336	TGCAGCGCGTCGGCGAGCTCCTCGA[A/C]GTCCGTGGCGTCACTCTTGAGGCTACGCTTCGGGTTGG
TP54347	TGCAGCGCGTCGTCGACCTTGAACACCACGAAGCGGTG[C/T]GCGCGGCCGCCGCGCAGCTCCTGGA
TP54357	TGCAG[C/G]GCGTCTGTAATCCCCATCTGTTGCATACGGTGTCTCAGCACACGACACGTCGACACCC
TP54362	TGCAGCGCGTGACTCAAGTTCAGCAAGTGGCGTCATCACTTGTCACTTCCATTGAAGAATC[G/T]AA
TP54363	TGCAGCGCGTGAGGGCCGACGGGTCGCTGGCGCGGGCCACC[A/T]CTGCGGCCAAAGCAGCCGCGGA
TP54380	TGCAGCGCGTG[C/T]GCCGCTCCTCCACTGGGGGCCACTGTGGTGCTGAAGGGAAGGAGAAAGGGAT
TP54392	TGCAGCGCGTGCTCGCACCGTGCCTCGGCAGCTCGCGCCCTGGCTTTGCCCGCGCTCG[C/T]AGCCC
TP54396	TGCAGCGCGTGCTTCACGGCGTTGACGATGCTGAACCAGC[A/G]GAGCGTGTGGTTGGGGATGGCAG
TP54399	TGCAGCGCGTGGACCGCGCGTCGGCATTGCTCCGCGC[A/G]CGCTGCGGCGGCGCGGCGGTGGTGGA
TP54403	TGCAGCGCGTGGCCCCCGTCCAGCTCGGCCTCGGCCGACGGCGGCATCGAG[A/G]TCGAGCTCGAGC
TP54405	TGCAGCGCGTGGCCCTGCAAGAAGACGCCGTCCGCGGGAACC[A/G]CGTCGCCGATGTTGAGCACGA
TP54411	TGCAGCGCGTGGCGTACCTCAACATGTCCACCTACCCGATCGTCACC[A/G]TCTTCATCCTGGCCTA
TP54414	TGCAGCGCGTGGGCC[A/G]CATCGGGCTCACTGACCGCCAGCACATCAGGGCCCTGCACGCGCTGGG
TP54432	TGCAGCGCGTTCGCGCGGCCGTCACCCATCCAGGCACACGCCTGGCCGTT[C/T]CTCCTCGACGGCC
TP54434	TGCAGCGCGTTCTCCTTGTCCATCAGGCACGC[T/C]TTCAGCTCCGCGACGTCCGTGAGCGACCTCA
TP54435	TGCAGCGCGTTCTGGTTGACGCTGGCGTTGCTCGAGAGCGTCAGGTCGGCGGGG[G/T]TCTTGTCGT
TP54436	TGCAGCGCGTTG[A/C]ACTGCACCTGCAAACGTATAGTACGTACGTTCCAGTGTCAGTGTAGCCGAT
TP54454	TGCAGCGCTACACGCACGCACGCGCAAGCGACGAGCGAGACGACGTCAGG[C/G]AACGGAGGCGACG
TP54473	TGCAGCGCT[A/G]CCTCAAGAACGGCGTCAAGCTTCCTCGCCGTCCTCTTTGTCCTTGCGTCGAGCC
TP54553	TGCAGCGCTCCAAGGATACAATAGAC[G/T]CATGCATGGGCCCGTTCGGGGTCATGATCCGATCCGA
TP54561	TGCAGCGCTCCATGCTCGAG[A/G]AGCAGTGGGAGCTCCCCTTCGAGGACGAGGACGAGGAGGACGA
TP54571	TGCAGCGCTCCCCGCGCCCAGACCGTAACCTGGGCTTGGGCTGGCATTTCTT[C/T]GTCCCGCCTGG
TP54576	TGCAGCGCTCCCTCCTGACGTAGCACCACCAGTGGATGCTGCCTTTT[C/G]TTTCTTGGGGATTGGG
TP54605	TGCAGCGCTCGCCACCTAGGAGCTTATGCACGGACGCAAACACACCCGATTTGCA[C/G]GCTATTAT

Table A2 (cont.)

TP54613	TGCAGCGCTCGCCTACTGCTCCTGCGCTTCCCACC[C/T]GTCTCTGCTCTGCTGCGAACCATCGCCA
TP54619	TGCAGCGCTCGCGCTACTGCTGCCGCTCG[A/G]CGCCTCCGACCGCGCTGATGACGAAGACGCCACG
TP54620	TGCAGCGCTCGCGCTACTGCTGCTGCTCGGCGCCTCCGACGATGACGACG[A/C]CGCCACGCACCCT
TP54622	TGCAGCGCT[C/T]GCTCCAACATGCCTGCGTCGCGGGTATCGACATGGACGAACTCAGACTGCCCCC
TP54628	TGCAGCGCTCGCTCTTCCCAAGCACAAGACCCGCCTCCTGATCCGTCCGTAGGTGA[A/G]CCATGCA
TP54633	TGCAGCGCTCGGTAAGCCCCATTCGCCGACCACCCATCTTTCGCTCGTTTCCCGTACCTCG[A/G]AC
TP54636	TGCAG[C/T]GCTCGTGCTGCTGGCTCTGGCTGCTGCGGCGCCTGGCATTGACATTGAAGAAGGGCAT
TP54646	TGCAGCGCTCTCA[C/G]ATTCTCGTGCCACCCACTGCTGACATGCTGAACCGCTCCCCATCTGTGGC
TP54662	TGCAGCGCTCTTAGCTTAAAAACAGCTCCGCTCGGG[C/T]GAGCGTTGGGTAGGTTGACGCCTGAAG
TP54684	TGCAGCGCTGACAAGTGGGCTTATGCTGGGCCCACATGCCATGGAGCAGC[A/T]CCTCGCGGTTATG
TP54696	TGCAGCGCTGATGG[C/T]CGTGAACTCGAACGGGAGCGGCGGCGACCAGGGTCCCGATGGAGAGATG
TP54727	TGCAGCGCTGCATCTGATCGATCTCGCTAGGTGCTATAGGCACAGGTTCG[A/T]ACCCGACCTCCTC
TP54730	TGCAGCGCTGCCAG[G/T]CTAGGACGACGTGACGACCAGCGGAGGAGACCAACAGCGGGGTGTCGGG
TP54749	TGCAGCGCTGCCTCCACCTCCAGAGACCGAGGAG[A/G]GAGGATGAGAGCGAAGAGAAGTAGGAGGT
TP54751	TGCAGCGCTGCCTGAACGAGCGTCCTGCACCTGGGGACTAGGACGAGGGGAACCCGCCGCG[A/G]CC
TP54763	TGCAGCGCTGCGGAGGCCGCGGCGGCGTGCACCGCGAG[C/T]AGCAACAGAAGCAGGCAACGGCGCG
TP54769	TGCAGCGCTGCG[G/T]CTCAAACGGCGGTGGCGGCGCCGAGACGCGCGAATGCGCAGGGGGTGCCGT
TP54776	TGCAGCGCTGCGTTGGC[A/G]GCCAGGTTACGGCGGAGCGGACCATTGGGTTGTGAGAAGGTTGGCA
TP54783	TGCAGCGCTGCTCGCTAGGTCGAGCCACGCTTCT[A/G]CGACACCGATGCAAATCGACATCGTGCCT
TP54788	TGCAGCGCTGCTGCC[A/T]CTGCAACAGAGAGCTCGCCGAGGGCATGGACATCTACATGTACAGGTA
TP54814	TGCAGCGCTGGAGCACTGAGTGGAAGGCGGAGCCGCGGAGGCAGCAG[C/T]CAGAAGCGCGGAACTG
TP54818	TGCAGCGCTGGCACGAGGGGAAGGCGGCGCCGACG[A/G]AGACGTCGTCGACGACAGCGACGAGGCG
TP54832	TGCAGCGCTGGCTGGGGCCTGGG[G/T]TGGGTGCGTCACGTGACTAGGACACCCGAAGCATCGCAAC
TP54852	TGCAGCGCTGGTCTGGAACACACCTTTTATTTTAGAACGTCTGCGACACACACATTGGAGAGA[A/T]
TP54855	TGCAGCGCTGGTGCGGCGGTTCATGAAGCTGTTGGG[C/G]AGGAGGAGGAGCTGCGCGAGCCAGTCG
TP54862	TGCAGCGCTGTAGTTGATGTAGCTGTTGGTGTTGAGTGCGCC[C/T]GTGGCTTCTGCCCTATTTGCT
TP54863	TGCAGCGCTGTC[A/C]AGAAGCATTGATTGGTTGTGCCTAAATTATGGTTAGGCTTGCGGGCACGGG
TP54876	TGCAGCGCTGTCTGTGCCCTAG[C/T]GCCGCCATCCGAGCTCGCCGAGAAGAAGCCGACGCCGTCAA

Table A2 (cont.)

TP54877	TGCAGCGCTGTCTTGATCTTCTTGATGGTGCAGGATAT[A/G]AGGTTGTTCACGGTTTCTACTGATT
TP54881	TGCAGCGCTGTGCCGCCACGGCCTACATACGG[G/A]TCGTCGCACAAACGCAAGGGTGAGCAGCAGG
TP54904	TGCAGCG[C/T]TTAATCTCAGCCGTTCATTCCACCTACCACGGCCTACTCTGGCCTTGCATCCACTG
TP54908	TGCAGCGCTT[A/C]CCGCCCCATGGGCTCCTCGAACGTGCCCTCCGATTCGTAGTAGGTGCAGGACG
TP54923	TGCAG[C/T]GCTTCCTCCTCCCAACCGCATGCCCACCTTTAGCAGCAGCAGCAGCGGCACTCCCTCT
TP54932	TGCAGCGCTTCGTGCGGCACGCGGGGCTCAAGGCGC[C/G]CGTGGCCGCCGAGTTCAGGACGCTCGA
TP54937	TGCAGCGCTTCTGTAATCCGCATCT[A/G]CTGTATACGGAGTCTCAGCATGCATTCGACACGTCGAC
TP54940	TGCAGCGCTTGAATCTCAGTGAAGACAGA[C/T]GCAGCCACCCTCAGCAGAGCTGAGCCTTGAGATG
TP54975	TGCAG[C/T]GCTTTCAGTGAAGCTTCCTTCGCCACATTACTTACTCGCTACTCGCTTAGCTAGCTAG
TP55006	TGCAGCGGAACACGTTTGAACAATAATTCAGATGAGACACACTGATGATC[A/T]ATATATATATTCT
TP55015	TGCAGCGG[A/G]ACGCGGAGGGAGCGGAGCGCGGTGAGGAGCGGCGGGATGAGCGGGAAGAGCCGCG
TP55062	TGCAGCGGAATACGCGACAAACTTTCTTTCTCCAGGATAAACGGGAGCTGTGTCG[A/G]CCACAAAT
TP55067	TGCAGCGGAATCGCCAATTCAAC[A/C]AGTGAGCACCAAGCAAGCACAAAGAAAGCTTTGTTGGTAG
TP55068	TGCAGCGGAATCGCCAATTCAACAAGTGAGCACCAAGCAAGCGCAAAGCTTTGCTGGT[A/G]GCTGA
TP55092	TGCAGCGGACACGTGGCTGGCGACGCACGGCGA[C/T]CTCGCCCGCGTGTTCCTGGTCGGCGACAGC
TP55097	TGCAGCGGACAGGCCCAGAAAACGCGGTGTGCGGACTGT[A/C]GGACGCCGCACTGTAGCATTTCCG
TP55115	TGCAGCGGACCTA[C/T]GTCGCGATGAGGCAGGGGAACGACGTGCTCGACAGGTGCGGCCTGAGTGG
TP55119	TGCAGCGGACGACGATGAGGAGCACA[A/C]GAACGCGCGGGGGCGGGGCATATATGCTAGCTAGCTG
TP55175	TGCAGCGGACGCGACGTGATGCCG[C/T]CCTCGCACTCCCACGCCAGGTAGGACCGACGACTAATCA
TP55191	TGCAGCGGACTCCTGAGGACGTA[A/G]GTCGAATCCCTGAGCGTGCGGAGCAGCTCGTCCGCCTCGT
TP55201	TGCAGCGGACTTCGGCGACCTCCATCGA[C/T]TTGGGCTTGGCGGCGGCACGGTTGGAGCGGTTGGA
TP55203	TGCAGCGGAGA[A/G]ACCAATTGCAATACGTACATGTTACACGTGTTTCCACGCGTGTGGGCAGCAG
TP55204	TGCAGCGGAGAAACCGATTGCAATTTGCAGTGC[A/C]GTGTACGTACATGTTACACGTGTTTCCACG
TP55236	TGCAGC[G/T]GAGCATCACCAGTTCAGAGTTCACCACCACGCCTTTGACCTCCAGCCCATAGCCCAA
TP55237	TGCAGCGGAGCATCATCAC[C/T]AGTTCAGAGTTCACCACCACGCCTTTGACCTCCAGCCCATAGCC
TP55253	TGCAGCGGAGCCGAAGCCTCGGCGGCTGCGGGGGCACAAGAAGGGCGCCGTCACC[A/T]GCTGCGTC
TP55263	TGCAGCGG[A/T]GCGGAGCGGACCCTCGAAGTCGCGCCAACGGACACGGCGACGGGAGACGAGGACC
TP55281	TGCAGCGGAGCTCGGCCAGCGCACAGCTCGCAGCGCTCCAGCCTC[A/G]CAGTGTTCCACTCGGGGC

Table A2 (cont.)

TP55296	TGCAGCGGAGGAGCGGAGCCAGGT[A/C]TGCCCCATGGTGTGACTAGGCCATCTGAGACTGCCTTCT
TP55298	TGCAGCGGAGGAGCTTCTCGACGGACGACGGGACGGGACGGAGTCAC[A/G]GAGACGACACCTCACC
TP55299	TGCAGCGGAGGCAACCCTGTGCCGCTTCCTACGGCCAACGCAGG[A/G]GAAACCCTCAGACCTCGGA
TP55366	TGCAGCGGATAGAGTAGTTATCATATAAACTGTAGAACTGACACAAACGGT[C/G]GTAACTGTAATG
TP55367	TGCAGCGGATAGTTACTTTGGTTCATAGAAAATGGCAT[C/T]GGCTGCTGCTCCTGCACTAGAGGCA
TP55377	TGCAGCGGATCAGCCACCGCTACCGAAGGTTCATACT[C/G]TACTCCCTCATCCTCGTCACCGCCAG
TP55379	TGCAGCGGATCAGCTTAGGCTTCGCCTCCATGATA[C/T]TCGCATCAGTCATCGCAGCACTTGTTGA
TP55381	TGCAGCGGATCATCAGGACAGGACACACGGCCTGAAAACAAGCGAACTCCCACACTCGACAGG[C/T]
TP55390	TGCAGCGGATCCATGACAAGTGGCTCAAGACAGG[C/T]GATTGCTCAACTGACAACACTGAGTTTGT
TP55405	TGCAGCGGATCGGCGTCGGGTTCGCGTC[C/T]AACGTCGTGGCGCTCGCCGTGGCCGCGGCCGTGGA
TP55409	TGCAGCGGATCGGCTTCGGGATCGTGCTCTCCATCGTCACCATGCTCGTCGCAGCCGCCGT[C/T]GA
TP55447	TGCAGCGGATGATACCGCCAGTATTTATAGAGCGAG[A/C]GAGAGAGCTGCCAATGCAACGACGAGG
TP55452	TGCAGCGGATGCACCCAAACAACGGCTCCTGGGAGCGGTGG[C/T]GCTTCGTCGGCGGCACGGGGCT
TP55455	TGCAGCGGATGCGGCAGCCATGTGCTGCGACCTGCACGCCACGAGTGCCGCCAGTGCGACAC[A/C]C
TP55456	TGCAGCGGATGCGGCAGCCATGTGCTGCGACCTGCACGCCACG[C/G]AGTGACAGTGCGACACACAC
TP55462	TGCAGCGGATGGCGGC[G/T]TCCGACGGGATCCTCGTCAACACCTTCGTGGAGCTGGAGATGCGGGC
TP55471	TGCAGCGGATGGGTGTGTTGGGTTGTGTGCTCTGTATAGTCGGGTC[A/C]ACCGTTATCATCCTCCA
TP55477	TGCAGCGGATGGTTCGCAGCCTGGAGGCCATCCTCG[C/G]CGACGCCAAGGAGCTGGCCGTGTTCCT
TP55483	TGCAGCGGATTACGACGACGATGAGGATGAAGAAGTGGA[C/T]GTGACGCTTGGTGTCCTTAGCAAA
TP55488	TGCAGCGGATT[C/G]GGGTGTTTGGCAACTGGCTGAGCCGAACAAATCCGCCCTTCTTTTTGCTGCA
TP55497	TGCAGCGGCAAACACTAGGAGAATA[A/G]TCCAGGATGGGATCGATGGGCGGCCTCGACGTGTACGT
TP55500	TGCAGCGGCAAACCTCGATC[A/T]AAGCCTAGTACTGTACTGTACTTGGCAGCAGTATTACTGCACC
TP55504	TGCAGCGGCAAAGATACAGTCATACAAAC[A/T]CGCTACCCTCCACGTCACTCCTGATGTTCACTGC
TP55523	TGCAGCGGCA[A/G]CCAAGGCCAGCCCGTCATCGTCCGCGCGCGTCGCCGTGCCTCTTCTCGCTGCG
TP55527	TGCAGCGGCA[A/G]CGCAACAGCGAGGCCGAGGCGGAACGCGAGCTGCACTGGCGAGGAGGAGCACG
TP55531	TGCAGCGGCAACGGCGTGCAGTGGTCGCTCTACCCCGACGGCTCCATCCG[A/C]CCGCCCGCGTGGC
TP55539	TGCAGCGGCAACTTGAGCGACGCGATGAAGTCCGAGACCGATGCCTGCTGGCCGA[C/G]TGGCGGCT
TP55562	TGCAGCGGCAATCCGTCGAGCGCGC[C/T]GCCGCCGCCATCGTCGAAGTGCTCGGGCAGCTTCTCGA

Table A2 (cont.)

TP55586	TGCAGCGGCACATACCTGATGCTCCTG[C/T]TCGTCAGAATCGCAAACCCATCCATCAGAAGAACGT
TP55612	TGCAGCGGCACCATCTGCTGCGTCAGCTGTTGCCGCGGCTGCC[A/G]CAAAATCATCAAGGTCACCA
TP55614	TGCAGCGGCACCCGAGGTGGTCGCAGCGGAAGAGGCGCCACGCCATGATGCCCCTGCCC[C/T]TGCC
TP55622	TGCAGCGGCACCGTGCTCCCCTCTGGCCGCACTCAAGCTCCCATCCGCT[G/T]CCACTCCCATCCGC
TP55632	TGCAGCGGCACGACGACGCGGACTCGCTT[A/C]TCAGCAGCGCCGCCGCGCCGAGGTTCGGCGTCGA
TP55633	TGCAGCGGCACGACGACGCGGACTCGCTTCTCAG[C/T]AGCGCCGCCGCGCCAAGGTTCGGTGTCGA
TP55638	TGCAGCGGCACGC[A/G]CGCACGCACAGGGAGGCGCACAGGCGCAGCGGCCGCACCGCACCGCAGCA
TP55642	TGCAGCGGCACGCGACCGCGGCGC[G/T]CGCAGCCGCGGAGCGGCTGGCCCGAAAAAAAAAAAAAAA
TP55653	TGCAGCGGCACGGGGAGAAAAAGGTGGGCAAAAGCGGGCACGA[A/C]ACCGAAGCGCTCGCCGACCC
TP55663	TGCAGCGGCACGTCGGGCTGCTGCCTGGCGCCCCTCACTTCCAG[A/C]GGCGTGCCCGTGCGCAATG
TP55674	TGCAGCGGCACGTGCAGCGGGACCACCCCACGCGCCGCGGT[C/G]GCTTCCGAGTAGGGCGCGCCCA
TP55679	TGCAGCGGCACTACATGCACCGAGCAAGCATGCCGAGCGTGCACCGTTCGAGGCTGCTGGC[A/G]GC
TP55680	TGCAGCGGCACTAGCTACATG[A/C]GCCGAGCAAGCATGCCGAGCGTGCACCGTTCGAGCCTGCTGG
TP55694	TGCAGCGGCAGAAAAGTCCGACAATAGTGAGAGACAGATGA[A/G]CCAAGCGGACGTAAAGCGAAAG
TP55708	TGCAGCGGCAGAGCGAGCGCGAGCGGCGAGAATGGCGGAACAGCCCGAATACCCGATCCAGTT[A/C]
TP55709	TGCAGCGGCAGAGGAGAAGGCA[C/G]CACGAAGGGCCACGAGGAGGGGCGCGGTGATGAGGACCCTT
TP55711	TGCAGCGGC[A/G]GATCGCGCGGCTAGTTGATGTGGATCAAACTGGGTTCATCAAGGGACGATCTAT
TP55725	TGCAGCGGCAGCACTCTAGGTTCACGGTGATGATGA[C/G]CGTCGGCATCTCTGCACAGCACATCAA
TP55749	TGCAGCGGCAGCCGAAGTACGTCCCGAATCGCATCGAGGTCGGCAACCAAGGTCC[C/T]GAATCGCA
TP55754	TGCAGCGGCAGCCTCCAGCTCCATTCAAGCTGACAC[A/G]CTCGGCGGCAGGGATGATCTTGGCGCC
TP55755	TGCAGCGGCAGCCTCTCGTCGCCGACGCCGATCCCCGACACGCCGACGTAGTAGAAGCTCGG[C/G]G
TP55760	TGCAGCGGCAGCGACATC[A/G]GTGGCGAGCACGACGGCATGCGGACGGAGAGGCGTGCGGCTGCGG
TP55766	TGCAGCGGCAGCGAGGA[G/T]GAGGAGGCGGAGGTCGCAGGGGCTCCGAGCCATCGCCGTATACACC
TP55770	TGCAGCGGCAGCGCCGCCGCCCGTCGAGAAAGAA[A/C]TCGACGAGACGTACTTTACCCACACAAGT
TP55776	TGCAGCGGCAG[C/G]GGCAAACGCGTTGGCGGCCTGCACGCACGCACGCTCGTGAGAGAGAGCGCTG
TP55785	TGCAGCGGCAGCGGCGGTGGCGCCGTGGTGGGCGCGT[C/T]GTCGTCGTCCTCCGCCATACCGCTCC
TP55789	TGCAGCGGCAGCGGCTCCGCCGACGAAGCCGA[T/C]CCGCACGAGCGGGCGCTCCCCAACGGCGACA
TP55797	TGCAGCGGCAGCTCGACGCGTGCAGGGTCAGGGCGCAGCTCTACCAGTCC[C/G]ACTCCGCGGCCAC

Table A2 (cont.)

TP55800	TGCAGCGGCAGCTGTCC[A/G]AGTCAAAGGTGACCGTTGGGCTGGGCAGGGCAGCGCGGAACGGGGC
TP55809	TGCAGCGGCA[G/T]GAGACGAGCCGCCGCCGCGCCGTGGGAGAAGCAGACGAGGAGGAGGAGCAGCA
TP55820	TGCAGCGGCAGGCAGGCA[A/G]GCGCCAGAGATCTCTCGGTTCCCGTGCCCGCGCGCGTGCCAAAAT
TP55823	TGCAGCGGCAGG[C/T]CGCTTGACGAATCGGCCCTTCATCCGCGGCCGCTTCTCCGCGTTGAGCTTC
TP55852	TGCAGCGGCAGTACTACTACTGTAGTAG[C/T]GCAGTGAAGTAGCGAGTGCAGTGATGACGCTGCTC
TP55861	TGCAGCGG[C/T]AGTGGAGCAGCGTTCGGGGGGCAGCGGCGGTGGAGCAGTGCACCCTGGCGGTCGT
TP55873	TGCAGCGGCATCAGCCACAGCCCGTGGAGCCCGTGCAT[A/G]GCGTAGGACACGATCCCAGCGTCGA
TP55892	TGCAGCGGCATGCGGGTGAGCTCGGCAGGTAGATGCAACGGCGAGGAGGAGAAACAGCAGC[A/G]CG
TP55901	TGCAGCGGCATGGGCGGTGCTCGTCTGCACATACGGGAAGCTGCGGGGGCCGCGGTG[A/G]TGGGGC
TP55916	TGCAGCGGCATTGGTG[A/G]TGGTGGGCAGTGTGGTGGCGAGTGGGTGGGAGTTGAAACCGAGCGCG
TP55933	TGCAGCGGCCAACTCCTCA[C/G]CATGCTGCTGCTTTAGATGCGCCACCTCGCCAGACAAGTCGGCA
TP55967	TGCAGCGGCCACTCGTGGATAGGTTCAGGATCCTC[G/T]CTGCTGACGTGGCGTCCCCTCGTTAGAG
TP55969	TGCAGCGGCCAGAGGGAGCAG[A/G]CTGGCTGGGTGTACGGCTGGCGCCCGTCGTAGTCGTCCGAAA
TP55984	TGCAGCGGCCATATCCC[A/T]GTGCAAGTGACTGCGCGTGCAGCTCCAAGCTGATCATGTCATCTTG
TP56005	TGCAGCGGCCATGGCATGCACGTTTCAGATAATGTATCACCCGT[A/G]TGCATTAATCAATCTCCTG
TP56019	TGCAGCGGCCCACCGCACTCGGCCGCGACTCCGTCGTCGCGAGATCCAGCA[G/T]CGCCGTCGTCGC
TP56030	TGCAGCGGCCCATGGTGGACGTGCGCACGCTGTTCC[A/G]CCTGGAGCGGAAGCTGGGGAGCGGGCA
TP56032	TGCAGCGGCCCCCACATTATTGTGGGTTGGTGCGAGGTGCGGTGCGCGACACGCA[C/T]GGGACAGG
TP56035	TGCAGCGGCCCCGCTTTGATG[C/T]GTCGTCCTCACAACTCCTGTGTGAGGTGCGGCCACGTCTGGT
TP56077	TGCAGCGGCCGATATATAGGTGGAGACTCGGGTGGCGAGACGGG[A/G]AAGGGGGAGACGGGGTGGT
TP56078	TGCAGCGGCCGATCGCGATCGCATTTGCGCAGGGTCACAA[A/C]CAAGCTGCTATCGATCCCGCTGG
TP56079	TGCAGCGGCCGCAAGTTCACCGAGCG[A/G]ACCAACTCCCAAACACGGAGGTAGTCACAGAGCACTT
TP56094	TGCAGCGGCCGCGAGCATGGGGGTGGTGCGGGAGGTCCTGGGCGCCGA[C/T]GTTGTCGAGGAGGTG
TP56102	TGCAGCGGCCGCGTCTGCTTCAGGCAGCTG[C/T]CTCCGCCTCCCGCTGGTGCCGTCCCTGCTTGGC
TP56112	TGCAGCGGCCGTCCCTTGAACGGCTGCATGCCTCTCGAAGCCTGCTGGCAGCTTGTTG[C/G]CAACA
TP56113	TGCAGCGGCCGTCCGCAGGAGCAGAAGCCCGTCGGCGAGGCG[A/G]CCGAGGAAGCCCGCGTGGACG
TP56148	TGCAGCGGCCTCCGTACACGGGTGGGTAGGGTCAGG[A/C]CGCCGTGGGGCCCCAGATCCGACCCCG
TP56157	TGCAGCGGCCTCGATGCGTCTCTCGCGACCCGACGGAGGCCCCTACGCGGCTG[C/G]CCTGCTTCGC

Table A2 (cont.)

TP56168	TGCAGCGGC[C/T]TCTCGACGGCGGCGTAGACGGCCTTGTGCCCGCTCTCCCGCAGCGTCAGGACCG
TP56195	TGCAGCGGCCTTGTCGCGACGCGCTTGGACTGGCGCGGAGCCTGCCTAGATGCCGTTTC[G/T]CGCC
TP56197	TGCAGCGGCCTTTGATCGGCGTCGCAGCATCGATGTGCGCGGCGCGGGGGGT[A/G]GTGGAGACGTC
TP56200	TGCAGCGGCGAAAACACTGTGCAACCAGAAGTTCAGGACCCTAC[C/T]ATGAATTCTGAGTTCGCCG
TP56201	TGCAGCGGCGAAAGGCGTGGCCGCGTCGCGGTGATGGGCCACCGTCGTCTGA[C/T]CCGCCGACGAT
TP56214	TGCAGCGGCGAC[A/T]AGACCAAGAGCGTGACGCGGGTCGTCGGAGGCGCGCGCGTCTAAACAAA
TP56219	TGCAGCGGCGACAATGGCGAGGGCGGTGCTGGTGGCCGTCGTGCTGCAAGCCTGCA[A/T]CATGATC
TP56220	TGCAGCGGCGACAATGG[C/T]GATGAGGGCGGTGCTGGTGGCCGTCGTGCTGATGCAGTGCTGCAAC
TP56233	TGCAG[C/T]GGCGACGAAGGCGGCAGGGTCGGCGCGAGGATGGATCCCGTCCTCCAAATCCCCAAAT
TP56256	TGCAGCGGCGACTCGATTGCGACGTC[A/G]TACACCTTGGACGACAGCACGCTGGTGAGGTACTCCA
TP56284	TGCAGCGGCGAGCTC[C/T]TGCCGAGCGACGCGGGAAGCTGCCCCGTCAAGGAGTTGTTCCACAGCT
TP56289	TGCAGCGGCGAGGACGCTCATAACTTGCACCGAGAAGACGAGTAGCAACACCACCTTG[A/G]CCATC
TP56291	TGCAGCGGCGAGGCCGATGTGCCTGAGAGACCGTACGTGCGAGACGATTGGGGA[C/T]GGGGCAATT
TP56292	TGCAGCGGCGAGGCG[A/C]GGCCCGAGGAGGTAAGGGCGTTTCTCGGCGAGGCGCCCAAGGGTGTCG
TP56313	TGCAGCGGCGATGAGTGCGGGAAAGACGC[C/T]GACCCACGGGCCCACGCACGCTGCCCGCCCTCAA
TP56343	TGCAGCGGCGCACACGCGTGGTGCTCTACTACCGCGCGGACGCTGGAGAGAAGGGG[A/G]CCTCACG
TP56364	TGCAGCGGCGCATACGCGACGC[C/T]GACGGCGTGCCGCCCGACAGCCTACTCGTCCGTGTTCAAGT
TP56376	TGCAGCGGCGCCACACTGCGCGC[C/T]CACACGTCCGACGAAACCTGCTGTCCGCTCCCGAAAAAAA
TP56398	TGCAGCGG[C/T]GCCCTGTCCTCCCACGCGCCGCCATCCCCGACCAGAGGCCGAAAAAAAAAAAAAA
TP56414	TGCAGCGGCGCCTACGCCAACCCAA[A/G]CACCTGCCGCCCCACCGCCTACTCGCAGCTCTTCAAGT
TP56417	TGCAGCGGCGCCTCGAGCAGACCTACGGCAAGCGCCGCCGACTCGTCGAGGAGGCCC[A/G]AGGCCG
TP56421	TGCAGCGGCGCCTTC[A/C]CCCACCGAGGGCAGCGTGGCTGTCCGTCCACCGCAGAGACGCGGCCGA
TP56423	TGCAGCGGCGCCTTCCCCCGCTGAGGGCAGCATGGTTG[C/T]CCGTCCACAGCAGAGTGCGCCCCGC
TP56427	TGCAGCGGCGCGACGCGATAGCGTGAGGAAGAAGGCCGAGCCACGAGCGCCCGAGACGTGGTC[C/G]
TP56434	TGCAGCGGCGCGAGGTGCAGCCGCCGAGATAAAGGGGAGTGGGGTTACCGATTTCTGCAAAA[A/G]T
TP56439	TGCAGCGGCGCGCACGTGCTCGAGTTCCT[A/G]CGCTACCTCGACCGCTTCGGCAAGACGCGCGTGC
TP56460	TGCAGCGG[C/G]GCGGAGGACGAGCCCCACGCCGCCCCGCTGGCGGCCGCCAACCCGAAAAAAAAAA
TP56467	TGCAGCGGCGCGGCGGACTTGGCGCTGAACAGGAACTGG[C/T]TTTGGTTCTGGCTCTGATTCGGAT

Table A2 (cont.)

TP56475	TGCAGCGGCGCGGGGAGTCATGGCGCGCGAC[A/G]CTGCTGCTCGCGTACCAGAGCCTCGGGGTGGT
TP56481	TGCAGCGGCGCGGTTGGTTGGTTGGTTGGGTTTGGATTTTGGCGTGGCCACAGCGGCGTTG[G/T]AG
TP56485	TGCAGCGGCGCGTACGCGACGCCGACAGCGTGCCGCCCGACGGCCTACTCGTCC[G/T]TGTTCAAGT
TP56510	TGCAGCGGCGCGTGCACGGCCTCGTCGGCGCCTTCTTCAAGTC[A/G]CCGCAGCTCAAGGCGCAGGT
TP56519	TGCAGCGGCGCTACTTGGCTCCTCCACTCCTC[T/C]GATGCATATGCATCCGTCAACGCGCACTAGG
TP56547	TGCAGCGGCGCTTGCTG[A/G]GCGGCGGCGGCAGCAGCGGAGAGGACGACTGGTGCTGGTGCCCCTT
TP56549	TGCAGCGGCGCTTGCTGGGCGGCGGCGGCAGCAGCGGAGAGGACTGCTGGTGCTGGTG[C/T]CCCTT
TP56554	TGCAG[C/T]GGCGGAAGCAAAAGCCACATAGCTGGTCAGCACCGACCAATGTTCAGCACCCATCAGC
TP56558	TGCAGCGG[C/G]GGAATAGCCTGCGGATCGCAGAGGCCGCCGCGGCTCTCATGACTCTTTACGCCAC
TP56577	TGCAGCGGCGGAGGCGGCGAGGGGAAGGGACTGGAGGACGGTGGACGCCGCGA[C/T]TAGCGAGGGG
TP56584	TGCAGCGGCGGATCGCGGAGGCGCTGGGGTACACGTGCACGGGG[C/T]TGACGAGGAAGGACAAGTA
TP56600	TGCAGCGGCGGCAGCTGGGAGAGCTTGGGACTGGTCGGCGGCGGCCGCGAGGAACTCACT[C/T]CTG
TP56615	TGCAGCGG[C/T]GGCCTCCAGTTCCATTCAAGCTGACACACTCGGTGGCAGGGATGATCTTGGCGCC
TP56619	TGCAGCGGCGGCGAATTGGTGCTCCAGCTCTGCTGCATCTGACGGCTCC[G/T]CCCAGACGAAGTAG
TP56632	TGCAGCGGCGGCGCATCGGAG[C/G]AGGCATCTGGGGCGTCCGACGACATGGCCGCCAGCGCCATGC
TP56661	TGCAGCGGCGGCGGCGACGGGCGCGACGTCGCAATGCCGATTGCGCAGTGACGG[A/G]TCCTCGGCC
TP56691	TGCAGCGGCGGCGGCGGTATCGCA[C/G]AGAGAGAGAGGGACAGAGACAGAGCGGACGCGTGGTGGA
TP56694	TGCAGCGGCGGCGGCGTGCGGTCG[G/T]GGGCACCCTGATAAAGCCGAGGACGTCGCTGCCGAATGG
TP56704	TGCAGCGGCGGCGGTGGAGCACTGACAACTTCGCCGTCGTCGTTGTTGCCCCAC[A/G]GTCCAAGAA
TP56721	TGCAGCGGCGGCTACATTGACAACG[C/T]CTTCCAGTACATCATCAGCAACGGTGGCCTCGCCACCG
TP56728	TGCAGCGGCGGCTGCGGCTGC[C/T]CAAAAGGTTAGTAAGAACATTGAGGAGCAGCAGAAAAAGATA
TP56798	TGCAGCGGCGGTGGTGGCGGGGGCTTGGCTTCTGCACGGGCTT[C/T]GCTGCTTGCCCTTGCTCCTC
TP56822	TGCAGCGGCGTCAACGGGTCGAAGAGGAATTACAGCGGCGAATGAAGCAGTTCCCCC[C/T]AGGGAA
TP56826	TGCAGCGGCGTCATCCCC[G/T]CGGAGCTGTTTAGCAGGTGGGATGTTGCGCTGTGCGAGCTGACGC
TP56837	TGCAGCGGCGTCGCCTAATCGGCGTGCGAGCTGGTG[G/T]CTCCACCTGCGGACACTGGCGACCCCA
TP56843	TGCAGCGGCGT[C/T]GTCAGCGCCGCCGCGGCCGCGGACGGGCTCTCGAGCGGGGGCAGCTTCATGA
TP56846	TGCAGCGGCGTCGTGTACTTGCATGGCGTGCCTGTACGCCATCGGACACAGACAACAGT[A/C]GTCA
TP56852	TGCAGCGGCGTGAACGCCTCCGCGCGGCCGAGGAAGCGG[C/T]GCGCCGCGGGCGCGACGGCCCGAA

Table A2 (cont.)

TP56882	TGCAGCGGCGTGGACGGCATCCCCGCG[C/G]CCGCTCCTGCGGCAGAGGCGGAGGCCATGGCCTGGG
TP56885	TGCAGCGGCGTG[G/T]CCCCGCGCCTCTTGACAGGCGGCACGCTGCTGGCGGCGTCCTCCTTATTCC
TP56908	TGCAGCGGCGTTGGGAGCGGGATGGCGGCGAGGCGGAG[A/C]GTGGAGGGGAAGGAGAGCACGGCGG
TP56979	TGCAGCGGCTAGTT[C/G]GCGGGTGGCGCGACCGAGGAGTCCCCGTGGAACGACGTCAGCAGGAGCT
TP56997	TGCAGCGGCT[A/T]TCATTAAAGCAATCAGGCCAGGCGTTAAGCCAATCAGCCCTCCCAATCCCACC
TP57008	TGCAGCGGCTCACGGCGCGCTCCAG[C/G]CGCTACCTCTGGGTCCCTGGCAGCCAGTGAGCACTAGT
TP57018	TGCAGCGGCTCATCGACGCGCAGCGGCGGAGT[T/C]TGGACGACAGCGACGACAGCGAGAAGAAGAG
TP57020	TGCAGCGGCTCATGACCCTGAAGCGCGAGAAGCCGCGGCGTC[A/G]CTGGCAAGTACTAACCCGTAG
TP57058	TGCAGCGGCTCGGAGTGGACTACCACTACAAGGA[C/G]GAGATCGATGCGCTGCTGCGTGCGGTTCA
TP57068	TGCAGCGGCTCGGTATCGGCCTCG[C/G]ACTGTCCGTGTTCGCCATGGTGTACGCGGCGCTGCTCGA
TP57071	TGCAGCGGCTCGTGGCCCGCCACG[C/G]CGCCCGCAACTGGTCCCTCATCAGCCGCTCCATCCCGAA
TP57075	TGCAGCGGCTCTCCGAAGTCCTCCAGACGCACGTCGGCGTCGGCCTG[C/G]ACGAACACCACCCCTT
TP57079	TGCAGCGGCTCTGCATGGTTTGGGCCGTCTTT[T/C]TTATGTGGTCGGCCGTAGTCAACATCCATAT
TP57083	TGCAGCGGCTCTGCTCGCGTGCTGG[A/C]AGGTAGCTGCGCCGAGTTCTCCCGCCGAGGAAGGGAGT
TP57102	TGCAGCGGCTGATCACACCACAACTGAC[C/G]GAGCAATCACTATCTCCGCGCCACACCGCGGAGCC
TP57134	TGCAGCGGCTGCGCCACGC[C/T]AGGCGGCAACACGGGGAGGGATGTCGCCAGAGGCGGCTGCGTCT
TP57143	TGCAGCGGCTGCGGCTCCGCCCGCTGGACT[A/G]CGTGCATGCCTTCTTCACCGCCGTGGTGTTCCT
TP57147	TGCAGCGGCTGCGTCCGCTCCGCCATCTCCAG[G/A]CTCTCCTCGCTCTGCGCCTGGGCGGTCGGCG
TP57155	TGCAGCGGCTGCTGCTCCGACTCCGAGGCGAGCAAGCGGT[A/T]GAAGCTGCATCCCCTGCTGAAGG
TP57166	TGCAGCGGCTGGAGACGCTGGTGCTCAAGCTCCGCTGCGC[G/T]GTCGAGGTGTCGGAGAAGCACGC
TP57178	TGCAGCGGCTGGCTCTCCATC[A/G]TCACCACCGCCGCTGCCTCCTCTCGCAGATGCAGATCTACTT
TP57207	TGCAGCGGCTTCATCGACTACTTCGAGCAGCGGGAGCGCCACCCCCGCGTGGC[C/T]GCATCGGCTA
TP57216	TGCAGCGGCTTCGTGGAGGTGATGGCGCCCGTGTTCACCAGGGAGGCCTGGGCGTGCGCCTGG[C/T]
TP57252	TGCAGCGGCTTTTGATTTCTGGGGTCTGGCGGTGTTCG[C/T]TCGGATGGATTTGGAATCGGAATCG
TP57253	TGCAGCGGG[A/G]AAACCCAATACCCATGCCAGCCTCTGACATCGCCGACCATCTCGGCCGCCTCCT
TP57257	TGCAGCGGGAAATTGTAGA[A/C]CGCTACGGCATGTCAAGTCGAAGTGGGAATTCGTGATTTTTTTT
TP57262	TGCAGCGGGAAGAAAGTCAATGGCCAGCGAGCAGAGGCAGAGCGCAACAAATGTCATC[A/G]TCGCC
TP57263	TGCAGCGGGAAGGGAAATC[C/G]GACCTGCTTGAGGTTGCGCAGCTGACAGTGGCGCAACCGACGGT

Table A2 (cont.)

TP57264	TGCAGCGGGAAGGGAACATCCACCAGCACATCATAGCAA[A/G]CACTGCTATGCGCTCCATTCCCTG
TP57271	TGCAGCGGGACAACCCAATACCCGTTCCAACCTCTGACATC[A/G]CTGACCATCTCTGCCGCCTCCT
TP57286	TGCAGCGGGACATTGGTGATCTCGAGACCAC[C/T]TGCCACCGCACCTCATACAAAGCGCTTGAGCG
TP57292	TGCAGCGGGACGAGCTGAGGGCAGCGTGGATCATCTCGAAGGCTGCTGCGAACGATACGCAA[C/G]A
TP57303	TGCAGCGGGAGACGAGATCCGCTCCTTGCACACAGC[A/G]AAAGCAACGGACTCCTCCAGCCTCCAA
TP57309	TGCAGCGGGAG[A/G]GGCATGTCGGCCGCGCGCACCCGCACCGACACCTTCCTGCTGCTGTCGTCCT
TP57313	TGCAGCGGGAGCACCAGCCGCCCAACATCTCGGAGATGAAGCCGCTCACGCGGGAG[G/T]CGTACGG
TP57319	TGCAGCGGGAG[C/G]CGCGGCGGCCGCAGCCATAATCATGGTGACCAGCCACGAGACCACCAGCTTC
TP57326	TGCAGCGGGAGCGAGGCCCCGCCGCGATGCCCTGGACGGTCCGCCTCC[A/G]CATCGCCGCCGAGAC
TP57334	TGCAGCGGGAGCTACAGCC[C/T]CAGCGCCGACGTCAGCGAGTCCGAGACCTCCAGCGACTGCTCCG
TP57338	TGCAGCGGGAGCTGCACCCGC[C/G]TCTTCGTCCCTGCATTTGGGCTGGTATGGTTCTTGAACAACG
TP57340	TGCAGCGGGAGCTGGGCCTGGAAGTGCGCGACGA[C/T]GTGCCGCTGCTCGGCTTCATCGGGCGCCT
TP57344	TGCAGCGGGAGGAGGAGGCGCCGTGGCCACAGACGG[A/G]GCCTTGCCGTGGTCGCGGGCCACGTCG
TP57353	TGCAGCGGGAGGGCAGGGGCGGCCAGCGCGGCGCCCTGCGGCAGTGCGGC[A/G]TGCGGCACCTCCG
TP57359	TGCAGCGGGAGGTGCTGTCGTCGCCGTCGAGGCCGAGGAAGGGAGGAG[C/G]GGGCCGAAAAAAAAA
TP57384	TGCAGCGGGATTTGCTGGCCTAGGTGATGATGCGAGCCTGTGACCAATGA[C/G]CATCTAGGCACTC
TP57400	TGCAGCGGGCAAGTAAAAACCAGCAAGCGAAAATACAAAAA[C/G]GGACTAGAAAAACCCAAGTCGT
TP57449	TGCAGCGGGCCACGCCCGTAGTACTTCTTCCCCAGGGCGCACGGCCA[C/T]TGTGAGCTCAGGGCGC
TP57452	TGCAGCGGGCCAGGCCCCACGGCACTGTCCTG[A/C]ACTCCTGCACGCAGACAGCGGTGCTCACTGA
TP57453	TGCAGCGGGCCATGCAAATAAGGAATGATCCGCGCGGCTCGAGGCGCGC[A/G]GCTACCAGGGGATC
TP57464	TGCAG[C/T]GGGCCCGCCATCTCCCCTCCGCCGCCGCCCTGCTGCTGCTGCTGCTTCACGCTGCCGT
TP57477	TGCAGCGGGCCGCGCCCGTAGTACCCCTGCATCGGGTAGCA[C/T]GGCCACTGCTTCTCACTCTCCC
TP57487	TGCAGCGGGCCTGGGAGGC[C/T]GACCCCAACTCCGTCGACGAGTCCTGGGACAACTTCTTCCGCAA
TP57489	TGCAGCGGGCGAAC[A/C]AGATGACGACGACCTTGAATGCCAAGCGGGTGTTCCCCTACGAGCTACC
TP57521	TGCAGCGGGCG[C/T]GGGCCCGTCACCTCCTGCACCGTCGTGGACACCGTCTTCTCGATCACCGCCG
TP57528	TGCAGCGGGCGCTTGGTGTC[C/G]AGGCGCCAGACGGCGCCCCACGACACGCGCATCGGCGTCCACA
TP57535	TGCAGCGGGCGGAGGCTGCAACCACCTCGACTGCCACCGTGGCCCCTTCCTCGTGGTCTT[C/T]GTG
TP57536	TGCAGCGGGCGGAGGCTGCGACCACCTCGACTGCCACCGTGGCCCCTTCCTCGTCGTCTTCGT[G/T]

Table A2 (cont.)

TP57566	TGCAGCGGGCGGTGTAGGACGAACAGCCAAAATGAACATCA[C/T]GCGGAAGATTAATGTGGAGACT
TP57572	TGCAGCGGGCGTCGTCACGCACTTAAGCGGACAA[C/G]CATCCGCGTGCTTATAAGCAGACCGTCCC
TP57574	TGCAGCGGGCGTGGCAAGGATGGAGCACGGCGTGGTGACAGGATGGG[A/G]TGCGTGGCAGGGAAGA
TP57592	TGCAGCGGGCTCCATGCCCCCGTCGGCCCCTACCCCTCCTCCTGAGCCGCCATTCACAGG[C/T]GTC
TP57630	TGCAGCGGGGAGAGGCCCTGCGGGTTGGCGGTGAGGCGGCG[A/G]GCGAGGGGCACGACGAGGCGGT
TP57654	TGCAGCGGGGCCCACAAG[A/G]AAGTCGATGGGCCTTTCAATTTCACCACTTCAGGCGGTGGAGCCC
TP57694	TGCAGCGGGGGAGC[A/G]CCCTGGCTGGGGCAGGCAGAGGAGCAGGCGAGTGGGGCGTGTGGCCGTG
TP57706	TGCAGCGGGGGGAGCAGTCGACGGGGTCTTCCTCGGCGCCGACCTCG[A/G]CGAGTCAGCCTCCCGC
TP57724	TGCAGCGGGGGTGC[A/G]GCGGCACGTACCTGGTGGCGCAGCGCGTGGAGGCGACGATGACAAGCTC
TP57728	TGCAGCGGGGTCGGCGCCAGCGCGCCGAGGCAGTTGAT[C/G]AGGAAGCGGATAATGTCTTCCCGCG
TP57739	TGCAGCGGGTACGCCACCACCACCGCGTG[A/C]GGCTTGCCGCCGCCATGCCTCGCCGTCTCTACTA
TP57804	TGCAGCGGGTGAGCTCTTTAC[A/G]AGTTCCCCTTGCTGTGGATCGGAGGAAGGAGGTTGGGACTGG
TP57806	TGCAGCGGGTGATTCGGGGCAGATGGTTG[C/T]TCTCCCGCACCTGCACCGCCGTTGATCGCGACAG
TP57816	TGCAG[C/T]GGGTGGCGGAGCGCAACGACGCCGCGGCAGCGGAGGGCAGCGCGGTGGTGGCGGCGCC
TP57823	TGCAG[C/T]GGGTGGGAGTGGGAGTGGAGGCAGGCGGCGCGGAGGAGCCCCGCCGCCGAGAGCATGG
TP57841	TGCAGCGGGTTAGATTTGCGGGGGA[G/T]GGGCCGTGGTTTTCCTGGCCGCGCCTAGATCTGGATCC
TP57852	TGCAGCGGGTTGTGCCAAGAGGAGGCAGCTCAATCGGAGGGGAGAC[G/T]TGCGAGCAGGGAGGGGA
TP57865	TGCAGCGGTACAGCAGGCTCAAAGCTCTATGGAGAGATACACCC[C/T]GAGGCCAGTGTCGTACCCA
TP57873	TGCAGCGGTACCAGCAGGTGCTCAGCA[A/T]GCTACTGGACTGGAGGGCCTCCACACTTTTGGGAAA
TP57886	TGCAGCGGTAGAAGGCGGCGAGGTCGGCGTTCACGCGCA[G/T]CGCCACGGCTTGGTGCTTGCTTGG
TP57910	TGCAGCGGTAGGGGGCTT[C/G]AGCCCCCCACGCCGTTAGATCCGTCCTGGGAGGTTGATAGTTGTT
TP57913	TGCAGCGGTAGTACCCCCTGCACAAACAGAAGCACAAAGCAAGCT[C/T]ACCAGGCTGCTGCTAATC
TP57915	TGCAGCGGTAGTAGCCGCG[C/T]GGGTAAGGGGACCCCTTGATGGGCTTCTGCCCGTACTTGCGCCA
TP57924	TGCAGCGGTATTGTACCAGTCTGAAAATGCCCTTCTGTGCACTTTGACTGCT[C/G]GAACCCGATGG
TP57952	TGCAGCGGTCCACGCTCACACGCTCTTCCAGATGCCGAGCCTCATCGAGACCC[C/T]CATCCGTGCG
TP57954	TGCAGCGGTCCAGCCGCTCATCAC[C/T]TCCCAAACGTGGCGCACTTCCTATCCCTCCGCCGCCGCT
TP57955	TGCAGCGGTCCAGC[G/T]CCGCGTCCAGGGCGCGCGCGGCGCTGCTCCTGGAGCGCGTCACGGCCGC
TP57965	TGCAGCGGTCCGATCCTGCGGCGCAACGTGGGATTGCCAATTTGCCATGCA[C/T]CATCTCGGCTGG

Table A2 (cont.)

TP57969	TGCAGCGGTCCTGGATCATCCTCTT[C/T]GCCTGCGCCATCGTCATGCTCCCGATCTACCTCTTCAC
TP57972	TGCAGCGGTCGACAGTCACC[A/G]CACGTATTACAGGGCCAGGGGTCAAGTCGAAGTCGTCGTCGTC
TP57984	TGCAGCGGTCGCGTACGGCGGCGGATA[C/G]AGCATGGGGTGCTGGCGAATCTCAGCGCTGCCATAG
TP58003	TGCAGCGGTCGTCGTCATCATCCGTGGCGCAAGTGGACGGAGACCGTGCTGCT[C/G]GCGGCATAGG
TP58005	TGCAGCGGTCGTGGATCATCCTCTTC[A/G]CGTGCGCCGTCGTGCTGCTGCCCGTCTACCTCTTCAC
TP58007	TGCAGCGGTCGTGTCGCTCGTTCTAGAGTCACTGACAATGTGTCCTGGTCTCCAGTC[C/T]CGCGGT
TP58037	TGCAGCGGTGACGGTAACGGCGACGGTGACGGCGA[G/T]CTCGAGGAGGCGTCCACGCCCACCGCGG
TP58130	TGCAGCGGTGCTAGCTCGCACTACTCGAGCACCA[A/G]ATCCCCATCCTACCACCAACTCCAACGGT
TP58134	TGCAGCGGTGCTGGCAGTCTGGCACTCATGCTCGCAAGGCTCCA[A/G]GACCTGATGACATGTATGG
TP58141	TGCAGCGGTGGACGACGGCGCGGTCGGCGCTCA[C/G]GCGCAGCGCCACCGCCTGGTGCCTCGCCGA
TP58152	TGCAGCGGTGGATCCGATAACTTTCGC[A/G]GCAAAACCGAATTTCGTATGTACACGCTTGTAATTA
TP58187	TGCAGCGGTGGCGGTCGACGAGCATGGGGGCAGCAAGGCAGGTGTGGCGCTTGCCTTGCAAT[A/C]T
TP58216	TGCAG[C/G]GGTGGTGCCTTGTCGGCCTGCACTGCCATCTTAGCTGCCGCTGCATCATGGGGCAAAA
TP58217	TGCAGCGGTGGTGGACGAGGCGTACATGGCGAGGCTGTC[A/G]CGGACCACGCCGCGGGCGGCGGCG
TP58221	TGCAGCGGTGGTTCCGCGCGCCTAGTCAG[C/T]GGCAATTGCCACGATACCCCTCGATGGCGGCGAC
TP58222	TGCAGCGGTGGTTCCGCGCGCCTAGTCGGTGGCAATTGCCATGATCCCGCTCGACGGC[A/G]GCGGC
TP58240	TGCAGCGGTGTCGGCGCCAG[C/T]GCGCCGAGGCAGTTGATCAGGAAGCGGATGATGTCTTCCCGCG
TP58261	TGCAGCGGTTACACAGTTCCCAGAAAATATCTTGTATACTA[A/G]TGTATTTAGCAAACAATCAACA
TP58267	TGCAGCGGTTATACGTCGCATCGTCGCCGTGGATGT[A/G]TGTAACCAGCCGTAAGTCGCTTCTTGG
TP58273	TGCAGCGGTTCAACGCCCCGTCCC[A/T]GTGGCCTGTGGGCGGGCTGCCCGTCGCGCCCGAAAAAAA
TP58275	TGCAGCGGTTCAAGGCGCT[C/T]GTGGCCGACTGCGCCGCGCGCAGCCGCACGCGCCTGCTGCTCCA
TP58297	TGCAGCGGTTCGAGATGAAGGCGTCCCCGAACTACGTCCACGCGCCGACCGTCCT[C/G]ATGCTCCT
TP58300	TGCAGCGGTTCGCCCGTACGATCGCCTACCTTGAG[C/T]TTGGTGCTCGCTGGGCGCACGTGCCTCC
TP58314	TGCAGCGGTTGCAAGTTAACGGATCGGAGCAGCTCCC[A/T]GACGCGGAAGTAGTCACAGAGCACCT
TP58356	TGCAGCGTAAAAGATTTGCACCCTGCCAAGTTGAGCTTCCAAATGCAAGTCCCA[A/T]GCAAGCTAA
TP58357	TGCAGCGTAAACAATTTCGACTTCAGCCCACGGGCTGGAAACTGAC[A/G]TTGCCGCAAGAAGAGTT
TP58359	TGCAGCGTAAAGCCGTAACCTAACACG[A/G]TAACACCCCGTGTGCGTTCCTCTACTCCCTTGTCTC
TP58363	TGCAGCGTAACATGTATACATCTACCTCAGTCCACAGCGGCGAGACCACAGCCGCGGCCCACG[A/G]

Table A2 (cont.)

TP58365	TGCAGCGTAACGCGCGTGGCAGAG[A/G]CACACGCACGAAGCAGAGAGCAGAGAGCGAGCCGCCGCG
TP58368	TGCAGCGTAAGCATTCCT[C/T]ACCTCCACCACACACCGCGACACCATTTGCACTCTCTGGCAGGGG
TP58392	TGCAGCGTACATACATACAACAATGCTTGGTTAGACTA[C/G]TCCTCTTCTAGTCGCCTCTACCCCG
TP58401	TGCAGCGTACCTCGGCTCCTCGCGACGCCAGTGA[A/C]GCTCAGGCTCCGCACGTGCGATGCTCGAC
TP58416	TGCAGC[G/T]TACGTACCTTTGGATCTGGCCGAGGCCACGGCTGCCCATGACGAGCGACTCGAGATG
TP58432	TGCAGCGTACTCGCCGCTGCTATCGCGGCAGCCGCAATCGCCGCCGCTCT[C/T]CCCTTCCCTGGCG
TP58433	TGCAGCGTACTCGTCGCTGCGGTCGCGGCAGCAAT[C/T]GCCGCCGCTCTCCCCTTCCCTGGCGTCT
TP58448	TGCAGCGTAGAACGCCGAGGTTTTCGCCCAATCGACTCAGGGGGTGTTTGCAAACTCTACTC[A/C]A
TP58452	TGCAGCGTAG[A/G]CATCCATGCTTCTACGACGAGATGCCCTGTCTGAAGTTCATACAAGGCTGGGG
TP58473	TGCAGCGTAGCGGCTAAGGCGGAGGCGCAGC[A/G]TGCGCGTCGTGAGCGGACGTGCGTGGTGTGCG
TP58483	TGCAGCGTAGGCACCTCCTTGACCAGC[G/T]CCTTGAGCACCGTCGTCATGTCCGCCGCCTGCTGCC
TP58484	TGCAGCGT[A/C]GGGGCGGCCACCGTACCACATGGCTTTCCTCCTCTCTGTAGCTTGCATCTACATC
TP58506	TGCAGC[G/T]TATAAGGGTCCACTGTCAGGCACGTATGCGTATAGTAAGGGATACGGACCTCAAGTC
TP58529	TGCAGCGTATCATTTGGGGGAGCGATCGCTGTGCTATT[G/T]CTTGCTTGGAGTAGGTTTGGGGGTA
TP58544	TGCAGCGTATGTATGTGACGGCATGCTGAGACCTACAA[C/T]GAAGTGTAGACATGGATATGCACGA
TP58563	TGCAGCGTCAACAACTATGCCTCCCGCGGCAGCTGCTTCAAGTGCGGCGCCGCCAAGA[A/C]CGAGG
TP58585	TGCAGCGTCAC[A/C]ATGGACCAGACCAAGCTCGGCAAGCCCGTCTCCCTCAACAACAAGGCCTGCA
TP58597	TGCAGCGTCACCAGCCCGCCCCAT[C/T]TGGCGTCGTAGAAGAAGCCGTTCCCCTGGAAGCTGCCGT
TP58620	TGCAGCGTCACGTTCCTTAGGTTGGGCCGTGTCGCAGTGC[A/G]CCATTCTTCACTAACTAGTCCAT
TP58630	TGCAGCGTCAGAAGAAAACTTTCGCTGCATGGCAGAGGTGCCGCCCCTGCTCGATGC[A/G]TTTGGG
TP58632	TGCAGCGTCAGAATCCGTCATCTTTCAGTTGACC[G/T]ATGCGAACTGGATTGCGAATCGCTTCCAA
TP58633	TGCAGCGTCAG[A/C]CGCATCTCCGCCATGCCATTGCTGAGATCGACGATGGCCGCCGTTGTCTGCT
TP58635	TGCAGCGTCAGATCCATCC[A/T]CACAACACTCGATCCATGGGCGATGCATGCATGGATCGGACTCG
TP58661	TGCAGCGTCAGGTATGATCCTTCGGAGCCGCTTTCGGTCCTCATGGAC[A/T]TGCATTTCACCTCGT
TP58671	TGCAGCGTCATACTG[A/C]GGTATATTTGAATTTGATGATCCTTTCTTCCTCGCAACACGAACAGAG
TP58690	TGCAGCGT[C/T]ATGTGGCCGCCACCGTGCCAGGCATAACCTCAACAACTACAAAGCGCCAATTCAG
TP58708	TGCAGCGTCCACGAGGAGCACTGGAGAGCTCGCGT[A/G]CCTGAGCTATCAGCGGAAAACGCGGGGA
TP58709	TGCAGCGTCCACGCACTGGCTGCGGACTTCATGTCCGCTGGCGCG[C/T]TCCATGTCTCCAAGAACC

Table A2 (cont.)

TP58717	TGCAGCGTCCAGCACATCGGTGGGGCTCCGCGGCACGGTGGCAGAG[A/G]AAGGAGAGGCTCTGCGG
TP58721	TGCAGCGTCC[A/C]GCGTTTCCACTGTGGAGGGAGGATGATGAGGAGGAGGAGTCCGCACGGTTGGG
TP58756	TGCAGCGTCCCCGTGCACGTGGTCGGCGACGCGTCGCACCTCCAC[C/T]TCTTGGTCGGCACGCAGC
TP58760	TGCAGCGTCCCGATCGAAATCACGTGACCGCGC[A/T]CGGAAAATGCCCCGCCTCCGACACACATCC
TP58766	TGCAGCGTCCCGTAGGACTTGTCGGCTTCGCCTTCTCGGCGAAGGCACGCACGTATGAAC[G/T]GCA
TP58767	TGCAGCGTCCCGTTGCCGCCGTCGGCGTGCTCCGAGATCGCCGCCACC[A/G]CGCCGAAAAAAAAAA
TP58843	TGCAGCGTCCGCACCTGCGCCGCCACCGTCACC[A/T]TCCACGTCGTCAACTTCCGCACCGATGTCG
TP58847	TGCAGCGTCCGCCACTCGTTCAGCAGGCGGTCGA[C/T]CACGTCCCCCGTGGGCAGGTTGCTGAGGT
TP58855	TGCAGCGTCCGTATACGGCCGCCACAGGGCCCATGGCCACGGGGCTCTGTCGGT[G/T]GCCGATGAA
TP58863	TGCAGCGTCCGTTCACCGCTGCCGTT[A/G]CTCCTTGTTTGGGTGGTTCGTTCGCCATGGATGGTGC
TP58873	TGCAGCGTCCTCCTGCTCGTCCTCAC[C/T]GCGGCAGCACTCCCCCACCGCCGCCTTCTCGACCCAC
TP58876	TGCAGCGTCCTCTTCGGCGCCCGTGCTCCTCCTCGGCTTACCGATCGGATTCACC[A/G]CCGCTGCA
TP58895	TGCAGCGTCCTTCTTCCCTGAATCTCCGAATCA[A/G]TGGTAGCCTGGTAGGAGAGGCCGATGGTGT
TP58906	TGCAGCGTCGAC[A/G]ACACCCTGCGGGTCCGCGTGGACCGCTTCCGCAGCTACGGCTTCTCCGAAA
TP58922	TGCAGCGTCGACTGCCAGCTGCG[C/T]AGCTGCTCGCTGGTCATGGGACCGCTCACGGCCAGCGTCA
TP58938	TGCAGCGTCGAGGTGGAGGCGCCCGTTCTTTGGGGAGAAGGCGTGGCCGAGTA[C/T]GCCGAGCGGC
TP58941	TGCAGCGTCGAGTGCGCCAAGAG[G/T]CTGGGAGAGCTCTAGATGCTACGCTACACTACACATGCAT
TP58984	TGCAGCGTCGCCTCGTCGTTCTCTTCTGTCACGGTGGC[C/T]GCTGCTGCCAAGGCGCCTTCAGCTT
TP58986	TGCAGCGTCGCCTGCCGCGGCGTCGCGCCCAGAGCCAGCGCCGTCTCCACCTGATTGATCGA[C/T]G
TP59010	TGCAGCGTCGCGTTGCTATCCGTCG[A/C]GCTCGCCAACCAACACACATGACACACCCCACGCAACA
TP59020	TGCAGCGTCGGAATGCGGAGGAGAGGAGCCT[G/T]GGCGCGACGGAGCAGGCGGAGAGCGCGGTGCA
TP59034	TGCAGCGT[C/T]GGCCCCATGGGCCGCGAGGCGAAGTCAACGTCGTGGGTCCTCAGGATCTCCCGCG
TP59076	TGCAGCGTCGGTACGCATGCCCTGGCTGCGGAGTCAACAACATGCCTGGGCT[A/G]GAGGAGGCTGC
TP59084	TGCAGCGTCGGTCG[C/T]CGAGCACGCGCAGGAAGACGTTGGCGCGTTTGCATCAACCGTCCGAAAA
TP59100	TGCAGCGTCGTCACTCGTCAGAGAGGGTAGAGGCGGGCAGTCAACGGTC[A/G]ACACAACGCAACGC
TP59106	TGCAGCGTCGTCCATGCCAGCAGCAGGCACG[C/T]CTACGTATACGTGCTTTGGGTTTATTTGGGGC
TP59114	TGCAGCGTCGTCGACGCCGACGACGATCGGCTGGAGGAGGGG[A/C]GGACAAGTGCCGCTGCCGCGC
TP59131	TGCAGCGTCGTCTACCACCTGAGGGCGCCAGTTATGAAGAACAAGTGCTGGTC[C/T]AGTGGTCTGG

Table A2 (cont.)

TP59137	TGCAGCGTCGTCTTCCCTGTTCTCTTGTCCTCGGACGCGTCCGAGAAAA[A/T]CCTGTCAAGCTAAC
TP59138	TGCAGCGTCGTCTTGGCGAGCCATCGCACTGCCATGGCCTCGCTCTTCTTCTCCGATCCAG[A/G]AT
TP59153	TGCAGCGTCGTTGACCCCACCGTGATGCTCTTCAGATTCAGATAGTAGTAGAAAGT[C/T]GAGGTCG
TP59176	TGCAGCGTCTCAACTTTCGCACCATTGCACTCCTCACCGCAAAAACCACATATA[C/G]GCGCCTTCC
TP59203	TGCAGCGTCTCCTTCTCAGAGCTCACACCATCATCGAGGAGGCCGAGGGACGGT[A/G]CGTGTCCAA
TP59207	TGCAGCGTCTCGGAGGCGAGGCGGACCTGCTGCCC[A/G]ACGGCGCCCATGCGGAACACCGACGACG
TP59238	TGCAGCGTCTGCCCAACTCCCCCCGCC[C/T]ACCGCCTCCTCGCCTCCGCCTCCCCACGAAGCCATC
TP59240	TGCAGCGTCTGCCCAACTCCCCTCGCCCACCGCCTCCTCGCCTCCGCCTCCGCCT[C/T]CCCACGAA
TP59248	TGCAGCGTCTGCTCGGCTTCTCACCTCCAGCTGCTAGTGGTTGCAGTAACAGTAACT[A/C]GTCGCT
TP59249	TGCAG[C/T]GTCTGCTCGGTTTCTCACCTCCAACTGCTAGTGGTAGCAGCAGTAACTCGTTGTCGTT
TP59287	TGCAGCGTCTTGCTCTTCCTGGAACTCTTGCATGGCGACCTTGCAGTTAGCTGC[C/T]GCCGCTGCT
TP59289	TGCAGCGTCTTGCTCTTCCTGGAACTCTTGCATGGCGATCTGCTTGCAGTTATTAG[C/T]TGTCGCT
TP59290	TGCAGCGTCTTGCTGACGAGCTCCACGTCGCCGCCCCCGCCAACGC[C/T]AACGCCGCCCCCGCCCG
TP59327	TGCAGCGTGAATGCCCAGACGTAGGAGAACATGAC[A/G]GGGATGTACCACAGCGAGATGGTCCCCG
TP59328	TGCAGCGTGAATGCTAAGTAGTGTGACTTGGTGCATGTATGCATGATTTCTCCTTCTCGC[A/C]TGT
TP59349	TGCAGCGTG[A/G]CGGGCCACAACCACAGACCGAAAAAGCTTGGACGGCGCCACACATGGCATGGCA
TP59361	TGCAGCGTGAGCACTGATGATGACTGATGAGCACCGCCACT[C/T]CTGATGATGATGCTCTGGCAAC
TP59370	TGCAGCGTGAGTCAAG[C/T]CGTGACTGCGTCTTTGAGACAAACAAAAACACATGCATGCACGAGCA
TP59382	TGCAGCGTGATCCCGAGCGGCGA[G/T]ACGCTGCGCACCTTGCCGAGGCGGACCTCCCGCTGGAGGT
TP59387	TGCAGCGTGATCTGCGCG[A/T]ACACGATGTGCACCTGCGCGCCGCGCCCGTCGATGGTCTTGTTGC
TP59425	TGCAGCGTGCAGAGGCGCCAGGGGTTGATCGGGTGGTTGGC[A/G]TCGTCGTCAGGGGTGCGCACGG
TP59446	TGCAG[C/T]GTGCATCCAACACACACACACAACCATGGCCCTGCATTTTATTTTTACAAATGTGGTA
TP59465	TGCAGCGTGCCACCGCCCCCACCTACAGCGGCCACGGGGTCCGTGTTTCCCATGGGCACCGAG[A/G]
TP59467	TGCAGCGTGCCACTTCCGTGGGGATGATGTCACGAGCAGCGTAGGCAGGTCCGCGCTGTTGA[A/T]G
TP59491	TGCAGCGTGCCGTCGTGGTCACTGCCGCTCTCGTACTCGCCGCGCGGATGCCCTGTTGC[C/T]CGCC
TP59492	TGCAGCGTGCCGTG[C/T]TAGATCGCCATTGCTTGCTACCGTAGGACCTGTTAGTTGTCGATTAGGT
TP59498	TGCAGCGTGCCTGCGTCCCAGTGCGGGTGCGGCCGAACTGAACGGCCCAGGCA[A/G]CTGCCGCCGT
TP59501	TGCAGCGTGCCTTGCATCGGTACGTACGTCGCTGTCGTC[A/C]GAAACAACGCGATGAACTGAAACG

Table A2 (cont.)

TP59523	TGCAGCGTGCGCTGAAGAGGCTGAAAGCACTCAACACGCG[A/C]ATGAGGAAAAGCAGTTCTTGTTG
TP59533	TGCAGCGTGCGGATGCCGACGGGCAACGGTGGTGGGTGGTGCGGCGGCCTGAGGTCGC[G/T]GGCGG
TP59534	TGCAGCGTGCGGATTATACACGACCCAAGTGAAAAATGACCACCCGCTCCCAGCCATGCCTCT[C/T]
TP59550	TGCAGCGTGCGGGAGCAGTGCACCTTCGCTGCCGCGGCGTGCC[A/C]GTGCTGCCATTCGTCGTAAA
TP59563	TGCAGCGTGCGTGCTGGGCGCCAAGAACTCACCAAT[A/C]AGGAACAAAAGATGCTTGGGTGGGCTG
TP59598	TGCAGCGTGCTGCCGAACACGGCCTTCCACTTGAG[A/G]ACGACGCCGTCGTCGGTGCCGACGTCGG
TP59627	TGCAGCGTGGAGACCTT[A/G]AGCTGCAAGAGCCGCGTCTCCGTGTCGGCGGTCGCGACGCGGCTCT
TP59638	TGCAGCGTGGAGTCGATGGCGGAG[A/C]CGAAGCTGGACATAGTGCTCTGGGCGGATAGTCGCCTAA
TP59642	TGCAGCGTGGATCATTGTGCACC[A/T]TGTTGTGCAAACTGCAAACAAGTTTCCTGAGCGGAAACAT
TP59643	TGCAGCGTGGATCCATCGACCCGTGTTCAGTGGTCGTCTCTGTCACCTGGCTCAGAGTTT[C/G]AAA
TP59666	TGCAGCGTGGCGAACTTGCC[A/G]CAGTTGGCGGCGCACTCCTTGAGCATGGCCTCGAAGGCCCGCG
TP59668	TGCAGCGTGGCGACGGCGGAGGACTGGAAGCGAAGGTCGGTCTTGAAGTCCTGC[A/G]CGATCTCGC
TP59686	TGCAG[C/G]GTGGCGTCGCTGGTGAATATGATGGAGAAGCTGTCTCTGAAGATGAGGATGAGTGCCA
TP59687	TGCAGCGTGGCGTGAGTGACCTGCGGCGG[C/T]GTGGAGGTCGGTCTGCGGCGACTCGGCCAGCAGC
TP59706	TGCAGCGTGGGAGCGGACCCACC[C/T]ACCGTACATCAGCATCCACAGCCCGCAGACAGGCCCACAG
TP59711	TGCAGCGTGGGCA[C/T]CTCCTTCACCAGCGCCTTGAGCACCGTCGTCATGTCCGCCGCCTGCTGCC
TP59715	TGCAGCGTGGGCCAGCTTAACGCCCAACAGACGCATGCTCCACTGCGCTGTCCATTCCAAT[C/T]GT
TP59717	TGCAGCGTGGGCCTCCCTTGCCAGCCAGTGTGATTCGCTGAAACCGTTTG[A/C]GTTGCGTGCTCGG
TP59722	TGCAGCGTGGGCT[C/G]TAGGGCCGCCCTCACATAGCTTGCGGTCTCCACTGCTAGCCACCGCGGTA
TP59728	TGCAGCGTGGGGAACGAATCGGCGATGGCGCTTAGCGTCGGCGAGGAGCTTGTGGCCGAGA[C/T]CA
TP59733	TGCAGCGTGGGGCGTGGCCCTCCGAGGCCTCCGTCCCCCACTCCCC[C/T]TGATACGGAAGCACCCA
TP59737	TGCAGCGTGGGTATCGCGGCGACCGCAGACGGCAAGATGCCGCGGAG[C/T]GAGTTCCCTTGAAGGT
TP59766	TGCAGCGTGGTGTTCCCGTAGCATGCGGCTGGACGCA[C/G]TGTGTGTGTGTGGGATTGTAATGGTT
TP59780	TGCAGCGTGTAATGTAACGAC[C/G]ACGACGACATTCCAATGAAGAAGAGATCGAGCATCAGGGGGG
TP59781	TGCAGCGTGTAC[C/T]GCTAGGCGTGTGAAGAGTGAGGCATGGCCCCCCTCCACGTATCCAGCAGAG
TP59808	TGCAGCGTGTCCAGTTGTAGCCGATCCTGGTCACGTTCGCGTGCAGCGCCGCCTGGA[C/T]GTCGGG
TP59813	TGCAGCGTGTCGAGGCGCAGC[C/G]CGAACACCATGGTCTTTGCATGCCAGTACACCACCTTGTGGA
TP59815	TGCAGCGTGTCGCCAGCAACGATTACAAGGTCTTTGGACAGGTTCACTCCTATTTCACC[C/T]GTGT

Table A2 (cont.)

TP59822	TGCAGCGTGTCGGC[A/G]GCGATGAAGCGCAGGTTCATGGTGTAGGGGTTGTTGGTGGAGATGAAGT
TP59824	TGCAGCGTGTCGGCGGCGA[A/T]GAGGCGCTGGTTCATGTGGTAGGGGTCGTTGGTGGAGACCATGT
TP59844	TGCAGCGTGTGCATGCTCTAGCGCCTGGATCTCATAG[A/T]CCATACCATAGGGCTCAGCAGCCTAT
TP59864	TGCAGCGTGTGGGGCGCGTCCAGCGACGCCA[A/G]CTGCGTGATCTGCTCCAGGTAGAAGTTGGCGC
TP59867	TGCAGCGTGTGTCATCTCATCCAATCCACCACCAAATAAAAATGAGTCGAAACGCA[A/G]CTCCACA
TP59873	TGCAGCGTGTTAGCCGAGGCTGTCACGTCCGA[G/C]GCGTCTTCGTTCTTCTCCAGCCAGATCTCGT
TP59899	TGCAGCGTTAAGCAAAAAGCAGGGGCAGGCAGCGCACTGGTGAG[C/T]GGTGAGCGGTGAGCGCCGA
TP59903	TGCAGCGTTACCAGAAGAACCAGCAGGATACAGGGATCCTGACGCAAGGGTTTCTG[A/C]GACCGAC
TP59954	TGCAGCGTTCATTCATGGAGAACG[A/G]CGAGGGAGGAGGAGGGGAGTACACCAAGGAAGGCTTCGT
TP59958	TGCAGCGTTCCA[C/G]CTGGTGTTGGCGGAAGCGGATTCAGAGTTCACCAGACTCGCAATATCATTC
TP59959	TGCAGCGTTCCACGCAGCTCCCACTCCTGCTGATGCCAAAA[A/G]CATAGAAGAAACGGAAATTATA
TP59971	TGCAGCGTTCCTAATTCCTATCCCAAATAGTTAAATCAGCAC[C/G]ACTAATCGACGATCAGCAGCC
TP59975	TGCAGCGTTCGAACCCTCAGCCGTGCTATTTTTTTACCTGTACGTGTGGA[A/T]TTTGCATGGCGCT
TP59978	TGCAGCGTTCGACGTGGGTGGAGGCGGCGCGGGCGTGGAACCTGTACTGGTACGC[G/T]CCCAAGGA
TP59979	TGCAGCGTTCGAGTTCCGCTACTGCTCCGCATG[C/T]CATCTCGCCGACGGGCAGATCTCCTGCGGC
TP59984	TGCAGCGTTCGCCTGCTA[A/C]CTGCTTGCATTGCATGGGCTGCGCGGACAGGCAGCGGTCCTACAT
TP59988	TGCAGCGTTCGCGTGTTTCACCAATCA[C/T]CAGAGAGATTATTAGAGAGTTACTGTTTTTCATGCC
TP60020	TGCAGCGTTGAACTTGACGATGA[C/T]GACCCCGACTGCTGCGGCTGCGGTGACTCCGACAGGACGA
TP60026	TGCAGCGTTGACTATGTAGCAGTCATC[A/G]TTCTTATCCCCCATTGCTTCCAGGCACACGCCGCTT
TP60043	TGCAGCGTTGCATCATCCGAAGATCCAATCATCATACATCATGTGAGCAATAACTCTGCATA[C/T]T
TP60062	TGCAGCGTT[G/T]CCTGCTGGACTGGGTGCCCTAGTGGTCGGAGTGGGGGGAGCTCTGCGTGACACC
TP60126	TGCAGCGTTGGGGCTGTTGGCTGC[A/G]CTTCTGCTGTGCTTGGTGAGGTACAAAAGGGATAAGAAA
TP60139	TGCAGCGTTGTAACGTAGCGATGCATGATGGGGGCAT[C/T]GGAAGCTGAAGCGAGGGAGCCTCTCA
TP60183	TGCAGCGTTTCGGCAAACAGGTGGTG[A/G]GGAAGCAAGGAAAGGGAGGGAGGCGCAGTACCTTTCG
TP60222	TGCAGCGTTTTAT[A/T]AAAAAGAAAAGATAGTAGGAAACGTAGCAGGAAAGAGAACATATGAAGCA
TP60231	TGCAGCGTTTTG[A/G]CATCCGTTGATGAGTGGTTCTTGGGATCAACAGTCCCTTGCAAACGCTGTC
TP60258	TGCAGCTAAAAACCCTGGAAG[A/C]GCGTGCAGAAATAGACTCGACTCGATTCTCGCGAGCCAGCAG
TP60316	TGCAGCTAAAGGCAAGTGACCGTACCCTCCATATGGCGACGGCAGCGAGGTCCTTCTC[C/T]AGCTT

Table A2 (cont.)

TP60327	TGCAGCTAAATGCTCCTCCATACTAGCAGTGAGAACAGCACCTGCA[A/C]AGGCATCCTCATCTAAC
TP60333	TGCAGCTAACAACGGCTCGATTCAT[C/T]CATCACAAACAACCACGCTCTAAGGGAAGGGAATGGTT
TP60337	TGCAGCTAACAAGACCACATTATTATCCTAC[A/C]TATACGCTTCTAAAGTAGCACTAGGACACGGA
TP60368	TGCAGCTAACCCAGCAAAGGCACAAGAAGTT[A/C]TATATATTACATAGGAACGTTTTAAAATGACA
TP60381	TGCAGCTAACCTCACGCCTGTGGACTCTAGCAAGACCACGAGATCTCGAACGATGGCCAAGCG[C/G]
TP60386	TGCAGCTAACGACCCCCAGTTTGTGCGTGCCTTTTAAACTGATCTGATGATGGTCGC[C/G]TTCCCC
TP60424	TGCAGCTAAGATAACCTACGCGTGAGCGGTGAGCCCACGGC[A/G]CCAGTCGCCAGCGGGATATTGG
TP60442	TGCAGCTAAGCCGCTCCAAAC[A/C]AATCTCTACTCCTAAAAACACCGAACTGGGGACGTCAACAGA
TP60461	TGCAGCTAAGCTGTCTTTGGTTGGTGCAGCTGGGACACTTGAGAGGCTCTATATA[G/T]ACCAGTGC
TP60499	TGCAGCTAAGGTTTTTTTTTTAATTTGTAGCGTTGCAGTTGC[A/T]GGCCACAATCGGCTGGTCATT
TP60503	TGCAGCT[A/G]AGTAGAGACGGTAACAGTGCCCAGGCCCTGTTCTTCCTGCTCTTCCAGCACGCTGG
TP60516	TGCAGCTAAGTTGCTCCCCTGGTGGTT[G/T]GTTGCTTTGTTTTTATATTCTGTCATACAAACTGAC
TP60519	TGCAGCTAATAAGAGAAATAAATAAAATTAGGACAGAGACGTGAGATCCATCTC[G/T]TCTCCCTTG
TP60567	TGCAGCTAATTAACTAGTTAGT[C/G]GCGCATGCATGCACGAATGCATCGTGGTCGTCTTTCCCATC
TP60596	TGCAGCTACAACACCAGAAGCTATTCTTGATCGCCATCTC[A/G]TCAAGAAGGGGAACACGGCCATA
TP60598	TGCAGCTACAACAGGCTGCTGGTCTGGTCTTTGTAGT[A/G]CAACAAGTGCAAGTGACAGCCTCCCC
TP60614	TGCAGCTACAAGAGGTGTTC[A/G]GTGCTCCGCTTCCACTCCACAGAACCAAGCCGAGCCGCAGGTG
TP60621	TGCAGCT[A/G]CAAGCTAAGCTCTGTTTGGGAACCATACGTATCCTATCCTCTCGTGATCCGTCGTC
TP60653	TGCAGCTACACCTCGG[C/G]CCGAGCTCACGCCCACACCGCCGCCACCCAGCTCGCCACTAGTGCCA
TP60668	TGCAGCTACACGGGGACGTACAGCGAGACCAAGTGCCAGACCAACTGCGGCGAC[A/C]TCTCCCAGA
TP60670	TGCAGCTACACGTTAGAAGAAGCTT[A/C]AAAAAACTATTTTAATTTATTCTTCTAGTGACTGGTGT
TP60700	TGCAGCTACAGCACACTGCCTCTTTATGCAATTGTAACCCAGGTGCGTGCGTTG[A/G]CAGTTTTCT
TP60706	TGCAGCTACAGCAGAA[A/G]GACAAAGAACAAAGTCAAGCTCAAGCAGGGAGAAGTGATCGGGAAAG
TP60711	TGCAGCTACAGCCCGCTGGGCAGC[A/G]AGGCCAACGGGAAAGTCCCTCTGCAATTGCTATGTCTGC
TP60736	TGCAGCTACAGGAGACCAAA[C/T]CCTAGGCGCGTTGAATCAAAAGGAAAAGGAGCATCGCCGCAGC
TP60753	TGCAGCTACAGGGGCAACCCATGGATTGCATGGCACA[C/T]CACGCGTCTCGTCTCGTCTCATCGCG
TP60786	TGCAGCTACATCACCTTCCCGCT[C/G]TACGCGCTCGTCACACAGGTACGTACTAAAGAGAACCATA
TP60788	TGCAGCTACATCATCCCACTGCCGCCGATCGACGAGAGCGAGGGAACGCGCTACC[G/T]CCACGAGC

Table A2 (cont.)

TP60789	TGCAGCTACATCGAACTTGCCATTGCCATG[C/G]GAAACAAGTCGCCGAGGCAACGATTGCATAAAT
TP60810	TGCAGCTACATGTGTCCTAGTACTGTCGCTCGTTTTGCCATCAGGTAACAAACAAGTCCACCT[C/T]
TP60836	TGCAGCTACCAATTGTGGCAACATACATGCATAGTTGCA[C/T]ACTGGTTATTAGGATCCAGAATTG
TP60846	TGCAGCTACC[A/C]CTACCACCCAACGCCGAAAGCTGCTGCCTTCTGGAAGTGTAGTGCTGGTGTAG
TP60860	TGCAGCTACCAGTTAACAGAACTGAAGCTGCGGGAGGA[G/T]GATGAGAAAAAGAAAATGAAGCAGC
TP60861	TGCAGCTACCAGTTAGCGAACTTTGTTGACTTTCTCAGCAGTGAGCATCAAAC[C/T]TATCTGGCTT
TP60874	TGCAGCTACCCAATGCTTGTATAAGTTACCCTCTAAAAGGG[C/T]GTACCCAGTGCAGAGAGCTCCC
TP60890	TGCAGCTACCCTCTTCTGCTCCCCCGTGACGCCCCCAGCAGCGTCATCATCCGCAGCAGCGC[C/T]G
TP60904	TGCAGCTACCGCGGCGGCGGCGTGACGGTGGTGGA[C/T]TCGCTCCGCGTCGCCATCGACAACTGCT
TP60945	TGCAGCTACCTGACTTCAGCAAGCGTTTCTTTGTCGATTGTGATGCTTCAGGGGCT[A/G]GGTTTGG
TP60952	TGCAGCT[A/G]CCTGCTGCATAAGCCCCAAGCAGAGCAAGCAGGTCCAGCACCATTGCTGTTTTCAT
TP60980	TGCAGCTACGAGCTTATTGTGCTGTGTCTACAGAAGATTACTGTTTAGCTGCCACAG[C/T]CACAGC
TP61009	TGCAGCTACGCGAGCGACA[G/T]GTCCTTGACTCCCTTGTACATTGGCAACCACTTTGTGTACTGCG
TP61012	TGCAGCTACGCGCCGCG[C/T]GCGGAGCCACGTCGTCCGCTGCCGCACCAGCACCCGCGTCACTTGC
TP61022	TGCAGCTACGGAGAGCAGAAGCGCCG[C/T]GGCGGAAACCAGCGTCGCGACGAGGACTAGCCTCGCG
TP61034	TGCAGCTACGGCCGCCGCCGCC[C/T]GCTGCGGCTGGCAGAGAAGAGCCCCCGTGCCTGCGCAGGCA
TP61043	TGCAGCTA[C/G]GGCTGTTCTCCAAGATACCAGCGAGGTTGCTAAGTAAGAAAGGGTTCTCCCACAG
TP61051	TGCAGCT[A/G]CGGTAGTGGTATTGGTAGCGCCACCGCCACCGCTGCTAGTACTGGAGCTGCTGCTG
TP61056	TGCAGCTACGGTTCCCACCCAGCACCACCGTCAG[C/T]CGTGCTCGCCGAAGCCCCCGCGAGCACCG
TP61064	TGCAGCTACGTAGTACGGCAACAGCAACCGAGCAATGCAAATCTCATC[A/G]TCAAAGAATCAGGCG
TP61070	TGCAGCTACGTCATCATCCTATATTCATGCACGACAAATCCTAATAGCCGTGTTGC[A/G]AGTAAAA
TP61111	TGCAGCTACTAGCTGGGCAGAGCGCGCGGGAGTGAAGA[A/C]GATCAGCAGCGTCGTCCCGAGTCCC
TP61130	TGCAGCTACTCACCTATAGCTACAGGTAGCTAGAGCTAGCTAGGGCTACCACTAGCTGATG[A/G]CT
TP61150	TGCAGCTACTCGACGCATCAGACTACGGTAAAAAC[G/T]ACTCCTAATTAGCATTTGTTTCTTGTGG
TP61161	TGCAGCTACTCTCTCTGCTTTGAGTTTATTTGACGAAGC[A/G]GAGGGTTGGCTCGCCTGAGGTTTA
TP61181	TGCAGCTACTGC[A/G]ACACCATCCTCGCGGTACGTACATACATACGGCATAGGGCATAATACATAT
TP61187	TGCAGCTACTGCGACACCATCCTCGCGGTACGTACGTAGATACGGCACAGGGCATAATACACA[A/C]
TP61219	TGCAGCTACTGGTCGGAACAGTGCGGTGCGCGCGAGCAGCAG[C/G]TCACGCGTGCACGCGCACGGC

Table A2 (cont.)

TP61291	TGCAGCTAGACACA[A/C]AGGCAATTATTTATTTTGGACATGTGTTCTGCCTATAAAGGTATGTTTC
TP61300	TGCAGCTAGACTAAGTGTCTAAGTTGGCGCTGGAGCTTGCCATCTTGCTGTGAGCTGAAC[A/C]GCT
TP61320	TGCAGCTAGAGCTAGTTTGGCATTGCTTGGCTAGTGTGCAGTTGTG[C/T]TTGTCTTAAGGGTGTCA
TP61323	TGCAGCTAGAGCTCCAAAATTTATATGCCGTATTTCAGGGACA[A/G]GGAGGAGCATATTGACTTGG
TP61379	TGCAGCTAGCAACAGCTGAGGCGCCGATACCGAATTAA[C/G]GGGTTGGGGATATCCACCCGCATAA
TP61403	TGCAGCTAGCACGTACCAACCTGGCTTTATTATTTCCTAATTTGACAACGTAC[C/T]AGCCGTATTA
TP61405	TGCAGCTAGCACTAGCAGTAGCAGGGGACCATTGACCCCCCGTCG[C/T]CGTCTTCCTTAATCCATC
TP61423	TGCAGCTAGCAGCTAGATCTCTCCTACGTCCCTGACGGTGTGCG[C/T]GCTGCGCGGTCAAGGGTGA
TP61424	TGCAGCTAGCAGCTAGCAGCCGACCGAGCTGACGCTGTGTCCGT[G/T]TGAACGCCGCAGGGTTCAG
TP61437	TGCAGCTAGCAGTCCTCCTGCTAGTAGCTCCTC[A/G]TACACGCGTATGTGCGCGCGAGAAGGGAGG
TP61473	TGCAGCTAGCCACGCCATGGC[C/G]GCTGGTTGTGACCCATGTTGGGTCACCACGAGGAGAAGGAGA
TP61475	TGCAGCTAGCCAGCAGCCCAGCATGGCGTGACTGGCTGGCTG[A/G]TGAGCAGATGGAGAGAGCAGC
TP61503	TGCAGCTAGCCCTGATACAGTAACCTGATACCACGACACGGCATCTAACA[A/G]GGGAAGGCTGCCG
TP61512	TGCAGCTAGCCGCGTGCAGGAGACGACGACGACGA[A/C]GCACCCAGCTAGAGAAGGCAGTGATGAA
TP61515	TGCAGCTAGCCGTCGAAGAGGCGGAGAA[G/T]CTCTTGGCCGCGGAGAAGCTGGAGGTGGTGGACTT
TP61523	TGCAGCTAGCCTCCCTCCTCGGCCTCCGCCCTTCTGTCTGCCGCACCAT[A/G]CTCAGCCTCCACGG
TP61524	TGCAGCTAGCCTCCTGCGGTC[G/T]GCGTGGGGCTACGTAGTCACCGTAGAGGCGCTGCTTGGCACT
TP61528	TGCAGCTAGCCTCTGACGAGGAGGAGGACGCGTCGG[C/G]GTCCAACAGAGAGAAGCAGCAGCTGCG
TP61531	TGCAGCTAGCCTGTGCTGGGAGGAAGCCACCGCTGCCTGGGAGGTGCAGCGTAGGGCGACAC[A/G]A
TP61552	TGCAGCTAG[C/T]GCCAGCAGATCGGATCTGACCGAGCCCTACGTGGGACGGGGCGGGCGGGGCGTT
TP61571	TGCAGCTAGCGGCAGCCCACGT[C/T]TAGATGCGCGTGCATCAGCGGTCGAGGGCTTCTTTTGGCTG
TP61589	TGCAGCTAGC[G/T]GTTGATCAAGCAGGAGGGTGGAACTTGGATTGGATCATGGCACAGGCGCAGTC
TP61611	TGCAGCTAGCTAACGATCACGACAGTCGACAG[T/C]GATACGGATCCAGCTCGTGTATTCAGAAAGT
TP61622	TGCAGCTAGCTACTGAAGTGAAGAAGCTGAAGCAAGCATCATGGATTCATGGCCACGGA[C/T]GCTG
TP61623	TGCAGCTAGCTACTGAAGTGGCGACGACGGGCGCAGCTATCA[A/G]TCTCAGAACGCCGACACACAT
TP61630	TGCAGCTAGCTAGCAGCAGCAACAGCCACACTCCAACCTCC[C/G]CCTCCTCTTTCTCTGGCTGAAG
TP61641	TGCAGCTAGCTAGCTAGCGCTCC[A/G]ACGATCCAGCCTCCATTCAGACGAATTGATGCTGCTGCGT
TP61645	TGCAGCTAGCTAGCTCCCAGCGCCTCTTCCATAGGTCCTGCGAGAATGTCTGCGCT[A/G]CTGGTGA

Table A2 (cont.)

TP61646	TGCAGCTAGCTAGCTGCAACGCTTTTACACCGTGAAGC[A/G]GTCGCGACAGACAGGCCGAAAGGGG
TP61657	TGCAGCTAGCTATA[C/T]GAGGAATTATGTGTAGGGAGGGGTAGGGAAGAGCAACCTGGTCCAGGAA
TP61669	TGCAGCTAGCTCCAAAG[C/T]AGCAGGCGCGCCCCCGCCCCCGACACCGCGCGGCGCGCATGCATGA
TP61684	TGCAG[C/G]TAGCTCGGCACAGTGGCGCGGCGCGCGGAGGCTGGCACTGGGCAGCACGGGCACATGC
TP61724	TGCAGCTAGCTGTGGAGAATGCGTGGGCCCCACTCGCAGGCCGAGTCTG[C/T]GGGTGTGGTGCAGT
TP61728	TGCAGCTAGCTTACCGTGGAGCCCATGGC[C/T]AGCACGTGCATCGCACGCTAGGATCCGCAGGGCA
TP61741	TGCAGCTAGCTT[G/T]GCTTCAGAGGCCATGGAGAGCTCTTCAGCTGCACAAAGGCTGAAACTGAAA
TP61743	TGCAGCTAGCTTTCCCGTCAATAATGGAGTTC[G/A]CCATACCAGTGATTATTTCCTTTCAATAGCT
TP61760	TGCAGCTAGGACATGAAGCCATTGGGCCGCAGGAGTTGGATCTTCACAAGTTGCTGGTACGGT[C/T]
TP61764	TGCAGCTAGGACGGACGGACGGA[C/G]GCACGGAGCACGTACGCGCAGTGCTGTGCGGGGGCAGGGC
TP61782	TGCAGCTAGGATAGCACTAGTAGCAAGCAGTGATGGTGCCAGCCGCCCAGCCTCAAGTGAG[G/T]AC
TP61784	TGCAGCTAGGATCGCGACGTAACCTGCCCGTTCCACGCACGCATGCA[A/C]ATATGCAACGTGCGCT
TP61790	TGCAGCTAGGCAAGGCAATATATGTCATGGTCCATGCATATGCATGC[A/G]TCATGGATCGTCCATG
TP61792	TGCAGCTAGGCAGAAGGAAACGATGAAGGAGAAGGAAGAAAATGCTGTGGCTGGCCAGAA[A/G]GAA
TP61793	TGCAGCTAGGCAGTGTGTATCGACTATCGTCGTCGTC[C/G]GTACCTACGTGGAGGTGGCGTGTCAA
TP61797	TGCAGCTAGGCCCCAAGTTTTACCTCACTGG[C/T]TTCTCCATGGGCGGCGAGATCATGTGGAGCTG
TP61851	TGCAGCTAG[G/T]GTTAGGGATTGGGGAGCCGCGCAAAGCGAATACGTGATGGTCGTGGCCTTGGGG
TP61859	TGCAGCTAGGTAGAGGTAGCT[A/G]CTGCACATACTCCACTCGTTCAGTTGCTCTTCGATCACATGC
TP61860	TGCAGCTAGGTAGCGGGGACAAGGTGCCGATC[G/T]CTCCATGTGACAATGTGCTGCCACTACACCA
TP61864	TGCAGCTAGGTGAGACCCCGCTGGTGGTGGTGTCGTCCAAGGAGATGGCCCGCAA[G/T]GTGCTCAA
TP61868	TGCAGCTAGGTGTCCAGCGTGACCAGGCTTTCATAAG[A/G]GATGAGCTCGAGATGATGCTCTCTTT
TP61869	TGCAGCTAGGTGTTGCTGTAGCCTGATTTGCA[G/A]GGTTATATGAGCAATAGAGTATATATAGTAT
TP61873	TGCAGCTAGGTTGTTAGGTTAGCTTCCTGTCAGGTGTCAC[A/G]GCTCTCCAATCGAAAGGCTACTG
TP61896	TGCAGCTAGTAGTGAGAACGCACAGGTGGTGTCTTCTGCATCAGCAGAGAAAAACAAGGCAAT[A/T]
TP61900	TGCAGCTAGTCAAGCTGCCTGCCGCTGTCCATCAACGTACGGGAGCTA[C/T]CATCAATTCCATCCC
TP61926	TGCAGCTAGTGGCCAGTGTT[A/G]ACTGACTGGTGAGCCTCCTGCGGTCGCCGACGACGTCGACGCA
TP61938	TGCAGCTAGTTAAAACCATACCAGACCTTGGACCACGGTCTCGAACCCGTT[A/T]GCCCAACCAATG
TP61967	TGCAGCTATAAACTGCTCGCTATCGTGTGCTGCCACGCCGCCGCACTCACTCAC[C/T]CGCAGACCG

Table A2 (cont.)

TP61986	TGCAGCTATACGTGATGGGTACTCGTGC[A/T]GTTGTCCACGGAAGTACTGATACTAGTATGCAACT
TP62003	TGCAGCT[A/G]TAGCCTTTTTCTCATATCTCAAATCACTGACAAGCGTGCTATAGATCACACTGTTT
TP62012	TGCAGCTATAGTGTGGAGTAGAGTATGCAGCTGCTGCCTGCTGGGAAACGTACAAACCA[A/G]CAGT
TP62049	TGCAGCTATCAAGACAACAACCGTATC[A/G]TCGCTTGCGCTCAGGATCTACACCCTTGACGACTGC
TP62064	TGCAGCTATCACTTCCCA[A/C]TCCCAATTAATTAGGCACGCGGAGGGATGGCGTGGCCACGCGTTA
TP62070	TGCAGCTATCATCAGTATTCAGTCGC[A/T]CGTCGGCACGTTAGCCGCGATCATCACTCGCACGTGT
TP62084	TGCAGCTATCCCTCGCCATTGATGATTGATGACGG[C/T]AGCTAGCTGACAGAAAGCTCGCGGAGTA
TP62086	TGCAGCTATCCTATACCTCTACAACAACCAATTCAAAACAATGCAAACAATCATTTACAG[C/T]CAC
TP62090	TGCAGCTATCCTGTCCTGTCCTGTGTG[C/T]TATGTTCTGAGATGTGAGATGGGTTAATATAATGGC
TP62119	TGCAGCTATCTATTCGGTGTTTTCTCAAAGAGGGC[A/G]AGGCCAAGACAGCGATAGGAAACACCGT
TP62130	TGCAGCTATCTGTGGCAGAAGAA[C/G]TGCCGCCTGGCCTTTCTTTTGTACCAGTCCAGCTCCAGCA
TP62140	TGCAGCTATGAAGTATGA[A/C]CAACAATTAATTAATCTTCATGGAAAGTCAGTCGGCGATGCAGAT
TP62155	TGCAGCTATGATCGCGACGTAAC[C/T]TGCCCGTTCCACGCACGCATTCAAATATGCAACGTGCGCT
TP62187	TGCAGCTATGCTGCGCTG[C/G]TTGAGGCATCCAACTTCACGTTCTTGACGAGCTATGCTACGTCGT
TP62252	TGCAGCTATGTCAGGGTCACCAATCATAGGCCTTGGT[A/G]GCTGGAAGCTGTCATTGCAGGTCACT
TP62326	TGCAGCTATTGTTTGAGCTCATGTTGGC[A/G]TGGTAGGTGGTTGCTTCGGCACGTTTCTTGGCATC
TP62378	TGCAGCTCAAAGCTCAACACCACTATAGAAGACTGGCAAGCAGCTTCAGCT[A/G]ACTGATCAGCCA
TP62379	TGCAGCTCAAAGCTTCG[C/T]TCGCCCGCGTCGCCGCCGAGCACTACCGCGCAGAGGCGCGCCAGGC
TP62424	TGCAGCTC[A/G]ACCCTTGCATTTGTTGCGATGTCATTGCAGCGGATAGCATCAATCAGAGCTTCAT
TP62427	TGCAGCTCAACGACCTCGCCCTCAAC[G/T]CCGAGTTCATCAACCGTAAGGTGCGTTTTCTTCCGCG
TP62441	TGCAGCTCAACTCGATGTTTCCAAA[A/C]GCGAGCGAGGACAAAGCGGCATAGTGGAGACAGACGGG
TP62445	TGCAGCTCAACTTG[A/G]CGACCTCCTCGCTCTGATCCGAGCCTGGGATCCCATGACACAAGACAAG
TP62447	TGCAGCTCAAGAAAGCCC[C/T]GTTTGCCCGTCATCACCCCTTCAAGCTCAGAGCCAAAGTGATCCA
TP62450	TGCAGCTCAAGACCTTCCCCGCGCAGCGCCGC[G/T]TGGATTTCGTCGCCGACGGCGTATGGGCCCT
TP62455	TGCAGCTCAAGAGGGGTCAACTGCTGAC[A/G]GTACCTCCATACCTGATGAAAGGAAAGAAGCAGCA
TP62462	TGCAGCTCAAGC[A/G]AAAACGACCAGGGGCACAGGACGCCTGGACGCGGGACGCCGTTGGCCTTGA
TP62471	TGCAGCTCAAGCCCTTCTCCTACGACGAGGAGGTCTTTCAGGTGCGC[A/G]ACCCGTCGCTATTCTT
TP62482	TGCAGCTCAAGCTCTCTGCCAGGTCAGG[C/T]GCCAGCCCATTTCTTGCACACAAGTTCCAGCAGAC

Table A2 (cont.)

TP62504	TGCAGCTCAAGTGGGAGGAGTTCAGAGC[A/G]TGCCACCAGTTCTGGGGCGGCGGCCTCGACCTGAT
TP62553	TGCAGCTCAATTGATGGATCACCAGTTCATTCGGAACCAG[A/G]GGAGCTGAGCTTCCATTTCCATA
TP62558	TGCAGCTCACAAA[A/G]GTCGAAACCTCTCAGAGATCCAGCGCGCCTAAGCCCCCAAAGCAACAAAG
TP62577	TGCAGCTCACACCACAG[C/G]CCACAGCACAAACGCAACGCAACGCACCAGCTAGCAGCAAGCTGAG
TP62623	TGCAGCTCACCATCCAGGAACCATCCGTCGGCCCCATCCGAT[C/T]CGTGGAGGCAACACGTGCGCC
TP62669	TGCAGCTCACCGCGTCGAGGGGGCCCCTGCGGAC[A/G]ACGACCTGCTCCGTGACGGAAGCGAGCGG
TP62682	TGCAGCTCACCTCCGCCTCCCATGTCACTCCCCCTCCCTAGCCCACGC[C/T]GCTTACTCTGCCCCT
TP62687	TGCAGCTCACCTCGCTTTCCATGTGGGTGAGGGGTCGGTAGATGCGACGCGAAGCAGAGCAA[A/C]C
TP62720	TGCAGCTCACGCTACA[C/T]GCCGTTCGGTCGCGCTGGCGCTGCGATCTGGCGAGTGCTGTAGCGAC
TP62722	TGCAGCTCACGCTCGAGATGGGCCAGGTATCGTGTAATTATTATT[A/T]TTTATTTACAGTCAATTG
TP62733	TGCAGCTCACGGCCTTGGCGAGCAACCATCACCGCTGCCATGGACGCGACGCTGATTTC[G/T]CTCT
TP62736	TGCAGCTCACGGGCAACAACAGCAGGAGAGAGTTTAAGTTTAACTA[A/G]CAGCATCTTTTCCGAAC
TP62809	TGCAGCTCACTCTCAACTTCCTGATACATGACGA[C/T]ACACACTGCACATTCTTTTCGTAGATCTT
TP62820	TGCAGCTC[A/G]CTGCCCTGCGCGGCTGCGCTCCACCACACCTGCCCAGCCACAGCTCGCTCGTCCA
TP62823	TGCAGCTC[A/C]CTGCTGCTCGCCTCCCTGCTCCTCATCGCCATGGCCATACTCGCCCTCGCCGCCG
TP62974	TGCAGCTCAGATCATAAAAGGACGCTAAATTCTTCCAATTTCA[A/C]GTATCAGTCTGTCAGATTTG
TP62990	TGCAGCTCAGCACATAAGTAACACAAAAATA[C/T]TATCAACTAACCGTTGGTGTAGGTGTGCCAGC
TP62991	TGCAGCTCAGCAGCAAAGCCAAAGGACCGAGCAGTCTC[A/T]GCAATCTGTGAACGTGACTACTCCA
TP63008	TGCAGCTCAGCCTCCAGACCGTGATG[A/G]CCAGTGTCAGCAATTGGAGTGGAAACAACCTCAGCAG
TP63009	TGCAGCTCAGCCTCCATCGACAGTGGCCTTTCGGACCACGAACCAAGATACTAACAG[G/T]CTCAGC
TP63010	TGCAGCTCAGCCTCCGACAAGCTCTCCAGCCGTTTCTGCAAGGACACAAAATGCAACAG[A/G]CCCA
TP63016	TGCAGCTCAG[C/T]GACCTGCACCGCCACGGCGGCCTGGGGGGCGAGGACAGCGGGGGCAACGGGTT
TP63024	TGCAGCTCAGCGGCCTG[A/C]TCCCCGAGGCCTGGCCGACGGGCTGTGTCAACCTACAGGGGAGGGA
TP63033	TGCAGCTCAGCTCCCCGCATGTGCCTCAGCTCAGCT[C/G]GAACCTGGACATCATGCATGATGCATC
TP63040	TGCAGCTCAGCTTGCATTGCATGCACGCTCGTACTCTCCCATTCCCGATCAGACCCTAGACGG[A/C]
TP63043	TGCAGCTCAGCTTTCTAAACAAGGCGGCCATCGTGACCG[A/C]CGCCGCCGATGAGATACGGCCCGA
TP63044	TGCAGCTCAGGAAACATTTCTTGAGGTGGTACGGAAGGTCATCGATACTCAAGTAGAGTAT[G/T]CT
TP63049	TGCAGCTCAGGAGCGC[A/T]GCAAACCCTGCGCTGTGCGTGCAGGAGCCAGGAGGCGCAAAAATTAC

Table A2 (cont.)

TP63072	TGCAGCTCAGGGATGTCCCTGCTGACAGCGCCACTCGCGACAT[C/T]GCTCTAGACTGCACACGGCC
TP63085	TGCAGCTCAGGTGGCCGAGCGGCCACACCGTCGGCGGCGGTAGCTGCCAGCCGAC[C/T]GAGCACGG
TP63090	TGCAGCTCAGTAGTGACATGCCAACAA[C/T]GTAGACTGAGATGTCGCCGTAAGCCCGCGCGTGCAG
TP63097	TGCAGCTC[A/G]GTCTCGGTGCAGTAGCCACTCATTCTTGACGATGACGACGATGCGTCGGCTGGCC
TP63109	TGCAGCTCAGTGTGAATTTTTTTGAAGCCAAAAAA[C/T]CAAGAGACTGGGAATTCATAACTGCTCT
TP63120	TGCAGCTCATACGATTCTTCTTGAGCAACGACGTGACGGTG[C/T]GCGGCCTGCGGATCGAGAACAG
TP63166	TGCAGCTCATCCTCAAGAACAAGAAGGGAGCAGTACTTCCCCCCTCG[A/T]CGGCCTTCGTCAATGG
TP63168	TGCAGCTCATCCTCGTCAACCTCCACGG[C/T]TTTTACAGCCACCGCCGCCTTCGCCGCCACAACGA
TP63174	TGCAGCTCATCGAGAGCATCCGAGACACGGTGCACAAGAGGTGCGGAGAAAGAAGCGTCTCGT[A/G]
TP63176	TGCAGCTCATCGAGGC[C/T]GCCGTCACCAAGCGCGCGGCGGTGGCACTGCGGGAGGAGAACGGCGC
TP63209	TGCAGCTCATGCCGCCGCGGCTCG[G/T]ACTCGGACCTTGACGCCGTCCTGCTGCCGAAAAAAAAAA
TP63246	TGCAGCTCATGTCCGAGCTCACCCTCGGGCCGCCATACACCTCGACGAAGAAGTCGCCGAC[A/C]GC
TP63249	TGCAGCTCATGTGGCTTTTGCTGCTGCTGCTG[G/C]TGGTGGTGGTTTTCCACCTGTTGCGTTTGTG
TP63256	TGCAGCTCATGTTGATTCCTTTTAA[C/T]AATAATTTTCAGGGTTGGAGATGCTCCGAACATATTCT
TP63288	TGCAGCTCATTTAGACCT[A/G]TTGGATACGTGAATCTCCAAGATTTTTTATTATTTTCGTGAATTT
TP63293	TGCAGCTCCAAAACTTGTTGTGATTGCCCGACACACAAGCTTGCGACTTCGAGCTG[C/T]TGGGTGT
TP63308	TGCAGCTCCAAC[A/G]CGGCGTCAGCCTCGCCGCGGTAGACCGCGGCCGCGATCTCGTGGGGCAGGA
TP63317	TGCAGCTCCAACCTCGGTCTTTGTCTCCCTATTGGGTGCGCCTT[C/T]GACTGTTGTCTCACTCCCC
TP63329	TGCAGCTCCA[A/G]CTGGAGCTGGGCGACGACGAGCTGATGTGCGGCCTCGACTACGACCTCCAAGG
TP63334	TGCAGCTCCAAGATCCATGAAAAGCAA[C/T]GGAGGTGTGGGTCAAACCCTAGCGGATCCAGAAACT
TP63360	TGCAGCTCCAATGCCCTCTCGTGGTGCCCTCCACGCACCGTCGAGGCCTCCATGTGCTCGAC[C/G]C
TP63370	TGCAGCTCCACAGACAGCCCAACAACATCGTGTCGTCGTCCCCGA[A/G]CGCCCAAGACCTAACTCA
TP63378	TGCAGCTCCACATCACGCTGGAGCTCACCGTC[G/A]TTAGAGTAGTAGACGTCCAAGTACTCTTTGA
TP63385	TGCAGCTCCACCACACC[A/T]CGCAGCACCACAGCAGAGAACGAAACCCGCCAACGAAACACCAAAC
TP63387	TGCAGCTCCACCACCA[C/G]CAGCAGCAGCAGGACGCTGCCGCGATGAACGGCGAGCAGCCCGTGGG
TP63403	TGCAGCTCCACCATCACCAGCAGCAGC[A/C]GCCGCAGGACGCCGTCGCGATGAACGGCGAGCAGCC
TP63420	TGCAGCTCCACCG[A/C]CTGATCGCCGACGCGACCATCGTCAGGCACGCCGATCGGGAGCACGAGAC
TP63425	TGCAGCTCC[A/G]CCGTCATTGTCCATGGACCTGAACGCGGGGCATGTCGTCACCGTGGACAGGATA

Table A2 (cont.)

TP63471	TGCAGCTCCACGACCACCTCCTCGTCGTCGCCATCGCTGGACAACG[A/G]CATGGGGATGTACGCGT
TP63482	TGCAGCTCCACGCGAGGAGCGACCTCGCCGTCGCC[A/G]TCGTCGCGCCATCGCATCGTTGTTGCCG
TP63484	TGCAGCTCCA[C/T]GCTCCCGTCTGCATTCGAGAATGCCGATCTGTCAGCAGTCAGGTCACGTGCGG
TP63496	TGCAGCTCCACTCCCGTCGTCCTCGGGCTCCGCTCCCACTCCGCC[A/G]CCGCCGCTCCAAGCCGAA
TP63498	TGCAGCTCCACTGCACGCGAGAGCAAGCTGCCACAGACAAGGACACAATG[A/C]CACCCATACCCAA
TP63526	TGCAGCTCCAGATCCTCATAACCATACACATAAAACTGGGG[A/G]TCAGTGCTGAATGGCTCATACA
TP63544	TGCAGCTCCAGCCGCGGCGGCGGCGGCAGCGGGTTTGG[A/G]CCTGGCTTCAGGGGAGCCGCCGCAG
TP63546	TGCAGCTC[C/G]AGCCGCGTCAGGGCGCCCAGGAGCGCCAGCTGCGGCGGTACCCCACCGAAAAAAA
TP63550	TGCAGCTCCAG[C/T]GCCTTTGAGAGCTCAACCATGGTGGTGTACAAGATGGTGTGCCTGTCGAGCG
TP63577	TGCAGCTCCAGCTCTACGACTATATACTCTAGTAGTACACATACATGTATAATAATAAGTTAA[G/T]
TP63582	TGCAGCTCCAGCTGCTCCCTGCTCCACGTAGTAGCAGCGTGTGGCGATGGCGATGAGTTCTT[C/G]G
TP63585	TGCAGCTCCAGCTTCTGCC[C/T]CTCACGAAACACTGTGCTAACAGCCAGCAGTTGGACGTATATAT
TP63590	TGCAGCTCCAGGAGAGCAGCC[C/G]CTGCCTGTTCCCCGCCGACAGCCAAACACGCAACGCCTTTGT
TP63619	TGCAGCTCCAGGTAGAAGGCGTCCGTGCCTCCCTCTCC[C/T]TGGCCGCGGTCGTCGTCGCGGCGGC
TP63623	TGCAGCTCCAGGTCCTC[C/G]TCGTCGTCGTCGTCGAAGCGGTTCCTCCGACCGCGGCCCCCGAAGG
TP63679	TGCAGCTCCATCGGTAATACGGCAATGGCGGCAATGCCATGACAGCGACGATGTCCCTGAA[C/G]CA
TP63697	TGCAGCTCCATGATTCAAGCATGTCAGAGATGAAGCACACAGCAG[C/T]GTGCACACGGACACGGCT
TP63705	TGCAGCTCCATGTGCTTTGCGTTCACGC[C/T]CTCCACCTCCAGCCTCAGCGCGTTGACGTCGTCCT
TP63726	TGCAGCTCCCAAATGAAGTGAAGTCACCAGGATTC[C/T]TTCATCAATCCTTTCATAATAACATTTC
TP63741	TGCAGCTCCCAGAGCCACCTGTCCAAGGGATCCGATCCATGGATGAG[A/G]TCCCTCATGTGCTCGC
TP63757	TGCAGCTCCCATGCGGATGCTGATAAATGGCTCAACGTGGGGGT[C/T]GGGGGCTGAAAAGTTTGTT
TP63765	TGCAGCTCCCCACGCCATCAATTGAAGAGCTTGC[A/G]TATAGATAAGGCCTAATCATCATACAAAT
TP63768	TGCAGCTCCCCATGC[A/G]GCAGGTTGGGCTAGCTGCCCCCACTTACCGCCGACATGGAGAACGCCC
TP63776	TGCAGCTCCCC[C/T]AGGCCCGCCCGCCAGCGCTCTCCTCCCGCTTCCTCGCTCGATCGATCGGGGC
TP63781	TGCAGCTCCCCCGTCGCGTTCCTCTCAGGTCAGCCAGTTTGGTCCCC[A/C]GCGGCTTCCCTCGCTG
TP63784	TGCAGCTCCCCCTCCCGTACCTCCCGCCGCCTCCTCCGCC[C/G]CCGTTATCGCTACCGCCGCTGTT
TP63861	TGCAGCTCCCGACGGGCATCTGGTCCATGGCGCAGTGCGCGGGGGACATATCGCC[A/T]GCTCAGTG
TP63864	TGCAGCTCCCGATAACGTCGTTGAAGTTCGGAGACTGC[A/G]TCATCTCCAGCACGGTATCCCGCCC

Table A2 (cont.)

TP63875	TGCAGCTCCCGCCCGAGCTGCGGCACAAGGCGATGCGGGTCGTGG[A/T]GGACGGCCGAAAAAAAAA
TP63902	TGCAGCTCCCGTCCAAAAACCTGAGTTTCTTAGAGTACATACCTTTTTTCAGGCACCCCC[A/G]CCG
TP63905	TGCAGCTCCCGTCCAAAGCGCCAACGTGCATGACAGACGCCACTC[A/G]CGGTACCAACGCGGCGGC
TP63928	TGCAGCTCCCTCATCTCGTAGCCGAAGGTGG[C/T]GGCGAGCCTGTCCTTGGCCTCGTTGATGACGA
TP63939	TGCAGCTCCCTCCGCAA[A/G]GCATCCACCTCCCCGCGCAGCCGCACCACCTCCTCCTCTACTGTCT
TP63940	TGCAGCTCCCTC[C/T]GCCGCCGACGGGAGCGGGCCGCGGACGTGCGCCGCTGATGGTGTCACTCCC
TP63944	TGCAGCTCCCTCCTCTCCTCCTCGCCGCCGCCGAA[C/G]TCGCAGAGCGAGTAGGCCACCATGTCCT
TP63946	TGCAGCTCCCTCGAGACGAGCTTA[A/G]CCTCCACGCGCGCGAGCGTGTCGTCGTTCTCAAGGCGAG
TP63965	TGCAGCTCCCTGCCGCCCCGCACGCGCACCTCCACGGAGGTATCCCCGC[A/G]CTTGAACGCCGCGT
TP63973	TGCAGCTCCCTGGGGCACGCTGT[A/C]ACACACACACGACACACAAAGCTTCACGCGTCATCAGAGC
TP63975	TGCAGCTCCCTGTGCTGCTGCCCGTACCGCAGTA[A/T]GTCGCGCAGGTTGCTCACCGTGAACACGT
TP63978	TGCAGCTC[C/G]CTTAGTCACAAGCTGTTCACACACATGCACACATATAGCGCCATATGCAAACGTC
TP63984	TGCAGCTCCCTTTGGCCGCCGTCAGCATC[G/T]CCAGGGGGAAGCGGTCCATCGGCGGCACCGTGGC
TP63994	TGCAGCTCCGACACGTT[A/G]TCAGCCTCGCCGCGGTAGGCCGCGGCCGCGATCTCGTGGGGCAGGA
TP63999	TGCAGCTCCGACAGCGCCATGGCGTGGC[A/T]AGCTCACGCGTCACTGACCGACGGCGGTGGCGGCG
TP64014	TGCAGCTCCGACGGCTCCCGCGATGTCGGACGCGCATCAGGCTCCCGTTTCCGAGAAGC[A/G]GGAC
TP64017	TGCAGCTCCGACTC[A/G]CCGACCAGCACCATCCACGGAATGCCTGATTGCAAGGCATACTTGATGT
TP64043	TGCAGCTC[C/G]GCAACGAGGTCGGCCACCAGGTCCTGCACGATGGCACGCTCCAGCGCGGCCGCGA
TP64049	TGCAGCTCCGCACTGC[A/G]TGCTGCTCCGACCTAGCATCGCTGCCGCCCTCCCTGCCCACCTGTCG
TP64052	TGCAGCTCCGCAGTCGTGCAGCTGCTCCTACTCTCGTACATCAGGTACGTGTAATAAAGTT[G/T]TT
TP64054	TGCAGCTCCGCATGAAGGACGAGGCGGCCAAGG[C/T]GGCTGCGCAGGCGCCGCCCGCGTTCGTCGT
TP64075	TGCAGCTC[C/G]GCCCGCTCGCCACTCAGGCGCGCGTTGTCGCGCAGCACGTGGTCAGCGTCCCTGA
TP64079	TGCAGCTCCGCCGCCGCGGGCGCGGGCACGGGCAC[A/G]CGCGCCCTGTGCTCGCTGTGCCTCGCGC
TP64081	TGCAGCTCCGCCGCCTGCGCGCAGCTCAGCCA[G/A]AGCCAGCAGGGGAACGGGTGCTCCAGCTCCC
TP64083	TGCAGCTCCGCCGCCTTCTCC[C/G]CCTGCTGCGACGCCATTGTTATCCCCACCCCACCACCAGCGG
TP64120	TGCAGCTCCGCGGCAGGCCGTGCCAGTAAAAGCTCCCTGACCCGTCGGTCCGTCCATGCTCCT[C/T]
TP64124	TGCAGCTCCGCGTCCTCATC[A/G]GCCTCGCCGTCCACTTCCTCGACTCCTTCTCGCCACGCCGCGG
TP64128	TGCAGCTCCGCGTCGCACGCTC[C/G]TTCGGACAGGATGGCGGACGCCGTCGCCACGGCGCCCGCGT

Table A2 (cont.)

TP64138	TGCAGCT[C/G]CGCTCCGCTCCACTCTTGGCGGAGATCCCGATCCTGCTGGAGCTGGGCTGCTGGAG
TP64165	TGCAGCTCCGTCGGTTCTTTACTTTTCCTAGTTGAGGTGC[A/G]ACGGAGTCGGAGCCGTTTTACCA
TP64168	TGCAGCTCCGTCTCGAGAGCCGCGACCTGGGTCATCGTCAAATCAAACAATCCGTTAGACT[A/C]TT
TP64171	TGCAGCTCCGTCTGCCCCGTGCGCGCT[C/T]GTCGTCCCGCCGCCGCCGTCGTCTCCCTAGCAGCCG
TP64205	TGCAGCTCCT[A/C]GATCTCGTCGATCGCCTCCCGCCCCAGCCGCGCGCCGAAGCACATGTGCGTCA
TP64254	TGCAGCTCCTCACCACCAGAGCCTGACCTGGCACCTCCCTCTATGTTGTCGCTGGCAG[A/T]GGCCC
TP64263	TGCAGCTCCTCATGCAT[A/C]TGATTCAAGGCAATGGGGGCCGTTCTTCAGCCCCATCGTCGTCCCC
TP64270	TGCAGCTCCTCCACCTAGTCGATCCAACTACACCTACGACACAAGCCCTG[C/T]TCTGCATGCCGTG
TP64277	TGCAGCTCCTCCAGACCTCCACCCATCTGCGCGCA[A/C]CGCCACAGTGTGAAGGCATGCATGCAGT
TP64284	TGCAGCTCCTCCAGCTTCCGCTTGTTCGCCTCTAT[A/C]TGCCTCTGCCGCTGCTCCTCGTACGCCA
TP64289	TGCAGCTCCTCC[A/G]TCCACACGCCCACGAAGGCCTGGCCGTCGACGCCCAGCTGCGTGAGCGCCA
TP64292	TGCAGCTCCTCCATGGCCTTGAGCCGCTGGAGCACCCTCTCAGACGCATTAACC[A/G]CCGTCGAAT
TP64310	TGCAGCTCCTCCGTCCTCTCCACCCATGGA[C/T]GACCACGTGCACGTAATCTGGGCCCTGCCCCCG
TP64311	TGCAGCTCCTCCGTCCTCTCCATCCATGGATGGCCACGTGCACGTAAT[A/C]TGGGCATGGGCACCA
TP64327	TGCAGCTCCTCCTCCTGCGGGTGCTCTCGCGGCTGCGGCTTACTCC[A/G]CTCGTTGCTCCTCGTGT
TP64332	TGCAGCTCCTCCTCGCCCAGCCAGCACACCACACCCACA[C/G]CGTCCCGTCTCCTCTCCCCAGCCT
TP64333	TGCAGCTCCTCCTCGGAGGGGCCGCCCTCGACGGCGGCGGCGGCGTCCTC[A/G]GCGGCGTCGG
TP64346	TGCAGCTCCTCGACCTGGTCGGCTGGTGTGCAGTGAGCCATGACAACCTGGATATATATTTT[C/T]C
TP64367	TGCAGCTCCTCGTCCTCAAGA[A/C]CACCTGACCAAGAACACAGCAGCTCGTTAAAATCCTGCATTT
TP64373	TGCAGCTCCTCGTTCGTCATGTACACGCGCGCCCACACATCTCCCTGATCGCCTCGACAAAAA[A/C]
TP64378	TGCAGCTCCTCTATGAGGC[A/G]GAAGATGCGCTTGCCCGTGTCGTAGCTCGTGTCGAACTCGGTGC
TP64386	TGCAGCTCCTCTCGCAAGCTCTCCTGCACTTCGAAGATCGCCTGAATGAATGAAAACACA[A/G]AAA
TP64437	TGCAGCTCCTGCAAGGAATGAGGGCTGGCGGCGCCAGAGG[C/T]GAGCTCGTTCTCAGCGCCAGGGA
TP64453	TGCAGCTCCTGCCGCAGCTGCTGGGC[A/G]CTGGGGTGCGCGGCCTGGGCGCAGGTGTGCGCGCCGT
TP64454	TGCAGCTCCTGCCGCATGTCAAA[C/T]GCGTCGACGAGTGACGCCGCCTTTATCTCGAAATAATCCT
TP64456	TGCAGCTCCTGCCGCTC[C/T]GCGGTGGACATCTCCGCCGCGCCGCCACCGCTCTTTGCGCCGAAAA
TP64459	TGCAGCTCCTGCGAAGGAACCGAGCAGTTTTAGCGTGAAGGATTGTCGTTATC[A/T]GTAGGAGGCA
TP64460	TGCAGCTCCTGCGCCCTGGAACTCATCCGCGCGCC[G/T]TCCTCCCCGCGCAGCAGCTCCTCCACGG

Table A2 (cont.)

TP64465	TGCAGCTCCTGCTCCTCCTCGCGTTCGCGTCGCATCCATC[A/G]GGTCGGGGCACTGCACTGGTACG
TP64470	TGCAGCTCCTGCTCGGCGTACGCGTGCACCCACG[C/T]GCCGTGCTCCAGTGACCGCAGCTGCGCGC
TP64471	TGCAGCTCCTGCTCGGCTTTGAGGACCAGGGAGTGCGGCCTTG[C/T]GGGCAAGCTGATGGATCGCA
TP64477	TGCAGCTCCTGCTGA[A/G]GGGGAAGAGAAGGAGGCGGAGGAGGGACTCGTGCAAGAGGTGCGGCGG
TP64480	TGCAGCTCCTGCTTGCTCATCAGCGCCGCCGCCT[C/T]CCGCTCGCGCGCCTCGTCCACCAGGATCT
TP64486	TGCAGCTCCTGGCAGTCGCTGGGCCTCCGTACGACACCTTAGAGGAGGTGATTGGGATCAGG[A/G]G
TP64494	TGCAGCTCCTGTATCCTC[C/T]TCTCCCACCGCTCGTTGTACTGCTGCCGCTGCTTCTTCCTCGTCA
TP64517	TGCAGCTCCTTCAACAGCCGCCTGCCGCCCAACGCTGACGACGGCACCATGG[C/T]CCCGTCGTTCC
TP64525	TGCAGCTCCTT[C/T]CCAGCCTATCATCGCCGCTGCGTTGGGAAGCAGAGAGATGGGGCGTCCGCGA
TP64532	TGCAGCTCCTTGACCTCAAGAGCAGGGGTCACCATCTCGGGCTCGGCTCCCC[A/C]GTTGGTTCAGG
TP64549	TGCAGCTCCTTGGGCTTGCGCGTCTC[C/T]AGCAGCCACCCCAGACGCGGCTTCTGCTCATCATCCG
TP64552	TGCAGCTCCTTGTAGCTGAATAT[C/T]CTCCACGTGCTGCTCATGGGCGACGCGCTCACGCACCTGA
TP64553	TGCAGCTCCTTGTCATTGCCATGGTTGCTCTTCCTGGTGGTGGTCCTTATTGG[C/T]GACGCTGCGG
TP64566	TGCAGCTCGAACAAGTGGC[A/G]GGGAACGGCGTCGAGCTAGTAGCGTGGAAACGCCTCTGACGTCT
TP64574	TGCAGCTCGAACGTCGCCG[A/C]GGGGAGACGCGCCGCCAGGCACCGCGCCACGTCGGTGCCGTTCT
TP64578	TGCAGCTCGAACTCAAGGCTCCATCGCCAGGCCTGACC[C/T]TCTTCTACCACATGACGCACATGGT
TP64580	TGCAGCTCGAAGAACCCGCTTGGCTGCTGTGTTGATCAGGAAGGAAGGG[C/T]GCTGTGCACCAGTT
TP64581	TGCAGCTCGAAGAAGCCGCC[C/G]TGGAGCAGGGTGTTGATGCGGACGAGCATGGCCGCCCTCGTGG
TP64582	TGCAGCTCGAAGAAGCCGTGCTCGATCCCCGCGATCTTGAACGCCTC[C/G]GCGGCGTCCACCTTCC
TP64585	TGCAGCTCGAAGT[A/T]GCTCTCAGTAAGCTTCACCTCCGTGAACCCCACCGTCGGGTCGCCACCGC
TP64593	TGCAGCTCGAATGCGAGTTATTCAGACT[G/T]GTCAACGGAGTTTGGCCACTGCAAGAGCAGCAAGG
TP64598	TGCAGCTCG[A/T]CAACTTACAACTCGGCCAAGCTACCACGGTTTGCATTTTGACACGAGACAGAGT
TP64604	TGCAGCTCGACACGGCCACACGGG[G/T]TTTTCCCTTCCCCACCTGGCCACCTCCCCGCCCCGTCCC
TP64616	TGCAGCTCGACCACGATGACGCTGATGTTGTCCCTGCTGCTGCGTGACATGGCCA[C/G]CTCCGTGA
TP64624	TGCAGCTCGACCGTGATGAGCGGCCTTATGTTGACGGCCACCTTCACGCT[A/G]TCCTTCTGCGGAT
TP64632	TGCAGCTCGACGAGCGGCTGCTGCTGCGCGCCACGGAC[A/G]CCGCGAGGCTCACGGGCTTCAACGG
TP64641	TGCAGCTCGACGCAGCCGCGGCGCTGGTTGGCCTGCGCGCGTTTGAGCGCGGCCAC[G/T]AGCGCGT
TP64646	TGCAGCTCGACGCGGCCACCAAGGCCGCGGCCAGCGCTGACGTGACCGTGCTGGTC[A/G]TCGGCGC

Table A2 (cont.)

TP64655	TGCAGCTCGACGGGCGTGGGGCGGTACGGGGACGGGGACGGCGACGGCGACCGCAGCCACGC[A/G]A
TP64656	TGCAGCTCGACGGGCGTGGGGCGGTATGGGGA[T/C]GGGGATGGGGACGGCGACGGCGAGAGCGGCC
TP64670	TGCAGCT[C/G]GAGAACAAGGACAGGGAGGTGGAGCGGCTCAAGGACCTGTGCCTGCGGCAGCGGGA
TP64674	TGCAGCTCGAGAGAGAGGAAGATG[A/G]CGCCCTTGAGCTCCCACCCTGCGGGCGTGCGGGAATCGC
TP64676	TGCAGCTCGAGAGAGGGAATGTAGTAGTAATTTAATTTAATTTAATTACTGTAGCA[A/C]CCAGGCA
TP64699	TGCAGCTCGAGCCGCGGCAACGTC[A/G]TCGTCGTCGTATGAGCAATCGTCGTCTAGGAACGCCAAC
TP64718	TGCAGCTCGAGGAACATCGCATCAACGAGTCAGAGAAACTCTAGGCTGTTGTGGCTC[A/T]CGTCGC
TP64727	TGCAGCTCGAGGCCTTCCACCTCGTGCTGCACGATCCCC[A/G]TGACCATGGTGTCGTCGCGGTGCT
TP64738	TGCAGCTCGAGTTGCGGCCCAAATTTTCTAAGAGTAGGTCCTTATCAGCAGCCCACGAAAGCT[C/T]
TP64748	TGCAGCTCGATCCGCGCTTCCGTTCCATCCATGGCTCCCAACCTCAGCTCCGACG[A/C]CCCTAAGT
TP64759	TGCAGCTCGATCGGGCAGGTCAGGCACGCACGGGCAT[C/T]CCCTGGCCCCTGCGCTGCAAGAGGCT
TP64800	TGCAGCTCGATGG[C/T]GTCCAGGTCCATCTCGAGGCGCGTGACAATGTCGTGGACGTGGTCTACGT
TP64808	TGCAGCTCGATTGGTTCAGCGGTGAGCCTCACCAGCACCTCCTCTGCCTCCCCCAAGCT[A/G]CGCC
TP64814	TGCAGCTCGCAACACCGACGATGATGATTATTGTGATCTTGA[C/G]GATGAGGGAGTAGTCGAACAC
TP64828	TGCAGCTCGCAGACCTCGCCGACGGAGCCAGACGGCGGGATGAAGCAGACCACCGACAGGAC[G/T]G
TP64832	TGCAGCTCGCAGCCATCAGAGGCCGCCGCGTTGCGGCTGTGCACGACGACGCTCCCAGC[A/G]GCGC
TP64847	TGCAGCTCGCCAAGCTCCTCCA[C/T]ACTCGCGGCTTCCACGTCACCTTCGTCAACAACGAGTTCAA
TP64849	TGCAGCTCGCCAATGTGCGAC[A/C]ACCTCACCTGGTCGTCTTGCGGCAAGCAGAACTGGGGAAACC
TP64850	TGCAGCTCGCCACCAAGCTCTCCGACCG[C/T]CTCGGGGTCAACCTCTGGATCAAGCGCGAGGACCT
TP64853	TGCAGCTCGCCACCGTACCTCGCACCAGTCACCACCATCCACCGCCGCTCATC[A/G]AGCAACGCCA
TP64863	TGCAGCTCGCCAGGCTGCTCGC[C/T]ATCGACCGACCCATCTGGCTGCTTGACGAGCCCTCCGTCGC
TP64936	TGCAGCTCGCCCTCGGAGAAGAGCGCCTCGACGATGTTGTCGATGAGGGA[A/G]TCGACGAAGGCGT
TP64950	TGCAGCTCGCCGC[A/C]GTCGCCTTCGAGGCCACGCGCCTCGTCCTCATCCAGATCCTCCTCACCTC
TP64954	TGCAGCTCGCCGCCGCCAC[A/G]CTGAGCGGGTCACTGGAGACGCTGTGCGGGCAAGGGTACGGCGC
TP64956	TGCAGCTCGC[C/T]GCCGCCACGCTCGGCAACTCCTGGGGCACCGTCACTGGCATCGCGCTCATGGT
TP64958	TGCAGCTCGC[C/T]GCCGTCGCCTTCGAGGCCACGCGGCTCGTGCTCATCCAGATCCTGCTCACATC
TP64986	TGCAGCTCGCCTTCGACGACGACAACTTCAAGGGC[A/G]GGTGCGACGGTGCCTTGGCTGATTACTA
TP64990	TGCAGCTCGCCTTTTCCAACGTGGCATGGCGCGCTAGGAGCTAGTATGCTATGC[C/T]ACACGACGC

Table A2 (cont.)

TP65001	TGCAGCTCGCGCAGGCAGAGC[G/T]CGCGCTCCAAGCACTCGCCGCCGACACTGAAGGCTTCCTGGA
TP65003	TGCAGCTCGCGCAGTTCCCCTACGACGCGGAGGCGATCCAGTCCGCGGACGCCGCC[C/G]TGGTCGC
TP65008	TGCAGCTCGCGCCCCTGCCTCGCAACCAGCACGGCCATGGATGCTGCTTCGTTCTCGGGC[C/T]TGC
TP65033	TGCAGCTCGCGGAGCACGACGGCCCTGA[A/G]CGCGTGGAGCTGCCTCTGGTGCGCGGCCACCTCCC
TP65036	TGCAGCTCGCGGAGCACGA[C/T]GGCCCTGAGCGCGTGGAGCCGCCGCTGGTGCGCGGCCAACTCGC
TP65040	TGCAGCTCGCGG[A/T]GGGCCACACGTGCCTGACCGAGCGCTGCCCGTCCGTGGAGGCCGAGGGCGC
TP65042	TGCAGCTCGCGGATCTG[C/G]TCCTCCGTGGCGCGCACGATGACCCCCTTGTCCTGCCCGCGCTTCC
TP65051	TGCAGCTCGCGGT[A/G]CGAGAACTGCACGGGCGCGCCCGACGCGTACTCCAGCAGCGCGTACTGCG
TP65052	TGCAGCTCGCGGTCGCGCTGCGCCGCCGCCGCTTGGGGTCGGCATGGGTGCAGCGTGCGGA[G/T]CG
TP65123	TGCAGCTCGCTGCAATAGGCTCGAAGGCGCTTCCACCAGC[C/T]GAGAGTTGTCGACGCAGGCTGTG
TP65125	TGCAGCT[C/G]GCTGCCACCAGGAGACGGAGTTGCGTGGGTATAGCTGGTGGACTCCATCGATCTCG
TP65167	TGCAGCTCGGAGGAACAGACTTGATAGGCTGATGTTCAGGACAA[A/G]TGAGCGGCTTCCTGGTGCT
TP65169	TGCAGCTCGG[A/G]GGATGCCAGGATGGTAATGCCAGGTGTCGCGAGTGGGTAGGATCACTGTCACT
TP65179	TGCAGCTCGGCAGCAACAGCCTCCC[A/G]CTCCCGCTCCCGCTGGGGGCGACGCCGCCAGGCGCCAG
TP65194	TGCAGCTCGGCCAGACGCCGCTC[A/G]TCGTCGCCTCCTCCAAGGAGACGGCGCGCGCCGTGCTCAA
TP65227	TGCAGCTCGGCGACGCCATTACCAACCACCTCCTTCTCCTTACTATCAG[C/G]TACCCTCAGCGCAG
TP65241	TGCAGCTCGGCGCGCGCCTCCTCGCGGCGACAAAGATCC[A/G]TTTCCTCCTTCCACGCGTCGACAG
TP65243	TGCAGCTCGGCGCGCGCCTCCTCGCGGCGACGAAGATC[C/G]GCTTCCTCCTTCCGCGCGTCGACGG
TP65250	TGCAGCTCGGCG[G/T]CGGCGATCGTCGACCACGCGTACTACTGGCCGCACTTCACGCACATCCCTG
TP65253	TGCAGCTCGGCGGTGAGCTTGTCGCTGAC[A/G]GGCTGGAGCTCCTTCTCGAGGTCCTGCGGCTGCA
TP65258	TGCAGCTCGGCGTACTGCTTAGAGTTATGACGCCTGAAACCCAACGGGATT[G/T]CGACGCGCGCGG
TP65265	TGCAGCTCGGCGTCGG[C/T]GGCCACCGCGGCGTCGGAGTGGTAGAAGTGGGCGCAGTAGCTCCGCA
TP65274	TGCAGCTCGGCTGCACCAAGAGCGCGGAAGGGAAGACGGATCACTGCATCGCCCATGG[A/C]GGCGG
TP65293	TGCAG[C/T]TCGGGCGCCGACGCCGCGGGCCCGTCCAGGTGCGGCGGCGTGGTGGCCAGGTGGTGCG
TP65297	TGCAGCTCGGGCGGCGCCGACCGCGGGCGACCACGGT[A/G]GTGAAGCGGAGCCTCAGCCCCGTGTG
TP65309	TGCAGCTCGGGGACAAGTTCTACGTGGTAGGGTGCTCCATGGGCGGCTACCCAGCGTGG[A/T]GCTG
TP65323	TGCAGCTCGGGGGGCAG[C/T]GGGGACGCATCCGCGAGGTGGTCCTCGCTCGACACGTTGCGGCTGC
TP65329	TGCAGCTCGGGTCACGTTTCG[A/G]GGAAAGCGAACGCACGCAGCAGCTGGTGCCGTCCGTGCGTTC

Table A2 (cont.)

TP65357	TGCAGCTCGGTGCAAAGCGAAGGAAAGGAGAGCAAATACCAGTG[C/G]CCAGTACTAATGCCGTGCG
TP65364	TGCAGCTCGGTGTTGACGAACTCGACGTC[G/T]ATCAGCTTGTTGTCGCAGCACTCCCGAAAAAAAA
TP65372	TGCAGCTCGTA[C/T]GACTTGGCGATCTCGTCGATGAGCTGGGTCTTCTCCTCGCGCGGGACGGTGG
TP65376	TGCAGCTCGTACGCTTCTGCATTAAAACAAATGGAGGCACACTAGAAACAAACG[A/G]ATGCTGCTA
TP65378	TGCAGCTCGTACTCCTCCTTCTTCTTCGTGCCGTAGTGCCACGT[C/T]GACATGGCCAGCAGCGTCA
TP65414	TGCAG[C/G]TCGTCCAGGTCGAACGCGTCCGCCACGGACGGGTCGACCAGCTCGTGGAGCCGAAAAA
TP65423	TGCAGCTCGTCCGTGCCTCCCACCGCTCTCATGGTGTAGTAGTAGACCCCGAGCAC[A/G]AAGGCAG
TP65424	TGCAGCTCGTCCTCCCGCTCCTGGAGGAGCTCCGCGACGCCGC[A/G]CCCCGAAAAAAAAAAAAAA
TP65431	TGCAGCTCGTCGAACACCTCGTGTC[C/G]AGAAGTGATGACGTGGCGAGTCTCCATATTTGCGGTAG
TP65436	TGCAGCTCGTCGATGAC[A/G]GCGCGCCCGCCCGCGTGGATGCAGAAGTGCTCGAACGCCGAGCGGA
TP65440	TGCAGCTCGTCGCCGTCCTCCTC[A/G]TTGGCAAGGCGGCCGAGACGCTGGCGTCGCACCACTATGA
TP65451	TGCAGCTCGTCGGCGGTGATGTACCCGCTGCCGTCCTTGTCGAAGTACTGGAACGCCGC[A/G]AACA
TP65457	TGCAGCTCGTCGTCGGCGCGCGACGCGCACC[C/G]CTCCAGCGGTACCCCGCGCTTCAGCGCCCGCG
TP65461	TGCAGCTCGTCGTCTTGATCGCGCAGCTGCCGTCCACGCA[A/C]GCGAAGTCGGAGCGCCCCGAGCA
TP65463	TGCAGCTCGTCGTGGCCCTGCACGC[G/T]CTCGAACGATTCGTGAATTTAAATAGGCAGTAGTTTGG
TP65474	TGCAGCTCGTCTTCCACG[C/T]GCATGGGTAATGATTAATGAATATTTAGACATTTGTCGTTGTGCG
TP65481	TGCAGCTCGTGAGCATGGCAATGCGATTGCTGAGGTGAAGAGGGCTGCGGCTGCTGCCA[A/C]GTCG
TP65484	TGCAGCTCGTGATGAAGAAGTCAAGTGCTCATGATGGACTTGTGAAGGGTCTTCGTGAGG[C/G]TGC
TP65486	TGCAGCTCGTGATGGCGAACTGGATGTCAGGCCTG[C/T]GGGCTTCTCCATCAATGCCGTGGCTCAT
TP65490	TGCAGCTCGTGCAGGGAGTGCGGGCCCGCCAGCGCGTTGGCGGCCATGCCCCC[A/G]CCGCCTCCAG
TP65492	TGCAGCTCGTGCAGTGTGTGTGTGTG[C/T]GCTGTGCTCAACTCCTTCTACCTCTAGCCAAAGTGAG
TP65500	TGCAGCTCGTGCCTCTGTTCTAACTGGGTTACTGGTGC[A/G]GCACTTCTCTACAATGGGCGTGGAG
TP65502	TGCAGCTCGTGCGACGGTATTACCAGCACACGGTTACA[A/G]CCTGCGCGGCGCAGTCGCTTGGGCC
TP65505	TGCAGCTCGTGCGTGATGCATGCATCTAACCTCGCGGAGACGGAATGAGCAGC[C/T]CAGCTCATCT
TP65516	TGCAGCTCGTGGC[A/T]GTGCTCCACCACCAGCTTGGTCACCTTCCACTTCCCGCCCGCCCCGTCCT
TP65524	TGCAGCTCGTGGTCGCCGCCTGCCTCGTCACGGCGCTCCTGGGCATCGCCTTCCC[G/T]CGGAGCTT
TP65525	TGCAGCTCGTGGTGGAGCTACTGGTGGAGGAACCTCATCGGTGGGATCAGGGG[A/G]TGCAACTTCA
TP65528	TGCAGCTCGTGTACG[C/T]GATGCTGGGCGATGTGCGTGCTTTGCTTTGCGTGGTGTGAGTGCCCTG

Table A2 (cont.)

TP65537	TGCAGCTCGTGTGCGGTCGTTGGTCGAGCTTGGTGGTTG[A/C]ATCAGGCGGTGGCCCTTGTGAGGC
TP65538	TGCAGCTCGTGTGCTGGTTCTACCGCTACAGGCCACGCAAGTCGATTAGACGAACA[A/G]TGAAAAA
TP65561	TGCAGCTCGTTCTTCGGGTGCAGAGACTCAAAGAGAGCGCGAGTTGCACGGAG[A/G]TCCAAGCTAT
TP65563	TGCAGCTCGTTGAGTTCAGTGCGCGCCATATACTGTATATGGCTTATG[C/T]CGATGCTTACGTTAA
TP65588	TGCAGCTCTAAGTGCCTAAGATTTTGCAGGTTTTGCAGCTCAGGTGGGATCTGCCC[A/T]GATAAAC
TP65592	TGCAGCTCTACAAAAGAGTAAGAGCTGCATGCAACTTGAGGAGAGGAGAGGAGGGCAATC[A/G]ATC
TP65594	TGCAGCTCTACAACT[A/G]AGGATTGGAGAGGAGGGCAATCGATCAGTAGCAGGTGCAGGAGCCATA
TP65595	TGCAGCTCTACAACTGAG[C/G]ATCGGAGAGGAGGGCAATCGATCAGTAGTAGGTGCAGGAGCCATA
TP65701	TGCAG[C/T]TCTAGGCGGCACCAAAAAAACACCGTGTTCCTCTGTTCGCGTTGTGTGCGTGTGTGCG
TP65702	TGCAGCTCTAGGCTGTAGCAGGCTACGCTACTAGCACCAACTCAACCTATAGTC[A/G]TCCTGTTCG
TP65721	TGCAGCTCT[A/G]TCCATCTCCATTGGCACTGCCGCTCTGCTCTTCAGCAGACGAGATTCCGCGCAT
TP65724	TGCAGCTCTATCTACTCCGATCGGCTACACACC[C/G]AATCACACTAGGACTAGGCACCTACTAGTA
TP65742	TGCAGCTCTATTCCTGACACTTTGATTATATTTTAATGGTA[A/G]GTGTGGTACGTGTACGTGTCTT
TP65750	TGCAGCTCTCAAAGCGCGCAGGCGACGGCACCTCCCAACGGCTGGCGGCCG[C/T]GACCGCGCGGGC
TP65766	TGCAGCTCTCACCCCC[A/G]CCGCTTACAACGCCCTTATGTCCGCCTACTCCCGCGCCGACCGCCAC
TP65767	TGCAGCTCTC[A/T]CCGCAGCTCCACTGCACGCGAGAAGACAAGGACACAATGCCACCCATACCCAA
TP65768	TGCAGCTCTC[A/T]CCTTACGACCTCAGCCAACGGTGTCAGATCAGTCGCGCCACAGCGAGCAGCAG
TP65771	TGCAGCTCT[C/G]ACGTCCTCGCAGCCCTCGGCTGTTGTTTCTGAAACCGAGACCGAGACGTGCATA
TP65790	TGCAGCTCTCCAAGGTATACCCGCGCCGCCGCC[A/G]CCGTACACGTGTGGCCGTGCACATTCTTCA
TP65804	TGCAGCTCTCCATGACTGT[G/T]GACTGCGGAGTGAGGACGACGGCGCTCCTCGCCTCCTCCTCTCC
TP65807	TGCAGCTCTCCCAATTTTTGGTGGGTTGCCCTAGCT[A/G]TGGCGAGGCACAGAGGGGGCTGGCAGC
TP65809	TGCAGCTCTCCCATCT[C/T]CCGAATCTTCACCAACTCTTGGCTATCCGTTTCAAATTTCACTTTGC
TP65813	TGCAGCTCTCCCCCCAATCCACCTGAGCGGCCAGACACGGCTGCCCGCCAGCGAT[C/G]CCTCCATC
TP65828	TGCAGCTCTC[C/T]GCATCAAACAGACCAGTACCAGCACCAGCCGCGGCAATGGCGTCCACGACGGC
TP65830	TGCAGCTCTCCTAATTAACGAGATTTCCATTAACAAAGGATCGATCTTTGTCCCATAC[A/G]TACCC
TP65838	TGCAGCTCT[C/G]CTTCCCCCTCCCGTTCCAATTCCAAGAACAGGGCAGCGGAGGAGAGGAGAGTCC
TP65846	TGCAGCTCTCGACAAGCACAGGCTTGCAGACGC[A/C]GAGAGGAGAGCGAGTGTTTGGATGGTGACT
TP65851	TGCAGCTCTCGAGGGGATGGACCTTGCTTTGGGCTTCATCCAGGACAT[C/T]TGGTCCGAGCAGCTC

Table A2 (cont.)

TP65858	TGCAGCTCTCGCCGCCCGCGACGTAGAGGCGGTTGCCCATGACGCACACGTCGAA[A/G]CACTGGCT
TP65867	TGCAGCTCTCGCTGGCGTTCCACGGC[C/T]ATGCGCGTGACGACGACGTCGGCGCGCGCCTGCGGCC
TP65876	TGCAGCTCTCGGGGCGCCCATGCATCCCTTGCTCTGCTAAGCTGTTTACTCTA[C/G]TCAAACTCGG
TP65887	TGCAGCTCTCGTGCTGTCGTGCATAGCGCCATTTGACCACCACACCCTCCTCA[A/C]CCTGTAGAGG
TP65934	TGCAGCTCTGACCCTAGCTAGCTGCTCCACCCACC[C/T]ACTTTGCCAGGCGCGCCGTCCTCTCCCC
TP65961	TGCAGCTCTGCAACTGTAACAGAAAAGGCCTGCGTGTCGTCTTCTCCCTCCC[A/T]CAGATCATAGA
TP65969	TGCAGCTCTGCACGACGTGGCGACGTAAATTGGG[A/G]GAGGGGAGCAGGCGGCGACCGTTGCTTGC
TP65982	TGCAGCTCTGCATTTCCCCAGTGGGCAGTG[A/G]CAGAAAATTAATTCAGGCGCACCTTCGTCAAGG
TP65985	TGCAGCTCTGCCACGCACGCCGCCGCATGGCGTACAGTATCGTCGGTCGATCGTCC[C/G]TTCCAAG
TP65995	TGCAGCTCTGCCGTTGCTGCTGCTGGTCGTCGGTCTTTGGCTAAGATAAGCAGTG[A/C]GCAGCGCC
TP66033	TGCAGCTCTGCTCGC[C/T]CTCTCTCTCTCGTCTTTTGTCTCTCTACGTCAGTGAAACAGTGAATCC
TP66063	TGCAGCTCTGCTGCTACCTCAAGCCATCTGACCGAGCATCCTTTGCCGTCCGACGACTGTT[A/T]GC
TP66092	TGCAGCTCTGGAGGAAAAGGAAATCACCCACGCCTGCCCTTCCTGCGCTTGCTTTGATCTTTG[C/T]
TP66100	TGCAG[C/T]TCTGGCACGTGCCGCGTCGCCAACAGGAACCACCCGCCCAACTGCCCCTACGTCGACG
TP66102	TGCAGCTCTGGCATGGGCACATCATTCGCCTCCATCTCTTGTTCTTCATTGAGCCCCTTCAA[A/G]T
TP66114	TGCAGCTCTGGGAGAGCTCAACTCTTTGC[A/T]CAAAGTCACAGCTGCTCTGGGACACCACAGTTTA
TP66121	TGCAGCTCTGGTAGACCATGCTGGTGACGAC[A/G]GTGTCAAGGACACAGATCATGGCGTGGATATA
TP66129	TGCAGCTCTGTAGGTTGGTGGGCTCT[C/T]GCGACCCTCTCTGTCTCTGTCTGAATTTCTCCGCCGC
TP66140	TGCAGCTCTGTCAGCCCACTATCCACCTGAACCTCAAACAGCCCGCTAAACAACCATGC[A/G]CTAG
TP66157	TGCAGCTCTGTGTTGACCTGGAGAGCGTTTTCTGATGACAGGATATGGCCTGCAC[C/T]GTTGGGTG
TP66162	TGCAGCTCTGTTCCGTGGCAGATATGCATCTCTTTCC[A/G]CTAATTATTTTGTTTCCAGAAAGGTC
TP66176	TGCAGCTCTTACAGG[C/T]AGTGCTCAAGGCAACAGTAGCGGTGGTGGCAATGAGCACCAGGACTGC
TP66184	TGCAGCTCTTC[A/G]AGCCTTGGCATGGCGCCCATGTGAAACTTGAGCGCTGTGCCCACATCACAGA
TP66205	TGCAGCTCTT[C/G]CCACACCTCTTCAGCCCTGCATGCAGTTTCATGAATCAGTTAATCATCGGTCA
TP66207	TGCAGCTCTTCCCCTACACCAGCAGCACCGCCACCTCCCACCCGCCACCGTGCGCCCCCAAC[A/T]A
TP66208	TGCAGCTCTTCCCGCACCGCAGTAGTCCTGTTCATTTCA[A/G]AGAGCACAAGCACGCGATCGAGTG
TP66212	TGCAGCTCTTCCTGCCCTGCCCTGCCCTGAGCTGCTGAGATGCCCTCTC[C/G]CTCCCTCCATCTCC
TP66223	TGCAGCTCTTCGGCGACCGCCTGTACATCAC[C/G]GAGAACGGTACTAACCTCTGGTGGTCAAGCGT

Table A2 (cont.)

TP66224	TGCAGCTCTTCGGCTTCGCCGAGGCCATCAGCATCGG[C/T]CGCCGCTCCCCTGAGAAGCTCTTCAA
TP66236	TGCAGCTCTTCTCCATGGCCGATATGTAAGCGCTCCTGGCCCTGCT[G/T]ACTGCCGTTGCCCCCTG
TP66248	TGCAGCTCTTCTCTCTTGTTTCGATCGGCCATGGCAGCGGCGGTG[A/G]CCACAGAGACTCCGTTCC
TP66264	TGCAGCTCTTGAGCAGGTCGC[C/G]TCCATTGTTGACCTGATGGGCAGCTTGCTCGACGTCGTCGTC
TP66266	TGCAGCTCTTGAGGATGACATGTGGACCTCTGCGTTGTCGCTGCTGCTCCGCAGAGC[C/T]GAGCAC
TP66276	TGCAGCTCTTGCC[A/G]CACCTCTTCAGCCCTGCATCATCACATCATGCACCGTCGTCCAACGCCCC
TP66282	TGCAGCTCTTGCCGCAGCGCAG[A/C]AGCCCCGCCGCCTTGGGCAGCGAGCGCCAGCACCCCTCCCC
TP66283	TGCAGCTCTTGCCGCAGCGCAGCAGCCCCGCGCGCCGCGGCAGCGTGCGCCACCGCCCCT[C/T]CCC
TP66288	TGCAGCTCTTGCGTTTTGTGGGAAATTTTGCATCCAACGGCGCGCGCGGGGGGCAT[A/T]TGCCCTT
TP66369	TGCAGCTGAAAGATAAACTTCACCCACTCCGATCTGGTGATCTCGGTCGTTGGGCTTAGGT[A/C]CT
TP66389	TGCAGCTGAAATGCAGAGC[A/C]TGCAAGCAACTGCATGGTACCTACATACCTGGACATGCGGCAGA
TP66401	TGCAGCTGAACAGAGCACCAATAG[C/T]AGGTGAGCAGAGCAGCACGGCCGAGAGCCATAGAGCACT
TP66426	TGCAGCTGAACGGTAGGTAGCACAGCCAGCGGCAGTCAGGAGCACGGCGGCCCCGC[C/T]TGCTCAG
TP66436	TGCAGCTGAACTGAACAGCTG[A/G]CGCTGCGTGCCGTCCATGACTCCGAAGACGTGCATGACGTGC
TP66441	TGCAGCTGAAGAAGAAAAG[A/G]CAGGGAAAAGGTTGGGTAGGTGAAGGTAGCAATTCTTGTGCTGG
TP66447	TGCAGCTGAAGAATCCTCTCCTCTCACACTCA[T/C]CACAGAGACACACAGAGAGAAAGCGGAGAGG
TP66482	TGCAGCTGAAGCTCCTCGTGCGCCGTCAGCTGGAACGCGCGCTTGCGCCGCCCGTCCGCC[G/T]CAT
TP66483	TGCAGCTGAAGCTCGCAAATC[A/G]GGGGCTCCACCTCGATAGTGGTTTAGGCACGCGTACGCAAAG
TP66484	TGCAGCTGAAGCTGAC[A/G]TCGTGTTCACGAGCACTGCATCTGAAACCCCATTGTTCACAAAAGAG
TP66488	TGCAGCTGAAGCTTGCATTGTACTCACCAGCAAGCAGTTCAGCGAGC[G/T]TGGGCCGTAGAGAGGA
TP66494	TGCAGCTGAAGGCTGACTGGAAGGTTGATCAGAATCAGACG[C/T]CGTCGGAGGATGTTGCTGCTGA
TP66517	TGCAGCTGAATGCAGGGCTCACAACCCAGCTGCTGCTGAGCC[A/T]GTTCAGGGTGAAGGGCATCGT
TP66522	TGCAGCTGAATGTT[C/T]TGCAATCTGATCCAGAGGGATACGAATTCCTCCACATGGGTGGTCGTTG
TP66538	TGCAGCTGACACCGTCCGCACCGCTACACGTTCAGCATGGGGACA[C/T]CCCACGGCCTCCATGATC
TP66541	TGCAGCTGACAGACTGTTCCAGGATGTATGTATTCCTCAGCCATGTATA[C/T]GCAGCTGAAGCTCT
TP66546	TGCAGCTGACAGCGCCCGAGGATTCAGAATTCCAGATATCAGATT[A/C]TGGGGCACTGTAGCTCAC
TP66551	TGCAGCTGACAGTGGAGGGAGCGGAGACGAGACGACGGAGGCGAGGACGGCGAGGCGGAG[A/G]CAG
TP66562	TGCAGCTGACATGTGGTTCCCGCTGGGTGATGCACATGCAGAGCGCAGCGACTCC[A/G]TATGCGTG

Table A2 (cont.)

TP66569	TGCAGCTGA[C/T]CACCAGCTCAGCCACCCAGCTGCCGACGTGGCGTGGCCATCGCCACCGTGGCAC
TP66571	TGCAGCTGACCACTTTAAAGCGGTACTCCAC[A/G]CCAGCTCGCTCCGCGAGCTTCTTCAGCGGCTC
TP66575	TGCAGCTGACCATGACT[G/T]CTTGGGCATGTTTGCGGATATGGACGGCGCCCTCGACGTCCTGTGC
TP66583	TGCAGCTGACCGA[C/T]GCCTCTCCTAGGGCCGTTGTCGCATAGGCCCCGCACACCTCTACCATGCT
TP66584	TGCAGCTGACCGATCAGGTCAGCCAACA[G/T]ATGATCCGACGGCCAGCGCCATCCACGCCACTCCG
TP66594	TGCAGCTGACG[A/G]ACGGGTGGAGGCCGTGGGGTCGTCGGGCTCTGCCTCTGGGTCTGGGGCGGCC
TP66612	TGCAGCTGACGCAGTAAAATTTAGTAGAACGAGGGAGAGATC[A/G]CAGAATCTCTGGCGCTGGTAG
TP66618	TGCAGCTGACGCGTGGAATAGTGGA[G/T]AGTAGAATAGGATAACGTGTGGTTGCCATAGCTATTTA
TP66627	TGCAGCTGACGGCCGCGTTGAAGTTTTGTCCTGTGGTG[A/G]TGTCTGTCGGTGGCGCTTGGCTCCG
TP66635	TGCAGCTGACGTCCACGAACTCCTCCCTCTCTTCGTCTTCGGCGAGAAGCAGATGCGGATTAG[G/T]
TP66663	TGCAGCTG[A/G]CTGGGATGGCCAGGGCGGGCGACGTCGTCGGCGAGATCGGGATGCTGTGCTACAA
TP66668	TGCAGCTGACTT[C/T]ATCTTCATTAACTTGAGTACGGGGTGAACACGAGTATAGTCCATTCTCACG
TP66689	TGCAGCTGAGAGCTGT[A/G]GAGCTCCTACGACACTGGAGACTTTCTAACATTGATACAACATTGTG
TP66703	TGCAGCTGAGCAATAGTAGACCGAGGATCGTGGCGTCCAGCGGCCTTCAGTCTCAGTCACGG[C/G]C
TP66716	TGCAGCTGAGCATGACACAACCCTACGCGACCATAATTCACAAGCACAAATCACACAAATC[A/G]AA
TP66719	TGCAGCTGAGCCACCCTCGCATCCATGATCCATCCGCGC[A/G]CATCGTGGGCAGCGCAGAGCACGG
TP66720	TGCAGCTGAGCC[A/G]CGGCGCTGCCGCCATGGTGGCCTTCGCGCATCCTGGCGCGGTCCCGAAAAA
TP66744	TGCAGCTGAGCTGACG[A/G]GGCTATAGATGCTCGCCCTCTTGAAAGCCCATGCCTTCATGAAGCAT
TP66746	TGCAGCTGAGCTGCCAAAGGCAATCTGTC[C/G]CACACCCACAGGCGCACGCCATCTCTTTACTGGA
TP66748	TGCAGCTGAGCTGCCGACGTCGCTCGCTCGGCTCGCCGTGCCAGC[A/G]CAACCGCGACCGCGACCG
TP66760	TGCAGCTGAGGAACCTCCTATG[C/G]CCTACCTCGAAGCACGACGTGTACCTGGCGCAGAACTACTC
TP66770	TGCAGCTGAGGATGCGCGGGTCTTTGGCCACGAGCAGCTGGATCTCGGCC[G/T]TGGAGAGGCCGAG
TP66777	TGCAG[C/G]TGAGGCCAGGCTCAAGAAACCGAGAGGCGAAGGGAAGCATGGAGCCTCCGCTGGAGCC
TP66797	TGCAGCTGAGGCCGAC[A/T]GGGCCCAAGATAAATGGCCAGGCCTCTTGCGGCTCCTTCCTATTCCA
TP66811	TGCAGCTGAGGCGAAGAAGCCCAAGGCCACAGAAACCGACGGTGCTGG[A/T]AGCAGTGGCGACAAG
TP66812	TGCAGCTGAGGCGC[C/T]GAGCTGAGCATCTAATCCCCAATTTCTTCATCTCTCTCTACATAAAACA
TP66831	TGCAGCTGAGGTCT[A/G]ACCGTCTGAGGCGGTGAGGCCTTATGGGTCGACCTTTCCTATTCTATTC
TP66857	TGCAGCTGAGTGTGTCAGCTACAAATTGGTTCAAGCATTTTGTGTGGTAT[A/G]TGTGGTCACTTTG

Table A2 (cont.)

TP66887	TGCAGCTGAT[A/T]GGGTGGGTACATTTTTCTTGACACGGGTTTCTCATCTCAGAGTAAAGAAACGC
TP66893	TGCAGCTGATATTACCCACCTCATCTACATCTCATCCAGTGAGCTTC[A/G]TCTCCCAGGGGGCGAC
TP66901	TGCAGCTGATCATCCTGTCGAGCCTGTTGCAAGCCGAGCCAGGGCATATGTAGCTG[A/G]ATCATGG
TP66902	TGCAGCTGATCCACCAGGGCCACGCCTTCAA[C/T]GGCAAGCGGACCAAAACGGCGCGCTCTCAGGG
TP66906	TGCAGCTGATCCCGAACGTGGTGACGTACGAGAACCTGACG[A/G]TGCCCGACGGCGAGGTGATCGC
TP66912	TGCAGCTGATCGACCTCTACTACGACTGGC[C/G]GCGCGGGCGCGACCTGAACATCGTCCGCGACCA
TP66925	TGCAGCTGATCGTTGGGCCGAAACATGGCGCTCCCCAGAGTAGCGACGAGAGAATCCACCA[A/T]CG
TP66931	TGCAGCTGATCTCAT[C/G]TGCGACGATCCGATACTACAGCGTCGTCCGTGGCCGTGCCCCATGTGC
TP66937	TGCAGCTGATCTTCTGC[A/T]CTTGCCTTGTAGTTCTCATGCCAATCCCTCCTTAGAAGCAAAGCCA
TP66939	TGCAGCTGATCTTGCAGGTGGGTGCTCGCTCCATTAACACGACCTGCCTCTGAGTCTAAGCCC[G/T]
TP66955	TGCAGCTGATGACGGCCCAG[A/G]GCGCGCGCGCCATCCTGGGGCCGCAGTCCTCCGTCGAGTCCGC
TP66960	TGCAGCTG[A/T]TGATACTGTGGAGGCCGTGGGACTGAAACTGTATGGATTTGTCAGGAACACGTGA
TP66966	TGCAGCTGATGCAGCTGCCATGATGTGATTTTATAATGGCAGTTGCAACT[A/G]GTTGTGGGGTTCA
TP67002	TGCAGCTGATGGATGGTCCTCAGCAGCAGACTGCTTCTG[A/T]CGTCGTCGTGCTCCTTCTCCTGGA
TP67011	TGCAGCTGATGGGTACGGGTACGGCTGCGCAGTGCGAGAT[C/T]GCAGCAGTGTAGTGCACACTGCA
TP67013	TGCAG[C/G]TGATGGTGAGCGTGGCGAGCCCGAGCCCGATGGTGCGGTCGGAGGAGGACCTGGGCCC
TP67015	TGCAGCTGATGGTGCAGGACGAGACGTCGGCGACGGAGCGCAG[A/C]GCGAGCGTCTTGGCCACCTG
TP67020	TGCAGCTGATGTAGACCGTGATCACAGAGCACTTCTGCACGGCTAACCTCTACATATGCT[A/G]CCG
TP67047	TGCAGCTG[A/T]TTGCCAAGTTAGACGGAGATGTGCCAGTTCTGGTGGTGTCAACGCTCAGTGCTCC
TP67059	TGCAGCTGATTTGTCAGCGTTACACTCTGTTGCCACTTCCTAGTTAGTTAGGGACA[C/G]AATACCA
TP67068	TGCAGCTGCAAAAGCAAGTGTCCTCTCACGC[C/G]GAAAGCAGATAAAGAAAGCCAACGGATCGGCC
TP67072	TGCAGCTGCAAAATCGTCTGAACATGTGGTGTTCAGTG[C/T]AGAACAATCAGAAACACTGTCACTC
TP67075	TGCAGCT[G/T]CAAACCAGCAATGGTGGATATCTGAATTCTGACCACTGCAATGCTACCAACCTCGC
TP67136	TGCAGCTGCAACTGCAAT[A/T]GGGGACCCGACCGCGTACTGCTTCGTGAATCGACATCGATTAGCG
TP67142	TGCAGCTGCAACTGTAGCGTTCACTCATTCACTCGCTCCCCTGGTCTC[C/G]TCTCCTCTGTCTCTC
TP67152	TGCAGCTGCAAGATTA[A/G]TTTCCGTTCTATGCTCGCAACAGGAGGTTCGGGAAACGAAGTTCTCC
TP67153	TGCAG[C/T]TGCAAGCAAATCCACAAAACCAACCGCGGGCCGCGCCGCCTCTCTAGAAGAAAACGGA
TP67155	TGCAG[C/T]TGCAAGCAAGCCAACAAACAAGATGAAGAGCAAGGCGTCGACGTTCTTGAAGCTGAAG

Table A2 (cont.)

TP67159	TGCAGCTGCAAGCAGCGGGGTGATCTCCACCAGCGAGCATCAACATCCATGGTC[A/G]AGCGAAAAG
TP67160	TGCAGCTGCAAGCAGGATATAGG[A/G]GTAGTAGTAGTGTGTAACGGAGATGGAGGAGGACTACGTG
TP67171	TGCAGCTGCAAGCGGCCAGGACGACGCCGACCGATGGCCGCCAGCAGCAGGAGGAGGCGC[G/T]CGC
TP67194	TGCAGCTGCAAGTGCAGGTCAGTGAGACAGCGACCACGTCCTCCCTC[A/G]CCGTGCAAGTCGATCA
TP67212	TGCAGCTGCAATGGATCAACGCGGGGAG[A/G]AGGAGGAGCATAGCTCCCAGCCGTCCCAGGAATCG
TP67215	TGCAGCTGCAATGGCCACCACCACCACCACGGCGGCAGCGTCCCTCACCACCCTG[C/T]CCCCCGCC
TP67233	TGCAGCTGCACAATCACGATGTGTTCTTGGTTTAGTTGGGCCTAAAGCCGAGCCTCC[C/T]CTGGCA
TP67249	TGCAGCTGCACAGCAACGGCTCATCGGCTTCAGC[A/G]GCGTCCTACGAGACGCAGGCGGACCACCA
TP67251	TGCAGCTGCACAGCACCACCCAACCAACTCCAACAGCACTAC[C/T]GAGGCATGTTCGCTTGAATTT
TP67253	TGCAGCTGC[A/C]CAGCCCAGCCGCTCGGCTAGTAGAGCCCAAGCAGGGCCTGCTGCACAGGCTCAA
TP67261	TGCAGCTGCACATCCGTAAACTTCG[A/C]AAAATTCACATGCAACCTCTTATTGAGCATATTGGCCA
TP67264	TGCAGCTGCACATTGC[G/T]AACGAAGTCATCATGCGCTTAGAAATAGCGCAGGAGAGAAGGCATCT
TP67277	TGCAGCTGCACCATGAACGGGCTGAACTCGTACAGCCTCTT[A/G]CTGACGCTCGTCGCCGCCGTCA
TP67280	TGCAGCTGCACCCACACCGCGCGTTAGCCGCCTGCATCTGCCT[A/G]CATGCCAAGGTTAGTGGTGC
TP67302	TGCAGCTGCACCGCCCTTGTGCTTCTTGTCGCGGACGATCATCTTG[A/G]CGCAGCGGATGAACTCC
TP67309	TGCAGCTGCACCGTCAACCCAGGCTGCAACAACTGCAAAGGCGCAAC[A/G]CAAGGCTGGGGCGTGG
TP67349	TGCAGCTGCACGCACGCGTACTCACACGAGGATGGGGTCACTCCGTCACTG[A/G]AAGTACTGTAAC
TP67354	TGCAGCTGCACGCCACTGATGACCATTCTGTTTCTCCGCATCGATACAAAA[C/T]AATGTGCGTGAG
TP67359	TGCAGCTGCACGCGAG[C/T]TGTGGAGGAGTTGCGATGCGGTTGGACTTTTTGAGGTGGCCTGGCTG
TP67368	TGCAGCTGCACGCTACCACCACC[C/G]CTGCACGCACGCTACCAGTCTACCACCACCGTCGAGCAGC
TP67371	TGCAGCTGCACGCTG[G/T]CGGTTTTGCCGAACGTGCCCGATGAAGAAGAGCGCGCCGCCGCCAGTG
TP67376	TGCAGCTGCACGGCACCGTGCGATCAAGCCAAGTTGTCACGTCGACAAAATGACAAAATC[G/T]GGG
TP67377	TGCAGCTGCACGGCACCGTGCGATCGAGCCAAGTCGTCACGACAAAATGA[C/T]ATAATCGAGCGGG
TP67385	TGCAGCTGCACGGGCAGCGACGCCGACGACGTGAGGTCCGTCTCCGACA[G/T]CTCCATGTACGGGC
TP67400	TGCAGCTGCACTACTGCACAAATCCAAACTGAAAGA[C/T]CCTGTAGATTCACTCCTGTGGCCACAC
TP67401	TGCAGCTGCACT[A/G]GAACCTGGTGTACACTGCGCTGGAGCACCCCTGCTGCTGGTTGGTTCCCAC
TP67406	TGCAGCTGCACTCCACGACCGCGCCCATGATGAAACCAGAATC[A/C]GCAGCGGCCAGCGCCCAAGC
TP67424	TGCAGCTGCACTGAGTTGTGGTGGGAGACAGAGTGAGCCGTAGGCAGCAGCAGC[A/G]CCGCTCAAT

Table A2 (cont.)

TP67427	TGCAGCTGCACTGCACAATGGGCATCTGCGTGTCGTGCGACGCGGCGGACGA[G/T]GGCGCCGCAAC
TP67432	TGCAGCTGCACTGCTACATGCCCGTGGTACACAAACCCAA[A/G]TGGCTCATCCTGTTGCTGCTGCG
TP67440	TGCAGCTGCACTGTCCCGTTGCCACGCGGTCACCCGAGGCCTTAATGCCA[A/G]TATAAGCCCATCG
TP67445	TGCAGCTGCACTTGTTACCGACCATCTACTCATGCTGTTGTCTGTTGACCTTC[C/G]TGCAACCACA
TP67453	TGCAGCTGCATAGAGGAAGCTCATGATCCGTGAATCAGC[C/T]GCTGACGACCACTGCCCATTGCTT
TP67456	TGCAGCTGCATATAGGGGCAC[C/T]CTTGTCCACAAGCTCCTTCAAGGACAGTTTTTTGCTGCTGGC
TP67460	TGCAGCTGCATCACCTGCATGCAAAGCAGCCAGACGCTACGGCCATGGCGCCA[C/T]TGACGCATGC
TP67465	TGCAGCTGCATCATCGCCTCCCTC[C/T]TGCTCTCCCTCAGGGGATGAGCGGCGGAGCCTCCAGAAG
TP67467	TGCAGCT[G/T]CATCATCTCCTGGGTGATGTCGTGCTCGTTCTCGGCGTGTTGCGCCACAAGGTGGT
TP67470	TGCAGCTGCATCCCCATGCCGACCATCAC[A/G]CACTACGCCGTGCTGGATCCCTTGCTTGAGACAG
TP67474	TGCAGCTG[C/G]ATCCTTATCCACTGGCTCTCCGCCACCGTGTATATGCACCCGCCTCCTGGCAGAT
TP67487	TGCAGCTGCATCTGC[A/G]TCTGCATGCCCGTCCCTCTCTGGCTCTCTTCTCTCTCAGTTCGCTCTC
TP67506	TGCAGCTGCATGCACACGTACAGGGGCACCGCGCACTCATGTCCCCATGCAT[C/T]GCCATGCAGTA
TP67507	TGCAG[C/T]TGCATGCACACGTAGTACAGGGGCACCGCGCACTCATGTTCCCATCGCCATGCCATGC
TP67522	TGCAGCTGCATGCATCTGTACTTGGTGGCGAGAGGGA[A/G]GGAGCTTTAAGCCTAGTCGTCTCCTC
TP67534	TGCAGCTGCATGCGGGCTGCGGAACGAAAACCAGAGAGCCTTTTG[C/G]CGTGACGCGTGGTGAAAA
TP67553	TGCAGCTGCATGGCGGCG[C/T]GGCGTCCGAGCCGCCCTACACCTGCGGCGCCGAAAAAAAAAAAAA
TP67555	TGCAGCTGCATGGCGGTCGGGCGCCTCGTTTTT[G/T]CGGTCGGTGCTGTGTGAGTACTCCTACTCC
TP67577	TGCAGCTGCATTGTCATCGGCCACTTGCTGGAAGGGAACCGATGGGTCAACGAGTCCAT[C/T]ACCG
TP67581	TGCAGCTGCATTT[C/T]GATATAGTAGTCGAACTCGCGCATATCCCTCGCCTTCACATCCTCGTCGT
TP67586	TGCAGCTGCCAAAACGCCAA[A/G]CCTGTGCAGGGCAAGATGTGATGTGATCGATCCCAAGGGCAAC
TP67597	TGCAGCTGCCAA[C/T]CCTTTGCCAACTATAAAGCCGCTGGCTCCTCTGAAACGGCAAGCATACGGA
TP67606	TGCAGCTGCCAATTTGCAGATGCTATTGCTGCACTCTGCCT[C/T]GTGCTGTTGCTAGTAGTTGCAG
TP67613	TGCAGCTGCCACCAGGACCCGCCGCTCCCTGCGCGCGAGGCTC[C/T]ACCAAAATGGGAAGGTTGTA
TP67632	TGCAGCTGCCACTCCTCCCGCTCGCACTACTCATGTCACCATCACAGTTTCCTTCACGCAT[C/T]GC
TP67635	TGCAGCTGCCACTGCCAGTAGTGCCACGCACCTGGCCAG[C/T]CAGTCACCCACCACGAATACGATC
TP67645	TGCAGCTGCCAGACCCCCCTCAGCGCCATC[C/G]TTCCGAAGCCCAGAGGTCCCCGCAGTCACCACT
TP67656	TGCAGCTGCCAGGATGGAGCTGAAGCGGAGGCTGTTTGACC[A/T]CTCGCACAGCGTTCTCATGGAG

Table A2 (cont.)

TP67677	TGCAGCTGCCATGGCTGCTGCCGCTCCCGTGTCTGTGCCCCGCATCAAGCTG[A/G]GCACGCAGGGG
TP67680	TGCAGCTGCCATGGTCGCACCATCGTGGGAGAGG[A/T]ACTTCCATTGGCACGTCGGCACACCTGCT
TP67687	TGCAGCTGCCATTTCGTCAATGGGGAAGAG[G/T]GGGATCCTGGAGCTGGCACAGAGGATGATGACG
TP67693	TGCAGCTGCCCACCCTGCCCGCTAGCTCGCGTGGCTGGCC[A/T]CCACAGCTTCCGACGGGCACGGG
TP67698	TGCAGCTGCCC[A/G]CGCCCAAAAATTCACGGCGCGCGCTTGCTCCTTCGCCGCGCTCCGCTCGCGG
TP67709	TGCAGCTGCCCATCGTCGCCGCCGCCTCCGCCGTGCTGCTGCTGCTG[C/G]TGGTCTCCGAAAAAAA
TP67720	TGCAGCTGCCCCCACAAACATGTTGAT[C/T]GCGACTCCGTGTCTGGTCTGTGTCCCCTCGCTCCCT
TP67729	TGCAGCTGCCCCGTGAGCGTCTGGATCAGCGCGTCCACGAACTGCTGCGA[C/T]GGGTCGGCGGTTG
TP67750	TGCAGCTGCCCGCGCGCCTCGTCTCC[G/T]CCGTCGACCTCCGCCAGGGCGGCGCGTGCGTGATGTC
TP67752	TGCAGCTGCCCGCG[C/T]GGCTCCTGCGGCAGGAGGCGAGCTCGTCGCCGCCATCCGCGAGATCGAG
TP67759	TGCAGCTGCCCGTTGCC[C/T]GTTGAGGGCGAGGCAGCGTAGAGGACCACCAGACGCCGACGTCCTC
TP67762	TGCAGCTGCCCTACTGCTCCCGCTCAGCTCGTTGCGCGACC[C/T]CCACATCTGGGGCAGCGAACAC
TP67776	TGCAGCTGCCCTCGCCTACGTACACGGATCTGTCCGTCAACAATGG[C/G]CATCCTCCAACGTCGAG
TP67786	TGCAGCTGCCGAAGGTTGGACCGTTGGAACCCTGGCTGA[C/T]CCTGCACATTTAACGGGCGCCTGG
TP67792	TGCAGCTGCCGACATCAAGCCCTCGGCCGCCCAAGTCAACAACAACCATGCTCTGCTGTC[A/G]TCG
TP67798	TGCAGCTGCCGAGCTGCGGCGCGCAGGAAGTCGTGAGGTGCATGTTGCTGCCTGCCTTGGC[A/G]GT
TP67803	TGCAGCTGCCGATATATCTTCGA[C/T]GTGTTCCAAACTGTTCAGGTAGATTCGGAATGCCCTGCTG
TP67812	TGCAGCTGCCGCACGGGGCTCCCTGCATCCGATGCGCCATCTGTGGGGCCATCACGCACGT[C/G]GC
TP67816	TGCAGCTGCCGCAGCAACAGCCACGGCACACCTCAGCCGCAGCAAGCAGCAGCCCAGAAACAA[A/T]
TP67824	TGCAGCTGCCGCCATTGGCCCAGAATGGCCAGGGA[A/G]TGTCGGCCGCGGTGGCACTGCTGGCTGC
TP67842	TGCAGCTGCCGCGACACAAGTGACAACCTGTTTGTTTGGCAGCTCGTTCGTTGCTGGATCGT[A/G]A
TP67849	TGCAGCTGCCGCG[C/T]GAGCATGGCGGCGGAGCTGCCGCCGCCGCCGAACCTTGTCTTGGACGAGC
TP67853	TGCAGCTGCCGCGGAGGG[G/T]TACTCGCGGCACGTCGGCGTCAGCGATGCGGTGGCGACACCTGCC
TP67860	TGCAGCTGCCGCGGTGCTCGGCGGCAATGGG[A/C]AGCGCGTCGCCGAGCCTGGCCCTGGCGGCGCC
TP67861	TGCAGCTGCCGCGGTGCTCGGC[G/T]GCAATGGGCAGCGCGTCGCGGAGCCTGAGCCTGGCGGCGCC
TP67862	TGCAGCTGCCGCGTAG[C/T]CACCAGCCAATCTGGCTTAAACAAAACCCACCCAAATTTAAGCAAAT
TP67865	TGCAGCTGCCGCT[A/G]CTGCTCCTCGGGCAGAGCAATGCGCAGACTAAAACACTGTCGAGAAAGGA
TP67878	TGCAGCTGCCGTACCACCACCATCCAGCCATCATCCACCGCTGCCCGCTGGTGCCGTGGTGG[A/T]T

Table A2 (cont.)

TP67897	TGCAGCTGCCGTTTCTGCGCCGCCTCCTGCTTCGACAGCTTT[A/G]TCTCCTCCCGCGCCAAGCTGG
TP67902	TGCAGCTGCCTAACCTGCCAGAATTCATAATAAACAGTTAAGTTATTCTGACGAACAG[A/C]CCTAC
TP67906	TGCAGCTGCCTAGGAGTACAAATTAACTG[A/T]ACTTGTTGGCTTGAGAATGTGTGTCGTCAGACGA
TP67914	TGCAGCTGCCTCCACTGCCCACAGCGCAAGA[A/G]GCTGAGCCGCCCTCGCCATCGGCGCTGCGGGA
TP67928	TGCAGCTGCCTCGCTGGGGCACCC[A/G]CACTTGAAGTACATGTCCATGAGCGCTGTCCCGAGCGTG
TP67935	TGCAGCTGCCTCTGCAACGCCGACTCCTCCCCGCCACCGCCCGCCGCGTCCACCCCACCGT[C/T]GG
TP67957	TGCAGCTGCCTGGTGCAACAGCTGAGCACAGTACCAGTAAAAA[C/T]TGCCTGTGTCTTGTGTGCGA
TP67962	TGCAGCTGCCTGTCCACTGAGTC[C/T]GCCATGTCTCCCAGTAGTGTCCTGCTCTTGCATCGCCTGT
TP67964	TGCAGCTGCCTGTCTGTGAGGTTCAACTGCACCGACAGCTCCGCCCGCTTCGTCTCGTTTGG[A/G]T
TP67975	TGCAGCTGCCTTCGCA[A/G]AACTTTGGAGCTTCTTCTTCCTCACCTTAGGAGCTCTTAATTTGATG
TP67995	TGCAGCTGCGACAACAGCCACGGGGTTGCTGGGCAGTAACTACTACTGCACCAG[A/G]AGGTGCGGC
TP68015	TGCAGCT[G/T]CGACCTGCTGCTGCTGGTCCTGCTCCTGCGCCACGACGACGACATGCACCTCGGCC
TP68020	TGCAGCTGCGACGACCGACGAGCG[C/T]GAGTGCGTGACCAAGACCGAGACGAAGACACATCGCTGT
TP68023	TGCAGCTGCGACGAGCTCTG[C/T]TGCACCGACGTCGTCGGCGCCGCTGACTGCGCGTTCGTCGTCC
TP68032	TGCAGCTGCGACTTGGTGGCCATGGCAATCGCCCTAAGGTTCGGACGTGGAGAAG[A/C]GTGGAAGT
TP68033	TGCAG[C/T]TGCGAGAATCCCTTTGATAATTATGACGGCCAGGTGGGGGCTTTAAAACTGGAAAGGT
TP68057	TGCAGCTGCGATTG[C/T]CGTGTCGGTGCCTCCGCGCTCGGCGGTGACGGTGGAAATGGTTGGCAGG
TP68061	TGCAGCTGCGCAATGGGAGAAGCAAAGACAGAGAAACCAAACAAAAATAGATGAAAG[C/T]TGCCAA
TP68063	TGCAGCTGCGCACGCCACGGGGTCAGTACCGCCGCTAGGGTTTGGGCGACCAACAAGC[G/T]GCGGC
TP68064	TGCAGCTGCGCACGCGACGGG[A/G]TCAGTACCGCCGCTAGGGTTTGGGCGACGAAGAAGCGGCGGC
TP68065	TGCAGCTGCGCACGCTCAGCTTCGGGTCCGCCAAGG[C/T]CGCCTTCTACGGCGGACGCGCCAGCAG
TP68067	TGCAGCTGCGCAGCCGCCGTGGAGGATGGGGACGTGCGGTGCAACCGCCCAGC[A/G]GAGTCCAGCT
TP68075	TGCAGCTGCGCCACCACGTCGGGA[A/C]GTCGGTCATGGTGGATTGGTTGGCCTCTCCGCCGACGCC
TP68078	TGCAGCTGCGCCAGCCAACAGCAAGCAGGCGCAGAGAAG[C/T]TTGCGGTTGCAGGCCATTGGCTAG
TP68080	TGCAGCTGCGCCAGGATGGTGTTGAACACGATGGTGCACGC[C/G]AAGATGGGCACCACGCACAGCA
TP68088	TGCAGCTGCGCCCCACGAAAACACAACTAACCATCGAGAGGAAAGTGC[C/T]CTCACTTAGTTCCTC
TP68090	TGCAGCTGCGCCCCGCGGCAGCGCCTGC[G/T]CTCGGTGGTGGCACCCGCATCTGCGTCCGAAAAAA
TP68105	TGCAGCTGCGCCTCCGAGGAGTAGAAGCATGTCACCATCACGGCGACAGCCACTA[C/T]GACGAGCT

Table A2 (cont.)

TP68107	TGCAGCTGCGCCTGCCAAGGGTCCCCAACGTCGCCACAATGCGTCAGGCAAAGCCAGTC[C/T]CGCA
TP68109	TGCAG[C/G]TGCGCCTGGTCGGCCTGCGGGAAGGGCTGGTGCCCGTAGCGGTACGACGCGGGGACGT
TP68112	TGCAGCTGCGCGACGCCGTCGTGTGCCG[A/C]CCCGTCTCGCGCCTCTTCCACGAGACCCTCTCGCC
TP68113	TGCAGCTGCGCGAGCACGGT[A/G]TTGAAGACGATGGTGCACGCGAAGATGGGCGTCACGGCGAGGA
TP68114	TGCAGCTGCGCGAGCACGGTGTTGGTGACGACGGTGCACGCCACGATGGGCAG[A/C]ACGGCCAGGA
TP68116	TGCAGCTGCGCGAGCGCCAG[C/T]GGCATTGCTGGCGGACGGAACAAGGCCGAGGACGGGTGTGTGC
TP68127	TGCAGCTGCGCGCGAC[A/G]TGCGGCGCGCGGAACGGACAGCACGTCGACGCGAGGCGGCATGGGCT
TP68131	TGCAGCTGC[G/T]CGCGCCCGCGGACGCCGCCTCCGTCGACCTCTGCCGCCGCCTCGTCCACCAGAT
TP68141	TGCAGCTGCGCGTACGCCGCCTTGACCGCCGAGACCCCCGCGAAGAGGTTGGC[C/G]AGCAGCGCGT
TP68159	TGCAGCTGCGCTGTC[C/T]CTCGATCCCTCCCTCCCCAGCTCCCTCTCCCATGTGCCATGGCTATGC
TP68169	TGCAGCTGCGGACGTCCAGGTGCGGGCGTCCATTTGGACGTTTGGGCG[C/T]TAATAATGTCGGAAT
TP68187	TGCAGCTGC[G/T]GCAAGCAGACCACGCAGCCGCCAGCAGCGCAGGTCGTCGTGCCCGCGCCGAAAA
TP68190	TGCAGCTGCGG[C/G]ACGTAGTCGCTGCTCCTGCACGGGCAGCTGCTCACCGACGCGGGTGGAGCAC
TP68195	TGCAGCTGCGGCAGCCGCTGCTCCA[G/T]CTCCTGGTAGATATGTTCCGAAGTTTAAACTCAGCGGC
TP68198	TGCAGCTGCGGCAG[C/T]GGCTTCTTCGCCATCATCATCGCCGTGGAGCCTGCTCCAGGGGCTCCTC
TP68233	TGCAGCTGCGGCGCCACGTCAGGGTGGAACGCGCCCGTGGACGGCGG[C/G]TCCGACTGCGCCATCA
TP68234	TGCAGCTGC[G/T]GCGCCATCGGACTAGTGGCGATGACGGAGTCTGGCGATTCGGACGGGGAACGCA
TP68243	TGCAGCTGCGGCGGCGGCAGCGCGGCTTCTCTCGCGCCTT[G/T]GCCCCAGTTAAAGAAGCTTCGAG
TP68246	TGCAGCTGCGGCGGCGGCGGCCGACATGGCGGCATCGGGAGGGCTGGAGCAGTGG[C/G]AGAAGGAC
TP68260	TGCAGCTGCGGCTGCAAC[A/G]GCACTAGCACTATGCTATAATATAATTTTCTATAGTTTTGATCTT
TP68265	TGCAGCTGCGGCTGCTGGCCGTAGTGCGCGCCGCCGTCCTGGGTCGGCGGG[G/T]ACGCCGAAAAAA
TP68271	TGCAGCTGCGGGACAAGCGCCGCCGCCGCACCCTCAC[C/T]CCCAGCCTTCGCATCCTCATCCCCCG
TP68299	TGCAGCTGCGGTCAGAAGTATGAATCGGTGTAGTGC[A/G]CCTGGACCAGATGGTTTCGGTCCTAGT
TP68305	TGCAGCTGCGGTCTGCGGG[C/G]AGCGCAGGCGCGTTTTATAGCGGCAGCCTTGACCTTGAGGCACC
TP68317	TGCAGCTGCGGTTGCAACTTGCATGCCAGCTTGA[C/T]AATAATAGAGATGGGTGTGTTTTACTTGT
TP68320	TGCAGCTGCGGTTTGATGACGTAGCTAAACTATTAACAGGAATAATACTCGTAGATAGAC[A/G]GAT
TP68321	TGCAGCTGCGGTTTTGCGGGGAGCGCAGGCGCGTTTTATA[A/G]CGGCAGCCTTGACCTTGAGGCAC
TP68355	TGCAGCTGCGTGACACGCACAAACACACCACGCTTAACCAAATCATTCGACGATCGA[C/T]GACACC

Table A2 (cont.)

TP68357	TGCAGCTGCGTGATGCCCCCCGTGTAGCCCGTGCG[C/G]CGCCGCAGCAGCGGCACGAGGAGCCGAA
TP68359	TGCAGCTGCGTGATGCCTCCC[A/G]TGTAGCCCGTGCGCCGCGCAGCAGCGGCACGAGGAGCCGAAA
TP68387	TGCAGCTGCTAAAGGTTGGAAGCGTTTCAACAGGCCTGGCTGAAACTC[A/T]TTCACGAACGAGCGC
TP68390	TGCAGCTGCTAACTACCAGTCAACCTATTGTCAGTACGACACACGCATCATCCCCCACAAAT[A/C]G
TP68405	TGCAGCTGCTACAACGC[C/T]GTCGTCCATATCGTTTCCTTTCAAGTTGACAACCACAAGGCCACAG
TP68411	TGCAGCTGCTACA[A/G]TTCGAGAAGACGACGGACATCACAACGGAGCCAGCGAAGAAGATGCATAC
TP68426	TGCAGCTGCTACATATTCGGGGCATATTCCT[A/G]TCCGCCTTGGACTTGCTCCCCCTTTTGGAGAT
TP68435	TGCAGCTGCT[A/G]CTACTACTACTGCTAGCGACGAATAGCGAGGACACGAGAGATCGATCATCGAT
TP68454	TGCAGCTGCT[A/G]GATTGCTTGGTGCAGACGAGAGGACCGTTGGAGCGGAGTCCACGAGGCAATGG
TP68459	TGCAGCTGCTAGCGAACGCCATTCTCTCTATGCAGAGCACCAGGTTGCAGGAGAGCGGTGG[C/T]TG
TP68463	TGCAGCTGCTAGCTAGTA[A/G]TGAAGCGTGCAAAGCATGCTGTAGCTGCGCACCGACACTAGCCGA
TP68502	TGCAGCTGCTAGTTCAATCTTTGTGC[A/C]AGACCTTGCCAAATGTTTGGCGACAAAATTGAGCGTT
TP68521	TGCAGCTGCT[C/G]AACCATGGACTTGTTCTTGTCGCTGGCCCCGCTGGACCACAGGCCGTGATGCT
TP68537	TGCAGCTGCT[C/G]AGCGGGCGCCCGCGTATGATCAGTGCGTGGGAGACGTCCAGGCGGCACGGACC
TP68543	TGCAGCTGCTCAGGGACAAGCAGTGGGGCTCGCTGGAGCTGCTGGTCGAGGACTTCAGG[G/T]CCTA
TP68544	TGCAGCTGCTCAGGGAGCAGGGACTGGTTCTGGCCGTGCTGCT[C/T]GGCCTCTCTGCCTTCTTCTC
TP68556	TGCAGCTGCTC[A/G]TGCCATCTCGGGGCCTTGTTGCGGAGGACCAAAGGTGTGTCCCTGCACTCTT
TP68565	TGCAGCTGCTCCACAGCCTCCACTGATTTCGCTTCCGACCTCCGCTCTGTCAACTT[A/G]TGCCTCT
TP68574	TGCAGCTGCTCCATGACGAGCACAAGCTACAGAA[A/G]GGCGTGAGGAAGCAGGTGCAGTGGCTCCA
TP68583	TGCAGCTGCTCCCCCATGTCCCCTGTCCCCGCAGGGTGATCACTGATCAGC[G/T]AAGAAGCCACGG
TP68585	TGCAGCTGCTCCCGCCGCGGGCCACTCAAG[C/T]GAGTGCTCGGTTGTCGCCCAGACGCCCACGACG
TP68586	TGCAGCTGCTCC[C/T]GCGCGCCCCTCAGCTCGTGGATGTAGATGGCGGCCGCCTGCACGATGGAGT
TP68594	TGCAGCTGCTCCGCGGCAGCCTCCCCTCCGTAGCAGGGCTCAAACGGGAAGC[C/T]GCCGCTCCCCC
TP68614	TGCAGCTG[C/T]TCCTCTGCTAGTATGCTCTGATCTTATAGGGGTTATTATATATATTATAATTATA
TP68623	TGCAGCTGCTCCTGCTGATCTCCGCC[G/T]TGGTGACAACCACCAGTGCAGCAGCAGCCTTGTATTC
TP68637	TGCAGCTGCTCGATCATGTTCTACTCGTATCCACCGAAAAGCGGGAG[C/G]GCGTGGGGCTGAAGCT
TP68641	TGCAGCTGCTCGCCGTCGCCGCCGAGGCCACCCGCCTCGTGCTCATCCAGATCCT[C/G]CTCACCTC
TP68652	TGCAGCTGCTCGG[A/C]GTCGAACAAATCCCATCCCGAGAATCAGATCAAATCAAGCGAAGAGGAGG

Table A2 (cont.)

TP68657	TGCAGCTGCTCGGTCGAGAGGCCTGAGGCCAGGAGCCCGCCCATCCGAAG[C/T]GGCCTCGCGCTCG
TP68663	TGCAGCTGCTCGTCGCT[C/G]ACCACCCAGCTCCCCTGCGTCCGCTGGATCTCGTCCATGGCGGCGT
TP68684	TGCAGCTGCTCTGATCCTCAGTTGTCAGCTCCTGTCTTC[C/T]AGGGGGCTGGGAAGGCCACCGCAG
TP68716	TGCAGCTGCTGACGCGGAGGGGCTGGAGGACGAGGA[C/T]GAGGAGGGCGGCGGCGGTGTACCCCAA
TP68746	TGCAGCTGCTGATCACGGACTACGCGGCGCACGGCAGCCTGGAGGCGCGGCT[C/G]CACGGCCGTGA
TP68758	TGCAGCTGCTGCA[A/T]CAGGGCTTCCGCGTCGTCGTCGTCGACAACCTCGACAACGCCTCCGAGGT
TP68777	TGCAGCTGCTGCATCATGACAGTGTCGTAGGCCCTGTCCAACTATCATAACCCCAATAA[C/G]CCAA
TP68780	TGCAGCTGCTGCATGCCACATGCCCACAGCCTCCTGCCTGGCTGCCTCCTCTCTTCT[A/C]TTCTCC
TP68790	TGCAG[C/T]TGCTGCCACGCCGCCGCCGCCCCGCCGTAGCTGGCGCCGTGGTGGTACAACGCGTAGG
TP68806	TGCAGCTGCTGCCGCATGTGCGCATTTTCATGAACCAACTGAGA[A/G]ACTTGCTTCTGAAGACGCT
TP68808	TGCAGCTGCTGCCGTCGCTGCTCGTGCACGCCGTCGTCCTCGCCGC[C/T]TGCTTCTTTCACCCCTG
TP68812	TGCAGCTGCTGCCTGCTGTGGCTTCAATCG[C/T]GGGATTGGCACAAGTGGGACATGGGAGCCATGA
TP68826	TGCAGCTGCTGCGCCAGCCAAGACGAGCAAGTAGGCGCAGAGAAGCTT[G/T]CGGTTGCAGGCCATT
TP68828	TGCAGCTGCTGCG[C/G]CATCGGCGCGTCGGGCCGCTGATGCGCGAACAGCGACGCTAGCTCGTCGT
TP68831	TGCAGCTGCTGCGCCTCCTTGGCCTTGGC[A/G]AGCATATGCGCCTCGTACCTCCGCAGCCTCTCCT
TP68842	TGCAGCTGCTGCGGATCAGGGGAC[A/G]ACGACGGGCAGAGGGGCTTGTGGGTGAGCGGGTCGATCC
TP68863	TGCAGCTGCTGCT[A/G]CCGCCGCCACCGCAGCCGCAGCTGAGGCTACTACTCGTCCTGTTGGGGTT
TP68869	TGCAGCTGCTGCTCCAGCTGCCGCTCAATCGCCGCCGCCTCGTCCTC[A/G]CCCTCGCCCGCCATAG
TP68873	TGCAGCTGCTGCTCCT[C/T]CTCGGCGTCGGCGTCGGCCTGCACCGCCGCCTGCTGCTGCATCTCCG
TP68881	TGCAGCTGCTGCTCTTGCATTTTTACAGTACCTATCATGG[A/G]CGCACTGTCACCGTCCGTCCTGT
TP68882	TGCAGCTGCTGCTCTTGCATTTTTACAGTACCTGGCTATCATGGACG[C/T]ATGGTCACCGTCCGTC
TP68905	TGCAG[C/T]TGCTGCTGCGTACGTGCAGGACAGCGAGGACGCGAGGCTGGAGCGAGTCCTGACGGCG
TP68911	TGCAGCTGCTGCTGCTGCAAGTCTGCAACCTGCAAGGGTGCCGCGGC[C/T]CGCGTGCGTGGATCCA
TP68913	TGCAGCTGCTGCTGCTGGGGCGCCGTGGGCCACCGTG[A/C]GGGCGGTGCCTGATGAGGCCGAAAAA
TP68929	TGCAGCTGCTGCTGTCCTCGGAAGGTGAAGACGACGACCTCCAGAGCTTCGCC[G/T]CTTTCTTCCA
TP68931	TGCAGCTGCTGCTGTCGTGCTTGGACGCTCCC[T/A]GGCTGGCTCCCTGCTGCCTGCTGCCTGAAAG
TP68936	TGCAGCTGCTGCTGTCTGTGGTGCTCCAGTGCTTGGGTTTGCAGGC[C/T]GTGGTCTGGCGGCCACT
TP68950	TGCAGCTGCTGCTTGGCAGTGTCTTGATGGTGGGCCTAGGCAGAGCACGG[A/T]GGAAGCAATGCGC

Table A2 (cont.)

TP68951	TGCAGCTGCTGCTTGGCAGTGTGATGGTG[A/G]GCCTAGGCAGAGCACGGAGGAAGCAATGCGCCTG
TP68952	TGCAGCTGCTGCTTTCCACAGATAAACTATCCATGC[A/G]TCCATCATTTCCTGACAGCTCAAGGTG
TP68981	TGCAG[C/T]TGCTGGCAAAGCAGAGTCGCGACTCCTGCTTACATTTAGTTCCTCTGGTTCTGAAGAT
TP69006	TGCAGCTGCTGGCGCGCAGCCCGCCGCC[A/G]TGGCGCGCGGCGCACGTGCAGCGCCTCGTCACGCT
TP69009	TGCAGCTGCTGGCTGGCCATACTACTAGAGAGGGACGCCCTCTCCCTTCCTCTCGCTTCGCTT[A/G]
TP69053	TGCAG[C/T]TGCTGGGGTCAAGCGAAGCCAGTGGCATGCAGACAGGTATGTGTACCCGTTCCTGTCC
TP69065	TGCAGCTGCTGGTACGACC[A/C]GCGGCGGCCGCGTCCTCCTCCTCCGCGCGACCCTCGCTACAGCT
TP69072	TGCAGCTGCTGGTGAAAGAAATGCAGAAAGAAAGCTGGTGTGTGTCCA[C/T]GACGACCAGGGAAAG
TP69083	TGCAGCTGCTGGTTGGTACCAAACTTAGCACAGGA[A/C]ATTAGTTTAGTCAAGTGATAGTCTGCAT
TP69100	TGCAGCTGCTGTCCGCGTCCTCCTGCGCCGCGCTCTCGCTACTCCGCCTCGT[C/T]CACCAGCGCTA
TP69103	TGCAGCTG[C/T]TGTCGTCGCTGGACACGACCAAGGTCAAGGACAAGAAGGACAGGGGCGTGCTCAG
TP69107	TGCAGCTGCTGTGACGAGGTGAGA[C/T]GGGTTGGCCTGCTCTCCTGGTGCGCTGTCGAGCAGGGGA
TP69123	TGCAGCTGCTGTGTGCCCCCGTAGGG[A/G]TCACGACACTACTCACGGGCGGAGGAACGGGAACGTA
TP69126	TGCAGCTGCTGTGTGTGTGTGTGTCGTGCGCAATTGCGAT[A/G]CGTGCAGATCCACTTCTGAAAAT
TP69129	TGCAGCTGCTGTTACCTCCCCGACAGCACCTGCACCGCA[A/T]GCCCCAGGAATAATTTTTCTGGCC
TP69148	TGCAGCTGCTGTTTTCTCAATGCAAACACAGGACAGCGATGTAGCTTGCTGT[C/T]GCCCGCGCCTA
TP69157	TGCAGCTGCTTATTGGTG[A/G]CGTGGCGCTCTGCGTGACCATGCAACCCAGCAAGCTGCTGCTGAT
TP69160	TGCAGCTGCTTCAAGACCCTCTCGTGCTGCAAACTCCAGT[C/G]CAGCCCAAACTGCTGCACTTGCA
TP69170	TGCAGCTGCTTCAGCTTGCCGTCCACGTGCTTGACGA[C/G]AGACCTCGTCGATGAACGCCTGAACG
TP69171	TGCAGCTGCTTCAGGTAGTCGATCACCTCGTCCAGCATCGACGCCTTGTCTG[C/T]CTGCTTTCATT
TP69179	TGCAGCTGCTTCCTCTTCTTCTTCTTGCTCTCGTGGTCGTGGCCATG[A/G]CTTCCACTCCCTCCCA
TP69181	TGCAGCTGCTTCCTGGTGATCCTGATCGTGACCTCCGCCGCCGCCGCGTGGTCCTGGT[C/G]CTTCC
TP69184	TGCAGCTGCTTCGAAAGGTC[A/T]CCCGCCGTGATGAGGCGGCGGATTGTGCTCGTCTCCTGGCAGG
TP69187	TGCAGCTGCTTCGCCAATCGCCAGGCTCTCTCA[A/G]GATCGGCCGCCAGGCTAAAGTGCAAGTGCA
TP69198	TGCAGCTG[C/T]TTCTCGGCCTTGGCCTGCTTCTTGAGCTTGGCAAGCTCAATGTCGCGCGCCATCT
TP69206	TGCAGCTGCTTCTTCGGCGGAAGCAGAGGCGGCGG[C/T]CGCGGCGGCAGCTGCTTCTCCCGCTGAG
TP69208	TGCAGCTGCTTCTTGGCCTTGGCCTGCTTCTTGAGCTTGGCGAGCTCGATGTCTCGGCGAA[C/G]GT
TP69209	TGCAGCTGCTTCTTGTGGCGCCATGGCAGGGCGAGACGGCAGCTCGAGCTCTCAACTT[A/C]ACCAG

Table A2 (cont.)

TP69211	TGCAG[C/G]TGCTTGAAGTTCTTCCGCCCACACCTTGGCCTTGTACAGCTTCTTGCCGCTGCTCGCC
TP69222	TGCAGCTGCTTGCCCTGGTGTTGTTCCA[A/G]TGCCGCAGTACGAATTTCATTCTGGATTCGAAGGT
TP69249	TGCAGCTGCTTGTCGGCCTTGGCCTGCTTCTTGAACCTGGCGAGCTCGATGTCG[C/T]GCGCCATCT
TP69264	TGCAGCTGCTTTGCCCTTGCGCCGCGGGGAGAAGCGTCGGTCCAG[C/T]GAAAAAAGTCGCGGCCTC
TP69284	TGCAGCTGGAAAG[A/G]CAAACACTGTTTACCAGCGGCACGGTCGCACGGGGGCAGTAGGTGGTTTG
TP69297	TGCAGCTGGAAGAAAGGCAGCGAGGTGGGCGGTGATGATGAAGTGAACAACAACTG[A/G]TGCTTCT
TP69331	TGCAGCTGGAATCATGCAGACTATACAGTGGCTAGCCTAGCCACCGTCAGAAAAGCTC[C/G]GTCGA
TP69340	TGCAGCTGG[A/G]CAAGATCGCGCCGCTGGCCGTGGGGCACATGCTGGGCACGGTGTTCACCAACAT
TP69378	TGCAG[C/G]TGGACTCCCAGATACTACGGGTGTAGTCCACCACCAGCAGCACTTGAACCGTCCGTCA
TP69379	TGCAGCTGGACTCCCAGATACTACGGGTGTAGTCCACCAGCAGCAGC[A/G]CTTGGACCGTCCGTCA
TP69393	TGCAGCTGGAGAACCCGTTCGCCGACGCCGCCGATGATGGCCAGGAGGGGGCGG[C/G]GAAGGTGCA
TP69396	TGCAGCTGGAG[A/G]ATGGTCACCTGCTCCTCCGACGGCTACGTCTCCGCCTTGTACGTTACGCTCC
TP69399	TGCAGCTGGAGACCAGAGCGCAGCGGCGCCATGCCTTGGCGAC[A/G]TGCGGCAGGGACGAGCGACC
TP69413	TGCAGCTGGAGCAGCAACAAAAGCTATTGTTGCAGCAGCAACTACTTTCTCAGATGGTACCT[C/T]A
TP69422	TGCAGCTGGAGCCGCAAGATTGTGACA[G/T]CCTAAGTTGGGCACCCCAGCACTCAGGAACAGAGGC
TP69425	TGCAGCTGGAGCCGCCACCGAAGCTGGACGACGCCGT[A/G]GCGCTGCGCATGCAACCATCCACCGA
TP69434	TGCAGCTGGAGCTCAGCCTCCGCGCCATACAGTCCTCTGGCGCCATAGCTGTGACATCGG[C/T]GGC
TP69437	TGCAGCTGGAGCTCGCTGGATGAC[A/G]GGTGACCTTGGGCCTCTCCCAGATTATTCTGGGCACCCA
TP69466	TGCAGCTGGAGGCGCCGCCACCCAAGTCGCGGCACTACATGCAGGGC[A/G]CGCTGTCGCCGTCCCT
TP69477	TGCAGCTGGAGGTGGAGCCCGCGGTG[C/T]ACGACGCGCGCGACGAAGGCACCGCGGACGCGTGGAT
TP69479	TGCAGCTGGAGGTTTCTGTTTTGA[C/T]TTTGGGGGACATGAGCCCTAGGATGTGGGGGATTTGGGC
TP69495	TGCAGCTGGATCGAACTCGACGGCGTGATCCACATGTTCATGGCTGGCGA[A/G]TCTGCGCACCCAG
TP69498	TGCAGCTGGATCGATCCTTCTCACGTGAGCAGAGCACCTCCGTTGCTATGC[G/T]CTGGTCTGACTC
TP69504	TGCAGCTGGATCTTTATCCACTGGCTCTCTGCCACTGTGTATATGCACCC[A/G]CCTCCTGGCAGAT
TP69547	TGCAGCTGGCA[C/G]TACTAGTAGTGCCCGATCTCGATCTGACAGCGGCATCAGCATCTCCCCGTCC
TP69567	TGCAGCTGGCATCTTC[A/T]GCATCCAGCAGGATATATTTGTTAGTACTTAGTACGGTACGGTGGTG
TP69579	TGCAGCTGGCCAGC[A/G]GCATAGAGGCGAGGCGGCGGCGCGTGGGGCCGAGGCATGGCAGCGGCGC
TP69599	TGCAGCTGGCCATTGGCGGCGGCGATGTGGAGCAGGGACAGACGGTCGTATGTGGTGG[A/T]GGCGC

Table A2 (cont.)

TP69600	TGCAGCTGGCCCAACATCCTCTTGGACTC[C/T]AGGTTTATCAGTTCTCGCATCATGTGAGTCGTTG
TP69618	TGCAGCTGGCCCTTGAGCCCCTCCTGGTAC[G/T]TCTCTACGAAATTCTTCATCGCGTCGGTGTACG
TP69622	TGCAGCTGGCCGACAAGATGGTTAGTCAAGGACTACACACACGC[A/T]TGCATCGCGCATGCCTTAT
TP69628	TGCAGCTGGCCGAGGGTGACCACGGCCATGCCGAAGATGTGGAACATGGGCA[A/G]GAAGCAGAGGA
TP69648	TGCAGCTGGCCGTCGTCGT[C/T]GACGATACGGTGTTCATCGATCGATCGAGGCTAGCTAGCTACCG
TP69658	TGCAGCTGGCCGTGTAC[C/G]TCTGCGCCGCCATGTCGCTGATGCTCTTCCTCGAGCGCCTCTACAT
TP69675	TGCAGCTGGCCTGTGCTA[C/T]TTGGGATGAAAAAATTGGTTCTTTCATCAACCATTGGATGAGAAA
TP69697	TGCAGCTGGCGAGGCTTGGAGGCTTGGA[G/T]CCCGCACCTCAGGTCGATTTGGAGCGGGAGCGCGA
TP69705	TGCAGCTGGCGATCTTTTGAGCTACCATCTTCGCCACAGCGAT[A/G]GCCACAAGAGTCTCAATGGC
TP69707	TGCAGCTGGCGATTCGTCAAGTGCAACG[C/T]GGCAGGGCGCGTCGTGAACCTTACCCTCGCCAGCA
TP69716	TGCAGCTGGCGCGCCGCCGACCAGGT[A/G]CGCGACACGCTCCATGAGAGCGAGCGGAAGTGCGCGG
TP69717	TGCAGCTGGCGCGCCGCCGACCAGGTGCGCGACACGCTCCACGAGAG[C/T]GAGCGGAAATGGGCGG
TP69718	TGCAGCTGGCGCGCTGG[A/G]GGAGGTCGTCCGCGGCGGCCAAGGCGGGCGGCGGAGCGGCGTGCCA
TP69726	TGCAGCTGGCGCTGAGCTGCGCGGC[C/G]GCGGCGCCCGAGCAGCGGCCCAAGATCGGGTACGTGGT
TP69730	TGCAGCTGG[C/T]GGATCGGGCGGTTCCGCTACCGCTGCGGCGATGGACATCTCGATCTGCTCGCCC
TP69749	TGCAGCTGGCGGGGTCATTGATGCCCACGTCCTCCAGGACGCCCTC[C/T]AGCCTCTCCCGCTCGGG
TP69756	TGCAGCTGGCGTC[A/G]GCGCTCATCTACAGCCACGCGCGCGGGGTGTTCCACCGCGACGTGAAGCC
TP69769	TGCAGCTGGCTATATGTGGAATTATGTGTAGGGAGGGATAGGGAAGAG[A/C]AACCTGGTCCAGGAA
TP69799	TGCAGCTGGCTGCCTGCACTTGCAGGCTGAAGTTACAGCTG[A/C]TGTTGGCCGCTCCGTGCTGTGC
TP69820	TGCAGCTGGCTGTACAAGATCGATTCTGTTGG[T/C]GTTTCAGCGCAGATGGAGTTTACTCAGCATC
TP69822	TGCAGCTGGCTGTGCACACAAGTGAGAATCCCATTCACATTTCTCTGGCTATAAAAAAA[C/T]TACA
TP69836	TGCAGCTGGGAAAACCCGAGTCGCTAAGTTGCGAACC[G/T]ACGTAGGAGGCAAGACCTTCGTCTCC
TP69848	TGCAGCTGGGACGGGGACTGGGAGACACTGAGGACAACTTTCAGGTGTTGATGATTGC[A/C]ATGAA
TP69849	TGCAGCTGGGACGGTTCGCCGTCGCCGCCGAA[T/C]GAGAGCCCGCGTCCCCTCAGCGCGGGAACGA
TP69863	TGCAGCTGGGAGGGCGTCACCTGCGGCAAGAGACACCCGTGGAGGGTGGTAGCTCTGG[A/G]CCTCA
TP69867	TGCAGCTGGGAGGGGGTGACATGCCGAGGCAAGCAGCACCAGCGACCGCGAGTTGTGG[C/T]GCTGA
TP69871	TGCAGCTGGGAGGGTGT[A/C]AGGTGTCGGGGCACACGCCGCCGAGTGGTGGCGTTGCGCCTCCCGT
TP69883	TGCAGCTGGGCAGCCGCCGTCAGGGATCTCGCAATGGCAATGCGTTGTTATAGC[C/T]GTGGTTTGC

Table A2 (cont.)

TP69889	TGCAGCTGGGCATGGCGAGCGCGCTGGAGACGCTATGCGGGCAATCCTA[C/T]GGGGCGAAGCAGTA
TP69899	TGCAGCTGGGCCCACGCGGACGTCATACCCTAAGGCTGCAATTTTGCATCAAGT[A/G]GTAACCCAC
TP69909	TGCAGCTGGGCCCTATGCTCGGACCCG[C/T]GGAGAGGCCCCGTGGCTGAGACCGCGCCTCTGACCC
TP69918	TGCAGCTGGGCCTAGAAA[A/G]AGTATTATACATATACAAGATATTAAAGAATATATATACTTGATT
TP69922	TGCAGCTGGGCGACGTGCTCCACGCGCG[A/G]GGGCTCGCGGTGACCGTGCTCCACACGCGCCTCAA
TP69923	TGCAGCTGGGCGAGGTC[C/G]CCGAGGCGGCTCGGGATGGGGCCAGAGAAGGAGTTGTAGCTGAGGT
TP69934	TGCAGCTGGGCGTCTACTTCG[G/T]CGGGCTGTACACCATCGCGCTGGGACACGGTGGCACGAAGCC
TP69945	TGCAGCTGGGCTCTTGCAAGATTGTGAGT[A/G]CCAATTGAAGGCCCTCTCTCTGCTACCACCTGTT
TP69952	TGCAGCTGGGGAAAAGAAATAAAAGAACGTCAATGAATCACCAGGATGAATGAACAGCT[C/T]AAGT
TP69958	TGCAGCTGGGGAGGCCAGTGCCCGTTGCCTCCGCCGACGGC[A/G]CCGCCGATCGCCAGGGACAGTC
TP69979	TGCAGCTGGGGCTGCGGCACAGCCGCGAGCGCTGCCTATGGTGGACGAAA[C/T]GGCCCGCCGAAAA
TP69995	TGCAGCTGGGGTCAAGTCGGTCGGTCGT[A/C]GGGCCACACGTCAGTGGCAGCGTACTGTACACAAG
TP69996	TGCAGCTGGGGTCAGGCCCGCTGGTGGATTACTGGCCGTCGCTGCTGTTCACGCACCTG[G/T]GCGG
TP69997	TGCAGCTGGGGTCGGGCCCGCTGGTGGGGTACTGGCCGTCGCTGCTGTTCACGCACCTGGGC[G/T]G
TP70013	TGCAGCTGGGTGATCACT[C/G]AAACGGTTGCTTTACTTGTCTCCGTGTGTGTTGCAGCATCAGGTC
TP70016	TGCAGCTGGGTGCCTTTGCCATGCCGAACTCGTC[A/G]GATCAGATGCCGCGTGAACGAACGCTGTC
TP70020	TGCAGCTGGGTGGCGGATAGCTTGATCACTTTTGATGAG[C/T]TGCTGAAGGACATCGGCGACAAGG
TP70033	TGCAGCTGGTACCACTGCGTCCCGAGCGTGCGGTTGTCGGCGTCGAG[A/C]ACGGCGGTGAGGGGCA
TP70039	TGCAGCTGGTACCTTGAGATCGGCGCCCGC[A/G]CAGAAAACCTTGGGCACCGAGCTCGCCACCAAG
TP70047	TGCAGCTGGTAGCCTGGTACTAGAAGCTGAGACGGTGGCGGTGGCGTACAG[A/G]ACATGTGGGTCA
TP70082	TGCAGCTGGTCGCCACGCTCGACGG[C/T]GCCACCGTCGTGTTCACCGCCATGCGGAACCACCCCTT
TP70093	TGCAGCTGGTCGTGGTGAGGCTGGCGCACTGT[G/A]CCTGACCTGTTGATGAGGGCCATGCTCGTTA
TP70095	TGCAGCTGGTCTACAGCATACAT[A/C]CATCCATTTGCACCCGTGCGCTGGCCACGGTGGTTACTAG
TP70097	TGCAGCTGGTCTCCCTGGGCACGCCGCGCGCGCAGGA[A/G]CAGGCGCTCGGGTGCCTCCAGCGCCT
TP70103	TGCAGCTGGTCTGGCA[A/G]TACTACTACTACGCAGAAGAGCCTGGGAGAGGGGCTGGAACTGGAAC
TP70106	TGCAGCTGGTGAAATGGAGACTCAGATTATTCTACCAGAGAAATGCCTAGA[A/G]CGACCAGCATCC
TP70107	TGCAGCTGGTGAACAAGCTCTGGACCGACCCCAACGACCC[A/G]ACGCACATCGAGGAGAGCGCGGA
TP70109	TGCAGCTGGTGAA[G/T]CAACTTACGAAGTGGAGACAACTGTGCTGACAGGTGGGGCTAGGAATGCC

Table A2 (cont.)

TP70113	TGCAGCTGGTGACAACAAAC[A/G]TGAAGACGGTGAAGGCGAAGAGGAGGAGGAGGAGGACGAG
TP70118	TGCAGCTGGTGAGCCTGCTCGTCCTGCGCCGCGTGCTCCTCCTCCTGCGCTTCGTCCTCCT[C/G]CT
TP70128	TGCAGCTGGTGCAAGCTGCATACC[A/G]CACGAACGGGACGCCTTGCTGGCCTTTAAACATGGCATC
TP70130	TGCAGCTGGTGCACTTTCACATCCGACATCAGAGGATCCTGCTGCCAAAACACCT[G/T]CTTCAATA
TP70132	TGCAGCTGGTGCAGGGGAGCCTC[C/T]CGAAGAAGGTCCTGGAGGCGATCCGCGAGCTGGTCACCGA
TP70145	TGCAGCTGGTGCG[A/G]TCGTGGCTCAGCAGGCTGCTGCCCCACCGTTGACTCCTCCGACCCCCTCG
TP70146	TGCAGCTGGTGCGCGACCCGCCCACCGTGTTCGCGGGCGT[C/T]GAGGGCGTCGAGTTCAGGCGCAA
TP70147	TGCAGCTGGTGCGCGAC[C/T]CGCCCACCGTGTTCGCGGGCGTCGAGTTCAGGCGCAAGCGGTTCGT
TP70151	TGCAGCTGGTGCGTCAGCTGGAGAAGTGGTTCGAGCTCATGAGCGCCGAGTACGCGTACATGG[C/G]
TP70161	TGCAGCTGGTGCTGCG[A/T]GATGAGGCGAGACGAACTGTAGGGTTCTGCTCACGATAGGTGCGGAT
TP70167	TGCAGCTGGTGGAATGGCGTGATCAGAAATGTTCCAATGGACAGAAGGAAAGGGCTAAAATCC[C/G]
TP70168	TGCAGCTGGTGGACCAGGGCGACATGCGCATCCTCGACAAGGG[A/C]GGCGAGCTGGCGTGGAAGGC
TP70184	TGCAGCTGGTGGCTGCTGCCTCCCCCCTGGGATTCACTGAAGTGCGCG[C/T]AAAATTTCCCCAGCT
TP70187	TGCAGCTGGTGGGCCGCCGCGGGCGACGTCAGCGACGATGG[C/T]GGGCTGACGATGACGCTCGTGT
TP70196	TGCAGCTGGTGGTGGCAGTC[A/G]GCAGAGGCCTGGCGCCTGGGGCGACGACGCTGCCATAGCGGAG
TP70217	TGCAGCTGGTTAGTTGCTGCTGCTTGA[A/G]CCTTGAATCGAGATGTGGAGTGCAGGATGCATGGAA
TP70222	TGCAGCTGGTTCACCGACGGTGGCTGCACCGCCTCGGCAGCAGC[A/C]GCCGCCGCCTGGTAGTAGT
TP70228	TGCAGCTGGTTCCAATTTCCAACCTCTGCGGCGGCCACCCAGCAGGACAGTAG[A/G]CACCACCACA
TP70246	TGCAGCTGGTTGGCCTCCGCGACGGTCTGGGCGTCGACCCCGAACCGCGCGGCCACGG[C/T]GGCGA
TP70255	TGCAGCTGGTTGTTGTGGTTCGTGGACAGGTCGTT[C/T]AACTTCTTGAGGCAGCCGAGGCTGTCGT
TP70262	TGCAGCTGGTTTTAAATAGCGGGCTAAGGTGCTTAATGGTGTA[C/T]CTTTAAATCGGCTAATAGCA
TP70263	TGCAGCTGGTTTTCCCAGCTTCTGTCTGCTGCCAC[A/G]CTTGCGTTGCATAATTCAGGTCGCTGCT
TP70296	TGCAGCTGTACATTTGGTTTGAAGGGGGCTCCGTTG[C/G]GTGGCTCGACGACGCCGTCAGCGACAA
TP70300	TGCAGCTGTACCTGTACGTACCTAACATGCAGCAT[C/G]TGCACAGATTCTACCAAACTGTCTTCCG
TP70342	TGCAGCTGTAGCTGTACCTAACCAAAGCAGCAGCCCAGCGCACGT[A/C]ATCTGGGCCGTCCGCCCG
TP70346	TGCAGCTGTAGCTTCTGAAGATGTTGTGCAAA[A/C]CGAAACCTCCCATGCCGCACAGTTTTATAGG
TP70364	TGCAGCTGT[A/G]GGTATAGCAGCGCCGTCATCCACGACGACGGAACGAGCATAGAAGCTAGCGACT
TP70373	TGCAGCTGTAGTTTTATTAAGTGTAAAGCT[A/T]AATTATAAAAACGTTGTGTGTAAAACTTAGCGA

Table A2 (cont.)

TP70385	TGCAGCTGTATCTGCATCTGCTGCTGCTGCTGATCATGTTGCAGTTAACGGCAAGCGTGCAGC[A/G]
TP70417	TGCAG[C/T]TGTCACGGCTTTTACTTGTATGCCATTCCTACGAACCTGAGGAGTATTAGCGTCACGG
TP70426	TGCAGCTGTCAGGCCGCCGAGCACATCTCAAGCGCCTGC[A/G]TGCGGCGAATGAACTGCGCGTCGT
TP70449	TGCAGCTGTC[C/G]CATGAGCGCCTCGGAGGTGGAGGAGCGCTGATGATGCAGGGGAGGGGAACATT
TP70453	TGCAGCTGTCCCGCACGA[C/T]CAGCAGCCACCAGCCGCAGGAGCTTCGCCTCACTCTCCAGTCTAC
TP70458	TGCAGCTGTCCGATCGATCACCCAA[A/G]ATGAATCGGGGGTCAACGTTCGCTGATTAGTCAGCCTG
TP70466	TGCAGCTGTCCTATTACCAGCTGCGGCGGCGGCGCTGATGGC[A/G]ATGGCGGCGTTGCAGCTCTCG
TP70480	TGCAGCTGTCGACCC[A/T]GCACAATGACCGCCTTGGTACTCCTTCGACAATTGTACCACTTCCTCC
TP70483	TGCAGCTGTCGAGAGCATCATAAATAGTTGAGCTGGTTTGCC[A/G]CTGTTATCAGGTTCAGAAACT
TP70495	TGCAGCTGTCG[C/T]CTGAAAATTTAGTTCCAGTGCAACCATGGATTCTACATATACCGAAGTATTG
TP70502	TGCAGCTGTCGGACTA[C/T]GAATCCAGCGACAAGGCAAGTACCTAACCATCCAAAACCTTTTTTTT
TP70524	TGCAGCTGTCGTCTACTTTATTGACGCCATTATTCCTAGGTAACCAGCTCGATGCCCGCCTCG[A/G]
TP70526	TGCAGCTGTCGTCTTTGGTGTCGGGGGATGGTGGTGACATCGCCGATTGGTGGCTGCTCCAGC[G/T]
TP70540	TGCAGCTGTCTCGCGGTAGGGCGCCGTTGCTCTGT[A/T]GTTGGTATGATGATCTGAGAACTGATCT
TP70574	TGCAGCTGTGAATGAGGGCAGCCGAACAGAC[G/T]AATTGTCCATTTCAAGTCGACCGTAGCACAAG
TP70580	TGCAGCTGTGACATGGAGTTGGCTCTCCCTCGAGCGGCAGCGA[C/G]AGCATGTGGCCCAGCGCGCC
TP70587	TGCAGCTGTGAGGACTTCCTCCACCGATGGCTGGCCA[A/G]GCTTCGCTGGCTCCTCCCTCCTCCCC
TP70589	TGCAGCTGTGAGGCTATTAACAAGGGCCCGAGCAGCGCCCAACAAGGCTCACCCC[A/G]CACCAACT
TP70591	TGCAGCTGTGAGGTTACTCACATA[A/G]TTATTGAACTTTGATCTTTTCGTCCACAGTATAAACAGT
TP70595	TGCAGCTGTGATAACGAGCA[A/G]CTGAACGACAACGCTTCCATATCATGTTTTATCAGTGGGGGTT
TP70600	TGCAGCTGTGATGTTGCACCTGTCTGTGCATAACGTGCATTTAGCTCGGGC[A/G]CAGGAGTGCGGC
TP70605	TGCAGCTGTGCAAATGACGACGGATCGGAGTCGCTGCTGATTAAGTGATGTACAGCGAC[A/T]TCCC
TP70614	TGCAGCTGTGCACGGGGGG[C/G]CCAAGCCACGCGTTGGATTAGACCACATGGTCGCTATTCTAGGC
TP70626	TGCAGCTGTGCAGGGGCGCCACAGACGATCGGGGAGCCCGAGATAAGAAGATC[A/T]CACTCGGGTG
TP70656	TGCAGCTGTGCGCTAACC[A/G]CAGATAAAGAAAGTCATCAGCTAAAATAACATAATTTCTATACAA
TP70657	TGCAGCTGTGCGCTCGTCAGCTTCGCCTCGCTGCCGAACGCCGCGTACACAACGGAGCCCCG[A/C]G
TP70658	TGCAGCTGTGCGCTGCAACCAGCGGCGAGCGCCAG[C/T]ACCGCCAGCATCGCCATTAGCGCCGCCA
TP70661	TGCAGCTGTGCGGCTACGACGAGGAGCTGAGGGAGATGGAGGG[C/G]CAGCCCAGGGAGGAGTACAT

Table A2 (cont.)

TP70677	TGCAGCTGTGCTGCTCCTCCCGTCCCGTGAACG[A/G]AGGAAAAGAAGAAGAACCAACTGCCCGTTG
TP70689	TGCAGCTGTGGACGCAAGACTTCA[C/G]TCCCAGACCTGACCCTCTATCCTTTTGTAAACTGCACAG
TP70694	TGCAGCTGTGGAGGACCCCGCGTCGACGAGGTAAGCAGG[A/G]GCGCCGTGGAACTCGAGGGACACG
TP70700	TGCAGCTGTGGCACGC[A/C]CTGGCCAAGACGCTGTCGGAGAAGACGGCGTGGGCGCTGGCCATGGA
TP70701	TGCAGCTGTGGCA[G/T]ACTTGCAGTGCTGCTTCTGAGCGTGGCCTGGGCCCTGGGGTGATGCGGTT
TP70705	TGCAGCTGTGGCCAAAGGACAAGGTACTTGCTT[A/G]CATATATGTCTCTTGATGCTGTAAATTTCA
TP70714	TGCAGCTGTGGCCTGTGGTTAATGCCGTGATGGCCCGATGCGACGATACCCA[A/G]GTGTAAAACGG
TP70719	TGCAGCTGTGGCGGAGGTCGCGATCGCGCCGCGCGTCGGGTCGTTTGCTCGGGCAAGGAACCT[C/T]
TP70722	TGCAGCTGTGGCTCTGCTCTCGGCGACCATCCTGACGCTGGTC[A/G]TCCAGCCATCCTGGGCGCCG
TP70746	TGCAGCTGTGGTATTACCAGCTGCGGC[G/T]GTGGCGCTGATGGCGATGGCGTTACAACTGTCGGCC
TP70753	TGCAGCTGTGTAACATGTTGAGTTGGTGAACCCCTCACGGTTCAC[A/G]CCGCCGTGAAAAAGTTTT
TP70768	TGCAGCTGTGTGACTGTGTCAGTGCACAAA[A/C]GGGCAGAGGTAACGACAAGTGGTTAGCTGGTTT
TP70769	TGCAGCTGTGTGCAATTCGACCGTAGCTCAGCGTTCCCCAAAACCCGAGAGAAACC[C/T]ATAGCTT
TP70770	TGCAGCTGTGTGCATGCGTGCGTGCAGAATGATCAGTCAGATCAGCAAGTTACCAGAAACA[A/T]GC
TP70777	TGCAGCTGTGTTACACGGATACGTCCCTGAAGCCGCGTATCGCGTATCCAATAC[A/G]TATCGGATA
TP70787	TGCAGCTGTT[A/C]ACCAGCTCAGCCGCCCAGCTGCCGACGTGGCGTGGCCATCGCCACCGTGGCAC
TP70794	TGCAG[C/T]TGTTACAGAAAGACCAGTGGCAAGTTAAAATGACAAAATGTTCGTTTGCTCAACGCCA
TP70810	TGCAGCTGTTAGTAGCAGGCAGTCCTAGGAGTACT[A/C]GATTCTACTCTACTCTAATCTCAATCAA
TP70855	TGCAGCTGTTCGTGAACGCCAAGCAC[A/C]TGCACCTCGAGTCCGCTCGCCTCGGCTCTAGCTTGGA
TP70876	TGCAGCTGTTGAGTGTGGACTTGCATGTCCAATTGTCCATCCAACTTCCAACCC[C/T]AGTAGCCTT
TP70895	TGCAGCTGTTGCGGTGC[A/G]TACATGTATCTTTCCTTTCCACACGCTGCTGTCGAGCTGCCATTGC
TP70900	TGCAGCTGTTGCTGGTGGCCGTCGTCCTCATCGACGACCTCGACGA[C/T]GTCGTCGTCGTCGTCCG
TP70924	TGCAGCTGTTGGCTTTTCAGCTTGGGTGTGTGCGTGTGTGCGCCTGTCTTCTGGGC[C/G]AGGCCCG
TP70943	TGCAGCTGTTGTACTGACATTCATTGCCCAT[G/T]TGAGAGGCGCGGGACAGAGCAGCCAAACTCAT
TP70969	TGCAGCTGTTTCCAGGTGCATCATCTTCACCAGAGCG[C/T]GGATGTTCCTGGCTAGGAAGCGACCA
TP70991	TGCAGCTGTTTG[C/G]CCGTCCCGAAGTCGGCCACCTTGGCTTGCCATCCGCCATCCAGCAGCACAT
TP71011	TGCAGCTGTTTTGGCACCGTCGGCGGCCAAGAACGTCGCCCTCGACTCTGCCACG[C/T]TGTCCTTC
TP71055	TGCAGCTTAAGCTCGCGCGT[C/T]GGGGACTCCAGTTTGACCACGGCGAAGGTGTGCTTAGATGGGC

Table A2 (cont.)

TP71056	TGCAGCTTAAGCTGCTCGACCTCCGACCGCAGCTCCTCGCGGAAACCGCCGTC[A/C]TCATCCCCGC
TP71064	TGCAGCTT[A/C]AGTATCTTAGTGCCTTCCTCTCTTCTTCTTTAGATTGTACCCTCATCAATGTTTC
TP71065	TGCAGCTTAAGTCCCATGATCCCACAATGGAAAAGGGGTTTTGCCATGATCCCC[A/G]ACGAAATCC
TP71070	TGCAGCTTAATCAGAATGTAGCACGTCAGTGCGGCATGTGACTTGATTGGTTCGAGCT[G/T]AATCG
TP71091	TGCAGCTTACAAACGCGTCACAATGGCCAGCTTTGCAAAGCCGAAGCATCTGCTGCTTGTCGC[C/T]
TP71106	TGCAGCTTACAGCTGGGCCCGATCGAGTCCGATTCCTTCTACTGGCCGCCCAATTCGA[A/G]CTCCT
TP71149	TGCAGCTTACTAGGGTAACGGTATACACCGCCAACATG[C/T]CAACATGGAGTATAATACAGGTTGG
TP71172	TGCAGCTTAGAAATAGGACAGATCGAGCAAAAGTTCGATTCCAGGGCGCTGTA[C/G]AAGGAATGGT
TP71173	TGCAGCTTAGAACAATAGTGGAGCGAGTATCTTTCACAAGCTCGTTCACTGCATCTTTC[C/T]TAGC
TP71178	TGCAGCTTAGAGAGAGGAGCAAGCTAGAAAGCGTTGCGGTCCGCGCCGCGCCG[A/C]GCCTATCTGA
TP71182	TGCAGCTTAGAGTAGCGTGAGTATTG[A/G]CATCGGTCAAAATTGCCTCCGTCACGTACAAAATCCA
TP71217	TGCAGCTTAGTGCGCTCTCTT[C/T]GCAAGGGTCACAGACCGCCATGGCCACCGCAGCCCCCTTCTA
TP71218	TGCAGCTTAGTGCTGCTGGCATGGTGCTGCTGCTCTGCTCTTGC[A/G]AGGAAAACATGGAGACCGT
TP71227	TGCAGCTTATAAATATAGCCCGCTGTAAAGCCCCTAG[A/C]CATCAGTACTTTGTTATTGAAAATCT
TP71240	TGCAGCTTATATCCTTATGAATCTTCCACCCTTTCTCGGC[A/G]TCGTAGACTCTGATGCGGCTTCC
TP71249	TGCAGCTTATCAGACTTCCTCAGCACCCAGCTGGCAACACCTTCGGAACAAACCTTCCTCTCC[A/C]
TP71251	TGCAGCTTATCATTACCACATCAAGAACACCATCTG[C/G]GTCGGCGAGGAACCCGCTCAGCTGGCC
TP71278	TGCAGCTTATGGAATTGGAAGGATGGGCAAGGAG[C/T]AGCTAGCTAGCTGGGACTGGTCACTGGAG
TP71280	TGCAGCTTATGGCGTCCACCTCGTACCCGATGAGCGTCGGCGCGTGCGGCGGCGACG[A/G]CCGTTG
TP71310	TGCAGCTTATTGGCCTTTTAACCACGGGAATCCAAGCACCCATAAGGAACCACGAAAA[C/T]GACGA
TP71347	TGCAGCTTCAAGCACCTGGATTGA[A/T]GTGGGGATCTGACACGGCAGAGAGCTCCGCCTCCTCGGA
TP71353	TGCAGCTTCAAGGGGACAGTCGCTGGCTTGCTGTTGC[A/G]CTGCTGCTTGACTCCAGGTCCAGGCT
TP71368	TGCAGCTTCAC[A/G]ACACAAAACACGCGGGAGAACGAAGAAATTGAAATCCCTGGCAAGAACAAGA
TP71370	TGCAGCTTCACAAGCGCGGTAGATTCCAGAGGACGGGTTCGGAATCATGAAGCTCCACA[A/C]GCGC
TP71399	TGCAGCTTCACCTTGTCAAAGAGTTTTGCGTCAAAATTGTGCGCGATCTC[A/G]GCTGTATCGGGCG
TP71403	TGCAGCTTCACGAGCGCCTTGAGCGC[C/G]CGCAACGCCTTCTTCGCCTGCGTGCGTAGAAACGATG
TP71406	TGCAGCTTCACGCGCGCTACTACTTCCC[C/T]TTTCAATTCCTCCCCGCCTTCTCCCGCCATTCCTT
TP71418	TGCAGCTTCACGTCGGGGGAGAGGAGGAA[A/C]GGCAGCGCCAGGAGCGCGCCCGTGGACGGGTCGG

Table A2 (cont.)

TP71422	TGCAGCTTCACT[C/T]CACACACCGTCGCCGCGTGCTGAAGAAGCACCACGACTAATCACTGACTGG
TP71435	TGCAGCTTCAGAATCCGCATGTTGCGCAGGATCTCAGACGTTGCCTTCATCCTGA[A/C]ATCCTTGC
TP71441	TGCAGCTTCAGATCTTGTCTCAAAACCTCAGAGAGGTAGAGGGCGAGGACGTCGACAGAG[C/G]AAA
TP71443	TGCAGCTTCAGCAGCATGCGAGGGCAGGGAGCGGGAGGGAGGAGGCGCTGGAGAGGAG[A/G]CGGGC
TP71480	TGCAGCTTCAGGGCCAC[C/G]CCCTGCTTCACCTTGCCACCAGAAACCACCACGGCGCTGTCCCTGA
TP71516	TGCAGCTTCATCTCGCAGGCACGCTGGCTCATCTCGTCCAGCATTTGGCGGAGCCTC[A/T]TTTCTA
TP71526	TGCAGCTTCATGGACGCGCTGGAGCTGAACACCAGCAGTGGTTTCTTGCGCGGCAC[G/T]GGCGCTG
TP71530	TGCAGCTTCATGGCCAAGTAAGTGGCCTTGTTTTTCCTC[C/T]CTGCTCTCGTCTCGGTTTCTTGTG
TP71536	TGCAGCTTCATGTGCGAGTGCGACCCCGCCGACGACAAGTCCCTCACCGTC[C/T]GCGCCCTGCCCA
TP71543	TGCAGCTTCCAAAGAACAAACTCCAGAAATGACCTCAC[A/T]GTCTCAAATGTGACCCTCCCTGTAA
TP71561	TGCAGCTTCCACCGCGCACGCGTCGTCGCTGTTCCCGTCGCTC[G/T]CCATACCGACCGTGAAGACC
TP71568	TGCAGCTTCCAGATCTCTGACAC[A/G]CTGACCTTGCTATCGCTGGCGTCGTCCTTGGTCTTTGCGC
TP71569	TGCAGCTTCCAGCAAGTCTCGTAGCTCCTTGTGAACATGCTTTCCCTC[A/G]TCGCTCGAGGGTTCA
TP71575	TGCAGCTTCCAGCGTTTCTGCATCTTC[G/T]TCCTCCCTAGTGAAGCATGGCGAGACGGCGGCCGCC
TP71594	TGCAGCTTCCATGCAGCATGCTTTTG[C/G]GTTGAGTATATTTGTGGGCACAGTGCCATTAACCTCA
TP71603	TGCAGCTTCCATTGTCTGCGCCGCCTATTTAGC[C/T]CACCCCCGCCTCATCTTCCCTCCCAAGTCC
TP71625	TGCAGCTTCCCCAGCCGCTCG[A/T]GGTGCTAGTGTGGGAAGGGGAAGGCAGAGCGGGGGATGTGGG
TP71628	TGCAGCTTCCCCCTC[C/T]GCTGCTTCCGCTGCTGCTCCATGGCTGTCAACAAACCAGGGCAATCAG
TP71632	TGCAGCTTCCCCGCCCAGGCGTCGGGCGCGGCGATGTGC[C/T]TGTAAACCTGCTCCCCGACGGCGT
TP71640	TGCAGCTTCCCGAGAATTTA[A/G]TACGCAGTCTCGCAAGAAAACCGAAAACCATCACCAGAATCTG
TP71662	TGCAGCTTCCGCACGCCCTGCGTCCGTACAA[A/G]TGTCAGGTCATCCCTGCATGCCATCGCTTCCG
TP71669	TGCAGCTTCCGC[A/G]GGGCCCCATGCTCCTGTGTCGTGTCCCTTCTCTCTCTCCGTGGAAGTCAAA
TP71674	TGCAGCTTCCGCCCAGCACCCTGCCGCCCTTTGGCGCGCA[C/T]CCCCTAGCCATGAGCTGCGCAAT
TP71675	TGCAGCTTCCGCCGCTGGACCTCAA[A/G]GACGGAGGCGGTGGCGGTGGTTACGGCGCCGCGCCGTC
TP71704	TGCAGCTTCCTAG[C/T]GTTGGTCGCCAACACCTTCCCCTCCTCCTCCACCGCGACGGCCCGAACTG
TP71708	TGCAGCTTCCTCAGGCATCCGACGACGCAGCCAGTCTGGTGCTGAAAGAAAACAC[G/T]CGCCGCGT
TP71709	TGCAGCTTCCTCAGGTAACGTCATCTCATCTTACATTTCCCTCCCCT[C/T]CCCACTCTGTTTCCCA
TP71712	TGCAGCTTCCTCCAATAATTCTCACCTTTTTG[T/C]TTCGCTTTCCAGGGAACAATTGTACTTGTGA

Table A2 (cont.)

TP71717	TGCAGCTTCCTCGAAAGCTCAGCTGAGAACTTGGCGGCGTTGTCGGAGGCC[C/T]CCCGAGCAATCC
TP71736	TGCAGCTTCCTGCCA[A/G]AGTTGGGAAGGAGATGAGGGCCATGACCAGCCTATTAACCCCAGGGAA
TP71753	TGCAGCTTCCTTCCGCGGAAGAAGGCCTCTTCCACCTTCACCCCCTCCACC[G/T]CCACACCTGTCA
TP71770	TGCAGCTTC[G/T]AATCGTTTAGAGAGCACACGAGAATGTCGTCGGTGCAGCTCTCTGGTGCTGGAG
TP71773	TGCAGCTTCGACGATTCCACAGGTGCGCGCCA[T/C]GGTGAAATAGGGCGCCAAAACCAAATATATC
TP71800	TGCAGCTTCGCCAGTATGTACTTCTGC[A/G]AATGGTTGTCACTTTTAATTTGCCCGTTTAATTGCA
TP71810	TGCAGCTTCGCCTTTGCTTTCGATTTCCGCGCCGTGTGTTCTT[C/G]ATCGCGCCCTGCGGCGTCGA
TP71819	TGCAGCTTCGCGGCCGCAGACGACGCCGA[C/T]GTCCCCTCGCCCGCGCCCGCGCTCGCGGGGGCCG
TP71829	TGCAGCTTCGCGTTCACCTCGGCGCACACGGCGGGCCTTCCTTCCGCGG[C/T]CGAGGCCGCCAGGG
TP71847	TGCAGCTTCGCTTTTCAACGGGGACTTGTC[A/G]ATGCCGCAAAACCTCGAGCACCTTGAGTGCAAG
TP71851	TGCAGCTTCGGAGGACGCGGCGTCATTGTGCTAGTGCTACAGTAGGGACAGGTGCT[A/G]TCAGTTT
TP71866	TGCAGCTTCGGTACAGTGAGCAACAGGCTTACACCAACAGTCGGGGAACCAAGA[A/G]CAGCTTGTG
TP71880	TGCAGCTTCGTCCATTTCAGAGCCCACCCGAGGCACTGCTTGCAGGGGCAGAGAC[C/T]CAGTAAAG
TP71881	TGCAGCTTCGTCCGCTCAAACTAGCTAGTGGTGGG[A/G]CCGCGCGCGGGGTTAGTGAACGAAACTA
TP71886	TGCAGCTTCGTCGTCGCCGCCGCCGCCGCGTGGGGTTCTTGCCGCAGGGA[C/T]GCGGTTGTGGTGG
TP71906	TGCAGCTTCGTTCAGACCTCTCGCGCGCTTCGCCTCTTGGCTAGCGAGCACGCGGGAACG[A/G]CAC
TP71909	TGCAGCTTC[G/T]TTCAGTCGCCCGCCGACGCCACCGCCCGCTCGGCTCGAGATCGCCGCCGTACTG
TP71915	TGCAGCTTCTAACTCCAGGTATAGTATTCCACTCCGTGGAGATGCCTGGTGACA[C/T]AAGAATGAA
TP71937	TGCAGCTTCTC[A/G]AGGTGGAGCTCAGCTAGGAGGGAATCCCTTGGGACGTCCTGGAGCACGATGT
TP71946	TGCAGCTTCTCCAGATCGCC[A/G]TACGCCGCCGCGGTGTACACGTCGTTCTTCAGCGACTCGTCCT
TP71948	TGCAGCTTCTCCAGCGCCATTATTGCCGCCGCCCGC[A/C]CGCTGCCTCGCACTCGCAAGCTTGAGG
TP71956	TGCAGCTTCTCCATGCCCTGCGAAAGGGCGTCCTCCGCCTGCGTCGACGTGTGCTGGAGGC[C/G]GC
TP71957	TGCAGCTTCTCCCCCAGCTCCTTCAGCTGCTCCG[C/T]GGCCGCCATACCAGGCCGCCGCGCCGAAA
TP71959	TGCAGCTTCTCCCTCTGCCTGCGTCGCCCTCCTAATGTCCGCCTCC[A/G]ACCGCCTCTCCTTCCTT
TP71988	TGCAGCTTCTCGTGCTGCCTTGCCGAAGCTCCTGGCGCCCCCACTGGCACTGTTCGGAGGAG[A/C]G
TP71993	TGCAGCTTCTCTCCCGTGATGGGGTCCCAGACGTCCATCTCGCTGCCATCCAAGGG[A/G]TGGACGC
TP71994	TGCAGCTTCTCTCGCAAAGCCGTTTATGA[C/G]CAGTGTTTGGCAGGGCTTTATCCGAAAAGCCAGA
TP72000	TGCAGCTTCTCTTGTTTGTTTTCCTGGTCCAGCTT[C/T]CCAGCCCAGCCAGCGTGGGCCTCAAAGC

Table A2 (cont.)

TP72003	TGCAGCTTCTCTTTTGCACACGTTGTTTCGTCAT[C/T]TTTAACAGGGGGAGCGGGGAGGCACCTCG
TP72007	TGCAGCTTCTGAACACGCGTCAGAGTCGCCAATTGAGATCGAGCAGAACGCGA[C/T]GGCGTCGTGG
TP72008	TGCAGCTTCTGAACACGCGTCGCCCATTGAGATCGAGCAGAACGCGACGGCGTCGTGGA[A/C]GGAG
TP72027	TGCAGCTTCTGCACGCGGTGGATGTGCA[C/T]GACCTTCATCTGTCGGGCAACCATCACTTTGCTTG
TP72036	TGCAGCTTCTGCCGCGACGGCTGCTGGTGGAACGGGTACCTATGCG[A/C]AACATTCCCAATCTGGA
TP72038	TGCAGCTT[C/T]TGCGACCCAGGTGAGTGAGATCGATCGATCCGCGGCGAGCTCTCGCGCGGTGCGT
TP72043	TGCAGCTTCTGCTCGTGCCGCAGGCGCTGGTGGGCAACACGCTGTTCCC[A/G]CCGCTGCTGGCCGC
TP72056	TGCAGCTTCTGGTC[A/G]GAGTCGGCGAGCCTCTCGTAGACAGCCCTGTGCTTCTTGTCCTCCACGT
TP72065	TGCAGCTT[C/T]TGTCGGTCGCCGCTGATCCTGTAAATGGCAATTATGACTCTGCTCCTGTGATTGT
TP72071	TGCAGCTTCTGTTCGAGAAGTGGCA[A/G]TTGCTCCTTGCAGGGTTGGTGTTTCAGGTGAGCTTCCC
TP72087	TGCAGCTTCTTCAGGTTGCCGATGCTGGGCGGATCGGCCCACTGAGCTCGTTGTCGTAGAG[C/T]G
TP72090	TGCAGCTTCTTCATCACCGACGGGTTCCGCATCAGCTC[C/T]GACATCCCCCACTCCATGGCCGACC
TP72098	TGCAGCTTCTTCCTCGCGCTCTTCGAGAGCTCTGGAGGCTTGC[C/G]CCCGTCTTCCGCTGCTACCG
TP72101	TGCAGCTTCTTCCTCTGCTTCCTGCTGCGCTCGTTCCG[C/T]GCCTTCTTCTCGTTGCGGCCGTACG
TP72106	TGCAGCTTCTTCGCCCTCTACAACTTGCGGACCATGGGTGAGCAAACGGCC[C/T]CTGAGTTGCGGC
TP72130	TGCAGCTTCTTGCCTCTCGACATGGCCACTGCCGCAGCTCCACGGGCAAGCAC[C/T]GAAGCAGCAC
TP72144	TGCAGCTTCTTGTTGTGGG[A/C]AAGGAGGGCGTCGTTCTCGGCGCGTGCGGCGTCCAGCTGCCGAA
TP72150	TGCAGCTTCTTTCTCAAGCTTCTCAAGGCGGCCAACATCCTGGG[G/T]GCCTCTCCCGCGTCCAAGG
TP72168	TGCAGCTTGAACACGGCCTTGGCCTTGCCGCCGCCGCGCCACCGCGACTTGAACATGT[C/T]GG
TP72230	TGCAGCTTGACG[C/T]AGGCGCTCATCGGGCGCGAGGTGTCGTGCGGGATGAGGTCCTGCGCGCCGA
TP72235	TGCAGCTTGACGCTGATGCCGCGGACGTCAAAGCTCGATT[C/G]AAATTCAGCGTTCTCGATGACAT
TP72236	TGCAGCTTGACGTGGTTGTAGTACCCCACCCC[G/A]AGGAAGGCGATCCCGTAGCCGAAGAGGTTGA
TP72251	TGCAGCTTGAGCAGTTGCTGTTGCTT[C/T]AGCAGATGGAACTGCAAAAACCAACGGGGGGAAGCGA
TP72255	TGCAGCTTGAGCCGCTGGGGGGATCCCTTGCTCAGGCAGTAGCGCCTGCACACCTGC[C/T]CATCAG
TP72258	TGCAGCTTGAGCGAGATGCCGCGGACGGGGCCGCGCTGGATGCGCCGCATCA[A/G]GTGGGTGGTGA
TP72262	TGCAGCTTGAGCGGGCACGTCGCGGCCAGCTTGCACTTGGTGACGTGCGCCTGGTACCT[C/G]ACCT
TP72267	TGCAGCTTGAGCTCCCACTGCCCCTTGGGCGGCGTCGGCGACGAGGC[A/G]GCGGCGGTGGAGGCGC
TP72308	TGCAGCTTGATCTTCTCGAAAAGGAACTGCTTCTCTGCCTCCGCCTCCTCCAGGCGCCGCT[A/T]CA

Table A2 (cont.)

TP72317	TGCAGCTTGATGACACGCATGTTACTGAGCATCTCGGTGATGTCTTCACGCGGCTGTC[A/G]CGGAC
TP72333	TGCAGCTTGATTCACTTCAAAT[C/T]GTGCCAATGCGATAGATAGGAAAGAAGCTATCTGAAATCGA
TP72356	TGCAGCTTGCAGCAC[A/G]GAAACAGGTGCATCCCATGGATGATGTATCCATTCTGTCGGTAGCCTT
TP72359	TGCAGCTTGCAG[C/T]AGCATCGGCGCCGCAGCGGTCTCCTCTCACCGCCTTCGGGTGCGGTGCTAG
TP72360	TGCAGCTTGCAGCCTTGCTCACCGATGCCATGCGCTCGCCGTGTTCAGCGAACTGAG[C/T]CAAAGC
TP72379	TGCAGCTTGCAGTATATATATTTGCTGTTAACCTGATTCCATTTTGCCATATT[C/T]GCTGAGAAAT
TP72395	TGCAGCTTGCCAACGGCGGCA[A/G]CCTCCTCGACGCGTGCGTCAAGGCGAAGGAGCCCTCGTCGTC
TP72419	TGCAGCTTGCCCTCTGTGCT[A/T]TCTAGCGAGGCCTTCAAGCTCTCCACTTCGACCCTTGCATTAT
TP72423	TGCAGCTTGCCGAGCAGCGACTGGATCTCGAACTCCATGGACTTCCAGGAGGAGCGGTCGGC[A/G]G
TP72441	TGCAGCTTGCCGTGTTGTGTGCCTT[C/G]CTGTGTGATCGGCACGGCACACCAGCCTGTTTTAAAAC
TP72443	TGCAGCTTGCCTACAGCAGACGTGGCACGCAAACAAGCTTATATTACCATGCTAAT[G/T]CAAGAGA
TP72452	TGCAGCTTGCCTGTCTCCTTTTCCTGTCTCCATC[A/C]ATGTACCCACACACGTGGACACCATCCAC
TP72457	TGCAGCTTGCGACCAGACAGATAGATGCGTACGGCACGACCGCACGAGAGATGAGGCATGTGA[G/T]
TP72465	TGCAGCTTGCGCAATCC[A/T]GCTACCTTCCTCGTCCGCCTACTCACCCATCCAAACCCTAGCCGCA
TP72481	TGCAGCTTGCGCG[G/T]GGGAGAAGGGCGAGAAGCAAGGCTCGACCTGCGGCGCGGCGGCTGAGCTC
TP72488	TGCAGCTTGCG[C/G]TTGGGCTTCAGCTGGCGCGTTGGTGATGTTGGACTTGAACAGCGCGGCCTCC
TP72490	TGCAGCTTGCGGAGCTTGCAGAGGCCCTCGCCGAGCTCCATCATCGCGCCGCGGTGGTTCTGC[A/G]
TP72496	TGCAGCTTGCGGCCGATGCTCTTCTCCACGCATTGTAGTCTGCCCCTCAGGCCC[A/G]CTAAGCAGA
TP72511	TGCAGCTTGCGTATAGAAGATGG[C/T]ACAAGCAAGTCAAACTAGCAATCTATCATCATGATGGTGG
TP72541	TGCAGCTTGCTCATGACCCTCTTGTTCCGCATCAG[C/T]TCTGACATGCCCCAGCAGAGCGCTGATG
TP72551	TGCAGCTTGCTCTCCCCCTCCACGTCTGCGAAGTCGCC[A/G]TCCGCGCACTTGCTGAACCCACCGA
TP72559	TGCAGCTTGCTGACGGAGCATGAATGCA[C/G]GAAGCTACTCGCTGTAGCTGATGATGATCTCTAAT
TP72597	TGCAGCTTGCTTCCTTTG[C/T]AGTGCTCGTCCCCTGTCGCATTGGGCCTGTATGGGCTTGTCCCCT
TP72679	TGCAGCTTGGCAGCTGCGGCAGCGGCGTTGGTGGATGACGCCGAAGGCGGAGTAGAGAAGAG[A/G]G
TP72681	TGCAGCTTGGC[A/G]GGGTCGCGGCCGACGAGGACCAGGTTGAGGCCCCGACGTGCGAGCTCCAGCG
TP72716	TGCAGCTTGGCGAGTCTCAAG[A/G]GCATGGACGTGAACAAGAATGGCAGTACGGTGCTGGCCTTCA
TP72719	TGCAGCTTGGCGATCGGCGAGGGCGCGAACGCCG[A/C]GGGGAGCGCACAAGGTGGCGATCGGCGGC
TP72728	TGCAGCTTGGCGCTGCCCCACTGGATGGC[A/C]TCCAGCTCCGACGACGGGGGCCCCGCGGCCGCCA

Table A2 (cont.)

TP72732	TGCAGCTTGGCGGCGAAC[G/T]CCGAGTCCATGTCCGAGGTGTTGCTAGGCGGGAGGCGGTCCCTGC
TP72751	TGCAGCTTGGGATTGGGACGCGGACGCG[C/T]GCGGCGGTTTGGCTTTTACCAATGGATCGGAGTTC
TP72755	TGCAGCTTGGGCAGGCTTCCAGGCGAGCTCCCAGGCTCAAAATTGAA[G/T]GGACCTGTTGATCAGA
TP72756	TGCAGCTTGGGCAGGCTTCCAGGCGAGCTCCCAGGCTCGAAATTAAAGGGACCTGT[A/G]GATCAGA
TP72762	TGCAGCTTGGGCCGCGCAATCGTTAAGCCTGGAAGGCTGGAACTCGCGAGCTTGTTGGGC[C/G]TGG
TP72785	TGCAGCTTGGG[C/T]TCCACCGCGGCAGCGGCCGACGCGGCGGGGGCGCCGCGGAGCGCGGCGCGTT
TP72855	TGCAG[C/T]TTGGGTTCGGCCAGAGCCGTGAACCGCCGCTACATCAGCGACTGTGTACCCCTGAAAA
TP72864	TGCAGCTTGGGTTTTAGCCAGCTCCTTGAAAGTCTCGATGGAACTCGTCGGCTGGGCTCAACT[G/T]
TP72866	TGCAGCTTGGTAAGCTTGGTAATG[A/G]ATGGCGGCAAAGTGGCTATGGAGGTGCCCCTGACATCCA
TP72867	TGCAGCTTGGTAAGCTTGGTGAT[A/G]GATGGTGGCAAAGTGACTATGGAGGTGCCCCTGACATCCA
TP72870	TGCAGCTTGGTAGATTTCATCATCACGCATCACAAACTGCCTGCGCAA[A/G]CTCGTGCTTTTTCTG
TP72893	TGCAGCTTGGTGGCCGCCTGGTCCAGCTCCACGCG[A/G]GGGCGAGGGGAGATGTACTCGATCATGG
TP72898	TGCAGCTTGGTGTCGAGCACCTCGGAGCAGATCTTGCCCAT[C/G]GTCCCGTAGAAGGCGGCGAGGT
TP72912	TGCAGCTTGTAAGAAGTCG[C/T]GAGACGCTCTTTGAGGTGCGTGCACGAGAAGTTGGAGCCGCGCG
TP72914	TGCAGCTTGTACAAAGCCGTGGTATAATACGCCTTCACGTGGCGT[C/G]CCGCGGGCGCTAATTACA
TP72920	TGCAGCTTGTACGAG[C/T]TCACGAGCTGCTCTCTGAGATGAGCGCACGAGAAGCTGGCACCTAGCA
TP72930	TGCAGCTTGTAGGATGGACGCC[A/G]CTGATAGAACTGAAGAGAATAGCTGAGAAGGACAATGTCAA
TP72956	TGCAGCTTGTCCAGATATATAGACGATAGCAGATATTTGGCCTAGCTGAAGAAACTCTGCTT[A/G]A
TP72964	TGCAGCTTGTCGAAGCTCCT[C/G]GCAACAAGATCATGCAAATTAAACACGTTACTGATTACTGAAT
TP72968	TGCAGCTTGTCGAGCTTGGCG[C/T]TCATGTTCCTCTGCTGCTCACTGACGGAGCCCTCCTGGGCCC
TP73010	TGCAGCTTGTG[C/T]GCGTTCTGGTGGCCGCCGAGCGCCTGCGAGCTGCGGAACTTCCTGGGGCAGT
TP73017	TGCAGCTTGTGCTCCGCCAACCGCTCCTCGTTCTC[A/G]TACTTCTCGGGGCAGTGGAACTTGGTCT
TP73021	TGCAGCTTGTGCTTTTAGTTAATTAGACGAAGCAAAT[G/T]TGACTTCTGCAAGCCACACTAACAAG
TP73036	TGCAGCTTGTGTCTGGAACATGGGAACATTGAGATTTGAGAAGATAG[C/G]AGTCTATCACAGCCAC
TP73053	TGCAG[C/T]TTGTTAGCCACCTAGCGTGAACGATTTGTTCAGGATAAACCAACAGATGAAGGAAGCG
TP73064	TGCAGCTTGTTCGGCT[C/T]GATCGTGGATTATAAGCTGAAATAATATTTTCTCTCGTACCAAATCA
TP73084	TGCAGCTTGTTGCGCCTCAGCTGCCACA[A/C]GGCGCTGGGCCGCCCGACGCGGATGCCGCCGAAAA
TP73104	TGCAGCTTTAAAGCAGGGGAGCTAGAGCCCAG[G/A]GGCCAGAGCAACAGGAGACGAGACGAGGCCC

Table A2 (cont.)

TP73155	TGCAGCTTTATGATAC[C/T]AAGTTGTTTTCATATGACAGTTTCCAACAGGTCTGGCGTTGCTTATC
TP73178	TGCAGCTTTCACTAGT[A/G]GTACAACTGTTAGGCGTGGTGGAGACTGGAGAGCACGCCCACGCAAG
TP73225	TGCAGCTTTCCTGGCGGCCTGTCGGGTTGGAAGTCATCAAACATATCAGTGATCTCGTA[G/T]GCCG
TP73228	TGCAGCTTTCCTTAAACAAACATTTTTACCGTA[C/G]CCCGCTCTTTATTCTGCCCCCAACGCGGCG
TP73237	TGCAGCTTTCGCCATTGACACTG[C/G]CCCCGCGTGAACCTGGTTGACCAATGCGCATGTGAATCA
TP73244	TGCAGCTTTCGGTTGCTGCTGCTGCTCAGCCGACGCCTCCCGCGCCTGCCGCGA[C/T]CGCAACAGC
TP73246	TGCAGCTTTCGTCGCTGATGCTAGCCGCGGAGGATGACGACGTCGGCGTG[C/T]GGTGGCTGCGCCA
TP73264	TGCAGCTTTCTCCCAC[A/C]ATGCAACACCCTTCTTCTTCATCTACATTACAAAAATTAAGAATACA
TP73285	TGCAGCTTTGAAAACTGAC[A/G]CAGCGCTGTTGACCCCCGACCCCAACGGTTCCAGGGTTCAGGAG
TP73295	TGCAGCTTTGAATGCGCAGGGCTCGGGCACAAAACCTTGTCGCCTTTTGGACACCTCGG[A/G]CACC
TP73296	TGCAGCTTTGACAAAAACATCTTTCT[A/G]AAAATCAAGTGGGAAGGCAAGGAACATGATCCAAGCT
TP73301	TGCAGCTTTGACGTGCAGTGCAGACATGACGTGGCTGCGGTTTTGGTCG[A/G]TCCACCTCACCTAC
TP73303	TGCAGCTTTG[A/G]CTCATTGCCTGCTGGCGGGCGTCCTGCACTCCTGGCAGCGTGTTCTTGCTCGT
TP73317	TGCAGCTTTGCAAACTGCGAGCTACGGTCGATGGTGTTGGTTGACAGAAGGTCAGTTTTG[C/G]CAC
TP73334	TGCAGCTTTGCCCTCTGCTTTTATTCCTCCTGGAAAACCTCGA[C/T]CTGTCCGCTGCGGCCTGCGG
TP73363	TGCAGCTTTGCTAGTAGGTTCTTGCCTATGACGAAAAAGACAAATAATTGGTCTAC[C/T]TAATTTG
TP73385	TGCAGCTTTGGAAAGATCAACCATAATTGACCGTGAAACAACACAA[C/T]GAAACATGACAGTAACC
TP73387	TGCAGCTTTGGACCTACTACACTCCATCATTACATATACGTGTAGTAATATTCCACGCCATGC[A/G]
TP73412	TGCAGCTTTGGTTTTGTGCAAACACCAGGACATGTACGCCGCGGACCCGACGACAAAGTAC[A/T]GG
TP73420	TGCAGCTTTGTCA[A/G]CTGGCCTCTTGCATTGTTTGAGCAACACCCATCTCTGATGATTGATATGA
TP73503	TGCAGCTTTTCGGCGAAATGCGCGTCGAATTTAGCCGCACAAGTACCAAAGCTTCA[A/G]CCGAATT
TP73510	TGCAGCTTTTCTCTCTGCCGAATGAAAAA[A/T]TAAATTGGATTTGGAGCACAAAAGGCTCCCTCTC
TP73513	TGCAGCTTTTCTTCCTCCGCTCGCCACGGCCACGGGTCGTCGGACGTCGGGTCAGCGGAG[C/T]TGG
TP73530	TGCAGCTTTTGCTCTTTTGGCAGTCGGC[A/G]CACACACATCGCTGCATGCTCACGTTTTTGCAATT
TP73541	TGCAGCTTTTGTCACCGAATTGTTCATGTA[C/G]AGCAAGTCATGCACGCATGCAGCATACGGCCAG
TP73566	TGCAGCTTTTTCCTTAAGCTCGAATC[G/T]TGCCACGAATGACAACTCAGTGTCTCCACCAATGGCA
TP73621	TGCAGGAAAAAA[A/G]TAAGGTGGCATGGCCCCAGTTGAAACCGTGCTTGTACAAACGGCGATGAGC
TP73628	TGCAGGAAAAA[A/G]GAACAGCACATTGTTCACTCGTCGAGCGAAGCAGGGCCTTGCCATGGCCGTC

Table A2 (cont.)

TP73647	TGCAGGAAAA[A/G]GGAGATGGATCGATCGATCGCGCGCTTACTTAATAATTAGACAGAAAAGAAAA
TP73666	TGCAGGAAAACATTTAGCGTTTGGAGTTCCTCAAAA[G/T]CCTCTTGTGAGATGGGCAGAGCAAAGA
TP73707	TGCAGGAAAAGGAGCGGGGGTATGGGGACGGGGAG[C/T]TGAGGGGAGTGGGCCCAGTCAGTGCAAG
TP73709	TGCAGGAAAAGGCCGTCAAGCTAGAGGGCCATGGACCTACGACA[A/G]CCTATACGTGGAAAGTCTC
TP73721	TGCAGGAAAAGTGGG[C/T]CACGCGGCTCGGACTCGGAGCACGCGAATACGCGAGATGGATTCCTCC
TP73741	TGCAGGAAAATGTATATCATGCTTTACAGTTCCCAATTTCCCAAGACATGGAACCTGTA[A/T]ACTA
TP73770	TGCAGGAAACACAGATTGACATTAAAGGATAGTC[A/G]CACGCGTATTATACGAGAAGAAAGACAAA
TP73771	TGCAGGAA[A/G]CACAGCAGCAGCATTAGTTTCAGTTTCAGCTTCGCTGCGCGCCACCGCTGCTGGG
TP73803	TGCAGGAAACCAAGGAGGATATAGGTAGCGATAGCACACTCATAGTGATGGCGAGGTGG[A/G]TTCC
TP73804	TGCAGGAAACCAAGGTGGGAAAGAGAGTCAGTTAGTTACATTACATATGC[A/G]CAAAGACTGGAAG
TP73812	TGCAGGAA[A/G]CCGTGGTGGCGGCGACCACGGGAAGCGTGACAGCCAGCTTGCGGCTCCCCGAGCA
TP73823	TGCAGGAAACGAAACAAGAAGTGCAATTCTACATCAGTTTCCATTCTCCCTGTGGCTTATAT[A/T]T
TP73848	TGCAGGAAACTCATGGCCACGGCGCCCCCCAGG[A/C]AGACCACGGTGCCGAGGATCTTGGCCCTCG
TP73861	TGCAGGAAACTGTTAGCC[A/G]AGTTGCTGCACGTCGCCAGAGCCCCGCGTGGAATCTGAGCTGAGG
TP73863	TGCAGGAAACTTGTAGA[A/G]ATTGTTTTACCACCATGGGAACCACTGGGACGCTGCGGTTGCCATG
TP73881	TGCAGGAAAGAGTCGAGAGCACTCCTCGCGCTT[C/G]AGGTCCAAGTATGCTATGCACTGTGGGTAG
TP73885	TGCAGGAAAG[A/C]TCATGTGAGCTACCACGGCAAAACAACTCGGCTTCATTACGAGCTCACCTCAA
TP73903	TGCAGGAAAGCATCCAT[G/T]CTAAGTGACGCTAAAGCCAACAGGAAAGCACCCCTGGCCTCGTCGG
TP73912	TGCAGGAAAGCGATGGGTCGGGCGAAGCAGCAGGA[A/G]GACGGCGATCGAGCTGGCGTCGCAGCGC
TP73924	TGCAGG[A/G]AAGCTGCATCGCGATCGCGGCCGTTCCGACATGAGATTGTCCTTGTCCGTATCCGCC
TP73966	TGCAGG[A/T]AAGTCCAGCTTGTATGCAACTTGCCCCACTCGCTGTAATATCTTGAACGGGCCATAG
TP73993	TGCAGGAAATCACTCGCGCGGGGAACGAGTGGTACAAGAAGGGCCGCCA[C/T]GCCGAGGCGCTGCG
TP74006	TGCAGGAAATGAACGGCTA[C/T]GATGCAGCAGCGGGATACGTGGATGATCTGAGTCGCCATAAGGC
TP74021	TGCAGGAAATGGAAATCCACGGCG[A/C]AGGCTTTGATTTGCAGTTCGGCCATTGGCCCGTTAGCGT
TP74025	TGCAGGAAATGGACACCCTGCACCGCTGCGTCAAGGAAACCCTGCGCCTCCACC[A/C]TCCCGCGCT
TP74034	TGCAGGAAATGGGAGGA[C/G]GGCGAGACGGAGGCTGCCACTGGAGATAGGAGGAGGTGAGCAGGCG
TP74035	TGCAGGAA[A/G]TGGGGGCATGGCCATGCCCCACGTTGCAGGTTGAGAGCAGTACTATTTGGTGGTA
TP74069	TGCAGGAAATTGCTGGCCATACTCGCTCTGGGCCCGCACAGTCGAGCAAGACACT[A/G]AACTTGGC

Table A2 (cont.)

TP74101	TGCAGGAACAACACGTCGCGGTCCCGCTCGGCCGCCGCGGCGG[C/T]GGCGTCCGACGCGTGCTGCT
TP74147	TGCAGGAACACCAGGCCGTCGCCGCCGAACGCC[G/T]CCGCCATGGCGCCCTCGTGGAGGCCGAGCC
TP74149	TGCAGG[A/G]ACACCATCGGCGCCGCCGATCGCCGCAGCGAAGACGAGATGGCTTCTTCGAGAAGAC
TP74156	TGCAGGAACACCTAACTACTGGATCTA[G/T]AGGTTTGTAAATTACATGGATCTAGAGGCCAGAACG
TP74164	TGCAGGAACACGCGCCGC[A/G]CGGCGTGCTCGGGGAGCCTCCGCGACGGCAGGGAGGCGAGCCGAA
TP74165	TGCAGGAACACGCGGAAGCTGCGCAGCTCGTCGTGGATCAC[C/T]GACTTGCACTGCGCGTACGCCG
TP74166	TGCAGGAACACGGTGGCAGAGTG[A/C]GCGATGTACACTAGCGCAACGAGGAGCGCGAGGCGAGATT
TP74167	TGCAGG[A/C]ACACGGTTTGTCTGTCCTGGAGCGTGCAAAGCACAAATTGGTGTTGTGCTCCGTGCT
TP74169	TGCAGGAACA[C/T]GTCGACGGCGTCCAGCCACGCGTCGCCGAACGAAGGGGCGGTGCACGCCGAAA
TP74176	TGCAGGAACAGAAGCGCGGCGAGCAACGTAGCCCCGCACGGTATGGCGACGTCCCACG[A/C]GACGC
TP74190	TGCAGGAACAGCAGCACGGCCAGCAACGCCACCCCGA[A/G]GAGGACGGCGACATCCAGCGCGACGC
TP74198	TGCAGGAACAGCGCCCGCCGCCGCTGCCGCTCCACCGCGCCCAGCGGCGCGTACCCCGCGG[G/T]CT
TP74206	TGCAGGAACAGGAAAAGAAGAAAAGAGCATGTGAAGCAGTGCATGCCGCCAAGGAGAAAAG[A/G]TG
TP74212	TGCAGGAACAGGAGGG[A/C]GTTGTGGTAGATCGCCTGCCCCGTCAGCGGCGCCACGATCACGGGGA
TP74230	TGCAGGAACATAATTA[C/T]ATCAGTTACTAGTTCGCCAAGTTCACTAATTCACATTGCTTGCCAAA
TP74231	TGCAGGAACATATGTCTTCCTTG[C/T]TCGCCGTGCAACAACATTTGCCGTCCGCCGACAGCGTATC
TP74233	TGCAGGAACATCAGTTCGCACGAGTTTCGTTGTATCCCCGACTTAATTGGGCACCAAGAACT[A/C]A
TP74270	TGCAGGAACCAAACCACGGAGTCATCAGTGATTCAGCATGACGTACTTGAACAAGAGAGATG[C/G]G
TP74281	TGCAGGAACCACGGAAGCTGTGGCTGTGGCTGCTTCTGCTGCTCCTCCTCCCCCTC[C/T]TGTGGCG
TP74299	TGCAGGAACCAG[G/T]GACCCCACAGGAGGTAGCGCAGGGGCCCTTTCTTGGGGAGGTGGATGTCGG
TP74313	TGCAGGAACCCCGA[C/G]GGGGTCTGGAAGAGGTCGCTGGTGGTGAGCGGGAACTCGCGGGCGAGCG
TP74316	TGCAGGAACCCCTGTAGGTAGTCGGTGATGCTGGAGTACGGC[G/T]GCATGAGCTCGGCGGTGGCGC
TP74322	TGCAGGA[A/T]CCCGCAGAGCTGCACCTTGATGCCACCTGCTCGACGAAACGACCGACAGCAGGGAA
TP74330	TGCAGGA[A/G]CCCTCCCGCTGTGCCGTGCTCGCTTCGCCTTCTCCATTCCACCGCCGCCGCCGCCA
TP74332	TGCAGGAACCGAAGC[A/T]GCCGAAACGCGGCGGGAGGCCTCGGAAACGCGGAGGAATACACGAGGA
TP74335	TGCAGGAACCGAAGTCGTCTGGACCCTC[A/G]CTGGGGTTGCGTCCCAACCCTGGTTCTCGTCTTGT
TP74357	TGCAGGAACCGTTGATCAAGACAGCGCCA[C/T]GTCCCCGCCAAGCCCGTCGTATCGATGACTCTGT
TP74373	TGCAGGAACCTCGGCGCCGCCGACCCCAC[A/G]GGCAGCACGATCACCCCGTTCGGCGCCTCCCAGT

Table A2 (cont.)

TP74378	TGCAGGAACCTGAACCACTCAGGCAG[A/G]GGGAAGAGCAACCGTTTGTCGTCTGCATGTTCCTTGA
TP74386	TGCAGGAACCTGGACGG[A/G]TGCTTCTCCTACCTCGAGGAGCTGATGGCCAGAGATGGGCCGTTCG
TP74387	TGCAGGAACCTGGCGTACTCCGAGTACTCCCCGTCGCCGCC[A/C]GCCAGCGCCAGCGCCTGCGACT
TP74389	TGCAGGAACCTGTCCCTATTCATACCACGCCACTCACTACCGAGTTCCGC[G/T]TACGCATCCTCCA
TP74392	TGCAGGAACCTTGACACCGCCATTATCAAGTCGGCGTGTGC[G/T]GCAAAACTTGGACAACCAGCTT
TP74397	TGCAGGAACGAACGTGCGCATAATTG[C/T]CGCTCGGGGCAACGTGCAAGTTTCTTTCCATTCCACT
TP74398	TGCAGGAACGAAGAAGGAAG[C/T]TTTGGCTCTCCGACAATGCGGAGATAGGAATCTACCTGTTTAA
TP74410	TGCAGGAACGACCAGCTCGGGATACTCGGAACCAACATGGGAGCAAGATGCAGCTTATGA[C/G]GCA
TP74430	TGCAGGAACGAGAGCGACATCGATGACGCTTCCATCG[C/T]GGCGTGAAGCTGGGTGGCCGCAGCGC
TP74455	TGCAGGAA[C/G]GCCCTCGGTGATGGCCTCCTAGAAAGAGAGCTGCCTCACTGGACACACACCTGTC
TP74459	TGCAGGAACGCCTCCGCTAGCAGCGACAGGTTGAGTGCTAGCTCCTCCCGTGTGTC[C/G]TGGCTCC
TP74465	TGCAGGAACGCGAGGTCCTGGCGGCGGCGGCGGAAATCGATGAAGAAGCGGCCGCGC[A/G]GGGCGC
TP74469	TGCAGGAACG[C/T]GGCATCCTCGGGGCAGTCCGACCAGGTGGCGACGCCAACGTGGGCGAGCACGA
TP74486	TGCAGGAACGGAAAGCAGCGGGCCGATTCAGATTGTTGC[A/C]CCGCCCAGGTGGGGTCAAAATACG
TP74491	TGCAGGAACGGAGAGAGA[A/G]AGGCTCAGGAAAAATCATCTGGGGTCGCAAGAGATTGTGGTCCGA
TP74515	TGCAGGAACGGCGCCACGGCGTCGGAGTTCATCGCGCCCAGG[A/T]TGGCCGACGGCGGCGCGGACG
TP74522	TGCAGGAACGGGAACCAGGTGTGCCACTTGTCGGTGGA[A/C]CCCGAGGAGTAGCCCAGGATGTTGC
TP74525	TGCAGGAACGGGCAGCTGGAGCACCCGCACTTCATGGAG[C/G]TCGCGCAGCACCCGCACCAGCCCC
TP74542	TGCAGGAACGTCTCGCT[C/T]TGCCCCGACGCGATCAGCGCCTCCACCGTCCCCTCCGCCGCCTCCT
TP74543	TGCAGGAACGTCTCGCTCTGCCCCGACGCGATCAGCGCCTCCACCGTGCCCTCCGC[C/T]GCCGCCT
TP74549	TGCAGGAACGTGGGGTCCGTGCCCTCCGACGGCAACAGCTCCCC[C/G]CCGCGGAAGTACGGGTGCA
TP74573	TGCAGGAACTC[A/G]ATGCCGAAGTTGGCCAGCGCGCGGTTCAGCGCCGCGCCTTCCTTCCTGAGGT
TP74578	TGCAGGAACTCCAGCAGCGGGAGCAC[C/T]AGGTGGCGGTCCAGGTGGAGCGCCAGGCGCGGCGTCA
TP74587	TGCAGGAACTCGAGCAGGAACGCGCCGTCGACGAGCATCATCCACGCGAGCGTCTC[G/T]CCGCTGA
TP74591	TGCAGGAACTCGATCCTGGCCCCGTCGTCGTACTCGATCGCGCTCGGCGTGTCGGGGGCG[C/T]CTC
TP74592	TGCAGGAACTCGATCTCG[G/T]TGATGAGGTGCTCGCGCTCGACGGAGAGCTCCTCGGCCTGCCTGT
TP74596	TGCAGGAACTCGTACTCGAC[A/G]CCCTTGAGCTTGAGCGCCGCGAACACGCGGATGGCGTAGGGGC
TP74597	TGCAGGAACTCGTAGTCCAACG[C/G]CCTTGAGCTTCAGCGCCACGTACACGCGGATGGCGTAGTGG

Table A2 (cont.)

TP74602	TGCAGGAACTCGTCCTCCTCGTCCAC[C/G]TTGTCCTGCCCGACAACCTTCACCGCCCAGGTGCTCA
TP74629	TGCAGGAACTGCGCGAACCCCGT[A/G]CCGTCGGCGACGATGTGGTTCCGCGTCACGCCGACGACGA
TP74631	TGCAGGAA[C/T]TGCGCGGCGACGGGAGCGGCGAGCGCAAGGCGTTCGAGCGCGTCTACGACTACGA
TP74641	TGCAGGAACTGGA[C/T]GCCAAGTATGTGATCTCAAGCAGGAGCAAGGAACGCTATGTCAGCCCAGC
TP74650	TGCAGGAACTGTCCTTGCCTCTATTGT[A/G]TACACCATCACCATGGCACCAGGTGTTGGCACCTAC
TP74651	TGCAGGAACTGTCGCGCTCCATCCTCAGGGGAGCT[C/T]GATCTAGAACGAAATCTCTCCGATCCCA
TP74679	TGCAGGAACTTGGACACAGCATAGACGGCGAGCGGGTCGTC[A/G]TCCCTGACGGTGGCCTGGATGG
TP74699	TGCAGGAAGAAACGTGTTGGCACAGTGTGCATCTGCGCGTCACTGTTGCAGCAAGC[A/G]GCAAGCA
TP74712	TGCAGGAAGAACCTTGTTCATCGC[C/G]GCCATGCGTTTCTCCATGGTGGACCACTGTTGCCGTCGT
TP74717	TGCAGGAAGA[A/T]GAAGATGGGGAGGTCCCCGTGCTGCTGCCACGACGCGGGCGTGAAGAAGGGCC
TP74740	TGCAGGAAGAATCATCGTTCGCGGGCAAGCTGTCGTTTTCGTCTGAGCGAGCAG[A/G]GGAGACCAT
TP74753	TGCAGGAAGAC[C/T]TGGTGGAGGAGGCGAGGGGCGCGACCGCGACCGCGCGGAAGGCGAGAGGAAC
TP74754	TGCAGGAAGACCTTCCCGA[C/T]GGGGCAGGCGCTGGGCGGCCACAAACGGTGCCACTACGAGGGCA
TP74766	TGCAGGAAGACTATAATACATTTGTAAGTGAATTTGCGGACACATGGTC[C/G]ATATGTACCCATGT
TP74776	TGCAGGAAGAGAAGGCGGAGAGGCGGGCGCAGGGCGCTGGCGCGTCGTCGTCC[C/T]CGCGTCTGCG
TP74784	TGCAGGAAGAGCAGCTTATCATCATCGCCCTGAGGTCCATATACGCAAGTGAGC[C/T]ACCATGCTT
TP74800	TGCAGGAAGAGGAAGAC[C/T]TGGTTAGTGCTCATAGGAAGCAGGTTGAAGAGACTCTGGACATCCT
TP74817	TGCAGGAAGAGGGAACGAAGAAACACATGGATGG[A/G]CCATGGGTGAGGAAGGATCATCAGGACGA
TP74826	TGCAGGAAGAGTTGCTCCTGGAGCAGTTCAGT[G/A]GTTTGATCAAATTCGTCAAATCTCGTCCAGG
TP74855	TGCAGGAAGATGGGCAAATACACATGATGTCTTTGATTTTATGTTCATGTGCTACTA[C/T]ACAATA
TP74879	TGCAGGAAGCACAGGTGTGGCTACCTCATTCAGAGTAGCT[C/G]GAGCAGTGGCCAGCGTAGTGGTT
TP74883	TGCAGGAAGCACCAGAGGAGGTTGAGTACGGCGACGGCCCAGAGGAGCGCGTAGTACGCGAC[G/T]A
TP74887	TGCAGGAAGCACGACACCAAACGAATGAGAAACCTTTCCACCCC[A/G]ACCCAAACAAAGAAGAAGG
TP74901	TGCAGGAAGCAGCATCC[A/G]CCGCCACCATGTCCGTGCTACCCACCGTGGTGCCACCTCCTCACAC
TP74904	TGCAGGAAGCAGGACCCCTGGGCGATGCTAGCATGGGC[A/G]TCGGGTGACCCGCCGCTGCCGCCAC
TP74919	TGCAGGAAGCATGA[C/T]ATTGAACCCAGGAACCCTGACAGCTACTTCAACCTCAAGAGAGATCCCT
TP74936	TGCAGGAAGCCA[A/C]GCTCGCCAACATGGCCTACGGGTTCGCCTACATCGTCGACTGCAAGCGGCT
TP74939	TGCAGGAAGCCA[A/G]TGACGGAAAGACTTGGGCCGATTACCACATTGCTGTGACCTGACCATGCGA

Table A2 (cont.)

TP74964	TGCAGGAAGCCCCTCGCCGCCACGAACGCCA[C/G]CAGGTGGATCCCCATCGACGACGACTGGACCG
TP74965	TGCAGGAAGCCCCTCG[G/T]TGATGGCCTCCTAGAAAGAGAGCTGCCTCAATGGACGCACACCTGTC
TP74980	TGCAGGAAGCCGCAGAGCTGGACCTTGATGCCACCTGCTC[A/G]ACGAAACAACCGACAGGGAAGGA
TP74982	TGCAGGAAGCCGCGCACCAC[A/G]GCGTCACGTGTGCGCTGCGACGGAGCCGTGAGAGACGGAAGCA
TP74985	TGCAGGA[A/G]GCCGTCTGGGATGCCGACATCGTCGTGAATGGGGTGCCGTCCACCGAGACGAGGGA
TP74989	TGCAGGAAGCCTCCCCC[G/T]CCCGTCGCCGCCCCCGCCACAGAGGCCGACGCCGCCGCCCACCGAA
TP74991	TGCAGGAAGCCTGGCTGACATCTTTGTCAAGCGTCCAACCAAGCTTGA[A/G]CAGGCGAAACTGGCT
TP75010	TGCAGGAAGCG[A/G]TCCACGGCGCCGTCGTCCGCCTCGGACTGCATGACGAGGAGCGCGTTCATGG
TP75013	TGCAGGAAGCGCAGGCAGGACGACGGACAGC[C/G]GCCATGGCTGGAGTATGTATCTATGGGTCGTT
TP75014	TGCAGGAAG[C/T]GCAGGCAGGACGACGGACAGCGGCCATGGCTGTTGTGTATCTATGGGCTTGTGA
TP75018	TGCAGGAAGCGCGGCATCAGCAC[C/G]GACTTGATGGCGGCGCACACCTCCAGGACCAGCTTGTGGC
TP75028	TGCAGGAAGCG[C/T]TTGAGCTCCACCAGCACCTCCTTGTCGTCGTTGCCACCGCCGTCGCTCTGCC
TP75040	TGCAGGAAGCGTCGGTTGCAAGCAGACGA[A/G]GTGAAGCAAGAAGATCGGGCGGCGGGACCACGGC
TP75072	TGCAGGAAGCTCAGTAAC[A/T]AGCAGTCACCATTTACTGAGATGTGTATGTGTACACGGTACACCC
TP75074	TGCAGGAAGCTCATGGCCACGGC[C/T]CCCGCCAGGCACACCACTGTCCCCGCTATCTTCGCCTGCG
TP75094	TGCAGGAAGCTGCGCCGAATCAGACCACCAGTCCGT[G/T]CCTTCTAGATCGCGCTTTGCAGGGGAG
TP75098	TGCAGGAAGCTGGTTGAGGAGAAGGCGTGGCGCGC[C/G]TACTGCAACGGCAAGGGCTGCGGGTACG
TP75102	TGCAGGAAGCTTGAAACAGCAAACACAACCTATGGCCACTATAC[A/C]TCCATGCATGTGTGATGTG
TP75136	TGCAGGAAGGAAACCGCGTGGACGA[C/G]GCCGTACCTGAACGTAGGCAGCTCGATCGATCATCATG
TP75158	TGCAGGAAGGACAGTGCCTTCTCT[A/C]CAGTAGTGCTAAGACTCCTTCCGCCCTGGAGGACGAAAG
TP75171	TGCAGGAAGGAGACCATGTGGACGAGGCCGTACCCGAA[C/G]GCAGGCAGCTCCATCGATCATCATG
TP75172	TGCAGGAAGGAGACCGTGCGGACGAGGCCGCACCCAAATGC[A/T]GGAAGCTCGATCGATCATCATG
TP75179	TGCAGGAAGGAGA[C/T]GGCGCGCACGAGGCTGTACGCGAACGCCGCTCCGATGCACAGCACGGCGT
TP75188	TGCAGGAAGG[A/G]GATGAGGTACGAGGCCATGTGCGTGCGGGACCGCATGGACAAGGAGGGGATAC
TP75189	TGCAGGAAGGAGATGGAGAGAGGTGAGCGA[A/G]GTGGTTGGCTGGCAGTTGGATCAGAGGCCATGC
TP75194	TGCAGGAAGGAGGAC[A/G]ACGTACGAGAGGGCAGAGCTCGAGGCGCTCAGGGACGCCCCGTCGAAG
TP75221	TGCAGGAAGGCATCCCTCCTGCCGACGACGTCCCTGATCTTGTTCCTGACGCC[A/C]AGCACGTCGA
TP75224	TGCAGGAAGG[C/T]CCAGTGCAACGGCCGCTTCTTGGGGTCCATCATCTGGCTGCGCCTCAGCTCGA

Table A2 (cont.)

TP75226	TGCAGGAAGGCCGCTGCCGCTCCGTCGAGCCCTACATCATCTCCGCCCGTTCCCCGTC[A/G]TCAAA
TP75230	TGCAGGAAGGCCTTGGAGAGGAGGACCTTGGTGCCCACGCGCTTGTC[G/T]TCCCAGCTGAAGGTGA
TP75231	TGCAGGAAGGCGAGCAGCACATCCCTGGTGCGCTTCCTGGGGTCGCT[C/G]ACCGACGCGCCAAACT
TP75233	TGCAGGAA[G/T]GCGATGAACTCGTTGAAGTTCTCCTCGGTGGGGAGGTAGTGGCCGCTGTAGGGCC
TP75239	TGCAGGAAGGCGGGGG[A/G]CCACGAAAGGGCGGTCCACGTCAGGGCGCCGAGCTGGAGGAGGTGCG
TP75243	TGCAGG[A/G]AGGCGTCGAGCAGAGGTAGTCGTGGAGAAGCTTGGCGCAGCGGCTCATGAGGTTGGA
TP75257	TGCAGGAAGGGATGAGGCTAGGCGATCGAGGTC[A/G]AAAACCTGGTGGCCGCAGCGAGGGCGAGGC
TP75261	TGCAGGAAGGGCACGAGCGTGCCAACGATGGTGGAGAGCGACCCCGACAGGTCCAT[C/G]TTGAGCG
TP75286	TGCAGGAAGGTCTGCAATTCTTCGATCAGGAACT[C/T]GACTTTTGTGGAATGGGAAACAAAAACAT
TP75295	TGCAGGAAGGTGTCCGATACGCCGACGAAAAACGTGGCGG[C/T]GGCCCAGAGGAAGGCCCCGACGG
TP75306	TGCAGGAAGGTTTCTACACGAGCAACACCAATTGCAC[A/C]GTCGACGTCGAGGCCACCGTAGGGAG
TP75311	TGCAGGAAGTAACAGGAGGTTCGGGTAGCCCCCAAAGTGGAG[C/T]TCTCGGAGGGAGGTGAGAAGC
TP75328	TGCAGGAAGTAGTGACGGCGCGTGTCGGCTAGCTAT[A/T]TATACGACTGTTTGGTTGGTGAGATAT
TP75345	TGCAGGAAGTCCTGATCGTTC[A/G]GGAGGAGAGAGTGTTCGAATGGTGGCTGAGAACTAGGAAGCT
TP75357	TGCAGGAAGTGAGCCCCATACCAACCAGCATGCTTCACTG[C/T]TTCTCAACCTGAAGCTGGTCACC
TP75367	TGCAGGAAGTGCTCCTGGGGAAGGAGGTGGTGGTACTCCAGCTCCACCTTGCAAGGGTA[C/G]CTGT
TP75378	TGCAGGAAGTGTACAGAAGGGTGTCGATGTTCTGGGTGCCGCAA[G/T]CCGTGCTGTGCCACTGGAT
TP75386	TGCAGGAAGTGTTACGCTCCACCTGGTCGAACT[A/G]TAGTCGACCTCTGACCAAGCGATGCGCGTG
TP75418	TGCAGGAATAAATGCAGGCAGCTTGGCAAAGCAGAAATCTC[C/T]AGTTAGACAAGAAGTGTCCACA
TP75442	TGCAGGAATAGCCGCATAGCTCCCCTACAGCAGGTCTCCACAA[A/G]AGCGCGGCGTCCATGTCGCA
TP75476	TGCAGGAATCACACGCTGATGTAGATCCTGATGAGGCGCCAGATGAGCACCAATTCAGCA[C/G]GAC
TP75479	TGCAGGAATCACGCTGACTAAGGTGAACGAATCTGGTTTCACATTTTCCA[A/T]CTGCATCCTAGCG
TP75487	TGCAGGAATCAGTGTCCCCTCTTCAATCCGTGCAGCCAGTGGGTGCGAGCAGGA[A/T]GGCCACACC
TP75494	TGCAGGAATCCAACATCCGTCAGTCTGAAATGTCAATCAGAAGCAGTGCCAAGACCTGTTCA[G/T]T
TP75507	TGCAGGAATCCTTAGACCAGAAAAGAAGAGCCTTTGAAGGACCTTAC[C/T]GTTCAAAGCTAATGCT
TP75513	TGCAGGAATCGCATCGATCGAGACGCA[C/G]GGGTCAGCGTCTAGCAAGCACACGAACGCGGCGCAA
TP75520	TGCAGGAATCGGGGGATACGGCTGGA[A/G]CAGGAAGTCTCTGCCACGCACTTGTGCTTACTTTGCC
TP75521	TGCAGG[A/G]ATCGTACATAAATGGGAATTATTCAATTTTCCTTAAAGAAAACTTAACACAGTAATG

Table A2 (cont.)

TP75528	TGCAGGAATCTGAATCTCGAGCGCACGCCGCGCGGCACAAGCAGGAGTACTGTAGAG[C/T]ACTCAC
TP75538	TGCAGGAATCTTCCAAC[A/G]CCCCCCTGCGCGTCGCTTGGAAGACGGAGCTGAAGCAGCCAAGAAG
TP75564	TGCAGGAATGAGGAGAGTCTCTTACTATTTTCAGCTG[A/C]CGAAGGACGTCAATGTCCAGCACTGT
TP75576	TGCAGGAATGCATGGATGGGAGAACGAAGATGTGTGTACATGTGCACGCACGTACCGCGTC[G/T]GT
TP75578	TGCAGGAATGCCAACAGAAGAGGCCCTCGCCTGTACCGCAGTTTGCCCCAAAGC[G/T]GTGAAACTC
TP75591	TGCAGGAATGGAGGTGTACGCAGTCGGAGTGTTGAGGCTGCTACCATGGCT[A/G]GCACTGGCAGCA
TP75601	TGCAGGAATGGCCTGAAGCTGCGTATCCCCCGTATGCCAATGGACCTGGCTA[C/T]GTTATCTCGGC
TP75617	TGCAGGAATGGTGGTGGTGGTGCTCCAACTCCGACTCCAGGCAGAGCAAGGAGGGGGTGCTTG[A/C]
TP75653	TGCAGGAATTATAATAAAATAATAACACACT[A/G]CTTCCAGACTACTACTCGCTATGCAGTCTGGG
TP75659	TGCAGGA[A/G]TTATGCTCCATGTCTACCTCTGTAATCTGCACAACTACGTACTACTGTCGATAAGT
TP75729	TGCAGGAATTTCGTC[A/G]CTGGAAGGAAACGATCTGAATCGCCAGCTCTTTGATGCATCGGCATCG
TP75734	TGCAGGAATTTGAGCTGTTTAAGCCAGGCCTAACCAAGCGAGGCCCTAGCCTGG[C/T]TCTTGAGAT
TP75743	TGCAGGAATTTTTCAGTATGGCCTGGCA[G/T]AGCGACACGTTCTAGGCCATCAGTGCAGCGTTCTC
TP75758	TGCAGGACAAAATTCC[C/T]CCCAAGAATCAGGATAAACTACTTGATGAGCAAGTACAGGCCAACAG
TP75760	TGCAGGACAAACAAGCA[C/T]GAGGCAGGAACAGACGATCACCATTCGGTTCACCAAGAAACGGATG
TP75784	TGCAGGACAACATACCGAAGCCCTAACCC[C/T]GTCTGATCCCCAAACCGCACGTCTCTAATCAAAG
TP75786	TGCAGGACAACCCACGGTATATCAAAATCGGTTAC[A/G]CTTACATGATGAGCTCAAATCAAATGTG
TP75791	TGCAGGACAACGCTGCCTGCCACCGCTGTTTTGCGCAGGGTGGTCCATCCTCCTAGCACTA[G/T]TA
TP75797	TGCAGGACAACGTCAGCTGGTCCATCGGCTACGGCATCCCCACGCTGGG[C/T]CTCATGGTCTCCAT
TP75799	TGCAGGACAACGTGCAGATAACTCCTTGGCCATATGGTCTCTTTCCCGTGCCAC[C/T]AAGGACCTT
TP75803	TGCAGGACAACT[G/T]AATGGCACGAAAATTTTCATGTATCCGCCGACCCTTGATGAAGGCCGTTTG
TP75824	TGCAGGA[C/G]AAGCTGTACGGGAAGGAGATCACGGTCGCCGACAAGGAGATGGTGGAGGAGGAGCG
TP75830	TGCAGGACAAGGACCTGGATCCACCGCAGTCAGTGATCGACGCCCGCTCCATCCTCTGCTAG[G/T]G
TP75853	TGCAGGACAATCAATTTTATTTAGGGTCAATATATACAGTCAAT[A/T]AAATCAGACGGACGTATGT
TP75890	TGCAGGACACCAAGCATGGC[A/G]CGGCGCGGCCTGCACATGGCCTCAAGAGGAGCCGCCCTCGGCA
TP75897	TGCAGGACACCATGGCGCTGCGGTCTCTGTCCCTGCTCGCGTCGTCG[C/T]TCGCTCTCATGATGGC
TP75902	TGCAGGACACCCTGAATTTCGTCAGTGGCGAGTGGCGGTGACAG[C/T]TGAATCTCTGTGGTTCAAA
TP75903	TGCAGGACACCCTGGGTGACCTCAGCAGCGACAAGGCGGCATCCCGCGGGCTCTGCGGC[C/T]TCGG

Table A2 (cont.)

TP75911	TGCAGGACACCTTCGAAGGAGGCAGCTGCGGGCGGCGGACC[A/G]TGGGTGACGGCAGCGGCAGCGG
TP75912	TGCAGGACACGAACCAGAGC[C/T]ACGTCCACGCCGAGGTGCGCCGCCGTCGGACACGGGCTCCCGC
TP75939	TGCAGGA[C/T]ACGGGCATTGAATTGAATTGCTGCTGCTCCTTGGGATAGGGGACGACTAGCCGAGA
TP75940	TGCAGGACACGGTCCTGCTCGACGACGTCGT[G/T]CAGGAGGCCGCCGAGGAGTGGTACCACGGGCG
TP75946	TGCAGGACACGTGCCTGGGCCTGGCCCTCTTCAAGCTG[A/C]TCCGCCGAAGGATGGAGGGCCACGC
TP75957	TGCAGGACACTCGTGGC[A/G]CACCGTGGAGGAGAGGAAAGCTTGCACGAAGCCATGGAGTGATGGA
TP75964	TGCAGGACA[C/T]TGTGGTTGTGGCTGTGCTTCTGGCGTCTAGGGTTCTTGCATTGGGTAGTGCCGT
TP75971	TGCAGGACAGAAGACCCGTGTGGAGTA[A/C]TTGCCCATGATGCGCGGCCGAGGGCTGTCAGCATTC
TP75981	TGCAGGACAG[A/C]GACCAGCCGACTCCAGGCAGCTGCTATTGCTATTTGCAGGGCCCTAGCTGCTG
TP75985	TGCAGG[A/G]CAGAGGAGAGAGAGACTGATGAGAGAAGGTGGTCGGCTGGTCGTGGCGTGGGAGTGA
TP75990	TGCAGGACAGCAAGCAGGAAGGGCCAAGAGAGGGTGTC[C/G]AATGCTTTAGAGATATCAATCTTGA
TP75993	TGCAGGACAGCACAAGAAGACGAT[G/T]TCTCTATGTCCATGCTGCATCACGTACGACGATTACTGA
TP76006	TGCAGGACAGCAGGAGCAGGACCGCCGCTGCTTGTTGCCTTTGCCTGTGTTGG[A/G]CGGGGGGAGT
TP76021	TGCAGGACAGCGATGTGTGC[A/G]CCTTGTGCAACCAGGAATCAGGGACATGCGGGCATCTGTTCCT
TP76022	TGCAGGACAGCGCAGCGGGAGCACGGTTTCTTGGTGGC[A/G]CCGAGCAGTGAATGCGATGAGGTGT
TP76023	TGCAGG[A/T]CAGCGGATGCCGCAGGTCCAAATAGGAGCAGTAGATGGAACGAAAACGCTTTCGTCT
TP76034	TGCAGGACAGCTTGAACTGCTGTCAACCGCTATT[A/T]TGGATGGATGGATGGCTGGTCTTGGTACA
TP76039	TGCAGGACAGGAAAGGAAAGCAACGTGTAGTG[A/C]CGTACCGTGCTCCTTCATGGTCTGATGGAAC
TP76053	TGCAGGACAGGCATTGTTCACAAAGAGGCAAAGCACGTGAACCTGCCT[A/G]GAGACCAGAGATCAC
TP76062	TGCAGGACAGGGCCT[A/G]TTGTCGGATCGGCAATATTGTGGCTGCTCATAAATCGATTCAGGAGTT
TP76064	TGCAGGACAGGGGAGGA[C/T]GTGGCACTATCCAGGCGCATAGCAGCAACGTTCCTCCTCATGACCA
TP76070	TGCAGGACAGGTCGCAGGACGAGGACGTGC[A/G]CGTGGGCGTGGACCGTTTCCCTGAGCGGCAGCC
TP76105	TGCAGGACAGTGGTGGTGAACTTGCTGAAGTAAAG[A/G]GCGGCATTCAGGAGTGCCTAATCCAAGG
TP76110	TGCAGGACAGTTTGGTTCGTC[C/G]AGGCCACACATGTCCCTGCTGCGTGCGTTTACGACGCTACCG
TP76113	TGCAGGACATA[A/G]AATCGAAACAATTAGACAGAGGCCGCTCGGAAAAAGTGCGAAGGGAGAGTTG
TP76126	TGCAGGACATCAATAGCAT[C/T]GAGCAAAGCTAACTCCGAGTCGAGCCCTGCGTTCTAGCACTGGC
TP76139	TGCAGGACATCCGCGTCAACGTCCGCGTAGGCGGGCGTTGGCGTCGCCATC[G/T]CCATCGAGGGGA
TP76140	TGCAGGACATCCGCGTCGACGT[C/T]CGCGTAGGCGGGCGTTGGCGTTACCATCGCCATCGAGGGGA

Table A2 (cont.)

TP76156	TGCAGGACATCTT[C/T]GCGCAGCTGGGGAGCAGCTCCACGATCGACCTGCCGCAGGTGGCCGTGGT
TP76166	TGCAGGACATGATCACGAACCCCT[G/T]CAAATACGGTGCGCGCCTCGCTTGCCTTGGCTGCCATCC
TP76169	TGCAGGACATGCAAGAAAACA[G/T]ATAAATAGGAAAACCACACAATTTTTCTCCAACATTTATAAA
TP76173	TGCAGGACATGCTGCCGTCCTTCGTCCACAGCAATGG[A/C]GGCAACATCCAGCCCTGAATTCGATC
TP76180	TGCAGGACATGGCACAAGACTTTGGATTGAGCAGGG[C/T]GAAGAGCTTGGCGATGATGAGGAAACT
TP76185	TGCAGGACATGGGGGTGACCAAGGTGGTGGTGA[A/G]CACGCTGCCGCCGTTCGGGTGCTCGCCGTG
TP76195	TGCAGGA[C/T]ATGTTTGCAGCAGGCACGGACACAACGTACCTGATCCTAGAATTTGCCATGGCTGA
TP76219	TGCAGGACCAAACAGACCCTCGTTAGAGAACACATAGGATACGGCCAGC[A/T]GGCGAGGTGGGAAG
TP76281	TGCAGGACCAGATCGCGACCGCCGACGACGTGCGCTCCGCC[C/G]AGCGCGCCGACGGCGCCGAAAA
TP76291	TGCAGGACCAGCGATGACGCTGCCGCCACGTGC[A/G]TTGACATGTTGCTGTCCTCCGACGGCCATC
TP76295	TGCAGGACCAGCTGTGGTGACGTGAGAGTTCCGTACCCC[G/T]TCGGCATCGGCCCAGGTTGCTCCT
TP76322	TGCAGGACCATCCCATGGTG[C/G]CCAAGAACCCAGTGCGCTCCATGGCAGCCAGCAGCGCCCGTGA
TP76324	TGCAGGACCATCTCCATTATTATGTACGCCAAGAAAGTAGGAGTTGAGT[A/G]GTGGAGTAGGAGAT
TP76354	TGCAGGACCCCAAGTACAATATCACGGCGCCT[G/C]AAGTCAACACACGGCAGACATCGTCGTCGTC
TP76360	TGCAGGACCCCCGCCTCAAAGTTGAAGCCCAC[A/C]AAGACAACGAGGAATGGGCCGCCGTGGCAGT
TP76368	TGCAGGACCCCTAAACCCTAGAATCGACCGACGCTAAGCGCTCGGAATCTACCC[A/T]TCGACTACG
TP76398	TGCAGGACCGACTGTTGTGTTCCCTTCACTATGCTATGTG[A/G]GTGTATATGTCTTCTCCTGATCC
TP76411	TGCAGGACCGCCTCGGGTACGACCAGCC[C/T]AGCAAGGCCATCGAGTGGCTCATCAGGGCCGCCGC
TP76414	TGCAGGACCGCCTTGGCCGCGTCGAG[C/G]TCACAGAAGCGCTCCATCCACGCGGCCAGGAGCGGCG
TP76416	TGCAGGACCGCCTTGGCCGCGTCGAGCTCGCAGAAGCGCTCCATCCAC[A/G]CCGCCAGGAGCGGCG
TP76454	TGCAGGACCTACCGCCGC[C/T]GCCTCCCCCAGTATCCTTTCCGCCTCGGCTGCCGCCGCCCACTGG
TP76479	TGCAGGACCTCCACGTCGCGCC[G/T]CGCGTCCACCACGGACGCCATCAGCAGCTCGTACGCCAGCA
TP76486	TGCAGGACCT[C/T]CCCGTCGTGCTCGGCGCCTGCTGCGTCCTCCACAACATCTGCGAGCGCGCCGA
TP76502	TGCAGGACCTCCTGCTCCGCCTCACCTTCGACAACATCTGCGGCCTCGCGTTCGGCAAGGA[C/T]CC
TP76505	TGCAGGACCTCGCGCG[C/T]GCCACCGATCAGGATGATCTATATCTACCATATCCTGTCGATCGACG
TP76513	TGCAGGACCTCGTTCAC[A/T]GATGAGGTGGAGTCCCTGAAGCACCGTGCGTTGCGCTCTTTCCAGA
TP76542	TGCAGGACCTGCTCAAGGCGACGGCGGAGGT[G/T]CTGGGCACCGCCAACCTCGGCGTGTGCTACTG
TP76549	TGCAGGACCTGGACCTGATGCTGATGCCTCCTCCACACACAATGTCAATGCCGC[C/T]CCCACTCT

Table A2 (cont.)

TP76553	TGCAGGACCTGGCACGCGGCAGCCTTGACGTACTGGTCCTTGCTCCTCTTCTCCGTGA[C/T]GCACC
TP76562	TGCAGGACCTGGGCGGG[G/T]GATCTGATCCACCACCCATCGGCCAAAGCTCTAGCTGCGAGTGAGT
TP76569	TGCAGGACCTGTCGCGGAAGCTGGAGACCACCAAGCTGCACGCCTTCACGCTGGACGAGCTCA[A/G]
TP76572	TGCAGGACCTGTTTGCGCAGGACTGTCCTGAACTAGATCAGGCAGAGAGCCTAAG[A/C]TCACTGAA
TP76598	TGCAGGACCTTTTCTACCCATGGCTAGGGCCCGATAATGAGCCAGCTCGGCTTGGCAC[A/G]GCTAG
TP76605	TGCAGGA[C/T]GAACACTTCGTTGCCGAATCAGAATCTCTGCCACATCGGCGAGGCGACGATGGGGG
TP76616	TGCAGGACGACAA[C/T]GGCCTCGAGTTCTCCGACGTCAACAGCTTGAGCCTGGTGCGCGAGCTGAT
TP76621	TGCAGGA[C/T]GACAGACGGCGATGTAGAGGCGCGGCAGGGGACTCCGACAAGCCAAAGTCGAGCAC
TP76624	TGCAGGACGACCACCGCGGCATAGGCCATCATGATCAGTGGCACAACCA[C/T]GACGGCATGGTGCT
TP76633	TGCAGGA[C/T]GACGACTGAACACGGCGAGGATACTGCGGATTATATGTGGTTGTGTGCGTACTCTG
TP76637	TGCAGGACGACGCGTTGAGCACGGGGGAGCTGGACTACATCAACGGAGGTA[A/G]CTGTGATGCGAT
TP76641	TGCAGGACGACGGGGACGAGGCCGTCCTCGTCGCCCTGCCACAGGTGCA[C/G]GGGGCACGGCGGCT
TP76647	TGCAGGACGACTCCACGATCCTTCTTCGAGGGCCTGTGGTGGCAGCCG[A/C]CCCTGTTCCACCTGT
TP76652	TGCAGGACGACTTCTACCTCAACCTCGTGGACTGGTCCTCGCAGAACGTGCT[C/T]GCCGTCGGCCT
TP76661	TGCAGGACGAGAGCGACATCACGTCGCGGGCGCGGC[C/G]CGCGGGGCCGACGGCGAAGCCGTTGGC
TP76691	TGCAGGACGAGGTTTC[C/T]GTTGTCGAGGAGAGAAGCAGCCATGGCGGTGGTGGTGCCGTTGGTTG
TP76707	TGCAGGACGATCTCGCCGTGGTG[A/C]GGCACGGACAGGTAGCTCTTCTCCGCCCTGCGGAGGACCT
TP76710	TGCAGGACGATGATGCTTGCGTCCTTACCAGAGAGCTGTGGTTCTCTCTTCTGGCA[C/T]CTGTTGG
TP76712	TGCAGGACGATGCCG[C/T]GATGAGCAGCACGAACAACCTTGCAGCTGCGGAGCGATGATGCATCGT
TP76716	TGCAGGACGATGGC[A/G]GCGGCCGTGGTGGCGTTGTCGACGAGGGAGACCTCAGATACGTCGCCAG
TP76735	TGCAGGACGCAGGAGTCGAAGAAGGTCTCGAGCTTGGCCACCAGGTTGCCCTTGGC[A/G]ACGGCCT
TP76748	TGCAGGACGCCCA[A/G]GCTGGTGGAGACGACCACGTAGTCCGCGCTGTACGACGAGCCGTCCTCCG
TP76749	TGCAGGACGCCCCAACACCTCCGCTCGCCGCACGCTGACCCGCTCGCGACCTCGCATACTC[C/G]CC
TP76774	TGCAGGACGCGCAGCGCCAGCTACTCGACACCGTCGCCGCCGCCTGCGCCTTGCCG[C/T]CGAAGAA
TP76778	TGCAGGACGCGCGCGGTGGTGGCGGCCACCTTGTAGCAGTCGGCCCGTGGCGAG[C/T]GGCCAGCGA
TP76784	TGCAGGACGCGGACGAAGAGCAGCGGGTGGATCGTCGTCACCCC[A/T]GACGGCACGGTGGCGCCGC
TP76803	TGCAGGACGCGGGGACCCAAAGGGCTGCACGAAGACGGGAAGCGCGC[G/T]CTACTGGGCTGAGGAG
TP76824	TGCAGGACGGAAAG[A/G]CACGCCCGCACGCATATGTGGCCGCACGGCTTATCCTGGCCGTCGGTTC

Table A2 (cont.)

TP76831	TGCAGGACGGACCATGTGAACTGTGAAGAACAA[C/T]CACCAGCCAACCATCCCCACATTTGGATTC
TP76832	TGCAGGACGGACGGGCCATGTGTGCACGCTGCCCTGTCG[A/C]TGTGGGGGTTGTTCGCAAGTCAAT
TP76838	TGCAGGACGGAGTGCGTGAAGGAGCGAAGAGTTACCATGCTCAGCGCGTC[C/G]TCCATTTTGGCGA
TP76843	TGCAGGACGGCAAC[A/G]AGCCCGAGCTGCGCATCGAGTACGGCAGCGGCAGCTCGGTGACCATCGC
TP76853	TGCAGGACGGCCACGCGGACCGAGCTGACCCCTATGCCGCCGACGTGTGGAGCCTCGGGGTGA[C/T]
TP76854	TGCAGGACGGCCATTCGGTTCCTGCGGTGCCCGTCCTCGT[C/T]GTGGACGACGCGCCACTCGGTGT
TP76873	TGCAGGACGGCGCCGTAGCGGCCCAGCCACCAGTAGTGGTACT[C/G]GAGCACCACGAACACCACCT
TP76874	TGCAGGACGGCGCCGTCAGCCTGCTGCACTGGAGCGGTAAAGGG[A/G]AAGCCTTGGGACCGCCTGG
TP76877	TGCAGGA[C/T]GGCGCGCCGACGGTGCCGCTGCACGTGGACACGCGGATGCTGGTCACGTTCGGCCT
TP76884	TGCAGGACGGCTACGTGTCCTACCCGTGGGAGAAGAAGATGCGGGAGGTGCTACCAAT[C/G]CCCAA
TP76889	TGCAGGACG[G/T]GAGAAACGACGACGACGAATCACGCCTACTGTTCCGAATCCGCCATACGTAGTT
TP76890	TGCAGGA[C/T]GGGAGCACGCCTGGCGGGCCGTTCGACGCCGAGTTGAGTGGGCTCGACTGCTGGAA
TP76917	TGCAGGACGGTGGCGCCGA[C/T]GACGAGCGGGAAGACGGCGAGGAGCACGAGCGCGAGGCGCCACT
TP76924	TGCAGGACGTACTCGACGGCGTCCTTGATGATGGAGGCCTTGTCCATCTGCAAT[C/T]CATTCCATT
TP76932	TGCAGGACGTCAACGACGCCATGAGCCGCTGCGCCGCCTCCAGCGC[C/T]ACCACCACCTCCGTCTC
TP76934	TGCAGGACGTCAGGATGGCGATGAAGGTGTTGCC[A/C]TTGTACATCCTGAGCTCCAGTGCGCGCTC
TP76941	TGCAGGACGTCGCCACATCCATGGCCAGGCTCGGCCCCCTGCTGCCGCCCGACTTTGAGGG[A/G]AA
TP76945	TGCAGGACGTCGCCG[C/T]CCGCGCCGAGCTCCGCGGCAACGCGGCGCCGAAAAAAAAAAAAAAAAA
TP76955	TGCAGGACGTCGTGCACAACGACAAGTGCATCTACCTCGTCTTCGAGTACCT[C/G]GACCTCGACCT
TP76968	TGCAGGACGTGCATGGCCTGCGCGACGGATGGCCGCTCGCTCTGGTCAGGGTGCGCGCAC[C/G]ACA
TP76969	TGCAGGACGTGCATGGCCTGCGCGATGGACGG[A/C]CGCTCGCTCTGGTCAGGGTGCGCGCACCACA
TP76976	TGCAGGACGTGCT[C/T]GAGCGCTTCGCGTTCGACAGCATCTGCCGCGTGGCGTTCGGCGACGACCC
TP76979	TGCAGGACGTGCTGGAGCGCTT[C/T]GCGTTCGACACCATCTACATGGTCGCGTTTGGGCACGACCC
TP76982	TGCAGGACGTGGACCTTAGGTACAAGGGGCAGGGTGGTACATCG[A/G]CCAAGTGCGAGAATGCCAA
TP76994	TGCAGGACGTGG[C/T]GGAGCGCAGGGCGCGGCGGCAGGAGCGCGCCGAGGAGCTGCCTCGCGTCGG
TP77021	TGCAGGACGTTGTGCAGCACCGTCATGGCCTCCAGCTCGCGGGGCCCCAC[G/T]CCCATGAGCGCGC
TP77030	TGCAGGACTAACCTATTCGGCACT[A/C]TGATGACTTTTCATGTGCGGTTGTCCAGTTTACGGGCTG
TP77074	TGCAGGACTCATTTAATAAGATTAAAAAACATTTCAGTTTGGTTTAATTCCACATAAGAG[C/T]TAA

Table A2 (cont.)

TP77076	TGCAGGACTCCACACTTGCATCCATTCTGCTGCGCCCATGGCCAGCCGCTCT[A/G]AGCACCGCCAG
TP77092	TGCAGGACTCGAC[A/G]CGTGATGGACGGCTATATAGGCGCAAGCAGGAAGCAGCTATACGCCGCTA
TP77121	TGCAGGACTCTTCGCTCTTGTCCCACCACCACCA[C/G]CAGCACACGGCCGCCGCCGCCCTGCCGAA
TP77126	TGCAGGACTGA[C/T]CTGATCCCTCCGTGCTCCGACTCGCCTGCTGTTGCTAGGAGCGATCGATTGC
TP77149	TGCAGGACTGCCTCCACGAGCAGGCGCACGC[C/T]AAGGTTTCTTTCACGCGGCAGGGCGTCGAACA
TP77152	TGCAGGACTGCGACAGTGTGGGCGGCCATACTTGCTGGCCGTGCGCAGGGACGG[G/T]GTCGACGGC
TP77171	TGCAG[G/T]ACTGGATAGTTAAAGGCTTAAAGCTATTGTCGACTCGGTGTTCAGTCGTCTATATATG
TP77172	TGCAGGACTGGATAGTTAAA[G/T]GCTTAAAGCTATTGTCGTCTCGGTGCTCAGTCGTCTATATATG
TP77175	TGCAGGACTGGCAGCGCCGCTACGGCGAGAT[G/T]CTGACGAGTAAAGGCAAGGACGTGCAGGTGGT
TP77177	TGCAGGACTGGCAGCGGCG[A/G]TACTGCGACGCGCTGCACGGCAAGGGGAAGGAGGTCAGGGTGCT
TP77184	TGCAGGACTGGGTCGCTAGCTCGCGGCCTGGACTGGTGCACGCGTCTCTCTCTCGAAAAAAAA[A/G]
TP77206	TGCAGGACTGTTCACATGATAACAGGCCCCATTCCTTCT[C/T]GGTTTATACACCAAGCAGAACCTG
TP77216	TGCAGGACTTCAAGCTGGGCCACTACATGAAGAT[C/T]CCGCCGCGCTCCATGTTCGCCGTGCAGCT
TP77252	TGCAGGACTTGGCTGATCCTTGTGCTCAA[C/T]ACTACGTGGAGGCGTACCTGAACCAGCCAGAGGT
TP77265	TGCAGG[A/G]CTTTGAGTTCGCAGAGGGAGTTGGAGTGGATGGGAGGCCCAAAACGCAGGTTGACGA
TP77272	TGCAGGAGAAAAACCAAAACAATGGCCGCTAAGCCGCCGCTGCTTCGACCATGGGGCC[C/G]AAAAG
TP77278	TGCAGGAGAAAACCTTTCCGC[A/T]ATGCGGGGCAGCTGGGCGCCTGACGAAGACGAAGGTAGTGCG
TP77287	TGCAGGAGAA[A/G]CAAGGCGCCGATGTGACCTTCAAGGTCCGAGACGAGGTCTTCCCTGCCCACAA
TP77293	TGCAGGAGAAACCATCAAGAACAAGCTTATGGACAGCATCTCTCAGGGCC[C/T]CATACTCTTCCCT
TP77297	TGCAGGAGAAACCCCAGAA[A/C]ATATACAAAATGCATAAGATAAACCGACCCAAAAAAACGAAATT
TP77299	TGCAGGAGAAACCGCGGGCAATGGATCAGGCAACATAG[C/T]CCATTAGCCTGTTAATCGTTAGATC
TP77327	TGCAGGAGAACAGTTTCCTCATCAACGACGCTATCAGGATGGCTTG[A/G]GTCGGCTGTAGCCACCA
TP77362	TGCAGGAGAAGAGGTCTAGC[A/T]TAGCTTAGTTTAATTAGCTCCCAACTAGATCGATCAGTCGATC
TP77367	TGCAGGAGAAGCAGCAAGCAAG[G/T]AGTCAGGAAAATGGAGGAGCAAGCCCCAAGCCCCCAACAGA
TP77370	TGCAGGAGAAGCGAGATGGCGGGGCGCACGTACCAGATCTCCTTCTGGACGCCG[A/T]GAAGGAGGC
TP77373	TGCAGGAGAAGCTCGGCCGCCTGGTGTCCTCCTCCAAGTCCA[A/G]CCCTTTCTTCCCGCTCGGCGG
TP77379	TGCAGGAGAAGGAAGAAAGGCGCAGTTCGCAAGGG[C/T]GGAAGCATGGTCTGGATGCCAGGATCTG
TP77381	TGCAGGAGAAGGACAAGCTGGTGGCGGAGGTGATGCG[C/G]TACATGCTCTTCAAGACGCACCAGAA

Table A2 (cont.)

TP77388	TGCAGGAGAAGGAGGCGACGGAGG[A/G]CGGCGCCAGTGCTGCCACCGACGCCGCGGCGTTGTTGCC
TP77405	TGCAGGAGAA[G/T]GCGTGGCCGTGGCGCGAGCCAGCGGCGGCGACGGCGCGCGGCCTCACCATCTG
TP77409	TGCAGGAGAAGGCTGCCAGGAAGGCGGCGCAGGCCGCGGGAGG[A/C]GGCGGCGGAGGCGCCGACGC
TP77411	TGCAGGAGAAGGGCGAGTAGGTGCTCGACG[A/C]GCTGGGGTCGAAGAGCGAGTCCGCCTCGGAGTG
TP77427	TGCAGGAGAAGTTCATGCAGCTGTGCGGGCAGATCGACGACATGGGCGGCGCGGC[G/T]GCGGACCA
TP77433	TGCAGGAGAATCCCCAAGTCGCAGCTCCCGAAGGCGAGGAGCAGAATCCTAAAGAGCTTC[C/T]AGA
TP77443	TGCAGGAGAATTGGTCCGACGAAGAGGAGCAGTGGGAGGCGTGCCCTAGCAAAACGAAGACT[A/T]G
TP77458	TGCAGGAGACACAGAGCGAGCTTCCTCAATCGACCCTCA[A/G]CGTCGGCATTTCATCGAGCAGCAG
TP77465	TGCAGGAGACACGCAGGCAGCCCAGTTTTTTACAATTTTATCTTTTTTTT[A/T]AAAACAAAATTAC
TP77469	TGCAGG[A/G]GACAGCAACAATAATAGCCCTCCCACTGAGCAGGGTGACAACCCCAATGCCCCTAGC
TP77478	TGCAGGAGACCAAACACGTCGGGGCAGATGCAGAAGAAGCAGGGATTTGGA[C/T]GCGGGGCGGAGA
TP77479	TGCAGGAGACCAACGCCA[C/G]GCTCCGCGCCGCGCTCGAGGACAATGTGGGTCGTGGCGTGCCCGA
TP77482	TGCAGGAGACCAGCACCCACCCTGATGG[C/T]GGGAGCCTTGTGGTGTTTGCGACTGTGGATGTGGA
TP77492	TGCAGGAGACCGAC[A/G]TCACCACCGCCGACGTCGCCGAGCTCCTGACGCCCAAGCGCGCCAACGA
TP77496	TGCAGGAGACCGCAGGCCCGCAGCGCAGGAAGGCAGGCAGGCAGGC[A/G]CCACCTCCACCTCTCTC
TP77507	TGCAGGAGACGAGCCGCATGGCCACCTTGTCACCGAGCGCCGCGCCAGCTCCAGCCATG[A/C]TTGC
TP77511	TGCAGGAGACGAGTGGAGTACTTGAGCGTAGCAAACATAGGATGTGATGC[G/T]ACGGTGTCACGAC
TP77512	TGCAGGAGACGAGTGGAGTACTTGAGCGTAGCAAAGATA[C/T]GATGTGATGCGACGGTGTCCTGAC
TP77515	TGCAGGAGACGCACGTGCGGCGGGACGAGTTCGAGGACAGCGGCGCCGTCG[C/G]CGCGCACTTCCC
TP77551	TGCAGGAGACTGCGGCGTCGATGTGGTGCCACCTGGAC[C/T]ACCCGCCGAAGTAGCTGTCCCAGAC
TP77561	TGCAGGAGAGAAAGTACTTGCTTTTAGTCAGTATATACTTCCCATGAAATTTTTTGAAC[A/G]GCTG
TP77563	TGCAGGAGAGAAAGTGGCTAGGTTTTATGGCCCTACCCTGCAATCTGTTGTGCATGGGT[C/G]GGTG
TP77585	TGCAGGAGAGAGGAAGCGGTGAAGACGGG[A/G]ACGAGCACTGTGTAGGTGGCGCAGGCTTCGCGGC
TP77594	TGCAGGAGAGATGCGCAGGCGGCGCGAGGTGCGGAGCCGACGCT[A/G]GCGGCGGCGTCGAGGAGCG
TP77601	TGCAGGAGAGATTTCCTGAAAACCCAAGCTTTTGTGAGCTACCAACCA[C/T]TACCAGTAAGCTTGG
TP77602	TGCAGGAGAGCAAGATCTTCAAGTTCTTGGGATTCATGTGGAA[C/T]CCGCTGTCCTGGGTCATGGA
TP77610	TGCAGGAGAGCAGAT[C/G]GATCAAGCAGGTTAGTGCTTCAATGACGGTGGGATGCAATAGTCCCTC
TP77611	TGCAGGAGAGCAGGTGGAAGTG[C/G]AATATCATATGCCACCCGTCTGTTCTGTTCGCATGATGGGG

Table A2 (cont.)

TP77618	TGCAGGAGAGCCACCGCTGCTTC[A/G]ACGAGGAGGCGCTGGAGGGCATCCGCCGCGCCGTCGTCGA
TP77632	TGCAGGAGAGCTGGTCGTGGCGCG[C/T]GTTGCCCGATCCGCCATTCGAGCGCAGGCATGTCGTCTC
TP77638	TGCAGGAGAGGCAGACACCGAAGCCAAGCATCGA[A/G]GTAGACGAGTGTGGAGCCTGTGGCCGTAG
TP77643	TGCAGGAGAGGCGGCCACTGCACGCCGTGCGCGGC[A/G]TCCAGGTCGAGGATGTGGATTCGGCGCG
TP77714	TGCAGGAGATATTGAAGTTTGAAAAATAATCAAATATCTCTTAGTTAAGTGAATTTG[G/T]GGTGGC
TP77721	TGCAGGAGATCAATATAGTAACAGCAAAC[A/G]ATGTCAGCACTTGAGAGCACAGACTGCATAGAAA
TP77724	TGCAGGAGATCAGCAAACGAGGCCAGGTTCACCGACAGCATGTCGCCGAGGGTCGCCC[A/C]GAGCT
TP77727	TGCAGGAGATCATCAACCAAACATAGTGAATAGGTCTCCTTATCAACCCCACC[A/G]TCCTTTGATG
TP77751	TGCAGGAGATCTAAAGCTCGTCGTGGGGGGCAGCGGGCCCGTTGGCTGCCG[C/T]GTGGTTCCGCAG
TP77763	TGCAGGAGATGAGACCGAGACCGACCCCCAGCGGGGACGAAGGGTGGG[C/G]CACGCCGCCCGTCAG
TP77774	TGCAGGAGATGCGCGGGCGCCTGATCCGCCTCTGCGCCGACGCGGAGGGCCTGCTGGAGGC[A/G]CA
TP77786	TGCAGGAGATGGAGGACGGCGACGTCGTGCGCGTGCTGCCCGCGTGCAGGCACTTCTTCCA[C/T]GG
TP77800	TGCAGGAGATGGTAATAATCTTACACTAG[C/T]AGTAGTGATGTGTCATTCGCCCATTCATACTAAA
TP77814	TGCAGGAGATTGGAATAGGGAGAGGAATAGGAGAATGTGAAGTGTACATTTAGCTTGTTCGCT[G/T]
TP77817	TGCAGGAGATTGGTGGTCTCTGAAACTCACGAATCAAGGAAGAAGCACGTGGAA[C/T]TCAAGCAAG
TP77827	TGCAGGAGCAAAAGCACTAGCAATGGCGTCGGG[A/C]ATGGAGGCCGTTGGCGCGCCTGGGAGCTCG
TP77835	TGCAGGAGCAAAGTACTAGTAGTAATTTTCACCAGGCAGATTAAGAAAAAAATG[A/G]CCAGGCAGC
TP77851	TGCAGGAGCAACTGATCATCACTCGCCCCGA[C/T]GACTGGCATCTCCATCTTCGTGAAGGCGGTGT
TP77869	TGCAGGAGCAAGTCGTCGTCGTACCTGG[C/T]GAGGAGCCTCTACTGGAGGCTGCGCGCGGGCCTCC
TP77870	TGCAGGAGCAATCGGCAGCTGCCTTGTGATGGAGCAAC[C/T]GCAAGAGGTGCGCGCGCGGCATTTA
TP77876	TGCAGGAGCACAACATATTGGCGTGTTGGACTGTTGGTGGGCCCAACGAGCGGACCTCGT[A/G]ATC
TP77905	TGCAGGAGCACGAAACA[C/T]GAGCGAAGGGTCTCATCTGGCTGCACGCATGCCCACCCGCCGAGAA
TP77916	TGCAGGAGCACGAGACCGCGTGGTACACCGCGGCGGGGAAGCGGCGGCTGCACCACAC[A/G]CGGGC
TP77921	TGCAGGAGCACGCCCCCGTTCTGCTCGAAGAACTTTTGCTTGGCTCTGATGAGCTTCCTC[C/T]TCT
TP77929	TGCAGGAGCACGGGCCCGCCGCGGACCAACCAGTGGACCACGAAGAGCATTTCCTCGTCCTC[A/G]A
TP77933	TGCAGGA[G/T]CACTCACTTCTTGCAAGAAGTCTGCAACACCTTTTCTCTCAGGACATTTGAAGCCC
TP77942	TGCAGGAGCACTTGTGGTATGGTATGGTCCACAAGAGCATTGATGCCCTCATGTAAAGA[G/T]ATTT
TP77944	TGCAGGAGCACTTTATTGGAGCAGAGCCGCCAGCGGTGCGGGTGTGGGGTCC[C/T]TCTACCGAGGT

Table A2 (cont.)

TP77955	TGCAGGAGCAGAGGCCAGAAGGTGAGGGTTGGCAACATCCAAGCGCCGTGCCG[A/T]GCGTGGCCCG
TP77956	TGCAGGAGCAGAGGGCCAAAACCCATCGAATTCCGAACAGA[G/T]GCACCTCCCAAGAACGCACGCA
TP77963	TGCAGGAGCAGCACGCGGCTGCCTGATAGGGACAACGCGGCATGGCATTCCTCCCTCGC[A/G]GAAA
TP77966	TGCAGGAGCAGCAGACAGAGGAGGG[A/G]CGCAGGGTCAGGAAAAGGGACAGGATCACGCGCGGGCA
TP77984	TGCAGGAGCAGCCAAGTAG[A/G]CCACCACAGCAGGAGCAGCCGAGCAGGTTGCAAGCCAGCAGGGG
TP77993	TGCAGGAGCAGCGCCTCCAGCTGCCACAGCTGCGTGCGTGCGT[A/G]CGTGGCCAAGGCCAGCCAGT
TP77998	TGCAGGAGCAGCTAACCAGCCGAGCAGGCCACTGACCAGCAGGAG[C/T]AGCTAAGCAGGTTGCAGG
TP78001	TGCAGGAGCAGCTCCCAAAGCCATGTACTCACCTCGATCTC[G/T]GCTTCCTCCACTTTTCTGTTGC
TP78010	TGCAGGAGCAGGACAGCGAGACTGAATCCCAAGACCGCAGC[A/G]GTGGGCGGAGCAGCACGCCACA
TP78025	TGCAGGAGCA[G/T]GAGCTGGGCAGCTTCCTCAGAACTCAGAAGAGCCCTGGCCCGTCCGTCCGTCC
TP78031	TGCAGGAGCAGGAGGTTGTCATTAGTGCCGTCTCCAAGGAGACCTTGCCCTTGTTGGCAGG[A/G]CG
TP78043	TGCAGGAGCAGGCCCGTGTAGCAGCACGCCG[C/T]CGCGACGACGAGCAGCAGCGCCAGGCTCAGCC
TP78053	TGCAGGAGCAGGGCCTGCTGCATCAGCTGCTGCTG[C/G]TGGTGGTGCTGCGCCGCGGCCGCGGCCG
TP78059	TGCAGGAGCAGGGTTAAACGTCAAAGAATGGGGCAACACGTACGGGGGGTTTACTGAAT[A/C]AAAA
TP78073	TGCAGGAGCAGTTCCACCTGAGCAGATCGGTGAAGGATCCGATGAAGGATATACTCCGTG[C/T]GAT
TP78074	TGCAGGAGCAGTTCGTGGTCATGCCGCTCGTCGTCGTCTTCTC[C/G]CTCTTGCCGCTGGCCGCGCA
TP78088	TGCAGGAGCATGAAGAACCTTTTGCTGTCGTAGCGGCGTG[A/G]AAGACCGTCGATGCCTTGGACTG
TP78115	TGCAGGAGCCAAACCA[C/T]GTCGAATCAGATGCAGAAAGAAGAAAAGGGATCTGGACGCGCGGCGG
TP78126	TGCAGGAGCCAATATACAACCTTCCTGACACGATCTCAATGGTGATCCAGACCAAGGT[A/G]TCTCT
TP78144	TGCAGGAGCCAGGAGGCTTACGTCGAAGAAGACGGTGTTCCTGTTGGCGTATCGGTCGTGCG[A/C]G
TP78164	TGCAGGAGCCCAAGCCAGCGGGCAGCAGGAAAGATCGGATACGC[C/T]CACTCGAGCAGACGGCCGT
TP78190	TGCAGGAGCCCTCCGTTTTGGTTGAGTAAGTGGAGAGGGATGATGGGAAGAAGTAGTGGG[A/C]AGC
TP78216	TGCAGGAGCCGCAGTAACACCTCCTCGCCACCACTGGAATTGCCACCGTTGCAACTGCCTCC[G/T]A
TP78217	TGCAGGAGCCGCCGCCTCGGCCAGATTACCTGGATCGCCTA[C/T]AGTATGGCACGAGGAGGCCTTC
TP78220	TGCAGGAGCCGCCTCGCTTGCGCGGCCACGAA[T/C]GGAATCTCGCGCGCCGCCGCCGTGAAGCCTC
TP78227	TGCAGGAGCCGCGGGTTATTAACGCCACGAGACCAACGAAGAGCGTGCCAGGG[A/G]CACGGCGAAT
TP78231	TGCAGGAGCCGTATTCTCGCCCTCTGTT[C/T]CTCACGCGGCGACGCCGTTATTCGTAGGTAGCCAC
TP78248	TGCAGGAGCCTCCACCTCCTAAACGAGGCGATGATGGTTCTGCTAAAGAAGACG[G/T]ACTCCCCAG

Table A2 (cont.)

TP78255	TGCAGGAGCCTCTGA[C/G]GCTCTGCCACAGGTTGATGTGACATGGAGCTCTACTGCATACGTGGAC
TP78258	TGCAGGAGCCTGAGCAGCAGATCGGTGTGGTGGACGTGCAGTACGTGGCGCAT[C/T]ACAAGGGGTT
TP78269	TGCAGGA[G/T]CCTGGCAGGGCGGAGGCCGACTTCGGGCGGTACGACGTGAGGCGCGTGGTGCGCAC
TP78284	TGCAGGAGCGACAGATAGGACGCACGGATAGCAAACATCGGGCCGCTGTGTGCAGGGCAC[C/G]CAA
TP78301	TGCAGGAGCGAGGAGGGCGCGGCGGGGGAGG[G/T]CGCCTGCGGGCGCGGCGGCGGCGCGGCGG
TP78305	TGCAGGAGCGAGGTGGAAGGAGAAGATCAGTTGGTGGATATGATCGATTAACCAAGCAG[C/G]TAGA
TP78322	TGCAGGAGCGCCAGTACTCCTCGTCGGTC[C/G]TCAAGTTGGGGGTGCACACGTCATGCAATACAGC
TP78329	TGCAGGAGCGCCGCCACC[A/G]CGTCCCTCGTCGTCGTCAAGCTGCCTGCTGTGTCTCCAGAGAACT
TP78332	TGCAGGAGCGCCTCCACGGCCTGCCGCGGCATGTC[A/G]TCGACGTCCACCCGCATAGCAGCAGTAG
TP78333	TGCAGGAGC[G/T]CCTCTACGGCCAGCCGCGGCATGTCGTCGATGTTCACCCGCATAGGAGTAGCAG
TP78353	TGCAGGAGCGCGCTGAACGAGTACGTCGCGGCGGTGCGGAAGGTGGCGGTGC[A/G]TGTGCTGGAGG
TP78395	TGCAGGAGCGGGAAATGAAAATGGAAGAATAAGCAGGAGG[A/G]TCTGGTGTAGGGATTGGGTCGAA
TP78429	TGCAGGAGCGTCGAGCAGCCTC[C/G]TCTCCTAATATCTCCCTCCATTAGATTGGACAAGATCCTGA
TP78431	TGCAGGAGCGTCGGATAGGAGAAAAA[C/T]GTGTCGCTGTCGCCCCGCCCGTCCCTCTCCCACCCTA
TP78435	TGCAGGAGCGTGAAGAACCTGTACGAGTAAACTACGGATCTTTG[C/T]ATTGGTATTTAGGACAAGT
TP78436	TGCAGG[A/T]GCGTGACGCTGACGGCTCCGTGACGACGACCACCAAGGGCCTGTACGGGATGCGCGG
TP78451	TGCAGGAGCGTTGCTACAAATACTCGCAGAAAGCCCTCGGGTTCGAGACCTGCACAT[C/T]TGTCGC
TP78452	TGCAGGAGCTAAACCATGTCGAATCAGATGCAGAAAGAAGAAA[A/T]GGGATCTGTACGCACGGCGG
TP78463	TGCAGGAGCTACGACGTGGACTGCCACC[A/G]CCGTGCCTGCCTGCGCCAGTAGCCCAACGGTTCTC
TP78465	TGCAGGAGCTACGATATGGAGGTGGGCGG[C/T]GGCGCTTGGGTGCGCGCGTGGCGCAATGGTCGTA
TP78473	TGCAGGAGCTAGCCACTGCACCATGGTGAATCTTGGTGG[C/T]TGCTAGGCTGTACTGAAGGTGGAG
TP78478	TGCAGGAG[C/G]TAGCTAGCCGAGAAGCAAAAACGAGGACGATGACGACCTCGCGCTCGTCTTGTTC
TP78500	TGCAGGAGCTCAACGTCGC[A/T]GCTTCGGGCGGTCCGATCTCGGTGAACTTCGGCGGCAATGTCAG
TP78511	TGCAGGAGCTCATCGTGTCTGGCAACGGCCTCGGCGGCGA[C/G]TTCCCGAGATCGATCCTGCGGTG
TP78531	TGCAGGAGCTCCCGCAGCGTGAGCCC[A/G]CGCTTGTTCACTGCCATGCCCATCCTCTCCGAGGCCA
TP78559	TGCAGGAGCTCGACGTCTCGCACAACAGGCTCAACGGC[A/G]CCGTGCCAGACGCGCTCGGCAGGCT
TP78587	TGCAGGAGCTCGTCCACTGCCTCTCCTATGTGTATGCTCACTGACATTGCATGTACTCAG[C/T]AGA
TP78599	TGCAGGAGCTCTCATCACTAATATCACTGCC[C/T]GTGCTCGCACGGCACATGCTGCTCTTCCCACT

Table A2 (cont.)

TP78616	TGCAGG[A/G]GCTGACGCCCAGCCGCCGCCCGCCATAGTTCCTTAGCGCATGAATGGGAGGAGAAAG
TP78662	TGCAGGAGCTGGAGAAGGCCATCGCCGCGCAGTCGTCGCAATGACCTGAC[G/T]CGAAGGAACGAAC
TP78670	TGCAGGAGCTGGAGGGCAGGAATGGCTGTACGT[A/T]CGGTACGCAAGGTCGGTCGTTGCGTGCTCA
TP78683	TGCAGGAGCTGGTAATTCCGAGTTCCGACTAGTTCCTCTCGCGTTTGCGT[C/T]TGTACCTGAATTT
TP78686	TGCAGGAGCTGGTCCCGAACG[C/G]CAACAAGGTCGGCCCCCCCTCTAGCTCCTTAATTTCTCCTCT
TP78690	TGCAGGAGCTGGTG[C/T]CCAACGCCAACAAGGTGAGATCAATTGCATACACGCTTGCTTTGAGAAG
TP78695	TGCAGGAGCTGTCGCCGTTCAT[C/T]AAGTTCGCGCACTTCACCGCCAACCAGGCCATCCTGGAAGC
TP78705	TGCAGGAGCTGTGTCAGAAGCGGCGATGGGCGCC[A/G]CCGTTGTACGAGCCTACCCGCGAGGGTCC
TP78721	TGCAGGA[G/T]CTTCCTCCTTCTCCTTCTCATCAGGAACTAGAGACGCCACATATTTGTCGGGTTGC
TP78729	TGCAGGAGCTTCTTC[A/G]TCTCGGCAGCGGGGTTTCTTCTTGTTGGCGACTTGTGTGGTGCTTCTT
TP78732	TGCAGGAGCTTGACGGATCAGTTTCGTGGTGCTGGTCCAGTGAAAGACGATCATATCGCCGAT[G/T]
TP78738	TGCAGGAGCTTGCCCTGCGACACG[A/G]CCAGCGCGGCGAAGGGCTGGCCGAGGGCAGCGGAGACGT
TP78744	TGCAGGAGCTTGTCGAAGGAGAGAAGTAGGCCACGGTCGATGGGAC[A/G]TCCCCAGTCCTCGTCGG
TP78756	TGCAGGAGGAAACA[A/G]GCGACTGACTTCCCAGTTCCCACGGATCAATCGGTAAATCTTAAACGAA
TP78760	TGCAGGAGGAAACTCCCAAGCAATTCCCCAAAACAACGA[C/T]CAAACTAATTTTCCGCAACACCGC
TP78761	TGCAGGAGGAA[A/G]CTCTAGACCGTACGCCATGGATGCGTTCATGGCTTCATGCTCGCTGGATGAT
TP78785	TGCAGGAGGAAGGGTTCCCGAGCTGGACGGGGAGC[A/G]GCGAGGAGGACGACTACGACCACGACCC
TP78787	TGCAGGAGGAAGGTGATGAAGGCGATGAGCCTCAAAGGTCACGAT[A/C]GCTCCTCTTCTTCTCTGC
TP78793	TGCAGGAGGAATGCCC[C/G]ACCCATGGCCGCCTCCCCGAGCCGCTCCTCCAGCTTCCGCACCTCAC
TP78795	TGCAGGAGGAATGGAGGATGGCTGAGATCGACTGCAAAGTGCAAAGTGACTGGAGGACTACTA[C/G]
TP78822	TGCAGGAGGACCTGGATGGCGAGCTCTGGGCTGACGGCCCCGCTGGAGACGAG[C/T]TCGTCCAGCG
TP78828	TGCAGGAGGA[C/T]GAGGCGTAGCACGACGGCGTTGGCGTGGCGAGGTCGAGGCAGGTCACTGCTAG
TP78831	TGCAGGAGGACGCCGAGAAGGTGAACCTGTGGTTCGAGGTGCCTGGGC[A/T]GTCCCAGTATGACCT
TP78832	TGCAGGAGGACGCGGAAGGTGTCGCGGATGTTGTTGCTGT[C/T]GAACTCCTTGAAGCTCTCGGCGC
TP78848	TGCAGGAGGACTTCGCGCACCACCACGGCGTCGGCGACGC[G/T]AGGTTCGTGCAGGCGTACGGCGA
TP78856	TGCAGGAGGAGAAGATGAGAAGCAACGACAGCGG[A/G]GAGTAAGTGGCCGACTCAGCCCCACCCCC
TP78867	TGCAGGAGGAGACGGCGCTGCACGCCGTCCTCGAGGGCGCCCTGGGCCGCGCCGCCGTCAC[C/G]CT
TP78878	TGCAGG[A/T]GGAGCAACCGCGCGTACGCGGCGGCGCGGTCGGGCTCCGCGGCAATCTCCGCCACCT

Table A2 (cont.)

TP78883	TGCAGGAGGAGCAGACCATCATCCAGCTCCACGCTCTCCTCGGCAACAGGTGA[A/T]CATCACCATC
TP78889	TGCAGGAGGAGCAGGGGGCCGTGCC[A/C]TGTGTTGCAGCGTGCAAGACGGTCATGTTTGACGCTGC
TP78901	TGCAGGAGGAGCTCGTCGCAGAGGTGGGCCAGGGCGGAGTAGGACTTGTCGGAGAGGGCGGCC[A/T]
TP78903	TGCAGGAGGAGCTGAGGAAGGAGAAAGAGGAGAAGGCGCGCGCCCTAGA[G/T]GAGATACAAGAGCT
TP78911	TGCAGGAGGAGGAATGG[C/T]GTTGTCACCTTGTATTGATGCACCAGCAAAGGATTTTTAAGAAGGG
TP78918	TGCAGGAGGAGGAGCCTGCGGCGGTCGACGACGGCGAGGCAGTAGT[C/T]TTCCCCTCGCTCCAAGC
TP78920	TGCAGGAGGAGGAGCTACCATTGCCGCTCCGTGCGCCCGTCACC[C/T]AGACGATGTGGCGATGTCG
TP78946	TGCAGGAGGAGGTCGAGGTCCTGCTGCTTCTGTTCATGTT[C/T]GTCTCCTGCCTCTGCCTGGGAGT
TP78951	TGCAGGAGGAGGTGGTACTG[G/T]CCCTCCACGCCCACGTGGTCCGCCGAGTGGAGGTGGAACAGCA
TP78957	TGCAGGAGGAGTGAGATTGCAGGGCGCACGTACCAGATC[C/T]TTCTGGACGCCGAGAAGGAGGCTC
TP78976	TGCAGGAGGATGAGTCGGGCCTCCTCCGTCCCAT[C/G]GACACCAAGACCCTCGTCCACGCGCAGTA
TP78983	TGCAGGAGGATGCGGTTAGCGAT[A/C]ATTTGTGCGGCAGGCGTCCGCGCAGCCCGCAAAAAAGACT
TP78989	TGCAGGAGGATTCCTTATGCCGTTGCGCTGAAGCGCAACCAC[C/G]AAGCGTGCGCGGCGCTGCTGA
TP79011	TGCAGGAGGCACCGCGCGTAGAGGTGGAGCGCCGCGACGAAGGCGACCGCCGCCGAGAGCGCG[A/G]
TP79012	TGCAGGAGGCACGGAGTCGGAG[C/T]CAGAGCTCCCTCGGTCTACTTCTCCTCCGCCCCCGAGCCCC
TP79036	TGCAGGAGGCAGTGCCAACCAGCAGTAGTAGTGTTGTCCAAG[G/T]CCAATGAGCAAAGAGAGGACA
TP79037	TGCAGGAGGCATATCAGCCCTGGTCCTGTACTTCGT[A/C]CACACTCAACTCCCAGTGAGACCTGTC
TP79045	TGCAGGAGGCATGGTGCGCGCGCGTCCGAGC[A/G]AGCGGCTTATTGCAACGTTGGATTCAGCAGGA
TP79046	TGCAGGAGGCCAATGCATTATCATTCGGTTTGCAGCGTCAGAAAAACTCTTGTTT[C/T]TGTGGCTT
TP79051	TGCAGGAGGCCACGGTCAGCTGGGACACCGCGACGTGCTATGAACTGAC[A/G]GCAGGACGTGGGTA
TP79063	TGCAGGAGGCC[C/G]AGAACTGGCGGTGCCCTGTGGAACTCGCGGTAGCTGCGGATGACATCGTCGT
TP79069	TGCAGGAGGCCCAGCGGCTGGTGGACGAGGTCGC[C/T]GAGCGGGTCGCCGAGAGGGAGCCGTCGCT
TP79075	TGCAGGAGGCCCGTGAAGTTGCGCATGGTGGC[T/C]GCGGCGCCGTTGGCCTGTCTCACCACGTAGT
TP79086	TGCAGGAGGCCGCAACACGTGGGACCCACGTTGGCCCCGCCCACC[A/G]CCCACTGTGGCGATCAAG
TP79090	TGCAGGAGGCCGCCATGGTCAGGTCGTCCATTTTGGTCGTCCTTCCTCTCATGCTC[C/G]CCACCTT
TP79099	TGCAGGAGGCCGTCTGGGACGCCGAC[A/G]TAGTCGTCAACGGCCTGCCCTCCACGGAGACCAGGGA
TP79104	TGCAGGAGGCCGTGAACGTGTCCCTCGCGAACCTCAAGACCTACCC[C/G]TTCGTCAAGGAACGGCT
TP79114	TGCAGGAGGCCTTCCAAAATCTG[A/T]ACAACAGCTCCCATGGTCGGCCTAGATGACTCATCTTCCT

Table A2 (cont.)

TP79127	TGCAGGAGGCGCACCGCTGCATGGACGCCTTCTTCACGCTCCCGCTGTCCGACAAGCA[A/G]CGCGC
TP79141	TGCAGGAGGCGCTGGAGCGCATCATGAAGGGCCGCACCGC[C/T]GTGCTGGTGGCGCACCGAAAAAA
TP79146	TGCAGG[A/G]GGCGGAAGGCGGAAAAACACAGTGGGTGAAGAGGGACGGCCCGAGCTTGGCTGATCG
TP79152	TGCAGGAGGCGGAGGACGAGGCGGCCAAGGA[C/G]TACCCGCAGTCGCTGCGCCACCGAAAAAAAAA
TP79155	TGCAGGAGGCGGATGACGCTGCGCCGCGCGTCGTGCCGAAACGGGCGC[C/T]CCGTCCCCGTGAACC
TP79161	TGCAGGAGGCGGCGCTCGATGCCCTAGGCCTGCTCGACTTCTTCCGCCTCGA[C/T]CTGCAATCCGA
TP79169	TGCAGGAGGCGGGCCTCGCCTACTTCTTCGTCCCGTTTACTCTCCGCG[C/G]CCCCCAAGTCACGTG
TP79172	TGCAGGAGGCGGTAGCAGCGGCGCACCTCCACTCACTTT[C/T]GCCGAGGGAAATGCCACCCTCAAG
TP79186	TGCAGGAGGCGTGCGTACGTGTGAGTCGCATCAATGGCACCAGGCCATGCAGGAGGAG[G/T]AGGAG
TP79198	TGCAGGAGGCTCACGGCGCCG[C/T]AACGGCTGCGGCCGCGGCCACGCGCGCAGCCATGCAGCCCAT
TP79214	TGCAGGAGGCTGTGAACGTGTCCCTCGAGAACCTCAAGACCTATCCCTTCGTCAAGGAAGGG[C/T]T
TP79237	TGCAGGAGGGAGAGGAGACGGTGGAAACGCGACCGCGAC[A/C]GCCACCGATCGGGTCAAACGCGAC
TP79248	TGCAGGAGGGAGGGTTCCCGAGCTGGACGGGCGGCGGCGAGGAGGA[C/G]GACGACTACGACCACGA
TP79276	TGCAGGAGGGCCACCAAGCACGC[A/G]ACTGTCCCCGCGCCATCCACACGGACAGCTGGGCTGGAAA
TP79279	TGCAGGAGGGCCTCGA[C/G]CCGACGAACTTCACGCTCGCCAGCGTGCTCAGCGCGTGCGGCGCCGT
TP79282	TGCAGGAGGGCGACGGCGACCTCCCCGACGACTTCGAGTTCGAC[A/G]TCCACGTGGACGTCACCTT
TP79286	TGCAGGAGGGCGCCAAGGAGAAGGTGA[A/G]GAGTGGAGGAGAGGGTGGGAGGGATGAGACGAACGT
TP79301	TGCAGGAGGGGAGCCCAGGG[C/T]TGGAGGCCGCCGCGCAGTACATCAAAGGGGAGCTCCAGGGTCT
TP79313	TGCAGGAGGGGCATCGC[A/G]ACACTGAGCGTACCCCACACGAGGCTGATGCAGGTGGCGATGCAAT
TP79321	TGCAGGAGG[G/T]GGCCCGTTAGGCCCACGTCAGCGTCATGGCCCGCCTCACCACGACTCGTTTATC
TP79322	TGCAGGAGGGGGCCGCGGGCGCGGCGTCGTACGCGCAGGCGCAGCGGTCCCCGCAGCAGGGT[A/G]C
TP79328	TGCAGGAGGGGG[C/T]GGCAGAAGCAGACCAGGCGGCGGTCCGCGGGGCTACGACGGAGCTGAAAGC
TP79333	TGCAGGAGGGGGGCCTTCTTCTAGCAAGCGGTATAGGCGGTCGTA[C/G]TCGTACGCGTGGTGCTCC
TP79348	TGCAGGAGGGT[C/G]AGAGAGGTGAGGTTCTCTAGGCAGGCTGGGAATGACCTGTCCAGCTCATTGC
TP79349	TGCAGGAGGGTCCGCCACGGGTTCTCGATGGCCTTGGTCGCCTCGCTGGCCGCCAGGAGGTC[A/G]T
TP79358	TGCAGGAGGGTTCAGGGCCACGTTC[A/G]GAGTTTCACAGCCCCACCATGCCCACCTACACAGGTTC
TP79386	TGCAGGAGGTCAGCGTCG[A/C]GTCGCGGAAAATGAGATATTGGTGCTTAGGTACTATCCTCGACGG
TP79390	TGCAGGAGGTCATGGCGAGGCGTGGG[A/G]CAGAGGCGATGATGGTGCGGGGAGAAGAGGGAGGGGG

Table A2 (cont.)

TP79396	TGCAGGAGGTCCTCGACGGCCCAACCGAACGGTGGCAGGAACGGCGACG[A/G]CGGCACCTCCCGTG
TP79403	TGCAGGAGGTCGAGTCGGCCTCCTCGGGCAAGCTGAAGCTGAACGCACGAAGAAGATGAAGC[G/T]C
TP79431	TGCAGGAGGTGAAAAGGAGAGGGTAGTATCCTCCACGTGATGAACCAC[A/G]CACTGCCATTTCCGT
TP79432	TGCAGGAGGTGATGACCTCCAAGGGCACCATGTCCGACGAGTCCCTCGT[C/T]GCCATGGACTAGTA
TP79449	TGCAGGAGGTGGATTGTGCAGCAGGCATAGCTCA[A/G]TCTCATAGCGCTCGGAAAACATGAGTTGT
TP79454	TGCAGGAGGTGGCCTACTGGCATGGGTTGTGGCTG[A/C]GGGGTCAGCACAGACAGACTGTTCGACT
TP79457	TGCAGGAGGTGGCGCGCCTCGCCCG[A/C]GAGCAGGACGCTCTCGCCCAGGAACGCACCATGGCCGC
TP79460	TGCAGGAGGTGGCTCCAGA[C/T]TCTTCGATCTACAACGCGGTCATCCACGGGCTGTGTTTGCGAGG
TP79465	TGCAGGAGGTGGTTCTGCTGCACTTGC[G/T]CCAGACTCGTCCAGCGAGGTTGTGGTGACCCCAAGA
TP79469	TGCAGGAGGTGTCCCGCGCCTTCACCGTCTGCCTCTCCATCATGAGCTCGCCCGCCCGCGC[C/G]CC
TP79484	TGCAGGAGGTTGGGCGACGCGTAGAGGCTGG[A/C]CTCTCGTGCGGTTGCTTCAGTTCCAGCATTGC
TP79499	TGCAGGAGTA[A/G]TCTACAATAATACAAGAGCTCTCTCTCATAATACAATATGAGCAACAGGGTGC
TP79526	TGCAGGAGTACTTCTACGAGCAGGT[C/T]CCCGACGGCATGCGCAGTCTGGGCATCGGCCTCTACCT
TP79533	TGCAGGAGTAGATAACAGTGCCATGATTAGTGCTGGACACAGCTTCTCTGGCGGAGT[C/T]GATAAA
TP79534	TGCAGGAGTAGATGTTGAG[A/G]CCGCGCACATTCTCAACGCAGCTTACCTTGATCCAGAAATCTGC
TP79537	TGCAGGAGTAGC[A/G]GGAGCGTTTTCACGGACGAGCTGGACCTGGACCTCGCTAGGTCGACCCCCC
TP79555	TGCAGGAGTATAGCATGTGCCTCCGAG[C/T]ATTTCGCATTAAGGTAGAGGGCTTCTCACCCAGTTC
TP79566	TGCAGGAGTATTATT[C/T]ATAATGACTTCGAGGACCACCGCTTGCAATTGCAAGTCACAATTTGGC
TP79586	TGCAGGAGTCCAC[C/T]ACGGTTCGCGTGCGCACCCACTTCTGCCCGTACTTGGCGACGCAGTACGC
TP79646	TGCAGGAGTGAAAC[A/T]AAATGCAGGGTACAAATTCGTTGGATCCTGCAACCAAACCAGCCATTAA
TP79647	TGCAGGAGTGAAACCAGAAGGATGACATCAGCTCCAAATCGAAGCACCTCAGCCC[A/C]CTCCGCCC
TP79653	TGCAGGAGTGACCACGACGCCCGAACAGCAAACACCGCATCGC[A/G]CGCCCATGTGCGGCCCTCGC
TP79662	TGCAGGAGTGAGGAGCGCAACAGCCAGCAAAAAAAACATT[A/G]GGATAATTATCTATTTGACACTG
TP79667	TGCAGGAGTGCAGATTACCTGCTTCCCTTTGAAGCAAGCAAAGCACAGATCATAGCTACTC[A/C]TG
TP79668	TGCAGGAGTGCAGCACGATTGCGTCGTCCTTCCATTCAATTCCGAGCCCT[A/C]TCGCGTAACGGGT
TP79670	TGCAGGAGTGCAGGGCGAGGGCGA[A/G]GGCGGTGCTGGCGGCGTCGGTGGACGCGGTTGCGAGGAC
TP79689	TGCAGGAGTGCCGCGATGAAGGCGATCAT[C/T]AGGCTGACACAAGGAGATCAGAGGTTGCGTCAGC
TP79694	TGCAGGAGTGCGCAG[A/G]AAAGGTAGTGTGGGCGTGTCGTTCTTGCTTCGACATGGAGGCTGCCTG

Table A2 (cont.)

TP79695	TGCAGGAGTGCGGCACGTCTATGGCACGCC[A/G]CAATTGCTGGAGGGAACCAAACACTTGCCTCAT
TP79775	TGCAGGAGTTCAAGACGGACTACAACCAGACCCACTTCGTGCGCAAC[C/T]CCGAGTTCAAGGCCGC
TP79776	TGCAGGAGTTCAC[A/G]GGGTGGCAGTTGGCGCTGCTGGGGTACCAGTCGCTGGGCGTGGTGTACGG
TP79799	TGCAGGAGTTCGTTGCGTGCAATTCGCACGTCTCATCAGGTAGCCGCGCGCGCGCTGCCC[A/T]G
TP79805	TGCAGGAGTTCTTCTACGACCAGGTCCCCGACGCGCTGCGCAGCCTCGGGCTGGCATT[C/T]TTCCT
TP79815	TGCAGGAGTTGATGTCCCAGTAAGGG[C/T]CTGTTTGACATGGCTCCACTCCAGAACTCCAGCAACT
TP79831	TGCAGGAGTTGCTGCACACGAACTCCACCATCTTCCACTTGGA[A/G]GGCTTCGACGCCGACTTGTT
TP79849	TGCAGGAGTTTAGCAGTACTATG[A/T]GCAAGACTCTGGGCTCCAGGTGCAGGCTGGAGATCGACGC
TP79853	TGCAGGAGTTTCTATCCGTTACTCCGCGATTACTC[A/T]TCCGTCCCGTTCCAATCTCCTGCATGCA
TP79881	TGCAGGATAACGACTGCCGCGGTTTGTGTGATCAGGAGAGCGAAACTGCTGATCATTTTGCTC[A/C]
TP79886	TGCAGGATA[A/G]CGGCGGCGAAGGCGACGAGCAAGGCGATCGTCAGCAGCGTGCACTTGTTGCGTG
TP79895	TGCAGGATAAGGACGACGGACGAGACAGACGATGGATCGGATC[A/G]ATCACGCGCACTGTGCACAT
TP79926	TGCAGGATACCTGTGCTGGGCTTTCCATAGCAGCAGGCGCAGCCGCAGCCGCAG[C/G]CGCAGGCGC
TP79956	TGCAGGATACTGCACAAGG[C/T]AGGCGACCAGTACAGCAAGCTGATGATGGTGAAGAGCCCCTACT
TP79961	TGCAGGATAGAAGCATGACAAAGCAGGAGGAGTCTTAGCTAGCTCCGATCCCATCCATCG[C/G]TTG
TP79973	TGCAGGATAGATGTGCGGCTCATCACGGGAGA[G/C]TCGCTGCACGGATTCCAAGCGAGAGAGCTTC
TP79975	TGCAGGATAGATTGCACTGTAGCACTG[C/T]GCTCTTGCGACCAAGCAGACTCATTCATCAACTCGT
TP80035	TGCAGGATATATGGGCCAAGGTCAGGCTTACAGAGAAGTGCAGCCACCACACTACTATGG[C/T]GGT
TP80046	TGCAGGATATCCGTGATCGGCTGCTGCTGGCTCAGGATGTCATGACTGAGCACCAGAACAA[G/T]AA
TP80086	TGCAGGATCAAAGACTAGGTGCTCCTTGTGAAAAAAGTTTTCTGTACCCAAATGTGGGC[A/T]TGGG
TP80089	TGCAGGATCAAATAAAGGGAGCAAAATTGAGGGCCAGATGGGATTATAGGC[A/G]CGGGTATAGGTG
TP80096	TGCAGGATCAACTTTCTGAGGTATACCAAGCAGGTGGCCA[A/T]GGGGCAGTGGGCTATGATGGACG
TP80105	TGCAGGATCAAGTTTTTTGG[A/G]ACAGAGGGAGTAACCTAATAATAGATTAAATAGCTGGTTAAGA
TP80111	TGCAGGATCAC[A/G]ACGTAGAAGGTGGGGATTTTTCTGAACTCTTCTACGGATCTGCGACACCAGA
TP80112	TGCAGGATCACAATTTTGGATGTGGAGAGATGGA[C/T]GCCGCCGCGGCGAGTCGAATTGCGACGGG
TP80130	TGCAGGATCACGTCCTCCCTGGGCGCGAAGTACTCGG[C/T]GTTCATCTCAGAGACCTGAATCGATC
TP80138	TGCAGGATCAGAGAAA[C/T]CCACGACCTCTATGGGCACGTCCATCTCGCCGTGGCAGAGACGACAT
TP80154	TGCAGGATCAGGCATTCTTGACACAACAGTAAGCCACTCGTGACCAGAGTTAC[C/T]GCTAGCTAGC

Table A2 (cont.)

TP80160	TGCAGGATCAGGTTCTTGAGCGCGTAGTT[A/G]GGCGCCAGCGACAGGTGCGCCAATGGCTGCCGCG
TP80172	TGCAGG[A/G]TCATATAGATTGTATGCATGGATTCCTCCATCAACTAACAATGCATACAATAGCTCA
TP80180	TGCAGGATCATCTCCCCTCAGAGAGAACA[G/T]TCCAAGAGGCTGCACAAACGCTGGTGGTAGCCGA
TP80203	TGCAGGATCCACACTGACGCTG[C/G]TGGTGGCGATGGTCCTCTCACCGTAGAGCCTGACCGATGAC
TP80210	TGCAGGATCCAGCGCGCCCAGCTGCGGGCCTGCGGCAGTGTCACATGGCGAGCCCAAC[A/G]GTTCA
TP80252	TGCAGGATCCCGTTATCTGCGGAAG[A/T]GGCCGATGCGCTCGGAGCTTCCGCCGCCGCCGCCATCG
TP80256	TGCAGGATCCGAGCGCATGCATGCATGCGCGG[G/C]CGCCGTACGGTGTGGTGTACCGACGCATGCA
TP80285	TGCAGGATCCTCATCAACTCCTTCGAGTCGCTGGAGCCGCGCGCGATGCGGGCCCTCAG[G/T]GACG
TP80295	TGCAGGATCCTGGACAGAGGGGTTCCTCAGAGAGCAGCGGCGCT[C/T]CGTCGGCGTCGGCGCTCGC
TP80309	TGCAGGATCCTTGCCCCCAGCGACAGCTTGCCCTTCACGGTCTCGTACAG[C/T]TTTGGCCCCAGAG
TP80316	TGCAGGATCGAATAAAGGCCGACAACCACAGTCATCGACGAATTTCCATT[A/C]GTCGTCCCCGTCC
TP80321	TGCAGGATCGACGACGATGCTAGGGTTTAGGTGTGATTC[A/G]TGTCGATTTAGCTGAGTGGCGCGT
TP80328	TGCAGGATCGAGCGGATTCTCAAGGTGC[A/G]GAGCAGCGACAGGACCGTGAAGAGGTTCGAGCAGT
TP80333	TGCAGGATCGATCCACATCGAGGACGAGC[A/G]GCATGCAGACGCAAACAAATCTCAACTCCGACGC
TP80343	TGCAGGATCGCAGGCTGCTCCTGGACATCATA[T/C]GGTGACTCGCGCCAAGGCGGGCATCTACAAG
TP80365	TGCAGGATCGGATAAAGGCCGACGACCACAGTCATCGACGAATTTCCATTCGTCGTCC[C/T]CGTCC
TP80372	TGCAGGATCGGCACGCTGCTCATAGTGACGAGCCTCAT[G/T]AGAGGGCAAGCCGCACCGCTCACCC
TP80376	TGCAGGATCGGCGGCCCCTGGAGACGGAGGCCGCGCCGCAGT[A/G]TTCGGCGAGCTGGGGCGGCGG
TP80392	TGCAGGATCGTCGCTTAGTACAAAACACTACTACTTACAAAAGG[G/T]ATTTGTCCACCAATTGTTG
TP80446	TGCAGGATCTCCTTCCCTAACAAATGACCTCTTCTCCCAGCA[C/T]CCTGTTCTTGATGAGAAGACA
TP80462	TGCAGGATCTCTCAATTTGAGTGGACAACATTCATATTCATCATATGTAATCCGTACGTA[C/T]GTG
TP80464	TGCAGGATCTCT[G/T]AAAGCTTGGCAGAGAATGCGGCATCGTAGGCTCGGTGCAGACAGGGCCGCA
TP80465	TGCAGG[A/G]TCTCTGAAAGCTTGGCAGAGAATGCGGCGTCGTAGGCTCGGCGCAGGCACGGCCGCA
TP80488	TGCAGGATCTGGCTGAGGCAGTGCAGGTCATCAGGCAGTGGTGCCGTTAGAACGACCAG[G/T]TCGC
TP80492	TGCAGGATCTTAACTGCTGTGTCCATAATGCTGTGGG[A/G]AATCGTTAATAAATGGGAATATGTTT
TP80498	TGCAGGATCTTCAGCCTCTCGTTGATCCTTTCCCTCCTCTTCTGCAAA[A/C]CCAAAGAAAAGAGCA
TP80542	TGCAGGATGAAGTG[A/G]TTGAGGTCCTGGTCGCAGGACACCACCGTGGGGGTGCAGAACAGGTGGG
TP80546	TGCAGGATGAATGCG[C/T]GAACGGCTAGTATCCGTGAGTCCGTGACCATGGTGGAGAGGGAGGCTA

Table A2 (cont.)

TP80556	TGCAGGATGACATCAT[A/G]TCATCCAAAAAATCAAATGGGCTCAATATTCTCTTTGTTCGGCGAGA
TP80557	TGCAGGATGACCAGCTGCCATG[C/T]GGGGCCCACGTCTGTTTAACGTTCACTCAGCCCGTATATCT
TP80560	TGCAGGATGACCGTATTCACTAAGGTTAAGGTA[A/G]CGTGAGAGTCAATCTTGGATCGAATTGATG
TP80561	TGCAGGATGACCTGGAGGCCCTGCACATAGCACAAGCGGACCTGC[A/G]CCGCCAAATCCTTGGGTT
TP80575	TGCAGGATGA[C/T]GGGATCCTTGCGATACCGACAGTTCCTGGTTCTCCACCAAAGCTGCGCATGGA
TP80587	TGCAGGATGAGCAGGGTGCAGTAAAGAAAAGAGAACGCGGCCTG[A/C]CACGAGGTCCCTTCAGTGT
TP80588	TGCAGGATGAGCCAGAGCGCGTAGAAGACGCAGCTGCTGATGCAGAGCAGCGAGCCCA[C/T]GACGC
TP80612	TGCAGGATGATGAGCGGCAGCGCGAAGTCCA[A/G]CGGGTTCTCCCCCTGGAACGCCCCGTTCGACG
TP80633	TGCAGG[A/G]TGCAAATGGAAATGGCCAGCCAATTCATCATTCCCAGTATCTTGGTGAGACCAGTAA
TP80640	TGCAGGATGCACAAGATAAAGTCTACTGATGAACTTCTTC[C/T]CCGAGTTAGCAAGCACTGTTGTC
TP80660	TGCAGGATGCAGCTCTGGCGTGAGGACGATATAGCAACCCAGGCGCCCAGGAGGGCCCGAC[A/G]TT
TP80671	TGCAGGATGCAGGTTGTCGTCGGGCGTGCAGTC[A/G]TGGTGGAGGTAGCACAGCCCGTGCGCCGCC
TP80700	TGCAGGATGCCCTTGCAGCCATAGGC[A/G]AGGATGGCGCCGAAGGCCGTGGGCGGGCGGTCGGCGA
TP80719	TGCAGGATGCGATGATGGGCGAGCTGCACTCGGAGGGCAAGACGGCCGAGGACATCAGAG[A/G]CAG
TP80739	TGCAGGATGCGGTCCCAGTCGACGCCGCGGAAGAAGGGGTGGGCCTTGACGCC[A/G]CGCGCGCCGA
TP80751	TGCAGGATGCGTGCGTGCGTGCGTACGTGCCGAGGGCGGGCG[A/G]GCTGCTGGACCATTGAAATTG
TP80774	TGCAGGATGCTGCTGAGCG[C/T]CATCTTGGCCTCGACCAGCGCGAAGTTCTGGCCGACGCAGATCC
TP80797	TGCAGGATGGAACTGTTATGAA[C/T]GACGTATAGGAATATGAAGTACACACGATTTAACGTGGAAA
TP80805	TGCAGGATGGAGAAGACGGCCGCCATGGTGCCGCGCAG[A/G]TAGTTGGCGTCCAGCGTCATGGCGA
TP80811	TGCAGGATGGAGGTGGTGGACGGGAGCACGAAGGAGACGTTGTT[C/G]ATGCTCGCCGCGAACCGCG
TP80820	TGCAGGATGGATGCATGGGTGAATCATTTGCCGTTGTCGCTTGATCCAGCATAGCCG[A/T]ATGGGT
TP80833	TGCAGGATGGCCCCCCTCCTGGTCCTGGCGCTGCTCCTGCTCGT[A/G]GCCGCCGCCGCGTCGGGCA
TP80836	TGCAGGATGGCCGAAATG[A/C]GCAGAAAAATGGACGCGGCCGTCGGTGGCTACCAATAAATGGACT
TP80865	TGCAGGATGGGCAGCCTGCGCCAGCCATCCGCCCGCGTGCG[C/T]GCGCGCTACCTGTACGTGTACG
TP80884	TGCAGGATGGGTAGGCAGTTCAGTATTGCGGAAATCAAAACAGC[C/G]ACCATGAACTTTGATGAGT
TP80898	TGCAGGATGGTTATGC[A/G]TGCACTTTCTGCGACCAGCATGCGGAGACAATCAGCCATTTGCTGCT
TP80900	TGCAGGATGGTTGATGTACAATCTATTGACATAGTTGGGGTTAGGATCAGGAACATAAAA[C/G]TCA
TP80901	TGCAGGATGGTTGCTCCGCACCCCGCGGCCGCATGCACGCGAGACGCGACGT[C/T]ATCCGTCGTCG

Table A2 (cont.)

TP80917	TGCAGGATGTACTCGATCGACTCCTTGGACCCCGCGCGCTAGCAGTGGGAGGTGCACGTG[A/C]C
TP80927	TGCAGGATGT[A/G]TTTGCTCGCAGCAGAGGTGACGACAATTGCACATTCTACGCTACAGCCAAAAC
TP80936	TGCAGGATGTCCCAGAAGCGCGC[A/G]ACGAGGAGCGTCTCGTAGTCCGCCAGGCGATCGTCCGCGG
TP80940	TGCAGGATGTCGAGCGCGCGCGAGGTGTCCTTGACG[C/T]GGCACCATCCGTCGGCCAGGGTGTTGA
TP80941	TGCAGGATGTCGAGGTCGAC[A/G]ACGTGCACGCGGTCCTCGCCGTGGAAGGCCTCGAAGATGGCCT
TP80947	TGCAGGATGTCTTAGCTGCGTATGTATAAGGTACCTTGGCGACGAGCTGCG[A/C]GCCAAGGACGTC
TP80955	TGCAGGATGTGCATCGGCGCCGAGACTGTC[G/T]GCGCCTCCGTTCTCTTGGAGTGGATGAAGTGGC
TP80971	TGCAGGATGTGTCGTGTGTGTGTGGCTGAGGAACTAGTGGCCATTGTCACCTACCTCTGG[A/G]GGG
TP80985	TGCAGGATGTTGC[A/G]CCAGGGGTGCGCCACCAGCTTGGACTCCTCGCTGGCGGCCACCAGGTCGT
TP80991	TGCAGGATGTTGCGGGTGAAGGAGAAGTAGGCCATGTCGGGGCGGCCCCAAGGCCC[A/G]TACACGG
TP80992	TGCAGGATGTTGGACAGGTCCCCTCCCTGCATCATCACATGATCCACCTGCGTATATGCAAA[C/T]C
TP81017	TGCAGGATTAATTGAATGGCTGAACATTCCAATCGCGACAG[C/G]TTCTCACCTTGAACTTGGTGTC
TP81026	TGCAGGATTACATCGAAGCCACACTTCAATCCATCAGGTACAGCAATTAATTAATAGCATTC[A/G]G
TP81031	TGCAGGATTAC[G/T]CCCAAATAAACGTGCTGGCCCGCTGGGTTTCCATTCTACCCTGCTTCGGGAA
TP81039	TGCAGGATTAGAAAGAACTTGTGCACTGTGTGTGTGATCGCAGTGACGAGCTAGTGCGTGGC[A/G]C
TP81040	TGCAGG[A/G]TTAGACATGCCAAACACACAGGAAACAGCAGGACGCGCATCCACCCGTGCACCAAAA
TP81065	TGCAGGATTATAATTGAATAGTAGCTGAACATTCCAATCGCGACAGCT[C/T]CTCACCTTGAACTTG
TP81071	TGCAGGATTATGTTATGATTCCC[C/T]TTTGCAAGCAGAGTATATGCTTCAGAAAAGATGGTGCCTT
TP81076	TGCAGGATTATTTATTTGACCACCCACACTTTTGGTTTGACTCCTCTTGCTGGTGGGTGC[A/C]TGC
TP81080	TGCAGGATTATTTGGAATATATGCTCTGGCCTCTGGACGACACCAGTCACCAGACGAGTGAGA[C/T]
TP81106	TGCAGGATTCAGATTCGATTTGAGGAGGAGCAAGC[A/T]GAGTACCTCGCGTCGAAGATCACGAAGC
TP81111	TGCAGGATTCAGGTAAACAATAA[C/T]TCAATCTGTAACTTGCAATAGCCATGACATTAGACATACA
TP81117	TGCAGGATTCATGGATGTAATGTAAAAATTTCAGATTAATACGCCCTTTTTTA[C/G]TTTCTGGATT
TP81168	TGCAGGATTCGGTCTTCTCCGATGAGGAGACCTGGTGTCTGTCTG[C/G]CTTTGTCCTCCCAGATAC
TP81183	TGCAGGATTCTCTCCCTGC[A/G]TGAGGCTTGATCCTGCTGACATGCCTGGCCTCTAGAAAGGGAAG
TP81188	TGCAGGATTCTGCCATGCCGAAGTCACCTCGTTGCCACCATTTGAAGGGAAAGCCTCCCATGA[A/C]
TP81204	TGCAGGATTGAACGCCAAG[C/T]CCGCGCCGCCGACTCGGCGCGACCAATACCGCCTCATCGGCGGG
TP81205	TGCAGGATTGAACGCCGAGCACGCGCCGCCGATTCGGCACGACCAAGACCACTTCATCGGC[A/G]GG

Table A2 (cont.)

TP81245	TGCAGGATTGGCAGCCACCT[A/G]GAAATAGATATTCAACTCCAACAACCCCCAGACTTGGAAACGG
TP81247	TGCAGGATTGGCATGCTGCTCATGGTGACGAGCCTC[A/T]TGAGAGGGCGAGCCGCACCGCTCACCC
TP81254	TGCAGGATTGGGACGCAACCCCGTCTCTGGTCTGGCCCACG[C/T]GAGCGCCGCTGCTGGTGTAGCG
TP81258	TGCAGGATTGGGTTGGCCAGAGGAAGACGGCGATCGGATCCCAGCTCTGGTGGAACTGGGAG[A/C]T
TP81270	TGCAGGATTGTTACA[A/T]TCAAACATTCAGTTAACAAGCAAAGTCAGCCTTGGTGCTGGGTCTCAG
TP81294	TGCAGGATTTCAGACGAGCGCTATCTCAAATGGATTGCGTATTG[A/G]CACTATTCTTTTGTTCTCT
TP81309	TGCAGGATTTCTTGTTGGGCGCGAGGAGC[C/T]TCGTGTTGGCGGAGAGCTTGGGCGACGGTCACCG
TP81310	TGCAGGATTTCTTTCTT[C/T]CCCTACAGATATTCCCAAAGAATCTTCTGTGTTGCTCTCCTCCTCG
TP81338	TGCAGGATTTGGCACCTGGTTTCAGGTTCGCCCCGAT[C/T]GGACTGGTTGACATGTTCAGCGGTGG
TP81350	TGCAGGATTTGTCTTGTTGCTCACGGCACTGCTGTGGTATCCATCTCGTGATCGTCCTCTCA[C/T]G
TP81363	TGCAGGATTTTCT[G/T]AAATTTTGCAGTGTGTTGGTCATGGTCTGTCTGTACTCTGTCCGAGCCCT
TP81380	TGCAGGATTTTTGTCTTTGCTC[A/G]TTCCTGTTGGTTTCTTCTCTGCGTGGTTTGCCTTGTTGCTC
TP81388	TGCAGGCA[A/G]AAAGGTGAAGAATTTGGTTTGGCTACCCGACAGCTCGAGCAATTTGTGGTTCTCA
TP81402	TGCAGGC[A/G]AAATAAACCCGTGGCTACCGTTGTCGGGCCACCACAACAACGACCGCAGGAAGACG
TP81427	TGCAGGCAAAGAGCACGAGAGTTTAACGGCGTTTGTCCAGACATGCAATAATTTCACGT[C/T]CACA
TP81428	TGCAGGCAAAGAGCGAGGCAGCGAGCCACAGAGGAAGGAAG[C/G]CGCTAGGCATACGCACTGAGAC
TP81429	TGCAGGCAAAGAGTACTCCAACCAT[C/G]GTTATGCGGTTCGGTGCCACTCCTTCAGATTTCATCAA
TP81438	TGCAGGCAAAGCGGAAGCACATAAATCA[C/T]TAGCCATCGTTCGTTCGTTCGCCAGTGTAAAACAA
TP81459	TGCAGGCAAAGTGAAGACCTGCAC[G/T]GTGCATCATCGGATTCTGTCATTCATTACCAAGATGGCC
TP81480	TGCAGGCAAATGTGATGCAGATTATTACATTTTT[G/T]GTGGCCGTTTCCATCATTGTCATTAGATG
TP81485	TGCAGGCAAATTCAGATTGGCTTTACATCGTGC[C/T]TTGGGGACTGTATAAAGCTGTCACTTACGT
TP81487	TGCAGGCAAATTCCCATCCTGGCCAATGGCCATTCATGTGAACTGCTTCCAC[C/T]TGCCCTCCCTC
TP81495	TGCAGGCAACAACAACAGCAGTAACGAT[A/G]CTAGCAGCGGCAGCGGCAGCCCCATCATCTTCGCC
TP81503	TGCAGGC[A/T]ACACAGCTAGTGCGAGGCCGTGACCCTTGTGTGGGTTCAGTAGCTGGCCACGATGA
TP81515	TGCAGGCAACAGGTCAAACACCTCTCTTGTGGGCGTCCTAGCGTTGATGGCGGACACTG[A/G]CGCC
TP81524	TGCAGGCAACCAATGCAAACCACCATGC[A/T]AATACGGGCAATCAGGCAGAAATGTTACAGGGAGG
TP81533	TGCAGGCA[A/C]CCGAGAAGCATCAGGACCTCGTCCACAGTGTCTTCCAGTGTATGCACGGTTCGGT
TP81535	TGCAGGCAACCGTTGCCACGTTCCCT[G/T]GGCCAAAAAGCCAGGGCTGTAGTTAAGGTTGACTGAT

Table A2 (cont.)

TP81538	TGCAGGCAACCT[C/G]AACTAACCTGCTGAAAGTAAAGGTTCCGAATTTCTTCAGCTCGAACTGGAT
TP81541	TGCAGGCAACCTGAACCGCTACTTTACTGTGACCTGCAA[C/G]GACAGTTTCCAGCCACCAAGGCCT
TP81552	TGCAGGCAACGCCTCTCTTCTTGTGTTTCCTATCGCCGTCTCG[C/G]GTTGCTACTCGCTGCGCGTC
TP81558	TGCAGGCAACGGTACACACACAGAGCTAGGCTTTATTGGAGCACTAC[A/T]AGTAGCATAGCAAGCA
TP81563	TGCAGGCAACGGTTCCGTTGCTTCTGCCAATGCCGCGTCGCTGCTCTCTGGGG[C/T]GCTGTCCCTC
TP81573	TGCAGGCAACTAGCGCTGCATGCGGGTCAAGTCAAGGCGTCCGTCAAGTTC[C/G]AGATCCAGCGCT
TP81578	TGCAGGCAAGAAAAAGTCAGAAAACCTTAGCATTCCGTGAAGAGGCAGAAAACCTTGCGGCA[A/G]C
TP81580	TGCAGGCAAGAAACAAATAGGGCATATACT[A/G]CCACTGACAATTAACTGCCGCACGCCGTTCTTA
TP81604	TGCAGGCAAGATAATGGAGAGCC[A/G]TGCACTGATGCACACCAACGCCGCCATCAATCCGTGGCAA
TP81609	TGCAGGCAAGATGCAGTCGCCGCCGACCCCATTATCGCCA[C/G]GGAACTGCCAGCGCCACCTTCTT
TP81610	TGCAGGCAAGATGCCAGATGCGGTAGTGGC[C/T]GAAGATTCGAACAAGCTGGGCCAGCCACCCGTT
TP81622	TGCAGGCAAGCAATCCTGATGGGCTCCTGGTCCGTCTCGTGTTTTTTAATTA[C/T]TTTTTATTCAA
TP81624	TGCAGGCAAGCACTGCGGCTCGATGAGAGAGCGAGGATAGGGGG[A/G]AAAAACAAGTGAAGAAAAA
TP81633	TGCAGGCAAGCGCGCGCGGCATTGTTCT[A/G]CACTGCCATCTGCCACGTTCATTCCATCCATGTCG
TP81639	TGCAGGCAAGCGGTCGTCGTCTCTCGACGTCAGTGAAGCGCGGGGAAGGGTAGG[A/G]CAATAGGAG
TP81640	TGCAGGCAAGCGGTCGTCGTCTCTCGACTTCAGAGAAGCGCGGGGAGGGGTAGGACAA[C/T]AGGAG
TP81643	TGCAGGCAAG[C/T]TGGAGGAGCGACGCCCATGCGGCATCCCATGGTTGTCACGATGATGAGCTCGG
TP81656	TGCAGGCAAGGCGAACAGGGGAGGCGGCGGCGG[C/G]CGACGGCTGCGCGCAGGGGAGAACCCG
TP81664	TGCAGGCA[A/C]GGGAAACCCAGGAAACCCGTCAGGCACACCCAAATCTGGGAACAAACAACGAAGC
TP81669	TGCAGGCAAGGGCGCCAAGAGGACGTTCGGCCGCGACAACGAACAGTCGCCGTCGCCGTC[C/G]CCG
TP81670	TGCAGGCAAGGGCGCCAAGGGGACGTTCGG[C/T]CGTGACGACGAACAGTCGCCTTCCCCGTCGCCG
TP81672	TGCAGGCAAGGGGTGGGCGCAATAAATATTCGTGTTGGGGCATTGGGGGCGGGGC[C/G]GATCCTTT
TP81678	TGCAGGCAAGTACCCAAGAACTCATCAGTCTTAAGC[A/G]CAGCCAGGCATCTGACCATAATGAGGT
TP81700	TGCAGGCAATAATGGCAACGCCA[C/G]TTCTTCTTCTTCTTCCACCATGTGCGGGTACAACTACTTG
TP81702	TGCAGGCAATACCAATTTGGTGGAGGTGGTACTACTGGG[C/T]GAACCCTGTCTCGTGGACCATCTA
TP81737	TGCAGGCAATGCTGCTGAACCGTGTATGGTGGTGC[C/T]ACCAAGGGCGGCGGCGGCGGCGGCAGGT
TP81739	TGCAGGCAATGCTGGCCGCCTGAGCCCTCTCTGGAAAGCATACT[A/C]CGTTCCAAGGGCAAATAAG
TP81740	TGCAGGCAATGGAAGAAGCCATGCACATGCATCTGTAAA[C/T]GCAAGCACGGAACGACGACCACGC

Table A2 (cont.)

TP81763	TGCAGGCAATTCGGAGCTCAGTTCAGTGCATGGCTGACAC[A/T]CTCCAGAGAGTCCAGAAATGTCT
TP81768	TGCAGGCAATTGATTGATAGGATCTTCAGCTTGGTTGGGTG[A/G]CGCCGATGAAGCCAGTGAGAGT
TP81771	TGCAGG[C/G]AATTTCCTCGACCGCATCGCCGCCCGCTCGCTCCGCCTCCATGGCAACCTCCGCCCT
TP81783	TGCAGGCACAACGGCGGCTCCCTTGCCGACCTCGTCGTCCTCCTCCTCCTGGATC[A/G]CCAGGAGG
TP81795	TGCAGGCACA[A/G]GGATTTGTTTAGGGGTGATTCCTTGTCGGCAGATCAGATGGGATCGACGAACG
TP81825	TGCAGGCACACCACCGTCGC[C/T]GCGCCCGCCATGAACCCCACGATCGTCGCGTGCGACAGGAAGT
TP81827	TGCAGGCACACCCACCGCGTGCTCCACCTGGGCACCTTCTTCTGCACGATGTA[A/C]ATCTCCACGG
TP81829	TGCAGGCACACCGAGCAGCACAGCGCCTGGCCC[A/G]CCGCGTCCACGGCGGTGTCCTCCGCGATCA
TP81839	TGCAGGCACACGCTAATTACATTTCTGAAGCAGTAGCTGGTTCATTCACTTTGTAGTCTTC[A/G]TC
TP81855	TGCAGGCACAGAACA[A/G]AAATGCGCTGCGAAACGACAAACTCACGCACTACACTGCGACGCGCTC
TP81856	TGCAGGCACAGACAATGCTTCGACTTGTGGTGCACGCGGCAGCATGCCGTGGTC[C/G]TTGTCAGTA
TP81870	TGCAGGCACAGCA[C/T]AAATTAAAGAAATAGTACACGCATGCAGAAACTTCAAAGTCCAGACGAGG
TP81873	TGCAGGCACAGCAGCGCGAGCTGCACGCACTTGGTGGCCTGGTCC[C/T]TGTCGTACCCGCCGTCCA
TP81884	TGCAGGC[A/G]CAGCGATATAACAAACACATAAAAAAAAGGAAAGGGAACAAAACTTCTCAAGTAAA
TP81893	TGCAGGC[A/G]CAGCTATTGAGTGAGAGGGACGCACTCGAGCTCCATTTCAAGCTGGCCACGCTCAA
TP81898	TGCAGGC[A/G]CAGGAGTTGTCCGCCCCGCCATGGCAGACATGGAAAGAAAGCAGGAAATGCTCATG
TP81908	TGCAGGCACAGGTTCCACGCCAATTGCATCG[C/T]GCCGTGGCTCGAGATGCACAGCTCCTGCCCTG
TP81909	TGCAGGCACAGTAGGACGTACACACAGCTGCTCTGCCGCTATTGGCCG[C/T]AGCCTGTGATGTGGG
TP81917	TGCAGGCACATA[C/G]CTCCCACATGCATTCCACACATTACTGGTAATAAGTGCCAAAGCACATCTT
TP81946	TGCAGGCACATGTTTGGTGGCCAC[A/G]AGTTTTTGCAGTGCCGCAGTGGTGTGTGGTGTGGTGTCA
TP81960	TGCAGGCACCACATGGCCGTCTTGACCATGCGCTCCACGGTGGC[A/G]ACGCTGGCGGCGTCGTCGT
TP81967	TGCAGGCACCACCGTCGA[C/T]CACGGCCACGGCCTGCATGTGGTACGGGCAGAGGCGCTGCGCCTC
TP81969	TGCAGGC[A/G]CCACGCCAGAAAGTGTACAGAAACACTAATCTTGTGATGAATTGAGAGGGGAGAGA
TP81976	TGCAGGCACC[A/C]GCTCGCGCCCGCGCCATGAAGTGCTGGTGCGTGCACGCGCCAAGAGGAGCAAT
TP82003	TGCAGGCACCGAAAGGCTGCCTGTTATCTACCTG[A/G]TTCAAACCATGTTGAGCAGCGCATCGTGC
TP82009	TGCAGGCACCGAGCTG[C/T]GCTTTACTTGGGACGGGAGGACTCCGCGATGCCTTCGCCAAGGGGTG
TP82026	TGCAGGCACCGCGTTGTTGCCGAGACTGGTGAGGTTGGGTGTTGCCGCCGTGCCCATGC[C/T]GCGA
TP82122	TGCAGGCACGCGGCCGCCGACGTTGTTGGCGTCGAGGA[A/G]CATTTCCTCCATGGCCTCGCAGGAG

Table A2 (cont.)

TP82127	TGCAGGCACGCGGCGCGCAGCAGCCCCGCCGACGACGGC[C/T]CCGTGGCCGCCGCCACCTGCTGGT
TP82137	TGCAGGCACGCTGTCCATGGCCAACTACGGGCCAGACTCCAACGGCTCCT[A/G]GTTCTTCGTCACC
TP82148	TGCAGGCACGGCCAATTCTCCGAGATCAGGATAGAT[G/T]AGAAGAACTAGCTGACCCCAGGCTTGG
TP82187	TGCAGGCACGTCAAAAGTCAAACCTG[A/T]GGCGCGTCAGAAAATTTCCAGACGTTTGACCGCATGC
TP82188	TGCAGGCACGTCAGGACTCTGGTCACCGAACGTCGAGTTTGCCTCGGACGTGGCTGA[C/T]GAGGAA
TP82203	TGCAGGCACGTGCGCGCAGATGGATCGATCGAT[A/C]GTATCGACGCAGGCAGCAGATCAGATAAAC
TP82233	TGCAGGCACTATGCCCCAAAGTTGTGCCAAGATT[A/G]CAATCATCTTCAGAAGGTATCGCTTCGGG
TP82247	TGCAGGCACTCCTTTGTGCTCCAAATGGTGGAATGGGCAAGGTGGGTGCTCACATG[C/G]CAATGCG
TP82270	TGCAGGCACTCGGCAA[C/T]ATTGCCTTCGCGTACACCTACTCCATGCTTCTCATAGAAATCCAGGT
TP82272	TGCAGGCACTCGGCGGCGTGCTCCTTG[A/G]CGCCCGCCACGGCGCCGCGGTCCAGCAGTCCGACCA
TP82275	TGCAGGC[A/G]CTCGTGCCCCACGTCACTGACAAGGTAAGGCTCTCGATCAGATGACACGATCGATG
TP82280	TGCAGGC[A/G]CTCTTCATCAACAATGACATCCACATGTACCATCGCGAGACAGACACGCCAGCCCA
TP82281	TGCAGGCACTCTTCCTTCGAAGTTCCACACCACCAAGAAA[C/T]GAAATGCGCGAGAGCACGGAAAG
TP82291	TGCAGGCACTGCAATCACGCACGAGC[A/G]CGCGGCCAGGGATGTGACACATTTTGGTGAACATTGC
TP82296	TGCAGGCACTGCGCCTACCCTGCCGCGGCGGTCACCGTCACG[C/G]TCCAGAACCAGCACCTCGCCG
TP82316	TGCAGGCACT[G/T]GCCGCCCGTGACCATGTACACCATGTCGCAGCCGAGCTGCACGATGAGCTGCT
TP82323	TGCAGGCACTGGTGCGCGACCTTGGCGGCCTTCTCCGCGGCG[C/T]GCGCCGAGTACTGCATCTCCA
TP82329	TGCAGGCACTGTTGCTTCTTGATCAGTTACAGTTGGTTTTGCCAATTCAGCTTTTCC[C/T]GAGTCA
TP82349	TGCAGGCACTTGGAATAAAAAAA[A/G]GAAGAGCTGCCTTTATTTAAAACGGTGTAATTATTTCACC
TP82360	TGCAGGCAGAACGCTTCGCCGTTGGGGATCCG[T/C]GCCGCCTCGGGCGCCGCGAAGGAGCTGAGGC
TP82367	TGCAGGCAGAAGCTCGAGTCCAGGAACAGCTCCAGCACCGCCGCGCCGTTGTCGGTGCA[C/T]CGCG
TP82389	TGCAGGCAGAC[A/G]GGTGGGCCCCACTAAACCCGAGTCTTCCTCCTGTCCGTCGCTTGGCCGTTTT
TP82391	TGCAGGCAGACCAGATCAGGA[G/T]ATCTGACACGGAGGAGCGGGAAAATCTTGAGATGTGCCCGCC
TP82393	TGCAGGCAGACCCAGTCCATGAGCGCGTCCACGTCCTTGGCGAAGTCCAGCAGGTACCA[A/G]TGCA
TP82401	TGCAGGCAGACGCACC[C/T]TGAATCACGGCCAGTTGGTGCATGTCTCCTGGGCCCGCCCAACGGAG
TP82406	TGCAGGCAGACGCATGC[A/G]GTGCACGGACCGTGGACATACCCGCCGTAGAGCGCAGAACAGAAAG
TP82429	TGCAGG[C/G]AGAGACGACACGAATTCCGTGTGTGGACAAGCATGTGTACCGTGTTGGGCCACGAGA
TP82438	TGCAGGCAGAGCCAGCAGAAGTGGTGGCCGCA[G/C]GGCGGCGAGCAGCGCATGTGGTTGCAGCCCT

Table A2 (cont.)

TP82440	TGCAGGCAGAGCCGTGTGCGTGG[C/T]TCCGTCTGCCCTGCCGCGTCAACGTCGTCGTCGTGGACGG
TP82443	TGCAGGC[A/C]GAGCGGAAGGCGCTGGGCGCGCTGTACGCCGAGCTGGAGGAAGAGCGGAACGCCGC
TP82450	TGCAGGCAGAGCTTGCTGGACATG[C/G]GATTCTGCTCAATGGTGAACTGAGAGTAACCCGAGAGCT
TP82455	TGCAGGCAGAGGCAGAGGGGCGTGCAGCGGCGCCAG[C/G]GCCAGGTGTCCCATTCGTCGTATCCTC
TP82461	TGCAGGCAGAGGCAGGGGCAGGCAGGCCCCAGGTCAT[C/T]AGCGCCTCTTCCATTTTCTAAGACTT
TP82464	TGCAGGCAGAGGCCGAGGCCGAGGCCGAGGCCAACGCCGCCTGCCCCTGCCAGCTGCCGC[C/T]GCC
TP82465	TGCAGGCAGAGGCCGTCCGCCGAGGCCAACGCCGCCTGCCCCTGCCAGCTGCCGCGTCCTCCT[C/T]
TP82484	TGCAGGCAGAGTCTTTTCGCCTACTGCGTGAATGAAAGAGGAAAAA[A/G]CGCGCGCGGCGACACCG
TP82500	TGCAGGCAGATGCATGACAGG[C/T]GCCTCCTGGATCCCATTGAAATGCCACGGGCATGGACTTCAT
TP82502	TGCAGGCAGATGCGTTTCTCGGATAGCTTGGCCTCGGGGCGTCGCGAC[A/T]GGGTCTCCGTCGGCA
TP82510	TGCAGGCAGCAAATTAAAAGCTTGTTCCGTGGTCAAGACGACCGACGTGACC[C/T]AACTAACCAAC
TP82525	TGCAGGCAGCACAGATGCA[C/T]CAGATGAAGGTGGAAGAGTCCAAAAAGTACCAAGAACTACGGAA
TP82527	TGCAGGCAGCACATTGGTGAAGTGCGG[C/T]TGGAGATGTTTGGTGCACTGCACGTCTGTCAGATCA
TP82530	TGCAGGCAGCACGATGCATGCCGCCGCCGC[C/T]GTCGCAGTCGCCGCCCCTGACGCCCGAAAAAAA
TP82550	TGCAGGCAGCAGCACACCC[A/C]AGAGAATGGAGTTTAAAGGTCTCGAACTGCTGCGCACCAGCCAT
TP82557	TGCAGGCAGCAGCATCCGCC[A/G]CCGCCACCATGTCCATGCTAACCACCGTGGTGCCACCTCCTCA
TP82569	TGCAGGCAGCAGCTCATCCATCTGCGGCTGGTGGGCAGG[C/T]AGGGCGTGCGCGTGGCCGCGCCTG
TP82572	TGCAGGCAGCAGCTGCACGTTGTTCCTGTGACGAGCGT[C/T]TCATCAGCTGGGAGCAAGCTCGAAC
TP82586	TGCAGGCAGCAGTGGAACGACACATTAGCCTCAGCTCCTTTT[G/T]TGCACATAGCGTATATGGAGG
TP82598	TGCAGGCA[G/T]CATCTCATGTCTTTAATCTAGCTAGTTTTGCTTTATCTTTTGCTGCCGCTGCTGC
TP82603	TGCAGGCAGCATGCAGGGCGCCGTTCCGTCCGCTATG[A/G]TAGAGTAGGGGCTTCGAGGAGGGCCA
TP82610	TGCAGGCAGCATGTGTGAGGCATGGGCGGATCGGCTCATCGGCA[A/G]TGTGCGAGGCTAGCGGCGG
TP82618	TGCAGGCAGCCACGGAGGAAGGGAGCAGTGGT[G/A]TGGTGGTCGGTCGCAGACAGGCACAGTCTGG
TP82620	TGCAGGCAGCCAGCAAGCAGTACCATGCACCACG[A/C]AAGCAGCAGGCAAGTAGTCCAATAACAGT
TP82626	TGCAGGCAGCCATGGGACT[A/G]CATCTGAGCGCAGGGCACGCGGGGAGAAGATAACATCAGTCATC
TP82643	TGCAGGCAGCCGCCGAGCGCGCGCACCGCCGCGAGGGCTGAGCGCAACGGTGAG[G/T]GGCAGAGCG
TP82657	TGCAGGCAGCCTGTTGAGCGTCTCCTGGAGATCAAAGTGAACAACAAATCTGAAGA[G/T]CAGCAGC
TP82660	TGCAGGCAGCGAAGGCCGAAGGGAGGGAAACACCCGTTCGAAACGCGG[A/C]GGGATCCAAGCCGCG

Table A2 (cont.)

TP82672	TGCAGGCAGCGATGAGCCAGGGGAATGCGCGGTGTGCCTGGC[A/G]GAGTACGCGGGCGGGGAGGAG
TP82680	TGCAGGCAGCGCGCCAAGGAATCACACGGACAACCAAATAACGCGACCAAA[C/G]AAAGCACCACAA
TP82684	TGCAGGC[A/G]GCGCGGCTGAGGGCGCGGCGGAGCGGCGGCAGTAGGGGCAGCTGCGGCGGAGGCGG
TP82704	TGCAGGCAGCGGGGCGAGAACAGCCGAGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG[A/C]G
TP82706	TGCAGGCAGCGGTAATAGAGCTTCATGAGCTCGTCGATCGAGCTGCGGTCAGCATCGGGC[A/T]CGC
TP82715	TGCAGGCAGCTACGGACCTGCGGTGA[A/T]GCCTGCCCACGCGGCCTGCGGCCACGCCGAGGCTGAG
TP82716	TGCAGGC[A/G]GCTAGCAGTCGATCGGTGCTCGGTGGTAGGCGTTTGAACACCACCTCATGTCTGTG
TP82720	TGCAGGCAGCTCAGATCTTACGATGCAATTGCAATCTGAGCTCGGCCC[A/G]TATGGTCGCAGGATG
TP82725	TGCAGGCAGCT[C/G]GCCGCCATTCGGGCTCCAATCCCAGCCAAGGAATGCAATGCCAACCGATGAT
TP82731	TGCAGGCAG[C/G]TCTTGTAATCCCTGGACAGCTTGCTGTAGCAGAGGAGCATCATTTGCTTGCGAA
TP82749	TGCAGGCAGGAACGAGGAGCGAGGTGGTTGATGACCGAGTTTGTAGCTGGCTTGCAAGTGA[C/G]CT
TP82755	TGCAGGCAGGACACCGCCTGCCTCAGCA[A/G]CTCGTTGTGGTAGCTGGACAGGTTGTTGTAGCTCT
TP82758	TGCAGGCAGGACCCGAGTGCAGGGAGCCAGGGACAT[C/G]AGCTCGTCGTTCCATTAGCTAAAGCCC
TP82768	TGCAGGCAGGAGCAGAGGGGCATGGACGCCGCGCTCAAGGCCGCCAGGCGCCGCCACCGCC[A/T]GC
TP82777	TGCAGGCAGGAGTCAGGACCGCAAT[C/T]GGACTGCCCTGAATGTCCATTCTTGTTCTTCAGTTAAG
TP82807	TGCAGG[C/T]AGGCAGGGGCGGCAGGTCGCCGTAGAACGGCACGGCGCTCGGCAACAAGGCAACGGG
TP82819	TGCAGGCAGGCC[A/G]CGCCCTCCCGTGGGCGGCAGGGGCACCGCGGACGGGTCGAGCAGGCTCGTG
TP82826	TGCAGGCAGGCCGATCAGCGTGAC[C/G]GTGACGGACGGACGGACGGGGATGGGGAGCCATGCCCAC
TP82830	TGCAGGCAGGCCGATCAGCGTGACCGTGACGGACGGGGATGGG[A/G]AGCCATGCCCACCTCCATGT
TP82833	TGCAGGCAGGCCTCAGCGTGGTGGCCCAACGCAGATTCACTG[A/C]TGGTCGCGCCGCCAACATCAT
TP82846	TGCAGGCAGGCGCCCTGCCCAGCTAGCTGCACTGGACTCCACGCAGACGCAG[A/G]CGCAGGCGCAG
TP82849	TGCAGGCAGGCGCG[C/G]CCAAACCGCCGCCACCCAGCCCCCAGCAGAGCACGCTGCCGCCCGCGCC
TP82874	TGCAGGCAGGG[A/G]TCGTGACGGTGACGGCGACGGGCGACCACCCACCCGCACCCCGCGCTCGGTG
TP82888	TGCAGGCAGGGCT[C/T]CAGCGAGAGGGGGAGCCGAGGAGGCGGTGGGTGTGGAATTTTCGTCGGGG
TP82909	TGCAGGCAGGGTGGGTGAATGCAAATATGGGTGAAGCTGAATGAAGCAGCAGGGCGT[C/G]TGATGA
TP82918	TGCAGGCAGGTGCACCGCCACTGCTTCGCGCTCGTCACGGAC[A/G]GCGTCGACTTCTCCGAAAAAA
TP82926	TGCAGGCAGGTTGTCTCCCTCCTTCCCACCTGCACCACCCTACCCCTGCCCCATCTCATCTT[C/T]C
TP82929	TGCAGGCAGTA[A/T]GCATGCCATTGCCACGCGTGCTTCCTCACGATCCAACAGCGCCCATGGCCTG

Table A2 (cont.)

TP82936	TGCAGGCAGTACTCGAGGTTCCACA[A/G]CACGTCGCCCATGGACGGCCGCTCCAGCCCGTAGTCCG
TP82938	TGCAGGCAGTAG[A/G]CGTCCGTTCCTCATCAAATTACTTATTTTTAACTATGCACCCGACCTTTT
TP82945	TGCAGGCAGTAGTCCAGGCGAACAGGAGGCTAGGA[A/G]CCGAGCGTCGGTCGCCGAGTCACGCAAC
TP82951	TGCAGGCAGTATGCATGCCATTGCCACGC[A/G]TCTGGGACAGGTCTTGAGTCTTGACGCACGGTGC
TP82952	TGCAGGCAGTCAAGCACTTTATACTTGT[G/T]CCTTTGGAATTTAATATTGTCAATGCCTCTACTTA
TP82957	TGCAGGCAGTCCATGCT[A/G]TAGCTCTTCTTTATGGACGCGGAGCCTGCGCCACCACCGCCGCCGC
TP82958	TGCAGGCAGTCCATGCTGTAGCTCTTCTTCATGGACGCCGATGAG[C/T]CTGCACCACCACCGCCGC
TP82976	TGCAGGCAGTGCCACCGTGCCAGCTT[C/G]GTTGGGCTATCCGATCGAGTGGGTCCACGTCGCAAAC
TP82982	TGCAGGCAGTGCTTCCGCAGCAACGCCAAGGACATCGGCTTCATCAAGGTACGCGCC[A/G]AAATCT
TP83003	TGCAGGCAGTTGCATTGTACCCCTTTTGTATCACGTATTTA[C/G]CAGTTTGTGTTTAAGCAAGTGT
TP83019	TGCAGGCAGTTTTGCAAAGGACACCCCCTGTCCGCCCAAGCCCCGCCGCCCCTCGCTGCT[C/T]GCC
TP83055	TGCAGGCATAGGTAACATAACATAACATGCGCGGCCTCT[G/T]CGTGCTCTGCCCCTTCCACACCAC
TP83064	TGCAGGCATAGTTGTCGACGCGGTAGGCGACGCGGCCGTCCTCGC[C/T]GTAGACGGTGCACCCGTG
TP83102	TGCAGGCATCAGAAATAGTGCATCCATGAATT[G/T]AATTGAAATGAAATGTGTGAATTCATGGAAT
TP83118	TGCAGGCATCATCAGCTGAGTAGTGCATGCTTGTGTTTGCCTTGGTTTTATAGA[A/G]TGCGCGTAG
TP83123	TGCAGGCATCCACCACGGTGAGTGAC[C/T]CTGATGGCGAACAATCGAACTGACAGCTTAGGATTTG
TP83155	TGCAGGCATCGCCCACGGCGCTCGGCTCCATCGCGCTGTCACGCTCC[A/G]TCGTGCAGACCGCCTG
TP83159	TGCAGG[C/G]ATCGGATCAAGACCCATCAATTATCCCGAAGCAACTTGCGAATCTGCCACATTGACC
TP83172	TGCAGGCATCTAATGTTAA[G/T]ACTTTCTTCCTCTTCACAGTGCAACGCAGTGACTTTCTCATCTG
TP83201	TGCAGGCATCTGTTTTCCTGGGCCTCCCTCGAGGCCTGCCACGGGGCGCGCCACTGCCACCGC[C/T]
TP83207	TGCAGGCATGAAAGGTACCAAATGTACAAAAATATA[A/G]TTAAGTGTTCATATGAAATGTCATATG
TP83222	TGCAGGCATGCAAGCACACGACACGATGGAGAACCCAGCTAGCTAACGCCGAGCGA[C/G]CACTCAC
TP83240	TGCAGGCATGCATGCCTCTGAAAATTCCTAATGCTTCCTGCTGCCTGTCTGCCTCCC[A/T]CGCAAA
TP83260	TGCAGGCATGCTGGGCT[A/G]TGGTGGGCTCGGCCTCTCCGCGCGGCCGCCGCACGCACGTACGCGC
TP83261	TGCAGGCATGCTGTCCATGGCCAACTACGG[A/G]CCAGACTCCAACGGCTCCCAGTTCTTCATCACC
TP83276	TGCAGGCATGGAGGACGCGAGGGGCTTGGCGCCGCGCGGGGCCGTCGGTCGTAAGCTTCCTG[A/C]C
TP83315	TGCAGGCATGGTGGAAGGAGGTGCGCGAGGTCGGGCACGGCGACCTCAAGGACGCG[C/G]CCTGGTG
TP83317	TGCAGGCATGGTGGAAGGAGGTGCGTGAGGAGGCGCACGG[C/G]GACCTTAAGGATCGAGACTGGTG

Table A2 (cont.)

TP83343	TGCAGGCATGTCTCCCTCCTGGACGGCCACCCAGACATCATTGTCCTTGGCGGCGGCG[G/T]CGTTG
TP83358	TGCAGGCATGTTTAAACTATCG[C/T]GTTCGTGTATGTGGCCTTGGTGTACGCTTTAACTAATCCAC
TP83359	TGCAGGCATGTTTCTCCTATATCATGTCACTACGGACAAAATTAAAGGT[C/G]CATGAGGCATCCTA
TP83365	TGCAGGCATTAATTCGGTACGCATTATTGTACTAGCAGTGAAATTAATTGA[A/C]GAATTGAAACTT
TP83376	TGCAGGCATTATGTATGCTAATATGCTAGTAATCCT[C/G]ATGATCACTCACGAAATCTTGGTTTCC
TP83377	TGCAGGCATTATGTATGCTAGTTAAGCTCATAATCTGCT[A/G]GTAATCCACACGATCACTCGCCAC
TP83385	TGCAGGCATTCGGCGACATCGCCTTCGCCTACTCCTTCTCAAACATCCTCATCGA[A/G]ATCCAAGT
TP83386	TGCAGGCATTCTGGTGAACAGCTTCGAGTGGCTGGAGTCGAGGGCACTGAA[A/T]GCGCTGCGTGAC
TP83404	TGCAGGCATTTCAATTTGTTTT[C/T]TTTTTCGCTTCCACAACCGTTGGTTTGCTCTCTCGTCTCGT
TP83409	TGCAGGCATTTGATCGGCTTCTTCGTCTTCCT[T/C]GCGCTCACCGTGTGCGCCGCCACGATGGTCC
TP83410	TGCAGGCATTTGTCCTGGGCACTTGGTGGGACGTCCAGGGCAGCCAGCGTTC[A/G]GGTGTTTCTCG
TP83415	TGCAGGCCAAAAATAGAGATGATGTCGTGAGAAAACTGACCGCGG[C/T]ACAGCTAGGCAGTGGCTT
TP83439	TGCAGGCCAAATTTGACGAAGTTGGAGTCATGCCACTGCCGCTTGCAAGAGCCCAAG[A/C]TGAGCT
TP83441	TGCAGGCCAACAAC[A/T]GGGGCCCTCCGCCGCCACCCTCGGCAGTTGCCCGACGAGCTGCGGCAAC
TP83452	TGCAGGCCAACATGTACATGTCACGTACGGTGGCGGCGATGGTGGCG[C/G]AGATGGCGATGGTGAG
TP83462	TGCAGGCCAACGCAGGCGTGATGGAACGCCGACGGGCAGTTGTCGCAGAGCAGCA[A/G]CTCGCCGC
TP83471	TGCAGGCCAACGGGTCGGC[A/G]GCGGACGCGGGGGGCGCCATGGTGGTGGGGCTCAGCCCGCTGAG
TP83488	TGCAGGCCAAGAAAGGTGGGAGAGAGCCTGAATTTCACATCCTGCAACGACGGCGG[C/T]GGCACGG
TP83489	TGCAGGCCAAGAAAGGTGGGAGAGCCTGAATTTCACATCCTGCAACGACGAAGGCGGCGGTGC[A/G]
TP83496	TGCAGGCCAAGACTACGAGTTCTCCAATGGTACAT[G/T]ACATACTCCTGTATAGTATCTTGGGTTG
TP83503	TGCAGGCCAAGATTGGAGAAGGCAAAGAGGACGGGAAGGGGTGGAGTCACACTAGGACGC[A/G]AAG
TP83538	TGCAGGCCAAGTCTCCTCCACACGCGGCCC[C/T]AGTGGTCTCTGTATTGCTCGTCGTCTGTCCTCT
TP83549	TGCAGGCCAATCTTTGCGCCGAGCAGCCGCCGTGTCAGCTCATCTGGGTGGTCATACTGTTGG[A/G]
TP83565	TGCAGGCCACAAGCTGCCCTTGTGGCCACAAG[A/C]TTTAAGGCACTTGCGCACCATAACAAATCAC
TP83576	TGCAGGCCACACCACAAACCAAAAAAAG[A/G]CCACCAAACTCAGTAAAACGACCAACCGCGCCCAT
TP83606	TGCAGGCCACCAAACGAAGAGACGAGAAGGCACCTCACCTGGGGGCCCATGAGCGGAGG[C/G]CGTC
TP83625	TGCAGGCCACCCTAATGACGCATGG[A/G]TGATGGGCCGTCGCTGGGCAGGCGGTTCCCGTGTGGAG
TP83646	TGCAGGCCACCGCTGCGGCCGTGGTGGAGCCTCGACATCAG[C/T]ACGGCGCCCTTGGGGTTGTTGT

Table A2 (cont.)

TP83720	TGCAGGCCACTACGACCCTCTGTGAGGCTACTGAAGTAG[C/T]GATCCATTTAACGTGGCAGTTACA
TP83726	TGCAGGCCACTCACCAGCTCGATGGGAC[A/G]GAGCGCGAGGGGACTGCTGCCGTAGAACATCCCGA
TP83729	TGCAGGCCACTCGTCGACTAGTGATTGGACGGCGCACT[C/T]CTCGGGCTCGTCAGTGAAGAGTGGC
TP83733	TGCAGGCCACTGATGACCATTCTGTTTCTCCGC[A/G]TCGATACAAAATAATGTGCGCGTGAGCAGC
TP83755	TGCAGGCCAGA[C/T]ACAGTGATGATGCCCACTGGCCCAGCGGACTGCGCGGCCTAGGCAGCCGCTT
TP83766	TGCAGGCCAGAGGCGCCGA[A/C]GCGGCCACGTCACGCCCCCGCGCGGGAAAGGTTATCCCTTCCGC
TP83777	TGCAGGCCAGCACAAATCTCAATC[A/G]CCGTGTCGGAAATGCTACAGTGCAACATCTATCACACTG
TP83780	TGCAGGCCAGCACATGACGACGGGGCCTTGGCGCCGTGGCGGCCGCGCCAC[A/G]ACCACGACGAGC
TP83785	TGCAGGCCAGCAGCGCCAGTGAACGACGCCACACATGACGCGCGCACGGCAGCGACAACAGT[A/G]C
TP83797	TGCAGGCCAGCCAGGTGGAGAAAGCGGGCGTTGGG[C/T]GGAGTGGTGAGCCGATGGGACCCCGCTG
TP83811	TGCAGGCCAGCGCGGGCACGCGCGGGCTGCCGTGCCTAGGAGCACGGCACGGCA[C/T]GGTTAACCT
TP83823	TGCAGGCCAGCTGGCGCGCATGCATGCA[C/T]GCACGCACGTGCGGCACGGTACGGCCGTGAGACGG
TP83825	TGCAGGCCAGCTTTGCCTGGAGCGGGGGATGACGTGGCGGATC[G/T]CCATTGGTGCCTGTGGCGTC
TP83845	TGCAGGCCAGGCCGCCA[C/T]GAGGGAAGAGCCTTTGGTGCTCTCGGCAGACAACCACTTCCACTTG
TP83848	TGCAGGC[C/T]AGGCTAACAACAGGCATTGGGCATATGCGTGTGTATCTGATCAAATACGTGGTGAC
TP83856	TGCAGGCCAGGGCGCGAGCTGCGGGTTCGGTATGCG[C/T]GGGCAGAAATCGCGCTCGGGGCCCGAA
TP83872	TGCAGGCCAGTCCCCCTGTCACACACAAGCGATTCCTCCCAATCCGTACTCGCAC[G/T]AACCAGTG
TP83878	TGCAGGCCAGTGATT[G/T]ATTGGTTGGTGCCGAGCAAGACTACTTGTCCTTCTCGCTCCCCGTGGC
TP83890	TGCAGGCCAGTTGGGATTCGGCACCATGGCCGCCTGTGACGACATGAGCACAACGCGG[C/T]CCACT
TP83924	TGCAGGCCATCATCATTCATCGTTGATTTAATAATGGTGAAAGGATC[C/G]GTTTGCGGCCGAAGAT
TP83927	TGCAGGCCATCATGTCGTGCCACCAGTGCGGCGGC[A/G]ACGTCGGCGACGTCGTCAACATCCCGAT
TP83935	TGCAGGCCATCCTCGCAGGCCTCCCGCCGCTCGCGCACCCGTCCCGCGTCCTC[A/T]CCGCCTCCGA
TP83936	TGCAGGCCATCCTCGCAGGCCTCCCGCCGCTCGCGCACCCGTCCCGCGTTCTCACAGCC[C/G]CCGA
TP83937	TGCAGGCCATC[C/T]TCGCAGGCCTCCTGCCACTCGCGCACCCGTCCAGCGTCCTCAACGCCGCCGA
TP83945	TGCAGGCCATCGGCTTGCATCTGCCCCAAGGAGCTCAGACAACC[A/C]TTACCTGGTGGAGGAAGCT
TP83949	TGCAGGCCATCGTCGTCACCTTCGTCATGGAGCGCCAGACCTCTGTCTGG[A/C]GGGTCGGCTTCGA
TP83964	TGCAGG[C/T]CATGAGCTTCGTCTGCCTCCTCATCTCCATCGCCGCCAGCATCGGCTCCGTGCAGGA
TP83969	TGCAGGCCATGCAGCTTGATCCGACCACAAGCGTTAGAAAT[C/T]TAACACTTGATAATGTTGTTTG

Table A2 (cont.)

TP83974	TGCAGGCCATGCCTCTTCCTGCGTTCGGCTGTCCAAATGCGACCATGTAGAGCCA[A/T]CCAAAAGA
TP83976	TGCAGGCCATGCGCGCCCTTAAGGGCTGCCCTG[A/G]CTGCTCCTCGTGTCCAAGGCCGACGGCTGT
TP83986	TGCAGGCCATGGACCGCCGCCTGCGCGCCGCCGAGAG[A/C]CGCCCGAAAAAAAAAAAAAAAAAAAA
TP83997	TGCAGGCCATGGCGGTGCCACGCAGAAACGG[A/T]AGTGGCGCGACGGCACTGGCCGCCGTTCTGGC
TP84006	TGCAGGCCATGGTTGGTCGCCAGCACTCGGCAGGGATTGCAAAGC[A/C]CCCTGCACCCGTGGACCC
TP84008	TGCAGGCCATGTAGGACTTTAGTTTTTTGCCCACTTCAAAATT[C/T]GACAAGGCATAGACCTTCCC
TP84018	TGCAGGCCATTCCTGGGTACGTGCTGACGAAATTCC[C/T]AGTGGACAAATTACTGATGTTAACTAA
TP84030	TGCAGGCCATTGTA[A/G]TGGTAGGGTATCTTCTTGTGTTATATAAGAAGGCAACAGAGGAAGACAG
TP84032	TGCAGGCCATTGTAGTGGTAGGGTATCTTCTTGTTATATAAGAAGGCAACAGAGGA[A/G]GACAAAT
TP84044	TGCAGGCCCAAATCAAGACGTGATTACTTGCAAGTTACTAGACCTG[A/G]GCCTGCGAGACCATGAT
TP84054	TGCAGGCCCAAGAGC[A/G]TGCTGCCTCTTTGCAAGCGGAGACGAGGCGGTCAATCTTTGGCTGCAT
TP84073	TGCAGGCCCACCACGGCCAGCACGTCCGCCACCCCCATCATGGC[A/G]TACTGCGGCACGATCCACG
TP84094	TGCAGGCCCACGGCGTCCTTGCCTCACTCTTGGGCATTCAG[A/C]GAAGATTGTCGTCACGGCGTCA
TP84102	TGCAGGCCCAGAACATCGTCAATCCTGTGGCATACAT[C/G]ACGTTGGCAGTGCTCATCTTCCACAC
TP84104	TGCAGGCCCAGACCGC[A/C]GCCGCCCGCGCCTGGGCCACCTCCGCCTCCACCTCCCCATCCACCGA
TP84114	TGCAGGCCCAGATGCTGAAAGTGTTCCGTACAAGTACTGGTCCACGG[A/T]TGCCACATGCTTCGTG
TP84118	TGCAGGCCCAGCCATTGGTCACGATTCAACTCCC[G/T]CAGGCCCATCTCGGCGACAACCCAACCCA
TP84144	TGCAGGCCCAGGATGGCGTC[C/G]CTGGAGGCGGCGACTCGAGCACCATTGACGCTGCGGTTGGATT
TP84159	TGCAGGCCCAGTAAGAAGAATCCCAGATACTATGGCGGCCCATGGGCTCA[C/T]TAACGCTTGCATG
TP84160	TGCAGGCCCAGTACGAGTGTCCATGGGCCGCAGTGGGAGTGAGCCACACCAGCTGG[C/T]ATGAGAG
TP84195	TGCAGGCCCATTTACGTTAGGTCTTCAGAGCTCGGACGCACGCCATTCAGTCCAGACCAGGAG[C/T]
TP84197	TGCAGGCCCATTTGCATTGCCCGTTGCGTTAGG[A/G]TGGAACCAGCTTAGCTTCTCCCGTCGACTA
TP84207	TGCAGGCCCCACCTGTCACAGGCCCGCACAGGTACTGC[C/T]CCACGGCGTCCTGGATCCTCGGCCC
TP84231	TGCAGGC[C/T]CCCCACGGGCTGCGGCCGCCGCCCCGCCGCTATCCGCCTAGCCGAAAAAAAAAAAA
TP84237	TGCAGGCCCCCGACGT[G/T]GTCCTGGCACAGCACCGTGAGGAAGTCGCTGTCCGTGTGGGGCACCA
TP84244	TGCAGGCC[C/G]CGAATGCTGGCACGCTGCCTGGCCATGGTCCGCACCAGGGAGCTGAGGCCAAGAA
TP84254	TGCAGGCCCCGCTGTTCGTGGACACCAAGATGGCGTCGAGCGTC[A/G]CCAAGGCCAAGCGCTTCTC
TP84276	TGCAGGCCCCTGCTGACGTCGACGACG[A/C]CGACCCTGCTGCCGCCGCCGCCTTCTTGTTCTTGCT

Table A2 (cont.)

TP84280	TGCAGGC[C/T]CCTGCTTGATCTTCCGCTGTGATCTCATCACCGCCGCGGCCGCGGCCGCTGCCGCC
TP84282	TGCAGGCCCCTGGCCGTGAT[C/G]CTGCCCGCGGACTCCACGGCGTTAAACACCTCGAACGCCCTGC
TP84293	TGCAGGCCCGAAGGACCTATATGTAAGGAGGC[G/A]ACAACACAGCCAAGAACAAAGGAAAGGCCTG
TP84297	TGCAGGC[C/T]CGACCGCTCGAGCGCCAAGCCGAATCCCCGATCACAACCCTACGCCACACCACAGG
TP84303	TGCAGGCCCGAGAAGACCTCCTGTATGTCATCGACGCGGGTCATGGCGCGGGCGCGGAACTG[C/T]T
TP84313	TGCAGGCCCGCAGCAGCGCATGTGAACGCTCACGGCTCAACTTGCA[A/G]CGCGGCGCGGGTCGTGG
TP84318	TGCAGGCCCGCCACCGCGAACGCGTCGCCCACGCCCAT[A/G]ATCACGAACTGCGGCACCAGCCACA
TP84326	TGCAGGCCCGCCGAGTCATGCACATGGACGCTTGCTTTCGCATGAC[C/T]GCGCGCATCCCCAAGCC
TP84332	TGCAGGCCCGCGAGAACAAGCTGCTGCCGAGGAACGCTATCCGTGGGAC[A/G]CCGTACTCCGCGGC
TP84341	TGCAGGCCCGCGTTATCTGCGTGCGTGGCTAAGTTTGCTTCAATGG[A/T]ACCAGTAACTTGAATGC
TP84350	TGCAGG[C/T]CCGTCACCTCCCGCCACCGTTCCCGTGATCGCCCCGCCGCCGCCCGCCGCGCCCCGC
TP84358	TGCAGGCCCGTCTCAAGCGCCGTGCCCGTGC[C/G]CGCCCGTCGCCCGCCCTGAGAGTGAGAGCCCT
TP84380	TGCAGGCCCTCAACAAAGGATATGAAGGTTGG[A/C]TGCTGAACACGGTGCGGCACACATGGAAGGA
TP84410	TGCAGGCCCTGCACCTCTCCCGCACGCGGCACGGGGCATACTCCCCTA[A/T]CCCTAGCGGCGGCGC
TP84411	TGCAGGCCCTGCACGGAGCCGTTGCCGTGGCACGACACGCCGTACCAGGAGGAGGAGTTGCCC[C/T]
TP84421	TGCAGGCCCTGCTATGCAGT[A/C]TGCACACATGTTGCGTTTTTTCAGTGTATATTTGAATGATTCG
TP84426	TGCAGGCCCTGGATCTGGTTGACCTGGAGGACGAGGGT[C/G]AGGAGGTCCGAGTCGGAGTGCGGGG
TP84474	TGCAGGCCGAACTACTCCCCACAGTCCACAGAGGAGCGAACCCTAG[C/T]GTCCTTCCGCACGCCGT
TP84476	TGCAGGCCGAAGACAACGGCAATGGCCGCGATGGTGAGGTAGGCAACGCCCTCAGC[A/G]GCGCCGA
TP84480	TGCAGGCCGAAGTCCTCCGCC[C/T]TGGGCAGCCGCGTCATGAAGTCCTCGAAGTCGTCGGGCTCCT
TP84497	TGCAGGC[C/T]GACATCGATCACGCCAATGCGCTGTGAGTGCAGGGAGCAGAGTTTCCTGTTCGTCC
TP84506	TGCAG[G/T]CCGACCATGGCGAACACGTCGGCGGCGCCGAACACGACGTACTGCGGCACCATCCACC
TP84536	TGCAGGC[C/G]GACTGCTCTGCACGGTGCGCGCGGGTGCTACGACCACAGTTCTCACCGAGTTTTCA
TP84551	TGCAGGCCGAGCAACCATGTACAAAGTACGTGT[A/G]TCGTGCAACTGCTATCTTTCAGGGTTCTGA
TP84566	TGCAGGCCGAGCCAGATCTTTTTGGACTTGGGCTGGTCTTTG[A/T]ACTGCCGCAGTGGGTCGTCAG
TP84581	TGCAGGCCGAGCTGGTCAAGTACCTGATGCG[C/G]AAGGAGGAGTGGAGGCGGTGGGGCGGCAAGAA
TP84582	TGCAGGCCGAGCTTTTGCAGCAGCAGAAACCA[G/A]AATTCCTGTGAGAAGGGGCAAGCACAGAGCA
TP84613	TGCAGGCCGATGAGCACGTCGACGAGGTTCTCGTCGACGTCCTCGGCGGCGGCGCCGCC[A/C]TTGA

Table A2 (cont.)

TP84646	TGCAGGCCGCACGAAATCGACTGCGGTGAGACG[A/G]ACGGGGAAACGATCAGAGCTCCGTGAAATT
TP84689	TGCAGGCCGCATGACGCGACCTGGCGA[A/G]CGAGAAGCCGAACCGACCAGCCTAATCCCTAGTGCA
TP84706	TGCAGGCCGCCATCCGCAACGTCGTCTGCCCCAACTG[C/T]GGCCACGCCGCCGTCCTCGGCGAGAT
TP84707	TGCAGGCCGC[C/T]ATGCATCTGTTTCGGGCGGCCTGCGCGCTGCCTGACTCGGTGACTCCTTCGCG
TP84714	TGCAGGCCGCCCAGCAGCAGCATGACGAAGAACATGGGCATCATCTCCAG[A/G]GAGTTCTGGTGCC
TP84721	TGCAGGCCGCCCCACGGCACGACCTGCACCACCGTGGCCCC[A/C]CGCGGCAGGAACACCATGTTGG
TP84727	TGCAGGCCG[C/T]CCGATATGTATCAAGCCGACAGATCTGGAGATGCCATCGAATCGGGTGAAGGCG
TP84733	TGCAGGCCGCCCTGGCCGCGGCGGCACTCGACGGCGACATCCA[A/G]GTGTCCACGTGCGTGAGGCT
TP84737	TGCAGGCCGCCGACCTGCTGGTCCTGGCAGAGCACGGTGAGGA[A/T]GTCGCTGTCCGTGTGCGGGA
TP84753	TGCAGGCCGCCGCCGAGGGTGGCGAGAGCGAGGAGGCGCGCGCCGACAG[A/G]TCGTGCCTGCGGAC
TP84756	TGCAGGCCGCCGCCGCACGCT[A/G]TAAACAAGACTGACTCGTGGATGCGCCACCGCCTGCTCCGCC
TP84759	TGCAGGCCGCCGCCGCCTGCCTGGACGCGCCGCCCT[C/T]GGGCATCACCGTCGTGTCGAGGCAGCA
TP84767	TGCAGGCCGCCGCTGCTGATGTCATGGAGCGTGCGGCAGAACCGAAAACTCC[C/T]CGTGTCCAGCA
TP84768	TGCAGGCCGCCGCTGGCGACCACCACACCACCTGATCTACTCTGCAAGGGCATCGAGGACAG[A/C]G
TP84780	TGCAGGCCGCCTTAAACACACCACCGCTCTCCTCTCGTGGGCTGCGG[C/G]TGCCGCTGCTCCCCTG
TP84782	TGCAGGCCGCGAACTCCTC[A/G]TGGAAGGCTCGGAACGCCTCCCTCAGCGTCGTCGCCCACCACCC
TP84786	TGCAGGCCGCGAGAGCACGCTGCACGCACGTCCGTCCAGTCGCCCCCATC[C/T]AACCAATCCTCGG
TP84787	TGCAGGCCGCGAGCTTCTTCCTTGTCTGGGGCTGCTGCGTGCTCA[A/T]CAACGCCACTGTCCTGAA
TP84789	TGCAG[G/T]CCGCGATGAGCCTGTTCAGGTCAGGGGGAGGCTGCGGAACACGACGTCGTGTCGATGC
TP84793	TGCAGGCCGCGCAGAAGGTCCTGGTAGAACTCGGGGTCGTCAGGCAGCTGTG[C/T]GGATTCAGTCG
TP84796	TGCAGGCCGCGCAGGATGAGCTTGTCGCCGCCGCAACCCGTCGTCGCCGCC[G/T]CCTCCGCCATGG
TP84798	TGCAGGCCGCGCATCTTCCCGATCTCCGTGGCTTCGCTGTCGCCGAT[C/G]CTGGACAGCCAGTGGA
TP84799	TGCAGGCCGCGCCATGACCTGGCTGCACCGTGCCCATCGCCTGACCAAGTCCCTATG[C/T]CTGGCT
TP84814	TGCAGGCCGCGCGCAAGAAGCCCGCCGCCGCCGCCCCCGTGTC[C/G]GCCGCGGGGCTCAACCATTC
TP84823	TGCAGGCCGCGCTCCTT[C/T]TTGCGGATGTGGATGAGGTCCATGACGGCCTCGTGGATGACCCTGA
TP84826	TGCAGGCCGCGCTTCATGGACACGAGGTACGG[T/C]GTCGCAGGGAACGCGAGGGAGACGCCGTTGA
TP84829	TGCAGGCCGCGGACGTGCTCGTCGGCGAGGAGGACGGTGAGGGC[G/T]CCCGAAAAAAAAAAAAAAA
TP84835	TGCAGGCCGCGGAGGAGGAGGACGTCCGC[A/C]GCCGCAGGGCGCTCGCGGAGGAGGTGCCCATGGA

Table A2 (cont.)

TP84850	TGCAGGCCGCGGCTCCGTGTCCGCCCCTGCCACTCGCCGCCTC[A/C]CGCGGCCGCCTCGCTGCGCC
TP84860	TGCAGGCCGCGTACCTAGTGGGATGTATGGGCA[C/T]GAGCTTGATGCGAAGTTAAGATACAGGTGA
TP84885	TGCAGGCCGCTCCTCTGTTCCTGGCCGAGATG[G/A]CTCTGTCGCGGTGGGGATGGCGCGTCTCCCT
TP84888	TGCAGGCCGCTCTGGTCATGGGGATCTTCGCCGCTGTGGCTAAAGAAAATGGTACTTTC[C/T]TTGA
TP84894	TGCAGGCCGCTGCTGCTCCGTTTCCCGTGGCCGCGAGCCACCC[A/G]ACGAGCCCGAGCAGGAGCAC
TP84898	TGCAGGCCGCTGGCAGTAGCAGGGGCATTGAACCCCTGCCTGATGGAGTCCTTGAACAC[A/G]TCCT
TP84914	TGCAGGCCGTAGATCCAATGGGCACGAGCGAGCC[A/G]AGCGAGCACGGACCGACGGCCAAGGAGAT
TP84932	TGCAGGCCGT[C/G]AATGGAGGAGGAACAAGCGCTGCTGCTGGTCTCATCCCTAGCCTCAACGCAGC
TP84940	TGCAGGCCGTCCGCTCCCACTGACCTCCCGCTCATCAGGCCGCCCCGCTCGA[C/T]CACGCAAGCAT
TP84941	TGCAGGCCGTCCTCCTCGGCAGGGCGGCTTCCTCGG[C/G]CGCGGCGTTGTGCGTGTCGATCGGCGC
TP84957	TGCAGGCCGTCGTACTTGTTCTGGAACTCCTGCACCCGCTGCAAC[A/G]ACGAGCTGAATTTCATCC
TP84958	TGCAGGCCGT[C/G]GTCAAGGAGTCCCTCCGCCTGCACCCGCCGACGCCGCTGATGCTCCCGCACAG
TP84960	TGCAGGCCGTCTCCCCCGCGCGCCATGGCGGATGGATACTAGCTGCCCTGCGAC[G/T]ACAAGAGAA
TP84967	TGCAGGCCGTGATGAGC[A/C]TGTTCAGGTCGGGGGGAGGCTGCGGAACACGACGTCGTGTCGATGC
TP84970	TGCAGGCCGTG[C/T]AAAGACGTTTGCGCTGCGGCCTGGGCAGGCATGGGCGCTGGGCGACACCCAC
TP84973	TGCAGG[C/T]CGTGCAGCTCACCGCAGAGCACAGCACCGCGGTCCAGGAGGTACGCCATGTCTTTCC
TP84974	TGCAGGCCGTGCAGGGTGCGCTGCGCCGTGGCCCACTGCGCCTCCCGCTCCTCCCG[C/T]CCGTAGT
TP85005	TGCAGGCCGTGGCCAGGAGCCAGAGCATGGCCGCCTCGCTCTCCATGGCGCGGAT[C/T]GACGAGGA
TP85017	TGCAGGCCGTGGTCGTCGCTGAGCCGCTCCGCGTCCGCCTCCACGCCGACGCCGAAGAAG[C/T]GGA
TP85018	TGCAGGCCGTGGTGGCGGACCGCGTGGGCGT[C/G]GCGCCGCACCAGATCTCGGCGTCCCTGGCGCG
TP85026	TGCAGGCCGTTCATAGC[A/G]TACAGCGACGCCGAGATGCGCCGCTCCACCTTGATCCGCTCGAACT
TP85031	TGCAGGCCGTTGACGTCGA[G/T]GCCGACGTGGTTGGCGTTGATGTCCTTGAACTCGACGCTCTGGA
TP85033	TGCAGGCCGTTGCCCAATGCGGGGCCCGCTTTGGCTAGAACGTGGCATGCTGCCG[C/T]CGCGCACT
TP85045	TGCAGGCCGTTTCCTC[A/G]GCCCAGTTCAGGGGTTGCCCGTTCTGTCGCCAACGTGACCTGCGCCC
TP85068	TGCAGGCCTAC[A/G]GTTGTTCTTTAGACACATTAGCAGCAACTCGTGATAATGTAGGATTTGCATG
TP85070	TGCAGGCCTA[C/T]ATTCGAACTCGATTCGGACCTGGGACGGGAGTAACGGGACCTGATCGACCCAG
TP85072	TGCAGGCCTACATTGATCAGCTTCTCAAGTGCACC[G/T]ACGACATCACTGTTGGATCCGACTCGAC
TP85074	TGCAGGCCTAC[C/T]AGCGCGAACCCGTCGGCCACGCCCATCAGCGCGAACTGCGGCACCAGCCACA

Table A2 (cont.)

TP85075	TGCAGGCCTACCGCAGCGCCATAATCGCAGTCGCAGTACATCCAGCAA[G/T]CTTAAACCCTATCAC
TP85114	TGCAGGCCTATGCGCGGCGCGGGGCAGTGGCGCGCGCGGC[A/T]GCTGTTCGACGAAATGCGGTC
TP85127	TGCAGGCCTCAGCCAGACACGTGAGACGGCGTACATATGTTCTTGCCCCTGTTTTTT[C/T]CCCTGC
TP85131	TGCAGGCCTCAGGGTACATGGACATCCTTATGGACGCGTA[C/G]ACGCCCCCATCCCACTTCCTGGC
TP85136	TGCAGG[C/T]CTCATGCTGCCATGATGGCTGTGCATGCATATCCATCACCATCGCCGTCGGACAGAA
TP85143	TGCAGGCCTCCACCGC[A/G]CGGCCTTCCTCCGCGAGCGCGTTGAGGAGCGTGTTGTAGCAGAGCAC
TP85161	TGCAGGCCTCCGCCGCCGCCAAGAAGCCGTCCTCCTCCTCC[G/T]CCGCCGTCTCCAGCGACATCCA
TP85188	TGCAGGCCTCGCGTCGCATCAGACGGGCGGCACGGCGG[C/T]TGCGATCACTTGTTAATCCTGGCAC
TP85191	TGCAGGCCTCGCTGTGGTGTGGGCCTGTGGCTCCAAGAAGAATTCTT[C/T]GAGGAGATCGGATAGA
TP85195	TGCAGGCCTCGGCCAACGAAAGGAACGCCACCACCTGTCTCACTG[C/T]CTCGGCCAGCATCGCTTA
TP85199	TGCAGGCCTCGTCACG[C/T]TTGAGCTCGGCCCATCGCGTGCCAGCAGCTGAAGCGGCGTCTCCTCT
TP85208	TGCAGGCCTCTCCGCCGCGGACACCGAGGTGGTAGCACAGGCAGATGG[C/T]CGTCCGCTGCTGCTG
TP85216	TGCAGGCCTCTCTGCTCCAGCCATATCCGCCCTTCATGCGGGCA[C/T]GGAATCGTCCCACTGCAAG
TP85219	TGCAGGCCTCTGCCTGCCGACGACCACCGACACA[A/G]CAACGGCGTCGTCAAGGCCGCCGCCGCCA
TP85225	TGCAGGCCTCTTTGGATCCGCCCCTAACTAGGGCCGTGGTGGATGG[A/G]ATGGGACGGTGCTTACA
TP85236	TGCAGGCCTGACAGGGGATTCCCAC[A/C]GATTCGGTGGGTGTTTGCCTGTTTGGGTGATCTCTGAC
TP85263	TGCAGGCCTGCACCCTCGCCCCCTTTACCTTCGCAGTCCTACCCCCATGCAGTGTTATCAGGT[C/T]
TP85275	TGCAGGCCTGCCCGATGCA[C/T]CTGGATGCTGGCGTCGGCCGCAACAGAAGGGGGAGGCAGGAGGA
TP85281	TGCAGGCCTGCCT[C/T]ATTTTTGGGCTTCACCTATAGGCTCAAGCCCACGCCATTCAGTTACCATG
TP85300	TGCAGGCCTGGAAACG[A/C]GCCTTCTACTCCGACCCCAAGGGCTACACCGCCAACTGGGTCGGCAG
TP85301	TGCAGGCCTGGAACTTGATTC[A/G]GCCGAGGCGTGACCTGAGAAGAGATGAACAGAAGCAAATGCC
TP85309	TGCAGGCCTGGGATGGACTCCCTGCAAAT[A/C]TCTGCGGCTGCACACACGGTGACACGGTTTAATT
TP85334	TGCAGGCCTGTGATCGATC[A/C]GCCATACCACCACCAGCCCATATCGACCATCCAGCCATGCCGTC
TP85372	TGCAGGCCTTCCTTCGCTGCTGCTCAGGGACGCTTTGCCGTGCTCGGCTATCCGCG[A/C]GCGGCGC
TP85390	TGCAGGCCTTCTCTTCTCACTTTTCC[A/T]GGAACCCTTGCCCTACCTACCCCACGGGCACGGCTTG
TP85396	TGCAGGCCTTCTTCCTTGCCGCCAAGGGCGTGTGGGGCGTCCGCCTCCT[G/T]GCGCGGTCCGTCCA
TP85444	TGCAGGCGAAA[A/G]CATACGTATACCAGGTAATACATGAATCATACCAAACGGTTCGAAATTCTAC
TP85448	TGCAGGCGAAACCGCAACATGAGG[C/T]CCATACAAATAGTAGCCACATCAGAGAGGGCGCCGTCGG

Table A2 (cont.)

TP85459	TGCAGGCGAACAAGCTGGAAGAAGAAGTGTATACGGA[A/G]TACTCTGCAAGGAACACAAAAAGGAA
TP85506	TGCAGGCGAAGGCTA[A/T]GGTGCAGAAGAGCAAGGCGGCTCAGCGGGACAATGCTGCACTAATGGC
TP85507	TGCAGGCG[A/T]AGGCTCTGGTGCAGAACAACAAGGCGGTTGAGAAGGAGAATGCTGCACTGATGGC
TP85516	TGCAGGCGAATTAACC[A/C]TGTTCGTTTGATCGTTTCTGTGGCTTATAAGCCAGCTGATGTTGTTT
TP85537	TGCAGGCGA[C/G]AGGTTGGGGAGCAGGACGGGATTAGACCGCAAAAACGAAACTCCACCGAAAGCA
TP85541	TGCAGGCGACATCCCGAGGTGT[A/G]CCTGGCGCACGCCATCGCACTCGCCTCCCGAAAAAAAAAAA
TP85545	TGCAGGCGACATTTGTATCACCTGGTTCGGACCAATTCCCAGGGTGGTTA[C/T]CACGGAGGCAGAG
TP85547	TGCAGGCGACCAACAACTTCAACGACA[A/G]CAACAAGCTCGGGGAGGGCGGATTCGGCACCGTCTA
TP85556	TGCAGGCGACCGCGGCGCGGACGAGACTCGCGGGGTCGTCGGGAG[C/G]GACGCGGAGGAGGACCTC
TP85558	TGCAGGCGACGACCCGTAGGTTCTTCTCCTCGCTGCCGCAGCGGCACGGGCAC[G/T]GGAGGACCAT
TP85562	TGCAGGCGACGAGTTCCTCGGCAGGGAAATACCTGG[C/T]GCCAGCAAGAAGGCGTCGCCGCCGTCC
TP85570	TGCAGGCGACGCGCATGTGCCGTGCCACTCTAGTACCCACTCACTTCACTCCACTC[A/G]CAGACTC
TP85577	TGCAGGCG[A/G]CGGCGACGAACTCCTATTCCTGTACGGTTCGATGTAAGCCAAGAGCAACAACCAC
TP85587	TGCAGGCGACGGTGGTGGTGCGCAAGTCCAAGAAGAAGGTGTTC[C/T]TGCCGCGCCTGGTCGAGCG
TP85589	TGCAGGCGACGTAT[A/C]CTTACGTGCCAGCTGCTGCTGTGTGTGGTACGAGATCAGTCTGTCACTG
TP85591	TGCAGGCGACGTCGTCGGTG[G/T]CTGCTGTCCCATCGATGAGTGGAGCAGCAGCATCACGCACACG
TP85598	TGCAGGCGACTCCCGCGCAGAAGCTGCCGTCGCCCACGTCCGCGG[C/T]GGCGGCTACTGCTGCTTC
TP85599	TGCAGGCGACTCGAGAGGCTTCCCCGCCGCCCGTTATTGAG[C/T]GAGGGAAGTCAGGCCAGGCATT
TP85603	TGCAGGCGACTGCGCGCGAGCCGTGCACGAGTGGC[C/G]GTGTGGGCGGTGGCATGCCACCAGACCC
TP85610	TGCAGGCGAGAAGAAAGTGCCGACGCCTCGTTTCCGTCGTACGTCTCCTCGTCCT[A/C]GGGCCTTT
TP85619	TGCAGGCGAGA[G/T]GCCTGTGGACGGCGGTGAACGTCGGCACCATCGACTACACCGACGACCGCAA
TP85628	TGCAGGCGAGCAG[A/T]GGAAGCCACATTTTTTCCCCTTCGGTGACGTTTCAAGAGGACCAGACATG
TP85630	TGCAGGCGAGCATGAGATCGGCGCGCTGGTTGGGGGCGAC[A/G]TACTTGTAGAGGGCGAGGGCGTC
TP85631	TGCAGGCGAGCCACCCTCGCCCGCCCGTACA[A/G]CAGCACCGTGCTCGAGTACATGTGCAGCCTGT
TP85638	TGCAGGCGAGCGCCACCAGGAAGAACTTGGCCCGCGACATCCTATTCCTACGTGAGCC[A/G]CCGCC
TP85654	TGCAGGCG[A/C]GGACGGGGGACAGCGACGGCGCGGGCGAGGTCAAGGTCGTGGGGTGGTGGGGCAC
TP85663	TGCAGGCGAGGCCGCCGCACATACATCACG[C/T]GGCGCGGAGTACGCGCGCCACCGCACGTCTCGG
TP85664	TGCAGGCGAGGCGACACATG[A/C]ACTCAGCCAGTTCGGACACTTTCGGTAAACAGTGTGCATGGAA

Table A2 (cont.)

TP85679	TGCAGGCGAGGGTTGGAGAGCACG[A/G]CGGGATTAGACCGCAAAAAAAACGGAACTCCGCCGAAAC
TP85681	TGCAGGCGAGGTCGAGCCTGCCCAGCGC[C/G]TCGAAGCAGCGCGCCCGCTTGAGCAGCGCCTTGGT
TP85689	TGCAGGCGAGTCCATACAAGGCAACGGGACACACGGGCACGGGCAAT[A/T]TGCCTTTCGTAAGCGC
TP85699	TGCAGG[C/T]GAGTTCGAAGGTGATGTCGCCCTCGCCCGTGTAGTGGTAGCAGCCGCGCCCGATGCC
TP85710	TGCAGGCGATATGTTTACTCCA[C/G]TACTGGTACTACCCAACCACCCTGATGAGTCTACTCGTGCA
TP85714	TGCAGGCGATC[A/G]GCGAGCTCGCGCGCGGGCGGTCCGCACCGAGCATCGTCCCCGTCAGGTGCGA
TP85719	TGCAGGCGATCGCAGTTTGAACATGACAGCGATCATGG[G/T]AGTATCTGGCTATCTGCAAAGCTAG
TP85722	TGCAGGCGATCGCGGCCTACGAGGCCAGGTTCAC[A/C]GACAGCATGTCGCCGAGGGTCGCCCAGAG
TP85724	TGCAGGCGATCGGCACCGCGGGCCGAAGCGGCACA[A/T]GTCCTCGGCGCCGTCGAAAGCGAGAGCG
TP85751	TGCAGGCGATGCTGGGGCCCCACGGCACCGTCTCCCTCGCCGAGTCCTGAAAGGCATCAC[A/G]ATT
TP85759	TGCAGGCGATGGGCGGGAGCGCTGCTGCTGATCAGCTGTCCACGTCGTGGTGCA[C/T]CAGCGACGA
TP85774	TGCAGGCGATTCGGGCATAAAGCAAGAGAGTGC[A/T]GGGGCGGAGCTCCACATCCTGCTCGCCAGG
TP85790	TGCAGGCGCAAGCCGACCTATGGCGCCACAGCCTCTACTACCTCACGTCCATGGCGCT[C/G]AAGTG
TP85796	TGCAGGCGCAATGCCGCGGCCACCGTCGCCAGCGCCGCCTTCCTGCTCCTCCT[A/C]CTCATCCTCT
TP85797	TGCAGGCGCAATGCGCGACAAA[A/T]TAGATCGAGCGGACAAAGCTGCTATGCAACTATGGGGGCGA
TP85798	TGCAGGCGCAATTGCTCTTCTTTAGTAAGAGGCTGC[C/T]CTGAAGGAGGTTCTTGGCCTGGGTTTG
TP85820	TGCAGGCGCACCAGGGGGTCG[A/G]GCTCGTCGGCGCCAGCCCCTCGACGCTGGTCACGCTCACGGC
TP85834	TGCAGGCGC[A/G]CCTTCAGGGCTTCCTCCTCCACTTCCCGTCCTTCCTCGCCAACTACAAGCGGGG
TP85840	TGCAGGCGCACGCACGCACGGTTCTCGAGGCGCCGCAGCCGCCGCCGTCACATGG[G/T]TTGAAGTT
TP85848	TGCAGGCGCACGGGTA[C/G]CGCAGCGGGTGGTCCTCGTCGCCGCGGTTGCGGCAGATCCGAAAAAA
TP85860	TGCAGGCGCAGAGCAAGAACGTCATCATCACCTACCTGGCATTGCTCAACCT[C/T]GGCCTCCACCT
TP85864	TGCAGGCGCAGAGCATCGTGGCGCCCAGCGCCTACATCTCCGCG[A/G]CGACGCTGGCTGTGCACCT
TP85871	TGCAGGCGCAGATCCAGTAAAGGACATGGGTGTGCGCATGTACACATAATGATTTTTGAAA[A/G]GG
TP85873	TGCAGGCGCAGATGGCGCAGCAGGCGGCCG[C/T]TGCCATGGCGCAACAGGTGGCGCCGCCGCCGCC
TP85885	TGCAGGCGCAGCGCGGCCACGTCGTGCGCCACCGCGGCCATCTC[G/T]GCCGACTCGAAGCTGCCGA
TP85895	TGCAGGCGCAGCTGACGCTCGTGCAGGAGGATCTCAGGAACGCGAGGGA[A/G]CACCTGGCCTCCAT
TP85896	TGCAGGCGCAGCTGCTGGACGGCAACCTGGGACTCATCGTGGAGGAGTGCATGCAGCACTAC[A/G]A
TP85898	TGCAGGCGCAGCTTCCCGACGGCAGCTGGGTCGACGTCCAGCCCCTC[A/G]AGAACGCCATCGTCAT

Table A2 (cont.)

TP85903	TGCAGGCGCAGGAGCTGCTCTCCAACATCTGCATCCTCGAGACC[G/T]CGGTCACGAAGCTGGAGGA
TP85909	TGCAGGCGCAGGCCGCGCAGCAGTTCAGGATGCAGGACCTCAGCAAGGTGATGG[A/C]CAAGCAGGA
TP85921	TGCAGGCGCAGGGCGAGGTCGGGGCG[C/G]TCGCGTGGATCGGCGCAGCCGCGCTGGCGGCGCACGT
TP85933	TGCAGGCGCAGTGACAAGTCCACCTCCTCGCCCTCCTAGAATGTGATAGCCTCATACTGCCA[C/T]T
TP85937	TGCAGGCGCAGTTCGGGAACAAGTGGGCGAGGATCTCCACCTACTTG[G/T]CGGGCAGGACGGACAA
TP85948	TGCAGGCGCATG[A/G]CTGCACGGCAGCGCGCAGGCAGCGCATGCAATGCAATCACCGTCTCATTAC
TP85954	TGCAGGCGCATG[C/T]GGCACAGAATAGCAGAAAGAGTGCAAGGCACAGGTCCAGGTGCGCGACCCG
TP85959	TGCAGGCGCATGGCGCACGCCTCGAG[A/C]CGCGCCTGGATTTGTCTCGCTCCCGCGGACTCGCACC
TP85968	TGCAGGCGCATTCCGTTACCGTGTCCTCGTCGGGA[C/T]GAAGGGCATCCCCTCCCATGCAAGGTCT
TP85969	TGCAGGCGCATTTGTAGTTTATCCGTTCAAATAAACAGACAAACACACCCTGGGC[C/T]AATCAGCC
TP85988	TGCAGGCGCCAGAGCCGCGTGTA[G/T]GCCTTGAACGCCTTTCGGCTGTGGTGGTCCCCGCCGCCGT
TP86004	TGCAGG[C/T]GCCATGGTTCAAGCAAAGAAAAAAAGAAGCGCATCACCTTCAAGACTTCAAGGTCGG
TP86013	TGCAGGCGCCCATGCCGCCCGCGGCGGCCCCACACCCGCACGAGGAGTTCAACTTCGACT[A/G]CCT
TP86017	TGCAGGCGCCCGACGCGTCGCGCTTCTGGCA[C/T]GCCGCGGTCTTGCAGCCCAGGTAGCCAGGGTC
TP86027	TGCAGGCGCCCGTCGTGTTCGGGTGCGGGCAGGTGCAGACGGGCTCGTTCCTGGACGGCGGC[C/G]C
TP86029	TGCAGGCG[C/T]CCTCCTTTCGATCAGCGGCAATGCGCGGCGCTGGCGCGACACGGACCAGGTAACT
TP86037	TGCAGGCGCCGATGCCTCCGAGGTGGGCGCGCTCCTCGCCTTCAAGCGTGCCCTC[A/G]CTATCCCA
TP86041	TGCAGGCGCCGCACTGTTGCAGGATTCAGAGACAACTAGTAGGTCAGTGCAAGTTGGTTGCAC[A/C]
TP86044	TGCAGGCGCCGCCGCCCTCCTGCTGCG[A/G]GTCCTTCATCTCCTCCGAGTACATCTCCTCCACCAT
TP86045	TGCAGGCG[C/G]CGCCGCGGCACTCCGTCGCGCTGCGGTCGTCCACGCTCGGGACGCTCAGCCTCGA
TP86046	TGCAGGCGCCGCCGCTTCGGC[C/T]GAGGACCCGCCGCCACCGCCTCCCTTCTGCTTGTTCCCTGGT
TP86052	TGCAGGCGCCGCGACACGGGGTCAAACGC[G/T]AAGGCGAAGAGGAAGGGCAGGGAGAAGGACACCG
TP86059	TGCAGGCGCCGCTATCCCGTACAAAGTGACAGCCATAGAGAT[C/T]ATAGGAGTGGTACCCTGAGGC
TP86068	TGCAGGCGCCGTGGCCATGGCGTCACCGCCCAGCGCAGGTCGTC[C/T]GCGAGAGCTCCATCTGCCT
TP86075	TGCAGGCGCCTCACG[C/T]GTGGTCTCTCCGCGAGTCCGCGCGCAACCGCGAGCAAGGGACGATCGA
TP86093	TGCAGGCGCCTGCTGCTCTCCGACAAGACCCCAAGAACTCGCCAACCAAGG[C/T]CAGCCACCCTTC
TP86117	TGCAGGCGCGAGGAACACATCATTCAGATGACTTGTGACCACCATCAGGCGAAG[C/T]GAATCCGTG
TP86119	TGCAGGCGCGAGGCGCGTCGCG[A/C]GCGATACGGTACGGTCGAACCAGCGAAGCTTCTGCTGGACG

Table A2 (cont.)

TP86120	TGCAGGCGCGAGGTCAGTACTTTGGTAATGATCTTCACAGGCCAATTCTG[A/G]AGCGAGACAGGCC
TP86123	TGCAGGCGCGATCATTTGGTAGTCGTGGTACCCGCACCGA[A/T]ACAGCCAGGCATGCGTTCGTGCG
TP86130	TGCAGGCGCGCAGCCTCTTCGCGTGCAGCGCCATTTTCCT[G/T]TGCGGACCCAATCTTCAGCAGTT
TP86142	TGCAGGCGCGCCACGAGCGCGTCCCTGGG[C/T]GTGCCGCGCACGGGCTCGCACTCGAACTCCCACC
TP86154	TGCAGGCGCGCCTCGCTCATGGCGACGCGCACGAGCGC[C/G]GCGTCGCCGTGTGGGCCCTGGTAGA
TP86155	TGCAGGCGCGCCTGGTACTCGTCGGCGATCCGCGCGGCGGCGTCCTCGAGCAGGGCGACGCAC[G/T]
TP86158	TGCAGGCGCGCG[A/G]CCGCGAGCCTCCAGGCGCGAGGGGCGAGCGCAGGGCCGCCTCTGTCGGGCG
TP86164	TGCAGGCGC[G/T]CGCGATAAAAGCCAAGTCTTGGTGCCGTGCATGGCGCGTACGAGCTCGCCGAAT
TP86174	TGCAGGCGCGCGCTGGGGCTCTGCTGCTCCCGCCTGATCAGGCTGCCGAGCGAGC[C/G]CTCGAACC
TP86175	TGCAGGCGCGCGGCATG[C/G]CGCAGGACCTCAGCTGGGACCACGCCGCCGTTCTGTATGAGGACGT
TP86177	TGCAGGCGCGCGGCATGGCACAGGACCTCAGCTGGGACCACGCCGCCGTGCT[G/T]TATGAGGACGT
TP86179	TGCAGGCGCGCGGGCCACCGTTTCCAGC[A/C]GCAGCCGCATCTGACGCCCAGCTGCGCGCAACCGC
TP86180	TGCAG[G/T]CGCGCGGGGAATGCTGCCCGCCTCTTGCTTTGCAGCCCGCGGAACCCACCGCCGTCGT
TP86184	TGCAGG[C/T]GCGCGTCGTGCCAATGGCGAGCTCGGCTGTGAAGCCTCTTTTTGTGGGGCGACCATG
TP86188	TGCAGGCGCGCGTGTAGTGACC[A/G]ACCGAGGTAATAATGGTGTGCTAGCTCATCTAGTGCTATAG
TP86190	TGCAGGCGCGCTCGGTGCAGACTCCGCGCCGATGG[A/G]AGCCACGCGTCTCGAAATTTGATCGAGG
TP86193	TGCAGGCGCGCTGGTACTGCTGCTCCTGCTCGTCGGGGCGGCGGCCAGAGCGCGTGACGCGGC[A/G]
TP86222	TGCAGGCGCGGCGCAGATTC[C/T]GTCTTCGCTCTGTTGCCTGGGAACTCTGGAAGGAGAGGAACGC
TP86228	TGCAGGCGCGGCGGTTTGAGCACCTGGGC[A/G]CACAGATCCGCCGCCACCACCATGTATCACATCT
TP86231	TGCAGGCGCGGCTT[A/G]AGTCCGCCCAGGAAGACCTGAAGAAGGCCAAGGACCAACTGGCATTCAT
TP86237	TGCAGGCGCGGGAGAGGTCGAGCCCCGTGGTGTCCGCTGC[C/G]ACGGAGTGCTCGCCGAAAAAAAA
TP86243	TGCAGGCGCGGGCAACTCGCCGACGACACGAGGCAG[A/G]CAAGGAGGTGACCTCCGCCGTCAGCGA
TP86252	TGCAGGCGCGGGCGTCCCT[A/C]GCCGAGCAGGCCTACGACTACGCCTTCGTGCACGTCAGCGCCGC
TP86255	TGCAGGCGCGGGGCG[C/T]TGACGATTGTGTCGGGCCTCTCGCAGTGGTCACTTCAGCTTCTGCGTG
TP86273	TGCAGGCGCGTCGCCTCCTCCTCA[C/T]CCCCTTCGTCTAACACGTCGCCGCCCAACATCACCGCCG
TP86300	TGCAGGCGCT[A/G]AAGCGGTCCATCACGGAGGACCCCAAGAACCTGACGACGAACTGGTGCGGCCC
TP86301	TGCAGGCGCTAAGTTCGGATC[C/G]AACAACGACCACCAGCAGCGGATCCACCACTCTTCCATCAGT
TP86305	TGCAGGCGCTACGCTCGGCGGTCGGCCGCTCGGCGCTGCCGTCGTGGAACAGCACGAC[G/T]CCCAC

Table A2 (cont.)

TP86306	TGCAGGCGCTACTGACCGAGAGACAG[C/G]ACAGCTGGAGAAGAAGACGCCACGGGTGAGGCAGGGA
TP86321	TGCAGGCGCTCATGAGGCTCCAGGCCAAGACGGCGTCGT[C/G]TCGGAAATCCGTTGAACAAGTGAG
TP86334	TGCAGG[C/T]GCTCCTGGAGCTGCATATTAGGAGCACAGAGTACTGCTGTGTCTGTGTATAACAACC
TP86337	TGCAGGCGCTCCTGTCAGCCGCCGCGGGCAACAAGCAGGCGCC[A/G]CAGCAGTTCCACTGCGCGGC
TP86345	TGCAGGCGCTCGATCATGAGCATGGCCTCGCTGGCCGCCGTCTCCGCGGA[C/G]GCCCGCTCCGCGT
TP86357	TGCAGGCGCTCGTCCGCGGGGCCGACCGCCAGCGCCGCGGCCGCGCAAGCGAG[C/T]TGCTCCTGCT
TP86361	TGCAGGCGCTGAAGCGCGCCATCACGGACGA[C/T]CCCAAGAAGCTGACCAAGAACTGGTGCGGGCC
TP86363	TGCAGGCGCTGAAGGCGGCCGTGACCGAGGACCCCAAGGGCGCGCTG[A/G]CGTCGTGGCAGGGCGC
TP86365	TGCAGGCGCTGAATCATGAGCATGGCCTCGCTGG[A/C]CGCCGTCTCCGCGAAGGCCCGTTCGGCGT
TP86368	TGCAGGCGCTGACAGCCGCCCAGGCTGGCACAGTTGTACGTGAGGTGGC[C/T]GTGGTACTGCGCTT
TP86370	TGCAGGCGCTGAGCAGCGTGCTCCAGATCACCG[C/T]GTTCGGTTCAACTTCCATGTCGCAAATGAA
TP86384	TGCAGGCGCTGCTCTCCCGAG[C/G]CCCCCCTCTCTGAGCGCGACTCCGCGCCGTCTACGCCGCTAT
TP86385	TGCAGGCG[C/T]TGCTCTCCCGCGGCCCCCTTGCCGAGCCTGACTTCCTCGCGCTGTTTGCTGCTGT
TP86386	TGCAGGCGCTGCTCTCC[C/T]GCGGCCCTCTTCCCGAGCCTGACTTCCAAGCGCTGTTCGCTGCTGT
TP86389	TGCAGGCGCTGCTGCC[A/G]CTCGTTTCGCCGCCGCCACAGTTGCTTGGGCAAAGGAGAGGGGAATG
TP86396	TGCAGGCGCTGGAGACCATCTTG[C/T]GCACCACATCCAACTTGTCGACGATGAGAAGCGATGATAC
TP86398	TGCAGGCGCTGGAGCAGGTGAACCTCTCGCCGAGGTGCAGCGCCGC[A/C]GTCGCCGCCTCCCGAAA
TP86418	TGCAGGCGCTGGGCGGCAACTACCACGCGCTCCGCGACTATCTGATGATCGACGGAGGC[C/T]TGTA
TP86423	TGCAGGC[G/T]CTGGGCTTCGAGTTCACCCGCGTCACCGCCGAGGAGGTGGTCGGCCGCCTCCCCGT
TP86430	TGCAGGCGCTGGT[A/G]AGCGTGGACATGCTGGTGCTGTTCCTGGCCACCATCTGCGGCGTGGGCGG
TP86435	TGCAGGCGCTGGTGCGCGGCCGCCGCGTGCGCAAGCAGCTCGCCGT[C/T]ACGCTCAAGTGCATGAA
TP86445	TGCAGGCGCTGTCCAAGGAGGAGGAGGCCGTGCGG[A/G]CGCGCCTCCGCCGCCGAAAAAAAAAAAA
TP86446	TGCAGGCGCTGTCCCTCGTGTCGGACGCGCTCGACACCGCCGCCTCGGGCTCGCCGTCCCC[A/G]TC
TP86448	TGCAGGCGCTGTCCCTTGTGTCGGACGCGCCGT[A/C]TCAGGCTCGCCGTCCACTGCGAGCCGCTGC
TP86449	TGCAGGCGCTGTCCGTCCATGGCGCACAC[A/G]CGTGGCAGGGCCTGGACCGTCCCCTGGAAAGTTC
TP86470	TGCAGGCGCTTGGCCCCCTGCAAGTCCTCCGCGC[C/T]GACCTGGACGACGAAGGCAGTTTCGACGA
TP86481	TGCAGGCGGAAGC[A/G]GAGGTGAAGCCGACGAGGACACCGATGGCGAGGTAGCCCTGGTGGTTCCT
TP86487	TGCAGGCGGAATTTTAGGCTACGAATTTACTTGGTTACGAGCGATCCAGCTGTGTTCGTCG[C/T]GA

Table A2 (cont.)

TP86491	TGCAGGCGGACAGCGGGAAGCT[C/T]GGGGGCAGCGCGGGTGGCTCCCCGTACTACCGATCGTCGTC
TP86493	TGCAGGCGGACATCTTCAACACGA[C/G]CTCTACTCCGCACGTCCTGGCCTCCCCGTGTACCCCGAA
TP86496	TGCAGGCGGACCCCAAACTCGCTTGTTGGGCCACTACTGTCAGCTCAG[A/T]AAATAAAAGTATAAA
TP86502	TGCAGGCGGACGAGCTCGCCACCGTGCGCCTCTTCCAGGAGAACACGCCCTC[C/T]GTCGTCTACAT
TP86512	TGCAGGCGGACTGTGACGCCGCCGTCAAGGAGGCGGCCCGCGCCGTGCTGAGG[C/T]TGCACTCCGA
TP86516	TGCAGGCGGAG[A/G]AGAAGCAGGACGACGGGTTCGAGCTCACCAGGGACGCCATCAAGTCGCTGCT
TP86517	TGCAGGCGGAGAGG[A/G]AGGACGACAAGGCGCTGCTGTTGTTGTGGTGGCCGTACCAGTAGTAGTC
TP86532	TGCAGGCGGAGCGGCAGGAGCTTCCCGTTGATGGGGCTGCGCGAGCACATGATGACGTC[A/G]TCGA
TP86544	TGCAGGCGGAGGACCTTGAAGACGCC[A/C]GACGGAGTGGCACGGCCAAGGATGGTGGAGTAGGTGT
TP86555	TGCAGGCGGAGGCGCTTCACGCCGAAGCCGCCCATGG[A/C]CCAGTGCGCCTCGCGCGCCCACTCGA
TP86556	TGCAGGCGGAGGCGCTTGGCGATGACGGCGCCGAGGTTGCGCACGGCGTCCTTCTCC[C/T]CGTCCG
TP86559	TGCAGGCGGAGGCGGAGGTAGGAGCGGAGGAGGAAGAG[A/C]GTGCGGTCGAGGTCCATCTGGTAGA
TP86563	TGCAGGCGGAGG[C/T]TTCGAAGGCGTCGGTACCAGGCGGGCCAGCTCACCAGGCGCTCGCTGCCGT
TP86591	TGCAGGCGGATCTGCTCCAGCAGCCGCTCCACCTCGG[A/C]GTCGTCCACCTGGTGGTGGCCCCCCG
TP86593	TGCAGGCGGATCTGCTCCAGCAGCCGCTCCACCTGGTGGTGGCC[C/T]CCCGTGGCGTCCAGGTAGC
TP86603	TGCAGGCGGATGCGGAGCGTGTCGAGCGGGTGGCCCGCCAGCACGCCCGCCATGCCGCCCAC[A/C]C
TP86606	TGCAGGCGGATGGCATAGTGGAAGCGGCCACTGCGGGC[A/G]GACGACGCAGTGAAAGCGGTAGCGG
TP86618	TGCAGGCGGCAACTAGCTCTCCATGAATCATGATGATGG[C/T]GGCAGCATGCATTGTTGAGAGCTC
TP86626	TGCAGG[C/T]GGCACAGCCTGATTTTTTTTAATTTTAACATTTTTTTAAAACTAATTTTAAATCTAA
TP86645	TGCAGGCGGCAGCTGGATCGATCACACTGACCGAGTCAAATCTCTTCACCTTAG[A/G]CCCTACCAG
TP86648	TGCAGGCGGCAGGTACGGGAGGAAAACGCTTGCAAC[A/C]TCACCAGGGTACATGCATACTGTCTCT
TP86656	TGCAGGCGGCATAA[A/G]AGAAACGCAGGGCTCACAGTTTGTCGGCTTTGCTCATGAGCTTGTCGGG
TP86667	TGCAGGCGGCCAGGGAGGCCGAGGCGGTGGCCGCCGT[C/G]GAGTGCTCGGGCCACGGGCAGGTGTT
TP86675	TGCAGGCGGCCCAGCTCACGCTGCGCTGCCTCGAGGGGGACCCCAGG[A/G]GCCGAAAAAAAAAAAA
TP86688	TGCAGGCGGC[C/T]GCCCAGGTGTGCAGGAAGTGCGTGGATGCAGAGCCGTCGCAGGCGGCGTGGTG
TP86717	TGCAGGCGGCGACGGAGCTGGACCCGACGATGACATTCCCGTACAAATATCGTGCCTGCGC[A/G]TT
TP86723	TGCAGGCGGCGAGGTGAGGT[C/G]GTCACCTGCGAGCGCTGAGGCCTCCATATTGAAACATACCCAT
TP86727	TGCAGGCGGCGATGGCCTCAGT[C/T]AAGCAGTGCTCCATCGGTGTGCAGCATTGTTGGCACGAGAA

Table A2 (cont.)

TP86729	TGCAGGCGGCGCAAGCTTCAAGCCGTGTGCAAAAGTGGGGCGGCAAAGGCACTGATGAAGT[C/T]AA
TP86730	TGCAGGCGGCGCAAGCTTCCATTG[C/T]GGTGGGATCCCAAGTTTGGGTCGAGGACCCCAACGTCGC
TP86741	TGCAGGCGGCGCGCGAGGAGCTGGGCTGGGGTGGCGTTCGCTGCGAACGAGTCGTG[A/G]TGGAGCA
TP86744	TGCAGGCGGCGCGTGCGGGTTCAAGAACACCAACCAGTACCCGTTCATGTCCATGACGTCGTG[C/T]
TP86750	TGCAGGCGGCGCTCGATCTGCTTGT[C/T]CATCATGGCGTGCAGCCGCTGGAACAGGCTCTCGATGC
TP86753	TGCAGGCGGCGCTGGACTACGCGTGCGGCCACGGTGCCGACTG[C/T]GGCGCCATCCAGCCCGAAAA
TP86771	TGCAGGCGGCGGC[A/G]CGGCGCTGCGAGCTGTGCACGGGGTGCGACGCATTGGTGAAGGAAGAGGG
TP86772	TGCAGGCGGCGGCAGCATTGAAAAATGGTTTTGTTG[A/G]GGGAGGGGCGGCGAGGAGGACCAGAGG
TP86777	TGCAGGCGGCGGCGA[A/G]GATCGCGGACTCAAGCCGCGGCGGCGGCATCGTGCTACAGGAGTACCA
TP86804	TGCAGGCGGCGGCTACACAAGCCTTTTTGG[A/T]CGCGATCGCCAAGGAAGCTGAGCGGGCCGACGC
TP86819	TGCAGGCGGCGTAGGGCTCGCTTGGGCATGCCCAGGTGGGGAC[A/G]GTGCGTGAGGGGAGGAGTTT
TP86821	TGCAGGCGGCGTC[C/G]AAGGAGAGCCATCCCTCCGCGGCCTGCCTCGGCCACGCTTGGCCTCAACG
TP86824	TGCAGGCGGCGTCGCTGTCGGTGAGAACGCAGGTGGCGACGACGGC[A/G]CCTGTGGCCACGCCGAA
TP86846	TGCAGGCGGCTGACCTTGACCTTGCAG[G/T]TTGCAGCTCCAGCCGATCGGAGCACGATGGCGGCGC
TP86851	TGCAGGCGGCTGCA[A/C]GCGATCTTGCTCAGGGCCTGCACGCGCGCACCCACACAAAGGGGGGAAC
TP86852	TGCAGGCGGCTGCACGCGATCTTGCTCAGGGCCTGCACGCACGCAC[C/T]CACACAAACGGGGAACA
TP86853	TGCAGGCGGCTGCCACAGCCCAC[A/T]GGCCATGCGCCCATGCGAGAGGACGAATCGACCCGACAAG
TP86872	TGCAGGCGGGAGCGGGACCCAG[A/G]CCCAGTGTCTGCTGCGTGTCCGCACAGCGACGTCGTGGACG
TP86958	TGCAGGCGGGTCATGTTGAACCTGGAGCTGACCTCCGTCACGAGG[A/C]TGCCGTCCACCCGCAGCG
TP86969	TGCAGGCGGTAATCTTCCTTCTGCACCTC[C/G]AACCCTTCGAGCGTAACTACAGGTCAGACCTGGT
TP86988	TGCAGGCGGTCCTGTGAAATACGAGAACCCCTGAA[C/T]CCCTAATTCAATAGACAACCAACCCAAC
TP86991	TGCAGGCGGTCGCCGTTGTCATCGCGTGGGTCGCCGTCGTCATCGCGT[C/G]GGTTGCCGAAGTCTG
TP86992	TGCAGGCGGTCGGCGCCCGCGCAGGAGAGCATCTTGTTGATGCGGAGGACGTGGAACGGGTGC[C/G]
TP86996	TGCAGGCGGTCGTGAAGGAGACGCT[G/T]CGCGCCCACCCGCCTGGCCCGCTGCTGAGCTGGGCGCG
TP87000	TGCAGGCGGTCGTTGTGGTCATCGGGTGG[A/G]TCGCCGTCGTCATCGCGTGGGTTGCCGAAGTCTG
TP87002	TGCAGGCGGTCTTACGTTCAGTGGACGAGTCAATCAATTTCAAGCCATTTGAC[C/T]TTGGCAAACT
TP87005	TGCAGGCGGTGAACACCGCCACCCTTTCCGTGAGCGCCAAGGGCCAAGGCCTGCTGCCATC[A/T]CC
TP87010	TGCAGGCGGTGATCCACAGAGCGGCG[A/G]CGGCCATCCTCATCGCGGTTCCTGGTCAGGCTTGGAG

Table A2 (cont.)

TP87012	TGCAGGCGGTGATGGG[C/T]GCCGCGGCGGGAACAAAACACTCCCAGACGGCGGTTGGCTCGTGGAT
TP87036	TGCAGGCGGTGGCGAAAGAGGC[A/G]GCAGTCCCTGTTGCCCTCGACGCTGGCACCGTGAGGCGGCG
TP87047	TGCAGGCGGTGGTCGATCGGATTCGGGGCG[A/C]GCGTGGCGTGGTCGTGGTGGCGGCCCGAAAAAA
TP87049	TGCAGGCGGTGGTCGCGAGTCGCAACA[A/G]GCGCTGGGCGTTGGCCGCGGCCTCAGTTGCCGAAAA
TP87054	TGCAGGCGGTGGTTGGAGTCGAGGCGCCAGATGGATCCCCAGGACTCGCGCATGGGCGTCCA[C/G]C
TP87062	TGCAGGCGGTTCTTGGTCATTAGTTCAAGTGTCGCTGG[A/G]CGATTTGGACAGACGACAGACAGGC
TP87077	TGCAGGCGTAAGGTTGGCACATACATGAGGGCACGTAGTTAATAACGCAACTGTGCCA[C/T]CTGCA
TP87082	TGCAGGCGTACACCATCGCCGCGGCCGCCGCGCTGTTCGTCAAGTACGAGAA[A/G]GAGCGGATCAG
TP87087	TGCAGGCGTACAGC[C/T]GCTCCTGCGCGCGTGGCAGCACGTGGCGCGCGCCGTGCTTGTGCAGCCG
TP87104	TGCAGGCGTACTACCTGCACCGCCTCGC[A/G]CACACCCTCCGCCTCGTCCCGCAGCCGCTGCTCTG
TP87116	TGCAGGCGTAGGGG[A/G]CGGATCCACAACGGATGTCTCGTCTCGCTGCTCCGCTCCTCATCGGCGG
TP87118	TGCAGGCGTAGTCCCTTTCCTCGATGAGGACACAATGCAAGTT[A/C]TTTTTCATGCATGGTAGGGC
TP87119	TGCAGGCGTAGTCGATCGCCGCCTGATATCCCTGGTCGG[A/G]CACGCCCGTCTTGCACACGCAGAA
TP87120	TGCAGGCGTAGTCGATCGCCG[C/T]CTGCAATCCCTGGTCGGGCACGCCCGTCTTGCACACGCAGAA
TP87122	TGCAGGCGTAGTTGTC[C/G]ACGCGGTAGGCGACACGGCCGTCCTCGCCGTAGACGGTGCACCCGTG
TP87142	TGCAGGCGTATCGGCGCCAGGTACGCGAACCCCTGC[A/G]CGAACGTGAAGTACCAGCAGCGTGGGG
TP87148	TGCAGGCGTCAACCAAGGT[A/T]ACTTAAGACCACTGCGCTTAAAAATATTTTCAGTGACAAGTACT
TP87162	TGCAGGCGTCAGGGACTCAGGGGCAATGCAAAAAGGT[A/G]GAGAAATCTAACGGATACCAAATCTA
TP87172	TGCAGG[C/G]GTCCATACTCCATAAACCACGGGAATCAGAATCACCACAATCAGGCATGCCAATTCC
TP87197	TGCAGGCGTCGACTTCAAAGGGAACCACTTCCACTT[A/C]CTGCCGTTTGGAGCTGGCCGAAGGATA
TP87208	TGCAGGCGTCGGAGCATCCTTTAGCCTCGTGTCATCGCTCGTGGCC[A/G]CATCGATCGTGGTCTCC
TP87231	TGCAGGCGTCTAGGTAGCAAGGAGTACATTCCATCACTTGCGGCTGTGAGCGTGCGC[A/G]CGTGTC
TP87242	TGCAGGCGTGAAGCTCAC[C/T]AGCAGGTCCCCTGCCGCGACGGGCGCTCGAGGAGCAGTTCGCGGC
TP87317	TGCAGGCGTGGAAGCACGCCATC[A/C]TCGAGGACCCCAAGAACCTGACCGCCGACTGGTGCGGGCC
TP87318	TGCAGGCGTGGAAGC[G/T]CACCGCCATCTTCTCCGACCCCTCAAACTTCACCGCCAACTGGGTGGG
TP87326	TGCAGGCGTGGACGTCGAGGATGGAGTCGAGGTCGGAGCTGAT[A/G]CAGGGACGCGACCCGAGGGC
TP87334	TGCAGG[C/T]GTGGCAAGAGCTGAATCTGGTGTTGAGGAGCTCACCTTCTTGGGTGTGACGAAAGCG
TP87339	TGCAGGCGTGGCGGCGC[A/G]CCATCCTCTCCGACCCCTACAACGTGACGGGCTCGTGGACGGGGCC

Table A2 (cont.)

TP87350	TGCAGGCGTGGGCG[A/G]CGCAACTGGTGTCGTGGCCGTCGTCAGGGCAGAGCACATCGGCGAAGTA
TP87360	TGCAGGCGTGGGTCCATGTCGAGATGGAGCGCGGGGCGGCCGCATGCAGC[A/C]GAGGAGGTCCACG
TP87362	TGCAGGCGTGGTAGCGCAGGTACACCGTG[C/T]GTCGTGCGCCACCTGCTAGCCCCCACGCCCGCGC
TP87374	TGCAGGCGTGTATATCAACAGTCAGTCA[A/G]TCAGTCAACAGAAACCCCACCATGCATCATAGCAT
TP87381	TGCAGG[C/T]GTGTGTCGCGTTCGCGTATCTTTCAGCTGCCGTGCGAGTGCCGTCGAATCGTGCCGC
TP87388	TGCAGGCGTTCAACACGCCGATGTACGCACCCGAGAGCGCACACGCCG[C/T]GAGCAGCGGCCGCGC
TP87397	TGCAGGCGTTCCAGCGGCGCGGCCGTGTGATGCACA[G/T]GCACCACCAGGCAGGACCGAACTGCGT
TP87403	TGCAGGCGTTCGAGTTCAGGCACCGCATCATGATGCACACCCTGCTCCAGCAGGGCCTC[A/T]GGTT
TP87411	TGCAGGCGTTCTGGACAGACGTGCGCAC[C/G]GTGGGGCACGGTGACAAGAAGGACGTGCCAGGGTG
TP87414	TGCAGGCGTTCTGGACGGACGTGCGCACCGTGGGGCACGGCGA[C/G]AAGAAGGACGCGCCAGGGTG
TP87424	TGCAGGCGTTGCAGAGCGCGCCCAGCCCCATCGGCTGGATCCTCCACTGTGG[C/T]GTCTCAGTGGC
TP87432	TGCAGGCGTTGGAGGAGACGTTCGGGGACAAGATCCGCCAGCTCAGGGAGGAAGAG[C/T]TCGGGTG
TP87445	TGCAGGCGTTTGATGCGAGTAACAACCGCCTCACGGGCGCGGTCCCGC[C/T]CGCCGTCGCCAACTC
TP87452	TGCAGGCTAAACAGACACGC[A/G]ATGAATTCTTCCCAGAATCACTGAACAAGATTTGCGAGTAAAA
TP87457	TGCAGGCTAAAGAGGTCCAGGG[A/G]GCTCCAAGGGTCCGAGGGGGCCTTGAGCCCCCACCCCACCG
TP87461	TGCAGGCTAAATGGCACAT[G/T]CCACTACCGTATGTTTCTACTCATCACGAATCATGCATCGCATT
TP87468	TGCAGGCTAACATCATCATGCGGCTCTGCCATAAGAATCCTGGATCGCTGCATACA[C/T]TGTCTCA
TP87469	TGCAGGCTAACATGACA[A/G]ACAGTGAGGCTACCATCCAGTATGACGTGGAGGATAAACGCAGACG
TP87496	TGCAGGCTAAGTTACAGCAGCTAGCTAGTGAATAAAAATTATTAAATCTTTAGCTGAGAG[A/G]AAG
TP87499	TGCAGGCTAATCCAAATTCGACCAAGAAATGTACACCTCTATAGCGCC[C/G]AAATCAAGTGGGATG
TP87512	TGCAGGCTACACCGCGTGCAGATCGTCTGCTGCTACCTCCTGCAC[C/T]GACCTGTGGTCGTCTCTG
TP87554	TGCAGGCTACGGGGGGCGGCGCAC[C/G]CCTCTCGTCTCCATCCGTCTCCGTCTCCTCCGTCTCTTT
TP87559	TGCAGGCT[A/G]CTACTAGCTCCTGGCAAAACGAGCTTGGGGCACCCTGCTATCTTAAGCTTCTGCA
TP87561	TGCAGGCTACTACTGAACCAGGAATCTACATCACCACACAGGTCT[C/G]TGCTGCTCGCGTACACGT
TP87582	TGCAGGCTACTTCCATCACATCGAAAC[A/T]GACCGAATTTGAGCTGGAACGAACGAATCCGACAGC
TP87590	TGCAGGCTAGACGACTTGGGAGCTAGGGAAGTGGTTTGGGCAACGTACGTAGATGTTCTAAC[A/G]T
TP87616	TGCAGGCTAGCTGTAGGTATACATACGCACTTCGTT[A/G]CAGTGGTTGATGGTAGTAAGTCACCTT
TP87617	TGCAGGCT[A/G]GGAACGACAGCGAGCGCGACCGAAAATATCAGAGAGCGCAAGGCAGGCTGGCAGA

Table A2 (cont.)

TP87621	TGCAGGCTAGGAGCAGAACGTGCGTTTTGCTCGGCGGCGC[C/G]CCGCTTTTGCGGTCAAACTTGCT
TP87631	TGCAGGCTAGGCAGAAGGGCATGGCACAAGGCACACA[A/G]TTGAATAATGCTAATACAGCTCAAGC
TP87642	TGCAGGCTAGGGCGCGAGGAAGGAAG[A/G]AGGCGGCGGCGGTGTAGGGTTGCACGACCAGGAACAC
TP87648	TGCAGG[C/T]TAGGGTACGGTGACAGCGGCATGCAGGCCGCTTGAGCGGCGACCTACGTCGTGTGGA
TP87659	TGCAGGCTAGGTTGGGGCCAATGTTGAGTTAAC[A/C]CCTAGCTCAAGCACGCGCTCCACAGATCAA
TP87664	TGCAGGCTAGTGCTTCGCCCACCTCAGCTTTGTCTATACCTTCAAGAACAA[C/G]GGCCGAGGCACC
TP87671	TGCAGGCTATACATGCATCTGCAATCTGCCAAGGAA[A/G]TCAAATCATACTTGTGTAGCCGTGTAT
TP87679	TGCAGGCT[A/G]TATAGCAACGACCTCCTGTCCAGCTCGTCGGCGATGGTCGGCATCAGCTTCCTCT
TP87705	TGCAGGCTATTCAGAGGACTGGTTCCTCTTTGGGGGCGACAGATTCCTTGTAA[G/T]CATGCCTTTC
TP87711	TGCAGGCTATTCGTATAGCACAGCTCTGACTGTGATCCC[C/G]TTCCTGGCTTCCTGTTCCTGCCGC
TP87720	TGCAGGCTCAAACGAGCGCCGACTCGTGCCCGCTGGCAGGTAGGCCCGCGCGACGAGGCCTAA[G/T]
TP87745	TGCAGGCTCACAGCCTC[A/T]CAAATCAACCTTTGCTCTACTCAATCGAAGTTTGTCCCCATTGAAT
TP87748	TGCAGGCTCACCAACATGGACGGCGGTGTGCACGGCCACCTGTGA[C/T]GCCTCGTCCCGTTCTACC
TP87766	TGCAGGCTCAGATGCAGCGGAACCTGTCTGCTGACGCTCTGCT[C/G]AAAGGCGCTGTGAAATGAGC
TP87767	TGCAGGCTCAGATGCAGCGTAACCTGTCTGCCGAC[A/G]CTCTGCTGAAAGGCTCTGTGAAATGAGC
TP87770	TGCAG[G/T]CTCAGCAAGCACACCACTGCTACTCGCACTAGCTAGCTAGCTCAAAAGCACAGCAAGA
TP87780	TGCAGGCTCAGCTCTGGACAAGGAGGGCGCCGTACCGTACTGCGA[C/T]GTGCGATGGGCCATTGTC
TP87797	TGCAGGCTCATCAGCACCCAACGTCTGTGCAGCATGAGCAGGCTTTCAGCA[A/G]CTGATGACCTCA
TP87811	TGCAGGCTCATGGTCCGCCCCAGGCCTAATCTGTACAAAGGACCCAGGGTTTCTC[C/T]GAGGAAGC
TP87830	TGCAGGCTCCACTTCCACCTGTTGG[C/T]CTGTCGTCGTCGCGCTTGGAACTGGACGGCGCTTGCGA
TP87838	TGCAGGCTCCAGCCAATGCAAGCACAGCT[C/T]AACAGCTCTTGTGGCTGAGATTTGCATTTGCATG
TP87862	TGCAGGCTCCCCAGGCACAGCGC[A/G]CCCCAGCGCGTCGAGGCAAGAAGCAACCACCACCACCACC
TP87864	TGCAGGCTCCCCGCCGTGGCCGCCGCGATGCCCAGCCCGCGGTGCAGCTTG[A/T]ACGTGACGCCGA
TP87892	TGCAGGCTC[C/T]GCCGCCTGCTCTGTTGCGCGGCGGCACGCGAGAGTTAATCAAACAAACGCGAGA
TP87898	TGCAGGCTCCGTCAAATA[C/T]CGTTTCTTGCCACCGAGTTCTACAACCACACTCACAAATTCCTTA
TP87903	TGCAGGCTCCGTGCACCCTACCTCTCTCTAGTGA[C/T]CTATTTTCACAACACAGCGATACCTCTTA
TP87906	TGCAGGCTCCGTGGTCCGTGCTGCTCTGCTCAAGCAGCAAAAGCACAGATGCTGACT[C/T]GCTGAG
TP87909	TGCAGGCTCCT[A/G]CTGGAAGAAGATGCAAGAAGGCATCGGAAAGCTACAATTCCGTCACGGAAGC

Table A2 (cont.)

TP87928	TGCAGGCTCCTTCCGATCCTAAAGTTAATTTTGGTAATAAAGGAGAAAAAAATGCTC[C/G]ATATAT
TP87929	TGCAGGCTCCTTTGGGACCTCGTAGAGCGTCACGGCACCTGT[A/G]ATACTGTTCTGGAGGAGTATG
TP87934	TGCAGGCTCGACCAGGCGCTCGTCCGCCACCGCGGGCTCCAGGACCTCCAC[C/T]TACTCTGCCTCT
TP87942	TGCAGGCTCGAGCGCACAACCGCGGCGTCCCTACCTGGCCGCAGCT[C/G]GCCGACTCGGTGCGCCG
TP87951	TGCAGGCTCG[C/T]ACACCACCACACCAGCGGGCGCGTGGTGGAATAGTCAATACGCCATGCACGTT
TP87953	TGCAGGCTCGCAGAAGGCAGCGACATGCTCGGTGTTACAGGCCGTGGCAAGTGATAATGGTGG[C/T]
TP87962	TGCAGGCTCGCGAGAAGAAAACATCTTGTATACATGGTCCCATAAAACAGTGGCGAATCTAC[A/G]T
TP87980	TGCAGGCTCGCTCTGCACGCAGAGGCATCGCACATTTCAGACACGGATCGATCGG[C/T]GGCGAACT
TP87992	TGCAGGCTCGGCGA[C/T]GAGGAGCGGGCGAACCACCTGCTCTTCGAGCTGCACCGCGCGAGCGTCG
TP88017	TGCAGGCTCGTCACCCTTCTTCCAGAAGCAGTTGAGGCCCAGGTCCTCAAGATC[A/G]ACATCGGCT
TP88019	TGCAGGCTCGTCACGCGCGGCGGCTCCGCGAACTCGTAGTCGTAGATGAAGTAGTCCA[C/G]CGCCA
TP88021	TGCAGGCTCGTCCACTGTTCAAGGACCG[A/C]AGGAAATTCCCTAAAATGGCTGATCCAATGCTTCA
TP88027	TGCAGGCTCGTCGTAGTAGTAAATCTTGAGTCCAACC[A/T]CGCCGCGGATCCAGCTGATGAGGCTG
TP88062	TGCAGGCTCTCAATCACACAGTTCCTCCTGCTC[A/T]CAGAAGGAAGATCTTCAGAGAGGGTCAAAT
TP88064	TGCAGGCTCTC[A/G]GGCAATGGGGGCAACTCATACATCTCTGAACTCGATGAAGGCTGCACGAAAC
TP88065	TGCAGGCTCTCATTTCCACCTCAACCTCCAATGCTTTGTTTCATAAGATC[C/T]TAATTACTATGTG
TP88067	TGCAGGCTCTCCACGTGTCCACCATC[A/G]GAAAGGAGTATGCACTGAGTTTTGGTGGATCCTGTAT
TP88070	TGCAGGCTCTCCCGCCGCCACCGCCTCGCGTGCCTCCCCCAGCCCCCCGCCGACGC[C/G]CTCCTCG
TP88076	TGCAGGCTCTCGAGTCTCGAAGTGCCTTGGCGCAAA[A/G]GAGACAGTTGTCTGCGCAAGTCGACAG
TP88079	TGCAGGCTCTCGCGCTCAGGCTCCAGCTGGGGAAGC[A/C]TGCTGCGGACTCTGAAGTCTGAACAGG
TP88080	TGCAGGCTCTCGCGTGCGCAGCTGCCGACGCATTTTGCGCCGTCGACGACCATGGGTG[C/G]TGGGA
TP88081	TGCAGGCTCTCGCTCGCCGCCCACGACCACGAGAGCAGCACCAGCATCGCAGCCATCCTCGGC[C/T]
TP88098	TGCAGGCTCTGACTGGGTGGGTTATTGACG[A/G]TGGCGGGGCCCTCTCACCCTCTCTCTGGTTGGT
TP88108	TGCAGGCTCTGCTTCTCAGCGTG[A/G]CAAGCCTGGCGAACAAGCTGCCATGGACCTGGTGGGATCC
TP88116	TGCAGGCTCTGGCTCG[A/C]CACCTTCGCCGCAGCGGAGGACGCCGCGCGCGCCCACGACGCCGCCA
TP88119	TGCAGGCTCTGGCTCGGCACATTCGACACCGCCGA[G/T]GCCGCGGCGCGCGCGCACGATGCCGCCA
TP88122	TGCAGGCTCTGGCTCGGCACCTTCGACACCGCGGACG[C/T]CGCGGCCCGCGCGCACGACGCCGCCA
TP88124	TGCAGGCTCTGGCTGGCTGAGCAACTTTTGTCTGTTCGCGAATCGGAAGAC[A/T]TGACTGGCGGCG

Table A2 (cont.)

TP88127	TGCAGGCTCTGGTGACGCCTTTTTCCGCCAGCGCCGCCCTTC[C/T]AGTTGCGCTCCTCTCTTCAAA
TP88148	TGCAGGCTCTTGACGTATTGCCAGGTGTC[A/G]CGGATGGAGACGTCGTGCCACCACCTGCTGACGT
TP88151	TGCAGGCT[C/T]TTGACGTGCAGCAGCACGAAGCCGTCCACCGTGATCCACATCTCGGGATCCCTGC
TP88152	TGCAGGCTCTTGATCTGGTCCCAACCAAGATCCACGAGAGATCCCCGATATTCCTCGG[C/T]AGCTA
TP88180	TGCAGGCTGAAGCTGTGCACTTGTTGCAGCCAGCAGGGCAGAGAGGCAGCGGCAGC[C/G]GCGGCGA
TP88196	TGCAGGCTGACGTC[C/T]GCTTCGAGACGGTCCGCGACGTCAAGGCCAACATCAAGCGCATCGTCAA
TP88211	TGCAGGCTGAGCATCAGCTGCTGGTTGTTGGCGCTG[C/T]CGCCGAGGCTCATGGACGGCCTGGCCG
TP88229	TGCAGGCTGAGGTGGATAAACTACCTGAGGCCAGACCTCAAGAGGGGAAC[A/C]TTCTCACAAGAGG
TP88243	TGCAGGCTGATCATGTGTCATTCTTAATCGACAGAGTCAGAGGC[A/G]CCTCAGAGCTCATTCTTAA
TP88274	TGCAGGCTGCAAGTGCTCAACATTTGGTGCTTGGGAC[C/T]TGAACACCACGTCACTGTGTTTCCAC
TP88292	TGCAGGCTGCACCTCAGGCCCAAGGCGGC[A/G]GCGGTGGCGGACGGAGACGACCGCCAGCAGCAGC
TP88294	TGCAGGCTGCACCTCAGGCCCAAGGC[G/T]GCGGTGGCGGCGGCGGACGGCGACGACCGCCAGCAGC
TP88296	TGCAGGCTGCACCTGCCTGCGG[C/G]CAGATGTGCATGTTGTATGTCTCTGACGTAGAAGCAAATCT
TP88312	TGCAGGCTGCATGCAGCAGGTGTCACCGCC[A/G]CGCCACCTTGTATGGGAGAATTGAGATTTTGTT
TP88339	TGCAGGCTGCCCTGTCCTTCCT[C/T]GTCGCCTCCAGGTAGATCGCCACGCCCTGGAGCACCGCTGA
TP88346	TGCAGGCTGCCGAACG[C/T]CGATCTCCGCCGCCGATGCCGAGCAGCCGCAGCCCCCTGCCACCGTG
TP88354	TGCAGGCTGCCGCCGCCCCGATGCC[A/G]ACTGGCGACGGCTGCTGCTGCACCGCCGTGTCCTCAAT
TP88357	TGCAGGCTGCCGCGAACGAGGCTCGATCGTCCGTTTCCCTCATTTTCCTGCGA[A/G]CTGCCACTGC
TP88358	TGCAGGCTGCCGCGAACGCTGGATCGTCCGTTTCCGTC[C/G]TCCTCCTGCGAGCTGCCACTGCGAT
TP88363	TGCAGGCTGCCGCTTGCCGATGCAATGCGAGTAATGAGGCTAGCTACCGCC[C/T]ACAAGTAGGCTG
TP88370	TGCAGGCTGCCTATACCCAGGCCGT[G/T]ATCTCAGATGGGCCGTTGAACGTCTCGCTCAGGCCTAT
TP88373	TGCAGGCTGCCTATACCCAGGCCGTTATCTCAAATGGGCCGT[A/T]GCACGTCTCGCTCAGGCCTTT
TP88384	TGCAGGCTGCCTCGGAA[C/T]GTCTGCTCCTGCGGCTGCTGCACGATTTGCATTGCACCAGAAAAAT
TP88395	TGCAGGCTGCGAATCAGCCATCAGATGGCTGACACCTTGGGGACGGCGA[C/G]GGGGTACCTGTCGA
TP88407	TGCAGG[C/T]TGCGCGGCGGCTACAACGGCGGTCGGCGCGCGGCATGTCGGGCAGGAGGAGCGGCGG
TP88412	TGCAGGCTGCG[C/G]TCCTTCTTGATGGCCGATGCAGGCGACCGTAGTAGGCGCAAGACGACCAGCA
TP88424	TGCAGGCTGCGGCACCAACGCGGCCTTCGCCGCGACCCCT[C/T]CCACCTCTCCCTCCGCCGTACCA
TP88434	TGCAGGCTGCGGCCGAGCATCCTTGGGTTGCTGGGATTGAGGGGCCAGTCCC[A/T]GAATTCATCTG

Table A2 (cont.)

TP88447	TGCAGGCTGCGGGGGGAGGCCGTACCC[A/G]TATCCGCTGATGAGGACGCGGCGCTGGGAGTCCACC
TP88451	TGCAGGCTGCGGTC[A/G]TCTTCCAAGGAGCCCGACCGCCCGAGCGCAGGGCCACCGCCGAAAAAAA
TP88454	TGCAGGCTGCGGTGGATGAACTAC[A/C]TGCGCCCAGACCTCAAGAAGGAGCCCATCTCCAAGCGCG
TP88456	TGCAGGCTGCGTAT[C/G]TAAGCTAGCAGAACATATACGCTCTGTTCTACCGCTACTTCAGTAATAT
TP88459	TGCAGGCTGCGTCGT[C/T]GTCGTGCATGGTCATCGCTTGCATGCAGCAGTGTGAGAGCGTCGGCAG
TP88471	TGCAGGCTGCTACTTATACACGAGCGGGAGAGGAGAAGGGAGATCAGAGATGAC[A/G]CTGGCGCTG
TP88485	TGCAGGCTGCTCAGCATCCGCGCCTGGCGCGCCTCCTTCCGACGCGCGCGCGCC[A/G]CCACGAAGC
TP88506	TGCAGG[C/G]TGCTGCAAGCCTGCATCTTTCTCGACCCGCCTTTTGATTATTCGTGCTAGTAGCTTG
TP88508	TGCAGGCTGCTGCACCGCACAAGCTCCTCGAGATTGAGACCTACA[A/C]GCACGAGGTCCCCCACAC
TP88519	TGCAGGCTGCTGCGGTTTCAGATGCGCCGCGCCGCCAGAGCAGCAGCCGCTCGCCTCGGAGA[C/T]G
TP88526	TGCAGGCTGCTGCTGCTTAATT[A/G]TTGTTGTTGGAGCCGTGGAGGATGAGGTTGTTGTAGCGAAT
TP88544	TGCAGGCTGCTGTGCGCCTC[G/T]CCTGGCGCCGTGAAGAGCCTCCAGAACCCGCTCTCCACCATCG
TP88559	TGCAGGCTGCTTGCCTGCCTACAAATAGGGCGCCAGTGACCTACAAAGCCAT[A/G]GCAGGTTGAGC
TP88563	TGCAGGCTGCTTGTGGGCTTATGTGGCTTGCT[G/A]GCAAGGGCCCAATTAAGATAGCGTCCAGGTC
TP88570	TGCAGGCTGGAACACAACATCGAAA[A/T]GCCCGTTGCTCTCGAACGGGCATGATGGCCAGGCGCCC
TP88577	TGCAGGCTGGACGCCAG[C/G]GACGAGTTCAGCGTCGGGTCCACGGAGCTCGTCGCCGTGAAGTTGG
TP88579	TGCAGGCTGGACTGCACTGGAAGCAATAGCAAGGAGCCCAAAAGTCCAAAGTTCAG[A/C]AGCGCAG
TP88584	TGCAGGCTGGAGCCGACAGCCCGTTCGTTCCCGTGGTGGAAGAGTGCAGGAAACGGGT[C/T]GAGCA
TP88585	TGCAGGCTGGAGCCGATAACAGCCCATTGTTCCCGTGGTGGAACAGTGC[A/G]GGAAACAGGTCGAG
TP88591	TGCAGGCTGGAGTTTTGTCTGGTGATGTTAGCGACATTGTCCT[C/T]CTTGATGTGACCCCCTTGTC
TP88593	TGCAGGCTGGATCCCATATGGCTAAAGGCTAATCGATATTGTTGTTGTTGATGGTTTATATTG[G/T]
TP88626	TGCAGGCTGGCGTTGGGCGGCGGAGCA[G/T]CGGGCTGGCGCTGCCTAATCTCTCTCTCCTCGGTCT
TP88634	TGCAGGCTGGCTGTGTGCCTGTGTTGGCTTGGCTAAC[G/T]CTTCTTTCTTTGTTTTTCTTTTTTCT
TP88657	TGCAGGCTGGGGGCTGGAGGGAGGGCTGG[A/G]TGTGAGCACGACAAGACATGGGCGGCTCACATGC
TP88676	TGCAGGCTGGTGAAGAAGTCGAGTGTCTTCTTGTTGGTGAGCCCTGC[G/T]CCTTGCAGGATACCCC
TP88681	TGCAGGCTGGTGCAGTTGGCAAGATGGTCCAGGAACTCCCAGCCTTGCTCGTCGCTAGCC[A/G]TTA
TP88687	TGCAGG[C/G]TGGTGGACGACAACGACGCAGAGCAACCACCTGGGCACGCGGGGACTGTGCACATAT
TP88695	TGCAGGCTGGTGGGATACAGTCCACCGT[C/T]GCTGATCACGCCGCCTCTCACATCGGCAAAGCCAG

Table A2 (cont.)

TP88715	TGCAGGCTGTACAAACATGACCAGATGCTAC[A/G]GTGCCCCTTCACCTGCAAACCCTGTTCTACCA
TP88729	TGCAGGCTGTAG[C/T]GGTGGTAGCCAGCGCAGGCAGGCACGGTCGGTACGGGGCGAGGCGGCACAG
TP88731	TGCAGGCTGTAGCTGCAACAATAGCA[A/G]AGAGAAACTTGAAGCGGCGTAACAGCGGATGCTGGAG
TP88740	TGCAGGCTGTATCGATGTGGCTTTAATACCTACCTGCTCTTTCTGCTGTTGCTA[G/T]GGCATGCCG
TP88755	TGCAGGCTGTCCAGTGGATGATCCAACGGCAGTCAGTTGGAGCTAGCTG[A/C]CCCTCCGTATGAGC
TP88780	TGCAGGCTGTCTTCCATGCCACC[A/T]TGCATTTACCGCGCACCGAGGCGTCCTTGCTGACCCACAA
TP88790	TGCAGGCTGTGCAGC[A/T]GTATCATCCAACAGCTCATGCCGTAGGCCGTACCACCACGTAGCATGC
TP88813	TGCAGGCTGTGGCGTGGTTCCAGGCGTGGTACCCTTCTCTACGTC[A/T]CCAGTTGAGAGGACACTG
TP88821	TGCAGGCTGTGTATGTCACCAAGGGCATCAGGGATCACACCAGAAAAC[A/C]TGTTCATGGTCAGGT
TP88845	TGCAGGCTGTTGAGTCACGCTGTGGGACAGTGATTGATGCTGTGGATGTG[A/G]ACTCAAGCGGTGG
TP88846	TGCAGGCTGTTGCTCGATCAGCACGGTCTCGACTGAGGCTCGGCACGAGG[A/G]GCAGGGCGGCCAG
TP88913	TGCAGGCTTATCTCATATGCCTGCCATGGACGATCTTATTCTCGGACCAGC[A/G]TATTATATAATA
TP88924	TGCAGGCTTATGGC[A/G]CCTGTGTGATCGGACCAGCAGTCCGCCCCATCTCTCCCTTAGCCCCCGC
TP88947	TGCAGGCTTCAGTCGATTCAGCGCAGGACGAGAGAGAGCGAC[A/G]ACGACGACGACGAGACGCCAT
TP88999	TGCAGGCTTCGTGAGCATCGACTGCGGCCTGGATGCCAGCTCGGGGAGCTACACGGACAC[C/T]CAG
TP89014	TGCAGGCTTCTGATCGATCCATCCATCATGGCCGCCACCACCACCACCAAGATGTACA[A/C]CGACA
TP89046	TGCAGGCTTGCAAAACCAACGGTGTTTTGTGTTCAGTGCTCC[A/G]AACACAACACAATCATAGGAG
TP89052	TGCAGGCTTGCAGCTAGACATGCATGTTTGTGTG[A/G]GCAGGCTGTCCAGCTGCCCAGCTGCCCCA
TP89053	TGCAGGCTTGCAGCTGATGTACATGGCCGCGGGTG[C/T]TGCCGTCCTCCATGATACGCCCAAAGAT
TP89065	TGCAGG[C/T]TTGCGAGCTCGTGGGCGTGGACTACATCGAGCAGTACAATCCTCACCGCGTCGCGAG
TP89067	TGCAGGCTTGCGCGCT[A/G]GAGCGGGGGCTTGGGTCGGTCACGGTCACCACAAGCCGTCGCGCGTC
TP89071	TGCAGGCTTGCGTTGAAAAGA[A/C]GGGGTCCTGAACAAGAAAAGCTGTTGTTCCCCGCAGGCGACG
TP89092	TGCAGGCTTGGCGGTGGATCCTGC[A/G]AAGCCTAGCAGAGCCCGCATGCCTTTGCGGCAGAGACGT
TP89116	TGCAGGCTTGTCTGAAGAGTTGGGTTTATAAACTAGCACTCTGCATGCTCCACCTACG[C/G]CCTAC
TP89126	TGCAGGCTTGTTACAG[A/G]GGCGGAAGAACAGGATCGAGTCGCTTTGGGTTAAGGGGAGCGAGTTG
TP89136	TGCAGGCTTTAAATT[A/G]AACACTGGCACACCGATGCAGCATAAGAATTTAGGAAGCAGCAGCATG
TP89171	TGCAGGCTTTCCTTGATCGCCTTG[C/T]GGCAAATCGCCTTGGTAGCAATGTCCAAATAACCAACGG
TP89172	TGCAGGCTTTCGAGCATAGAAAACTGGAATCCAGCCCAGGAATCTTAGCTCC[C/T]CTACGGCCCTT

Table A2 (cont.)

TP89174	TGCAGGCTTTCGCGCTCTTCGTTGCGGTATTCATCGCGGCTGA[C/G]GCGTCTGGCCGCCACGCCAA
TP89178	TGCAGGCTTTGACTTCCGATAGACTGC[C/T]TGTGCTGGTGGAAGACAGGGAGTGGTAGAACCCGCA
TP89188	TGCAGGCTTTGCAGCTAGACATGCATGTTT[G/T]TGTGGGCAGGCTGTCCAGCTGCCCAGCTGCCCC
TP89208	TGCAGGCTTTGGGTTCAGGTGGGGGACTGGGTCCCAGCCTCCCAGGGATCCGAATAT[C/T]CCCCTG
TP89254	TGCAGGGAAAACT[C/T]GACCCAGTTGTTGGCAGACAGGACCAGATTGAACGTGTAACCCAAATTTT
TP89261	TGCAGGGAAAAGTC[C/T]ATGCAAGGGAACTAAGTAGGTAGCAGAGAGAGAGAGAGAGAGAGAGAGA
TP89266	TGCAGGGA[A/T]AATCAGGCGCCTCCAGGAGCCAGCACGGAAATCGCTTTGCTTGGCTTTGCGTTGG
TP89283	TGCAGGGAAACGAAACCATCTACCACTAGTGTACAGATGAAACCACAAAGAGCACCACCCTGT[G/T]
TP89290	TGCAGGGAAACGTACAACCCA[A/C]TGAACACTGATGCATGGACTCCTCAGGCCTACGCTCTTTCCT
TP89310	TGCAGGG[A/G]AAGATATGACAAGCCTGTACTTATGGCATGTTCAATTTATGCCTTTCCACAGACTT
TP89322	TGCAGGG[A/C]AAGTAGCTCCCACCTTCTTGGGCAATAGGACAATCAGTGCGTTGTTTAGCTTCTCA
TP89342	TGCAGGGAACAAACTGGGCTAGCCAATTAGGAGCGGCATCAGCTGCCT[A/G]TGCGAGCTGTGCTGT
TP89349	TGCAGGGAACAAGTCCGCCAAGG[A/C]GAGGGTGACGTTCGCCAACGACGCGGGCAACTCCGAGCAC
TP89361	TGCAGG[G/T]AACCAAAGAAAACAAGAGCGCGCGATACACACCGATCAGCCACCCCACCCACGAAGG
TP89402	TGCAGGGAAGAAGGGATGAGTTGCAGAGGATGATGGAGCAGCGAGAGGAG[A/G]GAGACGCGCCGCG
TP89404	TGCAGGGAAGAAGT[C/T]AACGGTGTGCTGCTGCTGGGACGCCGCGTTGTTCTTCTTCATCCTCTTG
TP89405	TGCAGGGAAGACAGAAGCATGCAT[G/T]CGCTCAGCCACTCATCCATCATGCCGTGCGGCGCTTGAG
TP89412	TGCAGGGAAGAGATGAATCTATGACAAATGCCAT[C/T]CAATAAATCTGTAGAAACCAAAAAAGAAA
TP89431	TGCAGGGAAGCAGCGCTGATGTAGCGCAGGAACCTCGTCGATGGGCA[C/T]GGCCACACGATGCCCA
TP89452	TGCAGGGAAGCGGGCCGC[C/T]GCCACCAAACCTGCCGCACGTCGACCATGGCAGCTCCAGCGGCAC
TP89454	TGCAGGGAAGCGGTCGGCGACGAGAGCCATATGCCGAGGAGGGAGAGCAGGAATG[C/G]GAGGAGCG
TP89465	TGCAGGGAAGGAACG[A/G]AATAAACGATTCAATAATCTGAGTTTCCATTTAATTTCCTGCTAATAA
TP89474	TGCAGGGAAGGAGG[G/T]AAAAAAGACGTCTCCAGACCGTTTCGTGTCGCGCCGACCCGTGATGCGA
TP89481	TGCAGGG[A/G]AGGGAAAGGGATGGACCCACACCCACCAGCTGATGGAGGCGACGCGAGAGGTGACA
TP89490	TGCAGGGAAGGGGAAAAAAGAAAAACGTTTCAGACCGTTTCGCGTCGCGC[C/G]GACCCGTGCTGGA
TP89523	TGCAGGGAAGTTGGTAGTCGCCGATGGCCCGCGGAGTCGGCGGGCCTCGCTGTCGTAC[A/T]TCCTG
TP89531	TGCAGGGAATAGTATGTTTTAGTTA[C/T]GACAAATGGACTCGTTAGTTCAAGCATCAGGGATACCA
TP89535	TGCAGGGAATATCAGGGTACCATGTCGTGTCGGAGTTTCCT[C/G]GCCGCAGCCGCAACCGCATCCA

Table A2 (cont.)

TP89556	TGCAGGGAATCTCCGTACAAAACACTCGTCACCCTCCCTCC[C/G]AAAACCCCATCCTCCTCCTCTC
TP89572	TGCAGGGAATGGGCAATGTTGGCCTTACACC[A/G]CCCCCGCTGCCACCACAGCACCCTCCGCCTCG
TP89573	TGCAGGGAATGGTTCTATTGACACTTGCAGCAGTAATTCCAGCAAGCATTCATACAT[C/T]GGACAT
TP89581	TGCAGGGAATTCGTGAGTACGGTGTCCT[A/G]CATAAAGATACTCTCGCCGCAGGAGGTGCAGCAAA
TP89587	TGCAGGGAATTTTT[G/T]ACTCAAATCTGAAATGTGCATTACAGTGTTCAAATGATGTAATATATTT
TP89614	TGCAGGGACAATGGGATGTGG[A/T]CCGAATCCGAAGGCCGTATCCAGCGCTGCTTCCCGCCTCCAA
TP89652	TGCAGGGACACGGTGATGACCATCTGGCACTACCACGGCGGCTGCCACGTCGGGGGCGTCGT[C/G]G
TP89663	TGCAGGGACAGAACCGCTGAATGGGCCCCACG[A/C]TGCCCACGAGATCCAGCTCTGGGGGCTGTTG
TP89668	TGCAGGGACAGAGAGAAGTTGAGTTTTTTGCCCCCTTTT[C/T]CGATCGAATCGCAGAAAGATACGG
TP89680	TGCAGGGACAGCAGCTGCCGCCGTGC[G/T]ATGTCGGACGCCTCGGCGTCCGAGAGCGCGGCCGCCG
TP89726	TGCAGGGACATCGATGTCATGCCCTCACATTAGTGGAGTGGCTGCGCTCATGAAGGC[C/T]GCTCAC
TP89765	TGCAGGGACCCCTTCTGCACGCCTCCGCCATACGCCGCTTCACT[C/T]GCCGCCGCCATCGCTGACA
TP89771	TGCAGGGACCGA[C/T]GACGACGACGGCGAGCACGAGGCGAAGCACGCGGTGGCGGCAGTCCCGAAA
TP89779	TGCAGGGAC[C/T]GTCGGGTCAGCAAAGCCAACAAGAAATGGTGCCCTCCGATCCACGCGCGCGCGA
TP89796	TGCAGGGACCTGCAAGGGAGACGGGGAGCCGCCGCTGACGACGACCAGCATCCACGACCTCC[C/T]C
TP89804	TGCAGGGACGAAACCATGCTTTGTTAGACTGTTGCTGATAGGATTACG[C/G]ATCCTACCGCGTAGA
TP89806	TGCAGGGACGAAGACGATTCCTCGTGCTCATCAGAGT[C/T]GAGCGAAAGCGAATGCGAGGGGCAAG
TP89808	TGCAGGGACGAATTCAAGCTGC[C/T]GACATCAGAAAACGTAGATCCTTGAGTGAAGTCCTGAACCA
TP89816	TGCAGGGACGACGACGTTCTGGCATATATAGGCTGCTGAGAGACTTCAGAGA[A/G]GCTTCACGGCA
TP89838	TGCAGGGACGCGCGCCTCGTGTATTGCA[A/G]CCATGGGATCACTGGGCAGCGCTGCGCGGCCAGAC
TP89850	TGCAGGG[A/C]CGCTACGAGCTGGGCCGCGTGCTGGGGCACGGCAACTTCGGGCGCGTCCACGCGGC
TP89857	TGCAGGGACGGAAGAGCGAGGGCAAAAGAGGAACTTGCGTTGAGTG[A/T]GGTGGGACTAAACCCTA
TP89865	TGCAGGGACGGCAGTGGAAGAGGAAGGCGAGGC[C/T]GCGCGAGAACGACGACATAGCTCGAGCCGT
TP89872	TGCAGGGACGG[C/T]GCGGTGCGGCAGCAGTGCAGTGCAGGTTGCAGAAGCGAGCAGCGGTGGTGGC
TP89885	TGCAGGGACGGCTTGAAGTCGAGCAGGAGGTCTTGCGGCGTCTCTGC[C/T]GCTGATGATGATGATG
TP89888	TGCAGGGACGGGCTACGACTGTATCTTTTGATCGCAATGTTACTGTAGATTGAACTAC[A/G]GCAGC
TP89939	TGCAGGGACTAGGGAGTGTACTGGAGTCTGGAGATGACCTTCGCCGTC[A/G]CGCCCACGACACTTC
TP89968	TGCAGGGACTGCTTCCTGATGCTCCTGAACAGTTGCTGCTACATTTGGAACCAGTGAACTCG[A/G]T

Table A2 (cont.)

TP89969	TGCAGGGACTGGAC[A/G]GCCCATGAACGCCAAAACCGCTTGCGCTGCGTCCGTGACTCCAGCAGTG
TP89987	TGCAGGGACTTGTGTATTTGTGTGCTGCTAGCTTGCATGAG[C/G]TACGCGGCTGATCTCCATCTTA
TP90006	TGCAGGGAGAAC[A/G]GCCTCCAGGAAGGCGACACCTGCGAGTTCGAACTCAGCGGTAACTCTGAAC
TP90011	TGCAGGGAGAACGCGACGGGGAAGTGCG[C/T]GAGCGACGGCCTGTGGCAAGGCAGGCTTTTGAGCG
TP90015	TGCAGGGAGAAGAAGACCACTGACTTTTGTCTTGAG[C/G]TGTAAACAACCCATACGAAATTTGTAA
TP90019	TGCAGGGAGAAGGATGGGCTCCGAACCCAAGAGGACGGAGTCGAGTCACACCACGG[A/G]AGAGGAG
TP90029	TGCAGGGAGAAGTTGTCCA[A/T]GGATGTTATGTTACCCTGTCTGTTGCTGCACTCCAGTGCCTCGC
TP90030	TGCAGGGAGACAGCCGCGCCTAGGAGGATGTGGTGCGCTG[G/T]CTGCGCCCACGACGCGACACGAG
TP90034	TGCAGGGAGACCCCAG[A/G]AACAACTTCGTACTCTTGAATCGGGGCGACATTGTCTTCTCGATACG
TP90063	TGCAGGGAGAGATCCCTCCCAGCATCGGCTCCCTCAGGCGCCTCCGACGC[A/C]TTGACCTCGGCTT
TP90066	TGCAGGGAGAGCAG[C/G]GCCGCCATGGCGGAGACGGCGCTGGGCATGGCCACCACACTGGTGGGCA
TP90070	TGCAGGGAGAGCGAGCGAGAGAGGTGGTGTG[C/T]GGGTTGGTGTAGTAAGGAGGAAGGACGGCGAG
TP90071	TGCAGGGAGAGCGAGGATGAGAAGGATGGAGACCTGTACTGTCGTCGTCTCC[A/G]ACGAGGTGCAC
TP90076	TGCAGGGAGAGCGCGAAGTAGTCGAACTCCCGCTGCGGCTTGCTGCCCAG[G/T]GGCGCGCGGGCGG
TP90080	TGCAGGGAGAG[C/G]GGGTCTGCTGGGTTGCGTACAGGCGAAAGGCACGCGCCGCCGCTGCCGCGCG
TP90088	TGCAGGGAGAGGAGTCCAACAAGGAC[A/G]ACGACGCGAAGAAGGAGAGGCATGGTTGCTGAAGCGA
TP90099	TGCAGGGAGAGGGAGGGCAGAGCAA[C/T]GGCGGCAATGAATAGAGCCATGGGAATCCCCGTGTACG
TP90101	TGCAGGGAGAGGGGTGGATGGTGTGCGGACGTGGGGAACGGCAG[C/T]AGCGGACAGCAGAGTGGAC
TP90118	TGCAGGGAGATCACACA[C/T]ATATATATATTCGGTTTTCACTAACAGTAGCTTGCTGATGATCAAT
TP90122	TGCAGGGAGATCGTCTCCGTCGTGCACAGC[A/T]GCCACTCCATGGGGGTCATGCATCGCGACCTAA
TP90125	TGCAGGGAGATGAGGAGCTTGGTCGTGGTGCGGTCCTTGGA[A/G]TCCGCGGCAGCGGTTAGCGTCG
TP90140	TGCAGGGAGCAACTGGAGAAGAAAAAAATAGGCAAATGCGCACGGTTTTGGTGTACC[G/T]TCCATG
TP90143	TGCAGGGAGCAAGGAT[C/T]GCATGAAACCCTTGCTGACACCCAATTAACACAATAACCCTCGCCTC
TP90155	TGCAGGG[A/G]GCAGACCGCGCGAAGACACGATTCATCCCGCGCAGGCGCAGCCACCAGCGACGGCC
TP90167	TGCAGGGAGCAGGCGAGAGACGAGCAGGACACCCTACGCTATGAGCC[A/G]AAACTGAACTAGTGTG
TP90174	TGCAGGGAGCAGTCAAAAAAGGCCATGAAGCTCATAAGAACTTGCCTCAACTGCACCCTCAA[C/G]T
TP90177	TGCAGGGAGCAGTCACGGAGGGCGACGTCTCCACCGTCGCGTCGCCGCCGCGAC[A/G]ACTGCTCTG
TP90189	TGCAGGG[A/T]GCCATGTGATTGACGAGGATGGGTGCTCAGGTGGCTCGGCCTCTGTAGTGGACCTG

Table A2 (cont.)

TP90191	TGCAGGGAGCCCGCCGCTGGGCCATGCCGCGTGCGTCACTAGAGGACGCCTC[C/T]CACCAAGCCAC
TP90205	TGCAGGGAGCGAGGCCATGCAGTGCAGAGGCCCAGGAAGCTGATGCCGTGGGCCGAGGAGTCG[A/C]
TP90206	TGCAGGGAGCGAGGGGGGAGCCCAGCTGGGAGGTGAGCAGCAGAGCAGAG[A/C]AGAGGCGGTGGAA
TP90208	TGCAGGGAGCGCAGCTCC[A/G]AAAGCACATAGATGCCACTCTCGGCAGTGGAAACCTTAGGGAAGC
TP90215	TGCAGGGAGCGCTGCCTGTCCGCTATGTGTGATGGGAGCACCCAGGGGTGC[A/G]GCCGTGCGGGGG
TP90216	TGCAGGGAGCGCTGCTGCTCCCGTTGCCGCTGCTG[G/T]TGCTTGGGCTGGGGCTGACGCCTTCACT
TP90224	TGCAGGG[A/G]GCGGGCGCAGGCAGTGGGAAAGGTATGACTTTGCGGGGAGGGAGGGGATTTAGGAC
TP90225	TGCAGGGAGCGGGTGCTCAGGCGCCAGGCGGTA[A/G]CCGACGGAGACTGCGACGACGCGGGCGCTA
TP90226	TGCAGGGAG[C/T]GGGTGCTCAGGCGCGAGGCGGTAGCCGACGGAGACAGCGACGACGCGGGCGCTG
TP90227	TGCAGGGAGCGGTTGCAGCGGTAGTTCTTCTTAAGAACATGCGTCGAAGCCATGG[C/T]TGGTTATG
TP90237	TGCAGGGAGCTCCAGGAAGGTATCAACATCCATATATGTCTTCATCCTGATCTTTGC[A/G]GTTCTA
TP90240	TGCAGGGAGCTCGACGGCGGCGGCGCCGTGGCGCGTGAGGGAAGCGGCGACGGCGT[C/G]GACTGCG
TP90250	TGCAGGGAGCTGCTGATGCTGCT[A/G]GCTGACGGCCTGCGCGACCACCTCGCGGAGCTCGCGCAGC
TP90263	TGCAGGGAGGAAACCGCTCGTACGTGGTGAGCTGAGACT[A/G]AGAGCTCGGTCGCCGTCACTGCGG
TP90265	TGCAGGGAGGAAAGGCGAACAGAGCAAGGAGGAGGTGGAGCTCGCTGACGTCGCCAAGGA[C/T]CTG
TP90270	TGCAGGGAGGAAGAAAATA[A/G]CAACAGCGACGAGGACCCAATGCTAGCTGCTGTAGTAGTAGTAG
TP90285	TGCAGGGAGGAGAGGAGGAAGGCGGCGAGGACCGTGGACTCGCGCCCCTGCGGTTTCCCTTTC[C/T]
TP90309	TGCAGGGAGGCAGGGGGCTCCTGGGCACCGACCAGGTGTTGTACA[A/G]CGACCAGAGGTCCCGCGG
TP90313	TGCAGGGAGGCAGTGGTACAGCTA[C/G]GACCGACCATGTAGCAGCCCTCTGATCCCTGGGGTGGCG
TP90331	TGCAGGGAGGCGGCGTGGCGGGGCACAAGAGGAGCGGCTCCATGGACGGGTCCACCTCGTCGT[C/T]
TP90369	TGCAGGGAGGGCGCGCAGCACGCCGACGA[A/G]AGCGGCGACGGGGAAGACGAGGCTGAGGATGGCA
TP90375	TGCAGGGAGGGGAGGGGAAG[G/T]GAGAGGGAGAACTGAGCGCCTCACCATATCGTCGGATCGGAAG
TP90383	TGCAGGGAGGGTGAATCTGATCGGGGAGCACATCGACTACGAGGG[C/G]TACTCGGTGCTGCCCATG
TP90384	TGCAGGGAGGGTGGTATAGGTCCACT[C/G]AGGTTATTGTTGCTCAAATCCAAATGTCTCAACTTGG
TP90386	TGCAGGGAGGTAGCCGACTGCTAGGTGGAAGGTTGTAGCCCCTCATGCCACAGTCAAATC[A/C]CTG
TP90392	TGCAGGGAGGT[C/G]GCCATGTCCGCGTACATCCTGGCCCTCGTCGGCATGGTCTCCACCTACGTCT
TP90399	TGCAGGGAGGTGGTCGTGGCCGCAGGCGCGGCGTGCGCGGG[A/T]AAGGCGGCCAGACGAGCAAGGC
TP90411	TGCAGGGAGTAGGAGGCGTTCGTCTCCTTGGGGCAC[C/T]TGGACACAAGGATCCCGATGCCTTGGC

Table A2 (cont.)

TP90417	TGCAGGGAGTCAGTTCTGAATCAGGGACGA[C/T]GGTGCAGGGTGCAGTGGAGATGCCACCACGCAG
TP90421	TGCAGGGAGTCCATGCAGTGACATGAAGCTGAACCTGAGCT[A/T]CTCGATCCTGCCTGCACAACCT
TP90453	TGCAGGGAGTTCAGGTCCTCGCCTTTCAGATGCCTGCACCATCACAAGTTA[C/T]GGACATGCTAGC
TP90456	TGCAGGGAGTTCCACTCCGCCACGTACAGCAACCCCCCT[A/G]CAAGGTTGCACGGTTGCTTCAGCT
TP90464	TGCAGGGAGTTGGCATTGGGTCAATTCCT[A/T]CCTATCCTTTCCCTCTCCCACCTTACTGCTGTAG
TP90465	TGCAGGGAGTTGTA[A/G]CAGTGGTGATGATGAGCCCAGGAAATGGCCGTCGACGTGCAGCCGTGCG
TP90482	TGCAGGGATAATCGACGAGAT[A/G]AGTGACCTCCTGTCGTCCAAGCTGGGTAAACTGGACAAGGCC
TP90491	TGCAGGGATAGAAACATGGATCTCATCGTGCAAGTTGA[C/T]CAAGATCATAGATGCTGAGGACGGC
TP90495	TGCAGGGATAGACCATG[G/T]AACTCTGAGAAAAAGACAGGCCGTGACTGCCATTCCTTCACTGCCG
TP90500	TGCAGGGATAGCACACTACTACTGAATTGAGCCAGCGACATGATGCTTTCTTTTTCG[C/T]GTGAGG
TP90537	TGCAGGGATCAGCACGAGCTTCTCCTTCGC[C/T]AGCTTTTCCAAATCAAAATGACTGGCTCTGTTC
TP90544	TGCAGGGATCAGGTGT[G/T]GATCGAGTTGACAGGGAGTGATCGATCGAGGGAAGGGCTAAAGCTAG
TP90567	TGCAGGGATCGAAGGAGGGTGCAGACGCGTCTGA[G/T]TTCTAACGCGAGGGAATCAGCGGTGTGAA
TP90572	TGCAGGGATCGATCGTAGAGGTACGCCGCCTTCTTTGGCGGATCGGGCTACCAGGAGTTTTTT[G/T]
TP90586	TGCAGGG[A/G]TCGGCGGAGCTCTCGATCCCGCCGTTGGCGGCGGCCTCCGCCCCGACGGCAGCGTC
TP90596	TGCAGGGATCTCCCTTGTTCAGGACAACCAAGGCGGCAGTATTAATCTCTGGCCGCCCTGCTT[C/G]
TP90606	TGCAGGGATGAAACGTCCAGGCGTGACAGCTCCTGCTCAG[C/G]TTTTCCACGCAGGCAGCTACGTG
TP90618	TGCAGGGATGAGG[A/G]AAAAAATGCATAACAAAACTGAACAAAGGGCTCACCTGAGGATGAGGAAA
TP90623	TGCAGGGATGATCCGCTTCGGCTGCCGCATTGCTGCCATCGATGCGGATC[C/G]CAGCAGCCATGGC
TP90649	TGCAGGGATGCTACGATTAAATAGCGTAATCCGTACAGCGATTGTCA[C/G]AACCCTGGCTGTCTAG
TP90653	TGCAGGGATGCTCAGTGTTTTCTTCGGATATTAGGAGTCCTTATTATC[G/T]GACAACAGACACAAC
TP90660	TGCAGGGATGGAAAGCGCAGCGTGCCAATTGGTGGGCATCCCGC[A/G]TCCTATTTATTTCAACCCA
TP90673	TGCAGGGATGGCGACGGCGACGGCGCCCGATGCCCCGATCGGGATTATGCATTTGTGGCGGG[C/G]C
TP90682	TGCAGGGATGGGAAGATAACCAGCGCCGACGTGC[A/C]GCGCATGTCGTCGGTCGATCGCGAAACGA
TP90701	TGCAGGGATGTC[A/G]GAGATGTTGCCAGCTACGGCAGATGACGAAGAGTGCGCCTTCAACGCCTGG
TP90710	TGCAGGGATGTTGCCTGACATGGTTCGGTCAAGAC[G/T]AGGACGTTTCTTCGAGCGTCAGTGTGGC
TP90722	TGCAGGGATTAGGGAAAGGGC[A/G]AGACAATCGAATCGATCACCTCTGCTGCATGAACGTGACCAT
TP90728	TGCAGGGATTCAGATGTACAGACTGAAACCTAGAATGAACAGAGACCTTCGCTGCTTGT[A/C]AAAA

Table A2 (cont.)

TP90760	TGCAGGGATTTTCGTTTCGGTTCCTGCGCTGCGCCTCGGCGC[A/T]TCTTCGGCTGACGGCGGGACC
TP90763	TGCAGGGATTTTGTGAGCACAAACGGTGGCTGCTTGTTCTTCTTCTCCTC[A/G]AGGAACTGAGGCG
TP90778	TGCAGGGCAAAACGCGATGGCGTTCTCCAGCAAACCCCCCAGAT[C/G]GCTCTGTCATCACGTAAAA
TP90796	TGCAGGGCAAATCTCGTACGGCGGCGAGGCGATTTCCTCGGTATAAGCGTACGCTGCCAC[A/G]AAC
TP90803	TGCAGGGCAACATGATGGGAAGC[C/T]ACATAGAACTATATATTTGGCATATTCCACTTGGACTTTG
TP90809	TGCAGGGCAACCGAATGAGTAGCTTCTCGATGTAGCTGAGACCGAT[C/T]TCTCTCTCCTAACAAAT
TP90819	TGCAGGGCAACGCTGAACCAGGTGTTGTATTTCGTGGGGCTAAAGTCGACCAGCCCGAC[A/G]GTGG
TP90827	TGCAGGGCAAGAAGAAGAAGC[G/T]AGCGCACCAGGAGGATGGAGACGACAACCATGAGCAGGGAAG
TP90831	TGCAGGGCAAGAAGGCGAAGAAAGAACCACCAGGGAGAGGGAGAGGGGGTTAGCAG[C/G]GAGGCAG
TP90835	TGCAGGGCAAGCACAGCCAAGCGGGAGAGAGGGGAGAGCACGC[A/G]GTGATCTGATGGGGGACGAC
TP90840	TGCAGGGCAAGCCGATGGAATTGCCAGC[A/G]GGGTCTGTCATCCAGGTTCAGGCGCTGTCATCTGA
TP90848	TGCAG[G/T]GCAAGGACATGTCACGAGGATGCTGGATACAAATGCATATTTATCATGTTCATGGCAC
TP90858	TGCAGGGCAAGGC[A/G]GGGACATGGTATGACGCTGAAGCCTCGCCGTCCAGCCTCAAAGGACTCAA
TP90881	TGCAGGGCAA[G/T]TTGAATCCTTTGGCATGTACTACTGATGATGTAGACGATCGATCGATGATATC
TP90883	TGCAGGGCAATACACTCACCAACACCAGCAGCTTCTC[A/C]TCTGCACGCCGTCCTCGTAAGCTCCG
TP90898	TGCAGGGCACAATTGTGGACTGG[A/C]TTCAGAAAGAAAAGGAATCTGGAAAAAGAAAAGAGAAATA
TP90907	TGCAGGGCACAGCTGAAGCTAGCGATTGTTTATCGATCTCGCAACAGCAACGGGGCAACC[A/G]ACA
TP90914	TGCAGGGCACATCGACGACGTCGTTCTTGGCTACAAGGACATCGGATCTTACGTGGTGAGAAT[A/T]
TP90918	TGCAGGGCACATGCTCTCGCCCGCGTGCGGCATG[C/G]GTCCACCCACAGGCCTTTTGTAATGTTAA
TP90935	TGCAGGGCACCGCCGTAACTGACATCGCACCCAACCTAGCGCAGCTG[A/G]TCTCTAGAGGAATCCA
TP90941	TGCAGGGCACCTACCTGCCTGCTTGTGTCTGATGAGCTG[C/T]TTTGCCTTGTATGGCTTTCGCATG
TP90962	TGCAGGGCACGGAACATCCTG[C/T]TGTCCCGCCTCCTCCCTTGTTCCTCGTTGGACGCAGCTAGTA
TP90981	TGCAGGGCACGGGGATCCAGAGCTGCTGTCCGACGGCGACCCTGTT[A/G]GGGTCGGAGACGTTGTT
TP91021	TGCAGGG[C/T]AGACACCCCCGTGGGCCAGTCGGAGTTTAGCGTGATGAGAGACACGGTGGTTCTGC
TP91034	TGCAGGGCAGATCAACGACAACGCACGAGCAT[G/A]GAACAGCAACGGCCTCCACGCCCAGCGCTGC
TP91035	TGCAGGGCAGATCAATCTTAGAAACATTCAATTTCGCG[A/G]CTGAGGTGGTGCAGGCGTGCAAGAA
TP91042	TGCAGGGCAGCACGCGCGCATGTGGTTTTTT[A/G]CAGGACGGGACGGGGGCACGGGGCCGACGGCG
TP91052	TGCAGGGCAGCAGGGGCCCTCTCCTCCTCCTCTATAGTATTCTGCCACGCCCTCCAATCCCTC[A/G]

Table A2 (cont.)

TP91075	TGCAGGGCAGCGGCTGCGGGCCTGCGG[C/T]GTGGATCCGCGGTCGCCAGGCTGCGGACCTGGAGGC
TP91082	TGCAGGGCAGCTCGCCGACATCTTCACCAAATCACT[A/G]GGGCGAGTCAAGTTCGTGGAACTGAGG
TP91107	TGCAGGGCAGGGACGCGGTGCTCCTGCGCGCCTACGTCGGGGACAAGCCCAC[A/G]TGGCGCGACCC
TP91109	TGCAGGGCAGGGATGATGTCGGGTCAC[A/G]GCCCGTTCAGTACGGGCCGAAGGCCCAGCGAAACAG
TP91119	TGCAGGGCAGGGGGAGACCACGGCCACGC[C/T]CAGGCCCAGCGGTGGCTCGTGCTCGCTTTGCCAG
TP91133	TGCAGGGCAGTGTCCAGTGTGTTGCTGC[A/T]ACGTTCCTTCCTTGCCGCCTTGGTTTTCTTTTCTT
TP91142	TGCAGGGCATAATGAATATGAGCGAAGTAGAGTAG[G/T]AGGACATAACACAGGAGGGTATAGACAC
TP91160	TGCAGGGCATCAGCATGTAGGTATTGATAGCTGCGTTGAGGTGCCATGG[C/T]TGTGGCAGCAAAAG
TP91165	TGCAGGGCATCCACACGAACA[A/C]ACACATTTGTATGACACGTCCATTCTACACACACATTAAACC
TP91166	TGCAGGGCATC[C/T]CACATCCTTAACCGTATCTTGTCGTTCGCTAGCAGCTACTAGGGCTTTTACA
TP91170	TGCAGGGC[A/G]TCCTGGAACCTGCCGACCCACAGCCTGGATCGGGTGCGCGGGATGCGGATCTCCG
TP91172	TGCAGGGCATCGCCTCGTTCGTCGCCGACCGCGCCAAGTA[C/T]TCGGACTCGCAGAGCCATGAGAT
TP91175	TGCAGGGCATCGGAATCACACAAGCCGCAGTTGGCTCGAGGCGGACAATGCTCGT[C/G]AGTGACAC
TP91178	TGCAGGGCATCGGCAAGGGCAAGTCCGACGACGCGCTG[C/T]GGCTCTACAAGGCGCACGCCGACAC
TP91183	TGCAGGGCATCGTGCCCAAGAGCGCGGACGCGTACGACAAGATC[C/G]AGAAGGTCGGGCAGGGCAC
TP91193	TGCAGGGCATGAGCACCACCTGCCTAGGCCACCTGGTCACCGAGGCCAGCTGC[A/G]TCATCCGCTG
TP91194	TGCAGGGCATGAGCCC[C/T]CACACATGCAACCGTTAGATGCTCTTTGGGATGTGTGCCAGGACAGC
TP91203	TGCAGGGCATGCAGGCGACTCTTCTTCCTCCTCTA[C/G]AAACTGCCTAGCTAGCTATGGACGACAT
TP91214	TGCAGGGCATGG[C/T]CGCTGCCTTCGTCGCCGTCGACGGGGTGGAGGAGCTGGTGCGCGGCGGCCT
TP91223	TGCAGGGCATGGGTATTGCACCTTTTTGGGTGTGTGCTCTTTCCTGATGCGACTGGAGATA[C/T]CG
TP91235	TGCAGGGCATGTGCAGGGACCAAAACAACGTGAGACAGTATC[A/G]TGCACTGCTCTGAAACATTTC
TP91256	TGCAGGGCCAAACTTTACCTGTTGTCGCCATCCTCCATC[C/T]CCCCTGTGGAAGGGCGGGGCTGTG
TP91267	TGCAGGGCCAATCGCATGGCCGACAG[C/G]CTGACACTGCATCCTCGTCTAGTTCGCTGGTGCATAC
TP91278	TGCAGGGCCACACCAGCCCGATGCTGCTCCAGTTCAC[C/T]CGCCGCCTCGTGTGCCACGGCCTCCT
TP91295	TGCAGGGCCACCACGTCGGGAGAGAGGGAAAGAGGGAGAGAGAGAGCGGGGACGC[A/G]CGCGGCGC
TP91312	TGCAGGGCCACCTCCTCCGCGACGGCGGATTTGGCGTAGC[C/T]CAGCGCTCCGTCCAGCACGGACT
TP91315	TGCAGGGCCAC[C/G]TGACCCACCCCGTCGGGGAGATCATCTGCGACGCGCTCGACGCGCTCTCCGC
TP91326	TGCAGGGCCACGCTAGGGTCAGGAAGATCAAGAAGCCCCT[G/T]CCCATCTTCGACAGCAACCTCTT

Table A2 (cont.)

TP91332	TGCAGGGCCACGTCACCCACCCCGTCGGGGAG[G/A]TCATCTGCGACGCGCTCGACACGCTCGCCGC
TP91341	TGCAGGGCCAGAGGAGCTGAC[C/T]GTTCCTTCATTTTTTTTCTTCTTCGTTTTGTCACCTCGACTG
TP91358	TGCAGGGCCAGCGTGGCCGCGACGGCGAGGACGACCAGCGCCGC[G/T]GTTGGCACCGTCAGAGCCA
TP91366	TGCAGGGCCAGGAGGTCCCGCATCAGCGCGGCCGACGCCGACGCCGA[G/T]GACCCCGTCGGGCTGC
TP91377	TGCAGGGCCAGGTCAACGACATGGTGGCCGCCGCCGCCAACCGCGGG[G/T]CGTCCACGTCGGAGGG
TP91379	TGCAGGGCCAGGTCAACGACATGGTGGCCGCC[G/T]CCGCCAACCGCGGGTCCTCCACCACGTCGGA
TP91384	TGCAGGGCCAGTGAGCTCG[C/G]TAGCGGGCCGCGTGCAGCTCCCTCGTGAGAGTGGCATGGCCGTG
TP91391	TGCAGGGCCAGTTAACTGAACTGCCAGTGGGATCAGTCATT[C/T]AGCGGCCGTGTACTCTGATTCT
TP91407	TGCAGGGCCATCTCGCCGCACG[C/G]AGGCTGCTGCAACGAGAGCAGCGGCAGAGAATCGAGCGAGC
TP91408	TGCAGGGCCATCTCGCCGCACGCAGGCTGCTGCAACGAGAGCAGCGGCCGAGAAT[C/G]GAACGAGC
TP91417	TGCAGGGCCATGGTCGGTGGTGTGGGGAGCTTGGACCG[C/T]AGCTAGCTAGCCGAGTTCAGCTGGG
TP91444	TGCAGGGCCCAGTGCACGCCGCTCTCTGTAGGTGTAGGCAAGTG[C/G]CCACAAGCACGGCCCAGTA
TP91451	TGCAGGG[C/G]CCCACCTGTCAGGCGAGCCCTCCCCGAGAATCCTCCCCAAATTCCCCAATTCACAG
TP91464	TGCAGGGC[C/G]CCTAATTGGCTAACTCGGTAATTAGATTACAAAACTGAACATCTTCCATGATAAT
TP91465	TGCAGGG[C/G]CCCTACGTGTACTACCTCTACAGCCAGTACGGCTTCGACAAGGGCGACATCGGCCG
TP91466	TGCAGGGCCCCTC[G/T]GCCGTGCTGCCGCTGCTGCTGTTGGGCTGGTTGTTCGGATCCGAAAAAAA
TP91467	TGCAGGGCCCCTGCGTGGCGTTGTTGCCGA[C/G]GTCGAGCAGCCAGAATCCGACGAGGTAGACGCA
TP91472	TGCAGGG[C/G]CCGAGCGCAGCGGTGCCTGGTGCTGTGGTGCTTTTTTACTGGCACGCACGGCAGTC
TP91483	TGCAGGGCCCGCTCAC[C/G]CGCCTGCTCGGCGGCATCTTCCACCTCTTCCCCGCCGAAAAAAAAAA
TP91491	TGCAGGGCCCGTCGTCTCGTCGTCCGATC[C/T]GTCGTCATCCATCCCCATCGATGACGACACGACG
TP91510	TGCAGGGCCCTTGCGACATGAGAGCGAGCTCGCCCAC[A/C]AGATAGCCCAGAATATCCAGCACGCC
TP91518	TGCAGGGCCGAGATGGTGGTGCATCTGGTGGTGCTGGCCTGAGTTGCTGCCTCGCGAGGTT[C/T]GA
TP91538	TGCAGGGCCGCC[A/C]GCAGGTCGCTGTCCATCAGGTGCGAGCAGAGTGCGAAGCAGGGCAGCGGCG
TP91545	TGCAGGGC[C/T]GCCGCCGCCACCGAGGACGAAGTCGACGTCGTACACCTTCTGCTGGTTCGGGTAG
TP91547	TGCAGGGCCGCCGCGGACGATC[C/T]TGAAGAACCTGGCGAGGCAGAACCTGGAGCAGCCAAGGTGC
TP91572	TGCAGGGCCGCTGCAAACCTGGCC[C/G]TGGTCGTGTTTGGAGGCCGCGGAACGTGGAAGTGGAAGA
TP91574	TGCAGGGCCGCTGCTGCCCTTGCCACTGCCGCCGCCACCGCCGCTCTCTTTGCCC[A/T]CCTTTCCC
TP91582	TGCAGGGCCGTGAAGATGCACG[A/G]CAGCGTCGTGGAGACCACCAGCATGACGCTCTCCAGGTCCA

Table A2 (cont.)

TP91601	TGCAGGGCCT[C/G]ACTCACTCGGTGAAGCCCACTCCCCCACGCTCCATAGTAGTTCATACTCGAC
TP91615	TGCAGGGCCTCGATGTCCTCGAGC[G/T]CGGCGACGACGTCGTCCATGGAAGGGCGGCTCTTGGGGT
TP91633	TGCAGGGC[C/G]TGACCGATTTTCTTTTTGATTCTGTCATGAGAGGGCAATGATATATACATCGTAT
TP91647	TGCAGGGCCTGCGCGCTCGCCTTT[C/G]ATGAGGCTAGCTCGATCCAAGCGGGGAAACTGGGCGTGA
TP91668	TGCAGGGCCTGGTGGCCGCCGAGGTGGAGGGCGCCAAGCGCCTCGCCGA[A/G]TGCCTAGGCAAGGG
TP91673	TGCAGGGCCTGTGCACGGCAGCGACTTCAGACAAGTGGTACGCATA[A/C]GTACACTACAACGAGAC
TP91686	TGCAGGGCCTTCGC[C/T]ATAGCTGCATCTGTCTTAACACGGTGTGCTCGTATGCCGTCTTCTGCTT
TP91687	TGCAGGGCCTTCGC[C/T]ATAGCTGCATCTGTCTTAACACGGTGTGCTCGTTGGTCGGCTTCTGCGC
TP91695	TGCAGGGCCTTGGTCATGTTGAGCGAGATGCCCAAGTTCTGGCCG[C/T]TCTGGAAGACCTGGCAGA
TP91713	TGCAGGGCGAAGAGAAGTACATCATGGTTGTTGACGCGGT[C/T]CAGATGACGCTGTCGGCGGTGCC
TP91725	TGCAGGGCGACACGCTG[A/G]ACCAGCGCATGGGGTCCAAGTTCAAGATCCCCTCGGCGACGATGTC
TP91729	TGCAGGGCGACATGCATGCGCACGTATATGCTTGTGCACATGAG[C/G]AGGGCAGCCGCGTGCTCAA
TP91739	TGCAGGGCGACGAGGAGGAGGACGTGGAGGATGATG[A/G]CGCTGCGGACGACGACGACGCGACCAT
TP91748	TGCAGGG[C/T]GACGTACGGACGGAATGGGACGTCGAGGGCAGGGCACTCATGGCCATTTATTTACT
TP91753	TGCAGGGCGACTGGAATGGCGCTGGCGCTCACACCAACTACAGGTAC[C/G]AATCAAAAGAGAAAAT
TP91818	TGCAGGGCGATTGGCGGCCGACGGCGGAGC[A/G]TTTCTTGGTGGGGCTAGGCGTGCCGCGTGCAGG
TP91824	TGCAGGGCGCAGCAACAGTCAGGAAGGAAGAAGATACAGCAGCCCTAGGGCGGGGG[A/C]GCGAGCC
TP91826	TGCAGGGCGCAGCCATCCAGCCGCTCCTCGCCTCCCTCGCGATCGGCGT[C/T]CTCATCTGGTTCGT
TP91834	TGCAGGGCGCAGGGTGCGG[C/T]TGCGGCCGTAGGAAAACGCAACGCGCGGGTCAGGCAGGCTCATG
TP91842	TGCAGGGCGCCACTTGATCCTAACACGGCATTCGCTGGATCGGAAATAGTAAAAGA[C/T]CCCCCGT
TP91872	TGCAGGGCGCCGCCGCCGTGCTCGCCTTCTCCCGCACCGCGGAGTTCCTCTCCGACGGGCTCA[A/G]
TP91876	TGCAGGGCGCCGTGAACGTCACCACGGCGCACTCCCTGGACATCATGGGCACCTC[C/G]TACCCGCC
TP91886	TGCAGGGCGCGCACTGCGTCCAGATGAGGT[C/T]GCTGCCCGTGTCGGCGATGGCCTGGTACGACTG
TP91887	TGCAGGGCGCGCAGGCGTTCCTGGGCTCGGGAC[A/G]GAAACCATGGGCCATGGCCCATGGGATTGG
TP91896	TGCAGGGCGCGCTCGCACTCCGTGGTG[G/T]CGCGCGTGAGGAAGTAGACGCCCGCGCACAGCACCG
TP91901	TGCAGGGCGCGGC[A/C]ATCAAGCCGCTCCTCGCCTCCCTCGCGATCGGCGTCCTCATCTGGTTCGT
TP91911	TGCAGGGCGCGGGAGGCGGCGGCCTCCTC[C/G]TCAGCTCGCTGCTGCTGGGCTCGGTGTCCGCGTC
TP91917	TGCAGGGCGCGGTACCCGCC[C/G]TCGTTGAAGGCCCAGGTGCGGCACACGTTGAGCCCCGCGTCGG

Table A2 (cont.)

TP91920	TGCAGGGCGCGTATTGAGATCCCGTGCCGTTTCG[A/C]GGCAAAATACAACAAAGGCCTCGGAATGA
TP91932	TGCAGGGCGCTGCTAGCATTGGAAGTGTATCAAAC[A/G]CACCACTGTCTGGAAGAGTGCACCCGTC
TP91948	TGCAGGGCGGACATT[C/T]GCAAACCCTAAAATTCCATCATCCCGTAAACATCTCACAGCAGCAGGA
TP91960	TGCAGGGCGGAGGCGAGGGCAGCGCCGAGGCTGTGGG[C/G]CTGCTCATGCTCGCTATGTCCACGCT
TP91973	TGCAGGGCGGCAGAG[C/G]TCGGGCGGGCATGCAGACGGCGTCATCAATCGTGTACTGCGGCGCATT
TP91989	TGCAGGGCGGCCTCTTCAGTGAGTTCCCAAACATGGATGTAATTTAACGAAA[C/T]TTTCGAATATG
TP91993	TGCAGGGCGGCGACGCGTCCGAGCACTCGTTCGGCGGGACGCCCGA[G/T]AACTCCTCGGCGTCGTT
TP91994	TGCAGGGCGGCGACGGGCATCGTTTGTGCCGTTGCGAACTTGCAGTCACGGGCTGTTCC[C/G]TTCC
TP91997	TGCAGGGCGGCGCCCGAGTTGTACCTCCACACCGCGCCCCACGACCGCTGCATCGG[A/C]GCCCACG
TP92002	TGCAGGGCGGCGCGTTCATGTTGATCCCCAG[A/G]CCAATGCCGCCGCCGCCGCTGCTGCCGTGGTA
TP92007	TGCAGGGCGGCGGCGCCTCCGACTCCAACAGATACGAGCTGG[C/G]CGCGCAGTACTTCGGCGGGGC
TP92014	TGCAGGGCGGCG[G/T]CTCCTTGGTGTGGTATGAGGGGAACACCTGTAACATGCACCTGCTCCACCT
TP92033	TGCAGGGCGGGCCCAGCTGCTCTGGCCTCCTGGGCAACTTCTTCAAGCTC[A/G]GCCCCTGAACCCT
TP92053	TGCAGGGCGGTGAAG[A/G]CGCAGGACAACGTCATGGAGACCACCATCATGATGCTCTCCATGTCCA
TP92054	TGCAGGGCGGTGAGGTTGCCAAGGGTCGCTGA[G/A]ATGTGGCCCTGAAGGTTTCTGGAAGCCAGAA
TP92057	TGCAGGGCGGTGCGGTGTAGAC[A/G]GTGTCGTCGGAGGCGGTTGATGGCGTGGAATACGTGGCCGC
TP92061	TGCAGGG[C/T]GGTGGCGGTAGCGGTAGCGACGGAGCTGGCCAATCTTCTGGCCTTCCTGACTATAG
TP92069	TGCAGGGCGTAGCCTCACCTGTGCCGCGACGGTGTGGGAGCGCGTGGGGAAGAGCTTGGTGA[C/T]G
TP92075	TGCAGGGCGTC[A/G]GCGCCAGGATCATGGACCGCGCCGCCGTGCCGAGCGACGCGGACGACGACCG
TP92102	TGCAGGGCGTCGTGCTGGGCTGCACCGCCACGTACGACGGGCAGAG[C/T]TTCCAGTCCTCGGACGG
TP92123	TGCAGGGCGTGCTGGACGAGCGGCGCGCCGCCAGGTCCA[A/T]GGGGGTGTCGGGCTCCGAAAAAAA
TP92131	TGCAGGGCGTGG[C/G]GCGGCAAGCTGTGCAACGAGGCCCTCCTCTCCCGCCTCAACCGCGCGGAGC
TP92134	TGCAGGGCGTGGCGTCGACCACGTTGCAGACGCCGAACGCGCCGCACCTGCCGTAGCTGTCGC[A/G]
TP92140	TGCAGGGCGTGGTGGCGGAGACCGTCTTCACCTTCAGCCTG[C/G]TCTTCGTCATCTACGCCACCAT
TP92143	TGCAGGGCGTGTCCTTG[C/T]CCTTGTCCTTGTCACGTTAGGTGATCTGTTCTGCTGATCTCTCCCG
TP92147	TGCAGGGC[G/T]TGTTCAGCAAGATCCTGAGCACGGCGGTGGCGGGCGGGCTGCGCAGCGACATGAT
TP92159	TGCAGGGCGTTGAGGTCTTTATTAAGGAGGAG[T/C]TGTGGCAGCACAGCACAACTCAGCTGCGAAG
TP92167	TGCAGGGCTAAATATCAGAGATCACAGTCCTCCTAG[A/C]CTCAAAGAACTCTCTTAGAACCTCATC

Table A2 (cont.)

TP92187	TGCAGGGCTACCTAGCTAGACCTGCGCCTGC[A/C]CATGCATGATGGGCCATCGCCGATATAGCTAG
TP92194	TGCAGGGCTACGGGACATCGCGCTCATGA[C/T]TGCAAGCACGACCACTCACCCACTCGTGCCGCTG
TP92202	TGCAGGGCTACGTTGCGAGGATGAAGAGAACGAACGCGAG[C/G]TTTGATCGATTCCTGGAACATGT
TP92206	TGCAGGGCTACTGATCAACTGGACATTCGATGCAGACGTGGAGCTTGAAACTCCCA[C/G]CCACCAT
TP92209	TGCAGGGCTAGCGCCCAGAGGTAAAGACGAACGCCAGTGCCTGCA[C/T]TCTATTTCACGCGCCTCC
TP92212	TGCAGGGCTAGCTCGACGTCGA[G/T]TGCTATACGGGGAAGCGTCATGTCATAGTACTACTCGTACT
TP92226	TGCAGGGCTATCTGGACCCTGAATACTACATGTCTCA[A/G]CAACTGACCGAGAAGAGCGACGTCTA
TP92230	TGCAGGGCTATGTGCCGATCT[A/G]CTTGGGCACCCCCCGCACTGCGCTGGTCTTGTAGTGTGGTCG
TP92238	TGCAGGGCTCACCAGCGGTGGTCGAAAACAGGGCACGTAGCGCGGCGCTGGCTCGGCG[C/T]CGAGG
TP92242	TGCAGGGCTCAGAAATATACTTTGACTTGTCCGCGGCAGGTGAGGGC[A/G]CACTCCGTCGTCTTCT
TP92257	TGCAGGGCTCCATGAAGATGGCGATGCGGTGGGGCCTAGACTCCAAC[A/G]AACGCCTCGTCTTGAC
TP92259	TGCAGGGCTCCATGAAGATGGCGATGCGGTGGGGCGCGGCCTGGA[C/G]TCCAAGGAACGCTTCGTC
TP92261	TGCAGGG[C/G]TCCCAAATCTCGCTTGTTTTCTCCTATACCAGCTTACTCTTCCAATCCCTGTCAGG
TP92262	TGCAGGGCTCCCAGTTGTAGGGGATCCCA[C/G]TGACGTTGGCGTGCAGCGCCTTCTGCACGTCGGC
TP92264	TGCAGGGCTCCGCAA[C/G]TGAAGAGTCTTCGCCTCATCTCGTGCAAGAGCATCTCCAAGCACGGCC
TP92266	TGCAGGGCTCCGTGAAGAT[A/G]CCCTCTTTGTAGCTCTGGAAGGCGCTGCTGTGGCGTGCAAGCAA
TP92281	TGCAGGGCTCGACATGTACCAGGGCACCGCCACACCCTTCCCAGCGAGACCGTAGCCCAGC[C/T]TG
TP92286	TGCAGGGCTCGCCACGAAGAGCGGATAAAAGGTAGCCGCACGCAC[A/G]AGCAGGTAGCAAGATGTC
TP92321	TGCAGGGCTGATCAATTACAAGATAAACGTAACATTGTTAAGACCCAAACAAGCAGTGGACAA[A/G]
TP92326	TGCAGGGCTGCATCAACGACGTCCACGCCACGCGCACCGTCCTCCTCGACCGCTTC[A/G]GCTTCGC
TP92332	TGCAGGGCTGCATTACACCTTAAAAAAAACTTGGCTTG[C/T]GGTGGACAGACAGCCCCTACAATTT
TP92342	TGCAGGG[C/G]TGCGACGCCTCCATCCTGATCGACCCGACCAGCAGCAACACGCAGGTGGAGAAGAA
TP92345	TGCAGGGCTGCGACGGCTCCATTCTTCTGGACGA[C/T]GTTGGCAGCTTCGTCGGCGAGAAGGGCGC
TP92355	TGCAGGGCTGCGTGCCTACGTCGTCGTCGTCTGCAAC[A/C]GCACACGTACCTGCATGCACGGCTGT
TP92360	TGCAGGGCTGCTACTCCGCGTTTTGCATCATATCGTAGTTCGTGGAGTTGCC[C/T]GATGCCCGATG
TP92361	TGCAGGGCTGCTCAGGCAACTATTAGCCATGCTAGACATGATA[A/G]ACTGCTTCCAATATTTGCAA
TP92363	TGCAGGG[C/T]TGCTCGAAATTAAAGTTAAATGTCGTAGTAATTAATCTCTGTACTGCAAGTGTCAA
TP92364	TGCAGGGCTGCTGCGACCACGA[C/T]CAGAGGATCTTCATCGCCGCCGTCGGCGTCTCCACCGTCGT

Table A2 (cont.)

TP92367	TGCAGGGCTGCTGCTCCGCATTTTGCATCATATCGTAGTTC[A/G]TGGAGTTGCCCGATGCCTGATG
TP92374	TGCAGGGCTGGAAAAGCCTGGAAT[G/T]GGTATGGATTTCGCGCGTAGTCTTCACATCTTTTCTTTG
TP92382	TGCAGGGCTGGCGGGCTGCACGCTGACGCTGTTCCATTTTCGTGGATCCCGACGTACTCT[C/G]CAC
TP92394	TGCAGGGCTGTCTCGTTCTCGGTGGCCACGCTCACGAAGCTGTCAATGGTCACCACC[C/T]TTTCAT
TP92402	TGCAGGGCTGTGG[C/T]GGTAGCGACGGAGCTGGCCAATCTTCTGGCCTTCCTGACTATAGAGCTCG
TP92435	TGCAGGGCTTCCTCCACTTCCCGTCCTTCCTCGCCAACTACAAGCGGGGCGGTAAGTACGGGA[A/G]
TP92438	TGCAGGGCTTCCTCGTCCTTGGCGAGCTCGAGCTCGAGGTCGCCGCCGTCGGCGT[C/T]GGGTTTCG
TP92439	TGCAGGGCTT[C/G]CTGCTTTTGGACTTGGAATCTCGGAAATCAGGCCCGTGGGCTGTGCTTGTGCA
TP92464	TGCAGG[G/T]CTTGCTGTGCTGGAGCAGACCTGTGGGATTCATGCGCATGCGGTGGTGGTTGGGCTT
TP92481	TGCAGGGCTTTGGCCCCTCCAGTTTCATAAAAA[A/G]AAAGTGCTTCGGCAGCGCCATGTCGTCGTC
TP92482	TGCAGGGCTTTGGCCTCCGACGCCTCGTCATCC[G/T]TGCACGCGTCGCCCAGGATTTGCGCTTTCT
TP92487	TGCAGGGCTTTGTGATCACGGACTGGCAGGC[C/T]GTGGACCGCATCACGAACCCGCCGCACCAGCA
TP92491	TGCAGGGGAAAAAA[A/G]ATTGTCGGAGCGGTTGGTCAGCTGAGCAGGGGCTCAGGCTGCCCGCCCG
TP92509	TGCAGGGGAAACTTCATCAAGGGCCGCTGCTACT[C/G]CTTCTCGTGCTCCTAATAATCGTGTAATG
TP92512	TGCAGGGGAAAGACC[A/G]CCCCCACAGCATTGCATTGAGAAGAAACTTCTCGCGCGCAGGCTAAGA
TP92514	TGCAGGGGAAAGACGATCGATGCATCAGGGTAAGCAGACACTGATATCATCTCCGAGCATC[A/G]CT
TP92516	TGCAGGGGAAAGGGAGGCAGCGCCGCCCCCATCTCACCTGTGCGCGCTTCAGGTTTCGCC[A/T]TCC
TP92527	TGCAGGGGAACATGAGGAATTATCATAGCATACCTCATCTGCCCA[A/G]CACACCAAGCTATCCTTG
TP92533	TGCAGGGGAACGC[C/T]GCCACGGCGTCCATGGCCGACTGGAACGAGGCGTTCTGGATGCTGCACAC
TP92537	TGCAGGGGAACTCCAGCACACTTTGGGTGGTGCATGGAGCTGGATCCGTGCT[A/C]TCGCTGAAATC
TP92544	TGCAGGGGAAGACACGCTGCACGGCTTCGACGTCGTCGCTGGAG[A/C]AATGGATCGGGGTGATCGT
TP92545	TGCAGGGGAAGACACTCTGCACGGCTTC[G/T]ACGTCGTCGCTGGAGCAACGGATCGGGGTGATCGT
TP92551	TGCAGGGGAAGAGTTGTTAGCCA[A/T]TTGATCGATCGAAAACACGGGCGGTGGGCAGATAGAGTTG
TP92559	TGCAGGGGAAGCCCATCACGGTGTACCGCGGCA[A/G]GGACCACGTCGACCTGGCCCGCGACTTCAC
TP92565	TGCAGGGGAAGCTTCTTGTGACCACGCGGTACGGGAAGCCAGCCACCACTACGGAAGC[C/G]TGTGG
TP92591	TGCAGGGGAATGGCCTCTTGAGCACGCCGAGGAGTTGGCAAGACTAGCTCTGAAATG[C/T]TGTCGG
TP92596	TGCAGGGGAATTGTACCGAAAAGAACACCTG[A/G]AAAGACATGGGCCGAGGACGTTGCTCCACACC
TP92611	TGCAGGGGACAGCTGAGACGGAGCGAGGGCGCGCGGAGGAG[A/G]AGTGCAGCTCCGCCGCCGCCGC

Table A2 (cont.)

TP92624	TGCAGGGGACCCAT[A/C]TATCCATAGCTAGCTTATTTGTTCATTCGCCGCCACCGCAGCCGTACTT
TP92648	TGCAGGGGACGAGACGGCGTATCCCTGGAGGGCTGGACTGCTGCTGGAG[A/G]CAGATCGACGACGC
TP92656	TGCAGGGGA[C/T]GGAGAAGGAGCCTCTGCCTGTGGCTGTGCCATGAAGGTGGCAGCGACGACGACG
TP92657	TGCAGGGGACGGAGA[A/T]GGAGCCTCTGCCTGTGGCTGTGCCATGAAGGTGGCAGCGACGACGAGC
TP92680	TGCAGGGGACTGGTACAACCCGATTACCCGAGACCCAACTTGCTCAGCTC[G/T]CCTTCGTGTCTGT
TP92712	TGCAGGGGAGCAAGCGGCGGAAGCGTTCCGTCCCGCCTTCCTGG[C/G]CCCTAGGGCGCCGCTCGAG
TP92726	TGCAGGGGAGCGCTGCTGCTGCCGTGCTGGCTACCGCCTGGCCTGGTCTGGTCAAGTC[A/T]GATGG
TP92728	TGCAGGGGAGCGGCTACCTGGGGGCTCCGCCGTGCGTGGACAGG[C/G]GCAACGGCGACGGCTCGCC
TP92730	TGCAGGGGAGCGTGCGGCTAAACCGCCGCCGTCGCTCGTCAAGGAC[A/C]TCGGAGGAGACCAACGG
TP92731	TGCAGGGGAGCTAAACCCATCAGGCATCAGACTCGGCAAATGCAAGGTAA[C/G]CTGGCTATACACA
TP92735	TGCAGGGGAGCTACTACCTCCGCGAG[G/T]GCGTGCTGGGGCTGGACGAGGTCTACGGCGTCCTCGA
TP92743	TGCAGGGGAGGAAGAGGAAGCAGGAGG[A/C]GGCGGAGCGGGGTCTCCGCGGCGGCGGGGACGACAG
TP92750	TGCAGGGGAGGACGTGTGTGGTCGTGGCGCACCGCCTCTCCACGGTGCAGAAGGT[C/G]GACATGAT
TP92774	TGCAGGGGAGGCGAGGCG[A/G]GGCGACGTCGAGCTGCGCCTGCGCGTTACTATCCATCGAATTTTT
TP92805	TGCAGGGGAGTCAACACTCTCCAGCACGCAGCTCGGCTCGGCGGCTGAGTGTGCTTTCATAG[A/G]A
TP92811	TGCAGGGGAGTGCACCGCCTC[A/G]GGTCTCGGACTCGCCTTCCATTGAGGAGGTGGAGGAGGCCCT
TP92823	TGCAGGGGATACGGAAGAAGTCCGACGTGCTCAAGGAGCGGTTCAACCAGATGTTCGC[C/T]AGGAT
TP92824	TGCAGGGGAT[A/T]CTCAAAGACAATCTCAAATTCCTGAAATGTCTACTGCACGTGCTCCTCCAAGG
TP92831	TGCAGGGGATCAAAGGACAGGAGGACGACGGAGC[A/G]CATTCTGAAATAGGAAGGAATCTCTGAGC
TP92838	TGCAGGGGATCCTCGGGGAGGAGTGGGCGGAGGCGCAGAGCGCCAAGGC[G/T]CGGGCGAACGTGGA
TP92842	TGCAGGGGATCGACGGC[A/G]GCCGCTACGTCGTGCCAAGCGTGGTGGCCATCGGCCCCTACTACCG
TP92854	TGCAGGGGATGAATTCAAGAGTCTGATCACTCCATTGTTTGCTTTCATGGATT[A/G]CTGTACGTGC
TP92927	TGCAGGGGATGATGTTTGTCACC[A/T]TCTCGGCGTTCGTGCCCACGGCTGCGGTGCTCGGCGGCAC
TP92941	TGCAGGGGATGGACGCCGACGACGGGACGGGTGTTGGTTGCGCGACTGCGCCACGCA[A/G]ACGGA
TP92956	TGCAGGGGATTCAAGGAAGGGGAAGCGAGAACGTTAGCTGGATTTCGGTTTTGATAGCGTG[A/C]TT
TP93011	TGCAGGGGCACCTGGGCCGCTGGGCTCCCTC[A/G]TCGCAGTCAGAGTCAGTGAATCAGTGATACAC
TP93012	TGCAGGGGCACCTTGCCCGCCGCGCCGAGCCGTTCCTTCGCCTGGGCGACACAGGCGAC[A/G]GCGA
TP93019	TGCAGGGGC[A/G]CGCTCGAGTTGATCGTCTGTATGAGAGTGAGAGTTCGATGATGATGAGATGCTG

Table A2 (cont.)

TP93051	TGCAGGGGCAGCACAGGCGCACAGCAG[A/C]AAGAAACAATTAAGAGAGGAATTCAGAAAAGATAGA
TP93063	TGCAGGGGCAGC[C/T]CGATGTTTCGCTGCATCGGTGACACAACATATACCGATCAGATTGTTTGTT
TP93078	TGCAGGGGCAGGCATGG[C/T]GCCCATCGCAAGGAAGCTGACGCTACAGAGGTTCCTTAGGAAGAGG
TP93097	TGCAGGGGCAGGGCTGGAGACGAGGAGCCACACGCGGCTGGAGCCCGCTGCCCCTGTGCGCC[A/G]C
TP93115	TGCAGGGGCAGTGACTAGCTATGGAGGCAGCGGA[C/T]GGGATATACAGTATCCCTCGGTCGTCACC
TP93121	TGCAGGGGCAGTTCACGCAGGTCGAGCTCCGATCGCTCAAGGCCAAGGTGACGTCCGAA[C/T]CCGC
TP93124	TGCAGGGGCATAAATCAACACGAAGGCGGCGGCGAAGCAGTGGAAATGGATCCTTCAAAA[A/G]AAG
TP93130	TGCAGGGGCATCCCAAGTTAGCTTGCTTCCGCGGTGGAAAGGACCTC[C/T]AGCTCGGCCCACCAGA
TP93147	TGCAGGGGCATGGCCG[A/T]ATGGGCGCGCACTTGTGACTTGTCACTTGTGGTGAGTGTCGTGTTTT
TP93166	TGCAGGGGCCAATAGTGAGAGA[G/T]CGTCGCGAAAAAACTAGGGCCGACGATACACTGGGCCGCCA
TP93171	TGCAGGGGCCACCTCGTGTGCCTCGTGCG[C/T]ATATATATAATGGATGCATTATTGGTGACTGAGC
TP93201	TGCAGG[G/T]GCCCCCAGCTCCATCTCAGCACTGAGCTGAGCTCACCAGCGGTCGTGTGTGTGCTCC
TP93209	TGCAGGGGCCCTCT[C/G]TCGCTGGATATCACCTGTAAGACTTGCTTGAATTATGGCATCGTGTACC
TP93224	TGCAGGGGCCGATGTGGGGGCAGGGAGGGCAGGGGATGGTCGGTGCGTGTGGCGGACG[C/T]GACGC
TP93238	TGCAG[G/T]GGCCGCGGGCGCGGAAGTGGAGCGTGACGGGGCGGATGGCGGGCACGCGTGCGAGCGA
TP93258	TGCAGGGGCCTCGCCGTGCCACAGGCACCCATCGCCTCCACTGGTGCCATACCGTGCCTC[C/T]GCT
TP93283	TGCAGGGGCGACGAGCCGACGACTGCGC[A/G]ACCGCCGCCCGCCGACCTACGCCAGGTGCCGAAAA
TP93325	TGCAGGGGCGCATGGCATACTGGACTTCACCAGCTTATACCACGCTGATTAA[C/G]GATCAGCGTGG
TP93328	TGCAGGGGCGCCACC[G/T]CCATTCCTTCGTGCACGACATGCGCTCGCCGCGACCGCGGCCAGCTCT
TP93349	TGCAGGGGCGCTCGCGTGCTTGAGGGCAACCCGCAGGGC[A/C]AGAGCCGAGCGATCTGGCCGAGCA
TP93353	TGCAGGGGCGCTGTCCCTCAAGAAAGAGCTCAAACAAGCCAACGGGCATTGGGCCA[G/T]ACGCCGC
TP93357	TGCAGGGGCGGAAGATCGATCGAGTGAACAAGCAAAACGGACGCCGAGGT[C/G]CCAGCAAGGATGT
TP93364	TGCAGGGGCGGATCTTAAGCAGGATTTGGTCGGTGGAGCGCCGTTGGTGGAG[C/T]TACGTCGGTTG
TP93375	TGCAGGGGCGGCGGCGGCGGCGGCG[C/G]GGCAGAGGCATGAAGAACTTCCTCAGGAAGCTGCA
TP93385	TGCAGGGGCGGCTGCCTAACATCCGCAAGCTTCGAGTCACCAAGTCAACACTCAACTCCTC[A/G]GA
TP93427	TGCAGGGGCGTCGCGGCCTCACGGCAGATAGGTGAGCGTCTCGCAGGC[C/G]ACGGTGGAGAGGATG
TP93469	TGCAGGGGCTCAAGGACATGGCCGTCACCGTCGGGCTCTGGCCCGCCACCGC[G/T]CCCGTTGCTGG
TP93470	TGCAGGGG[C/G]TCAAGGACATGGCTATCAGTGTCGAACTCTGACCCGCCACCGCGCGCGCTGGTCG

Table A2 (cont.)

TP93471	TGCAGGGG[C/T]TCAAGGACATGGCTGTCACCGTCGGACTCTGGCCCGCCACCGCGCCTGTTGCTGG
TP93475	TGCAGGGGCTCACGCGGAGGAC[C/G]CGCGAGGTGCGGGACAAGTTCGACGCGCTGCTGGAGATCAT
TP93493	TGCAGGGGCTCGCT[C/G]TGGTGGGGGAGGAAGATGAGGATTTAGACTTCTCGGAGAAGATCGATGG
TP93506	TGCAGGGGCTCTGCCATCACCGTCGTCGCCTCTGCACTCAGCGCCGCCGTGATCCTGCT[C/T]GTCC
TP93508	TGCAGGGGCTCTGTCTGTCACGGTCAGGTATGTACTAGGGCGGCGCCGCAT[C/G]AGAGATGAGAAA
TP93585	TGCAGGGGGAACAATCCAAGTCACCACGGCATCGA[A/G]TCAGAGAGCGCCGCGCACGAATCGGCGC
TP93595	TGCAGGGGGAAGACGCCCTGTTCGCGGGACTCGGCGAGCTGCCCGAGTGCGCCGTCGTGTTCG[A/G]
TP93604	TGCAGGGGGAAGTCCGCGACGAGTTCCTGCGGTTCCTCGA[C/T]GAGTCGGCCCGCGGCGCGGCGGC
TP93606	TGCAGGGGGA[A/G]TGCGTGTGGCGGCCCTCGTAGGTGGTGATCACCATGCGGCAGTCCTCCGACAG
TP93620	TGCAGGGGG[A/G]CCGCACGGAGCTGTCAGGACTCAGGAGGGAGTGGGAGTGGAACAGAGACGGCGG
TP93626	TGCAGGGGGACGGCAGCGGCTGCAAAGGCCCTCCGC[A/G]GCATCCCGATTCAGTTTCCTCCACGGA
TP93628	TGCAGGGGGACGGCGA[C/T]GAGCGGGACGTCTTCGAGAAGTACATCATCACTGACCCCGACAAGTG
TP93632	TGCAGGGGGACGTCGTGGACGCGGCGCCCGCCGCTGTGGTGGTCGCCGC[G/T]GCCACCGAAAAAAA
TP93651	TGCAGGGGGAGCTGGAGCTGCGTTCCAGCCCCTGGAACACGATCTTGCCCGACGAG[C/T]TCATGCG
TP93689	TGCAGG[G/T]GGATTGAATCGGGCAGCAGGCAGGCCCTGTAGCTAGCTAGGCGTCGTGGAGAGGAAC
TP93690	TGCAGGGGGATTG[C/T]CCTTCAGTGAACATTTGGTAAATAACCATTGCTAAGCTGTACTGCCAACG
TP93695	TGCAGGGGGCAAGGAAAACATCGCACCTACG[C/G]TCACCATTCACTTGGAGCGGCTGCTCGACTGC
TP93706	TGCAGGGGGCAG[A/T]GCCTGGTTGGGGGGCAGGGGTCGCCTCTGGCCACTGCTGCCATTGCTGCAT
TP93711	TGCAGGGGGCAGGCAATTCGCCCAACTCTGACGTGGGATGTAGGCA[A/G]CCGCAGCACCATCGCAA
TP93763	TGCAGGG[G/T]GCGGGGGGAGGTGCGTACCAGGACGACGGCGTCGCGGGCGGCCATGATGACGATGT
TP93797	TGCAGGGGGGAACGACGAGCT[A/G]GTCCCCTGTCCGCCGTCATCGAGGCCGCGCCGAGGAGTGCTC
TP93810	TGCAGGGGGGAGCTGGTGTCCGTGTTCATGCGCAACGCCGCCGACCCGCCGCGGGTGTT[C/T]AGGC
TP93819	TGCAGGGGGGCAGGTTTATCTACTGCCATCCGAG[C/T]CAAATGCCTCCGCGCGTAGTACTATATAA
TP93829	TGCAGGGGGGCCGTGATGGTGGGGTAG[C/T]TAAGGTGGGACTCGCGGATCGGGAGATACCCCGAGC
TP93843	TGCAGGGGGGCTTGGCCAGAGCTCCAGAAGCGTACGTACGCACGTACTCCATGATCGGATCGA[C/T]
TP93885	TGCAGGGGGTAAGACAGCCCCCAA[A/G]CATTTTGCTAAGAAGAAGACCTCATGCAGGTCGAGAAAA
TP93901	TGCAGGGGGTCAGCGC[C/T]GTGTCGCGGAAAATGAGATACTGGTGCTGAGGTACTATCCTCGACGG
TP93913	TGCAGGGGGTCGGCGGAGGTGGTTCCGATCCCGACGGTGGCCACCGCG[C/G]CGAACAGCATCGAGG

Table A2 (cont.)

TP93953	TGCAGGGGGTTTGGTCTTCGCCGTAGTCGTCGTC[G/T]TCTTCTTCTGTTTCTTGGTGTAGAACTCG
TP93962	TGCAGGGGTAATCGGTTCGA[G/T]TAGGAACAGTGTGCTTCAAAGGCTGCATGATTTTATTAAAAAA
TP93966	TGCAGGGGTACATCAAGAGGATGAAGAGAC[A/T]GAGCAAAATGATCGACCCGTTGCTCGAGCACGT
TP93973	TGCAGGGGTACGGGCTCACCGAGAGCACGGCTATTGGCGCGTCCACGGACTCT[A/G]CCGAGGAGAG
TP93974	TGCAGGGGTACGGTACGTACTAGGTTCTCGGCGAGGCCCATCTGGATGACGCCGT[C/T]GCGGTTGC
TP94017	TGCAGGGGTCAG[A/C]AACAATCTGTCGGATCAGCGCAGTGCGCAGTCTAGTGTTGGTGGAGGAGGG
TP94038	TGCAGGGGTC[C/G]GCGTCGATGACGGCGTGCTCGTATGGGTTGCGGAGGCCCAGGGCGCGCGGGAG
TP94047	TGCAGGGGTCCTGCTGGGTGCTCGAGGATCGATCCAGCAGGCTGTTTGAC[A/G]TGAATGAAAAATA
TP94048	TGCAGGGGTCGCCGTCGCGCGGGCTCCAGCCCACCATGGCGCCATA[A/C]GGATCCTCCTCCACCCT
TP94051	TGCAGGGGTCGTACACGGGCACCCAGAAGCCCGTCTTCAGCTCCACAGAACGCTTGACTG[C/G]CCC
TP94055	TGCAGGGGTCGTCGTAGTACCCGTACAC[C/T]GCCTCGCGGTCGATGGCGGTGAGCAGGGCCTTCTC
TP94069	TGCAGGGGTCTGTGTCACGTTCAGGACAGTGGCAGA[C/T]TTGCAGTTGGGGGTCAGGCAATGTGAA
TP94100	TGCAGGGGTGCTCGCCGCGGCCGAGGAAGCGC[T/C]GCGCGGGGAGGAGGCGGTCGTGGAGAGAGCA
TP94102	TGCAGGGGTGCTGGAGTGGCCGATGAAGGGGTGACAC[A/G]GCGGCAGCCAGCAGGAAGAAGCCACG
TP94128	TGCAGGGGTGGTTGAAGGTGAGGTACCTCGAGTAC[C/T]CCCGCAGGCCGATGGAGCGGAGGAATAG
TP94131	TGCAGGGGTGTACCGTCGGCGCC[A/G]ACCGATGACCCGACGATTTGGCGCCCGTCTCTCTCTTTGC
TP94133	TGCAGGGGTGTCCGTTCACATCGG[C/T]TGCCGAAGAGACGTCAGCGTAGCGGAGCACTGCACTGTT
TP94143	TGCAGGGGTTAAGATACCGAGCTTGCAAACAACCACATGGGCCT[C/G]TGATCTGATGTCTGACATA
TP94157	TGCAGGGGTTCATCGAGCCCGACCACAAGCACCT[C/G]TACCCGCAGTACGAGGCGTGGGTGCTGCC
TP94169	TGCAGGGGTTCGACTCGTGGTACAGCGCGCGGCGGGAGAACCC[A/G]CACGACCTCGTCGGCGCCGT
TP94186	TGCAGGGGTTGGCGGCATTTGGTATGGCAGCAATTCA[C/T]GAGGACCAGCACCACGACAACATGCC
TP94207	TGCAGGGGTTTTCGTTCAGAAAGCAACCAGAACCAAATCAGTCACAAAA[C/T]GGCAGAGATCCATC
TP94258	TGCAGGGTACAGGTACAAACGCGTAGAATTGGATCGCAGTGTACAGCAATTC[A/G]ATAAGGAAACA
TP94275	TGCAGGGTACCACCTACAGGTCCAGGCCCTCAGTCCGTGTCTGCCTTCCTCGTAACG[A/G]CGGAAA
TP94286	TGCAGGGTACGAATTGGGGGTATACAATTCACTGAAGCCCCTGAAGCTGGGCAAGCGG[A/C]GCGGC
TP94300	TGCAGGGTACGGTGCTTCATGTTTCGTCCTCGGACAATA[C/G]AGAGCTTCCTAAAGCGTGCACGCG
TP94311	TGCAGGGTACTATAAGAGTAGCTAGCCCTGCCCACC[A/G]TCTTCAGCCGCGCACACCGTCTCGCTC
TP94313	TGCAGGGTACTCGCAGCCGTACCCGC[A/C]GCCGCAGGCTCCACCGCAGGGGCCTTACTACCCGCCG

Table A2 (cont.)

TP94315	TGCAGGGTACTGAAATAGTTTT[G/T]CCCTCCTCGACAGTTGTGTTCATCTCAGACACAATTCGACT
TP94317	TGCAGGGTACTGGTGACGGTGAATTTGAAAGGG[A/C]CGTCGGCTAGCCACGGTCCACGGGCCGATT
TP94320	TGCAGGGTAGAGCAGCTGCCTCCACCGCCCACGAGAAGG[C/T]TCGCTCCTCATCCTGCTCGAAGTT
TP94333	TGCAGGGTAGCGGATGCTCGCGTGCAGGCGGGCAGATGCAAT[A/C]GCACACGGACAGCAGAGGGAC
TP94336	TGCAGGGTAGCTTCGCGACTGAGAGGTGCTTAGCTAGCTTTGCCTGCTTG[C/T]TTGCGTTTGAGTT
TP94445	TGCAGGGTCACCAGCAGCACCGCCCACACCTGGAAGTAGTCGTT[C/T]ACCTTCCTCGCGCCCGATA
TP94459	TGCAG[G/T]GTCACCTTTTCAGCTGCTGCTCTGCTCACCCGTTTCCCCATGTGCTCATCATTGAGCA
TP94470	TGCAGGGTCAGATTTCTGTGGTTAGCTTAGGTCTATTGAGGAC[C/T]AGCAAGGAGTTCAGGCCTGT
TP94476	TGCAGGGTCAGCGCCGAGCCGCCGACGCCGT[C/G]GCAGACCATGACCAGGTGCTTGACGTACCTGC
TP94514	TGCAGGGTCCAAGAAGTTCAGGCACGCGATCCTCAAGAACCTG[A/G]TTCTAGGGCTCAGGAAGCGC
TP94581	TGCAGGGTCGAC[C/G]GATGGCAGCTTCGACAGGAGCGCCTCCAGGCTGCTCATCGACGGCACGATG
TP94585	TGCAGGGTCGACGACGACGTGCTCGAAGCCGTCGTGGCGGCCAC[A/G]CTTCCGAGCGGTTGCGGTA
TP94586	TGCAGGGTCGACGCAGAAGAACGCCGACGAAGCACACCGCTGGTGGTGGTC[A/G]CCGTACAGCAGG
TP94588	TGCAGGGTCGACGTCGCAGCACGGCAAGCAGCAGCACCGCACGGTGCTACC[A/G]CCGTTGCCGAGC
TP94605	TGCAGGGTCGCCTCCAGTTCGTCCTCCTTCCAGC[A/T]GCTTATAGTCCACTCATCATCACCAGCTG
TP94624	TGCAGGGTCGGCGGGGG[C/G]ACGACGACGTTGTCCTGCTGCTGACCCTGCGGCTGCTTCCCAGCGC
TP94641	TGCAGGGTCGTCGTCGACAATGAGACGCGCGAGGACTGCACGCT[C/G]GTCAAGGTTTGTTTGCTCT
TP94656	TGCAGGGTCTCATCAAT[C/T]AGCGGAATGAAGACCTTGTAACCCTCTATGGGGCGACAGGCGTTGC
TP94669	TGCAGG[G/T]TCTCGGCACGCTGGAGCGCGACGCGCTGGTGGTAAAGCAGGTGATGCGGCAGCTGAT
TP94670	TGCAGGGTCTCGGCGGCAAGCCCAAGGTG[C/G]TGACCAACGGTGTCCATGTGGAAGACTCCGCGCT
TP94674	TGCAGGGTCTCTGCTA[G/T]CTTAGTAATCCACCGTACCCACAGCCCACGGCACAATACAATGGTAG
TP94688	TGCAGGGTCTGGAAGC[C/T]ACAGCGAGTGATGCTGGAGAAAGAAAGGCACAGGAGGGCAGGCAATG
TP94702	TGCAGGGTCTTACTGAAGACGCTCCTGAACATATTTTGCTTCATGTTGA[C/T]ACGGCTGCATCATC
TP94705	TGCAGGGTCTTCCATGCGCGTGCATGCAACGTGTCTGTTTTACTG[C/T]TGGAGACGTTTTTCTATG
TP94707	TGCAG[G/T]GTCTTCCCCTCGCAGGGGCCCTTCTTCACTAGGAGCGTGAGCACAGGCGGCGGATCCG
TP94709	TGCAGGGT[C/G]TTCTCGTACGTGAGAAGTCCCCCCACATGCGAACGAGAAACTCCCCACAGCCACG
TP94722	TGCAGGGTGAAAA[A/G]GCCTTTTTACGCGGCTCCATGATCGTACGGAAGCAGGTGGTCGATGGAGA
TP94727	TGCAGGGTGAACCAAAATGCGCAATACGACGAGACAAAAGGGTTCTAACGCAAA[A/G]CATGCCACA

Table A2 (cont.)

TP94742	TGCAG[G/T]GTGACCACGCACCAAACGAAGCCGTATCACGCGGCCAGAGCAGCCTCAGCTAACGGGT
TP94747	TGCAGGGTGACGAT[C/G]ACGAGCGGGTTCATGCCGCCGTTCATGGCCACCTTGACGAGCGACACCA
TP94760	TGCAGGGTGAGCCCGTACGCCTCCTCCATGTCCAGCTTG[C/T]CCGCGGTCATGCCGTCGGCGAGGT
TP94772	TGCAGGGTGAGGG[G/T]CAGCTCGAGCAGCTGCTTCCAGAACTCGGAGGAGATTGGGTAGGCCTTCT
TP94797	TGCAGGGTGCAAGCTCGCTCAACGGACCGTGAGCGTGACCCGCAGGCCCGCGAA[A/G]CCGAGTGAA
TP94807	TGCAGGGTGCAGCTCCCCCTCCCCGCGGCGCTATCTGCAACTGCAACCGAA[G/T]CGCACCTCGATC
TP94811	TGCAGGGTGCAGGCGCACGGTCAGGGTCGGTCTCGGTCCGTCGGTGGCGTCTG[C/G]TGGCGCAGTG
TP94835	TGCAGGGTGCCATTTCACTGGCAGCTCCTGCGACCAAGACATCTAGAGTCCAGCTA[G/T]GCGCATT
TP94861	TGCAGGGTGCGGAAGTCCTTGAGCGGCCGCGCG[C/T]GCGGGTGCGCCACGTTGTTCTTGCACCCCG
TP94863	TGCAGGGTGCGGCAGCAGTGCAGAAGCGAGCAGCGGTGTGGCCCGCGCGCG[A/T]TGCTCACCTCCA
TP94864	TGCAGGGTGCGGCGCCAGAGCGCGCGGGGC[A/G]CCTCGACGAGCGCGGCGAGAGGGTTGGTGTTGG
TP94866	TGCAGGGTGCGGCGCTTGTTCTCCTC[C/G]GCGTGCAGCCAGGAGCGGATGGTGAGCTCGAGGATGA
TP94873	TGCAGGGTGCGGGTGGCGAACTCGACGCCGATGGTGGACTTGGACTCGAGGCAGAACTC[A/G]TTGC
TP94875	TGCAGGGTGCGGTGCAAGTTGCCTGGGGCGAAGATCCTGTTCCAC[C/G]TTGAGAAGGGGAGCAACC
TP94888	TGCAGGGTGCTGCCTGTCGCTGTGGTGGTGAGTGGGAGCTCGTTCTCTGATTTCTCGACTTCT[C/G]
TP94890	TGCAGGGTGCTGCTGCGGCGTCCCCCCTCTCGCTATGAGTAGCGCTGTGA[A/G]GGACCAGCTTCAG
TP94894	TGCAGGGTGCTGGCGAAGGACTGGCCGAACCTCCACTTGGGCGGCACGA[C/T]GTCGGTGAAGACGA
TP94919	TGCAGGGTGGAGGACCTGAAATTCTCAACCATGCAATTGGTTACTCACCGT[A/C]TCACATTTTTTT
TP94922	TGCAGGGTGGAGGGATGCAAATTTGAGAAGTTTTGTCACGAGGAAGCAACAGAA[A/G]GCTCAGATT
TP94925	TGCAGGGTGGATGTGATCGCCAAGGCCTCAC[C/T]GCCATGCACGCCGAAGGACGCCACATCGTGAG
TP94936	TGCAGGGTGGCCCACCGAACTAATGGGCCGAACTT[G/T]GGGTGCGGACCCACCAACCTTGGAACCG
TP94957	TGCAGGGTGGGCA[C/G]TTCCTCTACTAGCGCCTTGAGCACCACCATCATGTCAGCCGCCGCCTGCC
TP94982	TGCAGGGTGGGCGTGTCCTCGCGGCCCTCCA[C/G]GATGTTGCGCGGGGCGTAGGTCTCCTCGCCGA
TP95003	TGCAGGGTGGTCAATCCAT[C/T]CATGCATCGTACGTACGACCACGCCATAGGGCGCGAGAGATTTC
TP95007	TGCAGGGTGGTCCACGGA[C/T]CACAGGATCACCCTGTAGCTCCGCCCCTGACAGGAGAACAGGAGA
TP95012	TGCAGGGTGGTCGTCGGAGTTGG[A/T]CGACGCCGCGGCAGTGGCAGTGGCGTCACGGTCGGGCTCG
TP95014	TGCAGGGTGGTGAGAAGAGAAAGCGCGTC[A/G]TTGGTGGAGGAGATCGGGGTTGGGAGCGGCGGCG
TP95019	TGCAGGGTGGTGGCGACGATGGGGCGGCCGCGAACCGCGGGAACA[G/T]GAGAGGGCGGCACGCGGC

Table A2 (cont.)

TP95028	TGCAGGGTGGTGGTGGTGGTGACTACGTGTGGGCGGCCA[C/T]GTCGGCTCTCCCGCGCGGTGGCCT
TP95029	TGCAGGGTGGT[G/T]GTGGTGGTGGTGACTACGTGTGGGCGGCTACGTCGGCGCTCCCCTGTGGTGG
TP95057	TGCAGGGTGTCGTCCCAGGAGGTCGCTGCCGACCTCA[C/G]CGTCAGAATCGCCGACTCCGTCTTCC
TP95063	TGCAGGGTGTGACACGGGCCAACCAGCGCGCGACAGGCCCCTGCGCCAATGGAAC[A/C]TGGTCGGA
TP95087	TGCAGGGTGTTACCATCTCGGTCGATGAACGAAACTAAAGAGATTGCATGCAGATGACGCACC[A/C]
TP95107	TGCAGGGTGTTGCTAGGAGGTGCTCACCCCTTATAAACCGTGTTGAT[A/G]CTGGTGCCGAGAGAAA
TP95133	TGCAGGGTTACCACGCTAGGACCCAGGGAGCCCATGCTTCGCACCA[A/C]CAGCTGGCACCTGCACG
TP95134	TGCAGGGTTACCATCGGAGAAAGGAAACACACGGCGAGAGAGAAGTGGAGAAGC[C/T]TGAGGAGTG
TP95188	TGCAGGGTTCCGAGCTATCGGGTGTGGCGTCGCCCTGTCTGC[G/T]GCCGCTGCCGTCTTCGTCAAC
TP95201	TGCAGGGTTCGGAGGTGAAGGAGAAGGAGAAGGCGCGCCACCACAAGGACGAAAAGC[A/G]TGCCAC
TP95209	TGCAGGGTTCTACTGCAAGTACAAATAGCCGTGCACGGGAACGCGACAACAACCGCACT[A/G]CTCC
TP95213	TGCAGGGTTCTGCTCGGGCAAGTGCAGCGTG[A/C]GGTGCGGGCGGGCGAGCGCGCGGGCGCGGGGC
TP95216	TGCAGGGTTCTGTGCGGTTGTAACGGAGCAACGCCGATGCCATCCCATGTGC[C/G]GTTGTATTTGT
TP95243	TGCAGGGTTGAGTCGGAGACGGTGCAAATCAGCCTGACTAGAGAC[C/T]ACCTGTTCCTTCGTTTCC
TP95297	TGCAGGGTTGGGTTGGCAGCC[C/T]TAGACTTAGCTGCCAAGCGACGACTCCGCCTAGGAGAACCAG
TP95306	TGCAGGGTTGTCATCAGTGAGCTGTGCTTC[A/G]AGTGTAGTATAAGCGTAGTTGTGATTCATTCAT
TP95309	TGCAGGGTTGTGACGCCTCCGTTCTGCTCAACTCCACCGATGG[C/T]AACACGGCAGAGAAGGACGC
TP95310	TGCAGGGTTGTGACGCGTCTGT[G/T]CTGCTCAACTCCACTGCGGCCAACCTGGCAGAGAGGGACGC
TP95314	TGCAGGGTTGTGCGAGGAGAATGATCGATCGGATTTGG[A/C]TTTGGCTGCCTGCATCCATCCATTG
TP95351	TGCAGGGTTTATGAAGACGATCCAGATCTGGATGGGCTGG[C/T]GTGAACGGCATCAGCATGAGTGG
TP95369	TGCAGGGTTTCGCC[C/T]GCGGCACTGGCATTGTTCTCTCCTGCTCCGCTCCCCCACGCGTGCTCTC
TP95407	TGCAGGTA[A/C]AAATCCCGTTCGGTCGTTGTCTCTGTCCGCGCCGCGACGTCGCCCAGCTGACGGT
TP95410	TGCAGGTAAAAAT[C/G]TAGGAGCAGAGGGGGTGGTTCCAGAGATGGCGCGGGGGAGCGGATAAGTC
TP95433	TGCAGGTAAAATAGCCGCCACAGCTTCCACCTTAT[A/T]TTCCTCTTGCTGAGGCAGGGCGCAGTTC
TP95436	TGCAGGTAAACAAACAATCCTGCCGCACCACATC[A/G]ACTTGACCCAAGTGATCCTGTCTCGTTCT
TP95439	TGCAGGTAAACACAC[A/G]CATCGTATGACAAGAGGTAATCAAAGACCCCGAGGGCTGAGAGCATTC
TP95453	TGCAGGTAAAGATCGTGTTTCCTTCGGG[A/T]GGTGATGCTCATCTCCTCCATCATGTCCAATTCAC
TP95474	TGCAGGTAAATAATTGGTTCCTAAGCAAAAGACAGCATCCCTTATATAAAGG[A/G]AAAAAGGGAAT

Table A2 (cont.)

TP95516	TGCAGGTAACCTGATCTCCGCCCAAACCCCCGATCCACTGATTGGATCTGAT[C/T]ATGTCGGAGGT
TP95522	TGCAGGTAACGATGCAACCCACACAATCATGCAGAGGCAC[A/G]CGACAATGCAGGCCACACCGCCT
TP95523	TGCAGGTAACGCAAC[A/G]CAACAAGCCCTGTTCTTCATCCTCTTGGGATACAGACAACCTGCAAGC
TP95532	TGCAGGTAACGTTGCTTCCACAATAGT[C/T]TCTTCAGCCTAACTAACCTTCTGAGTCTCACTAATG
TP95538	TGCAGGTAACTCCACCTCTCTCTCCCC[A/G]TCCATCTTTGCCTTGGGTCATCTCCTGTGAACCAGT
TP95550	TGCAGGTAAGAAAGGAAATCGCGTGCCTTTAATTTCCTGGCT[A/G]AAGTTCCTTTGCCGAACTCGA
TP95562	TGCAGGTAAGAGTTCAGGAGGTGTAAAGCTGCGAGAGGA[C/T]GAGGAGGACCTGGAGGTGAAGCTC
TP95570	TGCAGGTAAGATCCTGGAGAACAGAGCACTGTTACATTGTAAAGTGCAGTAATAAATTCATTA[A/G]
TP95572	TGCAGGTAAGCAAGCAATCTCTGTCACTTGGGACGACCGTG[C/G]ATTCGTTCGTACGTACCAGGAT
TP95588	TGCAGGTAAGGAA[G/T]ATGAAAAGACGGGAAACGGAGAAAACCTAACCCAGGGTGGGCGGCCAGCA
TP95594	TGCAGGTAAGGCATGTATGGCATATTGGCAATTGACATGGTCACCGCCGTCATCAACTCG[A/G]TGG
TP95603	TGCAGGTAAGGCTCTGCAAAGA[C/G]GTACAACAGCAGCCAACAAGGTCACCATCCATCAGCGAAAC
TP95610	TGCAGGTAAGTCAAGAATTCATGAATCTTGAAAATGTCATATGGAAACACGCACCGTACAAA[A/T]T
TP95624	TGCAGGTAATAATTAGAGGGTGCACAATGGCGTTAGCAGGTAAGCCAT[C/T]CGACGGAATGCCCCT
TP95648	TGCAGGTAATGGTTAAAGTGCAGGGCTATTACAGG[A/G]CTATCTGTTTACACGAGGGAAAACAAAC
TP95655	TGCAGGTAATTAA[A/G]TGACCACTTCAGCACCATAGCAAGCATACGAAACTCAAGTAGCAATAGTC
TP95672	TGCAGGTACAAACTACGCTTGCGTGGAC[A/G]GTGGACATATGGACAGAGGTGGCCATGTGCGTCCG
TP95679	TGCAGGTACAACAGTCACAATCCAGGTGGCTTCCAAAAGG[C/T]TGTGCCTTACTTTGGAGGACTTC
TP95683	TGCAGGTACAAGCTAAGT[C/G]AGAAGCTCTAATGATAATTGAAACAAATGTGGTGGCCCGTGTCGC
TP95694	TGCAGGTACACAGTACTCCA[C/T]GCTTTTATTTACTGCATGCACAAGATCGACCGAGCAGGTAGCG
TP95708	TGCAGGTACACGATCGGA[A/T]TCGTTCTGATTCGATTCGATTCGATTTGGTTGGGTTTCCCGCTGT
TP95720	TGCAGGTACACTGCCGCTGCACTACAGAGCAGGTGCAAATGACA[A/T]CTTGTGGACAAGAGTAGCA
TP95740	TGCAGGT[A/G]CAGGAACAAAAATGGGGCGATCGCCGTGCTGCGACAAGGCGGCGGTGAAGCGCGGG
TP95764	TGCAGGTACATAAACTGCTTGGATCGAAGTTATAGATCCCTTTTTGGTAGA[A/G]GTAATTCTTTCT
TP95786	TGCAGGTACATCTGCATCATTATC[G/T]CTGGTAGAGTTGCTGTCGCTGCCTGATGTTGATCCAGAC
TP95791	TGCAGGTACATGGAAATGGTTGCACCGTAGCAATATACC[G/T]TACTAATTTTTCTTTTTCCCCCTT
TP95794	TGCAGGTACATGGAGCGGCACGGAGGAGTGAACGGCAGCGATGGCACT[G/T]CCGCGGCTGAGAGCG
TP95828	TGCAGGTACCCACGGT[A/T]GACTGATCCGAAGCCACCTTCGCCGAGCTTCTCCTCGTCGGAGAAAC

Table A2 (cont.)

TP95829	TGCAGGTACCCAGGCGGCGGGCGGCCACCACAA[C/G]AAACAGTGCTGATGGTCAGATATATAATAT
TP95838	TGCAGGTACCCTCGGTAGACTGATCCGAAACCGCCCTCACCGAGCTTCTCGTCGTC[A/G]GAGAATC
TP95849	TGCAGGTACCGCGC[C/G]TTGCAGCAGGGGAGCTCCTCGTCGTGGTGCACGGCGGACGCGTCGTCGT
TP95884	TGCAGGTACCTGAACAAGTGTTGCAGAAGCGCGTCGCCAAGGTGGGCACGGCG[A/G]TGCGCCTTCA
TP95887	TGCAGGTACCTGAGCACGTCCTT[C/G]AGAAAAGGGTGGCCAAGGTCGGCACTGAAGTGCGTCTACA
TP95904	TGCAGGTACGACGGCGGC[G/T]GGAACAGGTGGCAGCGCGGCGGCGTTCGGCGTGGCAGGCACAGCA
TP95910	TGCAGGTACGAGATTTTCGGTCACGCCTGCAAGACGGG[C/T]CCGTTTCACGGCGTGGCCCGTGGGA
TP95911	TGCAGGTACGAGGTCGAGCCTGCCGCCGCTGGACTGG[C/G]CGAAGCGTCTGAAGATCATCAAGGGC
TP95912	TGCAGGTACGAGTGCGG[C/G]CCATTTCCCGCGTCGTCCCCAAAGTCCTGCCCGACCGATGCCCCCG
TP95914	TGCAGGTACGATCTGGGCGGTTGGGCTGAATTG[C/T]CTCAGGATGTGGAGATCCAGCGGCCTGCCA
TP95917	TGCAGGTACGCACGAGGGGCCGTCTCGCA[A/T]GTCAATGTATCCACCTGTTCCACGGTATGCAGTC
TP95922	TGCAGGTACGCCATGCCGCGGAGAGCCAGTGACAGGAGCAGCAACAGGGTGGCG[C/T]GACACCACA
TP95924	TGCAGGTACGCCGAGTCCTTGCCCAGGCAGATCCT[C/G]GGCCCCGCCTGGAACGCCGTGAACTTGA
TP95929	TGCAGGTACGCCGCTTGCGCTCTCGTCGTCGTTTGGCAGCCAGGACAGTGTGCCC[A/T]GTGCGTGC
TP95937	TGCAGGTACGCGGC[A/G]AGCAGCAACCACGCCACCGCGCGCGCGGCCGCGTCCACCTGTTCCGCGA
TP95952	TGCAGGT[A/G]CGGCACGTTGGTGAAGCAGGAGAGGATGACGACCGCCGAGAGGAAGATGGCGGCCG
TP95959	TGCAGGTACGGGCTCAGCAGCGGCAGCCCCATCGCTTGCGCTGTTGGTCG[A/G]ACAAACACCAACT
TP95961	TGCAGGTACGGGTGC[C/T]AGTGACAGGAACCCAACGATGATAACGCGGGTACGATTCCGATCGGGC
TP95977	TGCAGGTACGTCATCCA[C/T]CCAGGACCAGATTGATTGATTTCGTCTGAGCTGCTCTTGGTAAATC
TP95980	TGCAGGTACGTCCTGCGCGG[C/T]GAGATGCTGGGCGACGACATAAGCCCCTCCACGTCCTCCTCGT
TP95993	TGCAGGTACGTGTGTCGACTGTGGAACCGTGGTCCGTG[C/G]GAGGTGGTGTGGAGAGATCAGAGAT
TP96028	TGCAGGTACTCCACGGGCTTCCCGAGCCCGAACGGGTC[A/G]AATCCGTAGTCGCCGACCAGCGAGC
TP96033	TGCAGGTACTCCATGGACA[A/G]GTAGTACGTCTGCTTCGGATCCGTCTTGTGGAAATGCAAGTACG
TP96038	TGCAGGTACTCCTCACAGT[A/G]CTCACTGCTGCCACCCTTCCAGCAGCCCAGCGGACTGCTGCTGT
TP96042	TGCAGGTACTCGGCCAGCAGCTGGCCGTCG[A/G]GTCCCACGGCCACCTCGCAGCCGACGTGGAGCG
TP96059	TGCAGGTACTGACGGTCCATTGGGGAAGAGAATGGAGAATTCGAAAACTCGGGTTGAGAT[C/T]GGT
TP96061	TGCAGGTACTGCATCGCCGTCGTCATGTTG[C/G]TCTCCATCAGCTGCGCCACCTCGTGCTCGAACG
TP96071	TGCAGGTACTGGCA[C/T]AGGACTTGGGTTGAGCGCACCAACAATGTCCCATGCCCATCGGTTGTGA

Table A2 (cont.)

TP96074	TGCAGGTACTGGTAGCAACTCGCAACCTAATCGCCATCGCATCGCCAGCCACCTAATGACACC[C/T]
TP96082	TGCAGGTACTTAA[A/T]GCGATAGTAACTGAAACTGGCATGGACAGGAAGTTTCTCGCGTCGTTCTT
TP96104	TGCAGGTAGAAC[A/G]AGTTGGGACGAACTGATGGAGAAGCTTTTCACCAGGGATGAAGATGGGAAA
TP96106	TGCAGGTAGAACACCACGCCCGACCCGAACACGCCCTGCACTCCGTCGACCTCAC[A/G]ACCAGTCT
TP96115	TGCAGGTAGAAGCGCGGGTGGGT[C/G]GGGCGCAGGACGAGGTAGATGATGAGCGCGATCACGCCGA
TP96118	TGCAGGTAGAAGGTGTAGGCTTCAGGAA[C/T]AGAGGGAAGCCGATTCATGAGATCGGACCACGCGG
TP96137	TGCAGGTAGACGCAGTACAGCAGGTGTTCCCCTG[C/T]AAGGTTCAGGACTTTCCCACCAAGGACCT
TP96143	TGCAGGTAGAGACTAGAGAGAGGTAGCTAGCTGCAAGAAGCAAGCTCATAATTAA[A/G]CAGACGAT
TP96150	TGCAGGTAGAGCCCAAG[C/G]GCCAGGCGGAGACCGCGGATCATCGCGCGCGCCTCGACGATGCCAA
TP96154	TGCAGGTAG[A/C]GGACGCCATGAGTGTACTTGCGAGGTGGCGACCGTCTCGGCGTGCGGCGCGCAC
TP96167	TGCAGGTAGATCCGAGGCGGCGCAAGGTCCTGCGCACCAGCCTCCGCCC[A/C]TCTCGAGCAAGGGG
TP96172	TGCAGGTAGATGCCCAGCATTTCGTAC[C/T]TGTGTGCGCCGTAGGCTTGGCCGCACAGGGTTTCCA
TP96190	TGCAGGTAGCAGAAGCCGTCGCCGCGCGTCGGCGCCGTACACAAACTGCGCTGCCGTACACCC[A/G]
TP96192	TGCAGGTAGCAGATGGTGCGGAACAGCACGCA[G/C]GCCATGAAGAACATGGCGGTGCGGTACATCC
TP96193	TGCAGGTAGCAGCAGCAGCAGCAGGTGCACGGGCAAGTCGCGGTGGAGGC[C/T]GCACGCCTTTCCT
TP96199	TGCAGGTAGCAGCTAGCTACCATACATGAATGATGAATAC[A/C]TCATCAGTCAAACAAGCTATAGC
TP96200	TGCAGGTAGCAGCTCGATCTATAAATACCTCACTGGTGCATAGCTCGCTTAACCACCA[C/G]CAGCA
TP96201	TGCAGGTAGCAGCTGACTTTTTCATTAGAAATTAGTGATATATAAAAGGGCGTACC[C/T]AGTGCAG
TP96209	TGCAGGT[A/T]GCATTATCATCATATACCTGTCTCGTCTCTCTCGCCCATTTTTATGGCCACCTATA
TP96222	TGCAGGTAGCCCTCCTCGCCGTTGTGGAATTCCGCGTCGCCCG[A/T]GGTCTCCTCGAGGCCGATGG
TP96242	TGCAGGTAGCCGCGGCGCTCTCCTAG[A/C]CTGCCAGCGGCCCCGTGGCCGTAGCAGTACTCCTCGC
TP96260	TGCAGGTAGCGCGTGCGCTACTAGCTGCGCGTGCGC[C/T]AGCGTTGGGCTATGCGGCGAGTAGGAC
TP96268	TGCAGGT[A/G]GCGGCGGTAGTCGGCGATGAGCGAGTCGGCGAACTGCTCGGGCGTGTACCGAAAAA
TP96270	TGCAGGTAGCGGCTGATGTCGCCGTCCGCGT[A/C]GTACACCTCGTCGGACATGGCTGCCGCAGCGT
TP96278	TGCAGGTAGCTAGCGCCTGGTT[C/T]GATCGATCGAGATGGCTGTGCAGATTAGCTTACCTGATGCC
TP96279	TGCAGGTAGCTAGTAGCACTAGAG[A/G]TCGATCGCAGAGCGGGAGCCAGCCGAAACCCCACGTCAG
TP96286	TGCAGGTAGCTCTG[C/T]ATGTAGTCGTCGATCTTGCGGTTGAGGACAGCCATGGGGAACGCCATAT
TP96290	TGCAGGTAGCTG[A/G]AATACTATTTTACCTAAATATGCCTATTAACTCCAGTAAGCTAAGCTAATT

Table A2 (cont.)

TP96294	TGCAGGTAGCTGATGTCCC[C/T]CTTTGGCGACTAAAGACAAAATATCACACGCATTGGCATATCGT
TP96297	TGCAGGTAGCTGCTGGGAGGGAGCTGTCGGCGATGTTGGTGGTGTCGGCTGCGGGCGGTTG[G/T]TG
TP96307	TGCAGGTAGCTTGCTAGCTACCTAGGACGCCAGAGAACGACCA[A/C]ATAAGAGACCAACATTATCA
TP96318	TGCAGGTAGGAGAAGGGAGCCAAGATCTGTGGGAGGGAGAAGCAGG[A/C]CAATGAGGCGAGGAATG
TP96320	TGCAGGTAGG[A/G]GCATACAGAAATTAGAACCCTTGTGTTTGAACAGTTTGACACGGCAGACCACA
TP96321	TGCAGGTAGGAGCGGTAGAAGTATCATGTGAGCTGTTGTGCAGCAGTGCCGAATGA[A/G]CGCGCTG
TP96326	TGCAGGTAGGAGTGAAAAAGTTACTACTGGGTTGCAGAAGTGGTTCACATGAG[C/T]AGTAGCAAAT
TP96332	TGCAGGTAGGATTCATCTCTTCTCATCATATTCTCATATCTGAATGATCTATGTC[A/G]CCTGTTCG
TP96345	TGCAGGTAGGCCCCACCCAAAGTCGGTAGCACGGAACGACAGCTGCGATCACGCC[A/G]TGGTGAGC
TP96355	TGCAGGTAGGCGAGGTGAGACACGTCGTCCGCGGTCACCAGGCGGGAGGTGCCCACGGC[C/G]GCGT
TP96358	TGCAGGTAGG[C/T]GGCGGCGGTGGCTCGAGTTTCAGGCAAGCACAGGAAGCAGCGGTGGTGACGGA
TP96366	TGCAGGTAGGGCAGGCGCGGGAC[A/G]TCCTGCTCCCCGACCAGGCGCGACGCGCCCACCACGGCGT
TP96369	TGCAGGTAGGGCCGCA[A/G]CACGCGTGTGCGGTCGTGGCGGCGCACGCGCAGCACGAGGCGGCCGT
TP96370	TGCAGGTAGGGCCGCAGCACGCGTGTGCGGTCGTGGCGGCGCACGCGTAGCCCGAGGCGG[C/T]CGT
TP96385	TGCAGGTAGGTAGACCAAACAACCTAGTATCCACCCTTGAGATCATTGACCACATCGTA[C/T]GGGA
TP96390	TGCAGGTAGGTGATGA[G/T]CACCAGCCACGCGTTCACGATCAGCAGCGGCACGGCGTAGACGCGCA
TP96403	TGCAGGTAGTACTGCCG[C/T]AGCCCCTCTCCCCCACCGCCGCTCCTCCCCTTCGCGGCCGCCGCGG
TP96405	TGCAGGTAGT[A/G]GAACAGAAAGCTGGAGGTGCCGTGCCCCTCGGTCAGGTCAGCGGGCGGTAGAA
TP96419	TGCAGGTAGTCGCAGGGGCTCGCCCCGTG[C/G]ACGGCGCTGGGTTGCACCGTCGTCATCGTCGGCG
TP96428	TGCAGGTAGTGTCGCCGCGCTTTATGTG[A/T]GAGTGTGATTCCGCGCCCGCCCGATCGTCTTTCGA
TP96463	TGCAGGT[A/T]TACGCTACTAGCACGCTGCAACACAGCGGACTTGATGCGCACGCACATCATTGCCT
TP96483	TGCAGGTATATATATTTAATATATTACTCCATATTCGTTTCCTTTTATTTATT[C/T]CTACTACGAG
TP96494	TGCAGGTATATTGCCACGCCGAGCACCGCCAGCAGCACCGCCGTGACGC[A/T]GAGGATGCACGTGA
TP96502	TGCAGGTATCACGCGGTTATTTGATCACAAAGTCAGAAAAGAATAT[C/T]AAGAAAAGGAAATTTGG
TP96509	TGCAGGTATCCACGGTAGAC[A/T]GATCCGAAGCCACCCTCGCCGAGCTTCTCCTCGTCGGAGAAAC
TP96583	TGCAGGT[A/C]TGCTCTCTTCCCTACGTGTCTAGCAGTAGAGTAAGTTGTAGCATTTTTTAGACACG
TP96585	TGCAGGTATGGACCCCAAAGAATTCAAAGAATGCATAGGTAGAACAG[C/T]AGACCTAATCACCCAC
TP96596	TGCAGGTATGTACTACTAGCCAGGCATGTTCAGATGGATC[A/G]CCTAGCTCTTCCTTAGCCATGCC

Table A2 (cont.)

TP96610	TGCAGGTATTACAC[C/T]GTTCCAGACTGGAGCATTGGTCGGGCTCGGGCTGGGCCAAAGAAAAGCC
TP96624	TGCAGGTATTCACCAA[A/G]GGGCCATCTTTGTATGCTTTCAAAGGGCTGGCTGGTCGGTATGCGCC
TP96640	TGCAGGTATTGGGCTTTGAGCCCACTGCTGCAACTACTGGGCTTTAA[G/T]TAACTCATCATAACAG
TP96659	TGCAGGTATTTTTGATCGTCATGAACTCGTGATCC[C/G]ATCGCACCAGGAACGAGATCCTACAACC
TP96660	TGCAGGTCAAAAACAATGTTGCTAAGCTACAAGGCGATCAAAATTAA[C/T]GTACATCCTTTTATCT
TP96669	TGCAGGTCAAACGCCCGACGT[C/T]GTGCTACTGACGGAGGCGAGCATCGCTGGAGGAACCTCCCGC
TP96675	TGCAGGTCAAATCATTCCAGCCACTTCATTCGTTTTCGTTCCCACA[A/G]GTCACAACCATGGAGGG
TP96713	TGCAGGTCAACGCCGCCGCCCAGTGCTTGCCTCCGTCG[A/T]TGTTTATTGATCTTGGCATGGCCTG
TP96714	TGCAGGTCAACGCTTCCGCTGTCTCAAGGTCTAAAACACCTTCCATC[A/G]CAACCGCAGATGCTCC
TP96734	TGCAGGTCAAGGACAGCCTCCGCGCGCACCACGGCCGCGCGGACATGGAGTTCGTCTACGT[C/T]GG
TP96738	TGCAGGTCAAGGCACCGCTGATGGTGCCTCCAACGGCTGCCGTCTCACGGTGAA[A/G]CAAGATGAC
TP96759	TGCAGGTCAATCTCCAGTGCATCTAGTAATGC[G/A]ATACTTGTTTCCTAATTTTAAAGCATGCATT
TP96763	TGCAGGTC[A/C]ATGCCATGCCATCACTCTCGGCGAAAAGCAGCGAGCAGATGGGGGTTGCACGCGC
TP96770	TGCAGGTCAATGTGGGCATCAACGCAGCCCCGAGCCGACGAG[C/T]ACGCACACATTGTCGCTGTCG
TP96778	TGCAGGTCACA[A/C]CACACGCACTTAACCGACGATCACAACGGAAGCCATTTGACACGATTGCATG
TP96801	TGCAGGTCACATTAAAGTAGG[C/T]GCTCAGGCTGATCACGGCACAGCCATCACTGATGCCAAAGGG
TP96810	TGCAGGTCACCACGCA[A/G]GCGCCGCCGCCGCCCATGTCGGTGGCGTCCGAAAAAAAAAAAAAAAA
TP96814	TGCAGGTCACCATCTCCGTCTGCGACGTGTCCGTCCGCGCCGACCGCGA[G/T]GAGCTCATGGCCAC
TP96845	TGCAGGTCACCTGAACAACTCTATAGCGCAATTCAAGATG[A/C]GGCAAAGATGTGGGTACGTGCAG
TP96859	TGCAGGTCACGCTAAACGCTCAGCTCCGAGGTGACGTGTAAAGGCTGCGACAT[C/T]GCAGTGTGGC
TP96861	TGCAGGTC[A/G]CGCTCGAGGTCCTCAAAGGTGGGGCCAGCCGCCGCCGCTTGAGATGGAGCCATCG
TP96888	TGCAGGTCACTCATGTCTGCAAGCCACAGCTTGGACGCATCCGTGGCGATCA[A/G]CGCACACACAG
TP96895	TGCAGGTCACTGATGGAAGCTGTGAGGGTTTTGATGAGTGTGGCCAGCTCGGCGT[C/T]GGTGGGCT
TP96897	TGCAGGTCACTGGAATCAGGTGGTCTATGAAGATTCTCACAGTTCC[A/G]AACAACTTTAGATATGG
TP96905	TGCAGGTCAG[A/G]ACCGTGCATTCTCCCAATTTGAATAAGGAGCGGATTCAGGCTACAGAAGTTTG
TP96906	TGCAGGTCAGAAGAGTAGTTGGGTTGCGTGGGCGGCATTGCCTGCCGCGTACCGACCTG[C/T]TTGG
TP96907	TGCAGGTCAGAAGAGTTGTTGGGTTGCGTGGGCGGCATTGCC[C/T]GCCGCGTACCGACCTGCCTGG
TP96918	TGCAGGTCAGCAA[A/G]GACGGCAGGTGGTTCCCCGTGCAAGCGCTCGACGGCGCCTTCGTTGTCAA

Table A2 (cont.)

TP96920	TGCAGGTCAGCAAAGCTGATTTTTTTGGCCAGGAGAACATGGGCTCCGCTACGATGGG[C/T]GAGAT
TP96925	TGCAGGTCAGCAC[C/T]CCGCAGTTACTGCTTCTCTTCTCTCTGCATATATACTGCCAGTGCCAGCC
TP96931	TGCAGGTCAGC[C/T]CCGACTTCCCCGACGTCGCCATGTAGTTGCTGTAGACGTTGGCGAGGAACGC
TP96938	TGCAGGTCAGCGGCGCCCGAGCTCT[C/G]CGTGGCGATGGACTACTCGGGCACCAAGGAGGGGGCTT
TP96945	TGCAGGTCAGCTCGTT[C/G]GGCGACACGGTGGAGATGGTGCGGGAGGCGAAGGCGGCCGTCACCAC
TP96947	TGCAGGTC[A/G]GCTGGCGAGAGCGCGAACATGCCTCCAAGGCACGTCGCGATCTCGCGGCAGTTGT
TP96960	TGCAGGTC[A/T]GGAGCGGCGGCGCGCGTCACGGGAAGCGGCGGCGGCGGCACGGCCATGTGCGCGC
TP96982	TGCAGGTCAGTAACAAGAGTCACGTGT[A/C]AGCTCTCAGCTTGTGCCTTGTAGTACGACTCCTGTT
TP96998	TGCAGGTCAGTTGACTCTCTCTATGGCTGCTCGCCATCCTCGCT[A/C]GTCAGGTGCTCGACGAAAT
TP97005	TGCAGGTCATAGCCTCTGTCCAACGATTCGTCAACGATGGC[C/G]TGGATGTTCCCGCTCTCGATGT
TP97012	TGCAGGTCATCAGCAACGCAAATTTACCGTAGTG[C/T]CGACAGCCTTCGTACAGTCATCATCAGAA
TP97032	TGCAGGTCATCGTGCTGCG[C/G]CTCCGCTCCCGCGGGAAGGAGGTCATCCAGTCGCACATCGGGAC
TP97044	TGCAGGTCATGGATTGCT[C/T]TGAAAAAAGAATCGCGGTCATGGTTTCTGAGCTTCCTGGAGGATG
TP97045	TGCAGGTCATGGCACCGATTTTTGCCCTCATCGCACCGAGGTATCAGTTCACGGCGTCCCAC[A/G]G
TP97069	TGCAGGTCCAAACAAAACGAAAACGAAACTGGCCACAGAGTATGCTTCTGTCTCCCTGTCT[C/T]CC
TP97071	TGCAGGTCCAAACGCCTGATCGAG[A/C]CTGCGCTGTGCCGCGCGATGGCTGGCATGGCGTTTGCTT
TP97082	TGCAGGTCCAAGCTAGAAGCTACCCCATTGCCGCAG[C/G]CCGCAGCTTGCAGCAGAATCAGGTATC
TP97086	TGCAGGTCCAAGTCGGTCGCTTGCTAAGCGTGGGACTCAATGTTACGTAGATTTAAGAGGC[A/C]TT
TP97087	TGCAGGTCCAAGTCTAGGTGTTCTGGTCCTTGAGACCGCCATGGCGTGCATCAACG[A/G]CGACGTC
TP97102	TGCAGGTCCACACGTCGTGTCATGCCAAACCAGTGCGTTT[A/C]GGGCAGGGTTGATCGATCCGTGA
TP97107	TGCAGGTCCACATCTATCTCTATGCGAAGCATTT[C/T]ACCATATGGCATCGCAACCACATTCCTCG
TP97111	TGCAGGTCCACC[A/G]CCTCTCCGCCGCCGTCAGAGAGGCCGCCGCCGCTGCCAAACCCTCGTCGGT
TP97123	TGCAGGTCCACGCCCACGCCCGACGTGGCGAGACCGTGGAGGAGCGCCAAGAG[C/G]CCGTTGCAGA
TP97124	TGCAGGTCCACGCGCATAACTAG[A/G]CTCATTTATTAGAGAAAGGGTAATGCTCTCTTCTGAGCAT
TP97125	TGCAGGTCCACGGAGCACGGACGAGGGACGGACCACGGCGTGTGGGCCCGTGGGCGT[G/T]GGCGTA
TP97133	TGCAGGTCCACTGCTACCTGGCGAGATCGTCATCAGTCCGTTCGGGAGATCCCTGGTCTGG[C/T]GG
TP97136	TGCAGGTCCAGAAAGCTGAGCCACGGGATCACGTCCCCGACGTTCACCCACTAG[A/T]AGAGAACAG
TP97147	TGCAGGTCCAGCACGCGCAAGCGCCGCTGTCCTAGCAAGTAGCA[C/T]CTCGCCCCAGCCGACGTGC

Table A2 (cont.)

TP97150	TGCAGGTCCAGCAGCAGCAGCAAGGTACGCACCACCAGCCGCTGCCACCGTCGCCGCCGCCGC[A/T]
TP97157	TGCAGGTCCAGCCGCGCGGCGCAGATCACGGGACCAGGTCGTCTCCTTCACC[C/T]TCGCCCTCGCC
TP97160	TGCAGGTCCAGCGCCGTCGCGCCCATCACCGCGAAGTTGGCGCCCTGGCT[A/G]AAGTTGGTGCCCT
TP97161	TGCAGGT[C/T]CAGCGGGTCGTAGTCGTCGGCGGGGCACGAGAAGAGGACTCCCATGGCGACGCGGC
TP97174	TGCAGGT[C/G]CAGGGATCGGAAGCTAGCCACACGTAGGCGCACGCAGATCAGCAGATGAAGCTGTT
TP97177	TGCAGGTCCAGGGTGATGGAGTCCAGATTCATTGACGAACGGTCTGGGACGGAGGTGT[A/C]GGTTC
TP97227	TGCAGGTCCATCGTCCACGACGCAAACAAAAA[T/A]TTGTAAGGTCCCAGCTATAGATTATAGATAT
TP97249	TGCAGGTCCATGTGTCATGGGTGTAGA[C/G]TAGGTCCACCGAAATTCCATTCGGGCGAGAGCGAGA
TP97265	TGCAGGTCCCAAGAACTGTGAAAGCTAGTATGGTGAGAGGCCGTTC[C/T]TTTGGGTCATCGAGTTT
TP97273	TGCAGGTCCCACATGCCCAG[A/C]GAGTAGCCCGCCGACATCAGCAGCTGCGCGGGGCCCCTGGGCG
TP97277	TGCAGGTCCC[A/G]CGGGTGGATGCTCTCGTCGGGCAGCGCCGCCCTCTCCATCTCCAACAGCTGTC
TP97282	TGCAGGTCCCACGTGAGGACGAGCGCCCCCAGCATCATGCAGG[C/T]GCGGCCAGAGTCCAGGAGCT
TP97286	TGCAGGTCCC[A/C]CTTGAGTCTCCAGTCTGCCCTGTCATGGCTGAGGAACACGCTGATGATGAAGG
TP97309	TGCAGGTCCCCGAGCTCTGCGTGGCGATGGACTACTCGGGCACCAAGGAGGGG[A/G]CCTGGTGGTC
TP97312	TGCAGGTCCCCGATCCAGAGGGTCCTGGCCTCGTCCCCCGCCCCGCCGCCCGACG[A/G]TGCCGAAA
TP97313	TGCAGGTCCCCGATCGCCTCCCGCG[G/T]GCTTTTTTTCTATGCCAGTGCTAAGCTGCTCATGGTGG
TP97327	TGCAGGTCCCGCTGCAATGGTCCATGGATATCGATCCAATCCAACACAACAG[C/T]GGCGTGGCGTG
TP97338	TGCAGGTCC[C/T]TAAAGCAGGCGAAGGCACAGCACGAGGCAACGGCGCTGACGCGAATGTACCAGA
TP97381	TGCAGGTCCGCCACGCAGATGTCCTGGAGCGGCGTCGGGTCCGACAGGGC[A/G]CCAGCGATGGCCG
TP97400	TGCAGGTCCGCTCTTGGCTGGCGTAGCAGGAGTCATTGCTGCTGGCATAGCACCAGAT[C/G]CCGCT
TP97402	TGCAGGTCCGCTTCGGAGGCCAACCCCCACCCCCGACGACGGAACGCAGAGACGACTTTT[C/G]GAG
TP97419	TGCAGGTCCGTTATTTTTTGGCGTTGCTTGCGGTCGGGCGGAGGAGGCAGT[C/G]TAAGGTCTGTCA
TP97421	TGCAGGT[C/T]CGTTCAATTTTCCTCCTTGCTGACCTCGTGCATTCAGTTTTATCTCCTTCGTTACT
TP97436	TGCAGGTCCTCAAGCTGTGGCAGAACAACTTCACAGGCGCCAT[C/G]CCCGCGGCGCTCGGCCGCTC
TP97444	TGCAGGTCCTCATCCTCACCCTCAACCGCCTCAACGGCACCATCCCCGA[C/T]GCCATCGGCCGCTG
TP97449	TGCAGGTCCTCCAAGTCGGGCCACTACTG[C/T]CACCCAGCGGCTTCGACGGTTGCATTACCAAAGG
TP97453	TGCAGGTCCTCCAGGCTCTCCCCCTTGCCGTTGTCCTGCGCGTGA[A/G]CCAAATGTGCACGTCGTC
TP97460	TGCAGGTCCTCCTACGCCGTCACCGACGCCGCCATCGCGCCG[C/T]CCCCGAAAAAAAAAAAAAAA

Table A2 (cont.)

TP97462	TGCAGGTCCTCCTCCCGCACCTCGCCGTTGGCGCCGCCG[A/C]CGACGCTGGACACCTCGTCCCGAA
TP97468	TGCAGGTCCTCGCGATCGGCCTGGGCGCGCTCTCGGAGGCGCGGCATCCAGACGT[A/G]TCGCACGA
TP97477	TGCAGGTCCTCGTACG[C/G]CCACCACGCCTCGTCCATGGATGCATCCTGCGCCTGCGCCTGCGCGG
TP97481	TGCAGGTCCTCGTGGATGCTCCGCGTTTTCACCGCGCG[C/T]CGCTTTTCCGCGCCGTCCTCGACCT
TP97484	TGCAGGTCCTCTCACCACCTCT[A/C]GTGCCCCTCCTACTACAGCCAATGCAATACTAGGATGATTT
TP97486	TGCAGGTCCTCTCCCATCCCGACGCCCAATGCCACGCCGCTCGC[C/G]ACGCCGCTCTCCGAGCTCG
TP97490	TGCAGGTCCTCTTAAGGTCCTCGAGGAAGCTGATAGCCCAATACCC[A/G]ACGTCGTGGGTGCTCAC
TP97501	TGCAGGTCCTGCACGATGCTCCAGGAGTC[A/G]TAGGGGTTCCGCGGGCACAACACGCAATGCACGT
TP97513	TGCAGGTCCTGGCTGCGCTCGCGCGTGTAGTCGTCGGTGGAGCGCGAAATCACCTTCACC[C/T]TCA
TP97539	TGCAGGTCCTTCAACTCCTTCAGGATCCTCTTCGACGCCATCGATCAAACCCTAAACAA[A/G]ATCC
TP97543	TGCAGGTCCTTCTCCTCGAGGAAGAGGGAGAAGCTCGGGGTGGGCACCTG[C/T]GGCCAGGAGCCGT
TP97546	TGCAGGTCCTTCTTCCTCAGGT[C/T]CTCCAGGCCCTTGGGCGTGTCGGACGGCAAGTAGGACTGCA
TP97558	TGCAGGTCCTTGCACACGACCACGCCCGACGGCGCGTGCGCCGCG[G/T]CCACGGCCGCGATGTTGT
TP97560	TGCAGGTCCTTGCCCTTGACAACAACAAGCTCGGTGGAGAGTTGCCAAGCTCCATTGGCC[A/G]CCT
TP97563	TGCAGGTCCTTGGGGTCCTTCCCATCGACAGTGCACCCAACGCTGACGCAGGTCCCCA[A/G]GATCT
TP97575	TGCAGGTCGAAGCGGGCGAGCCACGGGAGGTGGTCGGACCAGTTGAGCTG[C/G]CCGAGGAGGTCGT
TP97644	TGCAGGTCGACGTCGATCGCCGCAGTTGGAG[A/G]ACGAAACGAACGTGACCGACTCGTGGCGTCTG
TP97662	TGCAGGTCGAGCCT[A/G]GCGAGCACGGGGAAGAGGTCCGAGAGGTTGGGCTTGGTGACCTCCTCGA
TP97685	TGCAGGTCGATCACCACGCGCTC[C/T]TCCTCCGCCGAGAACTTGCAGCCCCTTCACACAGGAAACG
TP97702	TGCAGGTCGATCTTAGCCTGTAGGAGGATTTTCGTTGTACCACAGCGTGTACGGATCTTCC[A/T]AC
TP97713	TGCAGGTCGCAAAACATCCATAGCTTGCTCGATGGGCGGTCGCTGGATCGGGTCTCGATG[C/G]GCA
TP97716	TGCAGGTCGC[A/G]ACTACACGACAACAATGGAGTAGGACGGTGCGGCTCAAGGTGAGAATAGCCAG
TP97723	TGCAGGTCGCACGACCACGGCAGCGCGTACGGCGAGTCCCCGCGGCCGTAGCCGAAGTGG[A/C]CCG
TP97744	TGCAGGTCGCCAACTACTGCCGTGAGAGAATCCACAAGGTACTGGCAGAGGAGCTCA[C/G]CAAGGC
TP97781	TGCAGGTCGCCGCGGCCGCCGCGGCCGC[C/G]GACCCCGCCGAGCGGGAGACGCTGCTCCGCGTCAT
TP97785	TGCAGGTCGCCGTCCA[C/G]ATGGGATCCAGGCCCCGTCCAGAGCGGACCAGCGCTAGCTCTGCTGC
TP97790	TGCAGGTCGCCTACTGGAGGTATCTGTTTGCCCGTCGGTAAACCTGCAACGCC[A/C]GAGGATTTAA
TP97802	TGCAGGTCGCGACTACACGGCAACAATGGAGCAAGACGGCG[C/T]GGCTTGGTCAAGGGCAGGGCTC

Table A2 (cont.)

TP97803	TGCAGGTCGCGACTACACGGCAACAATGGAGCAGGACGGC[A/G]TGGCTCGGTCAGGGGCAGGGCTC
TP97813	TGCAGGTCGCGCAGCATGGCCCAGCACGTGTGCGTGCACGTCAAGG[A/T]GATCACGGAGGCCGCCG
TP97819	TGCAGGTCGCGCTGGACTACGCCTGCGGCTACGGCGCGGACTGCTC[C/G]GCGATCCAGCAGGGCGG
TP97829	TGCAGGTCGCGTATCGCCGATGAACCGTACCGTTGCACCTGTGGCCTGTTGGGGG[A/G]AATCCGTC
TP97836	TGCAGGTCGCGTGC[C/T]AGCTTCTTGGACGTCTGCGCCAGCGAGTCCCGCTCCTTGCTGAGCTTAA
TP97843	TGCAGGTCGCGTGGCGCTCTCCCTGCTTGCATGGCCGCCAGCTCCTCCTTGCTGTGCT[A/C]TGGTA
TP97853	TGCAGGTCGCTCCACTGGTCCCCGACGTTGCCGCGGATCCTGTAGCCTT[C/G]GTCCACGAGCTGCC
TP97854	TGCAGGTCGCTCGCGGCACGGTGTTCCTAGTCAATTTGCAAGGCA[C/T]TGCGTTTGCGTGCACATC
TP97856	TGCAGGTCGCT[C/T]GGCGCCTTTGGACGGAGACCAAGAACCTGGAGCATGTGAGGGAGAGCGCGTC
TP97864	TGCAGGTCGCTGGAGCCTCGTACGTCCTCTACAACTACATATACCTCGGCCACAGCGG[A/G]GCCTT
TP97874	TGCAGGTCGCTTTGGTGGGGTTGATTGGGGTGTGTGG[A/G]GATTGAGGGTCCGCGTTAATCGCCGT
TP97889	TGCAGGTCGGATTATTCAGACCCAGTCGTTGTCCCGTGCCGACCACAACCAGGCCATAG[C/T]CATG
TP97905	TGCAGGTCGGCCATGCCGCCGTCGTTCTCGTGCGGGAGCAGCAGG[A/T]TGTGTGGGGCCCGATTTG
TP97915	TGCAGGTCGG[C/T]GACGCCTTCGCTGTCGATCGACGCCAGGATCTCGTGGGGTAGCAGGGCGCCCG
TP97920	TGCAGGTCGGCGACGGTGGCGGAGGC[A/C]GAGTCTGGGACCGTGATGCGGTCCGTGCCGTCGCGGC
TP97946	TGCAGGTCGGGACAACTCATCGATCCGCGCCCCACCCATCTCCACCAATCTCCTTCCATCGT[A/G]T
TP97965	TGCAGGTCGGGGCGCTGCTCGACCTCGGGTCAACTGG[C/T]GGGAGGGAGTCACGGGCGTCCATGTC
TP97982	TGCAGGTCGGGTGCCCCACGAGGCGGCGGTG[A/G]CGGCGCGCGCGCATCACCACCACCAGCTGGTG
TP97983	TGCAGGTCGGGTGCCTCAGCCGCCGAGGACGACATTTGTCCTG[C/T]TCGTTTGACTTATAAGCTGT
TP97986	TGCAGGTCGGGTTCTACGAGCACTCGTGCCCGCAGGCCGAGGACATGGTGC[A/G]CAACGCCGTCCG
TP97989	TGCAGGTCGGT[C/G]AAGTCGCCACGGAAGGCCTTGAGCTCGTCGAGGACCAGCTGGATGTTAGGAT
TP97996	TGCAGGTCGGTGAGGTTCCCAA[A/G]GGACTGCGAGATATGCCCCTCAAGGCCCCTGTAAGGCAGCG
TP98004	TGCAGGTCGT[A/G]CCCTAGCCTCGCCTCCTCCCCGTTCCCGCTCCCAAATTTGTTGCGGCGGCGGG
TP98020	TGCAGGTCGTCAATGACACGACGAAACCTGCGCATCCAACTACGATGAAGGACGTCCTC[A/G]TTCT
TP98025	TGCAGGTCGTCCAG[C/T]AATCTCATCAGCATTCGATCGCTCCAGCTAGCTACACAAGCTAGCCTTG
TP98027	TGCAGGTCGTCCCAGTGGATGACCTTGGGCGCGTGGGC[C/G]CCCTCGACCTCGCTGGCCGAAAAAA
TP98033	TGCAGGTCGTCCCTGGTGATGAAGCCAGGACACTCCCAC[C/T]GCCACACCTGCGGGATCAGGCAGT
TP98057	TGCAGGT[C/T]GTCTCTGCCTTTGTAGTTTGTGCAGGTCGCTAGCCAGTCGTTCGGCGGCGTGACGG

Table A2 (cont.)

TP98064	TGCAGGTCGTGACTCTACCACAACGTGCCTGCGTCG[C/T]ACTATGCAGTAGCTGCTGCCGTACTGA
TP98076	TGCAGGTCGTGGCGGCGCTCATGGAGGATCCTGG[C/T]GGCGCCGAGCAGCATTGCGGTGTGCGCGT
TP98093	TGCAGGTCGTTGGCCCGCCTTGAGGTGC[A/G]GCGCTCGACGTTCCTGACGGAGAGGGGCTCCTCGC
TP98103	TGCAGGTCTAACAAGATCAGCCCCACCTGTCTTCTCTCTCATTGTACTAA[G/T]AATTCTCCCATGC
TP98112	TGCAGGTCTACAGCTGGGGCTGGGGAGACTTCGGGAGGCTGGG[G/T]CATGGCAACTCCAGCGACGT
TP98114	TGCAGGTCTACATCCATGCGGCGCTCGGTTCCGTCA[A/G]GAACGGATCGGACGTGCGCGGCTACTT
TP98123	TGCAGGTCTAGCAT[A/G]TATAGAGTATATATACATGTATATTTATTTGTAGTAAAGCAGAAAAACT
TP98134	TGCAGGTCTATACACCTTCGTTTGGCCCTTAGATTCAACTT[C/T]TGGGTCCATAATCTTTTTAAGT
TP98144	TGCAGGTCTCAGAAAACCGCATTCCGCAACCGT[A/G]CCGCCGCCAACGACAAGTGGGCGCGGTTCA
TP98147	TGCAGGTCTCAGTCGCTCG[G/T]ACTCGATGTCGTATCTCAGAACTCTGAAGCACTCGAGCCGCTCC
TP98148	TGCAGGTCTCATCAACATCTGCAAATCAGAACTATATA[C/T]ATACGTAAATGTTCTAGTATTTTAA
TP98160	TGCAGGTCTCCCTGTGTTGGGGTCTTGTTGTTCCTGCTCTATG[C/T]CCCGTGGCTTGATTTGGCCC
TP98163	TGCAGGTCTC[C/G]GATGTCTAACGCAGCCGCCACGTGCCCCGCAGACACTGAGACACAGTGTTGGT
TP98186	TGCAGGTCTCGGTTTCCCCGTGTTGCCCGACTTGA[C/T]GCCTCGCGGCGGCGACGGACCAGCCGTC
TP98196	TGCAGGTCTCTCGGTGTCGTCCTGGCCTCGT[C/T]TCGTCTCGTCATTTTCTAGCGCTTGATTTAGG
TP98203	TGCAGGTCTCTGCCC[A/G]TCCCCTGGTGCCTCGACGACCTCGCCTCCAGCGGCGGCGGCGTGTGGC
TP98207	TGCAGGTCTCTGTC[C/T]TCATCCTCTTCGTCCAGGTTGTCCCACCCAACCTCCACACTGCCACCCG
TP98209	TGCAGGTCTCTTCCCGTCGTGGCGTGTGGGCAAC[C/T]CGTTGGAAGTTGGAACGCCGAGAAAGCGC
TP98212	TGCAGGTCTCTTGAGGATAGCGGGTAAGCGGCGCTAAATCACTCGTTGCTTAGC[A/G]GATATCACG
TP98227	TGCAGGTCTGAATCACCTGCACAGCCTAGCGCCGCCGTTGATCCACAGG[A/G]ACTTCAAGACGAGC
TP98235	TGCAGGTCTGAGGGTCTGTGTACCATCCATGCATGTAATGTCAGCATGCA[A/T]GGGGACATGGGGT
TP98258	TGCAGGTCTG[C/G]CCCAGCCGTATCACACCTCCTATTCGCCGATGATTCTCTCATTTTGTGCAAAG
TP98262	TGCAGGT[C/T]TGCCTCTGCTGGCAGCCCCACGCATTCCGCGGCTCGGGCATCGTCGTCCTCTGGCC
TP98285	TGCAGGTCTGGCGATGTTCACGTGGCGTGGCCCGCCCGTGATACGAGTGACAC[G/T]ACCGCTTTTA
TP98291	TGCAGGT[C/T]TGGGAGCTGTTGCGGGTCGTGGTTCTTGAACCCCTACAGTGCGATCGATTCGATTG
TP98301	TGCAGGTCTGGTTGGGCG[C/T]GGGAGCCCGATTAGGTCTGCTTGATTAATCATGCGCGTCGACGTC
TP98343	TGCAGGTCTTCTCGCCGCCCTGGCGCAGGTGGACACGGGCGC[C/T]CACGGAACAGGGTTGGAGCCT
TP98348	TGCAGGTCTTCTTTTTAAGCATCATG[C/T]GTGCAGCGCACCAGACGTTCTTTGCCAACAGAGAGAC

Table A2 (cont.)

TP98423	TGCAGGTGAACCTCCCCACCACCAGCCATTGCGTCTCCGTCCCTGGAGAA[A/G]GACGTCCTCGTCC
TP98432	TGCAGGTGAACTCGTGGAGGT[C/T]GATGATGGAGCCCTTCTGGATGGAGCCGTTGTGGATGAGCAC
TP98437	TGCAGGTGAAGAAGTAGCCAGTCG[C/T]AGCAGTACAGCACGCACCTGAGCTGAGCTAGCTGAGCTG
TP98440	TGCAGGTGAAGATCAGCAGCATCGAGGC[A/G]AGCCCTGTGGCCATCTACTTCTCGGCCTCATGGTG
TP98442	TGCAGGTGAAGCACACAAATGAAGATGGCG[A/C]AGGGAGGAGCTACTGGGTGGACGTGGACATGAA
TP98446	TGCAGGTGAAGCAGGGATGGATCGGAGCACATGCATGGCTTCTA[A/G]CTCCTCTCATCCTTCCCTG
TP98452	TGCAGGTGAAGGAAGAGGGTGGGAGCTGTGACGGCCAGGTCAAGGGAGCTAGCTCGGA[G/T]GTCAA
TP98461	TGCAGGTGAAGGTGAATCTCAAGGTACTCCGTAGAATAGAAACA[G/T]AGAGGCTAAATGTGCGTGC
TP98464	TGCAGGTGAAGTGCAACTGGGTTTGAACCCTGTGCTGTTGG[A/G]CCCAGGTGTGGAAGCCCACAGG
TP98480	TGCAGGTGACAATTCGGATCACTTCCAGACTCCTCTTTCCTCTGCGACGG[C/T]CTTCTTGTTTCTG
TP98483	TGCAGGTGACACGACTGACGACGACTCAGGACGCCATCCACACGG[C/T]CGCCGCAATCACAAACAT
TP98493	TGCAGGTGACAG[C/T]GAGCTAGTGTGTGTGAGTAGAAGCAGCAAGCTGGAAAAAATGGCGCCTTGC
TP98505	TGCAGGTGACAGTGAGCTAGTGA[C/T]AGTGAGTAGAAGCAGCAAGCTGGAAAAAAAATGGCGCCTT
TP98508	TGCAGGTGACATCGTGCTAAGAGTTAGCTA[C/T]CCGAAGCGGTACCATATTTTCTTCTACTGCAAC
TP98514	TGCAGGTGACCAAGAGGGTCGAAACTGCTCAGACTGTCTGGAAG[A/G]GCTGGAACTGGAGATCAGA
TP98521	TGCAGGTGA[C/T]CATCAATCCCCCATTCGCTGCTTCTCGATCTAGATCTCGCCTCTCTCAATCCAT
TP98523	TGCAGGTGACCCACCCCCTTCTCCCTTTCCTTGG[C/T]GGTCTGGTCTGGTCCACTCCATCCGTCGG
TP98524	TGCAGGTGACCCACTTCA[A/G]GTGCGGTGGCGTGGCTATCGGCGTTGGCATGCAGCACCACGTAGC
TP98529	TGCAGGTGACCGAACCTCGAGTGCGTGCTTGTAGCGACGGACGCGGCTGAGGTCGCGTG[A/C]GATG
TP98532	TGCAGGTGACCGCTACCAGCAGCGGCAGCGGCAAGA[A/C]GGTACGGTGGTGGCGTGCAAGAGCGTG
TP98538	TGCAGGTGACGAACATCTTTCCAGCGGAGCTAATGAGAA[A/G]GACCTGTTGCCCACACACGACAAG
TP98540	TGCAGGTGA[C/G]GAGTTGTTCTGTACATGAGTTTGTTGTGAACTGTGCTGGAGCCTGCTGGGATCA
TP98553	TGCAGGTGACGCTGACTTCTTCCTCAGAGCCCCAATATCCCACACACGTACGGTCTGATCCA[A/G]T
TP98561	TGCAGGTGACGGTCGGTCAAGCGCCATCGCCAAGCCAATCTCGAGTGCGAGTGGGTGGGTCG[A/G]C
TP98563	TGCAGGTGACGGTGTTCGAGGGCAC[C/T]TTCGGGTACGTGCCGCCCGAGTACACGACGCACGGCGT
TP98581	TGCAG[G/T]TGACTCGGTCGGCCCATCAGTTCAGTTCAGTCCATGTGGACATGCATGCCCGTCCGCG
TP98587	TGCAGGTGACTGACGTG[A/G]GTTGTCGGGTAGCGGGGTAGCAGCGGCCTTCCAGACGCCACCAAGA
TP98597	TGCAGGTG[A/C]GACCATGCAGGATCCATGAGAGGCTCGTCCTCCTCCAGATCAACCCCTTCAATGG

Table A2 (cont.)

TP98620	TGCAGGTGAGCATGTTACTA[A/G]CTTCTGATGGGGTTAGGAACTGACCAGACTAGCCACCAGCTGA
TP98623	TGCAGGTGAGCCATGCCCGTCAGG[C/T]GCAGGGGAGGGAGCAGCAGGGGGTTGGAATATTTTGGTG
TP98641	TGCAGGTGAGCTAGATGAGCTGGCTAGAGAGTAGA[G/T]ACGACCATTTCCGTCCTGCAAGTCTCGG
TP98653	TGCAGGTGAGCTTCGGCTTCCTTCCTTCCTTCCTCGTCGCCCCAAAACCAA[A/G]CTCCAGCTACCC
TP98677	TGCAGGTGAGGGCATG[C/T]AAACCGAAGCTACCTAGCGTCAATTGCGGTTATGGTCACGCTGTTGG
TP98701	TGCAGGTGAGTCCCGA[A/G]GATGAAACCTCTCATCTCTCACTCACTTCCGTGTCATTCGAGCGCTT
TP98716	TGCAGGTGATACTGACACGCGGTTCGGACTTCACTCGGTGTGGTGG[C/T]TCTTGCCGATCGTGGGC
TP98717	TGCAGGTGATACTTACACCAA[C/T]GCATCTTATGATTGTGATGGAGTTTGCAGCAGGTGGAGAGCT
TP98718	TGCAGGTGATAG[A/G]TACTGACACGCGGTTCGGAGTTCACTCGGTGTGGTGGCTCTTGCCGATCGT
TP98741	TGCAGGTGATCGGCGAGGCCAAC[G/T]CCAGCGCCTACGTCGACGGCGTCCAGGTGGGATGCTTCGT
TP98754	TGCAGGTGATGAGCGGCCTTGTGCGGCGCGGCGGCCTG[C/G]GTGGACAGGGACGACACCAGGAGCT
TP98776	TGCAGGTGATGGTCATGACTAGAGTGACGAGAAGGCTGCTCGCAAAGCTCCCAGC[C/T]GACATGGA
TP98782	TGCAGGTGATGTGGAATGCGGGAGTGTGGAATCGAGCTCGAGCTTCCCTCGGCGC[A/G]AGTCGGCG
TP98794	TGCAGGTG[A/G]TTGCAACCATGGCAAATCCTATGTGTACATGCTAGTTATTTAGACTGTCATGTTT
TP98801	TGCAGGTGATTTGGGCACAGCGCAACTGTAGA[T/C]CGCCCGATACATCCCTCCTCGTACAATTTTG
TP98829	TGCAGGTGCAAGGAACACACGATTTCAGTTTCGTTGTTCCGAAC[C/G]CGAAAACGAGCCATTGCAG
TP98831	TGCAGGTGCAAGTACATTCCTGTTGAGATCGCCACAAGC[A/G]CCCAATGTTGAGCCCATATTCTTT
TP98841	TGCAGGTGCACACCAAACACACGACGACGCTGAGCGAATCTTCAGGGAGCGACGAACGCACGA[C/G]
TP98848	TGCAGGTGCACATGTTACTGTTTGAATGTTCTCGCTCATTGATTTTGTCGCGTTGTT[A/G]GCGCGC
TP98854	TGCAGGTGCACCAGCTCGTGCCCGATGCCTGTCGGGAGGTA[C/T]GCCAGGGCGTTGTAGCTCGCGT
TP98857	TGCAGGTGCACCATCGGCAGAGGAGCCGATGGAGCTCACGGAGGAGGTGCTGGTGC[C/T]TGTTCCC
TP98864	TGCAGGTGCACCGCGGCACCTACGCCGTGGTGGT[A/G]AGCACGGAGAACATCACCCAGAACTGGTA
TP98888	TGCAGGTGCACTCACTCACTTTACTCACTGC[C/T]GCACCAGTGTTAAAACAGACCGAACTGACTGA
TP98902	TGCAGGTGCAGACGCCCAGACA[C/G]AGCCACTGGTCTCTGCCTCTGCATTGCACACACATGGCAGG
TP98910	TGCAGGTGCAGAGCTGCATGAGAGGTGTGAGAGGATTGAATGAAAATCCTTGGGCACCA[G/T]GCTC
TP98914	TGCAGGTGCAGAGGTACGACAAGATGCAGATGCCTACAG[C/T]GGCCATGCGGGGGGCGATTGAGGA
TP98920	TGCAGGTGCAGCA[A/G]CAGCATCGAGATAGATAACAAGCCTACCATGGAACACCATTGGTCCAGCA
TP98941	TGCAGGTGCAGCCGTGCAGGGATTCGCCCCTCGGAAA[A/G]CTTTTTGCTCCCTTCCCCCGACCAAT

Table A2 (cont.)

TP98945	TGCAGGTGCAGCGCAGAGTAGTACTAATAGGAGGGTGGGTGTCAGTGGAATCCAGG[A/G]CGTGACA
TP98946	TGCAGGTGCAGCGCGATGTTCAGAAAACAGAACCACCTTACTATCTGG[C/T]GTTAATTTATAGCAC
TP98958	TGCAGGTGCAGCTGC[C/T]CTTCCTCCTCCTCCCTTTAGTTAGTTAGTTTCTGCCTTCCAATCCAAC
TP98960	TGCAGGTGCAGCTGCCTCCACAGGCTACTGGTCGCTCGCGATCGG[C/T]GCAATGCGTGCAGCCATG
TP98967	TGCAG[G/T]TGCAGGAAAAATGTCAGGTGGAGGCGACGAGCTGAAGCTTCTGAGCACATGGTTCAGC
TP98976	TGCAGGTGCAGGATCC[A/G]CCCGCCGCGGTCGCCTGTGCGCTGCTCGCCTCGGCCGCTCCTTGCCC
TP98997	TGCAGGTGCAGGGAATGGGAATA[C/G]ACGATTTCAGTTTCGTTGTTTCGAACCCGAAAACGAGCCA
TP99005	TGCAGGTGCAGGGTCCTGACGTCAGGTCGATCCTGTCGCGTAGCGGCGCA[C/G]GGACAGCAATGCC
TP99012	TGCAGGTGCAGGTAAAGAACAATTTGTACAGAGTGCCTTCCATGCAGAATTGCTTGGC[C/T]GCTTG
TP99019	TGCAGGTGCAGGTGAACGCTTGTCGCTGTGAGGCCGCGCGCGGGCAGGTCG[C/G]CCCGTGCACCAA
TP99026	TGCAGGTGCAGGTGGGGTGTGTGCTGGGTTGGTGGGCCGAGGCTGATGGCG[C/T]CCCGTTGGTGTA
TP99046	TGCAGGTGCAGTGGGTCGGTGAGACAAGCGTGTTCACATCATCAGTGGCATGGG[A/T]TCAGCGCGA
TP99072	TGCAGGTGCATCGCACGGCGA[C/T]GCGCAGCGCCTGCACCATCTCCTCCTTGTAGGGGCTCCACGC
TP99073	TGCAGGTGCATCGCATGTGTCTACGGGCCGAAGGGTGGTGCAT[C/G]CGATGGGGCCGTGGACCAAA
TP99074	TGCAGGTGCATCTAGCGCTAGCTAGAACGACGTCGGCGGTGGCCGCGT[C/T]ACAGCCGCGTGCCCC
TP99076	TGCAGGTGCATCTTGCCCCTGGCAGCAAGTTTGATTTCCAGAAGTACATCAA[A/G]CGGTCACTGGA
TP99150	TGCAGGTGCCCGCC[C/G]AACGCCTCGGCAGGGGCCTGCTTCTCGTCGGCGATGCCGCCGCCGCCTC
TP99155	TGCAGGTGCCCTCGACGTCCTTGATGAGCTTGGAGACGAGCTTGTCGCGGAGGTGCGGC[C/T]CGAA
TP99172	TGCAGGTGCCGAGGTCGCCAGCGCCAACGGTGCCCGCGGCGGCGTGCAGGATGGACCGCAGCA[A/G]
TP99177	TGCAGGTGCCGCATGCTCGGTGGGAGTAGACGAGTACTAGTGGC[A/C]AGTGGGGCACAGGCAGCAG
TP99179	TGCAGGTGCCG[C/T]CACCTCGCAGAGGGGATCGCCGAGATCCACTCGATGGAGCCACGCCCAAGCC
TP99182	TGCAGGTGCCGCGGTACAAC[C/T]TCCGCGTCACCAGACTCACCTCCGCCTCCTTCCTTGCGGACTT
TP99189	TGCAGGTGCCGCTTCACGGCATTCCTCCTCTGTATTTGCCCCC[A/C]TCCTTCCATCGCGCTAGATC
TP99194	TGCAGGTGCCGTCGGCGATGCTCCTGACGCAGGCGAGGTTGAGGGGCATGCTCATGAC[C/G]CTGTG
TP99221	TGCAGGTGCCTGACGAGGACGTTGAC[A/G]GAGCCGTCGATCTTGATGACCATGTCGACGTCGACGC
TP99247	TGCAGGTGCGAGCAGCAGATGCCCTTGCGTTGCGATCACGTGGGGTCCACCGC[A/C]GTGGTCGCCG
TP99250	TGCAGGTGCGAGCTGTTACGATCTGCCACCTCCATCGTCACCGACCTCAAGATCGACG[A/G]CTACT
TP99289	TGCAGGTGCGCCC[G/T]CGCCATGGGGATGAGATCCGCACCATGGCTGTGTGGGTAACTCCACCAGC

Table A2 (cont.)

TP99291	TGCAGGTGCG[C/T]GACCTCCCCTGCCTCATTAGCAGCTCGGGTAGCAGCAGCTGCTTGCAGGTGGA
TP99306	TGCAGGTGCGCGTAGGCCTGGGCAAGCCTCGGCGCCGCCTCTCGCCGCC[A/G]AGTACCCACCATGG
TP99316	TGCAGGTGCGCTCGGCCACGGCCACG[C/G]CCACCCCGCCTCGTGCCTTCTTCGTCTTCGGCGACTC
TP99324	TGCAGGTGCGGACTCCATGGAGAACGACGTGAAGGAGGCGAGGCAGGGGCA[G/T]CACCAGCTCAGG
TP99329	TGCAGGTGCGGAGGTCGCCAGCGGCGCCGCCGTGGGCAGCGTGCAGGATGGGCCGC[A/C]GCAGCAG
TP99345	TGCAGGTG[C/G]GGCGAGCGCCAGGAGGACGGCGGCGGCGAAGCAGGCAGCGAGGAGGGAAGTGGCG
TP99367	TGCAGGTGCGGGCACTGCGTGCAGATCGTTCTCCTGCCGCCTGCCGTGCCCTGGAGGCTGGG[A/C]C
TP99370	TGCAGGTGCGGGCGTTTGGCAGCCACCCTGTTCACTTAATCGAATTATCCAT[A/G]CTTATCAGCTA
TP99385	TGCAGGTGCGGTGCTCCCTGATGTTGAGGTC[A/G]CTGTCGCAGCGCTGTGGAGGGCGGCGCACTGG
TP99419	TGCAGGTGCGTGCTCATGGCCGCCTAATCTCCATGGACGAATCGATCTCCCCTCCTCCCC[A/G]TCC
TP99461	TGCAGGTGCT[C/G]ATCACCAACGTGGCGGCGGACGGCGAGGTGGCGGCCGTGAAGGTGAAGGGGTC
TP99464	TGCAGGTGCTCCAAGAAGAAGGCC[C/G]TCTACTACTGTCGTCCATCAGAGCCAGGCTCAGCATGTT
TP99468	TGCAGGTGCTCCACCACTACCTCGCCCACAGCCAC[A/G]GTATATATACCTTCTCAACCCGCTGACC
TP99479	TGCAGGTGCTCCCCTTCATCAGG[A/C]GCATGCTCATGGAGGACACGGACGACAGCATCTTGTACCA
TP99488	TGCAGGTGCTCCTTGATGATGCCGTC[A/G]AGGATCCCGAACACCGTGTCGCGGCACTCCTCCGCGC
TP99491	TGCAGGTGCTCGACGAAATGCCGA[A/G]CCTATGCCTCGCGCCAGAGAGGGACGCGTACCGCGCGAT
TP99504	TGCAGGTGCTCGCCTGCTTCTACAACCACTGGCAACGACGGCCGA[A/T]CGCCACCATCACGGCGCG
TP99509	TGCAGGTGCTCGCGTCGAGCATGGCGTACGCGCCGCTGGCCAGCAAGAAGGACGACCCCGTAT[A/C]
TP99522	TGCAGGTGCTCTC[C/G]GCGTTGGCCTGCGTCGCGCTCTCGCTGATGCGCCTCTGGAAGCACGACTT
TP99525	TGCAGGTGCTCTCGGCGTTGGCCTGCGTCGTGCTCTCGCTGATGCGCCTCTAGAAGCACGA[A/C]TT
TP99526	TGCAGGTGCTCTGCATGGCCCCA[A/G]CGGCGTCTGCGTCTAGTGCTGTAGGTGCTCTGGAGGCCGA
TP99536	TGCAGGTGCTCTTTCAAATAGACCAGAGGATC[T/C]GCGTCTTGCTCCAGAAGCTTGCCATAGTCAT
TP99537	TGCAGGTGCTGAAAATACAGCACGTTCATTGGGTCCTCAAAATGCACCTATG[A/T]TTGCTCCAACC
TP99538	TGCAGGTGCTGACAGCGAGACAATTCATCGAACCCTTAGTGGGCATCGT[A/C]GCCAAGGATGTTAC
TP99545	TGCAGGTG[C/T]TGCACCCATCATTCCCGAGCACGTACAACAGGTGCTGCGCCAAGTTGGTCGCAAC
TP99553	TGCAGGTGCTGCGACGGTACAACGACGAGCTGGAGAGGTTCCTCCGCTCCGTCGTC[C/T]CACGCCA
TP99555	TGCAGGTGCTGCGAGTTGTGAGTCCGTCTGCGTCTGATGAAACGAGGTGGGAGGC[A/G]AGGCGGTT
TP99592	TGCAGGTGCTGTCGCCGCT[C/G]GTGCCGATCCGTGAGGTGCTCTTCCTTCGGTTCTGCAAGCAGCA

Table A2 (cont.)

TP99594	TGCAGGTGCTGTCTGCTGTGGGACTCTGCGGTCATGCGTGCCGATCTCATCTGC[C/T]TCTGCCTGC
TP99603	TGCAGGTGCTGTGGGCGCCCATCCTCTTGATGCACCTTGGCGGGCAGGATGGCATTACTGCC[A/T]A
TP99605	TGCAGGTGCTGTGTGCTGGGTTGGTGGGCCGAG[C/G]GTGATGGCGTCCCGTCCCGTTGGTGTAACA
TP99638	TGCAGGTGCTTGTGG[C/T]CTGAGCTTCCTTCAGTTCTGCAACCTGAACAGCTTCAGGACCAAGTTC
TP99641	TGCAGGTGCTTTCCTCTGAGATCG[A/G]CGTCAGCTGGATGTCATCATCTATAGATATTATATATAC
TP99655	TGCAGGTGGAACGAGTTCCGT[C/T]GGCATGGGGCGCAGGCGGGGTGTAGCAGGTTACCGAGCTCTG
TP99661	TGCAGGTGGA[A/G]CTAGGATTGAACTGCAACGGATGGGTGGCGGAACATGCAAAAGGATGGAATTG
TP99665	TGCAGGTGGAAGAACTTTGTATTGGCATCCCCTTCAGCAAGGAACAGCAGCCGTGAGCGC[A/T]ACC
TP99669	TGCAGGTGGAAGCC[A/G]TGATCAGCACAAGGAAGAACTGAAGACTAGTGCCGCCGCGGATTGGTAT
TP99682	TGCAGGTGGACCCAAGCCAACGG[A/G]CCCACCAGGCAGAGAGACGCTCCCCCACCTGTGCTGCCTG
TP99687	TGCAGGTGGACCTCATGGCCGACCCAGAGTCGGGCATGGTGGACAATG[C/T]CGTATACACCCTCCA
TP99692	TGCAGGTGGACGAGGC[C/T]GTAAGGAGGAGATGGTGGCCGTGGCCACGCAGGTGCTCCTCCAACAC
TP99698	TGCAGGTGGACGGCTAACCTGATGCACAAGCACGGACGCAATGTAAGCAAGT[C/T]GCGAAAAGCGA
TP99704	TGCAGGTGGACTATGCGGGGGCGGTGTCC[A/G]TCGCCGCCTGCGGCCGCGACGGCGTGCAGTGGTC
TP99705	TGCAGGTGGA[C/T]TCCCTTTCTCCTCACTTTCCAATTCCTTCAGTTCTTCATTCACTCTGGTTTTG
TP99712	TGCAGGTGGACTTGGTGGGCGGGTACTACGACGCGGGCGACCACGTCAAGTTCGGCCT[A/G]CCCAT
TP99717	TGCAGGTGGAGACAGCACTTGCTCTAGGTGCGAC[C/G]CCACGCGATGCGACGCTCCAGCAGATGAG
TP99723	TGCAGGTGGAGATCGAGGAGCTTGCC[A/G]CGCAGGACAACAGCAACAGCAGCAGGGCCTCTTCGGC
TP99728	TGCAGGTGG[A/G]GCAGCGACCCGTGCGGCTCGCACTCGTCCGTGAGGTCCGAGCGGACGCATGCCA
TP99729	TGCAGGTGGAGCATCTGCAAGAGCATGAGCTTGGAACCGAGATCGTGGGGCACGC[A/G]ACCCTGGA
TP99742	TGCAGGTGGAGCTCGCTGATGAGACAACGGCCATCGGCAGCTGCCCTGGCTTC[A/G]TCGCCTCGAT
TP99748	TGCAGGTGGAGGAAGGGTGCGGCCTGGCGACGGCGGA[A/C]GACATCGCCGCCGCCGTGCACCACGT
TP99754	TGCAGGTGGAGGACTTCTCGCCGCAGTGGTGGGACCTCAT[A/C]ACCACCACCGCCTGGTTCCGCGA
TP99761	TGCAGGTGGAGGCGGAGGCGTTGGAC[C/T]CGCGGCGACGCCATGGACGCCCCATCGCGGTCGTGGA
TP99766	TGCAGGTGGAGGCTTACACTGCAATTTCACACACAGGCAC[A/C]GCACCGTTCGTTCATCTCCCTCG
TP99776	TGCAGGTGGAGTCATGGAGTATGGAGTTGCAGGGATAGCGGAGTTTCTTGTTTG[C/T]GATGGGTCT
TP99789	TGCAGGTGGATCACT[A/G]AAAGGGCGCGTTTGGTTACCTGTTTCTCCGCGGCCGTGGCCGCTCGGA
TP99812	TGCAGGTGGATGTGGATCCAAGGAACAAGAGCGCGATCGGGGTG[A/G]CCCTGAACCTCAGCATGAG

Table A2 (cont.)

TP99814	TGCAGGTGGATTAACAACACGATGA[C/G]TCGCCAGCGTTGGTCATTAACCTCACCTCGCTCAGATC
TP99824	TGCAGGTGGCAAGTTTCAGAAGAG[C/G]CGCCTGTGTTCCTGTGTAATTTTTCTTCGGAGTTCTTCA
TP99833	TGCAGGTGGCACGCACGAGTGGTCAGCGATC[A/G]ACGATCGAGCTCGAGAATGATGGATCTATCCG
TP99836	TGCAGGTGGCA[C/T]GTCAGTCAGCCCTCGGAGTACTCGTAAATTGCACCAGTATGATTGAAGCCGC
TP99844	TGCAGGTGGCAGCAGTGGCCGTTCTATGTGTGCAACCAGAACCAAGTTACAGAC[A/C]GCTGATTAC
TP99845	TGCAGGTGGCAGCCACTTAAAACATGGATCTTCATGAAAA[C/T]TGAATCGCCACAAATTTATACCA
TP99866	TGCAGGTGG[C/T]CAAGATGATGCGCCGTGTTGCACAGTCCTTTTGCTTCACTTCTCCCCATGAAGA
TP99872	TGCAGGTGGCCAGGAAGCACCAGAAGAGCACGCGCAAGTGGACCTGCATCGCCATCCTCAT[C/T]CT
TP99902	TGCAGGTGGCCGCCTCCGCGTGGTCCGTGCGCAACGGGCT[C/T]GCCGTGCCCATGGTCAACAGCAC
TP99954	TGCAGGTGGCGCCTGCGGGTTCAAGAACGTG[A/G]ACCTGCCGCCGTTCTCCGCGATGACATCGTGC
TP99961	TGCAGGTGGCGCTCAACCACAGCAAA[C/T]TCATCGACCGCCAGCTCAGGTCGCTCTATGCCGCGCA
TP99974	TGCAGGTGGCGGCCATGGTGACCGTGACCGCGACGGCGTCGATGCTGTC[A/G]ATGGGTGCGCAGTG
TP99997	TGCAGGTGGCGTGCTAATGCATGCATGGCGTGCATGGT[C/T]GTTGGTGACCGTACGTACGTCGTCG
TP100008	TGCAGGTGGCTCACACATGCCGCAGCAACCACCACTGCCGCTTTCTCATCCCCC[A/G]CCCACCACC
TP100012	TGCAGGTGGCTCTAACAATCTGCAAGAC[C/T]ACCATCGTTTGTGACATGGACTCTCGGTCATGACG
TP100017	TGCAGGTGG[C/T]TGACGCCGAGGTAGTGCCCGTACGGCTCCGTGATGCCCACCGCCGCCGAAAAAA
TP100041	TGCAGGTGGGAAAAAA[A/C]TTCGGATCTGTTATAGTTCTATGATTTCTGCATTTGGCATGCATGGC
TP100044	TGCAGGTGGGAAGGAAGAGAAGAAGCATGGGCCGCTGGATGTCAGTGTCATG[A/G]ACGATGATGAA
TP100049	TGCAGGTGGGACCAGAGAAGCTCA[C/T]CCGTGGCGTCGCCATCACGGTTTACGGTTGGTTCAGGAT
TP100070	TGCAGGTGGG[A/C]GTGGACCTGCTGCGCGCGGGCGCGCAGGCGCTGGACGTCGTGGAGGCCGTGGT
TP100078	TGCAGGTGGGCAGCA[C/G]CATGAAGCAGCCCATGTTCACCTGCAAGTTCGGATGCCGCAGCAACAG
TP100098	TGCAGGTGGGCCCTGCTTGCCACGTATCACCAGTTTCCTTGC[A/C]AGGAAAGTAAGGAAACTGCGT
TP100100	TGCAGGTGGGCCGCGTGGGGTTGGATGGCGCCG[C/T]GGCCCGTGCGATCTGGAACGGGCGGACACG
TP100117	TGCAGGTGGG[C/T]GTGCCGTGCAGCAGCTTGTTCCAGACGGTCACCGTGCGGTGCGGCCACTGCTC
TP100121	TGCAGGTGGGCTCACTCTGCT[A/C]CTGTTCATCTTCGTGCTGACGCCACTGACACTGAGGCTTGGG
TP100123	TGCAGGTGGGCTGCTGGC[G/T]GCGCCATTGTGTGCCGCCCACGCGGTGGGCTGTTCTGTTCATCAC
TP100139	TGCAGGTGGGGAGCGGAAAAAACCCTCCGCGC[G/A]ACCGCGCCAATCTGGCCGTCCACACCCTCCA
TP100152	TGCAGGTGGGGCCC[C/T]GCGAGGAGATGCCTTCGATGGCTGGTGCACGTGGACTTGGCACGGAGCG

Table A2 (cont.)

TP100158	TGCAGGTGGGGCCT[G/T]TAGGTCGACGGCTACCTCCCACGGTGGAAGGCCGCATCGCGATGGGCCC
TP100159	TGCAGGTGGGGCCTGT[A/T]GGTCGAGGGCTCTCTCCCACGGTGGAAGGCCGCATCGGGATGGGCCT
TP100162	TGCAGGTGGGGGACCGAAACAC[A/G]GGTTGCTTCCATGCCAAAGCACGACAAAGGGCGCGTACAAA
TP100186	TGCAGGTGGGTAGTATTCCTG[A/G]TCGCCTATGTCGTCGACGAAGCTGTTGAGCGCCCAGCTCGCG
TP100208	TGCAGGTGGGTTGGACGGCAGCTATGCTGCTGGGGCTCGCA[A/G]GGCAGTGGAGCAAGGAGGTTGC
TP100213	TGCAGGTGGTACAGCCTCTCTCGCTGGCGGACCACCTGTAGAAGTGCGTTCTCCAT[C/G]TGCTCAC
TP100214	TGCAGGTGGTAC[A/T]TGGCAGGCATCGTCACCGCTGAAATCTATGCCAGGAACGGCAGATTCTTCC
TP100217	TGCAGGTGGTAGCAACCAGGCATGGGA[A/G]CGCCTAATGAGGAGGTCCAGGTCGTCCAGGTCCAGC
TP100219	TGCAGGTGGTAGCAGCAGCAACCGCGCC[A/G]CTAGCACCAGCCCTGCCCCCTCCAACAACGGGGGC
TP100247	TGCAGGTGGT[C/G]GCAGTTTACTGTGACCTGGTGGAGGAAGATGAGGGGCCCAGAGTACGACGGCA
TP100252	TGCAGGTGGTCGGCCAGGAGAAGCGCGAGGC[C/T]GAGGCGATGAAGCTTCTCGAGGAGCAGCAGAT
TP100259	TGCAGGTGGTCTCCGTCTCCCTTGGCACGGCGTGCGTGCAGGAGTTGGCCCTCGG[C/T]TGCCGCCA
TP100260	TGCAGGTGGTCTCTGGTCGCT[G/T]ACATGAAGAATGGCCGCTTGGGAAGCTCTTGTGCCCTTCTTT
TP100262	TGCAGGTGGTCTTGCCGACGCCGCCCTTGCCGCCGAC[A/G]AAGACCCACTTGAGGGACTCCTGGTC
TP100278	TGCAGGTGGTGCAGGCTTAGAGGCGGTGGCGAATCAAGAGCAGAGAGCTGCGG[C/T]GTGCGAGTTG
TP100282	TGCAGGTGGTGCCGAGCTCGCAGAGCAGGC[A/G]GCCGCTGATGTTGTCGCAGTTGAGGAGGAGGAG
TP100284	TGCAGGTGGTGCCGTGGGGGCATATGGAGCA[C/G]CCGTCCATGGTGTTCTACGGCGGGCCGAAAAA
TP100294	TGCAGGTGGTGCTCGTTCACCTCTGTGC[C/T]GATCTCCTCCCCTGCTCGCCGCGTGCCATCCTTGT
TP100297	TGCAGGTGGTGCTGGGTGGAGCAGCGGTTGGGTTGCAGCTCGAGTAGCAGTTCACCGCTACGA[C/T]
TP100301	TGCAGGTGGTGGACGTGCTCGGCCTCG[A/G]CCCGCGGGAGAGGCGCGCTCTCCTGGAGCGCCTCGT
TP100312	TGCAGGTGGTGGCGCCTGCGG[C/G]TACGGCGACCTGGACATCTTCAGGTACGGCCGCTACACGACG
TP100325	TGCAGGTGGTGGTCGGCGTGGCGTGTGGCGTGCCGTGG[C/T]AAGGAGGCGATGGCGAGCGCAGAGA
TP100335	TGCAGGTGGTGGTGCTGGACCTGCTGGTGCGGT[A/G]GCTGCGGCACTTGGAAGTGCGGCTGCGGTC
TP100338	TGCAGGTGGTGGTGGTGCTTCTTGGAAATGGGCTTCTGGAGCTTGAACCGC[A/G]CGGAGTCCAGGG
TP100364	TGCAGGTGGTTGTCCTCGAACGGGACCTTGCCCGTCAGCAGCTC[A/G]AAGCAGATCATCGCGAAGC
TP100386	TGCAGGTGTAATAAGTGCCGCCGCGGAACGAGACGAGAGC[C/G]CCGTCGGCGTCAGGCATTTGCTT
TP100389	TGCAGGTGTACAACGCCCACACGACACGTAAAAACACATCAGCAACGTTTGATG[G/T]GTGCCCCAA
TP100481	TGCAGGTGTAGACAACCCCGACCTATTTTAGCTTAAGATATATAACTTCTCACCCA[A/G]TCCGAGA

Table A2 (cont.)

TP100494	TGCAGGTGTAGGC[C/T]AAAGCAAAAGCATCATAGCATGCATCGATCAGAACGTCTGATATGTGTGT
TP100502	TGCAGGTGTAGTGGTGCGGAGCACAGAGAAGAATAATTTTACATGGTA[C/T]TGTTGTATACAGTAC
TP100538	TGCAGGTGTATGTGTACACCAGAACCACGATGATCTTCACAGCTCGCTGTTACCGCT[A/G]CCTCAG
TP100562	TGCAGGTGTCCAACGCCTGGAGGCGTTCCTGATGCTGCACGACAGGATCGTGAAGCACCT[C/G]GGG
TP100589	TGCAGGTGTCGCGCACGAGGCGGCTGCGCAACTCCTCCGCGAGGTCATCTTCAAGG[A/G]GAGTCTC
TP100603	TGCAGGTGTCGTCGGCGACCGCGGAG[G/T]GCGGGAATGAGCGGAGCACGGAGGTCGGGGACGCCGC
TP100613	TGCAGGTGTCTCCATAGGAGCAGGACTAGGACGCA[G/T]CACTGCGGCTTACCACGGAGTGTCCAGC
TP100622	TGCAGGTGTCTGGGCCCGCCCCCGCCGCCGAGGC[A/G]CGCGGCGAGGATAGCACGCGCCGCCCGAT
TP100627	TGCAGGTGTCTT[C/T]AAAATCTAGATCCATACAACCTATCTGACCAGGATCTCAATCAGTGTAGTT
TP100637	TGCAGGTGTGAATGGATTTGTTTCTCGTTGGGACTTGTTAGGGAGATTGATCCAAATTAG[A/G]TAA
TP100711	TGCAGGT[G/T]TGCCCCTCGCCGCCCTTTCACATCCAGCCAGCCGCCTGACTCCAGGCGCGGCGGAC
TP100718	TGCAGGTGTGCCTGTTCCCGCAGGCGTGCAGCGTGCTAC[A/T]ACCTTTGCTGCCTGCCTTTTTTCC
TP100777	TGCAGGTGTGGTGGTGTTGCCGTGTCGTCCTCGCGGCCTTATTTGTAGTGCGTGTGG[C/G]TGGTGG
TP100781	TGCAGGTGTGGTTCTGGAGATGATCAAGG[A/G]TGTGGAGACCGCAGTCTCGGGCCGCAAGGGCAGG
TP100798	TGCAGGTGTGTATATC[A/C]CAAATCATGCCAGAAACTGACAGCACAACAAGATTCATCAGGCACAC
TP100805	TGCAGGTGTGTGGACAATGGCGGAGCAAAGCAATGGACGGGGAGCCATGC[A/G]TTGGAAGGAGATC
TP100816	TGCAGGTGTGTTGGCCGCTGATCCCCATA[G/T]GCTGGGACTTGCAGCACGACTTGTAGCTACGGCC
TP100826	TGCAGGTGTTACAGAACATCTCC[A/C]CTGACTGAGAAGCAAAGGTTTCTGATTGCATCGCAGTCGC
TP100828	TGCAGGTGTTAGCGTGTCGTAGTCTAGCACGTCGGCCTTGAACAGATGCAGATTCTCAGGG[G/T]CC
TP100829	TGCAGGTGTTAGCGTGTCGTAGTCTAGCATTTTCGGCCTTGAACAGATGCAGATTCT[C/T]TGGGGC
TP100839	TGCAGGTGTTCACCAGCTCACGCAGTTGGTGCTCTGCTCTTTTATCGCTGCTC[C/T]GCCACTGCCG
TP100846	TGCAGGTGTTCAGCGCGCCGACGTA[A/C]GCGCCCGAGAGAGCACACACCGCGTCGCCGCGAGCAGC
TP100850	TGCAGGTGTTCATCGCGCTGCTCTGCGCCATGAAGTACGC[C/T]GTCTTCCTGTTCTACGCCGCGTG
TP100860	TGCAGGTGTTCCAGGTGTCGGCGCCGCTGCTGTGGACTTCG[A/C]GTACCCGTCGCGGCCGAACGTC
TP100873	TGCAGGTGTTCGTCTCCATCGCGCTGATCCTGGG[C/T]GACGGCCTGTACAACTTCCTCAAGGTTAT
TP100878	TGCAGGTGTTCTTCCCAG[C/G]CAGCCCCCGATTTCACCGATTTCAGCACGGCACCAGTCTCATCTC
TP100880	TGCAGGTGTTGAGAACAACCAGACACTGGCTCACAACAATCTGTAGGGCACGTCCCGCAAC[C/T]CT
TP100881	TGCAGGTGTTGAGGTCCACAACAAAATGATGCCTGGTTCTCGAGCACAC[A/C]AGAGCCATCCTATT

Table A2 (cont.)

TP100886	TGCAGGTGTTGATGAGCCCTTTGTAAGTTGC[C/T]CGCCTGCTGTTTTGCTGCTTGCCACCATGGCA
TP100897	TGCAGGTGTTGGCGTACCTCCTCATGTCGGCG[G/T]CGTCGGCGGCCGCGTCCCGCCACCACCTGTG
TP100908	TGCAGGTGTTGTGGATGGTTGGTGGCTGGATTGGGCTC[A/G]TTCTTCAACCGATGACGGTGGTCGT
TP100928	TGCAGGTGTTTTGGACGATTGGTGGCT[A/G]GATCAAGCTCGTCCCTCCCTCGACGGCAGCGGTCGT
TP100945	TGCAGGTTAAAGG[C/T]GGCATACGTGCTGAATCAGGTGCTGATAACAGTGCCGAACAACAGAGCAA
TP100946	TGCAGGTTAAAGGTGGCGTACGTGC[G/T]GAATCAGGTGCTGATAACAGTGCTGAACAACAGAGCAA
TP100949	TGCAGGTTAAATCTAAAATAATTGTAAGGGGCTTTTTG[A/G]AAAAACGACGGCGTAGGGGTATCTT
TP100958	TGCAGGTTAACCATCTTCGATTCGCAGACGGCAGGCCAAAGAGGAGCTGCTAGTCCAC[G/T]TTGAG
TP100964	TGCAGGTTA[A/T]GATAGGATAGCACAGCAAAACTGAGCGTGGATGGATGCGAAACGAACCTCCACG
TP101005	TGCAGGTTAATTT[C/T]ATCGCCGTGCATTGTGTGGTGTGATGCTGGCCACGGCAGCAGAAACGACA
TP101052	TGCAGGTTACTGGCAGTTTGCCAGATGACAGTTACAGACAGCAAATGGAAGGAAAACAAATG[A/T]T
TP101093	TGCAGGTTAGCTATATATACTCCCT[C/T]CGTTCTAAAATACAAGTCATTTCAAGAATCTTGATATC
TP101101	TGCAGGTTAGGACTTAGAAAAACTCAGGGTCTCTTAAGCAAAA[C/T]TGCCACGCGAAGGGGTATCA
TP101108	TGCAGGTTAGGACTTAGAAAAGTCCAGGGGCTCTT[A/T]TGCAAAATCACCCGCGAAGGGGTATCTT
TP101119	TGCAGGTT[A/G]GGCAGCGTGCCGAAGCTGCTCGGGATGGGCCCCGTGAGCGAGTTGAGCGACAGGT
TP101142	TGCAGGTTAGTTGGCTAGTTGATCCCA[A/G]CACGTCCTGCACGGGGGTGTCGGGGTGATCGATCAA
TP101162	TGCAGGTTATATTTGGCC[A/G]AACTCGGGGGTCTCTTTAGCAAAACTGCCACGCGAAGGGGTATCG
TP101192	TGCAGGTTATTTATTGC[G/T]CGCACTGTTCCTCTTCTGTTCTACGCTCATTCCCTGTTTATATCCC
TP101209	TGCAG[G/T]TTCAAAGTTAGATACAACTAACAAATGTTTAAAACATTAATGAATATATAAATATTCT
TP101214	TGCAGGTTCAACACCTC[A/G]AGATCCTTCAGCCTGCCAATTTCAGGCGGAGCACTCCCCTGTAGAC
TP101218	TGCAGGTTCAACCCCGTGGTAAGACAAAGCAACCACAACGTACTTGGAT[C/T]CTGAGCTAGGTGAT
TP101221	TGCAGGTTCAAGACAAATGGATCGTTACGTTCAGCACCTCTGTGATGTAATGG[C/T]AGATGTGGTT
TP101223	TGCAGGTTCAAGCCCTCCAAACGCTCCTCCAGAGTTGGTTCGGGAGCACCATC[A/G]TCCAGGCCCT
TP101255	TGCAGGTTCACGACGTGCCCCCTGACCTCCCCGCGCAGCA[C/G]CGCGCCTCCCTCTACGCCTCTGG
TP101260	TGCAGGTTCACGTTCTTGAACAGGAGCCGCAGCCCT[C/T]GCCGTCCCTGAACAGGGGCTTGTTACC
TP101268	TGCAGGTTCAGAATAGTGAATCTTTAAGATTTTGTCTCCACTTACAG[C/T]TTTATCTTCAGGACTT
TP101272	TGCAGGTTCAGCAAAAAAATTTAAACATATCCTGATTATCAAACAGTATA[A/G]CACACTGTAAAAA
TP101285	TGCAGGTTCAGCGGTGCAGCAT[C/T]GGATCGCGATCGCCGAGCGAGACGCCTCTTGCTGCGTCGTT

Table A2 (cont.)

TP101302	TGCAGGTTCAGTTGCCCGACGCT[C/T]GCCAGTTGCCACCGTTGGAAGCATACCAAGCGCTCCATGC
TP101304	TGCAGGTTCAGTTTGCTGAACCGCAGGTGACCTTCTTCGGACTACTTATGACTCCTCAATGTA[A/G]
TP101312	TGCAGGTTCATCATACCCCGACGGATGC[A/G]AGGATATCGATGGACATGGATTCGTGCTGGACTGC
TP101321	TGCAGGTTCATGCATATGGCACCGCC[A/G]CAGCCGCAAACCATTAACAGGCCAAAGATATTTGGTC
TP101323	TGCAGGTTCATGCGGGATC[A/T]CCGCCCGCTGCGGTCTCTCGCGAGGGTCCCCAGACCGATCTCCG
TP101327	TGCAGGTTCATGGGGCATGAAGTC[G/T]AGAGCAGCAACGACAATACTGGCCCCCAGCTACACGGGG
TP101331	TGCAGGTT[C/T]ATGTTGCTATTTATCCCGCTAGTTTGCATGCGGCTGTGATTCGGCATGCTCAGCT
TP101332	TGCAGGTTCATTTACAGATTT[G/T]AGCTTCTTTCCAGCAGAGCGAGCTGTCATGGTTTGCGGCCCT
TP101355	TGCAGGTTCCAGGTCATTTTTAAGTTTAATTTGCCACGCCCACGAGAACGCTCAT[C/T]TTTATTCC
TP101359	TGCAGGTTCCATAGCACGTCCTCCACCGAGGGCCGCTGCGACGCCTCCTTGGCCA[A/G]GCACCTCT
TP101376	TGCAGGTTCCCACGCGCCACACGCATATGGGGCCGAGGCCGACGATTTTGGCAATTGAAAAAA[A/G]
TP101383	TGCAGGTTCCCCAGCAAGCCGCGGTTCTTTTGGCT[G/T]CGCTCTTGGCCGTCAGCTTCGGCGCCAC
TP101384	TGCAGGTTCCCCAGGTTATTCTTGGCCGTC[A/G]TTTTTGGAGAGATCGCGACCACACGGTGCCTCA
TP101391	TGCAGGTTCCCGAGAA[C/T]CCTGTCGGTGGACTTGGACGGCGATCACGCCGCCGCTGGTGCGGACG
TP101395	TGCAGGTTCCCGTCGCGTTGCCGCACCTGCAAGACTGAGGGGCACAGGGCTCGTCATTGCC[C/T]TC
TP101409	TGCAGGTTCCGATCGGCAGTGCACACAGTGACACAGGCCATGGCGAATGACGAG[G/T]CCTCCTTGT
TP101421	TGCAGGTTCCGTCCTCCTCGCCGTCGTCGGTGC[C/T]GTTCGCCGTGGGTTCGAACGATAGGTTGAA
TP101436	TGCAGGTTCCTCCTTGGGAG[C/T]GTGACGACGTTGGCGGCGGGCGAGGATGTAAACGAGCGCGGCG
TP101437	TGCAGGTTCCTCTCAAACTCCTTCAGGTAATCCAGGAGCAAGACGATCACAAAGAGGAT[A/G]AACC
TP101439	TGCAGGTTCCTCTTCAGCAGGTAGTCATAGATATACACGTCGAGCCTGC[A/G]CCACAAGCAACGGA
TP101443	TGCAGGTTCCTGCGCTGCCTC[A/G]GTGCCTCTACCTGGAAAGGGAGGAGGGGAGCGTCAGCATCGC
TP101446	TGCAGGTTCCTGGTGGAGGAATCGGGGTTTGATGTCAA[C/T]TCCGACTCCGAATCAGGTGCGTGTG
TP101484	TGCAGGTTCGCAAGTTCCGCGGTGGTGGCCTAGTGGTATTTGGCGGGCGACTTGG[A/C]CAACGCCA
TP101495	TGCAGGTTCGCCATCGCCAAGTCTGCTGGCGGCATTGCCTCCT[G/T]CTGCTGCTGCTCCGCCGTGG
TP101499	TGCAGGTTCGCCCAGGCGTTTCACGCAAAGCGACTTGGGACT[C/T]GCGGGCGAGACGCCGAGGAGT
TP101501	TGCAGGTTCGCCCGCGATTCTCCTTCTCCCGCACCATGAGTTCTCCTCCG[C/T]TCTGAATGTGCGA
TP101521	TGCAGGTTCGGGCGCACGGGCGTGTACCGAGGCTTCATGTTCAGCAGCCCGACGATCCTGGT[A/G]A
TP101541	TGCAGGTTCGTCGTCCGAGAG[C/G]GGTAGCAGGTAGCGGCGCACCTTGCGGCGAGACGGAGTGCGA

Table A2 (cont.)

TP101571	TGCAGGTTCTAGCCCAAAATCAAGCA[A/G]TGAGTAAACTGTATGAATGCATTCTGCACAAACTCAA
TP101572	TGCAGGTTCT[A/G]GGAATGCGACTGCAATAATCCATCCATCCGCATACTCAGTACCGAAGGCGAGC
TP101578	TGCAGGTTCTATAATGGCACAGCTCAGGGGCCTAATAGCAAAACAGCAGGGCGACAGCG[A/G]CTGA
TP101623	TGCAGGTTCTCGAACCTCACCTCGATCGTCGGCAAGTCCAGCCCAACCCTGCACGCGC[A/G]CGCAC
TP101629	TGCAGGTTCTCGGCCCAGGGCGAGAGTCCCTCGCAGGTCTTGAGCACCACGA[C/T]GGAGTCCCGCC
TP101630	TGCAGGTTCTCGGTGAAAGGCCCAAGGGCTTGGCTTGTGCTCATGATGTGAAGCCGTGATC[A/G]TG
TP101634	TGCAGGTTCTCGTCTGAGGGGCTCGTGTGTATCTTCCTTGGTAATGGTAAGACGCAGGG[A/C]CCGC
TP101657	TGCAGGTTCTGGAGTTTTGGTT[A/G]TCTACGTGATGGGCCTTGGGACAGGCCTAGTGCCATGCGGT
TP101663	TGCAGGTTCTGGTC[A/G]CGCTGGAACCCCTTGCCGCACACCTCGCACACGTAGCGGTTCGTCGCCA
TP101666	TGCAGGTTCTGGTGGATCTCCTCG[A/G]TCTTGGCAGCGCGCTTCCGTGCGGAGACGCGCGTGGGCG
TP101676	TGCAGGTTCTTAGGCTC[C/T]GTGTTTGGGGCGTTAGATGGGGGATGGCCAACATATATATAAATAG
TP101697	TGCAGGTTCTTCTTCGACTT[C/T]TCGGCGACGTACGTGGGCGTCGGGATGATCTGCCCTTACCTCG
TP101700	TGCAGGTTCTTGAAGGCAAGCCATACAATAGAAAGTGTGATGT[A/C]TACAGTTTTGGCATATGCTT
TP101701	TGCAGGTTCTTGCAATTAAATTGACACTTGCAAGAACACGTACATGCAGGTTATTGCTTTGCT[A/T]
TP101702	TGCAGGTTCTTGCTGGGCGTT[A/C]TCTGCCGTTGCGGCCATCGAGGGCATCAACCAGATCAAGAAC
TP101706	TGCAGGTTCTTGTAGTAGTGGTTGTCCA[C/G]CTTGAGCGCGCTCCACTGGTCGTCCAGGAACACGA
TP101722	TGCAGGTTGAAAGATAATTGCGCTG[C/T]TGAAAGAGAAGCCCACCAGAAATAGCTACTAGAGAAAA
TP101723	TGCAGGTTGAACACGCCCGTGATCTCGGCGGTCTCGGCGACAACG[C/G]TCCTCATCTCCTCGGTGG
TP101732	TGCAGGTTG[A/C]AGTTATGAGCTCACTTCCTGCTCTGCTGCTGCACCTGGTGCTGCTGCTTGTGCA
TP101770	TGCAGGTTGACTCCCTCTCCTTATCAACGCAACCGCGACGGCGACGCGACTCACGCGAGTTGC[A/G]
TP101771	TGCAGGTTGACTCTCCAGTTATTATCATCACAAAATACTGCCACAG[C/T]TCGGTAACGACAGGACA
TP101788	TGCAGGTTGAGCTCGGAGCTGGCTGCCGAACGAACGTGCGGTGAGCCCC[A/G]CCCGCCGCTGTTCC
TP101837	TGCAGGTTGCAAATATTTTGTCC[A/T]CGCGACGCGAGAGATGGTGAAGAAGAAGCTCATTCTCACC
TP101856	TGCAGGTTGCAGAATGCATCCACCATGTCGATGCAGTTCA[A/G]CGCAGTCGGTCTAGGAGCCGCCT
TP101859	TGCAGGTTGCAGATCCCGAGCAGCTGCTGCTCCGTCAGCGGGTCCAGCTGCGG[C/T]ATCAGGATCT
TP101871	TGCAGGTTGCAGGATCA[C/T]CAGAGATGAACATGGTTGTAACCGTGTGCGCGGGACATGGTTTTGT
TP101879	TGCAGGTTGC[A/G]GTCTCCCTTGGGGATCCCCAGCTCCTGAGCACGCGCCGCCGCGAGTTGGCCTG
TP101892	TGCAGGTTGCCAACCCGAAAGTTGTTTCGTATACCATCATCACATCATTAGTCAG[C/T]TGATTAGT

Table A2 (cont.)

TP101894	TGCAGGTTGCCACAGACATGTGCCTGGAACTGGAAC[G/T]GTCGCTGTTGGTGCGGGGAATTGGTCA
TP101906	TGCAGGTTGCCCATGACTGACGAATGAGCTCGCGGCTACCACCAAGGCTCCACGAGATCTCT[A/G]G
TP101919	TGCAGGTTGCCGCGACACCAGAAACCGACGGCGGTGGCAG[C/T]GGTGGCGATCTAGAAGAAGGGGC
TP101926	TGCAGGTTGCCTGTCGTTCTTCTGCCCGTGTATCCCGTTCGGACAGGTGGCAGAGGTC[A/T]TAGAC
TP101941	TGCAGGTTG[C/T]GTCAATGTCAACTTTGGAAGAGCGCGATCAAGTTGTGGATCCTGTCATTATTGG
TP101970	TGCAGGTTGCTTTTGCTTAGCGAGGGGGGAG[G/T]AGAGGACGGGGCGGCGGGGGATTACGTGAAGG
TP101979	TGCAGGTTGGA[C/T]ACCTGGCCACCCACGTAGGTGTCCTCTGGTGCCAACACCAGGTTGTGCGTCT
TP101995	TGCAGGTTGGCAAAGACTCCTGCAAAGGAGTCGATGGTTTCACATGACAAAAGCTGCAC[G/T]CAGC
TP102006	TGCAGGTTGGCCATCACCACGGCCCTCCGTGCCGCCTCCTCC[A/G]TCGCACACGCCACCGCGCTCC
TP102012	TGCAGGTTGGCCGTCTATCCTCT[A/T]CTCTATGCATGCATGCATGCATGAATATCGATCCGATCCG
TP102018	TGCAGGTTGGCGAG[C/G]ACGGGGCGGAGCGGCGCGAAGGGCACCTTGCGCACCAGCGACGCGTCCG
TP102025	TGCAGGTTGG[C/T]GGCAGCGGAGTCTTGGTAACAAAGCTGACCTACATATTCGATGAGGAGACGCC
TP102028	TGCAGGTTGG[C/T]GTGCGACGACCCGCCCACCAGCGCGGCCGCCGCCGCCTTGGCTGCCAGCGCGC
TP102035	TGCAGGTTGG[C/T]TGCGAGCCTGATGCAGTGGCATGCGGGACCCTCTTGTGTGCATATGCTAGGTG
TP102040	TGCAGGTTGGGATGGAAACATCAGGTC[A/T]TTCCAGAATTATGGTTTACCTATGCAAGTGTGACAT
TP102044	TGCAGGTTGGGCAACATCAGGGAGTCATCAAACAAACAC[A/G]AGAGAACAAATGCTGCGACGCGGC
TP102047	TGCAGGTTGGGCGAAAGCAGGAAGCAAGCAGCAGAGCTGCAT[A/C]GCTGAACAGTACTAAAAACTC
TP102058	TGCAGGTTGGGGCAGCTCGCGTCGTAGAACGTCGGCGACAGCTGCGCCATGGCGCCGAGCG[A/C]CA
TP102059	TGCAGGTTGGGGCAGGAGGACGCATAGAACGTGGTCGAGAGCTGTGCTTGG[A/G]CGGCACAGGAGA
TP102069	TGCAGGTTGGGTGGGGTAGTCATCTTCTCGCTAGTCTGTCTGCCGTC[C/T]AGCAACGTTTGTGAAC
TP102080	TGCAGGTTGGTCAGGCCGTCCAGCTCCGCGCCCACCAACAGAG[C/T]GTAGTACACCATCTCCGCCG
TP102088	TGCAGGTTGGTGACGACCTTGAGCGGGCAGAGCGG[A/C]GTGTCGATCATGTTGAGGCAGAAGCCGT
TP102089	TGCAGGTTGGTGACGACCTTGAGCGGGCAGAGCGG[G/T]GTGTCGAGCATGTTGAGGCAGAAGCCGT
TP102091	TGCAGGTTGGTGCCGTAC[C/T]GCACCAGCTCCGCGGCGTCGCCCGAAAAAAAAAAAAAAAAAAAAA
TP102101	TGCAGGTTGGTGGGTGAAAACGCCTCTATGCCCTCGGC[A/C]GTTCAGGCTTCCTCGTGCAGCGACA
TP102136	TGCAGGTTGTCAGTTGACAAATC[A/G]AAGAACCGCTGCAAGTCTCGGACGATGCTAGGGAGAACCG
TP102148	TGCAGGTTGTCTAACGCAGTCAAGAGCAGGCGCGCCCACCTGGGCACCGCCGCTGCCG[C/T]ATCCT
TP102190	TGCAGGTTGTTCAAAACACGGGCAATGTGTTTGGTTCACAGTACTGAATTT[G/T]AACTATTTCCTA

Table A2 (cont.)

TP102211	TGCAGGTTGTT[G/T]GCCTCCTTGGCAACGACGACATAAGTTTTGGCTAGATAAATCTGGTCCATGA
TP102222	TGCAGGTTTAAATCATTT[G/T]CGTTTGCGATACAGAAGACGGAACCAAACAGCTCGGTATATACAC
TP102230	TGCAGGTTT[A/C]AGAACGGCATCGCGCGGCCCTTCATGCCCTGGAGGTTCCCGTTTATCTCTGGTA
TP102238	TGCAGGTTTACACTTGATGGT[A/G]TTCGTAATGGGGACAGACAGGGTTAGGCCAAAGTTAGCCTGC
TP102241	TGCAGGTTTACCAGCAGCTA[C/T]CACCGTGAGGCGATGAACCAGAGGTTGAAGATAGCAGAAGCGG
TP102250	TGCAGGTTTACTGATTGGCTGGTGGTCTGATC[T/A]TGATGCTACGAGAGGAGCCGTGCAACTCCAG
TP102258	TGCAGGTTTAGCTGTCACTGTTCTTGTG[C/T]TGTCCCTCATCCACATATCTGGCTGCCACCTGAAC
TP102263	TGCAGGTTTAGGTGCTGCAACTGATCGGCTATGC[A/G]CTGACTGAGGAAAGATGAAGTACTGCCTG
TP102264	TGCAGGTTTAGTGGAACGTCTAGAAGGAGCGCGGTGATACCGTGACAGATTT[C/T]CAGTGCGCAGG
TP102269	TGCAGGTTTAGTTTGTATTGCAATTTTTTTCGAGAACACGTTCGTTGACGTGTTTTTCAT[C/T]AAG
TP102280	TGCAGGTTTATTCAGTCAAGGTTGCAGCGATGACAGGGGA[C/T]TTTCAGTGGCCGCTAGACGTGTT
TP102291	TGCAGGTTTCAACGTGGAGAAAGTTAATGTGGCCTTCACGGTGTGGG[A/G]CGTTGGAGGGCAGGAC
TP102300	TGCAGGTTTCACTGCCTGGCCGTGCTCGCTCGCTGCGGAGG[C/T]GGAGCGGAAGCAAAGCACACGC
TP102306	TGCAGGTTTCAGCAAGAAACCAGAGCCTGCCTCTCTTTGATGCAAA[A/G]CTAGAGCTGTGAATGCA
TP102314	TGCAGGTTTCAGTTAACAATCTCAGCGGAGCCATCCCTGCATCTCTCTCTAACATCACAGC[C/G]CT
TP102319	TGCAGGTTTCATCAGCTTGGACTGCGGGGGAGCTCGCGATC[A/G]CACGGATGCCATCGGGATCCAG
TP102398	TGCAGGTTTCTGTTCAAGCCAATCAGCGCCTGTGCTTTCCATCCGACGGCGCAGCACCACCT[C/T]C
TP102404	TGCAGGTTTCTT[G/T]CGGTAAGAACGCGCGCGCGCGCAGTGGCGGTGCAGTCAAAACGTAATTAAC
TP102410	TGCAGGTTTGA[A/G]CCACAACCCACGGCCAATAGTGATATATCAATGGTCAGTTAAGAAAATGCAA
TP102427	TGCAGGTTTGATTCAGCT[A/G]TTGCACTGGCTGAGAAGGCTAAGCTTATTGATCGTGTGAGCTCAG
TP102437	TGCAGGTTTGCATCACATAACAAATGTAACACCTGCTCGACCATCCGAGGGTCC[A/T]CTGATGACT
TP102458	TGCAGGTTTGCTGG[G/T]AGGGCACTTGACAGGGAGAGACTATTCAATTTGGGGAAATCATTTGCGT
TP102460	TGCAGGTTTGCTTTCTCGG[C/T]GATACTGTGCAGGCATGTCCTTAGTGTGTTCCTCTTGGCTGGTG
TP102468	TGCAGGTTTGGCAGG[A/C]GTTGTGCTGCGCGATGGAGCAGTGGATCGGTAGAGCTAGGCGGCAATG
TP102473	TGCAGGTTTGGCTCAGGAG[C/T]GGTGGGGCCAGCAGGGTCATGTTCCTCGCCACCTTCTTTCTTTG
TP102509	TGCAGGTTTGTGCATGCCGACGTGGGAAAGATCGCGGATCCCGTACGACGTTTTGACC[A/T]CTGCG
TP102510	TGCAGGTTTGTGCGAGCGTTTC[A/G]TCTGATTCAGCAAACATGAACGAGCTTCTTCAATGGAATGA
TP102515	TGCAGGTTTGTT[A/C]CTCCCATGCCACTGTTTCCTGAAGTTGGGACTCGGAGCCCACTGCGTTGAG

Table A2 (cont.)

TP102517	TGCAGGTTTGTTCATACGATTTCCACGCTCA[C/T]CCCCGTGGGTATCGGAGAGATACTTGTGGCAG
TP102534	TGCAGGTTTTACGTTACAGCGCACGCCGCACTTTCTCACCTGGGTGCTCCCACACAGGAGTC[A/G]C
TP102567	TGCAGGTTTTCGCAGCAGCAACAAGACAAGACAGACGACGATCTCAGCTGATGAACTTGGTA[C/T]G
TP102568	TGCAGGTTTTCGCAGTGCGGCAGTGGTCCTTTCACTG[C/T]TCGGGTGCGGAAGCGTCACGCGCTCG
TP102580	TGCAGGTTTTGATCCTCACGAATTAGAACCACT[A/G]CTCCAAAATTGGTCGGTGGATGGACAGCAC
TP102590	TGCAGGTTTTGGCAGCCACTCCGTTCTGCCACTCGGCTCCAAACCAAA[C/T]GGGAAAAGGGGCACT
TP102596	TGCAGGTTTTGGGAACTAATCGTGAAGGGCGCGAGGCCGAGGTCGGTGG[A/C]GGCGTCGGAGAAGA
TP102598	TGCAGGTTTTGTGCCAGGATATTTCAGGCAAGATGGTTCACTTGCAAAGTTCCGCTTGCGTGA[A/T]
TP102602	TGCAGGTTTTGTGGTCTACTTCTTCGACAAGATCTGTGCCAGGTAAATTAAACGCAGTGT[A/T]TGT
TP102668	TGCAGTAAAACAGCCGAGTGCCAGTGCACTGTAGCGGTGCAGTTGTAGCTACAG[A/C]CTAGTACAG
TP102678	TGCAGTAAAACTATATTATTACACATATAAAGGGTCATATATTCTAATAATGTTTT[C/T]TCATATC
TP102681	TGCAGTAAAAGAATGAACAAAGCAGAG[A/G]AGAGATCCACACCGACACCGCGCCATCGTCCGCGCC
TP102696	TGCAGTAAAAGTGGCACAGCACATTCCG[A/C]AGGCTCACAATGTCCAGGAACCCGTACCGCAGCAC
TP102697	TGCAGTAAAAGTGGGCATTGAAAATGGATATAATCACTGACAATTTGCAAACCAG[C/T]GGTGAAAA
TP102739	TGCAGTAAACACGGGTGACGTTGGGCTTGCATGCTGGGTGGGATTCGAAGCGTTTGC[A/G]TGCAAA
TP102810	TGCAGTAAAGACTGCAAAAAA[C/T]AGTGCTACCCTAGCACAAGTTCTCACTGAAACTCAAGCGTCT
TP102831	TGCAGTAAAGCAGGTG[A/G]AGAATCGAACGCCGAAAATGAAGCTAGCGACAAGACCACCATGATGG
TP102848	TGCAGTAAAGGCCAGGTTGCTGAGTAGTGACCCCCTGTCTGGACAGCAGCTCTCG[C/T]GCTTTGAG
TP102872	TGCAGTAAATAAATAAAATTAAATC[C/T]GACAAGAACCTGCATCTGATGATCTGTACGTGATGTCT
TP102893	TGCAGTAAATCATTGTGCTACATTCATATTAACTA[A/T]CAGATCAGACCTATTTCAAAAGTTTATT
TP102898	TGCAGTAAATCTGCAAATGACCCTCTCTGTCCACTCTAAATTTGTCTCTGACTTAT[A/C]AGAATTT
TP102949	TGCAGTAACAAGATCACAGAACAAATCGCAACCAACCCATTTCTCAT[G/T]GACAAAAACAGAGCAG
TP102950	TGCAGTAACAAGGCTCATGG[C/G]GACTCGTGCAAACTGCGCCGCTTTGGGCGCTGCTCCGCTGCGG
TP102962	TGCAGTAACACGATGATGCCATGTATATTAGCCAGCAAA[A/G]TATGACGATCACAGAACGGGAGGT
TP102972	TGCAGTAACAGAACCACGCCGAGGAAAAC[A/G]GCATCAGAAACCAAAACAAGTGGCCGAGTCTGTG
TP102978	TGCAGTAAC[A/C]GCTGAATTAGATGAGACAGCATTCAGAATCACGCGTAAACTTATTCGATCACCG
TP102983	TGCAGTAACAGTAAGCAGAAAAGGGGAGCAAGAATATC[A/G]AACCAGTAACAGGAACCTCCACGCT
TP102988	TGCAGTAACAGTGCCAGCCGAA[C/T]TCCCAATTCCAAGTTGTGGTTTGTTGTCTAACAGAGATAAG

Table A2 (cont.)

TP103003	TGCAGTAACATTCA[C/G]AAAACAGAATTGTGCTTGTTCTTGGGCCTTGGCACTGGCAGGCTCAGAA
TP103008	TGCAGTAACATTTTAGCTCTTGCTGCTTCGGAGTTCTCATTTCCGCTGCAATG[C/T]TTCATCGAGA
TP103023	TGCAGTAACCACAGGACTCTCGCCCACCAGCTCGCGCACCGCCTGGAAGTACACACAC[A/G]CGCCG
TP103032	TGCAGTAACC[A/G]TCAGCTAACTGATACGTATTGCTCTCGTCGTCAGTTCCGTTTCTATCTGTCTC
TP103042	TGCAGTAACCC[A/T]CTGCCTAGAGCCTAGCATTTTCTAGGCGTTAGCATATACACACATATATGTT
TP103071	TGCAGTAACCTCTCCCTGTCCTAACCTCTGTAGTGTAGACGACGACCTCCGTGGC[C/T]CCATTCCG
TP103093	TGCAGTAACGCAAAGACAGGACTACCAACAAACTCATATTTTCTCTTTGG[A/C]ACTCACGAGTTCA
TP103112	TGCAGTAACGGGATGGGAGCCTGAACCCCGCTGGAGCTGGATGCATCGAGC[A/C]TCGCCGTCGATC
TP103235	TGCAGTAAGCCCAGCATTCGAACGATCTGCGGTTTCCATGCGCCTCCGCCCTC[C/T]GCCGCCCCTG
TP103237	TGCAGTAAGCCGACCCTCCCTTCCCTCTCTCACTG[C/T]GTGTTCCATCTCCTGATCCTCATACCTC
TP103262	TGCAGTAAGCTTGGTAATCATGTCCTTCAAAACAGACGGGCAG[C/T]TTGTGCTCAGATGCTCGAGG
TP103297	TGCAGTAAGGGTACTTACGCTGAGCTGCTCGCC[A/G]CGCCCGACGACGTCGTAGAAGAATGAGTAG
TP103305	TGCAGTAAGGTAGG[C/T]TCTGATGAAATAAAACAACCAAACACAACGGTTGCATGCTCAGCCTGTC
TP103369	TGCAGTAATAATCGAGTGCTA[G/T]GCGTCTGGTCTGGGACGAGGTGGTGGTGGTGAATCGAATGAA
TP103383	TGCAGTAATAGAGAACTGTAGAGTGTCTTTGCCTGCAATC[A/T]GCATAACTAATTTGAAATGTTTC
TP103388	TGCAGTAAT[A/G]GCGATCCACACAAAAGCTACTCAGCTAGCAAGCAGTACTACATTCCAAACTACT
TP103441	TGCAGTAATCCC[C/T]AGGCATTCCCAAAAGCATGAGCCAACACTCATCATTGAACTCAGCCCGCCT
TP103452	TGCAGT[A/G]ATCGGCATGCAGGAGCTGGCCAGAGGATTCATGAACCCGCCGTCGGACTGGAGAGGT
TP103461	TGCAGTAATCGTTTTCCCTCCAAAAAGGCAGATGGACTTCAGCACA[C/T]GCATTGATGCATACCGT
TP103484	TGCAGTAATGCAATCTATCTTGTGTATTCATCGTTC[A/G]GTTGATTTGCCTGATCCAGGAAGATGA
TP103488	TGCAGTAATGCACTTTGAGGGTTTCGAGGGAGGC[A/G]AGCTCGAGGAGGGACCCAGGGAGAGTCGG
TP103493	TGCAGTAATGCTATTACGTTAATAAGGAGTACTGAT[A/G]TGATCCAAGTGCAGCACTAGTTGAGCA
TP103509	TGCAGTAATGGCGAATCCAAA[A/G]CAGGTAGGGTTTGCAAGGGGAGGGAGGATAATGAAGGAGGTG
TP103511	TGCAGTAATGGCTACGCACCTTCCCA[A/G]GCTGGCCTCGACAAGTGAGAACATGCCAGTGCCACGC
TP103539	TGCAGTAATTAAG[A/C]ACAGGAGCGCGTGTCAGTCGGCGTCGGCGGCGAAGCGAGGGATGGCCGAT
TP103551	TGCAGTAATTCCAACGAGCATATGTGATAT[G/T]TGTGTGTCGTCTACCTGGTTCACGTGTTTTTTC
TP103554	TGCAGTAATTCCGATAACCTC[A/G]GAGGCTCGTTTCGCAAATCCTCCACCACAAAGCCCTGGGGCG
TP103557	TGCAGTAATTCTTGGGGATGCTCCAGATCTTCCTGTCGGGTCTGT[C/T]ATTCAGTTGTGTATGGTT

Table A2 (cont.)

TP103560	TGCAGTAATTGCTGCCTCCCTGCCTGTAGCGGCAGCCGCGGAGGCGAGCGCCGCTCC[C/T]ACCGTG
TP103563	TGCAGTAATTGGGAGCTGGTTCAAGGACTTCAATTCCTCAAGCAAAGGGACCTCCCCTTC[A/G]TTG
TP103574	TGCAGTAATTTCT[A/T]TTGACATCGAGACAGGGAACCTGTACCAAACTGGAAATCCAGAAAGAAGG
TP103575	TGCAGTAATTTCTTCAAGCTACGGGCAGTATCTGTATCTCCTCTCCAATTTAATAA[C/T]TGTAATT
TP103580	TGCAGTAATTTGTTCCCTATACATCCGTAATCTCGTCTCTAGACTACT[A/C]CTACTCCACGTTCAT
TP103596	TGCAGTACAAAACTGAGGTTGATGTTCTCTGTGCAGCGTATATCCAAACGAATTTCGAA[A/G]GAAT
TP103620	TGCAGTACAAATTAAAAAAAAGGGGGGGCAGGGGTTAGTTCGAATTGAAAATCGTATAATTC[C/T]G
TP103701	TGCAGTACA[A/G]TTTATAGATCGTTTTGTTCACAGGGGGGAAAAGATCCCGTGTCACTTTTGTTCT
TP103710	TGCAGTACACAACAGAGGTTGGTGTTCGCTGTGCAGTGCACATCCAAAGGAATTTT[C/G]AGAAGCC
TP103720	TGCAGTACACAGTGGCAATGATGGGTTA[C/T]GGCCCTGAAGACAAGAACGCGGTGCTGGAGCTGAC
TP103731	TGCAGTACACCACCCGATCGATCT[C/T]CAGCGCCCCCATCGGTCGCGTCGCATGGACACTAGCTGG
TP103735	TGCAGTACACCCAAGCAAATGATCGAGTTTTGATTTTTTATCAACCACCTGCGTCGTCATA[G/T]AT
TP103743	TGCAGT[A/G]CACCTCAATGCATGACCCGAGCGTTTCACACTCGTGCACCTCAGTCCTCAAGGCTCA
TP103747	TGCAGTACACGAGCATGCTG[G/T]ACGCGCAGGTGGACGCGGTGACCTTCGCGGCGGCGCGGCTGGG
TP103764	TGCAGTACACTGCATGCATTTGATTCTCATCAGTGACCAG[C/T]TGTCCAGTTAATGCGTTCCATCG
TP103781	TGCAGTACAGACGTACAGTATGCAAAACGGTCCGCACGGCGACAAATGAAGCTAAGTA[C/G]TTCGA
TP103788	TGCAGT[A/G]CAGAGACGACGCAAGCAAGCAGCAAGCTGGCTCCGTCGGTGGAGCCGATTCATACAT
TP103795	TGCAGTACAGAGTACGCCGCCGCCGCGCTGTGCTGTGCACCGCCGCCGCCGCCGC[A/T]CTCCGCAC
TP103797	TGCAGTACAGATCGAG[A/G]CTACTTGTTACATACTTGGGAGATCCCATGGCTCAGTCTTATTTAGG
TP103807	TGCAGTACAGCA[A/T]GGGCATATTACCATGTGTACTTCATGCATGCAGTAACACGCTGCATGCAGT
TP103824	TGCAGTACAGCGGGAGAG[C/G]GACAGGGGAGGCGGGGAGTCTCGCGCGTGTGAACTGTAAAAATAG
TP103853	TGCAGTACAGT[A/G]CATGTGTACCCGCGGCATGGCGACGCCTGCGCTCGCATTCGTTGCGCACCAC
TP103857	TGCAGTACAGTAGAGAAGCAAGCAAACAG[C/T]GGACGAAGTCTCCCAGAATTATGGCTGACTGCAA
TP103858	TGCAGTACAGTAGCATGCACCCGATCGATCTCCAGCGCCCCCATCGG[C/T]CGCGTCGCATGGACAC
TP103875	TGCAGTACATAAAGAATGATCTGAGGAAGGCCAGGAATGCGAAGAAGAATTCCCAT[C/T]GTGGCAT
TP103876	TGCAGTACATAAAGAGTGATCTGAGGAAGG[C/T]CAGGAACAAGAAGAAGAATTCCCATTGTGGCAT
TP103882	TGCAGTAC[A/G]TAGTGAACACATTTTCGATGAGGCATAGACTGACACGCATCACATGACGTGATCC
TP103896	TGCAGTACATCAACCCAACAGTCTCAACATAAATCTCCACATCCTCACAAT[C/G]AGGCACTTCTAT

Table A2 (cont.)

TP103909	TGCAGTACATCCACGAGCACACCTGGCC[C/G]CGCGTGGTGCACAAGGACATCAAGAGCAGCAACGT
TP103921	TGCAGTACATC[G/T]CGGAGCTGGAGCGCAGCGTCACGTCGCTTCAGGTGCGTGCAGCGTGTGTGCA
TP103972	TGCAGTACATTCACCATCTTGAATGCACCCGTCCCA[C/T]GAGCTTTTCATCGCGGCAAAGGTATCT
TP103991	TGCAGTACATTTTTCGC[G/T]CTCGCTTGGCCTGCGCCCCTCCTTCACCACACTCGTCGGATATCCT
TP103998	TGCAGTACC[A/T]ACAAACCAGGCTGACTTCCTACTTTCGTAGCTGCTGCGGCTAATTGCTCCCCTG
TP104038	TGCAGTACCACTCGATCGATCGGTGTCTGGTTGATTCAGTCAGGGTGCGGTGTG[C/T]GCGCGCTAG
TP104054	TGCAGTACCAGCAGATTAGTGTTTTTTTTACAAAAGCATAGGCGCTGGATGGATG[C/G]AGCAAGGA
TP104064	TGCAGTACCAGGAGGTGGCAGCACTCTGCCTCGCCAACGATGTAGACGAGCT[C/T]TGCCTCGCCCA
TP104119	TGCAGTACCCATGAAAGGTCCTGCGAGCGAGATGAAGCAAAGGG[A/C]TGGTGGTGTGGTTCCAACA
TP104121	TGCAGTACCCCAAGTCCA[A/C]TATAACGGGCGTTCATCGGTTGCGATTTGAGCGAACGATGATCCA
TP104132	TGCAGTACCCCCCCATCCACCGCGCTCTTCACCTGGCTCCCACTTGTT[C/T]GACGTGTCACTCCAT
TP104147	TGCAGTACCCGCCACCGCCTCTGCTGCT[C/T]CCGCCGAAGAAGCAGCTGTACCCGCCACCGCTTCC
TP104154	TGCAGTACCCTAGAGTCCCGAGAAAGGTTGGTG[C/T]GGTGCTCTCGCTCCAATCCAATTTTCAGAT
TP104172	TGCAGTACCGAGGATGAGACC[A/G]TCGCTGTGGACAGGACGGGCATTGGTGTCCAGAGACATGAGG
TP104174	TGCAGTACCGAGGGGCGCAGATGCGG[C/T]GGCGACGCGAGGTCCCAAGGAGGCGAGGACAGGTCGG
TP104186	TGCAGTAC[C/T]GCACGATGGATGACAAATGGTGGAAAAAAAAAGGTCACTGAGTGTGTTTGCTTTG
TP104195	TGCAGTACCGCCAGCAGCTA[C/G]TAGCGGTAGGGGACTGACTGTACCTTAAACTGCACGTGCACGG
TP104209	TGCAGTACCGCGGCCTCGACATCTTTGGCATCAATGAG[A/G]AGGCCAACGGCACCATGATCTTCAA
TP104226	TGCAGTACCGTTTTACTAATTTTACCACTGCCAAGTGCCAACAACAGCCAAGTCCCGT[C/G]CTAAA
TP104234	TGCAGTACCTAACTACTGGGAGTATCCGTTACGATCCGAGCAGTGCTCGCCGCCACTG[C/T]TGTAC
TP104252	TGCAGTACCTCACCGTGACGCGCCTAGACTTGGCGTTCGCGGTGCAGCAGGCATGC[C/T]TGCATAT
TP104253	TGCAGTACCTCAGTGGCGAGCCAGCTGACCTCCTCAGGTTCCCGAAGTAGTTGGATCGACC[G/T]CA
TP104277	TGCAGTACCTGAAAGCATATGTCTGGGCCTGACTTGCTTCTTTT[C/T]CCACAATAACCGTGGTCAG
TP104289	TGCAGTACCTGATCATGGACAACAACCCAATCGGCGTC[C/T]CGCTGCCTTCCGAGCTCGGCAGCCT
TP104291	TGCAGTACCTGCACCTCTGTCATCTCTTTCC[A/G]TTGCCGCCGAGATGTCCCGTTACCGCTGAGGT
TP104292	TGCAGT[A/G]CCTGCACCTTCAGTCTCTCCTCACTCGCCAAGAGTAGATCACTAGACTGACGAAGAG
TP104305	TGCAGT[A/C]CCTGTAGCGGGGCCCATCCAGCAGAAAGGCAAAGCGGAGCAAAGGAAACGTGTTGCG
TP104323	TGCAGTACCTTGCATCACAAACAAGGCACGACTC[C/T]TTGCTCTCCCATTTCCTCTTCCCACAGCG

Table A2 (cont.)

TP104330	TGCAGT[A/T]CCTTTGGTTTCCTCTGGCCCCACGTCGCTTTTTTGTGGTCTTGTTTGCTGCCGCCAC
TP104346	TGCAGTACGACCCTC[C/T]GACTAGACCAAGTGTTGCCAATAGGCCACGGTTGAGAAGAGCACGCAC
TP104370	TGCAGTACGATCTAGATGGAGAAGAGGCGAGGTGCAGAAGCACTC[A/G]GGCAGGAATGAGCGGAGG
TP104394	TGCAGTACGCCCAGCGTTGGCCATCGTCCCGTGGCACATTCCAATTCCACCACGTT[A/G]CAGCAGC
TP104418	TGCAGTACG[C/T]GTCGCCGCTAATGGCCTGCGCCATGTCTCCCAGATTGACCAGCAGCGTGCCCGT
TP104430	TGCAGTACGCTTGCGCTGGCTGCATGTAACTCTATTGGGTCCAGAGAGGTGTTTTTGTAG[C/T]TGG
TP104434	TGCAGTACGGAGTAGCTTGCTGGCTTGCACAGGAACGAA[C/T]AGAACAGCACAGAGAGAGGCAAGG
TP104435	TGCAGTACGGCACCATTACATTGATCCCGTCAAGGCATTTGCTTCAGCGCAGCCCTGTC[A/C]TTGC
TP104437	TGCAGTACGGCAGAGAC[A/G]GCCATCGCTCACGCGCTTGGGCTGGACGACGGGAATCACGGAGAAA
TP104441	TGCAGTACGGCGACGACTACGGTACGTTCTACCGTGTACTACAAAT[A/C]TACAATCATCGTCGTCA
TP104455	TGCAGTACGGGCAGTCCACG[A/G]TTATAAAATCCGCTTCAAGTCCGTCGGGTCGCTCTTTTCTCTC
TP104459	TGCAGTACGGGTTCTACAAAGGCAAGTGCAACGGCAGCGACATGGAGGC[G/T]GTGGTGCAGGGCAT
TP104471	TGCAGTACGTACACCATCGCAGTGCGCCCCATAACTTGAACTCCGATTCCGCCAATGG[A/C]AACCA
TP104480	TGCAGTACGTAGATTTACAGTCAGAGGAACCAATTCCAT[A/G]TTCGACGTGTCTCAAGAAGTTTCA
TP104495	TGCAGTACGTCACCTCGCCAGC[A/T]TCCTGCTCACCACCTACGCCAAGTACATGGCCGTCAGCAAG
TP104509	TGCAGTACGTCGTCGCCAACTCCTTCATCGCCGCGCTCTA[C/T]GCCGACTACATGGAGGCCGTCAA
TP104515	TGCAGTACGTGAAGCGCTTCAGCCGCTACAAGAACCCCGAC[G/T]CCGTGCGCCAGGTCCGCGAGAC
TP104536	TGCAGTACGTGCTC[A/T]TGGTGGGCGCGGTGGCCATCGGGAGCCTCATACGGCGGAGGCAGTCGGG
TP104544	TGCAGTACGTGGTCGCCAACTCCTTCCTCGCCGCTCTCTTCGCCGACTACATGGAGGCG[A/C]TCAA
TP104550	TGCAGTACGTGTCCAA[C/T]GTGATCATCCACAACGTGCACGTCCACGACTGCGTCCCCGCGGGCAA
TP104551	TGCAGTACGTGTGAATGG[A/G]TTGCCCTGCAAGGATGTTAAGGATGTGAAGGTTGACGACTTCTTC
TP104567	TGCAGTA[C/T]GTTTACCGTTACTCACTATACTCACCTCTACCATTTCATTTCTCGTTTAATTGCGC
TP104603	TGCAGTACTACTAGAGTTTGGTGGTTGACTTTTGAGGGTGGGGGTTCAGCCGTTCAGGGC[A/T]GCT
TP104619	TGCAGT[A/G]CTAGCATTCTTTACCCTGAACATGGCACGCAGTAGTCGCGGCGCGACAGGCTCTTCA
TP104626	TGCAGTACTAGGACCCAGTGCACTGACGTATCCTA[C/T]TTTTCTTCAGTGTTTTCTACGCTTTACA
TP104647	TGCAGTACTATATGTGAAAATAAACTGAGCGCCGCCTCG[C/T]CGTCGCGGTCGTGGCCGCGGTTCG
TP104650	TGCAGTACTATCAGTGAAGCGTGAGCCGTGATATGATACCAGTGCTATTTCCCACTCTTAACC[A/T]
TP104661	TGCAGTACTATTCATTTATAGTGTGTTCAGATT[A/C]CCAATTCTGTCTTCAAATGTTCATATGACT

Table A2 (cont.)

TP104668	TGCAGTACTCAAGCATAGCTGTCATGTTCTTGGGTGTTCTGTTTGC[A/G]GTCGCTGAGCTCCGAGG
TP104713	TGCAGTACTCTAAGTAACATTTCAGTAATCCACTCGAATTATTGGAGTATCTTTTTC[C/T]TTCTCC
TP104725	TGCAGTACTCTGTAGTCTGTACACTTGTACAGGACGCCGCGGG[A/C]GAGCCCGTGCCGTGGTTGTT
TP104739	TGCAGTACTGACGGAGTGTACTCTGCATGTGCAGTGCA[G/T]AGCAGCAGAAGGATATTGGCGCTGC
TP104744	TGCAGTACTGAGCTCCAG[C/G]TTACCCGATCGATGGCAGCCACGAACACGACGACGACGCTGA
TP104776	TGCAGTACTGCACTGCGCTTCACACTGCTGTC[T/C]CGCGTCGCTCGCTGGCACCCGTCGTTCCTCG
TP104788	TGCAGTACTGCCTGAACGAGCGTCTTGCACTTGGGGACTAG[C/G]ACAAGGGGAACCTGCCGCGGCG
TP104804	TGCAGT[A/G]CTGCTTCAACGCGTGCCACTGCCGCCGTGCCCAGCAGGCGGCGGCGTCGTCGCAGAG
TP104808	TGCAGTACTGCTTGCGATTGCGACGGCCAGCCG[C/T]GGTTGTCAGATTCGGAGAAGCCAAGAAAGC
TP104824	TGCAGTACTGGGTCG[C/G]GAGACTGGGCCCTGTCTGGCTGCCTAATGTCCTCTTCTTCTTCCTTCC
TP104825	TGCAGTACTGGTACAGTAATGTCCTCCGTGTGGACACACTAATTTGCAACTTGATCCAGAAGC[C/T]
TP104848	TGCAGTACTGTGTACTGGCCTGTGCGTCCTTTTCCGCCCTC[G/T]CGAAAACCGATCTGCTGTAACT
TP104894	TGCAGTACTTGGACTGACAGCCCAGCCCATGGTTGCAAAGGATCTGTCTTTTGTGCCCACAA[C/T]C
TP104896	TGCAGTACTTGGAGTAGGATTGATACGCGCGTAAATTGGGGTTCGGAACAAG[C/G]AACAAATGGAA
TP104900	TGCAGTACTTGGTTTCTGGCATCTCTGATCAACCAGCTTCCGCGTT[C/G]GCGTTGGCGTTGTGTTG
TP104950	TGCAGTAGAAATCTC[A/G]CCACACTTGGAGTACATGTCAACAAGAGCTGTACCTACGAAGACATTG
TP104952	TGCAGTAGAAATGCGCAAAAGGATTTACAC[C/T]GTATTCCTGCTAGGAAGTTAGTTAGGAGTGCGG
TP104957	TGCAGTAGAACACCATGGGCATTGGTCCTCACC[C/T]GACTGCCATGGCCTCTTGATCAGCCAGATG
TP104958	TGCAGTAGAACACCTAGGTACCTTAGACATTTGAGACTTCGCTGTTC[A/T]TAGTACATACCTTTAG
TP104990	TGCAGTAGAATACTCTA[A/C]GAGTACTATGCTATTGCAGTATTGCTGTTGCTGGCACCAACCTTTG
TP104997	TGCAGTAG[A/C]ATGTCGCTGTCGTCTGTCGCGTCGATGGCGGGCGGCGCGGAAGACACATTGGCAG
TP105029	TGCAGTAGACCTTC[A/G]GCTGTAGTTGGACTGTCTAGAGTCTCGACAGAACTCGCGCCGCGTTGCA
TP105057	TGCAGTAGACTTCAGGTGTGCAGATAAGGCCATGGTTCTTCAGGCAGAAGTC[A/G]CCGAAGGCCCT
TP105086	TGCAGTAGAGATTACAGGGGGCCATCAGGTTG[G/T]AGTTGGAGTACATGCACGGACGGCTGATGGT
TP105089	TGCAGTAGAGCAAGAATTGTCAGCTAC[A/G]AAGTAGAAGTGTATGACCATCCAAATAGCATGCCAC
TP105102	TGCAGTAGAGCGCGCACGCACAGAAAAGCGAGGAATCAAA[A/G]CATCAAGCCCTTTCTGGCTTCCT
TP105106	TGCAGTAGAGCTAGAGCA[C/G]TTTGGTTGTTGCTTACTGGAGCTAGGTAGCTGCTTGTGCTTGAGG
TP105113	TGCAGTAGAGGA[C/T]GAGGAGCGTGGAAGGGGTAAAGGCGGGAGCGGAGCGGAGCAGAGCCAGGCG

Table A2 (cont.)

TP105119	TGCAGTAGAG[G/T]AGCTCAAGTGCAAGTTGAGCTGTTGGCCTGAGAACCTCACTTATTTGAGCTGT
TP105160	TGCAGTAGATAG[C/T]ACATTGACATTTATTGGTTCGAACTGCTGGGAGCGGGCGAGGCAAAGGTAG
TP105167	TGCAGTAGATCACACGATCAATGA[G/T]CAACGTTGACCGTTGACTTGGTCAACGCTAGGTCTGGTT
TP105219	TGCAGTAGATTGGAATGACCGAGATTTGGAGACGGAAACG[C/G]TATACATCAACCGTATGATTTAT
TP105225	TGCAGTAGATTTGGTGCCGCTCCTTTTTATCTGACGACACTA[A/G]CTAGCGTCAGAGGAGAAAGCA
TP105229	TGCAGTAGATTTTTGCGTGTCCTCAGAATTTTGACATT[G/T]CCCCATCATGTAGGCTCAGTTTGTT
TP105231	TGCAGTAGCAAAAGAAAGCAAG[A/C]ATGAATCGTTGAGGATACTACGTTGAGATGGATTGGTAACG
TP105243	TGCAGTAGCA[A/G]CAGCAGAGAATGAATTTAATTGAGGAAGGAAGAGCAGTACATACAGTAAATAA
TP105246	TGCAGTAGCAACCGCCCGAAAGGCATGGCGACATGGACGCGGA[A/C]GTGAGCCAGGAACATGCTCA
TP105250	TGCAGTAGCAACTCCAACGGCTAAGCAAGGGTAAAAAAAAG[A/G]GCATCCGTATTGCAGGAGCATG
TP105266	TGCAGTAGCAATCTGCACGGCTTGCGCGCACCACGCCCAACAGCGACACGACG[A/G]CTGTGGCTGC
TP105272	TGCAGTAGCACACACGTCAATGCCCCCAATGACTCGCCAAGTCAGCGCCTCGTAAAGTA[C/T]TGTA
TP105276	TGCAGTAGCACATACCAACTTCCC[A/G]TTACAAAGTAAGGATACACACACAGCTACCCCTTAGCTA
TP105295	TGCAGTAGCACGTTATGCTTGGAGACTGGGCCAGAAGAGAGATGATCATAAGAGCACC[A/G]ACGGA
TP105307	TGCAGTAGCAGACTGCGATTATCTCATCAGCTAGTGCAATAATATTCATGCGAGTTAAAT[A/G]CAC
TP105324	TGCAGT[A/T]GCAGCAGACGAGGAGATGGAGATCAAAAGGAGCAGCAAGCAGGGCAAATGGCATAAT
TP105331	TGCAGTAGCAGCAGG[C/T]GTGTATGAATGTTCCTGTCTATTCCTTTTTAATTATGGGAGATTTGAG
TP105363	TGCAGTAGCAGGCAGGAAGGATCTGCCTGTCCCAATCGCCAATC[C/G]CCAATCCCCAATCCCAAGT
TP105364	TGCAGTAGCAGGCAGGAAGGATCTGTCTGCCCCAATCCCAGAGCGGCCAGCATTATCAGG[C/T]TAG
TP105366	TGCAGTAGCAGGGGCCACTGCCTCCGATCCAGACTCCAGCACAAAGGGGTTGTC[A/G]CCTCCAGCC
TP105380	TGCAGTAGCAGTAGATAGCGCGCAAGAAACACG[C/T]ACTACAAGGCACAAGCAGAATTTTTTTGCG
TP105385	TGCAGTAGCAGTCTTCCCCCCAGA[C/T]CCCGCCGACATTCTCCAAGCCAGTCGTGCCAGCGATGGG
TP105419	TGCAGTAGCATTCTCAT[C/T]TCTCGAACTCTCTCCAACTTCCTCTCCCTTATTCTATCTTCTTGTT
TP105442	TGCAGTAGCCACAGGATAACACACCTACGGCTCTCGTCA[C/T]CCGCCTCACTCCCTTCTCAGCTTG
TP105461	TGCAGTAGCCAGTTTTGCTTGCAGAGCATGTAGGCAAACCAGTGGTGTCCAATGTAAGGCACT[A/C]
TP105467	TGCAGTAGCCATGACGACTAAGCGCTGCTGCCTGTT[C/G]TTTGCCACGCTCCTCGCGGCGCTGCTC
TP105476	TGCAGTAGCCCAGCCGACAGCTCCCGTGGGCTCTGGTGTTGGCGCCAGGTC[C/G]TCTCCTGCACCA
TP105497	TGCAGTAGCCGAGCGAAGATCGAAGCCCCCCAGCGTGTCTGAGTTGGAGTC[C/G]AACTCAGTCGTC

Table A2 (cont.)

TP105510	TGCAGTAGCCGTCCTCGGCCGACGACATCGATCAGATCC[C/T]CTCCTCTCTGGCTCTCTTGCCGCC
TP105514	TGCAGTAGCCGTTTTCTTTATGTAGACAAGGCAGCGATG[C/G]CTAGATTAGGCCTGCATGCATGAG
TP105520	TGCAGTAGCCTC[A/C]GTGGTACGCCGCCACATCCATCGTCAGTCGCCACATCGCGTCGCCTCCATA
TP105521	TGCAGTAGCCTCCAAAGCAACCAC[A/G]TCCAAAAGCAGGCACTGTCAGCAGCGACGAGGCAGCGGA
TP105525	TGCAGTAGCCTCCTGTCTCGGTCGAGGCAGGCA[C/T]ATGGCAAGGTCGTCCTCGAACACCATGCTG
TP105532	TGCAGTAGCCTCTCGGCGCGGCGCGTTGATTTGTTGTGACCGCGATCGA[A/G]CCCCGCCGATGCGA
TP105534	TGCAGTAGCCTGAGCGACGC[A/G]CAGGTGGGGAAGATGCAGTGGGTGCAGAGCAGCTACAGGATCT
TP105580	TGCAGTAGCGCGACGAGGTCGGCGCTGGTGAGCTTGCTCAGATCGGG[C/G]AGGTCCTTGGCCTTGA
TP105581	TGCAGTAGCGCGCGAACACGTCGGCGCTCAGCACGCCTGCACAG[C/T]CGAATTAAACGCCCGTGAG
TP105583	TGCAGTAGCGCGCTGCAACCAGCTGAACTGGGCACAACGTAGTTCAT[A/C]AAAAAACTGGGCACGA
TP105602	TGCAGTAGCGGCCGCGAGAAAGACGGTAT[A/C]TCCCTGCGACAGCGGCTAGGAGACAGCGCGTTCC
TP105614	TGCAGTAGCGGTTGGAGCTGCGTCCTTCTCGAATGTCA[A/G]GTCTCTGCTCCCCATATGGCCATAT
TP105642	TGCAGTAGCTAGCTATAGCTTC[C/T]AGCTTAGTAGTAGTAGCCTGTGGAAATGGAGACGGATCGTA
TP105665	TGCAGTAGCT[C/T]CTCCCTCTCCAACCACCACCACCATCCGCGCGCCGTGACCTGGGATCCCGAGT
TP105692	TGCAGTAGCTGGCT[C/G]TCATCTTGGTGCGCTTGTGGTCTTCTCCTTGGCTTTCTTGCTGCCCCAC
TP105697	TGCAGTAGCTGTACCATTTAGGAT[C/T]GTAATGCATGCGCGCTGACATCGATCCACCCGTGCGAAG
TP105715	TGCAGTAGCTTGAGATGGTCTCTGCTGCAACATAGCAGTAATCTGGGAGTGGAGT[A/C]TGTGACCT
TP105729	TGCAGTAGGA[A/G]AAATCAGGCGAGGAAGGACGGACTACAGAGGCAGGCAGGCAGGAGCAGATCTC
TP105735	TGCAGTAGGAACAGCTCGCGACAAGC[A/G]GTGCCCTCGGGGAAGACAATGACGACATAGCCCTCCT
TP105738	TGCAGTAGGAACTTGCAAGAAACCGTGAAGAAAGCTAGCGAGGAGTTACT[A/G]CTACTGCTTGCTT
TP105768	TGCAGTAGGAGAGGATGATGGAGTTGAGGGTGAGGGT[A/G]TCACCTGGGACGGGGCGGAAGCGGAC
TP105773	TGCAGTAGG[A/C]GCCGTTGGACAGAGAAAGCTGTGGGGGCTGTGCGTCAGTGAGAGAGTGCTGGAG
TP105811	TGCAGTAGGCAGAACATCATGGCGTTCGGTAACGTTGCTAGTCCCTAGC[A/T]GGACGGACACAATG
TP105842	TGCAGTAGGCCTGTTCAAGTTTGGTTTGAAACTGCTCAGACCGTCAAACCGTCCTAGACTG[A/G]CC
TP105887	TGCAGTAGGGAGGAGGAGGAAGAAGAGGACG[C/T]GGGGGCTTTGTTGTTTTGCATTAATGCCAAGT
TP105926	TGCAGTAGGGGTGATCC[C/T]GATCTTCTGTCAGGTGATGATAACTATCGTTTTGTTGGAGCACGAC
TP105975	TGCAGTAGGTGCCCTTGAGCCACCCATCCGCGATGGAACGGTAGGC[A/G]GCTTCCGTGAGATGGAT
TP105993	TGCAGTAGTAAAGCTTATTCAACCAAACCCAGGCGTGAACGTGCGTGATTGATGAT[A/C]AAAAACA

Table A2 (cont.)

TP105994	TGCAGTAGTAAATCTTATTCAACCAGTCGTGATTGCGCGAACGTGATGATAAAAAACAGAGTA[A/C]
TP106005	TGCAGTAGTACACACCCTTCGTGGTAGGAAGTTTCTAGAGA[C/G]AAGTAAAACAGAAGTTACCGAA
TP106016	TGCAGTAGTACGACTAGTAGATCTGTATGTATA[G/T]ATGAACACCACACACCACTGAGGGCTAGAT
TP106022	TGCAGTAGTACTAAGAACA[G/T]ATATCCGTATCAAACAATTCCTTGGTTGGACCCATTGCGATGTA
TP106065	TGCAGTAGTAGTCGGCGTGGTAGTGGTGC[C/T]AGGGTTAGAGGCTGCTGCTGCCCTGTACAGGAGA
TP106126	TGCAGTAGTCCTCGTCCGACCAGCAGTCTTCGTCGACGAC[G/T]GCGCCATCGGGGATGTTGGGGTT
TP106127	TGCAGT[A/C]GTCCTGCATGCAGGCCCGCTCGAGGAGGTTCCATGAGTCCCAAGAATGTCACGGTTG
TP106131	TGCAGTAGTCCTGTCAATGTGGTACCCATGCGGCCTAGG[C/T]TTGATAGGCAGTTTCTCCTCACCC
TP106156	TGCAGTAGTCTATAATCTATATATATTGAGGAAACTAATTATAATATAACCACGCCGC[A/G]CCTTG
TP106160	TGCAGTAGTCTGCACCCACGCCAACCACACA[C/T]CCCCACACGTATCCATAAACTGGGGAACAAAA
TP106199	TGCAGTAGTGATGACGCGTCTTCCAGGGATGGTGCTGCGAGGTATGC[C/T]TGCTCCTATCTGGAGA
TP106202	TGCAGTAGTGC[A/G]AATCAAACAAAATCTGTGAGGCGCCTTTTGTATACCAAAACAAAATGTTAGA
TP106204	TGCAGTAGTGCAAGGCGCCCCATGAGCCGCCTA[A/G]AGGGTCGGCGAGACGCTCGCGCACGGGTCC
TP106207	TGCAGTAGTGCAATTACATGCTATGAGGAGTTTTAGGAT[G/T]TGTTTCAGATAGCTGAAGAAGTGC
TP106211	TGCAGTAGTGCACGCCAAAGCTGCGTTGACCTGACCACCTGCTACTGCTAGGCTGCTACCCAC[A/G]
TP106222	TGCAGTAGTGCAGTAGAATCAGCACTGTTCTTCGAGCCC[C/T]GTTCGCTGGTCTGAAACTTGGCTG
TP106244	TGCAGTAGTGCCAGAAGA[C/T]GGCGCGGGCAAGGTGTGGCAGTTCTGGTACTTGTACTGGGCCAGC
TP106339	TGCAGTAGTGTTCTTAACTTTTG[A/C]TCTACTGGGATTTGGAGATCCGTCATCGTCACAGGTCGCA
TP106340	TGCAGTAGTGTTCTT[C/G]AACTCTGAAATTAATCAGTTCAGTTACTACTAGCTAGCCACGGAGGAC
TP106347	TGCAGTAGTGTTTCGTCGAACCAGTGCGACGGAAACAGCAACTCCTCCGAG[A/T]CCTCCTCCGAGT
TP106363	TGCAGTAGTTCAGGGATCAAACAATTTA[G/T]CAGAACAGAATACCTTTCTCTTAGTTTACTGAAGT
TP106371	TGCAGTAGTTCTACACCTTCAAAATGTACATACAGGT[C/T]GGTTCTACTTCTCATTGCAGGACAAG
TP106383	TGCAGTAGTTGAGGGTGGGGTG[A/G]TCCGCTGACGCAGACGGCTCGAGAGGCGGCACGTGCATGCG
TP106425	TGCAGTAGTTTGAACAATGGAATGGCGAATTTTCGAGAGTAGCTA[C/T]CTCGATCTGAAGCCAGAG
TP106445	TGCAGTATAAAACGTAAACGTACGCGGCAGCCTGCCCTGCCGCCACCTGGGCTCGA[C/T]CCTGACG
TP106461	TGCAGTATA[A/G]CCCAGGCTGTTGAGTGTACCCTTGCTTGGACAGCAGCTCACGTGCTTTCATCAC
TP106492	TGCAGTATA[A/G]TGGTAATGCCCGCGTACGTGTGCCACACTCTGCGGCAATATCGTCGTTCATTCC
TP106504	TGCAGTATACATACAGACAGCTGTACGCTGTATCCAGACGACTGAGCCACG[A/T]ATTTCGGTTGCC

Table A2 (cont.)

TP106520	TGCAGT[A/T]TACTACTAGGCTAAAGCAACGACCCAGAAATCTAATTCAATTAAGTTCACAGAATCC
TP106593	TGCAGTATATATAAAATGAACCAAATAAAACGT[A/T]GCTAAATTCCACTTTCACGTACGGTGTGGA
TP106594	TGCAGTATATATACACCTATATAC[A/G]TTTTCAAATTCCAACCCAGCTTATATATATTTATTTAGA
TP106623	TGCAGTATATGAACATCTCAGATGATTCCTCGTCTTTCTTCAGACCCTGC[A/G]CTTGTCAGCACCA
TP106647	TGCAGTATATTCGGCGGCCGTCACCTCCAACGACGGCAAGTGAGGACG[C/G]TGATGGCAAACCAGA
TP106651	TGCAGTATATTGCAGATAAAACCTTCT[A/G]TCGCTAAAACCCTCTGCTGTTCTTCGGTGCTTCACC
TP106661	TGCAGTATCAAGCC[C/T]CAGCTTCTTCTGATCATTCAGGACTGCCGCTTTCGCTTCGCTCCCACCC
TP106693	TGCAGTATCAGCAGTACGGCACCATTTAGTAGTAGT[A/G]TCTCTTTACAGAAACAGTGAAAGATGG
TP106720	TGCAGTATCATGCTTGTGCCTCTTGGCGGGTTGCTTCTGAAGTTCTGAATTCTGATGT[C/T]TTTTT
TP106736	TGCAGTATCCATCAAATTCCCGATGGGCCACAAGCTAACAAGAAAGCAAGCT[C/T]GGAAGGCGTCT
TP106760	TGCAGTATCCGCGCCAGGGCG[C/T]CCTTGGTGCCCTCCCTCTCCAGGATGGCCCTCGTCTCCATGG
TP106767	TGCAGTATCCGTGGTGTGGTTCGTTCTGTTTGTCCGAGAGAAGAGAAC[A/G]TGTGCTCTGCTGTGC
TP106799	TGCAGTATCGG[C/G]CACAAGCTGTTCAGGGTAGCGTTTGGTTTGATCCGTGGCAACCCCTGGCTCC
TP106820	TGCAGTATCTATATCTATTAATTTACAAACTAGAACGCCACTCATGTCTCTCTGGC[C/G]GAAAAAA
TP106831	TGCAGTATCTCAATTTATGATTCAGGCTGGCACTTCAAATGGGACCAACTGATTGCA[C/G]TCAATG
TP106839	TGCAGTATCTCCCTAGTAATCCTCATATCATCCAGATGGCT[A/G]GAGACGCACACCCACATGAGGG
TP106844	TGCAGTATCTCCTTGAGAA[C/T]ATCCCCAGCGTCCTTGTCCGATGCACGAACCCAAATCCGCGGGC
TP106852	TGCAGTATCTGAAACTTGTGCAAAGTAGAATGAAGCGCT[C/T]TCAAACTCCCTAGTGCCGTTAAGG
TP106865	TGCAGTATCTGGATGTGGCTTCCCCTCGACTTCAAA[C/T]ACATGGATACTTTGCTCAATCTGTATC
TP106889	TGCAGTATGAACCATTTGGAATTATGCCCTGTGCTCGCTAATTATTTTTCCCA[A/T]TGCAGGTTTA
TP106916	TGCAGTATGAGTGTGATTAGTAGGCCGAACCGAGCCGTCCCCGTA[C/T]TGTTTAGTTGTCTCACCT
TP106925	TGCAGTATGATGCCGAGTGCAGGAAGC[A/G]TGGCCTTGAGGTTGTCACCAAACTTGCAGCCGAGCT
TP106927	TGCAGTATG[A/C]TGTCCTCGGTTGTCCTTTTTGCTGTGCCGTGCGTGTAATACTCCTACGAATCTG
TP106930	TGCAGTATGATTGTGATCAAGCATGAC[A/G]AAGCTGAAAATGCAAGAGCTTTTGATCTAGACCGTG
TP106937	TGCAGTATGCAAATCTGCAA[A/G]ATCAGAGATGAGAGGCATTGCCTGCTTCTGCTGCTGCTACCAG
TP106980	TGCAGTATGCCTTGAAATGTTCCATCGGCCTATTTTGTGAAAGAAATCA[C/T]ATGACGTGGGGATA
TP106982	TGCAGTATGCGAGTGGGTCGAGGGGGAGGAGTAGGAATGGCGAGGTCAGATTTGAATTGG[A/T]GGG
TP106985	TGCAGTATG[C/T]GCAACACATAAATACATGTGAGCAAGCTGTTGCGTATGCTAGCAACGAGTGAGC

Table A2 (cont.)

TP106998	TGCAGTATGCTCCGCTTTATCCGATCCGCACTTTTTTATCCGTCCAAGCGTCCACACCACGCT[A/C]
TP107009	TGCAGTATGGAATAGCTTCACAGATG[C/T]TGAGAACAAATGTATTTTGTGGATAAAATACCCGCAG
TP107013	TGCAGTATGGACGTATGCTTGGTCTGTCAAAATGTGTTGTCTGTGTTGACTGCTA[C/T]GTGGATGG
TP107018	TGCAGTATGGACTTATGGAGATCTGGGACTAATAGGCTGCTCGAGCCAGGCAGCCAGCCAG[A/C]TT
TP107056	TGCAGTATGTACACTAGTCTTTCAATCGATTATTTTTGGGAAAATGCCGTACCCGAAAGTACC[A/G]
TP107058	TGCAGTATGTACGTTTATTAAACAGATATGCATGATTTTCTTCTTATTAT[A/C]GTGAAGTGATCCA
TP107059	TGCAGTATGTACGTTTATTAAAC[A/T]GATCTGCATGATTCTCTTATTATAACAAGTTAAGAAATAG
TP107068	TGCAGTATGTCAGTATCAGTGAATAAGTAAAGAAGCCATAGCCTCACCTTCAGCT[C/G]GCTTTCTT
TP107098	TGCAGTATGTTATCTTAAGTAAAAATGCGTGCTTTG[C/T]AGGGTTCCTTGCGTGAAGCGTGGTGGG
TP107102	TGCAGTATGTTCTCTTCTGGGACACC[A/G]AGGTAGATCAATGACATGGTCTGCTGCTGGATTTCAC
TP107118	TGCAGTATTAAGGGAGAACAATGCATCATAATGGATCAGTAAGGCTGTCAGGCGTCTAG[C/T]GCAG
TP107174	TGCAGTATTCGCCTGTTCCTTGTCGTAGTGCTCCTCCAGAAGGAGATAGGAGCGCGCCG[A/T]GAGG
TP107183	TGCAGTATTCTCAATCACGTGAACTGACG[C/G]GATGCAGCATCGATCGTCGTGCCCCCGATTAACG
TP107185	TGCAGTATTCTCCAATCAAACACCTATCCATGCG[A/G]ACTCAGAAGCATCAGTCCTGATCTAGCAC
TP107194	TGCAGTATTCTGGGGTGGAACCAGCAGTTTTGTTA[A/T]AAAACAGAATGCAATCTAGAAATTGACC
TP107201	TGCAGTATTGATCCACAAAATAGCTTGAAACTCTCCATCGCTGTTCC[A/C]TGGAGGTAGCAAAGGC
TP107209	TGCAGTATTGCAGAGGATTCCTCTCAACAACAA[A/C]AAAAAATGCCGAGGATTTGTTTCCGTTGTA
TP107227	TGCAGTATTGGGTATATCTTCAACTTCGAGCATCTTTCATCCTGAAAGGGGCATAATGCAA[A/T]AA
TP107245	TGCAGTATTTACAAGGACGACGTCATCCTGTTTGTGCACC[C/T]AGATGTGGCAGAGGCCAGAGTGG
TP107259	TGCAGTATTTCAGTGGTGAGGACCT[C/T]AAGCAAGAGCTAAACGATATTGACAACCTGACGGTAGA
TP107265	TGCAGTATTTGACACGAGCTACCAAGGAGGGGG[A/G]AAAAACAAGGGATTCGAGCACGAACTAGCA
TP107270	TGCAGTATTTGCAAAAAGGTTTTAGCAATGTCGTTTTGGTTGCTGAATA[A/T]GAATTAAAGGCCAA
TP107283	TGCAGTATTTTATATGACCAAGAGGCCATGGCACACAGGC[A/G]CAGCAATGGACACCACTCCATGC
TP107289	TGCAGTATTTTGATCCTTGAATGTTGAG[C/T]TTGCACTTCTGCTTATTGCGTTGCGGCGTTGCCCC
TP107318	TGCAGTCAAACAGAGGAGACTGAGTTCATTGGT[A/G]CCTCGGGTCTCTGGGGCGTGGGCCACGGCA
TP107329	TGCAGTCAAACGCCAATAAATCCACAGCCATGCCCCCAG[C/T]TCTACCCATACGCTTCATAGCTCT
TP107339	TGCAGTCAAAGCACCCAGCACCACCACACGACGC[C/T]CGCGCGCACCATGTGGGTCACGTTCCTCA
TP107366	TGCAGTCAACAACCAAATCCAACACCAT[A/G]CAACCAACCTTTGACACACCAAATCGCATAGGATC

Table A2 (cont.)

TP107371	TGCAGTCAACAGCAGCAAGCACGACAGCATCCCTCT[A/G]CCTCGCGCGGCTCGGTCCCCCCTCAGG
TP107395	TGCAGTCAACCTATTAACTTGACCACTCATATGCATATAAGTATTTAGATTT[A/G]CCGTGTGGGAA
TP107399	TGCAGTC[A/G]ACCTGGTTGATCTCCTTGTGGCTCCACATGTCCTGCAATGCGAAATTCAGAGACAT
TP107400	TGCAGTCAACG[A/G]ACTCCAGGAGCCATGACTGATCTTTGCTTGCCAATTTCTCTTTAAGAATTTT
TP107404	TGCAGTCAACGACTTCGCGTCATGTCTGCA[C/T]GATGCAGCGATCCGCCCGCCAGCAAGGTTTAAG
TP107407	TGCAGTCAACGCGCGTGCTCGTTGACGAGTCTGAAGCAAGCTAGAAGAAATTACAGAAC[A/C]ACCA
TP107410	TGCAGTCAACGGCTCCCCGCTGGCCTGGTTAGCAT[C/G]GTCTCGTCGGAAGGAAGGAGCAGGTGAG
TP107414	TGCAGTCAACGGTATCCACTATCC[A/G]ACTCCAGCGCCGTGATTCATGAACATCATATCATAGCGA
TP107421	TGCAGTCAACT[A/G]CCAGACAAGATGTTTCCTGCTTTCACTTCCCAGGACACAACAGAGGAAAAGC
TP107453	TGCAGTCAAGCAACTGAGCC[A/G]TGCATTTCAGATCCAACCGTGAGCCCACAAAACGCTAGAACCA
TP107465	TGCAGTCAAGCGTATCTGACCTTTCG[C/T]TTCAATCGAACGGCGACCACGTCGCACCAGACTTTCA
TP107490	TGCAGTCAAGGTCTTCGGGTGGCTCCTAACTCAGAATAGGAT[C/T]CATTGCAAGACAGCCTTGGCC
TP107500	TGCAGTCAAGTTGCCGTTCACAGGAATGACAAAGTCAATATGCATCGTCGTCCCACCAGCCA[A/G]C
TP107511	TGCAGTCAATCAATGACTAAATGCATCAGGTGCCTACAACCATGACGC[A/G]TAAACCAACACGTTG
TP107513	TGCAGTCAATCACAGCCAACCACCCACAAATGCCGCCGATCAGAAACAGCAACAAAAC[C/T]AAACC
TP107527	TGCAGTCAATGGCGC[C/T]GAGTCCAGATTAGTGCCAACGCTATTTGCAGGAACTTCCTCAAGCAAT
TP107588	TGCAGTCACACCACAGATGGTGAGACTAGGGAAGAA[C/G]TCGAAGGTTGAAGTCGATGATCTAACA
TP107602	TGCAGTC[A/G]CACTTGCACCCCAGAAAATTGCATAATTGCCCCTCAAAAAAGAAGACGTAATTACG
TP107633	TGCAGTCACATCAAAGGATCAATCTAAACA[A/T]GGTTATATGTTATTGCCTTGTAGCCTTGTACTG
TP107636	TGCAGTCACATCGCCGCCGCCAT[C/G]GACCTCTACACCAACTCCTCGCCCCTCCCTCTTCTTCCAC
TP107654	TGCAGTCACCAACCGACCCCTTTGCTGTTGGCTGTTGCA[A/G]CAGAACGCCTAGGCAACCTGAACT
TP107655	TGCAGTCACCAATAGATTTGCCACCTAAGAACAATGCTTTATTTTAGAGAGTTTTAC[C/T]ATCGCG
TP107661	TGCAGTCACCACCATGCCGCT[A/C]GTCATTCCATCTATCCCCGCTTCCACCATCTCAGCCATGGTC
TP107682	TGCAGTCAC[C/G]CACCGCGCGCATTTTGTAACTCCGCTCCTGATTCTGGAGATGCATATGCTATGT
TP107685	TGCAGTCACCCCGATCTGGAGCCAACGCCACCAGAAGACACGATCTGAGC[C/G]AAAGCGCGCTACC
TP107688	TGCAGTCACCCTACCCTATCTCATCTGGTTTACCCATATATACTTGGCCCTGGATGTCACA[C/T]GT
TP107703	TGCAGTCACCGAGCA[A/G]CACAGAGCGGCTCCACCTTCGGCGTCCCCCGCCGCCGCCGCTCCGTCG
TP107708	TGCAGT[C/T]ACCGAGGCTGGATTTTGGGACTATCTTGGATGATAAAGGACTGGAAACGATTTGCCT

Table A2 (cont.)

TP107724	TGCAGTCACCGTGCAGACTGGAACGCCAATCGCAGTC[A/G]CTGTGGTGTTGTCATGGTCCATCATC
TP107729	TGCAGTCACCGTTAGATTTTAGTACATGTCACTAGCCAGTCAGTTTT[C/T]TGGTGCGGTAACGTGA
TP107744	TGCAGTCACCTTGTCCTCCACAGAAGTGTCAACTTCTCCCGCAGATCCGA[A/G]CAACGCCGCGCCT
TP107748	TGCAGTCACGACGGTGCTCGTGGGCTTCCAGCACTACCTGGTGATGCTCGG[C/T]ACCACCGTCCTC
TP107753	TGCAGTCACGATATCTCTTGCTGAACATTAAGTCTCCAAGGGCTCGAGAGCTGAGTC[A/T]ATGGAA
TP107761	TGCAGTCACGCCACGTCGCCACAGCCGCCCTTCTCTTCCAT[A/G]TGCGTGTGCCAGCACGCCGCGG
TP107762	TGCAGTCACGCCATCT[A/G]TGCCGTCAACTGAGGATCGGACGTCTGCGAGCATTGGCCACTAATTT
TP107778	TGCAGTCACGGATCAATACCGT[C/T]CATTTTCCATCCAACCGTGGCCCCGCAAAACTCCAAGCCAC
TP107793	TGCAGTCACGTACACACCACGGGGGTGAAGACTGAAGAGTGAAC[C/T]GCCTCCTCAATTCTGACCT
TP107809	TGCAGTCACTACTATAAAAAAAACT[C/T]TTGTAATAACGGGATAATTTTTTTAGGAGCGGCTGGT
TP107812	TGCAGTCACTACTTACCTTCGAGCACCTCGG[A/C]GAATACGAAGGTGATGAGAGCTGACGTGACAT
TP107849	TGCAGTCACTGAGGTGCGGAAACCCTAGCGCGTCTGGGTGGGGGTGC[G/T]TGCGGCGCGGAGGTGG
TP107871	TGCAGTCACTGGGTCAGCGACAATAATCTGGCGGCC[A/T]GCACTAGCACTAGTGCACTACCCGTCA
TP107893	TGCAGTCAGAAGTGTTCGCCGTCCCGTCCGTGTGCTGCATGCCGATGCCGTGCCGTT[C/G]TACTCG
TP107898	TGCAGTCAGACGCCATCAACATCTCCTTCCTCCATCCTCCAATCCAACTG[A/G]TACCGCACCGCGC
TP107901	TGCAGTCAGAGAAGGGGTCCACACAGACGCCACCACGGGAGGAAGGGTC[A/C]CGCCGTGGCGGTGG
TP107919	TGCAGTCAGATCCAGGAGATCCAGCCATGTCGGCCG[C/T]GGATCCAGCTACGCCTGCTGTGGAACA
TP107937	TGCAGTC[A/T]GCACAAACGCAAGGCCCAGCCCTCCTCGGCTTTGGACAGAAAGAAAGAAATTCACG
TP107943	TGCAGTCAGCACCGAAGATCGGCCCTTTTGCCATCTTCCCCTG[C/G]GCGGCTGCCATGATCGCGAC
TP107949	TGCAGTCAGCAGCAGCAAGCAC[A/G]ACAGCATCCCTCTTACTCGGCGGCTCAGTCCCCCTCCCAGC
TP107962	TGCAGTCAGCAGTCCT[A/G]CTCCTTTTGCATCGCATCTTGTGTCTCCCTCGTGCGCTCTTTTCCGA
TP107973	TGCAGTCAGCCAGCCCCCCTGAGACCGAGACGCGC[C/G]CCGTCCATGTCCATCCATCGGCAATAAT
TP107974	TGCAGTCAGCCAGCCGCTCTGCAAGGCAGCAGAGCGCGGAGCTGCAC[A/G]CTTTGTTTGTTCGTCT
TP107979	TGCAGTCAGCCCCCACCTC[C/T]GTGCTCCTCCCACCAGCAGACCAGCACCACTAAACAAAAAAATA
TP107985	TGCAGTCAGCGAGTCCGCGGTGAAAAGCGGGCCGTCCTACAAACCTACGG[A/C]TCTTGCACAAATT
TP108028	TGCAGTCAGGAAACTCAGGACAGCGGCAGCTGGTAACTGCACAACATGGG[C/G]TGTTGCTTTGCAT
TP108034	TGCAGTCAGGAGCAGAAGCTGCGCCGCCGTTGCAAGCGTGCAGTGC[A/G]GCCGATGGAGGCTGCCG
TP108061	TGCAGTCAGGCTTGCTCCACGATGTGTCTTCAGCCGCAG[C/G]TCTTCTTGCAGCGAAGCCTGGCTG

Table A2 (cont.)

TP108065	TGCAGTCAGGGACATCGGACCCTTCGCTAAAGATC[C/G]AACGATGAACGGCTCCCACCAGGCTTCC
TP108079	TGCAGTCAGGGTTGATGAAGCCCTCGGCGGCGCCTTTCTCGAACAGGGCAAGCAGC[G/T]GGTCGTA
TP108085	TGCAGTCAGGTAGCCGTTGGGTCTGGCTCTCTCTGGCTGCTCTG[C/G]CCTCGCGCCCCCGCCAGTT
TP108094	TGCAGTCAGGTGCCTGCGTTCAACGAGGAAGGCCACCAT[A/G]CGCGTGACGCCGTCACTATCGGCG
TP108097	TGCAGTCAGGTTGCCATCTACAAAAGTAT[C/T]AACATTTAAATATTTTGAATAGTAAATAAACATA
TP108104	TGCAGTCAGTAGATAAGCCGTAAGCG[A/C]ACTAGCCTATTTTACGTAACCTGCGCGATTCTCTTCT
TP108116	TGCAGTCAGTCAGTCAGTACTGACAAAGGAAAAGGAGGTAGGTATATACCCGCGGTTAAGT[A/C]GA
TP108132	TGCAGTCAGTCTCTCGTCAATC[C/G]TTTTCTTTGTTCTCCCTCCAACTTTTATTTAGCTACGTGGT
TP108142	TGCAGTCAGTGATTTGCATCGATTCGTCGATCCATCTCTAGATT[C/G]TTGCTGCTTGGACACATAT
TP108146	TGCAGTCAGTGCGGAACGCGTACGCCATGGGCAAGG[C/T]GCGGATGGTGGCGTCCGAGTTCGAGAC
TP108152	TGCAGTCAGTGTCACTGAATCAGCTGCAAACCCTGATTTTTGCATCTGAT[A/G]AACGAGCAACAGG
TP108219	TGCAGTCATATCGCAGGAGCA[A/G]CCTAGAATGGTCATCGTCTACTACCCCTGTACCGTACACCCC
TP108226	TGCAGTCATATTGATTAATCGAGTCAATTGGAAGTCAACTGTGCCGAAATGGTCGTTTTCTGT[C/T]
TP108242	TGCAGTCATCAGCTTGCCAGAATCCCTTTGCTTCGACCTCAGGGCAGGACCAGTCGTCT[C/T]GTCC
TP108247	TGCAGTCATCATCCAGCCTCTGCACGAGTGTCGCTAATGGTACATGCCAAGG[C/T]GCGCTAGGCTG
TP108289	TGCAGTCATCGGTC[A/T]GTGACTCACCGAAGAGCTCCCTCCTGAGGTTCTCGTCCATGGTGTCGTT
TP108292	TGCAGTCATCGTCCTGGAGCTCGAGCAC[A/G]CCTCTGGAGAACACCACCATGCTGCTGCTTCTGTT
TP108294	TGCAGTC[A/G]TCGTGCAGTGCATCGTCGTCCTCGTCCGAGAGAGCAACGCAATCGACGTCCTCGTC
TP108307	TGCAGTCATCTGGATGGATGGATCGACGTTGGCTGAATGGCAGATGACTC[A/G]CTCACTTCGCACA
TP108343	TGCAGTCATGCAGATGCATCTATCCTG[C/T]GCCGTCGGTACGGTCGACGAACCTTCCAGCCGATCA
TP108346	TGCAGTCATGCCAACAATAAACTACGGGATCAAGCATTGGGTGCTCC[A/T]CCATTGTGGAGATAAC
TP108351	TGCAGTC[A/G]TGCCGTACGCTGCGACTGCGTTGACCAGACCGTGTGTTTGCGATGCGAGGTCAGAT
TP108404	TGCAGTCATTAGAGCACAAACAAAATCAGCAACC[A/G]ATGAAGCAATTAAAAAAAAACTGCAAATC
TP108429	TGCAGTCATTGGCGTATGCGTACAAAAAGATACAGGTAAAG[C/T]ACGGTAGCCGCAGCTGGTACGA
TP108432	TGCAGTCATTGGGCGGCGCAAGACCGAGAGTGGAGAGCC[A/C]TCTTTCATGGCGGAGAAGGTAAGC
TP108475	TGCAGTCCAAATGCATATCCAGAT[C/G]AATAGGCCACCAAATGGTCGAAAAACTCATAAATTCAGC
TP108478	TGCAGTCCAAATTAAAATAAATGCGTT[C/T]TAGAAACCACAGGAAGAAATGGACGGAAAATGGCGA
TP108479	TGCAGTCC[A/C]AATTCGACACGGTGACGCAGCAGCTTCCTTTAAATATTGCTGACTACCGTTTTCG

Table A2 (cont.)

TP108539	TGCAGTCCAAGGACGCGCCTCCACACCCCGCT[G/T]CCAAATTCATCTGGGAAACCCGTGCACCCCC
TP108552	TGCAGTCCAAGTTC[A/G]ACAGCCAAAGTCGCTCCTTCGCACCTGATAAGGAAATAGCAGAAGCTCT
TP108554	TGCAGTCCAAGTTTGACAGCCAAAGT[C/T]GCTCTTTCGCACCTGATCAGGAAATAGCAGAAGCTCT
TP108574	TGCAGTCCAATGGCACGGCGAATGCTGATTGTGATGTGATATGATGCGCGGTAGCACA[A/G]AGAAA
TP108591	TGCAGTCCACACACGGTTTTGGATGATGAGCCAAGCAAAGAACTTGCATTTACTT[A/G]TTGCATAA
TP108600	TGCAGTCCACACTCCGCAGAGACACATCAGGCATACACGCTGTGATCACT[G/T]ATCAGGCGGCCGA
TP108609	TGCAGTCCACAGCGCCGTGA[A/G]CAACCGTGGTGTCACGTTCCACGGCCGAGCAGCGGCGCCGTTC
TP108623	TGCAGTCCACATCAGCCCCAGC[C/T]AATACGACAAATATTCTGATAAACAACTGGTGCATGAAACT
TP108630	TGCAGTCCACC[A/G]CCGCGGCACCGCCTCTAATTTTCAAATAAAGCAGGCTGACGTCGTCGGCCCA
TP108666	TGCAGTCCACGAAATCCTCGTACTTGCGTTGGCACTTGGCCCCCGATTGCCCGTCT[C/T]GTAGCGC
TP108670	TGCAGTCCACGAAGTCACTTCACCAGTGGACAGA[C/G]AACCTCAAGGTGGTGAACCACTGCGTCGA
TP108690	TGCAGTCCACGGATGGAAGGGAGAGGGAGGGGCATGGCATGCGTGTCTGTTTGTCAGGTAGCT[A/G]
TP108692	TGCAGTCCACGGCCCTACAGTTGAATGGGAGGAATTTAGCATCCATCGCTAAC[C/G]CTTTGCAAGG
TP108695	TGCAGTCCACGGGGACACGTCGCGGAGCTGCCCACGACCACACC[A/G]CCGATGCCATCTGCGTTCG
TP108697	TGCAGTCCACGGGGTCGCCGCT[C/G]ATGCTCAACGTGTACCCGTACTACGACTACATGCGCTCCAA
TP108707	TGCAGTCCACTAAGACCATCGGGTAATTGTCTGATTCTGATGAAATCCAACAAAAC[C/T]GCTTTGG
TP108752	TGCAGTCCAGAGCGTAGAGG[C/G]GCACGAAACCTGACCTCGCTGCGAACGGGGCTGATCGTCCTGC
TP108760	TGCAGTCCAGATGCATGACGAATGTTGGGCCATGAACACTGAAGAACGCACGCGACGGAGCC[C/T]G
TP108766	TGCAGTCCAGCACCTATTGTGTGCCACTAACCACATGAAGAACTTGCATTTGCCT[A/G]GTGCCCAG
TP108778	TGCAGTCCAGCATCAGGTCACGCAGCGTGGCGTACTCGTAGTCGTAGCTCCGCCCGCCGCCG[C/T]T
TP108787	TGCAGTCCAGCATTGCAGTACCTAAACCGACCTTGCTTCGTGCTATCTCCTGCT[C/T]AGGATTCAA
TP108791	TGCAGTCC[A/T]GCCAGGAGTGGATAGGAAAGCGTGGTCCTGAAAACTGCAATCCCCTGCACCACAC
TP108808	TGCAGTCC[A/T]GCGCCACTCCCGCACACGCGCGAACACCTTGCCGTATGTGCCGAGCGCCGACCGA
TP108818	TGCAGTCCAGCGC[G/T]TCCGCGAGGCCGTTGTTGTCCCGCGCCCGCCACGGCCTGCGGCGCTTGCT
TP108824	TGCAGTC[C/T]AGCGTCTCCTCCACTCCGTACTTGAACCTGAACCCCAAGTCCTCCAGCTTGCTGGT
TP108837	TGCAGTCCAGCTTGGATCGTAGCCGCTGGCGA[A/C]GCAACAGCATATCCTCGCGGCACACGGCCGC
TP108847	TGCAGTCCAGGCCGAATCACAA[A/C]CCCCTCCTTCTCCAGATTTACATCCCAGACGAACCAGCGTT
TP108857	TGCAGTCCAGGGGCCCTCGGCACCTCCCCCACTCGGCACTCGCTCACT[A/G]GTACTGCACTGCCTC

Table A2 (cont.)

TP108864	TGCAGTCCAGGTTCAGCTGACGGCTCCACCGTGACGTCACCGCCGTTTTGCCAAAAAT[A/G]GTAGC
TP108892	TGCAGTCCATACACCACCGTGATTTGCCATGGAAG[C/G]CTGTCTGCTCTCATTGTGATCGTCGCTG
TP108942	TGCAGTCCATCGGTTCGTTTCTCCCCAC[G/T]TCACATGGCCCGCCGCGTCTCTCCCACGCCAATCT
TP108945	TGCAGTCCATCGTCTACAACCG[C/T]GGGTCCCTCCGCCTCCTTGATCAGGTGCGTTTTCTTTTCGT
TP108946	TGCAGTCCATCGTCTACGCC[A/C]GTGGGTCGCTCCGCCTCCTTGATCAGGTGCGTTTTCTTTTCGT
TP108981	TGCAGTCCATGGCCACCGCCAGCCTCGCGCTC[T/A]CGCTGCGCCTCGCGCCGTCGTCGCGGCCGCT
TP108987	TGCAGTCCATGGTGTACCCTTCCGAC[G/T]CCGTCATCGCCGCAGCCGCTGACGCGCCTCGGAAGAC
TP108989	TGCAGTCCATGTAAAACTGTTCTGCTTCTTGAGCAATCTGAAGAAGGGCATTGCTCGTTCCC[C/T]G
TP108995	TGCAGTCCATGTCGCTTTCTCCTGTCCGAGGTCCATAGCCTACGGTGCAGCGCAAGC[A/C]AGAAGA
TP109063	TGCAGTCCCACCTTT[C/T]GGAACGAGATCGCGATCGCGCCGCTGCCGTATCTTCCTTGGTTGTTCC
TP109097	TGCAGTCCCAGGGCCTCCGTGGCACCACGTACCGCTTCCCGTTCGGCGACCTCAAGGAGTT[A/C]GC
TP109141	TGCAGTCCCCCGTGGAGAGGTCGCCCTCGCACTGCGCCATGG[A/C]GTAGACGGCCTGGTAGCTGGT
TP109193	TGCAGTCCCGAGTTAGACTCGGCGACTCCCAAATCCC[C/G]AAGTCGCAACCCAAGGCCGAGAAGCA
TP109207	TGCAGTCCCGCCTCGGCTTCTTCGCCTTCAA[C/T]CTCACCTACCTGCTCTCCTCCACCACCGAGGC
TP109212	TGCAGTCCCGCTCGACGGCCTCCCCGCCGACGCCCGCATCGAGACCGTGCTCCTC[G/T]AGGTGATC
TP109224	TGCAGTCCCGTTGCAAATTGCACGACGCGACACCGACAAGGCGACCCTGGTAAAGT[A/G]TTGGACA
TP109242	TGCAGTCCCTCACCCACCTCAACCTCTCCAACAACGTGCTCAACGGCACCTTCCCGCCGC[A/C]GCT
TP109259	TGCAGTCCCTCCGTTTAGCATGCGCACGAAC[C/G]TAGTCGAGAGGTCTCGTACGTGGCCAAATATA
TP109267	TGCAGTCCCTCGCCTTCCTCCTC[A/G]AGTCAGGCCTCCACGCCAACCCGCTCGTCCTCACCAGGCT
TP109287	TGCAGTCCCTGCGATCCTACAACGCTGCAAGCAT[A/C]TGTGCTTGTGTGGGAGCTTCTCCTATGAA
TP109294	TGCAGTCCCTGCTGGTACAAGCAGCAAGCGGCATGCC[G/T]CTAGAAAGTGGAAGCGCTCGCTGAGT
TP109302	TGCAGTCCCTGGGCCCTTGGTTCGATC[G/T]TGGAGCAGCGCGTGCTTTCACATGACAAAAGTGATC
TP109304	TGCAGTCCCTGTCACA[A/T]AAGAGGGCTGCGTGCTGCTCCTCGTACATTTGGCCTTGTTTGTTTGT
TP109317	TGCAGTCCCTTGCTAGCTCTCTGCTCTAGCTTG[C/T]TGACTGCTTCGCTTGCTCTGTTTCTCGCTT
TP109329	TGCAGTCCGA[A/G]GCAGTGCAGTCACACACACACACACGACTACTAGCAGGCAGCACGCAGCATCA
TP109339	TGCAGTCCGACAGCTCTAGCGGATGGCAGGAAGGCAGCAGCAACCCCTGAGCGGGCAGCAGGC[C/T]
TP109359	TGCAGTCCGACTGTCGTT[G/T]TGGCGGATGGTCGCGCAGGCCTGCGGCCAGTTTACTGCATCTGCG
TP109360	TGCAGTCCGACTTCAGGGACGTCGCCA[A/G]CAAGTGCGTCGACGCCGCCAAGCTCGCTGGCTTCGC

Table A2 (cont.)

TP109372	TGCAGTCCGAGCCTCCCAGCCAACAGCAATTCAGCCTGTTC[A/G]CTGGTTGGTTTCTGGACTGATA
TP109373	TGCAGTCCGAGCTC[A/G]TCTTCCTCGGCACGGGCACCAGTGAGGGCATCCCGCGCGTCAGCTGCCT
TP109375	TGCAGTCCGAGGAAGCCGACTCTGTTCCTGATGAGCGAAAAGCCTGATCGAAGCTCGGCCCAA[G/T]
TP109378	TGCAGTCCGAGGCGGTACTCGGCCATGACGCGCGGCGGAGCGGGCGAGGGCGA[A/C]GGGAGGATTG
TP109389	TGCAGTCCGATGC[G/T]CTCGTACGCATCCGCCCATCAATCAGATCAGCTGACGCCAAGGAATCCCA
TP109393	TGCAGTCCGCAAAAGTAGCAGACGTTTCGCCGATGCGAAACGA[C/T]GGCCGCACGCGCAAAGTCGA
TP109395	TGCAGTCCGCAAGGCAACAGCAACCAGGGGCG[G/A]ACCAGGACATTGGTGTACACATGTGCACCCG
TP109439	TGCAGTCCGCC[A/T]GGGCCTCCGCGAAGTAGACGCCGTCGGCGGTGCACCGAAAAAAAAAAAAAAA
TP109448	TGCAGTCCGCCGCCAAGCGCAACCGCAAGATCCGCAACCAGTTCAACCACCGCCG[A/C]GGACCCCG
TP109468	TGCAGTCCGCG[C/T]AGCGGACGAGGGGCGGATGGGATCAGCGGACCCGCCAATCTAGGAAGCAGGC
TP109473	TGCAGTCCGCGCCGTTGGCACAGGCATAGCTCAACCCATCCAGGAGCCGCG[C/T]GTCCCCGACCGC
TP109481	TGCAGTCCGCGGACCATCGGCGCCGC[C/T]AGCATCGCGGCACTGGGCAGGGCGACACCAATTGGAC
TP109497	TGCAGTCCGCGTCGGCGGCCGTGACGGACGGCGGGGCGTCGTACGGCAACATGTTCGACGC[C/T]AT
TP109513	TGCAGTCCGCTGCCACTGCCCCTGCCCGCTGGCCGCCCGATGTCCTGGCTGCTGGCTGCCGCC[G/T]
TP109531	TGCAGTCCGCTTTGCCCGCCTGCG[C/T]ATGGAGAGGCGACACAATTACCTGCGCAAGGTTGCTGAG
TP109545	TGCAGTCCGTCCGTCAGCCAGTCAGTTGCGGAACACTATGTGAGTGAGGCAAATGCTA[G/T]GAACA
TP109572	TGCAGTCCGTGATGCGCTGCTCGTCTGCTGCTGGCTAC[G/T]GGCCGCAGCACCGCAGTCCGCAGCA
TP109586	TGCAGTCCGTGCTCTTCCTCGAGTCCTCCGCTGAACATTCGGGCTCCGTC[A/G]GGGTGCAGCCCGA
TP109587	TGCAGTCCGTGCTGGAGAAGGCGCAGGAGGC[C/G]CTGGCCAAGCAGAGCGTCCACCTCGACGGCGG
TP109592	TGCAGTCCGTGGGCCATC[A/G]TAGCACAGAGCATGACGTGAGGCCACGAGCGATGTGGCCTGCGAG
TP109600	TGCAGTCCGTTCCCGCTGTGCTGGCGGCGCTCGTGCAGTGCTTCGACTGG[G/T]CCACCGTCGACGG
TP109609	TGCAGTCCGTTTCCACGTCCCATTTCGTGCGTCCATGTGGGGCATGTGCTGCTCGGACTTT[C/T]GC
TP109621	TGCAGTCCTAAATGGTGTTAGTTGAGATTGGACGATATTGTGCGCACTGAACA[A/G]CACCCATGTA
TP109660	TGCAGTCCT[A/C]GAGGCGGTCGAGGAGGTTTTCGGCGACGGCATCCACGAGCCCGTCGGTCTCACG
TP109695	TGCAGTCCTCACCA[A/C]CTCAGGTGAGGAGGGGATCCCTCACCCTCCTCCCCTAGCTCCTCACCGC
TP109708	TGCAGTCCTCATCCTCGTCCCCC[A/G]CGCGTCCTCCACCTCGGGCTCGGAGGAGATCCACTGCCAC
TP109767	TGCAGTCCTCGGCAACCATGACTACACGGGCAACGCGCTGGCACAGCAGGACCCCGCCATCC[G/T]C
TP109768	TGCAGTCCTCGGC[A/G]GTCGGGGCGCACCGCCGCCGCTCTAGCATTCGACGGTGCTGCTGTGGGCT

Table A2 (cont.)

TP109776	TGCAGTCCTCGTCCCC[A/C]CGTTCCCTCCCCACGCGCTCTCCGCCTCTCGCGACGGCAAAACCCCA
TP109827	TGCAGTCCTGATTCTGGTATTTTGTCTGAGATTTGTTGAGGGGGGTAGGATTTTTG[A/G]AGGGGTA
TP109828	TGCAGTCCTGATTCTGGTATTTTGTCTTAGATTTGTT[G/T]AGGGGTAGGATTTTTTGGAGGGGTAT
TP109842	TGCAGTCCTGCACCTA[A/T]AGCTAGGGTTGGGTGAAGAATGCACGGGCTGGTGGGCTTCACAGAAA
TP109856	TGCAGTCCTGCACTCAAC[G/T]AGGAGAAGTGGAGGCCGACATGTGGACCTGAACCATCTGCCTGAG
TP109859	TGCAGTCCTGCACTGCACTCTGGTACGTGCACGCCCGCAGCCAATGCAAGTAG[C/T]CAACTCGATG
TP109863	TGCAGTCCTGCACTGGAGGGGGGAGGATTTGGCCATCTGAGTTGACCTGACCT[C/G]ACACAACGCA
TP109864	TGCAGTCCTGCACTGGGTTGCAACTGCCGTGCCT[C/T]TGTTGTCGGTGGAAAGGCCGCACGGGGAC
TP109894	TGCAGTCCTGCCTGTGCCTGACCGCCGCAGCGAGCAA[G/T]CATCTGGGCATCTGGCCCCTACCCCT
TP109895	TGCAGTCCTGCGCCTAGCCTACGGCCGCAGCGCGGCGCGCGCTGACGTCTGACCACTCCGACA[C/G]
TP109906	TGCAGTCCTGCGTTCCAAAGAGGCTTTGAATGCTTTGACGACAACTTCAACTGTAA[C/T]AAGCTCA
TP109912	TGCAGTCCTGCTACTGTCGATCGTGGTAGTGCGTGTTGATCTCTGTAGAACGTGGCC[A/G]ACGGAG
TP109921	TGCAGTCCTGCTCCACTGTCGCTTTGCACCGACGTGACACTGCCTCGTAAACCGAGCCACCC[A/T]C
TP109934	TGCAGTCCTGCTCTGCTCAGTGCTCCCACGGCAACCCCAGTCCCCAGCCAA[C/G]TAGCCTCACAGT
TP109945	TGCAGTCCTGCTG[C/T]GCCAAGGGAAGAAGACTAATCAAAACTCTGAAAGAGTGTGCTGTGTGTTA
TP109948	TGCAGTCCTGCTGGCCCCGATCTGATGTCTC[G/T]GTCAGGCGTCAGCCCTCGGACTCGGAGGCCGT
TP109954	TGCAGTCCTGCTGTGCCGAAGGCCGAGGCCCCTCGGCACGTGGCCCGCGCGGCGCTTTTGGCA[A/T]
TP109984	TGCAGTCCTGGCTGCTGCCGCTGCCGCTGCCGCTTCG[C/G]CGCTGCCACTGCCACACCACCCGCCA
TP109989	TGCAGTCCTGGGCCTCCTGGCGTCCGCGAGAAG[G/T]ATCAAGAAAGAAAGAGCTAGCTTCCGTGAG
TP109993	TGCAGTCCTGGGGTTCATCAGTAGGGACAGTCTTCGGGTTCTCCGACGACCTAA[C/T]GGCGTCCGC
TP110010	TGCAGTCCTGTCACT[G/T]TTGTTTATTTCGTGCCGCGGAGACGACTGGATCAGAGACAATTCATAC
TP110018	TGCAGTCCTGTGTCCTGCTCGCCCGACGACCGCTCGGCAGTTTGTGT[A/G]ACATCCGACGGCTGGG
TP110019	TGCAGTCCTGTGTCCTGCTCGCTCGAC[G/T]ACCGCTCGGCAGTTTCTGTGACATCCGACGGCTCCC
TP110079	TGCAGTC[C/G]TTCGACATCATTGAGCTCTACTGCAAGCGACTCGTTGAGCATGCCACGCAATTAGA
TP110154	TGCAGTCCTTTGCACGCTTG[A/G]ATTAAACCATGCTGAAGAACTGAATTGAAGTCCCTGCATCCTT
TP110175	TGCAGTCGAAACCAGAGAACATCAGGGAGAAGATCGTCGAAG[A/G]GCGGATAGCAAAGAGGCTCGG
TP110185	TGCAGTCGAACGGGTGTGCCGCGGCGGCCGCGCACTGCGACGGCGGGCGCTG[G/T]GCCGAAAAAAA
TP110191	TGCAGTCGAAGACCTTGACCGCCACGGGGAG[A/G]CCGTTGGGCAGCACGCCCTTGTACACCGTGCC

Table A2 (cont.)

TP110205	TGCAGTCGAAGTGCTGTCACTGCAAAGCCTGCATGGCCAGCGCCCTG[C/T]CTCTGCCTCAAGTGCT
TP110209	TGCAGTCGAATGTACAC[A/G]CGCGGTGGAGGTGAGACGCGTTCGGTTGACGCGACCCCGCAGCGCA
TP110230	TGCAGTCGACAGCAAAGGAATTGTGTCCAGCGGGCCGCCACCAGGTGCCGAAGTGCGCGCG[A/C]GA
TP110235	TGCAGTCGACCAGGTTCTTTGATATACTCTACAGAAAG[C/T]TACTGTCGTTCAATCTGTATGCTAA
TP110245	TGCAGTCG[A/G]CCTCGCCGTCGCCTCCCGCCACACCATGGTTGTTGCCGACCTCCTTGCACCCCGT
TP110246	TGCAGTCGACGAAAATCTTCCAGTCCGAACGTTCGGACTGGAGCAG[A/C]GCGCCGATAACTCCCGC
TP110258	TGCAGTCGACGCCGTCGTCGGTGT[A/C]CCCACATCTGTCGGCGCCGCCACCGTCCCCCATGCCCGT
TP110259	TGCAGTCGACGCCGTCGTCGGTGTCCCCACATCTGCTGTCGGCGCCGCCACCGT[C/T]CCCCATGCC
TP110263	TGCAGTCGACGCTCGCTCCACAGCAACGCCTCCACCTCTCTCGC[A/G]TCATCCAGATCCAGTTCGA
TP110301	TGCAGTCGAGCACTGCACCACGAGAAAATGGATGCAGCTTGTTCGGTTGGCTGG[G/T]TTGTATTGT
TP110310	TGCAGTCGAGCCTGACCTCGCCCTGCG[C/T]CCCCGTGAGCGGGCTGATGGCGCCCATCCTCACCAT
TP110323	TGCAGTCGAGCGTGCAGGTGCCTCAGCTCCTGGGGAGCCTGCTGTTCCTGGTCGCCGCGGC[A/G]CT
TP110342	TGCAGTCGATAGCACAGTAAATTCCGCGGCATTCCATTCCCTTCC[C/G]TTTCGAAACGCACCCTGC
TP110348	TGCAGTCG[A/G]TCCACTGCACGAGGAAGAGGAAGAAGTGGGCGGCGGGGCTGTAGGACATGCGCAT
TP110353	TGCAGTCGATCGAT[G/T]AATCAATCGCAGGAGTTCATCTTTTTCCTATGGGGATTGGTTGGTTGGT
TP110372	TGCAGTCGATGTGGTAGAGGCACTTGATTCTTCTTTCTCCTCCTCGTCCTGGTCAACAAAA[C/G]AC
TP110373	TGCAGT[C/G]GATGTGTTCTGTTAAAAAAAGTACGCATTTGTTTCGTTCAGAAAAGGTGCTGTATGC
TP110398	TGCAGTCGCAATGGACTAACTAGAACAAGGG[C/G]AAGCCTTTCGCTTCCATTTATGGCTGCGAAAA
TP110401	TGCAGTCGCACAGCTCACAGAGCACCTCAAGAAGGAGCG[C/T]GCGGCCGAGGTGGCTAAGCTCCAG
TP110421	TGCAGTCGCACTTGTACTCATCGGAGGCTAGCACCTGGAG[C/T]TCATCTGCCCATCAAGGTCCTAG
TP110423	TGCAGTCGCAGACGGCGGCGCTTCAT[G/T]TAGCACAGCTGATCAGGCTGTATCTATCCCCACGGGA
TP110426	TGCAGTCGCAGAGTCGAGCATATCCTCGTCTTCAGGCAACAGTGAGTGGCTACGACCCGC[C/T]CTC
TP110439	TGCAGTCGCAGGAGGCCAATCCGAAAGAATCGGC[C/G]GCCTATCCTGAGCTCAACTTCAGAACGAT
TP110454	TGCAGTCGCAGTCTGATTGGTATCATCATGACCCTCATCAACTTCAGCCTGC[C/T]GCTGACTCGGA
TP110463	TGCAGT[C/T]GCATCTGGACTCTGGCGAGCTAAGTGCAACTGGTCGACAAGACCCCGTAACTTGCAT
TP110472	TGCAGTCGCC[A/G]AATCGCTCCGTTACCGACGGATTCAAGCAGCTGGACAGCGCTCCCTCCTCCCT
TP110502	TGCAGTCGCCATGACAGATCACAGGTAGGC[A/G]GGCGAGGCGAGCGAATTGGACGGTTGGAGCTCC
TP110527	TGCAGTCGCCCTGCGCCTGCGCGG[C/T]GGCCGTCTCCGTTAACGAGGGTGCGGCGGCGGAGGACGC

Table A2 (cont.)

TP110541	TGCAGT[C/T]GCCGAGCTCCTTGGGGATCACTCCCTCCAGGCTGTTGTTGGCCAGTTGCAGCACGGC
TP110549	TGCAGTCGCCGCACTGCCAGTGCCAGAGATGATGAGTAGTGCAGTG[C/T]TCTGAGGTACAGTACAG
TP110554	TGCAGTCGCCGCCGACGCAGCAGCAGCAGGAGCTGGTGGGCA[A/G]CCTGGACACGGAGCTGAGCGA
TP110557	TGCAGTCGCCGCCGCTCTCGACGCCATTTCGCGCACCAAATCGGCCATGACTT[G/T]CTAGCTCGAG
TP110558	TGCAGTCGCCGCCGTGGTCCCACGTGCCGTTCTCGAAGTG[C/G]GACATCGGGGACAGCATGCGCAC
TP110560	TGCAGTCGCCGCCTTGCAGGAACTCGAATGGGCAGGA[A/G]AAGCTCTCACCACCCTGCACCTTTCC
TP110563	TGCAGTCGCCGCGCACGCTGCGGCCTCGCTCGC[C/T]CGTCTCGCCGCCTCCCGCCCCGACCTCCTC
TP110571	TGCAGTCGCCGCTAGCGGGGACGAAAGGGGGCGGCGATTAAGGTC[C/T]GACCAGGTCGGCGGCACT
TP110582	TGCAGTCGCCGTTCATCAGCCGATCGATCCCGTGAC[A/G]AGTCACGGACGGGATGGAGCGGCAGAA
TP110587	TGCAGTCGCCTCCAGCTCGCTCCAGTGTACTAGTGCAACGCACAGCCGTTCAAAT[C/G]GAGATCTG
TP110591	TGCAGTCGCCTCTGTCCGTATGTCGTCGCACGGAGATGTCGTGTCGTC[A/G]TTGTTGTCGGAGCTG
TP110604	TGCAGTCGCGAGCCCCGCCGCCAAGTGTCACCACAT[G/T]CTGCCTCCGCTTGCAGCGCCAGCGTAG
TP110611	TGCAGT[C/T]GCGATGGGCAAGTCGGATTTTGGCATCTCTGATTCCGTCCGATCCAACAGCGAGAGC
TP110637	TGCAGTCGCGCGG[A/T]TCGATTTCTCGTGGGGGGACGCGGCGTACCACCAGGAGACGCTGGAGAAC
TP110656	TGCAGTCGCGGCGGAGGTGTC[C/T]GCCGTCGTGGCCATGGTGGTGGTGGTGGTCGGGATCGCCGTG
TP110663	TGCAGT[C/T]GCGGGCGAGGTCACGGACCTGCTTCATCCACGTGCGCACCTGCTCGTCGTGCCCGCT
TP110665	TGCAGTCGCGGTAATCGACGAAGCTGAGGGCGTAGG[C/G]CGAGGCGGCGGCCCAGCGGTCGCGGAG
TP110681	TGCAGTCGCGTGGAAGTT[A/C]CAACCGCCCTCCTGTTCCTGTCCGCACATGCGCATGTTTCCTTTC
TP110693	TGCAGTCG[C/G]TAGCTGTGATGGTACGCCCTTGACATCGATCGCTGCCGCGAATGGCGGACGATTT
TP110750	TGCAGTCGCTGCC[A/G]CCTAACCAGGACGTGGACGCGCTCCTTCAGGAGTACTACCGCCTCGCGAG
TP110755	TGCAGTCGCTGCTCAGCTGGCGCGACCCGAGGGCGAC[C/G]TGCCTCTTCGTCATATTCTGCCTCCT
TP110756	TGCAGTCGCTGCTGAGCTGGAGGGATCCAAGGGCAACTGCACTGTTC[A/G]TGGTCTTCTGCTTCAT
TP110766	TGCAGTCGCTGCTGGGCGCTGGCCATCCCATCAGACCGCGCGCGTGCAAACGG[C/T]GCTGTTCGCT
TP110780	TGCAGTCGCTGGATCCT[A/G]GCCGTTCACTGGTATCCAACGGTGACCAGGATTCCTGGAGCATGTG
TP110797	TGCAGTCGCTGTCGTCTCGAGGGCGACGGCCGAAATGAGCTGGTCCCTGT[C/G]GACTGCCTCAACG
TP110822	TGCAGTCGCTTTCTTTTGAGT[C/T]CTAAGGAACTGGAGACTGGAGTCCTGAAGCTCTGCACGACCA
TP110831	TGCAGTCGGACAGGTTC[A/G]TCTGGCGTTGGACCGAGAGTGGCCAGTACTCCGCGTCTTCTGCGTA
TP110844	TGCAGTCGGACTCCTTGTACAGCGGCGCGCGGGACTCGTCGTAC[A/T]CCCAGCGGCCCTTGTACAG

Table A2 (cont.)

TP110849	TGCAGTCGGAGACAGCCCTCCTCGCCTCTCCTCTCGTCGGCGCCGAGCTTA[C/T]GAGTGGAAGCAG
TP110851	TGCAGTCGGAGACG[C/G]CGTCGCCGAGGAACAGCGCGGCCGCGCAGAAGCAGTCGCTGAGGCAGTA
TP110859	TGCAGTCGGAGCAGCAG[C/T]CGTCGTCCTTGCCGCTGCACCAGCCCTCGTAGAACGCCATGGTCGG
TP110882	TGCAGTCGGATCGTTTCATCTA[C/G]AAGTGGTCAAAAGATGGGAAGTACTCTGCCTCATCGACCTA
TP110884	TGCAGTCGGATGGCAGAGCAACGAATGAATTTA[C/G]TAGTAATTATTCAGACTAATGTACACCAAG
TP110893	TGCAGTCGGCAACCTGATCGA[C/T]AATATATGCAATCCAGTCAGGATTTGTTGAAGACCAGTGCTA
TP110894	TGCAGTCGGCAACTCGGTATGCATGCATGGTCC[A/G]TCGATCAGCTATAGGAGTACTCTTAGGGCG
TP110901	TGCAGTCGGCACTTGCATTTTAGGAGCAGGTATGCT[G/T]CTTTTCCATTTCAGCGCCGAGCAGATC
TP110905	TGCAGTCGGCAGTGCGATCCATTGGAGGCAGA[G/A]CAACCAGTAATCTGCGGGAGCAGGATCATGT
TP110931	TGCAGTCGGCGAGAGCCAGCAG[C/T]GCTGCTGTTGCCGCGGCCCTGCTGCTGCCCCGCGGCGCCTT
TP110933	TGCAGTCGGCGCACTGCCAGTGCCAGGGATGA[T/C]GAGTAGTGCTCTGAGGTACAGTACAGAAGAG
TP110936	TGCAGTCGGCGCATCTGAGACGTTCATTGTGATCCAACGGTGA[C/T]CCTAACTAAACTCATCTAGC
TP110944	TGCAGTCGGCGCCGTTCCTGTTCCTGCGCCCCAGCGCGCCGCC[C/G]TACCACCTGCTGTGGTGGGC
TP110947	TGCAGTCGGCGCGCGGTTACTTGAGCACCAAACGGAGCAAGGCTGTCCACACTCC[A/T]ACGGCTAC
TP110955	TGCAGTCG[G/T]CGGCGGAGGATCGGATCACGCATCAACGTGCATGTCCGATACATACATGTATGAT
TP110956	TGCAGT[C/T]GGCGGCGGCCCTCCTGGCGCTGCTGCTGCTGTTGGTGCCTAGGCCCTATGGGTCTAG
TP110961	TGCAGTCGGCGGCTCTGG[C/T]CTTCCGTTTTCTTCAGGGAACGCCGCCGCCACCGTAGCTCTTTCC
TP110964	TGCAGTCGGCGTC[G/T]TCGGACCCGAAGAACCAGTGCGTGTACACGGTGTACGTGCGGACGGGGTC
TP110969	TGCAGTCGGCTACGTTGATGCTGGTG[A/G]CCTCCATCCTGATGAGCACCTCGCCTTTCTTCGGCGA
TP110989	TGCAGTCGGGAGCGGTACGTGTTTGGGCATTGCTGCCTAGTGCCTAGGCTA[A/G]TTGCTGAGCCTT
TP110999	TGCAGTCGGGGAAAGC[A/G]GGGCGGCGGCCGTTGTCGGGGCCTGGAAGTAGACGAAATGGCGCCAC
TP111003	TGCAGTCGGGGACAGTCCAAGCGAGAGTGGACTT[C/T]GGAGTCTGGACAGAGACTCACGCTCTCTC
TP111029	TGCAGTCGGTCACGGCGGTCAACTTCGGCGCGGAGCTGGACATGATCGG[C/T]TCCCTACTCCCGAG
TP111050	TGCAGTCGGTGGCGCAGAGCACGGGGTGGACGTACAG[C/T]CTCCTCTGGCGCCTCTGCCCGCGCCA
TP111053	TGCAGTCGGTGGCTGAGGTTTTGGTCGTCGC[C/G]CAGGCGCTGTGCATGCGCTCGTCGGCGGCGTC
TP111071	TGCAGTCGTACAGAGACGCAG[A/G]CACGAGAGGGAGGGAGGGAGGAGACGGGGAGTGGGAGGAGGT
TP111077	TGCAGTCGTACCTTGGAGATCGCCCAGAGGCTGAAGTG[C/G]ACGATGTACTCGCTGTTCGTCATGC
TP111132	TGCAGTCGTCACGCAATGTGACGGTCACGGTACTACGAGATGAGGCGATGAACGGGTCC[A/G]CCAC

Table A2 (cont.)

TP111134	TGCAGTCGTCACTGTTGCAGTTGCAGCCGTACCACCCTTCTC[A/G]TTGGTCTCATGCGTCGTCGGC
TP111138	TGCAGTCGTCAGTGCTCTGAACATAC[A/T]TACAACAAGTAGAGTAATAAGGAAGGAACAATCCAGT
TP111150	TGCAGTCGTCCAGTAAAATCCTTACCGAAAGGCCTTTCCCACCAAAGTATTTGGTGCC[A/G]CGTGA
TP111157	TGCAGTCGTCCCATCCCTTACCAACCACCATGGTGGCATTCAGCGTGTCAGGCACC[C/T]TGACATG
TP111163	TGCAGTCGTCCGTGCAGAACCCCAGGTTCGTGACCAACACCACGGTGCGGCCGCT[A/G]TGCATCAT
TP111164	TGCAGTCGTCCGTGGGCGCGTGGCTCACGAGTACGGCGCGC[G/T]GCGGCCGCCACCACCAGCGACG
TP111182	TGCAGTCGTCGAGGCGGATGGACTTGCCAAGGGCGCGACGGG[A/G]AGGCTAGCCAGAAGAAGTGAT
TP111189	TGCAGTCGTCGCAGTGCTGCTCAG[C/T]GGCGCTTGCGATGATCTTCACCTCTTGTCTGTCTCTGTC
TP111190	TGCAGTCGTCGCCAAGAACGGCCACGGCGCCGTGGTCGAGGAGATCCACGGCCTGATCCGCGT[C/G]
TP111204	TGCAGTCGTCGGCGCTGGAGCGGAGCTCGGCCGAGGTGTT[C/G]CACTGCGCGAGGGGCACGTGGGA
TP111220	TGCAGTCGTCGTCGTC[C/G]GCCTCCGCCGCGCTGCACGTCGTCGACGTCGAAACCAGCACCCCGTA
TP111248	TGCAGTCGTCTTCATTTTCTTTCCATTTTC[A/C]ATGTGGTTGCTTTGCTTGAGCAGCAATTAGCAT
TP111259	TGCAGTCGTGACAGGCGCGCGATCCAC[C/T]ATTCCACTCCATGCTGCCAAACAAACGAAAGAAACC
TP111273	TGCAGTCGTGCCCGTCGACTCCTCTGTGCAGTCGGCTGATCTGCGCC[C/G]TCCGTTAGCATCGAAC
TP111281	TGCAGTCGTGCGTGCCTGGGGTTGGTGTGAGGCAACTGA[A/G]CAAGCAACTGGTCCGTCGTCCCAA
TP111288	TGCAGTCGTGCTGCCTGACCTTAGGCCTCGTGCAGCTATCGGGACTGCATCGGCATCGCATGG[A/C]
TP111295	TGCAGTCGTGGAGCATCTCGGTGAGGGGCCCGCTCTACTCCGC[C/T]ATGTTCAACCCGCTCTGCAC
TP111296	TGCAGTCGTGGAGCTTGCGCAGGGACGCCATGGGAGGCGGCACGGCAGGCGGGCACTGGG[A/C]AGT
TP111316	TGCAGTCGTGGGCGCCCGAGCAGAGGAACCCGTTGA[A/G]CTCCCGATTTACGAGATGGTCTCTGCC
TP111318	TGCAGTCGTGGGCTTAGGACATTATGATGGAGCATGGATGCAACGCACCCCCG[C/T]AATCCAGCGG
TP111319	TGCAGTCGTGGGTCCCACACGGTCAACTATAGGTTCTCACT[A/G]GTTTGTGCCAGGCAAGGCGAAG
TP111324	TGCAGTCGTGGTGCGACGCCCATGCATTGGTCACATGC[C/T]GACGTGCATGCGCGTAAAATGCTCT
TP111341	TGCAGTCGTTACCTGCATTTGTCATTGAAGCGCAGGTTGGCAGCATCC[A/G]AAGCAACATTACCCA
TP111404	TGCAGTCTAAAAAAAATCACCGAAGCAGAGCACACGCTCCACCCACGGAGCTCGCGG[C/T]GGCCGA
TP111425	TGCAGTCTAAGGAGCAGATGGAAGCCGTGCTGAAGATGAAGCA[A/G]GAAGCCGCTTCAAGGCGGCA
TP111451	TGCAGTCTACAGCAGTGGTCAGTGGAGAGGGAGGGGAGAGGCAGTTGCCGACTT[A/T]GCCGTGCGG
TP111459	TGCAGTCTACAGTCCACAG[C/T]TTAAAGACCAAAGAACCTCTCCTGTCACCCTCCTCCGCCACCGC
TP111471	TGCAGTCTACCCACCCGCGCTGCGATCTCGGCCACAAACGGGCACGCGCGCTC[G/T]CTCAGGGGCG

Table A2 (cont.)

TP111472	TGCAGTCTACCCACCCGCGCTGCGATCTCGGCCACA[A/G]ACGGGCACGCGCGCTCGGTCAGGTGGC
TP111481	TGCAGTCTACCTTACTGCCTAAGAAAACAAA[A/G]AACCGACTTACATATGTTGGCAACTAGTAAAA
TP111487	TGCAGTCTACGGCGATGTCCAGTTTACACAACCAGACACGACTGCACTCCAAGAT[C/T]GCTGACGC
TP111525	TGCAGTCTAGACTCTAGATGCTCAATTGGCGGATCCATCATCGCCTG[A/C]GCCGTGGTGCTCCGAC
TP111562	TGCAGTCTAGGCGAC[A/C]CTCAACAGCAGCAGCTACCTAGGCATAGCATGCAGTAGTACTAGGAGT
TP111564	TGCAGTCTAGGCTG[C/T]TCGTCGTCCGTATCATTACGCGGCGATCATCCGCGTGTGCAATCTGTAC
TP111573	TGCAGTCTAGTAATTCAAGCGAAAAGGGGTACGTTCGCTCGTGG[C/T]TTGCACAGAGCTTCCAGTG
TP111578	TGCAGTCTAGTAGCCATATATGTCACGCACGCCTCACCTCGTCGTGCGCACGCTCTATGCTAT[C/G]
TP111579	TGCAGTCTAGTAGCCATATATGTCACGCTGTCTGTCCTGAAGACCCTGAAGGCGC[A/T]ACTAAAGA
TP111637	TGCAGTCTATTGGCAAGAA[C/G]TTTTGAGCACAGCTTGTAGATAACATTGCACAAAGATATAGGTC
TP111656	TGCAGTCTCACCAATGAATCGATGGTGCGGTAGATGCCCACA[C/T]AGCACGGGGATGGGAGGAGAG
TP111657	TGCAGTCTCA[C/T]CAATGAATCGATGGTGCGGTAGATGCCCACACAGCAGGCGGGATGGGAGGAGA
TP111659	TGCAGTCTCACTCGCATAGGAGTACA[A/G]TATCTTTCTTTCCTTTTCCTTTCCACACTGTTCTTAT
TP111661	TGCAGTCTCACTGTTCGGGTGTGTATTTGTAACATGGTGCAGATGGGGGAGA[A/G]CGGTGTGCCCG
TP111676	TGCAGTCTCAGTTTGTTGTGCAAGGAAAGATTTTCACTGCTCACCTTTGACAAACGAGAGATG[G/T]
TP111682	TGCAGT[C/G]TCATGAAAACCGATGATTAGCGGAAAGATCTACCAAGAAGTTGAAAAAAAGGAAAGG
TP111732	TGCAGTCTCCATCAGC[A/G]ACCCCTTCAGTGAAATCTGAGTGTGCATCGCCGAGGAACAGTGGTCT
TP111737	TGCAGTCTCCATGGATAGTGCAGCAAAATGGCATGGCACGACGACGATGG[C/T]CGCATTGATTCCG
TP111766	TGCAGTCTCCGTGGCGCCGACACAATTTTCGATTCCAAGC[A/G]GGCAGAAGCAGCTTGTGACCTTC
TP111775	TGCAGTCTCCTCCCGCGGTGGGAGTCGCTGCGC[G/T]ATTCCTCCAAGGTAGATGCCCCTGTTTCCC
TP111794	TGCAGTCTCGACCTCTGTCCATCAGAGTGCACCAGCACCGCACC[C/G]ATCACCTCAAAGCTTGGGT
TP111801	TGCAGTCTCGCA[A/G]TAGCGCCAAGATCTCTCCTTTGACCTCCCCCTTCGCCCTCCTGCCACTGCC
TP111818	TGCAGTCTCGGTGCAGTCACGACAGGATCGGGCAGGTGCCCACCGTCCAGAGGATGGGGA[A/G]CGG
TP111832	TGCAGTCTCGTTGACATCTCGCGGCTTCGCGCTCACACGGGGGTGCGCGGCCTCTCAAGCGG[C/T]G
TP111846	TGCAGTCTCTACTCTGTAGTAGCATGTGAAC[A/C]CAAGGATATCCCTATCACTCGGATGACCGCAA
TP111881	TGCAGTCTCTCTGACTCATCAAGCCATA[A/G]CCAGCTAGCTGGATATATATGCCTGAACCTGAACA
TP111917	TGCAGTCTCTTCTCATAATCATCAGCAGCAGCAGCAGCAGC[C/T]AGGAGAGGTTGCCTAGCACAAC
TP111920	TGCAGTCTCTTCTGAAGATGACCCCACTTTGGAAAGAAAGTTCTGAAACC[C/G]TTGAGAGCATGAC

Table A2 (cont.)

TP111953	TGCAGTCTGAATAAAGGG[C/T]GTACCCAGTGCGGAGAGCTCCCGCTCTGTGCGGGGTCTGGGGAAG
TP111966	TGCAGTCTGACGTTGCCGACGCAGGAAGCGCGCCAGCTCCTGAGCGCCTTG[A/G]CCAGCGCTCGTA
TP111973	TGCAGTCTGAGACAGCCTGACGCTACGCAA[C/T]TCCGCTGCTGCGGCTCCCGAAAAAAAAAAAAAA
TP111988	TGCAGTCTGATCAGCCACCTC[A/G]CGACGCCGCCGCGCGGGAGGGGAGCCGCGGCGGCACGGGTGC
TP112031	TGCAGTCTGCACAAACATTTCAGTTCA[A/G]GCGTCGATAAAATATTCCACAATTTCACTCAAAATC
TP112039	TGCAGTCTGCACAAGGCGGCCATTATGCTATGCCGAGCCCGTACACAC[A/C]GAAAGAAGCGCAGAA
TP112041	TGCAGTCTGCACACAAGTTGAAGTTGAAGCTGAAGCTAGGCAGCTAGCTATCCCACTGAACTA[C/T]
TP112054	TGCAGTCTGCACAGATCAGAGGTAGTGCCAAACCTCCGATTATCAGATGGCGATTTGGTCACA[A/C]
TP112055	TGCAGTCTGCACAGCGCGTGGGGGCACGCCGCACGCGCGCGCTTCCAACCG[C/T]GCCGCGCCCACC
TP112059	TGCAGTCTGCACATCAGCATTTGTACAGT[A/G]TTGCCTGCAATGCAACGCCATACCTTGTTGTAGA
TP112064	TGCAGTCTGCACATTTAACTTGAAAGGACCAATTTTCTTT[C/T]ACTCTATCTAAAACTAGTTCCTG
TP112070	TGCAGTCTGCACCACCCCTGCGGCGTATCCGAGTCCCCCGAGAGA[A/G]AAAAAAAATCTTGGACGC
TP112083	TGCAGTCTGCACCGATGGGAATGAATGGGATTTG[A/G]GCACAGTGAGTGCAGTGTGGATGGATCTT
TP112099	TGCAGTCTGCACGGCGGGGCTCCAC[C/T]CATCCACCACGCCATCGCTTCTACAAGATCCCACCCCA
TP112104	TGCAGTCTGCACGTATAGGAGTACGAGTAGTACACAC[A/T]GGGAAGCTACCATGGGCCACTGCCCA
TP112105	TGCAGTCTGCACGTCC[A/T]CTCCCACGCACTCTCGCCGTCGTTTCTCACGGGCTCTCACCGCAGCA
TP112131	TGCAGTCTGCACTGCATGTGCTCTTGGCCCAGGAAGGAGAGGACCGCATGCAGCCACCGCG[A/G]GG
TP112139	TGCAGTCTGCACTTGGTCTATTTAAATCGATCGCCCCGCATGCACGC[A/G]CCAGCAGCACCCATCG
TP112153	TGCAGTCTGCATC[C/T]TGCATCCTGCATGCATGATCTACGGCCTCTACCTCGATCGTAGTACTTGC
TP112157	TGCAGTCTGCATCTCACGTCATCGTCCAAGAATTTGCACGTTGTGCAGAAGTACTC[C/T]CCCATGC
TP112176	TGCAGTCTGCCATGGCGGTGATGGGTGACATGGAGAGA[A/G]AGGGGATCGGTCTAGATGATGTTAG
TP112202	TGCAGTCTGCGCTCTATCGATCTACAGCCTGCAACACCATTGGCATCAG[C/G]AGTAGTCACCACTC
TP112213	TGCAGTCTGCGTGC[A/G]CCGACGAGCGCTAGCACGCTACATCGCCGCTATTATCCTCTCCGTACGT
TP112218	TGCAGTCTGCGTTCCCAGCCTGCTTGCGTTTGTTGGTTTGCACGTCACTTG[G/T]TGGCAGGAGAAA
TP112224	TGCAGTCTGCTACG[C/T]CAACGGCAACGCCCTCCCCCGACTTAACGTTCACCTTCCTATTTATTTC
TP112246	TGCAGTCTGCTCGTTGCTGATTGGGAAATCAC[T/C]GCGGCCCCGTCTCTGGGTTCTGGCACGGTGC
TP112252	TGCAGTCTGCTCTGGTGGACTGGACTGGTGGTAGCGGCGGC[G/T]GCCGAGATAGGGAATAGGGCCC
TP112276	TGCAGTCTGCTTGC[C/T]TGCACTGGACCTATATGTCTATATCTATCCCTCTGTGCTTGCCATGGCT

Table A2 (cont.)

TP112278	TGCAGTCTGCTTGCTTGCA[C/T]TGGACCTATCTGTCTATCGACCCCTCATCCCCTGTGTGCTTGCC
TP112287	TGCAGTCTGGACGAGAGCCCGATCGAGCCTCAGCCGTTGAGAGACCTGAGACCGCCTCCTGCG[A/T]
TP112291	TGCAGTCTGGAGCACATAATGTCATTCCCTTCAGAGTTTCAAACTGGA[A/G]GCGAGATGCTGAAGC
TP112327	TGCAGTCTGGTTGTTAATGAAAATTTTGAAGACCCGCTGATTGATCTTGGTGAT[C/T]GGGTACTGG
TP112334	TGCAGTCTGTACGCGGCATCATCACAGGGGATCCCTGCCTCTCGCCCTC[C/G]CATTTGAGCACAGC
TP112344	TGCAGTCTGTAGCTGGAGAATGGGCGACTCGCGGGTGAGCGCTGCCCGTGCTCGGTGT[A/C]ATGAG
TP112353	TGCAGTCTGTATCCTGCTAATC[C/T]GATGTTCTTCAGTCTTTGCGGCAGATTAGATTAGAAGGAAT
TP112384	TGCAGTCTGTGTGGAAGTAGCAAAGCTCTGC[C/T]TGCAATGCAACGCGATGCGAGCAGTGCCATGG
TP112406	TGCAGTCTTAAACCGCAGCTTAATCTGTCCTTTTGTTTCCGTCTCACCAG[A/C]CACCTGCATTGTA
TP112422	TGCAGTCTTACCAACCATGGTCCATGGGG[C/G]CGCGATCAGATTCAGACCATGCAACCCCACGGGT
TP112474	TGCAGTCTTC[C/G]CCTCGTCCACGAGAGAAACCACCAAATAAGGAGAGCAGCAGAGGAAGCCCCTT
TP112511	TGCAGTCTT[C/G]TGCTGCTACCTGATCTAACACTGGTTCCATGGATTCTTTCGCGCCCGTTACAGG
TP112526	TGCAGTCTTCTTGGTTTCTGACTAACGTCCATGTGGTTTTCCCTTATTTAGATTCA[A/G]AGTCGAA
TP112543	TGCAGTCTTGAAGACGGGTGGCGGTGCAGCGGGCTG[C/G]TGCTGCTCTGCCGTCCTCGTCGTTTTG
TP112549	TGCAGTCTTGAGCGTGAAGTTCGGATCATCGT[T/C]GGTTTCCTTTCATGCTCATACACATTTTGAG
TP112581	TGCAGTCTTGCTTCCTTAACAGCCTGACATCGCAGCACCAGGAGC[C/T]AGCATCTTAGCAGCCATG
TP112601	TGCAGTCTTGGTGCTAGCGTCGAGCTGCA[C/T]GCCTGCACCTGCAACTGCATGCATCGGCCATCGG
TP112624	TGCAGTCTTTACTTGCCTG[C/T]TCGACGCGCCAGAAATGCGCAAAACCAACAACGCAGCAGAGTCT
TP112633	TGCAGTCTTTCCAGAACCTGTCTCAGC[A/G]ATACCAATAACATCACGCTGCTGTAGACCTAGCGGA
TP112676	TGCAGTCTTTTGGCCA[C/T]CGCGCAATTCCTGATAGCCTGTAGTCATGTCGAGACGGTGGAAAGGT
TP112728	TGCAGTGAA[A/G]CACCACATGGGGGGTTATGATGAGTAGAAGGAATGCTTTCACATGGAATTCAGA
TP112746	TGCAGTGAAAGATGAAGAAATCAGAATACTTGCACTCCACCGCGTGCGA[C/T]GCGCAAAGCCTTTA
TP112748	TGCAGTGAAAGCATGCGCAGGCACCGAATAAAGTCGTCCCTACCC[A/G]TCTCATCATTGATCACGC
TP112750	TGCAGTGAAAGGAGCAGTGAGGGCTGTGGTT[A/G]TTGTGGGCAGACCTGTGTAAAGTGACTGAAGA
TP112775	TGCAGTGAACAAACTTTTAGCACTCCCAA[G/T]TACCAGTGGGGCGCGTGTATAAACTTTCTACACT
TP112779	TGCAGTGAACA[A/G]TGCAGAGGAAAATCTGCTGTTCTGCTAACGTGCATTATATTCATGCGTTTCA
TP112788	TGCAGTGAA[C/T]ACTAAAAGTGACTAGTCAGAATTGTTATTCCGAAGCGATTCTAATAGATGATGT
TP112799	TGCAGTGAACATTGAGGAGGTTCATGGCAGAGGAAGTGGTGATGAAGGC[A/G]CTGTTTTCCAGCTA

Table A2 (cont.)

TP112807	TGCAGTGAACCCCAGCAAGGGTACAACGGCCCGCCATGATCCATCCCGC[C/T]TCTGGAAGCCTTGG
TP112862	TGCAGTGAAGA[A/G]TCATCCTTCAGGGGGAGGAGGAAAGGGGACGACGGCACGAGTTTAAGCCAAC
TP112869	TGCAGTGAAGACAGGTGC[A/G]CAACAAGATTGCGGACGTATCATCAGTGACAGTGATCGATGCATG
TP112887	TGCAGTGAAGCAATCTTAG[C/T]TTGCTTGCTTTACTTTGGTATCATCTGTCTCTGATGAAAAGAAA
TP112937	TGCAGTGAAGGAGGGTCGCTGT[C/T]TGTGTCTCGCTTCGTCCACGGTACGGTTGGGTGTTGGGGGC
TP112956	TGCAGTGAAGTATGGGCGGGCCCAGATTTGATGCGGCGAAGCCCAAAAGGCCC[A/G]TCGCGGGGGC
TP112963	TGCAGTG[A/C]AGTCGACCTTCGCTCATTGTTCTCTCTCAAGTCTCGAATCAAATAATGTTTATACA
TP112969	TGCAGTGAAGTGACGCTGTTTCCGTGCCTTTGGTGCAGGCACTGACGGAGCGGCAGCCGCAG[A/C]T
TP112986	TGCAGTGAAGTTGTTCCTAGC[C/T]AGCGCGAGTCGGCGCAACGCATGGAAGCCCCCCAGGAACTCT
TP112998	TGCAGTGAATCAACAAA[A/C]AAGAATACCTGTCAAACTCAGTTGAGGCATCATGGCTTTCCTGTCC
TP113008	TGCAGTGAATCTAAT[A/T]TCCCACAAGAAAAGAACGGCACAAAGTGGAAATCAATCCTGAAATCAA
TP113016	TGCAGTGAATGACGAACAGAAT[A/C]ATCGATTCCATAATCTGGGTTTCCATTTCCTGCTAGCTACC
TP113017	TGCAGTGAATGACT[C/T]GGCGGTCGTCTGACGCGCACTGGCTCCGATCGTTTGTAGTACTTGTCTT
TP113031	TGCAGTGAATGTGAAA[G/T]AATTTGGTCTCACCCCTTCACTTTTCATCAGGCAGAAGACCTTGAGA
TP113032	TGCAGTGAATGTGAACGAATTTGGTCTCACGCCTCCACTTTTCATCAGGGA[C/G]AAGATTTTAAGA
TP113033	TGCAGTGAATGTGTTTGTT[C/G]TGTTAAAAAGGTACGCATTTGTTTCGTTCAGAAAAGGTGCTGTA
TP113036	TGCAGTG[A/C]ATTATTGGTAGTGTATTAGAACTAGAACGGGCGGACGCAAGCACGGGGACGGAGAT
TP113037	TGCAGTGAATTCAAGCACGACAAC[A/T]ACGGTCATGACAGCCCACATTGCATTCTTCCCGATTCCT
TP113056	TGCAGTGACAACCCTATCGCTCTTGCT[A/G]AGAGAGGCATGGAAGGTTGGGAGGATGGGGAATGGG
TP113058	TGCAGTGACAACGC[C/G]GAGCATGCCGCAGTAGCTGTACCCCCTTCAGTTCGCCAGGCGGTGCATA
TP113068	TGCAGTGACAAGGTTTCCAACCTGCGTTCAACTTCCCAGCTCGAGAGCGTCCATTGCTGA[C/T]CCT
TP113085	TGCAGTGACAC[C/T]ACCAGCCGAGCTGGTCAAAGCTGAGCCTGGACCTGGTGGAGTAGGACTACTC
TP113104	TGCAGTG[A/C]CAGCAAGTGAGTACCCTGATGAGGTTTTTGATTGGGATGACCCCTTTAAGCCAGGT
TP113105	TGCAGTGACAGCATGACACCGATCATGCCCAT[G/C]TTCTCGTCCGCCGAGTCACTGGCATCGACCT
TP113114	TGCAGTGACAGTAAGCA[A/G]AAAAGGGGAGCAAGAATATCGAACCAGTAACAGGAACCTCCCCGTT
TP113115	TGCAGTG[A/G]CAGTGCCAAGCCGAGTTGCGCGCACGGCACACGCCGAAGGGCACGCGGGGCGCTGG
TP113124	TGCAGTGACATCACACGGAACGCGCCAGCGTCGTCGCCGTTTGGGAGCAAACACAATGTG[C/T]GGC
TP113129	TGCAGTGACATCTC[A/C]ACGGACGCGCAGTGCTCCATCGTCAGGTTCACGGGGCCCGACTCCAAAG

Table A2 (cont.)

TP113153	TGCAGTGACCAGCAGGTAACTAAACTAGACTAGAAAGGCAAAGGCA[A/G]CTACCATATCTCCATCT
TP113162	TGCAGTGACCAGTGAGGCCATCAGCTGATGTA[A/C]AGTGACATCTGCCATCAGGTCGGTACGGCTA
TP113172	TGCAGTGACCCATGTGCCACTGTGCCAATGTCACTCATTGCT[A/T]GCATGTTCTCTTCTCGCTGCT
TP113199	TGCAGTGACCTCCTGGTAGTGCTTTTTT[G/T]AAAACTGTTTAAAACGTTAGCAAAATAAATGAAAA
TP113207	TGCAGTGACCTTTATAATGTATGATGGGGCTAGTCGGCTAGAAATCGAAAAAGC[A/T]AAATTACCA
TP113213	TGCAGTGACGACACTGCACGGCCCTGCACAGCGCTGCACAGGAG[A/G]ACAAGGGCGCCTCGCCTGC
TP113214	TGCAGTG[A/G]CGACCACACCATTATTATTTTTTTCCTCCAGTGATCGTCGATCCATCTGTTCTTGA
TP113216	TGCAGTGACGACCGCCTCAGCGCCCTCACCGA[T/C]GACCTACTGCTCCTCATCTTGCGCCGCCTCG
TP113229	TGCAGTG[A/G]CGATGTGACCTGTATAAGCAAGATTCTTCTCCACCCAGAGCGAGCGATAATTGCAA
TP113249	TGCAGTGACGCGGCGTCCTCGCGCGATCGTACGGT[A/G]TGGATCGCCGTCTTCACTCGGGTCACGC
TP113276	TGCAGTGACGGGTGAGATAGGGGGCAAGTGGACT[A/G]GATAGAGACCTGCGGCGGATTGGTATAGG
TP113279	TGCAGTGACGGTGGTTACAGTGATTCACAGTGCCAC[C/T]GCCATCGGCCTAGTGTGTGTGCAACTG
TP113283	TGCAGTGACGTACGTCGCTGACACTGATATGTA[G/T]GAGTACTTTTATTTATGTTATTGTTATCCC
TP113297	TGCAGTGACGTGGCAACGGCGGCGGCGGCGGCGGCGCGGAGGAT[G/T]AGGTCGTCGAAAGCGGGGC
TP113317	TGCAGTGACTCCCACGACCGTTCGTCCGCGTACGCGCGCTCCCACGCCTCCAGGACGCGGCCC[A/T]
TP113333	TGCAGTGACTCTTATC[C/T]GAAGCTCTGGTCGCCGCCTGGCCTGATAATGCGCGTTGCCGCCTCCC
TP113336	TGCAGTG[A/G]CTGAACTACCCATGCTTATACAAATTAATGTCTTTACGGCCCATGTGTTTTAGCGC
TP113340	TGCAGTGA[C/T]TGAGGACCAGACGGAATAGCCGCTGCCCATGTCTGCTCTCTAAGAGGTCGCAGGC
TP113354	TGCAGTGACTTATAGTGGAAATTGGC[G/T]CCACAGCGGGTACTCCATACCCCATGGTAAACGCCAG
TP113370	TGCAGTG[A/G]CTTTTAGCTTCCTTCCTTGCTTGCAATTGCAACCCAGCCTTGCAAGAAACCAATCC
TP113381	TGCAGTGAGAACCTGGAACTTCTCGGCCGCGTGTGGGTCGTTGGG[A/G]TTCTTGTCAGGATGCACC
TP113394	TGCAGTGAGACTGCACCAGCGGGATCCAGAGCAATTAATCAAGCGAGA[C/T]ACAGAACTACCGTAA
TP113410	TGCAGTGA[G/T]AGTCTTGGGACTAGTATGCTGTTCAGACCAGTTGAGCAGACCAAGTGAACTGAGG
TP113436	TGCAGTGAGCAAGCATGCATGACATGAGATCGTCTTCGTCAACAAT[A/G]GAACCAACAATTGCTCT
TP113437	TGCAGTGAGCAATAA[C/T]GCAGGCCTCGTCAAGGAGGCCAAGGCCATCATCCGTCTGTTCCCGATA
TP113446	TGCAGTGAGCAGACGGCACGGAGGGAGCGGAATGAGTAGGCATGCGGTCAGCATCAGCGATCC[A/C]
TP113459	TGCAGTGAGCATGATTCAAAGTTTAAAGATAATCCATCAGGTTTCAGAAAGAAATG[A/G]TTGGAAT
TP113468	TGCAGTGAGCCACCTGAGCTGCCAAGCGAGCC[G/A]CCCGAGCTACTAAGCGAGCCGTCCGAGCCAT

Table A2 (cont.)

TP113540	TGCAGTGAGCTTGGAGCAG[C/T]GTTGTTGTTGTTTCCTACATGAAGATGAGAGAGATCCACACCTG
TP113542	TGCAGTGAGCTTGTACTTAAGGTATGCTCTGATGAA[A/G]GGATCTAACTCTCCGTCCATGACGCCA
TP113543	TGCAGTGAGGAAAACAATAAGGGTCC[A/T]TGTCAGTTTATTTTCATGTGGCAACAAATAACAAATT
TP113544	TGCAGTGAGGAACA[C/T]AATTGCAGGTGTCAAGTCTGAAACTCTGAATCAGTGAAGGCAATCATGA
TP113547	TGCAGTGAGGACATCCCTCCTTCCTTGTGATTGAATCCGAGGACCACCTTT[C/T]GAAGAAAAGCTC
TP113549	TGCAGTGA[G/T]GAGAGAGAGAAAGAGAGGAGCGGCACTGGAGGAGTGATATAATTATTTGATACCA
TP113551	TGCAGTGAGGAGATGGTGGCCACGGTTCAACAAGTGTTCCCCTGCGTGGTCAGC[C/T]CGTTCCCTT
TP113601	TGCAGTGAGGGTGAGGAAAA[A/G]ATAAAAATAAGGGCACGTGGTGCCAATCAGACCCCAAAGCTAC
TP113611	TGCAGTGAGGTGGTA[C/T]GGGATAAGCAGGGCAGCTCGTCGGCCTCAAAGGGGTTTATAGACTTTT
TP113619	TGCAGTGAGTACAAACAGAGGAGGCCTTCAGGTAGT[A/G]TCCCTCAAATTTGCATGCGGAATTGGA
TP113668	TGCAGTGAGTGTCAGCCACTTCCCAGCAGTCCTC[A/G]AGCCGTGCGTCTCGGACCACGATTTCAGG
TP113678	TGCAGTGAGTTGAATGGGCTCGATGTCGGCGGCAAC[A/C]ATTTCATGGATTCTTTCCCGTCATGGC
TP113693	TGCAGTGATAAGACTGCTGCTAAACCATGCACGCTCAAAAGCGC[A/G]GCGTGAATGACAGCGATCA
TP113748	TGCAGTGATCAAGGAAATTAAGCATG[C/T]TATTTTATTTTGTACAATTCTTATTTAGTACAGTTCT
TP113753	TGCAGTGATCACTGAT[C/G]ACATCGGATGGTGATGATGACGGCCGTCATACGTACACGTACACCAA
TP113762	TGCAGTGATCATCACGTG[A/G]TGGATCGGAATCCGAAGGCAAGCGTGGCCGAGGCCGAAGACGCAG
TP113764	TGCAGTGATCATCCACTGAACCTCCATGTCAGCTGCATCTGCCTCCTTCGCCAGGGC[A/T]GCAAGG
TP113767	TGCAGTGATCATTCTCAG[A/C]GAAGGTGCTGGGGCATTGGCTTCGGTCTGCGGTTCAGAGTGGTCT
TP113772	TGCAGTGATCCCTGTCGGTGCCGCAGCACGCAGCGC[A/G]CTAGCTTAAATTGGCCAGCACCATCAT
TP113775	TGCAGTGATCCTGTGAAGCCCAGCAGCGTGTTGATGTCTGTGGAGAAGCCA[C/T]GTCGGCAGTCCC
TP113777	TGCAGTGATCCTTTTTACTAATTAGCTCCCTCTTCTATACGT[C/T]GACGCTATTAGCGTGCATACA
TP113784	TGCAGTGATCGCCGATGGCA[A/T]CGCGCGAGGACACAAGGAGAAGTTGCACATACAGCCTGCTAAG
TP113785	TGCAGTGATCGCGAGCGTGATGCAC[A/G]CAGCACAACACGCACTCATATCATTTCATCGACTATAC
TP113791	TGCAGTGATCGGCGATCGCCATGAGGCTCCGCGTCGTGTTGCT[A/C]GTCCTGGCGCTCGTCCTGGC
TP113802	TGCAGTGATCTCA[C/T]GAGGACGAGGACGTGGACGGCACCACCACAGACAGCGGCAGTGATCGAGT
TP113807	TGCAGTGATCTCATTATTGCCTTGAGTTTTTTTAGAGTT[C/G]TCTCTTATGGAGAGTTTTCAATCA
TP113809	TGCAGTGATCTCGCGCGCGCGCGCGA[A/G]CCAGCGATCTTTCGGGCGCTGATAACCGCTCTGTTAT
TP113821	TGCAGTGATCTTGGAGATCCTGCTCGACAAGCGGCCT[C/G]ATCTTATCGACCTGACCGACGACGAT

Table A2 (cont.)

TP113822	TGCAGTGATCTTGTGGT[A/T]GTTGGTTTGCGCGGCTGTGCGGCCTCCACGTACAAGGAACCACGTT
TP113875	TGCAGTGATGCAGTGGCAAGCCCTATGCTTCCCCAAGAGGCCAAGACTGCTAGGGT[A/C]GTGTGCT
TP113898	TGCAGTGATGCTTAACAGGGGACAGCCATCAGCGCACCCCGCCCGTGTTGGAACCGAGGATC[A/G]A
TP113903	TGCAGTGATGGAAGCCAATAGCGAGATGACGGGGTCCAGCACGCCTC[A/C]GTCGGCGGCATGCGCA
TP113905	TGCAGTGATGGAGATCACAGATCACAAGGCGTGCGTGTTGCAGTT[C/G]TTGGCACAAAAACCGAAC
TP113964	TGCAGTGATTACTGATTAGTGAAAGAACTATATGGCTAAAATTGAT[A/G]TAGTAGGATGCCAAACA
TP113991	TGCAGTGATTGTGACTGCG[C/G]CACGTCTGGTAGGGCGCAAGACTTTTAGCGCAGACTGGTCCATG
TP114037	TGCAGTGCAAACGGCCGCTGCTAGTTCCCCTGCTCTTGCTTG[C/T]CCCTTTTTCTTCTGCGCTAGC
TP114038	TGCAGTGCAAACGGCCGCTGCTAGTT[C/G]CCCTTCCCCCCATGATCTCTGCCCCTTCCCCTACCTT
TP114042	TGCAGTGCAAAGAACAGAGGAGGAAGTTGC[A/G]TCGTAAGTGATGGATGATGCTGTAATTACTTTC
TP114064	TGCAGTGCAAATGGACAGTTTCCCTGCCCTAATTAAACCCGAGACTGGAAACCTTAAATT[A/G]AAT
TP114065	TGCAGTGCAAATGGGATGCGCG[A/T]GCGATGTCCGTCGGCGAAAATGAGACCTCAGCTCGTCACTT
TP114069	TGCAGTGCAACACTACTGGTGCTGTTGACGCCGTGCACACGACATG[C/G]GCGCCACGTATCATTGG
TP114074	TGCAGTGCAACATGCAA[A/G]GCAAGCCTGCGGCTGCCTGCGACGGCACGTTCTGTGCGCATGCTCG
TP114110	TGCAGTGCA[A/C]GACACACAGGTGAGCCGTGAGCGTGCACGGGCAGGACAAGATCACAGGACGGGA
TP114114	TGCAGTGCAAGATAGCGTTCAGGTAGCGCGCGCACGTATTAGTG[A/G]CCAGTGGGTGGGGAGACGA
TP114122	TGCAGTGCAAGCCGTGCCAACTGTGCTACCCTCAGTCAGGGCCCGTGTTCGACCCGCGG[C/T]GCTC
TP114155	TGCAGTGCAATGCAGATAT[A/C]TGTGCATGCAGTGGGTTTTGTGTTGGCCTCGTCCTCACACCTGT
TP114229	TGCAGTGCACCAGTGCGAACGTCCATCGATCTCGTGTTGACCAGTGAGCACCGCACCCGAG[A/C]TC
TP114236	TGCAGTGCACCCCCAAAATTAAC[A/T]GAGCAGGGGTCGGGGCCGTTGGTAGGTGGGAGACTCAGCG
TP114241	TGCAGTGCACCCTCAATCATGTGGCGTGGTGGC[C/G]ACATGGTCCTTTTTTTCGCAAATAAAAAAA
TP114248	TGCAGTGCACCGCCCAAAACCCTATAAACAATCTCCCATCTCTCTGG[C/T]TCACCTAGCAGCCTTC
TP114280	TGCAGTGCACGCAAGTCCTGATC[C/G]ATCAAGATGCAGGGAGGAGGGAGAGCACGAGGTCTGGCTG
TP114285	TGCAGTGCACGCAGAGAG[A/C]CAATCCAATCCGCCACCATCTTTGTGCAAATAAATAAAGCTTTCC
TP114286	TGCAGTGCACGCAGAGATCGGTACGGTACGGTGGAGCAGCAGCAGGCATGGAGCGAGGTTA[C/T]TA
TP114290	TGCAGTGCACGCAGTACGGGCAGCCGCCCAACACGCTGGCCGAGTACGGGCTGAAC[A/C]AGTACGA
TP114298	TGCAGTGCACGCCGCTTGTGTGAATTCCTGCTTCGACCACGAGG[C/T]GCTGCGCTGCGTGCGTCCA
TP114311	TGCAGTGCACGGGTTACGGGCGCGCCCCCAACAC[A/G]CTGGCGGAGTACGCGCTGAACCAGTTCAA

Table A2 (cont.)

TP114333	TGCAGTGCACTGCACCGAAATTACTCACCCACCAGCG[A/C]CACGCCCGTCCGTTCCACTGCCACTG
TP114338	TGCAGTGCACTGCGAGGTGGCAGCAGCAGGTTTCAGGTTCT[A/G]TCCGATCCGTCTGTGCCGTACA
TP114357	TGCAGTGCAGAAAAAGGAGCAGACTTTGTATGAA[A/C]CATTCAATTCTAAAGCTAATACTCTAGTT
TP114372	TGCAGTGCAGAAGTATCCTTCTACTGGGGGTCCACGTCTTTTTTTC[C/G]CACATGATTACAGCGC
TP114393	TGCAGTGCAGAGACGACGCAAGCACGCAGCAAGCAGGCTCCGTCGGTGGAGCCGATTCATA[C/T]AT
TP114397	TGCAGTGCAGAGATTGCGC[A/G]GCTTGACGCCCTTCAATTCCTTCCTCCGTCAGAAGCCAGAACTC
TP114401	TGCAGTGCAGAGCGCTGACACACGCATGGCGCGCGTCCAACGGGAAG[C/G]ATGGGTGGTGGCGTGG
TP114404	TGCAGTGCAGAGGAAGAAAGATCAACGA[G/T]GAATATTAATAATAATTACATAGAAGATGCATGTA
TP114429	TGCAGTGCAGATGAATGCAGATGTCCT[A/G]CGATGTGCGATGAGTAAAGGGCCTTCCATTTCGAGC
TP114445	TGCAGTGCAGCAATTAGAAAAGAGGAGAAAAAACATAC[C/G]AACAAGGATTGTAATCGTTGCTTTT
TP114458	TGCAGTGCAGCACTCGAGCTATATATG[C/T]ACATCTCATTGACCATCCCAGCTACCGCGCGTCGTC
TP114462	TGCAGTGCAGCAGATCGATCGCCGTCGTGCGTGACTCGTGAGTT[A/G]TAATGCATGGCGTCTTCTT
TP114466	TGCAGTG[C/T]AGCAGCAGCAGAGGACAGCGCGGCGCTCGCCTCACGGGGGCGCGAAGCTTCGGCGA
TP114480	TGCAGTGCAGCAGTGCTGACCGACCGAAGGAGCGAATCTCTGCGAATG[A/G]ATTGGGTTGGCAGGC
TP114493	TGCAGTGCAGCCAGCGATGGGATA[C/G]GAAACTGAAAAGCGTTGGGCAACCGCGTACCTCAATCGA
TP114495	TGCAGTGCAGCCAGGTGCTGCGGAACGGCGCGACGAGCAGCTGCACGCTGGG[G/T]CCCGAAAAAAA
TP114502	TGCAGTGCAGCCGAGCCAGGTTGGAGATACGGTCACTGCCCCGCGGGTCCC[A/T]CCGTCCAGTCCA
TP114508	TGCAGTGCAGCCGCATCATCTGGACCAGCTGTAGTACTTA[A/G]TGAAAATTGATGGCGAAAGGAAC
TP114511	TGCAGTGCAGCCTATCGTTCTGCACGTACGCCGTCACCGTCAGTGGCTTGCGTT[C/G]CGCCGCACG
TP114512	TGCAGTGCAGCCTATCGTTCTGCACGTACGCCGTCAGTGGCTTGCGTTGCGCCGCACGC[A/G]CGCC
TP114525	TGCAGTGCAGCGCCTGGAAGAGCACGGAGGCGTGGATGTC[C/G]ACGAGATCGGAGCTGGCCTGGCT
TP114546	TGCAGTGC[A/G]GCTCCCAAGTCATGACACGCCCAGCGCGCAGCACGACACGGCCAAGTATTGTGTA
TP114556	TGCAGTGCAG[C/T]TGCTTGGATGCAGCGGCAACAGCTTCCTTGGCAAACCTCTCCTCCTCCCTTTT
TP114575	TGCAGTGCAGGACATGGGGCTTGCAAGCATTGCCT[C/G]GCCAGCGTACGTCTTCGGAGCCTCTTTT
TP114580	TGCAGTGCAGGAGGCCAAAAGCTGTTGGTCAGC[A/T]TGTGCTGTGCGGTTTTGCCTTTGTTGCAGC
TP114582	TGCAGTGCAGGAGGCCACACAATATATGTGCAGGCACGAC[A/G]AAGCGCGCCCACTTTTCTTGTAT
TP114594	TGCAGTGCAGGCAATGCAGAGACCAAAGATAAAAACACACCATCATCGCATGACATGACATGA[C/G]
TP114595	TGCAGTGCAGGCACCTTCGGAGAAGTTGCCCCTGTC[C/G]CTGTCGGGAGCGGAACGCAGGCACGCA

Table A2 (cont.)

TP114602	TGCAGTGCAGGCCAGTGGGCATGGCGATATCATCACATTGTTAGTCGATCTCGCTCGAT[A/C]GCTC
TP114605	TGCAGTGCAGGCCCGCCTGAACCATGTCGTGCACATGGATAGACATGCATGCTGCGGGCGCG[A/C]C
TP114607	TGCAGTGCAGGCGAGGTCAGCATTGGATTGGAGC[A/T]GAACCTGAACGGCGGCTGAGCCTGAAATG
TP114618	TGCAGTGCAGGCTTTCTGCATTCTAGTAGCAGTAGTATCTGGTTGCAGATT[A/G]CAGACTTTCAAC
TP114631	TGCAGTGCAGGGCCTTGCCTGCTGGTAGTGCGATGCTGCCCAGGACACGGGC[A/G]CTTTCGCATGC
TP114645	TGCAGTGCAGGGTACTGCCATTTCCATCCATCATTACTGTATA[A/G]TATTTTGCTAGCTGCTTCTC
TP114649	TGCAGTGCAGGGT[G/T]CTTCCTTTTCCATCCATCATTACGGTATAATATTTTGCTAGCTGCTTCTC
TP114660	TGCAGTGCAGGTCCGTCACCCCCTCCTCCAGCCCCCCG[C/T]CCTATGCTTCTCTGTGCTTGGTGAA
TP114666	TGCAGTGCAGGTGCTGCCGATGATACAAGTAGAAGTAGAGCA[C/T]CACCCAACAGTGCTCAATTGA
TP114670	TGCAGTGCAGGTTGCTCATCATGGAATGTAGCGGTGGCCGTAGTAGT[A/T]GGAAGCACGAGGGTTG
TP114693	TGCAGTGCAGTCGC[G/T]GCCAGGGATCTGTCCAGCAGTGGCTATGGCGAGGAGGCTATGACGGCGA
TP114714	TGCAGTGCAGTGCAGGCATTAGTAGTGTACTGGTGTCATCTGATCTCATCAG[C/G]ATTCTGATTAA
TP114731	TGCAGTGCAGTGCGAT[C/T]GCCGCTGTCTCCTCGTCGCCGTCCCGCCCCGCCCGACGACGACGACC
TP114732	TGCAGTGCAGTGCGCGCCATTTTCTGCGCTCCTGC[C/T]CTGCCTCGCAGCTCGCCTCGTCCTCATC
TP114742	TGCAGTGCAGTGGCACAGGACAGGACGCAAGGCGCTTAGGCGGTCCAAGGGG[A/C]AAAACTGTCAA
TP114751	TGCAGTGCAGTGTGCAGAGG[C/G]CAGAGGCACGCAGCCAATGTGCCATCATGGTCAGACCGTCGGA
TP114756	TGCAGTGCAGTGTGC[A/G]GTGCAGGAAAGCGCAGCCCAGCACTTGCACTCGATGAGTCCAAGTCCA
TP114770	TGCAGTGCATAACGCACAG[G/T]ATTATTTTGCCCTCGGCAGTATAATTTGCCCCAGGCGGTGTGTT
TP114785	TGCAGTGCATAGCAGGGTAGCTGAA[C/T]GAAACCCCCAAGAAAACTCCGCAGTGCAGAGGGCATGC
TP114789	TGCAGTGCATAGTATCGCACCCCATGATCTTCTCGA[C/T]CACAATCTTACAACTGGGGCGCTGGGC
TP114794	TGCAGTGCATCACCCGATCTCCAGCGCCCCCATCGGTCGCGTCGCATGGACACTAGCTGGTCT[A/G]
TP114811	TGCAGTGCAT[C/T]ATTGTGCACTCTGTATAGAAACCTTGGCAGGGGCAGGCCAGGGGGGACCAGCA
TP114823	TGCAGTGCATCGGCGTTGCTACGCTCTTGTCCAGGTTTGCAAAAAGACCAGACGCTAA[A/G]CCGAA
TP114828	TGCAGTGCATCTCATGCTTCCTTGTCGGGTCACCAAAGTTCAGTGTGCTGACCT[G/T]GCACATGCC
TP114829	TGCAGTGCATCTCCAAGGGCCGCAGCGAAGGA[T/C]GGAAGGAGGAGGAACGGAGACGACGACAGGT
TP114853	TGCAGTGCATGCATCCAGTGGCGTGGCATCC[A/T]CCTCAGCGGAGAGGTTGCAGAGTTGCATGCTC
TP114888	TGCAGTGCATGTGTC[A/C]ACTCCCAGCTGACAACGCCCAGCAATGATCATGAGATGAGAGAACCAT
TP114911	TGCAGTGCATTGCTACAAAAATACTGTTTAGGGCACTTCCACGCATAGTTTTGCTACAT[C/G]ATAA

Table A2 (cont.)

TP114945	TGCAGTGCCAACCTCGGTCGTGGCGGTAGAATTTGTTGTTGGACAAGCCTTTG[A/G]AGCTCGGCAA
TP114972	TGCAGTGCC[A/G]CCACCGTCTCAGGTGCATCACGAACTTGCCCTTCTCGTCATAGTTCGCCAGGTG
TP114974	TGCAGTGCCACCATCAGGGGGGTCTCGA[G/T]ACCGAACATCCTCGCGTCCATCTCTCGCTCTCGCT
TP114984	TGCAGTGCCACCTCACGGTCACGGCGCCGTCGGTG[A/C]CCCCGTCCTCTTCCTTCTTTTCCTCGTG
TP114986	TGCAGTGCCAC[C/T]TGTGTGTCAGCAACCTTCCTGCCCACGCTGCTGCTACAACTGAAGACGGTCC
TP114989	TGCAGTGCCACGCCAGATCGCCGTGCGC[A/G]TCACACGAGCGGGTGCTGCCACCGCGCGCGGCCAA
TP114993	TGCAGTGCCACGGCGTGACGGTGCGCGGGGTGACGGTGGAGGC[A/G]CCGAAAAAAAAAAAAAAAAA
TP115010	TGCAGTGCCAGAAGGACACTGATCTGGAAGGCGGTGAGGTCACGCCACATGGCGTTATTGA[C/T]GA
TP115014	TGCAGTGCCAGATGAAGAACTTCGCCAACGCCGCCGCCTCCGC[A/C]GTCGCGCTCGCCGTCCACGT
TP115019	TGCAGTGCCAGCATCCACGGGTACAGAAC[A/G]CCACGATGCTCGAGAATGGTTCGGGCTCGGATTG
TP115020	TGCAGTGCCAGCGCAAGAACTGGGTCGCCGCGGTCACCACGGCCGCGGCGTTCCCCGT[G/T]CACGT
TP115028	TGCAGTGCCAGGGCAAAAGAACCATGGT[A/G]AGCTCCTTGTCAGAAGTTTCTCACTCATGGTCTAT
TP115030	TGCAGTGCCAGTCCTCGCGCACCCCAGACACA[T/C]CTCGCTTTCCTTAACAGATCAGTCTGCAAAG
TP115051	TGCAGTGCCATCT[A/G]CCGAGCTAGGCAGCTACAGCACCCCGCCACGCGCTTCCGTCCCCAAATCC
TP115052	TGCAGTGCCATCTACTCGATCCCCTGCAATGGCGCCACCA[A/G]GGTCCCTTGCCTTGGCGCTCCTC
TP115059	TGCAGTGCCATGCATGCACGC[A/G]AATACTCCCTCCCAGTCAGCTAGTCTGGCTTTGGTTTTTCGA
TP115109	TGCAGTGCCCATCGATCAGCGTAGTGTATGTGTTTGTGTTC[A/G]GGGCCAGTCCCTGCTCAACCAT
TP115123	TGCAGTGCCCCAGATGGAAATCACAGGAAGGTCCATGCCACTGTC[A/G]GCGAGCAGAGCACGGATG
TP115127	TGCAGTGCCCC[C/T]AGCTACGCGTGCCTGCGTATCCTACCAGCCGTATGGCGACCGTCGGTGCGTT
TP115142	TGCAGTGCCCCTTTCGT[C/T]GTCGGAGCAACGTGCGGTGGTCATCTGTCGTCCATGGGGCGCATCC
TP115152	TGCAGTGCCCGCCCCAGGCAGAAAACCACCTGCATGCAGCCTACCACGGC[A/G]GTTTCCCATGCAT
TP115154	TGCAGTGCCCGCCCGCTGCCGACGTTGAGGAGTTCTTCCA[G/T]CCCTCGAGCACGGGTGGGTCGCC
TP115159	TGCAGTG[C/T]CCGCGGGCGCGGCCACATGCGACGGTGGCGGCGGCTTCGCGTAGCTCTGGTAGGCG
TP115169	TGCAGTGCCCTC[C/T]TCCAAGTACACAAAAGTCTTGTCTTTTTCATTATAATTAGCTATTGGCACA
TP115175	TGCAGTGCCCTCTCTCCTCTCTTCCTCTCTG[C/T]ATATATGCGGCGGTCACAGCAGCCTGACGGCA
TP115181	TGCAGTGCCCTGCACACACTCCATCTCC[A/G]TCTCCATCTCTGGAAGCATGCAGTTTGGTGCTCAT
TP115201	TGCAGTGCCGACGTCTTGCGCACCGCTTGTAGGATCGTCG[G/T]CTAGCAGGGCATTGTGTGTAGGA
TP115211	TGCAGTGC[C/T]GATTGCATCGATCTCCACCCTGCCTTCTTCAACACACTCTCGAATGAAATGATAC

Table A2 (cont.)

TP115235	TGCAGTGCCGCCCAATCGATCGGC[C/T]ACGTCTGGCGTGGAATAACGAATCATCTCTCCGTTCCAG
TP115236	TGCAGTGCCGCCCAGGATTGCCAGTGGCAGCATCGA[A/G]GGGGTCACGGCAGAGATGTTTGTGGAA
TP115241	TGCAGTGCCGCCGCCAGGCTAGGACGACGTGACGACCAGCG[A/G]AGGAGACCAACAGCGGGGTGTC
TP115253	TGCAGTGCCGCGCCTCG[C/G]CATTGATCGGTGCATGCATCATCCGTCTCGTGGGGCACGCGGGGCA
TP115266	TGCAGTGCCGCTCCAATTAAG[A/G]TGAAGATGCAGGACCTCCCCTTGCCGCCTGCTGCGTGATGCA
TP115270	TGCAGTGCCGCTGATCAAACGGCGAG[C/T]GACCCTGCGGTCCGATCCCGCGTCGCAGCGTATCCGC
TP115280	TGCAGTGCCGTCCACCTCCCGAACAGCAGGC[C/T]GATGCATTCCGCCATTGCCGCCGCCCCCTCCT
TP115288	TGCAGTGCCGTCTTGAGATCACGCGCCCTGTCTCTCTTATGGCT[G/T]TGGTGCTTTGCGCCAACCA
TP115293	TGCAGTGCCGTGCTTAATTGCAAATTGACGAACTGTCACAGGCATGGCA[G/T]CTGTGGAGGGAAGG
TP115300	TGCAGTGCCGTTGCGATGGGTGACAAGGCCAAA[C/T]TGACTCGGTGTCTTCTTCCTCACGTCAGTC
TP115302	TGCAGTGCCTAACAAAAATC[A/T]TGAGGCTGGAAGCAAGGAGGAGGAAGTGCGCAGGGCTAGGGAA
TP115308	TGCAGTGCCTAGATGTCTACCTCGTGCGTCGTTGCATTAGAAAAAAGGATA[C/G]TGTGGTCATTGT
TP115324	TGCAGTGCCTCCATGGCC[A/G]TCGAGCCTCCTCAAGGACTGGCGGACGGCAGCACTCGAGGGAGGC
TP115333	TGCAGTGCCTCCGTTGGAATCATAGGCATGCAAAACAACGCTTCTGCC[A/T]CGGCAAATCAGTGGC
TP115337	TGCAGTGCCTCCTGCCGCCTGCCGCGCGGGGTTGGGACGGTTGTTGTTGACTTG[G/T]TGGTGAG
TP115352	TGCAGTGCCTCTACTACCTGTCGCTGGGCGTCGCCATGGCGCTCCTCGTCGGCACCCGC[A/G]TCCC
TP115374	TGCAGTGCCTGCCATGCACGCACAGCCTGCAC[G/A]TGCCGCAGTCGACGGTCAGGCACAGACGGAT
TP115379	TGCAGTGCCTGCCGATCACGATCGATGTCGGCACCAACAACGAGACCTTGCTCAACGA[C/T]GAGTT
TP115396	TGCAGTGCCTGGGACTCTGGGACTGGGAGTC[A/G]GCACGATGGTTCGTCTACCCTACGAGCTAGCC
TP115413	TGCAGTGCCTTCTCCGTGGTCGA[C/T]GGCCCACCTCCCACGCCGCCCGTGGCCACGGCCACGGCTG
TP115424	TGCAGTGC[C/T]TTGGCCTCACCGTGCTCCACCTCAACGTGACCACCACCGCCGATCACCTGGCCTT
TP115443	TGCAGTGCCTTTTCTAACATGCTGCATGGCCTTGTGTTTCGCTGA[C/T]GACTAGCAAAACTCCATG
TP115459	TGCAGTGCGACGTGATGACGAACACGAGCAGGAGGAAGACGA[G/T]CGTACCAATGTTGCTCTCCGT
TP115467	TGCAGTGCGAGCCCCAGAGTGGGCGCACGAAAAGAAGGTG[C/T]GGGGAAGGGGCTTGCTGGCACGG
TP115482	TGCAGTGCGATAAGAGGACACACCAATGTGATTTGTCGCGAAATGCAGTTCCAG[A/G]CCGTCGCAG
TP115484	TGCAGTGCGATCCATATTCGGACAGGTGATGTAGGCATCGTTGAGAGGA[C/T]GGAAGAATCTATAC
TP115515	TGCAGTGCGCATGCCAGTCAGAAGCTTGCTTAACGG[A/G]GCAGTGGTCAGCAGAGGCGTGAACACG
TP115519	TGCAGTGCGCCAACATCTACTCCGCACCCAGCAGCGCATA[G/T]GAAGGCCCAAGCTGATAAGCACC

Table A2 (cont.)

TP115524	TGCAGTGCGCCACTGCCCCGTACGCTTACGGCAAAACGGCTGGCTCTGG[A/C]TGCCTCACAAGTAT
TP115528	TGCAGTGCGCCATCAAGCTCGGAATCCCCAACATCATCAGCCGCCATGGCGGCGC[C/T]GCCTCTCT
TP115540	TGCAGTGCGCCGT[C/G]GAGCTCGGGATCCCCAACGCCATCCACCGCAGCGGCGGCGCCGCCTCTCT
TP115554	TGCAGTGCGCGCCGTGCCTGGACTGCTTCGAGCAGCTTGGCCCCGTGTTCGACCCCGC[C/T]GCGTC
TP115568	TGCAGTGCGCGGCGCACCTGGCCGCCGCGGCCGTCGTCGCGCACGAGAAGCGGTTCC[G/T]CGCGGC
TP115579	TGCAGTGCGCGTGGAGGCCCATCCTGGCAGGC[G/A]GTGTGTTTGGCGGCCAGTGAGCTCTGTTCCT
TP115589	TGCAGTGCGCT[A/C]GCTCGCGCGCCGCGTGCGCTAGCCCGCCTGCCGCCGCGCGTGGTCGCCAGAG
TP115606	TGCAGTGCG[C/T]TTCATCATAACCGTGTCAACGAAGTACAATTGGCCTTACAGCAGCAGCTCCTCT
TP115609	TGCAGTGCGCTTCGCGAAAAAC[A/G]CTAGATCCCGATGCGACCTTGGCACCCGAGCCGAGATCCGC
TP115614	TGCAGTGCGGACGGCAACAACGGCGCGTG[A/G]CCGTAGATGGAGCGGCAGAGGCGGAGCTTGCACG
TP115642	TGCAGTGCGGCCGATCGATCGAGCCGAGCAGGCAACTAGC[A/G]AGCTTATGTGCAAACAAACTTTC
TP115651	TGCAGTGCGGCGGCGGCGG[C/T]GTAGGCGGCAAGAGGCAGCTGCTCGTGGGCGTCAAGACGGCGCT
TP115661	TGCAGTGCGGCTGCAACCTGGCTGCATATATATACTCCGTACGAAGAAAACCT[A/G]TGTTGTGCAG
TP115663	TGCAGTGCGGCTGGCCGTCGTGCCCCACCACCCCGCCTCCGTCCACGGAGCAGGT[C/G]GCCGAAAA
TP115693	TGCAGTGCGGTGTAGCTTCTCAATGCACGTGTGCATGGCTACTGATTTTTT[A/T]TATATATTCAGT
TP115703	TGCAGTGCGTACGC[C/G]GTCACCCTACATACACAGCAAGTGAAGCAGCAGCAGCAGCCATGTCATG
TP115705	TGCAGTGCGTACGTACGTGCGCGATTCCTTTGCGAATTTCTCGTTGCC[C/G]ATCGTTTTGAAAAAT
TP115707	TGCAGTGCGT[A/G]CTAGTACACAAACATAAGTGGTGAGAGGAGGGTGGCTGCGGCAGTGCCGCTGC
TP115711	TGCAGTGCGTAGCTCCAGGATCTAATCAGGTTTGTGTTTCTC[A/G]CGCCCAGTTCCGCAGAATTTT
TP115720	TGCAGTGCGTCAGTCAACAAG[A/G]GCATCAGCTGTTCCTCGACAGAAAGGGGAGATCAACCCGCTG
TP115731	TGCAGTGCGTCGCGCACCACCCACAAGAAAGGCTTGCTGGTGCTGGCCAGGCCCTCCGCCATG[A/G]
TP115744	TGCAGTGCGTGAAAAATACTGGGCCCACGCCGTACGCAGCACGCCTGAGCTGAGC[C/T]ACGGCTAA
TP115766	TGCAGTGCGTGGGTTCTCGCGCGCGCTGCCGCCTGCCGCTGCGGCGCTGCCC[G/T]CTGGTCACTGG
TP115781	TGCAGTGCGTGTTTTGGTTTCTACCAAGTGATT[A/C]TGAGCGAGTGGATTACAGCTAGCTAGCGCC
TP115812	TGCAGTGCTAATGATCTCAACTGAAGCCGATGCTAAGGCCCCGTTTAGTT[A/G]AAGCCAAAAACCA
TP115839	TGCAGTGCTACGTACCCTGACGAAGCAGTCGTGGAAGTGGGT[A/G]CGGATCAGGGTGGCGGCGACG
TP115845	TGCAGTGCTACTCCATAAGATTGGGGTTAGTGGCTCCTAATTA[A/T]ATGGGCAGCAAACGACACGG
TP115850	TGCAGTGCTACTGAGATCGGGATCGGAGGAAAC[A/G]GAATTGTGTGCTCTAGTGACCGTGATCCGA

Table A2 (cont.)

TP115875	TGCAGTGCTAGGCCTGCTGCTTGTCGTTACGAAGAGCAGTGCACGGAGCGGAGCCTGGC[C/T]AGCT
TP115889	TGCAGTGCTATATGAAGAGCACCACAGA[A/T]TGTGCAATGGCGGCCAGAGCAAAGGCGATCACGAC
TP115913	TGCAGTGCTCACACGTTTCTCACCTCCCGCCGCCGCCGCCGAGGAAGACACTAGCCATA[C/G]CAAG
TP115937	TGCAGTGCTCCATCACCACTCTACACC[A/C]AACTCATCAGTGCTACTCACCTTGCCTTTGCTGAAA
TP115946	TGCAGTGCTCCCCAGATCTACCGCGCGCCTGC[G/T]CGTGCCCGTGCTCGTGCTCGGATCTAACCCG
TP115948	TGCAGTGCTCCCCTCCCACACCCAGACAGCCGCTGCC[C/G]CTGCTGAGTGATCCATGCAGTGGTAG
TP115962	TGCAGTGCTCCTCACACCGCCTCGCTTTCATCCATCCGCAGCGCCTGCACTGTGCA[G/T]TGTGCTG
TP115975	TGCAGTGCTCCTTGGTGTCACCCATGCGCCGCCCGATGTCCGCCGAGAACCCGATAAT[A/C]ATCAC
TP115991	TGCAGTGCTCGGCTCAGTGCACCAGAGCAACTCATCCTGCATCCATC[A/T]TGGTGAGCGAGCGAGA
TP116012	TGCAGTGCTCTCGTGTCTTCCA[C/G]CCTGGAAGAGTACCTAGCCTCGATCTCGAGCTCTTGGAGAC
TP116037	TGCAGTGCTGAGCCACTTGCCAC[A/G]CCTTTCCTTTGCTTCCACAGTTCCACTTGTCGTTGTTGCC
TP116044	TGCAGTGCTGATTATCTTCGGTTTT[A/G]GAACTCAAAATTAGCAATCCCAGATGCAGGAGCATACC
TP116054	TGCAGTGCTGCACAAGCGAACAACAAGCA[A/G]CCTGCCTGGAAGCGCATGCGGCATGTCTGAGACT
TP116066	TGCAGTGCTGCACTGCA[C/T]AGGCGTCGTCCAGCTATGTCCTCCGCAAGGGGCAGAGGTGACACGG
TP116079	TGCAGTGCTGCCACACTGTCTCTCCTCTTGCTGCTTCTCGCTAGCTCGT[C/G]TTTTGGCGCTCTCG
TP116090	TGCAGTGCTGCCCCTTGCGTTGGGCGGCCTCATTGCACCCTCG[C/T]CAAGACGCCGTCGTCCGCCG
TP116109	TGCAGTGCTG[C/T]CTGGTTCGTGACAAACCTCAGACAACACACGTCTCTTGACCTCTGTTCGCATT
TP116142	TGCAGTGCTGCT[A/G]CGATGGCGATGCAACACGGCCACCAGTAGCCGCTGCCTGCCCCTGCCCCTG
TP116154	TGCAGTGCTGCTC[A/T]GCTCAGTGCTCCCACAGCAACCCCCGTCTCCAGCCAACTAGCCTCACAGT
TP116158	TGCAGTGCTGCTCCTCCTC[C/G]GTCCTCCTGGCGGTGAAGCCAGGACACGGTGGTGGCGCTGTGCG
TP116168	TGCAGTGCTGCTGCCTCTCCGTTCTCCA[G/T]CGTGCCCCAGACGTCCAGCCAATGGTAAAAACCCA
TP116170	TGCAGTGCTGCTGCGTGGTGACTGGCGCAGGATCGGATGCTCAACTCAGCT[C/G]GTGTGTTATGAC
TP116173	TGCAGTGCTGCTGCTCCATCACGACGACGCCAACCACCTCAC[C/G]TCACTAGCTCCCGCGGTCCCG
TP116182	TGCAGTGCTGCTGTACTG[C/G]CGTATCTGTACAGTGCAGTGCACGATATCCAACGGAAAACGCTCT
TP116188	TGCAGTGCTGCTTAGTGCTTACATACA[G/T]ACAGGACCCCAAAAGCATAAGCAATGGTTGTATTGT
TP116193	TGCAGTGCTGCTTGAACTTTGTCTTGGGTGGTTTTTGCGATGCGGATGGTGGGATTTGCGG[A/G]CG
TP116208	TGCAGT[G/T]CTGGCCCCACCCGTGTCTTCAGTTACTGACAGGGAAGCCCGCCTAGACGTGGGCCAC
TP116241	TGCAGTGCTGTAGCACCAGGGTCAGTGAAAAGGGAGCGCACATT[G/T]GTACCAATTCCTAGCTTTG

Table A2 (cont.)

TP116242	TGCAGTGCTGTAGCACGGGCGGCTATTGCCCGTGGTGCGGTCACACTGGC[A/T]CTGGCGGTACAAG
TP116244	TGCAGTGCTGTCCTTGGTGTCGCTGGAGTAGCCCTCTGCAATCCATCG[C/T]CTCACCAAACGCCTC
TP116248	TGCAGTGCTGTCTG[C/T]CGAGCAGAAGTACTGTTGACTAATTTGGTGTGAGAGAAAAATAGTGTTC
TP116251	TGCAGTGCTGTGCACTGCTCCCGCGTCG[A/G]CGGAAAGCGATTGATCGATGCTTGCTGACTTGGGG
TP116252	TGCAGTGCTGTGCA[C/G]TGCTCGCGTCGATCGATGCTTGCTGACTTGGGGAGAGATCCATGTCCTG
TP116264	TGCAGTGCTGTTGCGCGCAATGA[G/T]ATCAAGGAGATTTTAGATGTTCATAAAGAGGCTTTGAGTG
TP116303	TGCAGTG[C/T]TTCGCCGAGCTCATGAGCATTGCGGGCGTCTGCAAAGACTGGCGCAACGCCGTGCA
TP116313	TGCAGTGCTTCTGAATACTTCCTAAATTCAATTTGCATTTGCTTTGGT[A/G]CAACAGATGAAGGCT
TP116317	TGCAGTGCTTCTTCGTCGCC[G/T]CCAAGTGCGTCTGGCTGCTCCACCTGCTGGCCTTCTCCTTCGG
TP116320	TGCAGTGCTTCTTGGACTGCACCACCCCCACCGTGGAGACGCACATTCTCCCCAAGGTGACGC[A/G]
TP116340	TGCAGTGCTTGCGCAAGAACTGGGTCCCCGCGGTTGCCACGGC[A/G]GTGGTGTTCTCCGTGCACAT
TP116347	TGCAGTGCTTGGC[A/C]GCCTTCACCACCCGTCGCTGGAAACAGGCCCAACGCGCTCAATCTGGGCA
TP116348	TGCAGTGCTTGGCCAGTGGATACGTACGCC[A/G]ATAGCTAATCATTTGAACAAAACCACCATACAG
TP116350	TGCAGTGCTTGGCCGCCTTCACCACCCGT[C/T]GCTGGAACAGGCCCAACGCGCTCAATCTGGGCAG
TP116383	TGCAGTGCTTTTGCCAATTGGCAGCACAGCATAGATCCTAGAGTAGTTTCTGATTCTAGTG[A/G]GA
TP116405	TGCAGTGGAAAGCTCT[A/G]ACTCAGAACAACCAAGAGTCCTCTTAAAGAACTCAAGCTTGGCAGCG
TP116438	TGCAGTGGAACGGAGCGAGAGGCGGCGACGACACGC[C/T]GAGGACACCCGTGAGGTGCATGGTTGC
TP116441	TGCAGTGGAACTGCACCAACGTCAAGGGGGTCACCTCCGACGTCTCGCCCAAGCCGTGC[C/T]CAGA
TP116453	TGCAGTGGAA[G/T]CATACTGGCCATCGTACAAAGGATCGGAGCACGATCCATCCATCCATCACGCA
TP116485	TGCAGTGGAATTTCCCACCTGGGCA[C/G]GCATGCAGCCGTCAAGGCGACCCTGCTCGCTGCAACAA
TP116503	TGCAGTGGACAAAGCCAAGCAAAACAAGATTGGTGGCGACAT[A/G]TGCATTGTCGTTTTTGTATAG
TP116506	TGCAGTGGACAACGAACTTGGTTACTGCTGTTTAT[C/G]AGCGATAGAAGGGCTTGATGGTGGCGAC
TP116516	TGCAGTGGACACGTCACATACTCACAGGTACCTCCATTTTACCAAATTGTCCTTTTTTT[A/T]CCCC
TP116551	TGCAGTGGACCTTGACGGCGCCGAGCCGCGAGGAGGAGGAGG[A/G]GAGCGAGGCGAGGTACACCGT
TP116570	TGCAGTGGACGCCTCGATGGCCCTCGTCTTCCTGCCCACGCTCGCCTCTGCCACGGAT[C/T]ACGTC
TP116576	TGCAGTGGACGGGTACTGAG[G/T]CGGTCGCAACAGCAGAAACCGCCGCGATTTCAATGCTGCCGCA
TP116579	TGCAGTGGACG[G/T]TTATTACCAGGTTAATTACCCATGCATACTGATGCATTAACATGCAGAAACA
TP116605	TGCAGTGGAGAAGCAGGCAACAGAAACACCTGCGCTGGTATCTTCA[A/G]ATAATAAAGTAGACGAC

Table A2 (cont.)

TP116632	TGCAGTGGAG[C/G]AAGCCTGCATTTTTTTTTGCCTCTGTATGTCCCGAAGAAGAGCACATGATTCC
TP116641	TGCAGTGGAGCAGTA[C/T]CCGTCGGAAGCTATGCGGCTGGAGCTGTCGGCCAAGATAGGGCTGTCG
TP116644	TGCAGTGGAGCAGTTTCACTCAGCGGCACCGCTTGCTATCCTTCGGAAGAGAAATCTAGG[A/C]ACG
TP116666	TGCAGTGGAGGACGGGCTAGCGTGAGAAGGCACGCTAACATGTGCAGCGTGCACTACAGGCA[C/G]G
TP116668	TGCAGTGGAGGAGAAGATTGGAGA[C/G]GGAGGAGACGCGTACGATGCGATGCGCCGCCGACGTCAC
TP116716	TGCAGTGGAGTCAGAGCTGCTTCATTGGGAGC[G/A]TAACGAAACCCAGCAACGATGACGTGTGGTA
TP116758	TGCAGTGGATCAAGTCCCCCGACGCGCAGGCCAACGCCACCGTCTT[C/T]CTCGCCAAGTTCTACGG
TP116764	TGCAGTGGATCATGGCCGAGCTTGT[A/C]AAAAACACAGCCATCCAGGAGAAGCTTCACAACGAGGT
TP116766	TGCAGTGGATCATGGCCGAGCTTGT[A/C]AAAAATCCAGCCATCCAGGAGAAGCTCTACAACGAGAT
TP116767	TGCAGTGGATCATGGCGAACCTAGTGAAGCGGCCGACGTG[A/C]AGCGCGCTTCGGAAGGAGATCGA
TP116778	TGCAGTGGATCGCAGGGATGAGCAGCAGCTGGAGCGGCTCCGA[G/T]CAGAAAGGAAGGCTAAGATT
TP116785	TGCAGTGGATCTCATGCAACCCACGCATGTGCCAATTTG[A/C]TCTTGCAGGTTCCATAGTCCGACA
TP116804	TGCAGTGG[A/G]TGAGTGTGAGTGAGTTTATTAGCACCATAACGACGACGGCTTAGCGAAACAGGGT
TP116813	TGCAGTGGATGGAATCCAGCCTGATATGCGCGCAGTGCGCTGGCAGGCCGCAGTGGCA[G/T]TTTTG
TP116816	TGCAGTGGATGGC[A/G]AGGGCGGACTACGGCGACCCCGCGGAGGCGATGGGGCTCAAGTACATCCA
TP116864	TGCAGTGGCA[A/T]AGTCAGAGCTGGCGGCAACGATGACAAGCTGCGTTCACTTTCCTTGGAGGTTG
TP116945	TGCAGTGGCACTGGCACGTCGCACACGGACGATTACAGTTAGAGATGGCAGTTCTAGG[C/T]CCAGA
TP116977	TGCAGTGGCAGCGCATGGTCGACGACATGCGCGCGCTCGGCAAGCT[C/G]AGCAACTGCGTCGCGGT
TP116988	TGCAGTGGCAGCTTGTTTG[A/C]CTTCTCTTCCATTCTTCTGCACGTCTTTCGGCACGCACAGGTGG
TP116991	TGCAGTGGCAGGCAGTGCCAAAACGAATCATCAGACCAAGCAAACATCCAAAGCTCGTCT[C/T]TTG
TP116998	TGCAGTGGCAGGGACGAGATGCGGGAGCGGCTGATCTCCGCCGTGGGCGGCGGC[A/G]GCTGCGCGG
TP117010	TGCAGTGGCAGTAGTACCAGC[G/T]TCTAGTAGTGATCATGGTGAAGGAAGAGGAGATCATGGCCGA
TP117014	TGCAGTGGCAGTGCAGGGCCCAGGGCACCGCA[G/T]CATCATCATCATCACAATTCACACCTCGGCC
TP117027	TGCAGTGGCAGTTCCGTTTCAG[C/T]CCGCCGCGGCCGCGCGGAGGCCGCTGGTTGGCCAGGAGACA
TP117041	TGCAGTGGCATATGCGCACCCCTGATCAGGTTACCGTTGTTCACCCCCCCGACATTGCCTAG[A/G]G
TP117076	TGCAGTGGCCAATAGTGTGTTGTCAATTCGCTGTTGAGCATTAGCACAG[A/C]AACAGATGGGAAAC
TP117100	TGCAGTGGCCAGTGACAGTTAGATCCGATTGGTAGAAGCTCGTCTCCAGCACACATC[C/T]CTGTTC
TP117110	TGCAGTGGCCATTTCAAACTCGGCCGCGGACCAGCCCACT[A/G]ACGAGCGAGGCATAGACGACCGA

Table A2 (cont.)

TP117122	TGCAGTGGCCCAGGAGGCTGTTAACCAAGTCTTATCAAGAATCAA[A/G]GATGGTTGTCACCATAAG
TP117131	TGCAGTGGCCCCGACTGAAAGGGAAACTA[C/G]AACTAGAAAGTTCTGAAGTCCAAGCGACCATGCA
TP117137	TGCAGTGGCCCGCGTGGTCGGCCATGGATCAAGTTGAAGTGGCGATCGGG[A/G]CGAGAGTGAGGAG
TP117139	TGCAGTGGCCCGTGGAGGAAGC[C/G]GAGACGCTGCGCACCAACTCCACGGACCTCAGCGGCATCAC
TP117140	TGCAGTGGCCCTCCACCACCCCAACAAAGACAGTGGCGGC[C/T]GTCCCAACCCCTACCCCAATGGC
TP117148	TGCAGTGGCCGAATACCTCAGACTCTGG[C/G]ACATGCCGACCGAGGTCCAGATCAACGAGGGGGTC
TP117169	TGCAGTG[G/T]CCGCGCCATGGGCCGAGGGCTAGCGCTAGGGTGAGTCACGAGTGGGCCTTTGACCC
TP117175	TGCAGTGGCCGCTCCATGCCCTACGCAGCATGCAGGCGCAG[C/G]TTGGGGCAGACCAGGCGAGAGA
TP117176	TGCAGTGGCCGTACGCCTAACC[C/T]AATCTAAATTCAGAAAAGGAGCAGCAACGACGTACGCGCGC
TP117178	TGCAGTGGCCGTCAGTTCGACCGCTGGCACGAGGGC[C/T]ACGTCGCCTTCGCCCCGACCTACAAGT
TP117210	TGCAGTGGCCTGGGCTCGGACCTGAAGCTGCCTCTCCTGTCGGA[A/C]AAGCCACAGGGGAAGCAAG
TP117215	TGCAGTGGCCTTCCAGCACCCC[A/G]ACGGAGACTGCGGCGGCCGTCCCAACCCCTACCCCGATGGC
TP117218	TGCAGTGGCCTTGTGTGCTTCCCCTCCAGGATCATTGGGTCCCCTCCTAGATC[C/G]AAAAACAATT
TP117251	TGCAGTGGCGCAAGGAGTTCGGCGCCGACACCATCATCGAC[A/G]ACTTCGTGTTCGAGGAGATGGA
TP117254	TGCAGTGGCGC[A/G]CCATGTTCTCGGCGGGGCTAGACGACGCGGCGGCGCGGGCGCTGCACGACGC
TP117268	TGCAGTGGCGCATGGGTGCGTTCCTGAACAGCTCGAA[C/T]GCCGTGGAGGGGGCAGGGGACGATGA
TP117270	TGCAGTGGCGCCACAGGCGCATGCATGCATGCAGTG[A/T]CCACTAGAGATGGAGCAGTCTGCGGTC
TP117272	TGCAGTGGCG[C/G]CACGTAGGCGAGAGGGATCTCTGCGGAGTGGTGGAGGTTGATGGTATTTTTGC
TP117279	TGCAGTGGCG[C/G]CGAGACGGACGCGGACGCGCACCTCGGCCTCGAGCCTCACGCTCTCCCACTGC
TP117302	TGCAGTGGCGCTCGCTCGGCGGCGCGGACGCTTGGCTGGGCGATG[A/G]CGGTGACAGGGCGACAAG
TP117323	TGCAGTGGCGGAGCTGAACGAGCGGCTGAC[C/G]ACGCTGGGCATCGCCGTGAACCTGGTGACGTAC
TP117343	TGCAGTGGCGGCGAGGGCGTGACGGCATCGTGCAGTACCCTCA[C/T]CTCTTCTTTGCGGCCCTGGC
TP117360	TGCAGTGGCGGCTCA[A/C]GCTGGTGGCGCTGCCGTCCGTGCTGCTGCTCGTCATCCCCGAAAAAAA
TP117381	TGCAGTGGCGGTGCTGATGACATGAACACGGGCACAGGAG[G/T]CTGCGTTGTGATGTCGCACTCGA
TP117400	TGCAGTGGCGTCGCCTGTTGTCGAGGCCGCAACGGC[A/G]CGCGACGCTGACAGGATGCTACCTCAC
TP117414	TGCAGTGGCGTGGGCGGGCTCGACGACGCGTACGTCAGCGG[C/G]TCCTCAAAATTGCACGCGCACA
TP117451	TGCAGTGGCTC[A/T]GGAAGGATCTCACAATCCCAGGACAGAACCAACCGACGATACTGAGCTTCTA
TP117503	TGCAGTGGCTGCGCGTACTGCGGCGGCGGAGGAGCGTACTGCTGCGGCAGCGG[A/C]GGAGCGTACT

Table A2 (cont.)

TP117505	TGCAGTGGCTGCGGTACGTCGGCGAAACCTGATTGATATGGTGACGGGCAGCATC[A/G]CTCCAATG
TP117506	TGCAGTGGCTGCGGTACGTCGGTGAAACCTGACATGCTGACGAGCGGCAT[C/G]GCTCCAATGGTGT
TP117511	TGCAGTGGCTGCTTTCTCCTAGGGCCTTTATTCCAAGCGTTCTC[A/T]GAACATTGTTCTATTTTGT
TP117514	TGCAGTGGCTGGCCCCGCCGCAGACCGCCTCCGC[C/G]CAGCCCTTCGTCTTCTCGCAGTGCCAGTC
TP117575	TGCAGTGGGACCGCGAGGCGCTGTCG[C/T]GGGAGCTGACGCGGCTGCGGCGCGAGCAGGAGGAGGC
TP117582	TGCAGTGGGACGGTTCAACCGAAGCGCATGCAGGCCAGGCCAGATTAGATTAAAAACCCAGC[A/G]C
TP117584	TGCAGTGGGACTGGTCGCCCGCGCAGGACGACGACGAGAAGGACGGCCTAAGCCCCGCGCAC[A/G]C
TP117597	TGCAGTGGGAGCGCATGGTCACCGACCTGCGG[G/T]CGCTTGGCAAGCTCAACAATTGCATCGCCGT
TP117599	TGCAGTGGGAGCGCGTGGTCGGTGACCTGCGGGC[G/T]CTCGGCACGCTCAGCAACTGTATCGCCAT
TP117602	TGCAGTGGGAGCTAGTACTCGTA[C/G]TAGTATCCATCAGTATATATAGATCGGTCCATTCCATTGC
TP117611	TGCAGTGGGAGTG[C/T]GTGGTCAGCGACCTGGCAAGACCCTCTGGGAGAAGACAAGCTTCATCCGT
TP117620	TGCAGTGGGATCGGCCGACTGCGGGA[C/T]CGAAAGCGACGGCGGAACGATGGCGACTACGGGACCA
TP117650	TGCAGTGGGCAACCAACGTCCAGCGACA[C/G]AACGGACGACGCTGAAGTTGTTGCCACCAGCGTCC
TP117652	TGCAGTGGGCAAGCGGCGCCGAGTT[A/C]GATCACGTGAACTTGCTTGCAGTCCAGACTGACTGCGT
TP117730	TGCAGTGGG[C/T]GCCCAGCCAGCAGATGGAGGCGCCATCCTCCAAGATGGCGTCGACCGCTGGATG
TP117733	TGCAGTGGGCGCTGCTCTGCTCCGTCCCGCTCCGCGAGACGCAGCGCGC[G/T]CTCGTCGCCTTCTG
TP117757	TGCAGTGGGCTGCCTCCCTGGAAGATGTTCCGCTCGGTGCCCGTGGTCTG[A/C]GGGACCACGTAGC
TP117761	TGCAGTGGGCTGGC[C/T]GCCTTCACCTAACGCTCTGGTTCGTCTCCCACTCCCACCTCGCGCCGCC
TP117783	TGCAGTGGGGCGGGCGGCAGGGTCGTCGCCAATTT[C/G]GATTGGTAGTCCCGCGCGGCGAGGGCGA
TP117788	TGCAGTGGGGCTGGGGCG[A/T]AGGGGCCGAGGCCGAGCTCCTGGTGGTACTGGTGCTTGTTGCCGT
TP117799	TGCAGTGGGGGCCCTTTCGTCGTCGCCTTCGTCGGCGTGGAGAACATACTGGAGA[A/G]CCATTACT
TP117866	TGCAGTGGGTCTA[A/G]GAATTCATCATACATACCAACGACGGTTGAGCATGCTGTCTTTCTCCAAC
TP117868	TGCAGTGGGTCTCATCAGAATTTTTGTTTGTTTATTGAGTGT[C/T]ATGTGAGGGCTAGTAGTGCTA
TP117876	TGCAGTGGGTGCTCGTCTCCAAGGTGAAGCTCACCCCCGAGCCGCGCCGCGGGGACGGCTC[C/G]TC
TP117899	TGCAGTGGGTTCACCCCCTTTGGGCAAAGAAGGCAGCATCACTGGGAGCTTC[A/G]GCTGGCTGCCC
TP117902	TGCAGTGGGTTCCTGGGGCGAACATTGTCACCTGGAACGCGGTTGC[A/G]GCTGGAAATTTTAAGGC
TP117920	TGCAGTGGTAAGTGACAATGGCTTCCCGTTCCCCAGTCGCCGACCCATCCAGGTTCGCCATCG[C/G]
TP117931	TGCAGTGGT[A/G]CATCTCGTACGAAACGGGAGAGAGAGGAAAGGAAAAGAGGAAGAAGATGAGGG

Table A2 (cont.)

TP117935	TGCAGTGGTACCTGAAAACT[C/G]CCCCCTCGAATTGACATTTGACGCCCATTCTAGAATTTTCAGG
TP117951	TGCAGTGGTAGAGGCAAGGCGCGGCCATCTGCTGTCTGCTCC[C/T]TGCCAAGTGCCCGAACACG
TP117976	TGCAGT[G/T]GTATATGGTGCATGGCTAGGAGTTGGGTAAGCAGGGTATGCGTTTGCAGCAGGATAC
TP117977	TGCAGTGGTATCAAGGTACGGAGTACAAGCAAAGGTAGACTTC[A/G]CTTCATCGCTCTGTACTCAT
TP118021	TGCAGTGGTCAGTGGTGTGGTCCG[C/T]ATTGGCCTCCAGCATGGCTCCGTAGGGGAACGACAGGTT
TP118024	TGCAGTGGTCATCATTCATC[A/G]GCACCCGTGACAGCCGAGAGCCCATGAAAGTACCATGAACGAT
TP118026	TGCAGTGGTCATCGTGGCCCGTGCCCCTCGTCGGCTTCGTACTCATCTTGCACG[A/C]CGCCGCCGT
TP118029	TGCAGTGGTCCAGGACCGACCATGAGGAGCTCCA[C/G]CTGTCGGCGTTGGGCAAGAAGCTGAGCAT
TP118072	TGCAGTGGTCGGTGCTGGGCACTGGGC[A/G]GAGTGGGCACGTACTGGTCGAGCGCGACGTGGTGGT
TP118093	TGCAGTGGTCTGTCGCCATGGCGGTC[A/C]CCACGAGCATGGCGTGCTGGGTGGTCCAGAGCGCGCC
TP118095	TGCAGTGGTCTTGATTATCTGCGTCACAAAAATTGCAAAATCATCTCTGGAGAAGGC[A/G]TTGGCC
TP118119	TGCAGTGGTGACTGAATGTGGTGCCTGCTGGA[T/C]GATACTCAGATCAAGGAGCATCAAGAAGAAT
TP118122	TGCAGTGGTGA[C/T]TGGAGGGGGTAAATAACTGACTGCACCACGACTCAATTGACCAATGAGTCAT
TP118143	TGCAGTGGTGATTTATTCACGGATTGCCACCCTATCGGAAGACAGACGCCCGCGTCGCTC[A/G]CCA
TP118174	TGCAGTGGTGCGTACCTTGCTTGTCCTTGA[C/G]CTGCGCCAGATATATACTTCCCCGTCGACTTAA
TP118179	TGCAGTGGTGCTCCTCCTCTCTGTTG[C/T]TGCTGCTGTCCGTGCTGCTCTGCTGCTGTGCCGATCT
TP118183	TGCAGTGGTGCTCTCGATCT[A/G]GTCCTCTCTTCTTCCACTCCGTTCTTCCCCCGTGGCACGGACG
TP118194	TGCAGTGGTGCTTGATGGCTTGTGTTTCCAGCGACCGAA[G/T]GACCCCCTGCTCTCTTGCCGTGGA
TP118209	TGCAGTGGTGG[C/T]CGCCTCGATGGCCCTCGTCTTCCTGCCCACGCTCGCCTCCGCCACGGATCAC
TP118239	TGCAGTGGTGGGTCAGAAAAGCCACGCGGCCTGGAGGGAGAGGGCAACGGAGCGCTGA[C/T]GCTCT
TP118244	TGCAGTGGTGGTAGGACGAGCTGGCAGGTGGACGGTGTGGCGCGTAG[C/T]GGGTGACGGTGGATGC
TP118250	TGCAGTGGTGGTGCTAGTGCGAAGC[A/G]TTTCCACCATGGACACTGATAGCAAGTCTTCAAAGGAT
TP118271	TGCAGTGGTGTACACTAGACAACTGACAACGGTTCTTC[C/T]ATGTGTCTGTGTGCGCGCGTGTGCT
TP118281	TGCAGTGGTGTGCAGCAGAGGCGACCACGAATGTTGGGCGCTTTTCTT[G/T]CCATCAACCTCCAGA
TP118288	TGCAGTGGTGTTCGACTCTGTTTTCTTTAATTTAGCAGACAAATGTAAACTTG[A/G]CAGTGTTTTA
TP118290	TGCAGTGGTGTTGACGCGGACTGCGAGTAGTTGGTGGAAATGGTTTGAGTGG[A/C]CATAGGGGCCA
TP118307	TGCAGTGGTTACATATATATGCATC[A/G]ACTTTGGAAAACAGCCGCTTGCAGAGCTAAAGAACTTC
TP118325	TGCAGTGGTTCAAGGAGGAAGGGCCGCAG[A/G]GCAGCAGGATCAGGGCGCACTCGTCGGTTCGTGC

Table A2 (cont.)

TP118332	TGCAGTGGTTCATCACCGCGACGGGATTC[A/G]TCTACTTCGCCTTCGCCTACTTCGTGCCGACGAT
TP118347	TGCAGTGGTTCGAGTCTCTCAAGCCCTC[A/G]CTCTGCGCCACGCCCAAAGGTGAATTGCCTCTCTC
TP118349	TGCAGTGGTTCTCAGTCTCGTCTAATAGTTTCACTGGTAAAATTCCAACTGGGCTAGCAG[C/T]GTG
TP118350	TGCAGTGGTTCTCTGTCGCGTCTAATAGTTTCACTGGTAAAATTCC[A/T]ACTGGACTAGCAGCGTG
TP118370	TGCAGTGGTTGCGCCCGTCGGGCGTCGTCGGCTCCTTGGAAATGAGGAAGCCCAGCTCGTCCT[C/T]
TP118371	TGCAGTGGTTGCTCGCGCACTGGAGGAGACCGTAGAGGCTGACCATCGCGTTCTT[G/T]CGCCCGCG
TP118400	TGCAGTGGTTTCATGTCCAATTTTCAACATTCC[A/C]ACGTGTTGAGTTTTACCCGCATGAAATTCA
TP118405	TGCAGTGGTTTG[C/G]GATGTTGTCCGTCACCTGCCTCGCAAGGCGCCGCCGCATGCACTGCCGCGG
TP118409	TGCAGTGGTTTGGTCGTGTTGTGTACAAGGCGGCGCCATTATTACTGTTACTCT[A/G]AACTGTCCA
TP118453	TGCAGTGTAATCATTCACTCTGCCAG[G/T]GTCGACCACCGAGGCTGTTGCCGAGAAGCGTCCAACG
TP118466	TGCAGTGTACAGTGCACACAC[A/T]TGTCGTCCTGGTGCGCTTAAAAAGAGAAAACGACCGCTCCAC
TP118483	TGCAGTGTACGGCACCGTAGGAGGTTAGT[A/T]TGGTTTTTGCAGATGATGCCTGCTTATGTTGCAC
TP118494	TGCAGTGTACTACTCCCGCTTTGCTTGTCGACCGCAGATGGCC[A/G]ACGACGGCGAGGAGCATCAA
TP118504	TGCAGTGTACTGTAATGGATAGGACAA[C/T]AGACTTGATATGGCACCACTTCATCATCAAGTTACT
TP118507	TGCAGTGTACTTGTACCAAGTGAAGAAGTTGGGCCCAGGCCCAGCGTT[G/T]CCTTCCTCGCAGCGG
TP118515	TGCAGTGTAGACCATCTAAATGCTTTTGAGCATGGTACACTACCACTTGGGTCATGG[C/T]ACGCGT
TP118562	TGCAGTGTAGTAT[G/T]GTCCGAGGTCGAGGACGTACAGCGAACGCGTTGGCTGATTCAGCGGCTCC
TP118579	TGCAGTGTATAACCTTGTGTGTTTTCCTCTCTGAGTT[A/C]TACCTGATATAATTTGCACGGGTATA
TP118591	TGCAGTGTATAG[C/G]GAAAAAAGAAAGTGGTTCGTACATTTGAACTGGATTCCCTTTCCTAGTTTC
TP118616	TGCAGTGTATGCATGTAGCTCTGTCCCTCCCCTAGCAGTTCCACGTAATTGCGG[C/T]TGTCCACGA
TP118627	TGCAGTGTATTATTATTATGTTCATCGATAATAACGAGCTTT[A/C]ATGTTTCTGAAACATTGGTTA
TP118644	TGCAGTGTCAACACGACAACGTCTTCTCCTCCCACCATGCTCCTTCCTCCCGCACCTAC[A/G]CGGC
TP118646	TGCAGTGTCAACCACTGCAAGAGGAAGAGAATCGTTCGGGTGATCAGGGAA[A/G]CTTTGTTGATCT
TP118649	TGCAGTGTCAACGTTATCTCTCTCTAAAAAGGATTCGTGCACCAAAAGACGGGCAG[C/T]AGATCGG
TP118669	TGCAGTGTCACGGCAAAATCGCTCCGCCCCGCCAAAACAGAACTGCCA[C/T]GTACGGCATAGTCGG
TP118671	TGCAGTGTCACTACCAGCCAGTAGTATCGATCCAGCT[C/T]CCCTCTGTTGAGGTTGTCCTGAAGCC
TP118673	TGCAGTGTCAGAAG[G/T]CCGAGCAAGCTGACATCTTGTTCTTGTCGGAGACCAAATTAGACACGAA
TP118684	TGCAGTGTCAGCGTGCGA[C/T]GGCTGGGGGGCTTCCAGCATCGATTGCAGAATGACCTCTTGAGCG

Table A2 (cont.)

TP118685	TGCAGTGTCAGCTGACCTTGGCAC[C/T]CACAGCTCTTTGAATGGCAACTCCCGAGCACTGGCCACT
TP118688	TGCAGTGTCAGCTTTGCGCAG[A/C]GCCGCCTCGACGGCGCGGACGGTAGTAGCGCCGCCGTGGGCC
TP118704	TGCAGTGTCATGGGTCC[G/T]AGTTTGGCCACTGGAGGCCGTACGTGCGTGATCGTGAAATTCGACG
TP118721	TGCAGTGTC[C/T]ACAGGTTTCTTGTGCAATGCATTGGTCAAGTCCCCCTTTGGCATGTACTTGTAA
TP118728	TGCAGTGTC[C/T]AGGCTACCATCGCGCTTGAGCAAGGGACTGCATCGTCTGTCTTTCTGCTCCGTT
TP118766	TGCAGTGTCCGCCATGGCGCATCTGC[A/G]CCAGGCAAGCGGCCGCGCAGAGCATCTCCACGCACGG
TP118767	TGCAGTGTCCGCCGCCGCTCAACGGAACTC[A/C]ACTCCTCTCCCCACAGCAACCGCGGGTCCGATC
TP118806	TGCAGTGTCGAGGTCCATGAGGC[A/G]GCCACCAGGCTTGGTGTGGCCTAGGCAGAGGTCCCCCGTC
TP118809	TGCAGTGTCGCAGGCATAGGGAGC[A/C]ACAACCACAAGCTGCTGCTGTCACGAACACGATGTGACG
TP118813	TGCAGTGT[C/T]GCGATCGAACACGTAGGAAGAAGATTCAGAGTTTGAGACATGGGGAGGTCGCCGT
TP118824	TGCAGTGTCGGCCGAGGTGGGGCGGGCAA[A/G]TGCGAGGAAGGAGGGACGGGACATGGCGGCGGCT
TP118832	TGCAGTGTCGTATTCCTATATGATGGGTCTGGCTTCACATGTGATGGCATGAGGTCCAATTAA[G/T]
TP118838	TGCAGTGTCGTCGCTTATTGTGCTCGGCGGCGGTGGGGATTCC[A/G]TGGAGTAGCGAGGAATCTGG
TP118850	TGCAGTGTCGTTTACAGGAGGAGCTGGAGCTAGTGAATCTGTACCGAAGGG[A/G]GCCTGATTGACA
TP118867	TGCAGTGTCTATGGGCCAGGGCATGTCTGGCCATGAG[C/G]ACATACGTGCCCGCACCCCTGTGCGT
TP118873	TGCAGTGTCTATTGGACACGATTT[C/G]GCCTATGGGGTGCGGTGCGTGGCCCAGCGTCGAACATAA
TP118875	TGCAGTGTCTCAGCAAAATCCTGCAACTATTCGCGGG[A/T]GCCTCGGGTCTTGTCACCAACTTCGA
TP118877	TGCAGTGTCTCATTGAGAAAGAAAAGGCCCATCATGCCTCAGCTATCTCCCAGATC[A/G]TCGCCGC
TP118882	TGCAGTGTCTCCTGTATCTG[C/T]CATGGACCTGGAACGAGCTAAAGATCCGACCAAAACAGCTAGT
TP118915	TGCAGTGTCTTAGTGTTCATTGCTTCCTTGCT[G/A]AACAACCTTTACTTGTTGCAAGTTCAAAAAA
TP118917	TGCAGTGTCTTCCAGGTACATGGACGCGACACTGACCCAAATAGATGGGTC[A/G]ACAGTGTTCATG
TP118928	TGCAGTGTGAAAACGCGAACCCGATCTGGATGGAAGGACCGACGCGTCGG[C/G]CTCGGCCAGCCAA
TP118940	TGCAGTGTGAATGGCTTTGCTCC[C/T]GTCCACACGGGCAGTACAGCTCGCCACGTCATCCTGGAAT
TP118947	TGCAGTGTGACCAC[G/T]CACCAAACGAAGCCGTATCACACCACCTGCTGGACCCACTGCTCAGCGA
TP118962	TGCAGTGTGAGAATTCCAGGTACGTTTTTTTT[T/C]CCTGTTATAAGACCATGATCCAAAGAATAAG
TP118974	TGCAGTGTGAGCGGATAAGACCGTGAGAAACAAGTGGAGGA[A/G]GACACGCGGCGCCGTATCGAAT
TP118984	TGCAGTGTGAGGTGAGAGGACAACTGAGTGAGGGGAGTGCGAGGGCTG[C/G]GGCCTGATGAGGGCG
TP118996	TGCAGTGTGATGACGGATGGATGACGCGTTG[A/T]AGATGCACGCACCGACGCGTCTGATGTGTGCG

Table A2 (cont.)

TP119026	TGCAGTGTGCACCGATCGTCCGTGCATCGGCGTCCAG[C/T]TCCTCCTATGGATTGGGAATGAATGA
TP119040	TGCAGTGTGCAGCCA[A/T]AGCAACAGCAATTGCCATGGCAGAAGTAGTGTGGAGCAACGTCTAGCT
TP119042	TGCAGTGTGCAGCCATCGGTTCTCGCGACATGCCT[G/T]GGCGTGCCTCCGCCTCGTTCGCGACGAC
TP119050	TGCAGTGTGCAGTCCAAACGCCACACCGTCTGTTGGATTGGATGAGCAGTC[C/T]GACCAACACCTA
TP119054	TGCAGTGTGCAGTGAGCT[C/T]CTTTCACTGTGATATCTGCATCGAGCACCGTGAAGCAACAGCAAT
TP119062	TGCAGTGTGCATC[A/G]ACCAGTACAGTGTAAGTTACACAGTTGGGAGTAATATTATCCGACTGAGC
TP119068	TGCAGTGTGCATTAAATCT[A/G]TGGATCGATCGACTCCAATCCAAGTCTAAAAAAGAGCCCAACAT
TP119075	TGCAGTGTGCCAACGAGCTGATCCCCAGGACCCAGGTGCGTTC[C/T]GCCGTCAAATCCTCGAGTGT
TP119096	TGCAGTGTGCCTATCCTGGCGAGCTTCTCCCTGGACCAGATG[A/G]CCACGGCGACGGCCCTGGAGG
TP119103	TGCAGTGTGCGCGCGCGCGC[A/G]CACACACATGCCTATAGCTACTCTCTCTCTGGGTCTGGGCCTC
TP119157	TGCAGTGTGGAAGAGGAGTTGGCT[A/G]TATGCATCAACAATGGCTCACATCGTTTTTGACACCATC
TP119179	TGCAGTGTGGATAGTCCTTGTAAAGAAAGCAAACATTAACTAGAAAATGATTAAAATGGTACT[A/G]
TP119183	TGCAGTGTGGATGCTGCCTACAGGTTGTCTTACTCCATGAACCAGCCTCCAGTGA[C/G]TAGACATA
TP119191	TGCAGTGTGGCGCCTTGTGTGCTTCCCCTCCAGGATCATTG[A/G]GTCCCCTCCTAGATCCAAAAAC
TP119243	TGCAGTGTGGTTTGGCAAATTTAAGTTTAAACAGGCTCTAATGGG[A/C]CTTCAGTAAGGACATCGC
TP119264	TGCAGTGTGTAGTCCCTCGTCGTCC[G/T]CCATATACGATAGAAGCAAACGCCAAAGAGTGCGAGGT
TP119266	TGCAGTGTGTATGGAAAAGGACAACTGCTATCCACAAACAAGACGCTTTTGGGCCC[A/G]ATAAGTT
TP119269	TGCAGTGTGTATGTCG[A/G]CGGTGGAGGAAAATATCACTGACAGGCATGGCCCACGCCTGCGAAAC
TP119270	TGCAGTGTGTATGTCGGCGGTGGAGGAAAATATCACTGACAGGCATGGCCC[A/G]CGCTTGCGGAAC
TP119276	TGCAGTGTGTCAGCACGTTGCCCAAATGCGAAGGAGAAGCGAGGTGGGGAAAGTTCTGAC[A/G]ACA
TP119286	TGCAGTGTGTCCAGTTGTAGCCGATCTTGGTCA[C/T]GTTGGCGTGCAGCGCCGCCTGGACGTCGGG
TP119295	TGCAGTGTGTGACCTCACTGGAAAGAACAAATCAAGAACACACGTTGATGAATGATGAGTAAC[C/G]
TP119296	TGCAGTGTGTGCATGCATGA[A/G]CATGATCCTTTCGTCAGCTAGCCTCAGCTAGGACGACTAGGAA
TP119301	TGCAGTGTGTGGCACAAACAGATTTTGTTTATTTAT[C/T]CATTTATATTGTTTTTGCGAACGAGGC
TP119347	TGCAGTGTGTTTTGCGCGACACTGTCACTGTGTGAATAACTGAAAAAGG[A/C]CTCGGTGCCCGTTG
TP119361	TGCAGTGTTACCCCCACCACTCAGCCCA[C/T]TAGTATGCCCTAGATCTGCTGCTGAAGAGGTATAT
TP119368	TGCAGTGTTACTTAAAACCAATATGGGTTCAGTCATTCGGCAAGCACA[A/G]TTAGTCCTCCATGGC
TP119395	TGCAGTGTTCACAGTTTGATTCTTTGCGCCGATG[A/G]TTCGATTATTCGACACACTAGAGATGCTA

Table A2 (cont.)

TP119399	TGCAGTGTTCACGTACGGGCCGCCGCACACCGTCAACGA[C/G]CTGCCGTCGGAGGCGGACTACAAG
TP119406	TGCAGTGTTCA[G/T]GTACGACCCACCGAACGCGACGGTGCACGCGCACAGCGTCTACCTGATGCGC
TP119441	TGCAGTGTTC[G/T]ATTCGACATTCGAGGCGGGATGCTTACTGGATCGCTTGATGAGTCCTCGACAC
TP119459	TGCAGTGTTCTACTGCTAGTAGGCGTAGTA[A/C]CAAAAGAAGATAAAGGCAGGGGTAGGGGTATAC
TP119471	TGCAGTGTTCTCTGGCGGCCTCGCCATCGGCGTCG[A/G]CGTCGACGGAGCTCGCGCGGGCGGAGGC
TP119538	TGCAGTGTTGCTTTTCCTTTGCATGATGGATGTACT[C/T]GCAAGCAATGCAATAATGCGATGCAAT
TP119574	TGCAGTGTTGTACTTGTTACACATGCGAGTCTTCACAG[A/C]AGGTGAAGGTGGCCCATCAGGGCCA
TP119576	TGCAGTGTTGTAGAGAGTTTGCTCTCTCCAGGCCTCTTCTCTCCCACCGCATTCT[C/T]TGCGCCAC
TP119577	TGCAGTGTTGTAGATCGATGACCATATGCGGCACGGCGTGGACGCCCACTCC[A/G]CCGCACGTGAA
TP119581	TGCAGTGTTGTCACGTACTACGAGAGCTAGC[A/G]ACGCGCGCGGCGCGGTAGATGGATGATGAGCA
TP119591	TGCAGTGTTGTTGAAGATTCTCCTTTTAACCGC[C/T]ATGTTCGCTTGGCTGATAAGTTATGGTTGA
TP119595	TGCAGTGTTTAACAACGAGC[A/T]CCACAATGGCCATTTGGGCGACCTACCCTGTGAACGCGGAAGT
TP119609	TGCAGTGTTTATTGGTGGCCAATTTGCCATG[C/T]GATGATCTTGATCCGTCGGCCTGTTCGCTGGT
TP119640	TGCAGTGTTTGACATGATGGATGCAGTGGCGCCACGGGACAACAACGATCGCATATTG[C/T]TTGAG
TP119652	TGCAGTGTTTGCTTGT[C/G]CAGGCAGGAGACCAGGGACAGGCGCGCGCTGAGACGACGATAGCAGC
TP119658	TGCAGTGTTTGGCGGAGCCAGTGGCCTCCACCGCCGCCGCTGCATG[A/G]TATAGGGCATGTAGCAC
TP119663	TGCAGTGTTTGGTTGCTGCCGCGCACTGGGCGAGCCAAAAGTGCGGC[A/G]CCGTTTCCTGTCTGCT
TP119752	TGCAGTTAAATAAATCAATCTGGTGTTCATGG[T/C]TATTACTGAACCTCGGGGGTCTGTTCATGCT
TP119770	TGCAGTTAAATTCTCACTTACTAACCAAGTAACCAAA[A/G]GTTTTGTTTCTTTTCCCAAATAAAAC
TP119786	TGCAGTTAACCACAAGCGACAA[C/G]AAGAAGTAACTGCTATTACAGATAGGTGGGCAGCTCAACGG
TP119793	TGCAGTTAACCTGACAGTGAAATTCTGTAACCACATCAGAATCCACAGCTGGTCTGGCCACC[A/G]T
TP119800	TGCAGTTAACGATGAGCACGTCGATCTCCTCGGGCTTGACGCTCGTCCTGGC[A/G]AACACCTCGTC
TP119836	TGCAGTTAAGCTCTGTCTGGTCG[C/G]CTTCTTGTTGACTTTTCTTCTTATTACCAACAAGGAACTT
TP119856	TGCAGTTAATACAAGAGACCAGCC[A/T]TTGCTCCGACTAAAATTGTTGGAAGAGTTTGTGACTATA
TP119884	TGCAGTTAATGATGAACTTA[A/C]GTAGAGTGGTTAGCCAAGCAGTATAATTGGTGTTTAATCATAT
TP119891	TGCAGTTAATGGCCCCTTCAT[C/T]TCGGTAGGTTCTTGATGGCGAAGGCACATACATATATGTACG
TP119895	TGCAGTTAATGTCAAAATGAGCTACGAGATGAAGCTTTGACCAACAACTTCAATGAAATGTGA[C/T]
TP119932	TGCAGTTACACAAACTTACACGTCTTGGTGCGGAACAAGACA[G/T]GAGTGCGCGTGCCGATCGCTT

Table A2 (cont.)

TP119939	TGCAGTTACACGACGAGGCAGGACGCCACCAAGGGCTGGCTAGCTCGGGGCACTCGGCGAAGC[A/C]
TP119942	TGCAGTTACAGAAGGAAGGTACCTCTC[A/G]ACCTCAAAGAGAGGAGGAGGTGGTGGGCGTGGCCGC
TP119943	TGCAGTTACAGACCAAGTTAATTGCTGCTGTTCATGACAGTGTGTTGGGTGGTCACTCAGGGG[G/T]
TP119948	TGCAGTTACAGCCTGCACCTTCTA[C/T]AAGTACAGCCGCGAGCCTCAGCTGCAAATTAACTAGCGC
TP119963	TGCAGTTACAGTCTCGCAGAGCGGTGTCGTTGC[C/T]ATTGTCCATATGACCATATATATCAGCCTC
TP119965	TGCAGTTACAGTGCGGACTTAGGACACGGTGTGGGCGTGGGACATGGA[G/T]CGACGCGGGCCCCCA
TP119976	TGCAGTTACATCCAAC[A/G]TAACTGCAAATTAAAAGAAAATGTTGCGCTGCAATTCCCATACCTCG
TP119998	TGCAGTTACC[A/T]CCGCAGGAGACGCCATCAAATCCGAGGACGACGCTGCTGCGGCGGCGGTGGCG
TP120001	TGCAGTTAC[C/T]AGATAAACATGTAGGAGAGAAAGAATTGGTGGAATAGTTGATTCTATTGCTGAG
TP120002	TGCAGTTACCAGCATAACCATCTAAAGCTTTGCCCCCAACAACCCATCCACA[C/G]CCAACCAACAG
TP120011	TGCAGTTACCGACGCGCAGGC[C/G]AGTTGCGGTCCTCCAGAGGTGGCGCCAGCGCCGAGCGAGAAC
TP120027	TGCAGTTACCTCC[C/T]CATCATGAACTTGGAGACCGAAAGGTGTGGTGCCTAGCTACCCCGTACTG
TP120047	TGCAGTTACGAACGGCGGCAGGAGTGAAGTAGTGAACTA[C/G]TTGCTGCCGTGCTTTGCGCGAAGT
TP120057	TGCAGTTA[C/G]GATTACCATCTCATTGATTTTCTTTTTCTTTTTGGTGTGTGTTTGGTGGGTGGGT
TP120068	TGCAGTTA[C/T]GCGCACGGCATCTTTGAGACGTTGATGCACCCGACCAAGTTCCGCACCGTGATGT
TP120080	TGCAGTTACGTAGGTGTGGGCCCTCGTCGACG[G/T]TTTTGGGTACAGGGGCACCGATTCGAAAGAT
TP120086	TGCAGTTACGTCCTGGAGG[A/C]CACGATGCTAGAAGAAGGTTTGTGAGATATTCCCCCGCTCTGAC
TP120121	TGCAGTTACTCCATTTGGATCCATCAACGCGAG[A/T]GAGATCATGACGGGCAAGTGCATTGCTAAG
TP120122	TGCAGTTACTCGGCTCAAGGCTCAATCGATCAGTGGTACTGGTG[G/T]TAGTGTCCTTTTCGCTTGG
TP120141	TGCAGTTACTGTCATTTACCTACTACACTGCTGGCAGAAGCGCTG[C/G]GCCTGGTTGGCGACGACC
TP120161	TGCAGTTAGAACTTAG[A/C]AGAGGCAGGCAACTAGGCAAGGCAAGAGCTCGTGTACCTGAAGATGG
TP120183	TGCAGTTAGA[C/T]GGGCATTGTTTAGCCTTTCTTGCGACATATCGGTGCAGTGATAGTCGTCGGTA
TP120187	TGCAGTTAGAGAAGACGGTTGCCTGGACTGGCCGAC[A/T]CGCCTGCGCGTGGCGGTCGGCGTGGCC
TP120188	TGCAGTTAGAGAAGCTGAAGATTTGGACTGGCCTGCACGGCTGCGCATCATCATGGG[A/T]GTAGCA
TP120195	TGCAGTTAGAGG[A/C]ATCAAGCAAGCAATGAGTGAGGGGTGAGGCACTGAGCCCGATCGTTCGGCC
TP120205	TGCAGTTAGATACGGGCACAGACCACAGGCCCAAGTGCAACCCAACA[A/C]ATCCTTCCAAGTTCCA
TP120214	TGCAGTTAGCAAATTAATTTCTTAACTGCCCCACTACGGCACTAAAAATGAAACATTTA[G/T]TGCC
TP120229	TGCAGTTAGCAGCATTGTCCCCAGGA[C/T]GTTCCGTCGCAGCCATATCAATAACTGGCATGGATCC

Table A2 (cont.)

TP120232	TGCAGTTAGCAGTGACAGCTTCTCTCAGAGA[C/T]TCATCAGACTGCTGTCTGCTGAGGCCTTCACT
TP120250	TGCAGTT[A/C]GCGGAACATCGATCGATGTGAATTGTGGGTTAGCGCGCGCTCGCGCATATGGCA
TP120252	TGCAGTTAGCGGACAACGGGTCCTGCTCT[A/G]GGCGCGGCTGCTGCCAGGCCTCCATCCCAGCAGC
TP120288	TGCAGTTAGGACGCAGGTAGCTGCTAGCTCACTGCTCA[C/T]GGTCAAACTCAAATCTATCCCGCGC
TP120309	TGCAGTTAGGCTCTGAAACACATG[C/T]AGATGCATGTACACAACATACAAATGCAAGGAGGGGAAA
TP120318	TGCAGTTAGGGCCGCCGCCACCCTAGATGCGCCCCACCC[C/G]CACTGGATCTGGCCGCCCCTCCTC
TP120337	TGCAGTTAGTACTAGTTTCACGAAGATCAATAG[G/T]TATGTTGCATTGCATACACAGCTATTCTCT
TP120341	TGCAGTT[A/C]GTAGCCAATTCTTGCACCAGATACCTGTCAACAAGCTCACCAGGCTACGTGAGCAC
TP120410	TGCAGTTATAGA[C/T]TTCTACAAGAACTTGGGATTTGAAGTTGATCCTCAAGGCATCAAGGGCATG
TP120428	TGCAGTTATATGAAGGGACAATGCTAAGGTACAAAC[C/T]TTACCTCTGAGGAGGTAATATTTCAAA
TP120452	TGCAGTTATCAGTCACACCGCTGATTGGACGCCTGCCGTCAAAAGT[A/C]AAAAACTACCTAACCTC
TP120459	TGCAGTTATCCAGCAAGATGGAGATGGAGGCGTACCTCCACCAGTCCACCACCTCTTCCTG[C/T]TG
TP120533	TGCAGTTATGTCACTGACAGGTGAGCCTGATTGCAATCATGCCCTGTGAG[C/T]GACACAAGTGCAA
TP120544	TGCAGTTATGTGATTGGTGCCTTGGTCGTG[C/T]GGTGCCGAAAGATATGAAAGACCACGCGAGTCT
TP120555	TGCAGTTATTAGGAAGTTAACAATCCAACGGACGGGCGCGTAGAATCGAAGAAAGA[C/T]GGTCCTG
TP120595	TGCAGTTATTTG[C/T]TGTGAGTACTGAACATCAAAGCACAGAGGATCAAGATCAGCAGGGATCCCA
TP120632	TGCAGTTCAAATAGACTAAGGGCGCGGCCACGTGGGCTGGGCCGAGTTGA[A/T]GTCGTCGGCCGTG
TP120677	TGCAGTTCAAGAAAGACATAACTCATGCATGTCATCCAACCGAAAAACAATAGCAGGAGCTT[C/T]G
TP120688	TGCAGTTCAAGCACAGCAA[G/T]AAAATCTTGCAATCGTGGAGCTAGAGACAAACATCACAAACATC
TP120695	TGCAGTTCAAGCTCTATCTGGT[G/T]AACACTTACTCGGATGTCATTGGCCCTCTAGTTAGTCAGGC
TP120735	TGCAGTTCACAACAAAGCACAAACAATATAATAGA[A/T]GTTTCCGAACTGTGTGATCACAGTAATA
TP120740	TGCAGTTCAC[A/C]ACCAGGATGTCGATGGCGCGGGGGCTGATGCCCGTCTTGGCGAGCAGGTCGTC
TP120744	TGCAGTTCACAAGAAAAAAGAACTCGACATTATGGATCACTTTTTTT[A/G]ACCCAAAAAAGAAAAG
TP120748	TGCAGTTCACAAGATCTGGACACACTCAGCTGC[A/G]CGGCAATGCGATAATGATCACCAGCACAAT
TP120777	TGCAGTTCAC[C/T]ACCAGGACGCCCACGTCCTTGGGCCGCACGCCCGTCTTGGCGAACAGCTCGTC
TP120781	TGCAGTTCACCACGAGCACGCCAACGTCCTTGGGCTTGA[C/T]GCCCGTGGACCTGAACAGGTTGTC
TP120783	TGCAGTTCACCAGACCGTCCGTAGAATCCGATCAGACAATTATCCAGGAACTCCTTGCC[A/G]ACCA
TP120788	TGCAGTTCACCCGTGTAAAAATAATAATAAAGCGCGGTGCGG[C/T]GCATGTGCATCGCACGCAGCT

Table A2 (cont.)

TP120828	TGCAGTTCA[C/T]GGCCACGGCCCACGGCCTATGGAGCTGCTCCTCTCTCTTTCACCACACTAAGCT
TP120830	TGCAGTTCACGGCGTGGAGTACGCGTACGGGGCGCACGACGGCGC[A/G]AGCAGCGGGATCTTCGAG
TP120835	TGCAGTTCACGTTTTTAGTTTGT[A/G]ACTATGTATGAACAACAAATATCTGAACTAGTACATTACC
TP120874	TGCAGTTCAGACTTCAGACATGACATGACAGGCTACTCTGCCCTT[C/G]GCTGTTTCTAAAGACGAC
TP120885	TGCAGTTCAGATAAGTCAGCCTCAATTCATCAAAAACCCCAAAAATAATAATGCTAT[C/T]GCTAAG
TP120889	TGCAGTTCAGATCTCCAGAACATCTAGTACGTAGCGA[G/T]ATTAACACACATGAAACTATGAAAGG
TP120961	TGCAGTTCAGTGCAGTTCTTCCATTGGTTGAACAGGTCAAACTTGCTC[A/G]GTTCTTCATCAGTAC
TP120972	TGCAGTTCAGTGTATTGGCACTA[C/T]GGGTAAAGCAAGCATCTCTATGCCGAAAGGTGCAGATCCA
TP120983	TGCAGTTCAGTTGGACTGCGGCAGCAGCCCCAATCTGA[A/T]GCGATCATGCCCTTAGTCCGAAAAA
TP120988	TGCAGTTCATACA[A/G]GCAGGATCATTCTGTGTTTCAAAGGTGCAGTTTTCAAGAACCAAATGTTG
TP121002	TGCAGTTCATCACCAGCCGCGCGTGTCTTGCTGCC[A/G]CCGTAGAAAAACGACGTAGTAGCTATAA
TP121028	TGCAGTTCATCCTGGCAGGTACGGACGGCGACCTCGGCATCGATGTAAAACTGTCGGGCGTAC[A/G]
TP121068	TGCAGTTCATGCTC[C/G]CCCACCGTGCTGCAAGCCTGCAAGTACCTGGGCGGACCTTGATTCAGGT
TP121077	TGCAGTTCATGTGTCTCCCTCCCCACAGGTCACGTCACGC[G/T]GACGCACTCGGTTCCTCCGATCC
TP121118	TGCAGTTCCAACAGTGTTCAGAA[A/G]CACTGCTCACCTGACCCCTCCACCTCCAGATGCGTTGCGA
TP121135	TGCAGTTCCA[A/G]TGCTTGCAGTGGTTTGAAACCTTTGTGTGACTGTCTGAAATTATGCAGAGAAG
TP121144	TGCAGTTCCACCACCATGACGAACGAGATCTAGGTCGCTTCGGCTAGAGGCCT[A/G]CTCCTCCGCC
TP121155	TGCAGTTCCACCTGGCTGCGCCGACGA[C/T]CGCCCCGCGAACTCGATCAGGTGCAGCGCCTGCACC
TP121163	TGCAGTTCCACGCTGGATCACCATACCTCGTGCCTTAGTTTTTTTTTTTGACGAACCGA[A/G]CTAT
TP121170	TGCAGTTCCACTCTGGAAGA[C/G]CGTTTAGACGGCGGCTCTCCACATCATGATCATGAGAATGGAG
TP121175	TGCAGTT[C/G]CAGAAAAACCAACCGTTCGTCCTGGCGACATGAACCAACAGAGGGTGCAGATGCAG
TP121176	TGCAGTTCCAGAAT[A/G]TTCCCAACGCAACTGCCAGTCCAGACTAGCAAAATTTGCCGACTCGCCA
TP121179	TGCAGTTCCAGAG[A/G]AGACACCTCTTCTGTTGTGCGTGTATCTACTGTATCAACTTAGCAGCAGA
TP121191	TGCAGTTCCAGCATGGGAGCACTGCGCA[C/G]CTGATACTTCCTAGGCCTGGAGGTGGCCTTCAAGG
TP121208	TGCAGTTCCAGTCGTCCCGAGAGCCACCTCGCCTGCTGGCCCGAGAGCCGAGCTGG[C/T]CATCCCG
TP121241	TGCAGTTCCCA[C/G]TCCAGAAGCTGCCGAGAGAGCCTGCGGATTACACGCATCTCGCTGCCGCCGC
TP121246	TGCAGTTCCCAGTCCAAGGGCAACAAGGGCGGCTTTGCTTTTCTTACTGTG[C/T]GCAGCTCCCACA
TP121263	TGCAGTTCCCCCTTCTTGTTGACGCTGGAATCATATCGCCTCGGCTCCT[C/T]GAGTCCTCGTCACC

Table A2 (cont.)

TP121270	TGCAGTTCCCCGTCGGCCGCATCGCCCGCTACCTTAAGACGGG[C/T]AAGTACGCTGAGCGCGTAGG
TP121274	TGCAGTTCCCCTGTAGGTTCCTCTCTTAGAAGCGAAGTTGCCATCCTCAGGCCACG[A/G]TGCACAG
TP121283	TGCAGTTCCCGTCCTCGTCCTCGTCCGCGCCGTC[G/T]GGCGACAGCTACGGCGCGCCCCCGCACAG
TP121297	TGCAGTTCCCTCTGCGGGTGTGCCGTCAAGAGCGACCAAT[A/G]ACCAGGTGGTTTCTTTCTTCGTT
TP121314	TGCAGTTCCGACGGTTGCCGCGACGTC[C/T]GACGCGCATCAGGCTCCCATCTCCGAGATGCAGGAC
TP121329	TGCAGTTCCGCAAGGGCGCCGCCGTGGGCGGGTGCCGCTACGCCGACGTCGACGA[C/T]GACGACGT
TP121332	TGCAGTTCCGCATGCT[A/T]CCAAAATGTATGGGTTCAGTCGTTTTCTCATGGCGTCTGGCGTTAAC
TP121335	TGCAGTTCCGCCGCCTGCGCGCAGCTCGGCCAGGAAGGCAACGGCAACGGCTGCT[A/C]CACGTCCC
TP121344	TGCAGTTC[C/T]GCTAGAGCACATTTATAAGGACTAGGTGCCCACCAGGTCTGCTTAGCAGTTGGCA
TP121354	TGCAGTTCCGTCCGTCGAG[C/T]AGCCACGACACGACGGTGACGACGACGAACGCGGGAGCGCCGAA
TP121355	TGCAGTT[C/G]CGTCTCGTGGTCTCCATCGGGCAGTTGTGTCTCGTAGCCGTGAGAGGAGACCAGGC
TP121365	TGCAGTTC[C/T]GTTCGCTATCCTCTGGTTGCCGCAAAACATCGAGCAGCTTGCGTGCAAGCTCCGC
TP121371	TGCAGTTCCTAAAAAAAACACTTTTGTGTTGTGCATGT[A/G]TCTACTGTATCAACTTAGCAGGAGA
TP121384	TGCAGTTCCTAGAAGGACAGGCATGGGACAGTGGT[A/G]ACTGGTGAGAGCTGTCTCACTGAGTCAC
TP121387	TGCAGTTCCTAGGCGTCCTGGGCATCTACCGCTTCTCGGC[C/G]GAGATCCTCCGCGGCCAGCACCG
TP121402	TGCAGTTCCTCACCAACGCCTGCGTCGTCCTCTTCTTGGTCCAGAGCGTCGA[C/T]CGCATCGTGCT
TP121418	TGCAGTTCCTCCTACAATCCCCAGTGCGAGCGAGACCAGCGACACTA[C/G]CTTTTGGGAACACAGA
TP121423	TGCAGTTCCTCCTCCTCACCGTGCGCCCCGTCGTCGTCATGCAGCT[A/G]CGGCACCGCGCCGAAAA
TP121425	TGCAGTTCCTCCT[C/T]GCAGGGTTCCACATTGTCTCCAGGGCGGCGCTCAACATGGGCATCAGCAA
TP121439	TGCAGTTCCTCTACCGCACCCAGAAGGAGCTCGCCGCATGTACGTCGGTCATCGCCACTTC[C/T]TC
TP121441	TGCAGTTCCTCTACTCTACTGCTATAGA[C/T]AGGGCAGTGGTACAGGCGTACAGCCGCAACCATTG
TP121442	TGCAGTTCCTCTCAAGGCAAGGCGTGGCGTCGCG[C/T]TGCGTCGTTGCGTCCCCTCCACTTCACTC
TP121461	TGCAGTTCCTGCCGCCGAAGAGCGAGGAGGAGCAGAGCTGTTCTGGGTG[A/G]TTGTCGTCGTCTTC
TP121465	TGCAGTTCCTGCGCCCTTTATCCAGCCCTTTACCC[C/T]CTTCATACACCCAGCCGCTGGTATATGC
TP121477	TGCAGTTCCTGGGCCAGGCCCAGCGGCTCCAGAATCT[C/T]GGTTTCCTCGCCGCCGCCGCGCTCCA
TP121484	TGCAGTTCCTGTACTCTACTGCTAGTCTAGAGCCACAACCATTGTAC[C/T]AGTAGCCTAGCAGGAG
TP121505	TGCAGTTCCTTCTCACCAGTTACCAGATCCTATATGGCGACTTTGTTT[A/G]GCACGCTCAGACCCC
TP121513	TGCAGTTCCTTGCAGTTTCAGACCACTGTTGTCTGAA[C/T]ATGATAACCATGGTCAAGCCATTCAT

Table A2 (cont.)

TP121514	TGCAGTTCCTTGCCCCGCGGATCGGTGAGGAGTTATTTAATGATTGGTGGGAACGAATC[C/T]AAAC
TP121539	TGCAGTTCGAAGTTCGAACCAAAGC[A/T]AGTGCTTCCTTCTCTCTACTCTACTCCCTCACTCTGGC
TP121559	TGCAGTTCG[A/G]CGGCTCGAATTCGTCGTCGCCGCCGCCGACGGACCCGCTGTCGTTCGCCAACAC
TP121567	TGCAGTTCGAGAGGAAC[A/C]ACCATTTCCTTCATTGGGAGGAACTCGTCTACATTCCCACAAGCCT
TP121581	TGCAGTTCGAGGGCAGTACATCC[A/T]GAGGTCACCACCACGCACCCCCATCATCATCATCATCAGG
TP121582	TGCAGTTCGAGGGCGCGACGCTGGACCTGCCGCAGGGCAACTACGTGT[G/T]TCCTCAGGACAACAA
TP121600	TGCAGTTCGCAAGAAATCATTCACTTTCCCTTGCTCCGTCAACAAAAGTCTGCTCTTGGTAGT[A/G]
TP121620	TGCAGTTCGCAGTGCAGCACAGCTTGGTTTCGTAGCATCAGG[A/C]CAGAAGAGCGTGGGACTCGGA
TP121634	TGCAGTTCGCC[A/G]TTAACCACTGGAATATGGTTCTTCAGTGATTCTATCTGAGGATCGACGACCT
TP121645	TGCAGTTCGCCTACAACGGCAGCCTGCCCGTCGTGGACGGCCTGAGCGTGGAC[A/G]GCTACAGGGA
TP121647	TGCAGTTCGCCT[A/C]GCTGAAGATACATGTTTTGTTTAGGATCCTAGATTAGGATTTCCTGTTCCT
TP121649	TGCAGTTCGCCTCCGACGTCTGC[C/T]CGACGCATGGCCCAGCCATGTTCTTCAGGTGTGTGGGGGT
TP121657	TGCAGTTCGCG[C/T]ACCGCGAGCCGCTCCAGCCTCTCCAGGTCCTCATGCGCCGCCCGCGTCGCCT
TP121706	TGCAGTTCGGCACGCACAATGAGCAACA[A/G]GAAGGGACGAAAGCGAAGCGCGCGGCCGTGACGGC
TP121715	TGCAGTTCGGCCGCGCGCGCAGGGACTTCGTGCTGCGCTCCCACGGCGGCGCCGCGTAC[A/C]AGGT
TP121722	TGCAGTTCGG[C/T]GAGCTTGCTGCTTGGCGGCGGCGGTGGCGGCGGCGGAGGGACCATCGCTGGTC
TP121725	TGCAGTTCGGCTACGCGGGGTTCCACGTGGTGTCGCGGCTGGCGCTCAACATGGGCATCAGCA[A/T]
TP121739	TGCAGTTCGGTAAGGTTGATAATGATATCTTCA[C/T]CATGGATTATCGCCAGCCGCTCTCGGCATT
TP121752	TGCAGTTCGGTGGGTTCAAGGAGCGCCTCCTCGCCGACGACCTCTTCCTCACCAAGGTCG[C/G]CAT
TP121761	TGCAGTTCGTACGTGGTAGTGGTACGGAAGCCTAAAGTGGGTCAAGTTCAGCGTTGA[A/G]TGATAT
TP121764	TGCAGTTCGTAGAAGGAGTTGATGAGGACATGATCTGCAACCTCGAGCCC[C/T]TGGCACTGCTGCA
TP121765	TGCAGTTCGTAGGAATGACTACATCCATGACAGCCAAGTGCACCTGGACGACAAAAGCGC[C/T]ACC
TP121785	TGCAGTTCGTCGCCATGGTCGCCGCCGCCGTCGGCGAGGCG[A/C]CCCCGCCCCCGAAAAAAAAAA
TP121788	TGCAGTTCGTCGCGTGCAATAATTTGCAGTCGGCAGCT[A/G]GCATGATGCTGGAGCTAGGTCATCA
TP121806	TGCAGTTCGTGCTACAGATGCTGGGG[G/T]CCAAGGTCAGTGTCCTCCTTTCTTCTGTGGTGATCTT
TP121834	TGCAGTTCGTTTCGCTCGCCAGTCGCCACCGCCCCGTTTAACACCAGTAGG[C/T]CCATCGGTCAGA
TP121848	TGCAGTTCTAAC[A/G]CCTGCTCGGTCGCCGTGTTGCTTCTGCACTGCATATATACGAATCACAGCA
TP121850	TGCAGTTCTAAGAAGAACAT[A/G]CTCCCTTTGCCTCCTGCTCGCCTTAATCCCGAGCACCCTCCTG

Table A2 (cont.)

TP121877	TGCAGTTCTACTCCAAGGAGGTGAGCCGCCGCCTGCTCGACTTCGTCAAGT[C/T]CCGCTCCGCGGA
TP121904	TGCAGTTCTATCGGTAGACTGGAGGAAGTCGGAG[C/T]TTCGAAAAGCATGTTCAAACATTACGAAT
TP121907	TGCAGTTCTATCTCGCTCACTCCTTCTCCGAGTCCGACCAAACCCTCTC[C/T]GCCTCACACTCGCT
TP121928	TGCAGTTCTCACCCCATATGCCTTCTCTAAGCTACAAGATGAGCTTGTTGCGTCTGCT[A/G]AATAT
TP121936	TGCAGTTCTCAGGAAGGTGGAGAGCCTGGGGTGGCTCGACGC[C/T]GTCTATCTTGCGGTCATGTCG
TP121946	TGCAGTTCT[C/G]CAACCTGTGAATCAGCATGGTCATATGTATGTGCAGAACCACTGGAGAACCTGC
TP121950	TGCAGTTCTCCACATCAAACA[G/T]ACCAGGCCAGCACCAGCCGCGGCAATGGCGTCCACGACGGCA
TP121953	TGCAGTTCTCCAGATGTATATGGGTGCAC[C/G]AACCACACTTAAACAAATCAACAAAGTGGCTTAT
TP121968	TGCAGTTCTCCTCCAGCGCCTGCCCGACGCATGGCCTAGCCATGTTCGTCTGTCCC[A/G]TGGGGGC
TP121971	TGCAGTTCTCCTCGCTGAGGAGCCGCGCCGCAGCAAA[A/G]GAGTCCCGTGGCGCTCGCGCGACCTG
TP121981	TGCAGTTCTCCTTGCTACCAAGAG[C/T]CCATATGAGTAGTAGCACCGCACCCTTTACCTTCTCAGC
TP121984	TGCAGTTCTCGC[A/G]GAGAATATGTCGAGCAGGCGCTGTAAACTGCTCGTTCCCCTGACAAGGACG
TP121985	TGCAGTTCTC[G/T]CAGGAGCTCAAGGCCACCGCCAGCCGCGCCAAGCAGTTCTCGCAGGACCTCAC
TP121995	TGCAGTTCTCGGCGTT[C/T]GGATCGCTGTCCAACGTCGGCGCCATGGTCGGGGCGATCGCCAGCGG
TP122006	TGCAGTTCTCTGAGGCCTCGCCCAGGGAGG[A/C]AATTCCGCTTCACCCCACCGCCGCCCGAGGTCA
TP122021	TGCAGTTCTGAAGCATGTTATTTCCTGA[C/T]AGCTTATGCATTTATGCTGCTTCTTACATGAATAC
TP122032	TGCAGTTCTG[A/G]CGACCCCCTCCAGTCCGACGACGTTCTGCTCGGCGCCCGCCGCAGCTCCGACG
TP122048	TGCAGTTCTGCACACGATGCAAAGCAAACATACCTACCTACAGTCTCACAAACGTTCAGC[A/G]TGC
TP122052	TGCAGTTCTGCACCACAAAGGAGCAAGGGGTCTC[A/G]GCGTCTCGCCGTCTCAGCATCAGAGACGG
TP122083	TGCAGTTCTGCGACGAGCAGCCATCTTCGGCTGC[C/G]ACCAATAATCTGGTGCAGAGGCTCCTCAA
TP122089	TGCAGTTCTGCGCGGCGGAGTTCTGGCACACGTCGCTCGTGCACCG[C/T]ACCACCGCCATTGTGGT
TP122093	TGCAGTTCTGCGGGTAGGAGCCGTCGTCGCGGTTGGGCCACAGGCCGTGGATCCCAAAGTC[C/T]GC
TP122100	TGCAGTTCTGCTAGCTACTGTTGGTGTGGATAGAGAAGAAGGGAGCCTGGTCGCCTCACCCC[A/C]T
TP122104	TGCAGTTCTGCTCAATCAGCTAGTATATTTCTCTTTCTGTTTTCTCACTAAGTT[A/T]AGCACTCAA
TP122107	TGCAGTTCTGCTGTT[C/T]AGCAGAGTTTAGACTACAGCTCGTTGCCCCGTCCTGCTCCTTGCCGCT
TP122120	TGCAGTTCTGCTTTTCCTGGACACATGAGCTTCCTAGCGGCTGGCAGCTGTGC[A/G]ATGGATATGG
TP122129	TGCAGTTCTGGCTGCTGCCGCTGCCACTGCCACACCACCCGCCAGCTTGGTTGG[C/T]TACTTGCCG
TP122146	TGCAGTTCTGTCATCT[G/T]TGGGAATTCTTGAAGCAAAATTTAATTACATCATTCATCAGTTGTGT

Table A2 (cont.)

TP122148	TGCAGTTCTGTCATGTTCCCAATCTC[A/C]GATGGGATCGCTCCGTTAAGCGCGTTGAAGAAAAGTG
TP122172	TGCAGTTCTTAGCAACAAATCTTGG[C/T]TCGCCACGATTCCTGCGCCCGTGTTCTGCTCCTGCTTT
TP122173	TGCAGTTCTTAGTTATTCTTAGCATTTCTTGATTCTATCTGTTCGATTTCACTCAGCTCA[C/T]CGT
TP122185	TGCAGTTCTTCAGCACGCCGCCGCTGCCGTGCGACCTCTCGCCGATCCCCGTCGTGTACAAGG[G/T]
TP122187	TGCAGTTCTTCAGCACGCCGCCGCTGCCGTGCGACCTCTCGG[A/C]GCTCCCCGTCGTGGTGGAGGA
TP122197	TGCAGTTCTTCCAGCAGGCGTCGGG[A/C]ATCGACATGATGGTCCTGTACGGCCCGCGGATCCTCGC
TP122200	TGCAGTTCTTCCTCACCGTGCTCGCC[G/T]CCAGCTTCGCCTACTACATTGTGCCCAACTACCTGTT
TP122204	TGCAGTTCTTCCTGAACCTGGGAAGCTGATAGTGCCATCGCGCGCC[A/T]TACTATACCCCTTCACG
TP122205	TGCAGTTCTTCCTGATC[C/T]CCAACTTGTTTCCCTGGGCTGGCAGGCTGCTGAGCTTGGCCATGGC
TP122211	TGCAGTT[C/G]TTCGCGCATGCCAAGTCCCATCGAGGACGTACAAATTTGACGCATCTCATCTTTGG
TP122214	TGCAGTTCTTCGGCTCAAACGTTTCAGACTTTCAGTGCAGTGCAGTGCATT[A/C]CACTCCCTTGCA
TP122215	TGCAGTTCTTCGGCTCAAACGTTTCAG[C/T]GCAGTGCAGTGCATTCCACTCCCTTGCATCCTGCAT
TP122243	TGCAGTTCTTGCACGAGATCAGCAGATCCTGGACATGTTG[C/T]TCCACTTGCAGACACCATCGAGG
TP122257	TGCAGTTCTTGGCACGGCGTTGTAGCTGACCATGTGAGTTCCA[A/C]CTTGCTAAGTGCCATGTGAG
TP122274	TGCAGTTCTTGTTGCTACCCTGCTGTCAGTAATGCACGGTAGTGCCAGTATATC[A/G]CGTGCCATC
TP122309	TGCAGTTGAAAATCCCACTCCAATTCTTCCTGGGACGCCTGCATTGCTACCTTCTGTTC[A/G]GGCT
TP122312	TGCAGTTGAAACAAGACACGCATATGCATTGTATTGTATCGATGAAACG[A/C]CAACAAAGACGATG
TP122313	TGCAGTTGA[A/G]ACACCGCGCGGGGAAGACGCAATCCGCCTTGACGTGGTTGCTCGCCAGACAATT
TP122318	TGCAGTTG[A/C]AACGCAGGCAACTTGCTTCTGTTCACTTGCCAATAAATTAAAAAGAAAATAATGG
TP122325	TGCAGTTGAAAGGCGAGACACGGCTAGGGCTAGAGAGAGTAGGAGTCGTCGGAGTAGA[C/T]AGCAG
TP122332	TGCAGTTGAACACGCTACTACTGGCGCGCGACACGCAATGCTAC[A/G]GTGCGGTAGATGTACGGGA
TP122340	TGCAGTTGAACCCCAATCACCAACTCT[A/C]TAGTCAGTCGCCACGGCATATAACCATTAACAATAA
TP122344	TGCAGTTGAACGACGACGTCTTGAAGCGAAAGATCTCGTTTCGGAGAAACCAAAGCCT[A/G]GAAAC
TP122364	TGCAGTTGAAGAGCCGAAGGGGGTGCATGACGCGAATGCCAGTCACTGGCCCTTGGACCTCA[C/T]G
TP122366	TGCAGTTGAAGAGCCGA[A/T]GGGGGTGCATGACGCGAATGCCGTCACTGGCCCTTGGACCTCATGG
TP122374	TGCAGTTGAAGCCGCTCCCCCCGCCTCTACGCCGCCGACTC[A/T]TTGACGCCAAATACCCGCGAAC
TP122444	TGCAGTTGACGA[C/T]GACGATGTCGATGGCGTCAGGGCTGATGCCCGTCTTGGAGAACAGGTCGTC
TP122447	TGCAGTTGACGACGAGCGCGCCCACGGC[C/G]GACGGCGGCACGCCCGTCCTGGCGAAGAGCGCGTC

Table A2 (cont.)

TP122448	TGCAGTTGACGACGAGGATGTC[A/G]ATGTCCTTGGGCTTGAGCCCCGTGCGGCGGACGAGGTCGTC
TP122459	TGCAGTTGACGCCCATGTACGGATACGGAGACGGAGTAATAAC[A/G]CACTACATGGGCATGCAGTT
TP122460	TGCAGTTGACGCCCGACGACGTGCCGTGGGAGTACCACGACGAGGTGGACATGGAATTC[C/T]TGGG
TP122464	TGCAGTTGACGCGCGATCCTGGTATACCCGCGTCACGTCCGTCGTCGCCCACGCTGCGCAC[A/G]CG
TP122484	TGCAGTTGACTGTCGCTGCACGGGGTTCATCAGCATGGCGC[A/G]ACGTGAAGGAGGCTGGAGTGCC
TP122525	TGCAGTTGAGCCCCAGGGCAGGGCAAGGTCACACTCACTCATGCTTTCATGCGGCAGACAGG[C/T]C
TP122528	TGCAGTTGAGCCT[A/G]ATCTCCCCCGCGGAACCCGTGAGCGGGCTGATGTTCCCGAGCCTGACCAT
TP122532	TGCAGTTGAGCCTGATCTCCCCCTGCGT[G/T]CCCGTGAGCACCTCGATGTTGCCCATCTTGACCAT
TP122550	TGCAGTTGAGGAACTGACC[G/T]AGCACAGGGACGCAACGCAAACAAAAAGACAACTTTTTTCCCCA
TP122581	TGCAGTTGAGGTGCGGCATCCCTC[A/G]GCAAGAACCAAACGCGCTCTAAGTGCAATATTTTGGTTG
TP122607	TGCAGTTGAGTTGGAGACAACAATGGTAATGAATCAGCCAATCCTGCTCAACTTCTTAT[C/T]GATG
TP122627	TGCAGTTGATCCGCCACACCACGTTGCCGATCACCTGCGGGAG[C/G]AGGAAGAAGTCCTGCGCCAT
TP122628	TGCAGTTGATCCGCGAGAAGATGGACGTCATCGACGTGGAGGA[A/G]GAGACTATCGACGTGGACGT
TP122635	TGCAGTTGATCGGGAGGAGGGCCGAC[A/G]GCGGCCTAGGGGTCGCTGCCGTGAAGACGCAGTCGAA
TP122642	TGCAGTTGATCTTCTGACTGACCAACAAGTTAA[A/G]CTAATTTGCTTGGTCCCATGCATGCATGCA
TP122681	TGCAGTTGATTCAATGTTCCAACTCTTGAGT[C/T]ATGGCATAATCCGTCAGGCTTCAACCACAGCA
TP122689	TGCAGTTGATTTACCGA[C/T]CTGACACGGGTGAAATTCTTGGGGTTCACATTTTGGGTTTGCATGC
TP122710	TGCAGTTGCAAC[A/G]TGTCTATTTTGGTCTTCGGATGGCTTTGGCGTTTGATCATATCATATGCTG
TP122717	TGCAGTTGCAAGGAAATTGCACTGCACTAGCAAGGAAATTGGTCTGCGGTTGCAG[A/G]CTTCTGTG
TP122723	TGCAGTTGCAAGTCGACGAATACTCATGCAGTCGTGCTATAATTGCACATGCCTCATGGTTT[C/T]C
TP122729	TGCAGTTGCAATGGAACATATCTTGTATATAAGGGCGTACCTAGTGCAGAGAGCTCCCGC[A/T]CTG
TP122732	TGCAGTTGCAATGTTTGGTTCATCAGTTCAG[G/T]TTAGTCCAGTGCGTTCGTGCTCTTGCTATTAC
TP122737	TGCAGTTGCACAAGCAAAATGGCATCACTTGATCTTGACGACGGCGG[C/T]GGCGGCGGCGGCGTGC
TP122739	TGCAGTTGCACAATCAAACAAAACTGTTCAGGACAATCCCACACACTAGTGATAGATAG[C/T]ATCA
TP122743	TGCAGTTGCACACCAAACGATGATGAACGTTGAGCGACGAATCTTCAGCC[C/T]TTCAGGGAGTGAC
TP122753	TGCAGTTGCACATTTCACACAAGCCTTTGCGGAAAGGGTTC[A/G]CGTGCGCCGTGCGGCGTGTGAT
TP122758	TGCAGTTGCACCCAACAACCAACTCGATCGGTCACAGCACAGGACG[A/G]TGCCAGCCATTGTTAGC
TP122763	TGCAGTTGC[A/T]CCTGAGCTTAATTGGATCGAGATCTGGTTCCTTGATTCAGTCTTTTGAGTGTCT

Table A2 (cont.)

TP122765	TGCAGTTGCACGAAAGAAATG[C/T]CTTTCATGGCGCTGTTAGGGCATCCAACATCATGCTGGAACC
TP122780	TGCAGTTGCA[C/T]TAATAATACCTTGTGCTTGTGTTAGCTAGCTGTGCCCCAATGGGCCCAATGTC
TP122792	TGCAGTTGCAGAGAGAGACGGAGCTGGCCGCTGGCGCCTTGGGA[C/G]TTGGGACGCGATGGTAGTC
TP122794	TGCAGTTG[C/T]AGAGGATATTCGCCCAGACCTCGTCGGAGATCACGCCGTGGCTCCACATGAACTC
TP122803	TGCAGTTGCAGCACGAGCTAGTTAC[C/G]AGGAACGCAGCCATGGCAAGCAGTGCCGTCGTCGTCCC
TP122816	TGCAGTTGCAGCGCGTGCTCGCCGTTCTGGCGATCGCCCGACCGCCGTGTGCGCC[G/T]CTGCCTCC
TP122835	TGCAGTTGCA[G/T]GGGAGCAGACACAGACAGACAGGCTCAAGGACGGGAATGATTCGGTGTCCCAC
TP122838	TGCAGTTGCAGGGGTCAGCAGGTGGAGACAGGGATGTTCTTGGGAAAAGTTTA[A/T]AACTTTGGTT
TP122854	TGCAGTTGCAGGTGGTCGCGCGGCAAGCTCCCTGTGGGAGCATGCGACATCGAAAGCCTTGA[C/T]G
TP122861	TGCAGTTGCAGTACTACTGCCATTTTCCCATTTGACGGTGCCTAGTACCCATGA[C/G]GACGACGAA
TP122864	TGCAGTTGCAGTCAGTCGATCACTAGCTGTTTCCGTCTGATTGC[A/G]TCGTCTCCATCCGATCCCC
TP122865	TGCAGTTGCAGTCCCTTACGGTTGGTTGCCTGCATTCC[A/T]GGTACGGTTGTGTACTCTCATGTGT
TP122871	TGCAGTTGCAGTGCCCTTGGAAGGCGTCCCTACGTAGGATGCTGGTATGCTCG[G/T]TGCTCCTCGT
TP122878	TGCAGTTGCAGTTAACTTTGTCGGCCGCCTGCACGTTCGTAGCACCAGC[A/C]GCCACCGCCGCCGC
TP122897	TGCAGTTGCATCCAACGTAACTGCAAAGTAAAAAAAAAATGT[C/T]GCGCTGCAAATTCCATACCTC
TP122904	TGCAGTTGCATCTCTGCGTGGGAGCGTAGGCAGATGCAGGCAGCAGGCAGCAGGCAGCAGGCA[G/T]
TP122913	TGCAGTTGCATGCCTCATCAAGTA[C/G]GTCTGATCAACTCATCGTCAACTAACTAACTATGAGTGT
TP122925	TGCAGTTGC[A/G]TTCTCTGGGGTGCCATAGCTGACTCTTCTGCCTTCATTTTCAAATTGGTCAATT
TP122938	TGCAGTTGCATTGGGATTTTT[G/T]ATGTCGGCCCAGCCACCACGAAACCCGCGAGGGAAAAGGGGA
TP122945	TGCAGTTGCCAAACTTTGCTCGTCTCATCGTCTGGTGTGTCGTACTACATC[A/G]CTGTTGAGTTCT
TP122953	TGCAGTTGCCACAAACACGTTCCCAGCAATCCCCTCCTG[C/T]TCTGCCACCCTCCACACAGCCTCC
TP122989	TGCAGTTGCCCTGGGCGGCAGGGGTTTATAAACCCTACGGGCAGG[C/T]GCAGCAGGAGAGGAGGCG
TP122993	TGCAGTTG[C/T]CGAATCCGAGCGCGACCACCAGGAGCGAAAGGCGAACTCCCTTGCAACTTGGGTG
TP123001	TGCAGTTGCCGATTTCGCGCAATAAATCGGCCATCGCTTCCAC[A/C]GTCCCGTCCGCCTGGGCAAC
TP123012	TGCAGTTGCCGCCGCGCCCGTTCACGGG[A/G]CGCACCGTCACGGGCAGGTTGAATCCGTCCACCAG
TP123022	TGCAGTTGCCGTCGTGTTTGGTTTGCGT[C/G]GCCGTATGATCCGATCCAAAAACCAAAGCTAGCCG
TP123028	TGCAGTTGCCTAAAGCCCTAACTTCAGATCGGGCAATGCAAG[C/G]AGCCGTGTTTCCCTCAAAACC
TP123041	TGCAGTTGCCTGTCATCCGATCCGACAAGCACTCTTTCGCCGCGATCGTGATACAGTAATA[C/T]AG

Table A2 (cont.)

TP123053	TGCAGTTGCGACTTTGCGTCGGCGCTCGGCGAGTGGCAGCAGGCA[A/G]CCAGCGCAGGCATTCTCT
TP123076	TGCAGTTGCGCCTGATCTCGCCCTG[C/T]GTCCCTGTCAGCACCTCGATCTGCCCCATCTTGAGCAT
TP123108	TGCAGTTGCGGAGGCG[C/T]GGCTCCATGGACGGAGCGCAGAGCCTCCCTCGGCAGTCGACGATGGT
TP123113	TGCAGTTGCGGCAGCGTCGGGTGGCGGTCTTGCGGAGCTTGTGGAGCTC[A/G]AGCGCGTGCGCGCG
TP123129	TGCAGTTGCGGTGCGGTAGATCAACTCGGGGGAAAATGACCGCCCAACCTTTTCCTAATTCC[C/T]C
TP123150	TGCAGTTGCGTGGCAGCGCGGCA[C/T]TGTTCCTATGGCTGCTACGCAACGAAGTCAGCCTGTTCGC
TP123157	TGCAGTTGCGTTTCCGCACTGCTCCTGAGCCTTTTTTTA[A/G]TGGAATCGTTTCTGATTTCGGCGC
TP123169	TGCAGTTGCTACAGCGACCGCAACTTTGGCTGTTGCGCCATCCTGGAC[G/T]CCCAAAATCAATCCA
TP123175	TGCAGTTGCTAGACGCCAG[C/T]GGTTGACGTTGACAGGCGATCTCCACAGCGCCAGTCAACCGCCC
TP123177	TGCAGTTGCTAGCGAGTGGCGTCTCCTATTTCTCGTTCGGCAAATGACACACCAAC[A/C]CGTGTCA
TP123200	TGCAGTTGCTCACCGATTCCCCACTCCTGCGTTCTGGTCGACCTGCAAAGTACACAAATCG[C/T]GA
TP123237	TGCAGTTGCTCTG[A/C]ACGGCTAGGTACGGGTAGGCCGACTCCTCGCTGAGCCCGCCGTTCCAGAA
TP123256	TGCAGTTGCTGATGTCGGCGGCCAGGGAGGCGG[A/G]CCTGCACGAGCTCACAACGAGCGCGTTCTG
TP123259	TGCAGTTGCTGCACTTGCCGCTTAAGAGCTGCC[A/T]GCCAATGTTCGCATTGCAGAACAGAGAAGT
TP123260	TGCAGTTGCTGCATCATGACAGTGTCGTAGGCCC[A/T]GTCCAACTATCATAACCCCAATAACTCAA
TP123269	TGCAGTTGCTGCGGTCCCAGGCCTCCCC[A/G]ACTTGGCACACGCCTTTCCATCGTGAAGGCACGGG
TP123274	TGCAGTTGCTGCTCCACCCGCGTGTGCACGGAGG[C/T]GTTGACGGCGTGACAAGGGGACAGGCTTG
TP123281	TGCAGTT[G/T]CTGCTGCTTCAAGGGCGTCCCAACAACAGTCGACGTCGCCAGCTGACTCGGATTTC
TP123292	TGCAGTTGCTGGCATGGCCTACTTCATCGCGGCGGA[C/T]AAGAAGATCCTCGCGCTGGCGAGGCAG
TP123294	TGCAGTTGCTGGCGGGGGCGGAGGAGGAGGGCGCACGTCC[G/T]CGGCGCAGCTGATGGCGTCGAAG
TP123316	TGCAGTTGCTGTCCTTGGGGATCTCGCAGACACGCTTGGCCAGAGCTC[A/G]AAGGATCTGTTCAAG
TP123320	TGCAGTTGCTGTGCTGCGTACGTGCAGGACAGCGAGGACGTGAGGCTGGAG[A/C]GAGTCCTGACGG
TP123338	TGCAGTTGCTTCTCACAGTCACA[A/G]GCCACTGAGGCACTGAGGCTTCCCACTTCCCAGCCAGTCA
TP123352	TGCAGTTGCTTGTAGAAAGGAGGTGTG[A/C]TTGTGATGTTGATGTTGCTGTTGCTGCCTGGTTGGA
TP123356	TGCAGTTGCTTGTTCAATTAT[C/T]TTGTGTGATGAGAGAGATTCCTACCGATCCAATCCTGGAGTT
TP123368	TGCAGTTGGAAAAGGCATACCTTGCAGTGTGTCGGTCAACTGCGT[C/T]TGCTGTTGGGTGGTGTCC
TP123375	TGCAGTTGGAACCCTAAAATTCACAGCAACCAAAACATTTCCCCAACAAAGATACATTGTTAT[A/G]
TP123379	TGCAGTTGG[A/G]AGGAGGAACTGCCATGCGAGCGCAGCCTTCAGCTACGCTGGGAGGAGGAACTAC

Table A2 (cont.)

TP123380	TGCAGTTGGAAGGCGCGGCGGTGGCGCCCTCCGAGGCTTCTCTTCCTCCCTTCGC[G/T]TCCGCAGC
TP123392	TGCAGTTGGACGAGTACGTCGTGTGCAAGATCTACGTGTCCCCACAGCACAAAAA[A/G]AAGGCTGA
TP123416	TGCAGTTGGAGCAGAGCCAGCCTTGCGAGGCTGAAGAACATCC[C/T]TGTAGCTTGCAGATGGAGCC
TP123420	TGCAGTTGGAGCCTAGCCTAAAGGTTACTCCAGGTCCAGGGCTTGAAAGAAAGCCT[A/T]GCTAGCG
TP123421	TGCAGTTGGAGCTCCCTGCATACTGTCCTTCGGCTACCGTCGGAATGGACTCCGAGA[C/T]AGGAAC
TP123435	TGCAGTTGGAGGTGGTGTTCACGTACT[C/T]GGGGCCGCTCGGGGCCGTGCCGTTGTTGCAGTCGTA
TP123438	TGCAGTTG[G/T]AGTCCATGGCGAAAAGGGCAGCCGAGATCTCATCCATGGTGAAGGGAAGGGAGAG
TP123468	TGCAGTTGGCACCGCCGATCTGGTGGCACCT[A/T]TGAATGTGATGATGCATCGTGGCTGCATGGAG
TP123489	TGCAGTTGGCCAGAGAACTTCTGTCTACGGTTGCTGAAAATCTAGCCGCCCATTCC[C/T]ATCTAAC
TP123504	TGCAGTTGGCCGCGCTACGCCCAGAAGCCGCG[T/C]AGCTCCCCGCTCCTCACATGCGAGCATTTTG
TP123524	TGCAGTTGGCGGCGGCCGAGGAGGAGGACGACGCCACGAGCAAGATGGTCGAGCA[A/G]CAGCCCCC
TP123568	TGCAGTTGGG[A/G]GAGAGAGAGACGAGAGACAGACAGCGCTCGCTTATCAGTGACACCTCTAGCTC
TP123605	TGCAGTTGGG[C/T]GTCCCTGACGACGGCATGAGGTTGCCCATCTTGATCATCGCGGAGACGAAGTC
TP123611	TGCAGTTGGGCTC[A/G]GTAGTAGGCCTTTAAAAACGCTCAACACCCATCTCTAAAAACCCATTTTT
TP123612	TGCAGTTGGGCTCGGTAGCAGGCCTTTAAAAA[T/C]GCTCAACACCCATCTCTAAAAACCCTTTTTT
TP123636	TGCAGTTGGGTCAAGATAAGACATGGTTGGCAGCAGGATGGGTCAGGCCCAA[A/G]GTCGTCATGAG
TP123653	TGCAGTTGGTACAGTTATGATTA[A/G]GGAGCATCTGTCCACCTTGTGTCAATGTTTCCCCTCCACT
TP123658	TGCAGTTGGTAGTTTATGTCGCAAAAGGCCTCAC[C/T]CAGATGGTGAGATAGGGATGATGGATGGC
TP123663	TGCAGTTGGTCACGGGGACGGCACCGAGCGGCGGCAGCGTCCCGC[C/T]GCACCTGGACATGATGTA
TP123690	TGCAGTTGGTGACCAAGAACTTCTCAGAGAAG[T/C]TCGGCGGCGGCGCCTTCGGGTCCGTGTTCAA
TP123692	TGCAGTTGGTGATCTGAACCACTTGATCAGTGCCACCATGAGTGGTGTCACCTGCTGCCTTCG[C/T]
TP123695	TGCAGTTGGTGC[A/G]CCAGCATCTGCTTCGCGCCCAAACACGCATGAAGTGCCAAGCTGATAAGCG
TP123753	TGCAGTTGTAAAGCTCTCTACCAAAGTACCAAGTGCAATATATAGACATCACAGCAAGCTCC[C/G]A
TP123788	TGCAGTTGTACTGCGCCATCCTTTCTGAAGATTGAACATTTGAACA[A/G]CGTCGTGGCCACTTTCC
TP123820	TGCAGTTGTAGTTGTT[A/G]TTGTTGTCTGAAACTGGATCCTTGGTGTTGGTGAGCAGCAGCCACGA
TP123831	TGCAGTTGTCAAAGAACGATGCTACAACATGTTCTGGCTTAGCATGATCTTTGGGCA[C/T]GTCAGG
TP123869	TGCAGTTGTCCTCATTGGCGGCCAGACCCTGAAGGATAC[A/G]TAGGCCTTGCACCACCAGACCTTT
TP123877	TGCAGTTGTCGAGTTGGGGGAAGGGGCATGGAAGGAAGGCTGGAAGG[G/T]GCCACTTGGTTGATGT

Table A2 (cont.)

TP123938	TGCAGTTGTGATCGAAAAGCAGGTACTT[C/T]ATATGCCATTTATGTTTTGATCAAAGTTTCAGATT
TP124025	TGCAGTTGTGGCT[G/T]CAACCTGCAAGCGCGGGCTGATCTACCGACCAGCTGAACATGCTGTGCAC
TP124054	TGCAGTTGTGTCTCGTAGCCTTGA[C/G]AGGAGAGCAGGCACCCTGGCCAAGCGATCGCATGCAGCC
TP124064	TGCAGTTGTGTGGGCAGCGCGGCACTGTTCCTATGGCTGCTACGCAA[C/G]GCAAGTAACCAGCAGT
TP124067	TGCAGTTGTGTGTATCATGGCTTTTTTCGCTGGCTTGCACCCCCAG[A/G]GCACGTCTGAGATTGGT
TP124085	TGCAGTTGTTAAGG[C/T]CAGTCTTAGTGGGGATTTGTGTTGGAAACAGTGTGGACTAGTTTCATTC
TP124125	TGCAGTTGTTGAGGAACATGGCTCTGTCCTACGCCCCTGCCCTGTGAA[G/T]GATACTGAGTAGGAG
TP124143	TGCAGTTGTTG[C/G]GATGCGTTGGACGCCGATTGAAGGGCTGGCTGGACCGTGTGACGCGGGACGG
TP124192	TGCAGTTGTTTAATTCCTGAATGTGTGGGAGCACAACGAATCAA[A/T]AATCACAGGGTGATGCCTT
TP124193	TGCAGTTGTTTAATTCCTGAATGTGTGGGAGCACA[A/G]TGAATCAATAATCACATGGTGATGCCTT
TP124219	TGCAGTTGTTTTCAGTGTCTC[C/T]GTCCTTTTCCCCTAATGTACTTTTCAGTATTTATCTTCTCTC
TP124221	TGCAGTTGTTTTCCTCATGCTCA[G/T]GGGTGCAGCATGTCTTTATTTTGCCGTTCAGGAGGGATTG
TP124228	TGCAGTTGTTTTTGA[C/T]GGTGAAGGTGGCCGCGCTGGCACTGGCGGCGAAGGTTGCGACGAGGAG
TP124295	TGCAGTTTACAAAGCTAGCTTGTCGCCGTATCC[C/G]AGCACTTGTCTCGCAGCACGGAGTCGGAGT
TP124325	TGCAGTTTACCTGCCCGTAAGCAAACATGCAGCTGTTATAGCCAGCTATGCAGTTCT[C/G]CACCAT
TP124367	TGCAGTTTAGCATCTTGCGAAACACAGGGAATGCATCCTTATGGAGTTCATTG[C/T]GGACAAACCC
TP124371	TGCAGTTT[A/G]GCGGGCTTCCGCTGGGCCGCCGCCGCTCTGCTGCTGCCGCGGAGGATCTTGGAGA
TP124405	TGCAGTTTATACTTTGATCTGCCATTTTGAAATGG[C/T]GTAACCAGGTGATCTGTATGATGTGGTT
TP124427	TGCAGTTTATCGGCGTTTTGTCTACGCTGATGTTGAC[A/G]CTCGCTGAGTCTAGTCCGATGCATCT
TP124510	TGCAGTTTCACATGTACAATTGCTTAATGTAAGCATGAGTCAAATA[A/G]CCACGCTCGCTAGTGGT
TP124511	TGCAGTTTCACC[A/T]GAATAGTATAAAGGCAGGCACAAGTTGATCACATGATCCACAGCAGCAGTG
TP124512	TGCAGTTTCACCTGCATTCCTGTA[A/G]ATTGCGTTCTCGTCCTGTCGCTTTGGTTGTCTGATGTTT
TP124544	TGCAGTTTCAGCCATGATTGCAG[C/T]CGCGAGCTCTTGCAGGGCGAACGCAGTTTTGTCATCGGTA
TP124546	TGCAGTTT[C/T]AGCTTGCCAAGATCCATGGTTAATTTGCAATTTATCTATTGTAACAAAGTGGCTT
TP124548	TGCAGTTTCAGGCACGCATGCTCGGCTGGAGAAGAAGGGCG[A/G]GAGCCTGCTGGTGACGGACCTG
TP124570	TGCAGTTTCATCATAATCATTTGTGTTAAGACCTAGAAACAGCCGTCGTCTTTTCTCG[C/T]CGTGT
TP124585	TGCAGTTT[C/T]ATGTGAACTTGGCACAAAGAAAAGCGGACGTACGTCGCGCCAATACCAGTCCAGT
TP124619	TGCAGTTTCCAGAGAAGAGAATCAGCTAGCAACTCCTGAGCAA[G/T]ACTGCAACCTTGCGGGTAAC

Table A2 (cont.)

TP124628	TGCAGTTTCCATATTTCTCATTGTACCCTTTACTAGAACGCTAGGCTCTGTTTTC[G/T]GCCTTTCG
TP124643	TGCAGTTTCCCCAGTTCTCAACT[C/T]AGTAAGCAAAATGATGCATACTCATAACAGGTTAGTTAGG
TP124654	TGCAGTTTCCCGCTC[A/G]AGTGCTGAGGCTGAGCAGCGTGCTATGGCGTTTGTGACTGCGGAGTTG
TP124657	TGCAGTTTCCCT[A/T]ATGTGGTTACTTGTAGCTTTCCAAGGAAAACCAGCGCCGTTGCCGAAGCTG
TP124668	TGCAGTTTCCGTCAGCGAATGCCTGAATGGCAGCCATGACCTCAGGTTGAATTATG[A/G]GCCATGC
TP124672	TGCAGTTTCCGTGTGTTTGTGCGTCATTTTGCTCGCAATCCGTTATCGTGTTTT[C/G]CAAATTTTG
TP124685	TGCAGTTTCCTCGTCCTCGGTCGGTGACATGCTGGTCGTCATCGG[G/T]CCTGGCTGGTGGTCGACG
TP124704	TGCAGTTTCCTTCATCTTAGTGAGAACAAATGCACCAATCTG[A/G]CTAGGGGAGTACTGCTGGCCA
TP124712	TGCAGTTTCCTTCGCTCTGTAGCCT[G/T]CTCGAAGGCGAGGACGGAGAAGGCAGAACAGCAGGATG
TP124734	TGCAGTTTCGCTACCGAACGCTCTATCAT[C/T]ACACTACGGTGGTTTGCTGGCGCACAAAGCGTAG
TP124746	TGCAGTTTCGGTCTGCGAGATGAGCCGC[C/T]GCTCTCGTCGTTTTCATCTGGCGTGTGTTGTGCTT
TP124758	TGCAGTTTCGT[C/T]GCTTCTTCCTCTGGAGGCTTCGTCTCAACTTGTCAAACAGGCCGAGAAGGAG
TP124781	TGCAGTTTCGTTCGTTGGATCGCGCGTACTCGTAGTCAGGTAAGGG[A/G]CGCGAATGGAAGTGGAC
TP124797	TGCAGTTTCTAGTATGATCGGTGAAACGAAAGAAAAGAAAAAA[A/T]ATATATATCTCAGCATATGT
TP124819	TGCAGTTTCTCATCCACATTAGCAC[G/T]ACGATGATCTTGACGACGATCATCAGGCGGCCGTTTGT
TP124831	TGCAGTTTCTCGTAAAAGGAATTGCTAATCTTC[A/G]TGCCCATGCAACCACAGAAGTTTCGATATC
TP124834	TGCAGTTTCTCTGAACTCTGATGCATCAAACTGGGTTATTTCCATTTG[A/G]CTCTGGATGGTTTTA
TP124837	TGCAGTTTCTCTTA[C/T]TGTCACCAACTGACTATGTTAAAGTACTATGCTACTACGTTATTAACTC
TP124869	TGCAGTTTCTGG[A/C]GTGATGTTGTTTCCTGGTTGTAGAGCTTGAATGTGGAGCGCGATCTGTGCA
TP124883	TGCAGTTTCTGTGCAA[C/G]AACTCGTAGAAGCCCAGCATCACCCTTTCTACCAAGCCCGCGCCCTC
TP124899	TGCAGTTTCTTCACTGCAAATTCAAACAGAACCAAGGTGAAATCA[A/G]TGAGCTTGAGAGTAGCAT
TP124923	TGCAGTTTCTTGTACGCATCATATATATGCTTCTTCTGC[G/T]ACTACGACCATACCAGCAGTATTT
TP124931	TGCAGTTTCTTTGAGATG[C/T]ATTTGTTTTTCCTTCGTCCAAGAGTTGAAAAGATGGGTTGGCCTG
TP124938	TGCAGTTTGAACACAATAAACAGCAAGATTACAGGTGAGTCGTTGTTACTA[C/G]TGATTACCTAGA
TP124942	TGCAGTTTGAACATTGCACTATAGATCAAGGGCGTACCCAGTG[C/T]AGAGAGCTCCCGCTCTGTGC
TP125029	TGCAGTTTGATAGAGAATTGATGAATTCCCATCCCTCCTTATCATT[A/T]GCTTCAAGCTTGTTTTC
TP125051	TGCAGTTTGATTGGTCGCCTCAG[C/T]AACTTCTTCCGAATTACCCTTCTCTTCTACCTCTGCTTCC
TP125071	TGCAGTTTGCACAGCCGACCAGCTGTTT[C/T]TCTCTCTCTCTGGCACCCGCCGCTAGCGGAGATGA

Table A2 (cont.)

TP125095	TGCAGTTTGCATGCACGCCTGCGCCTCGGTGGGTCACCT[C/T]TGGGAGGACTGGGAGTGTTTCGTG
TP125103	TGCAGTTTGCCACCATTTCGCAGAGGAATTAACCTATGATACGATTGACGAAGC[A/G]GTGATTATT
TP125113	TGCAGTTTGCCAGTTTTGGGTTCC[A/T]GTCCACATGGATGGGTGGAGATGGATCGGCAAAGCGGCT
TP125123	TGCAGTTTGCCGCCTCATCGAATAGCTCCTTGACCTCA[C/T]CAATCGCCTCTCTGACATCCCTCGT
TP125125	TGCAGTTTGCCGCTTGCCAGTTGAAGGCAGCAATGTAAGTGAAGTACCAGAGTGCCCATG[A/G]AAC
TP125148	TGCAGTTTGCG[C/T]GTACCTTCTCGTCTGCGAACCTGGCCCAGAACCTCGCCTTGAGCACGGTCGT
TP125150	TGCAGTTTGCGGGCGGCGGCGTTCGTG[A/C]GCATGGTGTTGGTTGGGCTTGGATGGCTTGAGCGAG
TP125153	TGCAGTTTGCGGTTGGCATGGACTTATTTTATCCAGCT[C/G]TAATTACCCTATCTTCTTGAATTGT
TP125224	TGCAGTTTG[C/T]TTTGAGGACAATGTAAGAATGCATACGAGCCAACCAAATAGGGACGAAGTGCAC
TP125228	TGCAGTTTGGAAATCAA[C/T]GTCTGTCAGCACTGAAATAGTAGTATTGGTGCGCTAAGAACTGGAT
TP125270	TGCAGTTTGGGAATTTGCC[A/G]TATGGATTCCGTGCAAACACATGGCTTATTCCTCCAATATATGT
TP125272	TGCAGTTTGGG[A/G]GGCCGCGCCACCGCCGTGCGAAGGGCCTGCCCGTCGACCTGTGTAAGCGCCG
TP125292	TGCAGTTTGGGTTTGTAGGGAAGCCTAGTGGGTACTGATGTGTGCC[G/T]CCACCACCGCGTGATGC
TP125294	TGCAGTTTGGTACGCGTGCATCCGATCC[A/T]TCGTCGTCCATGGGCTAGTTTTGTCGTGTTCATGT
TP125297	TGCAGTTTGGTCAA[C/G]TTTGTAAATATTAACAAACAGTGGAGAAGCGATCATGGTCTTGTTAGAC
TP125361	TGCAGTTTGTCCACCAGCAGCACCCAACCC[A/T]AGATAATGGGTTTGGTAACATCAAACTCAAGAT
TP125382	TGCAGTTTGTGCCTGTCGACGAACTTCAATGAGA[G/T]GAGACATCGACTCGTTGCAAGAACAACAA
TP125431	TGCAGTTTGTTTGCATTCTCTGGGAAAGAGTTA[C/T]ATGGATGGGAAGTTGCAATCTTAGGCATCA
TP125529	TGCAGTTTTATTGAAGAAAATTTGTTGGATGGCGACTGGAAATT[A/G]AGGTCCTTGACAGTGGCAC
TP125567	TGCAGTTTTCAGTTTCAGAA[A/G]CTTGTGATGGACTGCTCTGGTTGTCATATCTCGATTGTCGCGG
TP125596	TGCAGTTTTCCTACGAAACCTGCATGCTTACTTGTCGCATCAAC[C/T]TTTACTGTACATTTTCACT
TP125619	TGCAGTTTTCGGTTCCTACTGTCCAGCTTGCAATT[A/G]GAAGAACAAATATGTGAGTTCACAAAAT
TP125624	TGCAGTTTTCGTTCTTGCAAAGCAAGCCTGCCCCAGAGAAGACA[A/T]ATTGTGCAGTCTGACCCGA
TP125629	TGCAGTTTTCTAAACGCAAGTGTAAAACGC[A/G]ACTAGTCGCGCTGGTGCACGACCGCGTGACGTA
TP125665	TGCAGTTTTCTTGCTCCTTCCACCCCTTC[A/G]ACCCCGAGCCCCACGATCATCCCAGGCGTCCTCT
TP125677	TGCAGTTTTCTTTTTTTCCACACGAACCTCTTCATCGCCGCGCGTCGTCGTC[A/G]TCGTCGTCGTC
TP125697	TGCAGTTTTGACAATGAATATATG[C/T]TTAAGATATATAGCGTTTATGAGATATATGGTGCAATGA
TP125724	TGCAGTTTTGCAACAAGTTGCTCA[A/T]GCTCAACGTTAACAGGATGGAATTCTCGGTTGTTGGCCT

Table A2 (cont.)

TP125731	TGCAGTTTTGC[A/C]GCGCGTTCGCGTGACGTTTTTGAGCAGCGAATCCCCGTGTTGCAAAGCCTTT
TP125768	TGCAGTTTTGGACGCTACTGAATTGTCATGTACCGTCGCGACG[C/T]CAAAGCAACGCAAAGTTACC
TP125770	TGCAGTTTTGGAGCAGAAAGCAACAGCTACGAGCTACCTACCTTTGCAGTTCGC[C/T]GTGGCGCGC
TP125786	TGCAGTTTTGGGCAGGCCGTGTCCTTACAGC[C/G]AGCAACTAACTCCTGTAGGAGCTGCACAAGCT
TP125817	TGCAGTTTTGTCT[C/T]GCCTTCAGTGACAGGACGCTGACTGCACCAGTACTACAAATGCATACTAG
TP125850	TGCAGTTTTTAAACACAACCGTACGCAGTTCATCACTCGTCG[C/T]GGTGGGCAAATGCGTGTAGCC
TP125885	TGCAGTTTTTCCATTTGTCCGCCACTGATTTCAGGGTCGTCAAGCC[A/G]CCGTGAAGGCCGTCGCT
TP125918	TGCAGTTTTTGCCCAGTCCGCGGCTC[A/G]GCGCGCCCCGCACTCCTAGCCCTCGCATCGTCTCCCC
TP125923	TGCAGTTTTTGCTCAGCGTTACCTATG[A/C]CATGCATCAGAGATTCAGAGTTCAGTCAGGCAGCAG
TP125925	TGCAGTTTTTGCTCCCATCGTGTCCGTGACTGGTGGTGACGAGGAGAA[A/G]GTCCCTGTTGAGCGG
TP125971	TGCAGTTTTTTCTCA[C/T]GCTATCATGCTTCATCGCCATTGGCGTCAATCTGAGCCAGTTCATCTG
TP125977	TGCAGTTTTTTGTTTCT[G/T]GGCATGTTGAGCCACAGGTTGCTTATCGACACTAGAGCATCAGCGG

Table A3 All RAD-seq and GoldenGate markers mapped in an F_1 population of *Miscanthus sinensis* 'Strictus' × 'Kaskade'.

Marker names	**Marker type**[*]	***Miscanthus* LG**[†]	**Position on Female Parent Regression Map (cM)**	**Position on Male Parent Regression Map (cM)**	**Position on Composite Map (cM)**	**Sorghum LG**	**Position on Sorghum LG (bp)**
TP72511	<nnxnp>	1	NA	0	0	NA	NA
TP58635	<nnxnp>	1	NA	3.967	8.368	NA	NA
TP111737	<nnxnp>	1	NA	6.431	19.967	1	1391861
TP116405	<nnxnp>	1	NA	12.263	35.698	1	2554232
TP34632	<nnxnp>	1	NA	14.276	44.254	1	2494672
TP75786	<nnxnp>	1	NA	15.48	69.204	1	2911264
TP44017	<nnxnp>	1	NA	16.891	51.69	1	2811058
TP18261	<nnxnp>	1	NA	17.921	64.381	1	2911329
TP59728	<nnxnp>	1	NA	19.354	79.378	1	3697488
TP49833	<nnxnp>	1	NA	20.744	59.381	1	3071325
TP26510	<nnxnp>	1	NA	23.876	97.003	NA	NA
TP34939	<nnxnp>	1	NA	24.552	90.023	1	4227898
TP110933	<nnxnp>	1	NA	25.584	152.364	1	4682103
TP122215	<nnxnp>	1	NA	26.804	104.873	NA	NA
TP122214	<nnxnp>	1	NA	27.427	114.542	4	4512194
TP5489	<nnxnp>	1	NA	27.882	110.549	1	4560204
TP52864	<hkxhk>	1	4.082	28.645	142.06	NA	NA
TP65461	<nnxnp>	1	NA	29.461	120.448	1	4901072
TP117010	<hkxhk>	1	2.767	30.247	157.707	1	6382765
TP40349	<nnxnp>	1	NA	30.431	130.86	1	4990077
TP71603	<nnxnp>	1	NA	31.083	127.016	1	5316957
TP33854	<nnxnp>	1	NA	32.244	169.124	NA	NA
TP16393	<hkxhk>	1	7.111	33.206	186.632	NA	NA
TP19030	<hkxhk>	1	8.399	34.014	195.917	1	7576879
TP1086	<nnxnp>	1	NA	34.283	162.059	NA	NA
TP45249	<nnxnp>	1	NA	35.005	240.826	1	7347962
TP111562	<hkxhk>	1	11.462	35.56	233.912	1	9520056
TP42401	<nnxnp>	1	NA	36.08	181.623	1	8574544
TP32260	<hkxhk>	1	12.46	36.491	207.261	1	9191372
TP16023	<nnxnp>	1	NA	37.142	177.753	NA	NA
TP19473	<hkxhk>	1	10.105	37.32	174.848	1	8571233
TP49957	<hkxhk>	1	13.416	38.202	223.36	1	8932450
TP19029	<nnxnp>	1	NA	38.949	250.965	1	9919630
TP50291	<hkxhk>	1	18.546	39.399	271.009	1	10103661

Table A3 (cont.)

TP53511	<hkxhk>	1	14.754	40.02	215.211	1	9154418
TP92321	<hkxhk>	1	15.539	40.538	265.261	NA	NA
TP15824	<nnxnp>	1	NA	41.332	317.664	1	11526386
TP76853	<hkxhk>	1	16.474	41.675	257.462	1	65618406
TP36421	<nnxnp>	1	NA	42.027	312.863	1	11490691
TP64549	<nnxnp>	1	NA	42.353	333.234	1	12046656
TP54684	<nnxnp>	1	NA	42.87	293.223	1	11656296
TP104234	<hkxhk>	1	17.463	43.29	278.275	NA	NA
TP121263	<nnxnp>	1	NA	44.015	325.321	NA	NA
TP119652	<nnxnp>	1	NA	44.434	338.485	1	13174804
TP68544	<hkxhk>	1	30.067	45.606	370.081	1	14875607
TP41720	<hkxhk>	1	24.118	45.959	307.417	1	12187360
TP123831	<nnxnp>	1	NA	46.511	355.566	NA	NA
TP14536	<nnxnp>	1	NA	46.76	348.708	1	14250425
TP54763	<nnxnp>	1	NA	47.325	416.997	1	16771336
TP43313	<nnxnp>	1	NA	47.674	481.01	NA	NA
TP52985	<nnxnp>	1	NA	48.103	465.79	1	16778195
TP115337	<hkxhk>	1	36.395	48.308	454.883	NA	NA
TP40830	<nnxnp>	1	NA	48.534	387.146	1	17704316
TP67194	<hkxhk>	1	26.759	48.747	340.226	1	12950837
TP123169	<nnxnp>	1	NA	49.026	381.398	NA	NA
TP51905	<nnxnp>	1	NA	49.571	425.092	1	17539551
TP96369	<nnxnp>	1	NA	49.981	409.428	1	17167396
TP92824	<nnxnp>	1	NA	50.481	394.501	1	19036370
X423	<hkxhk>	1	NA	50.662	NA	1	14076523
TP117270	<nnxnp>	1	NA	51.069	402.481	NA	NA
TP44040	<hkxhk>	1	39.001	51.401	431.604	NA	NA
TP8184	<nnxnp>	1	NA	51.488	437.351	NA	NA
TP47125	<hkxhk>	1	33.839	51.975	379.034	1	14993393
TP1243	<nnxnp>	1	NA	52.354	656.117	1	23805316
TP87360	<nnxnp>	1	NA	52.643	663.196	NA	NA
TP76354	<nnxnp>	1	NA	53.181	530.051	1	27996842
TP65243	<nnxnp>	1	NA	53.504	672.83	1	21861455
TP99789	<nnxnp>	1	NA	53.788	682.447	NA	NA
TP116079	<nnxnp>	1	NA	53.963	677.833	NA	NA
TP47417	<nnxnp>	1	NA	54.237	650.497	1	24846634
TP77611	<nnxnp>	1	NA	54.474	669.086	NA	NA
TP9765	<nnxnp>	1	NA	54.851	541.087	1	25246670
X499	<hkxhk>	1	41.526	55.107	533.176	1	24003332

Table A3 (cont.)

TP12266	<nnxnp>	1	NA	55.123	536.486	NA	NA
TP104567	<nnxnp>	1	NA	55.321	545.222	NA	NA
TP98442	<nnxnp>	1	NA	55.71	644.669	NA	NA
TP5675	<nnxnp>	1	NA	56.103	444.731	1	49641893
TP99150	<nnxnp>	1	NA	56.278	520.066	1	43859258
TP66594	<nnxnp>	1	NA	56.449	516.026	NA	NA
TP67902	<hkxhk>	1	43.268	56.554	524.888	1	50860488
TP58938	<nnxnp>	1	NA	56.746	638.181	1	50936213
TP32968	<nnxnp>	1	NA	57.025	634.38	1	50031939
TP28986	<nnxnp>	1	NA	57.202	492.29	1	3581699
TP83997	<nnxnp>	1	NA	57.53	511.777	1	51708701
TP26125	<nnxnp>	1	NA	57.858	551.56	1	50776684
TP71851	<nnxnp>	1	NA	58.075	619.349	NA	NA
TP6171	<nnxnp>	1	NA	58.305	614.728	1	51889379
TP105521	<nnxnp>	1	NA	58.684	608.889	1	50299224
TP16994	<nnxnp>	1	NA	58.892	593.013	1	52864531
TP46239	<nnxnp>	1	NA	59.179	597.614	1	53279738
TP69100	<nnxnp>	1	NA	59.604	601.963	1	52586399
TP33076	<nnxnp>	1	NA	59.803	577.145	1	54508767
TP101391	<nnxnp>	1	NA	60.257	558.215	1	54091684
TP95562	<nnxnp>	1	NA	60.468	695.601	1	54925403
TP117169	<nnxnp>	1	NA	60.87	560.96	NA	NA
TP54832	<nnxnp>	1	NA	61.069	505.838	NA	NA
TP84421	<hkxhk>	1	42.62	61.396	499.952	1	53377166
TP38836	<nnxnp>	1	NA	61.806	584.647	1	52593494
TP16579	<nnxnp>	1	NA	62.102	626.873	1	49142700
TP98960	<nnxnp>	1	NA	62.925	569.213	1	53812166
TP47527	<nnxnp>	1	NA	63.212	690.243	6	58888159
TP99522	<hkxhk>	1	52.362	63.571	762.01	1	58114188
TP113822	<nnxnp>	1	NA	63.684	708.463	1	56212524
TP30470	<nnxnp>	1	NA	64.051	702.519	NA	NA
TP16508	<nnxnp>	1	NA	64.621	756.057	1	56840092
TP59711	<hkxhk>	1	44.907	65.194	749.511	1	56707030
TP44244	<nnxnp>	1	NA	65.541	900.556	1	58539478
TP36709	<nnxnp>	1	NA	66.187	716.75	1	57821068
TP72267	<hkxhk>	1	46.561	66.622	724.819	1	57420365
TP90011	<nnxnp>	1	NA	66.789	726.117	1	58625149
TP22521	<nnxnp>	1	NA	67.019	722.492	1	58493850
TP22631	<nnxnp>	1	NA	67.648	906.057	1	57680575

Table A3 (cont.)

TP40406	<nnxnp>	1	NA	67.972	912.608	NA	NA
TP26887	<nnxnp>	1	NA	68.497	770.445	1	58217851
TP96895	<nnxnp>	1	NA	69.009	893.269	NA	NA
TP113785	<hkxhk>	1	49.75	69.421	884.965	NA	NA
TP39479	<nnxnp>	1	NA	69.993	926.158	1	59508338
TP33960	<nnxnp>	1	NA	70.343	929.625	8	53828845
TP57536	<hkxhk>	1	51.748	70.617	875.238	2	1806523
TP53240	<nnxnp>	1	NA	70.942	733.9	1	59682275
TP5562	<nnxnp>	1	NA	71.364	782.932	1	60022144
TP23749	<hkxhk>	1	53.066	71.802	869.404	1	59419757
TP45753	<nnxnp>	1	NA	72.935	921.351	1	60371314
TP96279	<hkxhk>	1	56.204	73.445	791.949	1	60813667
TP112327	<hkxhk>	1	54.528	74.215	860.771	1	59892689
TP45261	<nnxnp>	1	NA	75.163	799.305	1	60806190
TP55483	<hkxhk>	1	59.872	75.964	832.605	1	61573968
TP17357	<hkxhk>	1	58.16	77.051	842.477	1	61754518
TP97946	<nnxnp>	1	NA	77.698	959.467	1	62699923
TP73420	<hkxhk>	1	61.811	78.155	849.072	1	61658774
TP34835	<nnxnp>	1	NA	78.457	947.12	NA	NA
TP69148	<hkxhk>	1	60.794	79.205	941.176	1	62413515
TP110557	<nnxnp>	1	NA	79.685	951.388	1	62431178
TP67798	<hkxhk>	1	59.122	80.168	813.496	1	61835513
TP62070	<nnxnp>	1	NA	81.157	955.384	NA	NA
TP104441	<hkxhk>	1	63.156	81.486	961.6	1	62663963
TP30205	<nnxnp>	1	NA	82.718	982.809	1	64000619
TP72441	<hkxhk>	1	65.468	83.347	968.572	1	63518110
TP48453	<nnxnp>	1	NA	84.42	994.724	1	64659497
TP35472	<nnxnp>	1	NA	85.293	1019.238	NA	NA
TP85396	<hkxhk>	1	67.672	85.52	979.126	NA	NA
TP90572	<nnxnp>	1	NA	86.159	1014.036	1	64614971
TP75520	<hkxhk>	1	69.341	87.336	1007.492	NA	NA
TP118984	<nnxnp>	1	NA	87.904	1027.741	1	65543275
X252	<hkxhk>	1	71.461	88.372	1017.123	1	64629127
TP115515	<nnxnp>	1	NA	88.543	1034.444	NA	NA
TP8376	<hkxhk>	1	71.068	88.972	1023.402	1	65619832
TP121461	<nnxnp>	1	NA	89.579	1042.341	7	8852922
TP86305	<nnxnp>	1	NA	90.119	1039.645	1	65751242
TP112422	<nnxnp>	1	NA	91.092	1046.098	1	65926432
TP20436	<nnxnp>	1	NA	92.106	1086.755	1	66004730

Table A3 (cont.)

TP59766	<nnxnp>	1	NA	92.49	1082.685	1	66088939
TP79460	<hkxhk>	1	73.946	92.759	1097.91	1	66455662
TP95917	<nnxnp>	1	NA	93.083	1101.107	NA	NA
TP100622	<hkxhk>	1	75.133	93.533	1092.2	NA	NA
TP68033	<hkxhk>	1	76.524	94.666	1078.389	1	66325518
TP97723	<nnxnp>	1	NA	95.68	1063.435	NA	NA
TP78305	<hkxhk>	1	78.217	96.402	1118.486	NA	NA
X67	<hkxhk>	1	77.871	96.634	1115.797	1	67724596
TP123420	<nnxnp>	1	NA	96.77	1071.694	1	67750815
TP24115	<hkxhk>	1	79.583	97.533	1106.863	1	67449668
TP66436	<nnxnp>	1	NA	97.912	1124.561	NA	NA
TP91973	<nnxnp>	1	NA	98.289	1054.368	1	67488606
TP79090	<nnxnp>	1	NA	99.976	1132.382	NA	NA
TP28602	<nnxnp>	1	NA	101.062	1163.612	1	5091743
TP23614	<nnxnp>	1	NA	101.937	1172.861	1	69096248
TP66797	<nnxnp>	1	NA	102.291	1139.91	NA	NA
TP59873	<hkxhk>	1	84.704	102.788	1189.953	1	69663683
TP56219	<nnxnp>	1	NA	103.132	1112.664	NA	NA
TP78848	<hkxhk>	1	86.228	104.079	1181.995	1	69229942
TP33857	<nnxnp>	1	NA	104.903	1149.107	NA	NA
TP34713	<hkxhk>	1	88.56	105.747	1204.886	1	70025451
TP96960	<nnxnp>	1	NA	106.864	1253.522	1	71474014
TP77835	<nnxnp>	1	NA	107.588	1247.593	NA	NA
TP93973	<nnxnp>	1	NA	108.311	1291.429	1	71251609
TP108942	<hkxhk>	1	91.467	108.736	1226.664	1	70752061
TP77515	<nnxnp>	1	NA	108.885	1229.55	1	71879757
TP48234	<nnxnp>	1	NA	109.766	1269.263	10	3128537
TP51161	<hkxhk>	1	93.17	110.534	1234.071	1	71209561
TP121283	<nnxnp>	1	NA	111.026	1280.302	1	71183229
TP62577	<nnxnp>	1	NA	111.583	1285.844	1	71101340
TP54646	<hkxhk>	1	94.459	112.425	1219.465	1	70565357
TP98902	<nnxnp>	1	NA	113.541	1259.633	1	71663040
TP91615	<hkxhk>	1	96.194	114.18	1240.125	1	71318799
TP33358	<hkxhk>	1	99.165	115.754	1295.795	NA	NA
TP75939	<nnxnp>	1	NA	116.769	1305.062	NA	NA
TP7244	<hkxhk>	1	100.557	117.604	1310.278	1	72045756
TP59780	<hkxhk>	1	106.045	122.499	1324.605	3	53255805
TP68127	<nnxnp>	2	NA	0	0	1	2590159
TP92805	<nnxnp>	2	NA	3.867	41.826	1	1892914

Table A3 (cont.)

TP77021	<nnxnp>	2	NA	5.971	28.211	1	2041927
TP72359	<nnxnp>	2	NA	7.542	23.376	1	1893817
TP114462	<nnxnp>	2	NA	8.663	34.529	NA	NA
TP17261	<nnxnp>	2	NA	10.907	16.924	NA	NA
TP98801	<nnxnp>	2	NA	12.366	11.116	NA	NA
TP110209	<nnxnp>	2	NA	13.491	51.138	1	3037162
X237	<nnxnp>	2	NA	14.117	18.631	1	3149279
TP44016	<nnxnp>	2	NA	15.263	66.207	1	2811058
TP57166	<nnxnp>	2	NA	16.986	59.012	1	2542270
TP47253	<nnxnp>	2	NA	20.232	74.518	1	51816021
TP93620	<nnxnp>	2	NA	23.616	87.219	1	3697552
TP13305	<nnxnp>	2	NA	25.471	98.95	1	4584260
TP45740	<hkxhk>	2	7.211	32.43	131.385	NA	NA
X646	<hkxhk>	2	17.394	37.28	149.537	1	17065308
TP89402	<hkxhk>	2	22.712	41.466	165.209	NA	NA
TP86418	<hkxhk>	2	28.207	46.675	186.698	1	20084912
TP83625	<hkxhk>	2	33.892	49.821	219.602	NA	NA
TP64079	<nnxnp>	2	NA	51.331	199.515	1	49348728
TP14446	<hkxhk>	2	35.689	52.914	283.776	NA	NA
TP81076	<hkxhk>	2	40.509	53.968	280.115	1	47509359
TP34323	<hkxhk>	2	38.916	55.042	230.085	1	51127885
TP66426	<hkxhk>	2	37.216	56.591	292.256	NA	NA
X454	<hkxhk>	2	46.075	59.459	320.126	1	54126459
TP1828	<hkxhk>	2	44.923	61.561	306.772	NA	NA
TP58483	<hkxhk>	2	50.377	65.193	345.656	1	56707030
TP84768	<nnxnp>	2	NA	66.05	370.494	NA	NA
TP71886	<nnxnp>	2	NA	77.043	409.974	NA	NA
TP54190	<nnxnp>	2	NA	80.474	446.053	1	65478588
TP30341	<nnxnp>	2	NA	82.216	546.721	1	67569444
TP114770	<nnxnp>	2	NA	84.974	533.256	1	66995849
TP70614	<nnxnp>	2	NA	86.264	526.649	1	67077188
TP7780	<nnxnp>	2	NA	86.923	483.302	1	66369500
TP89431	<hkxhk>	2	73.345	87.181	498.746	NA	NA
TP101376	<nnxnp>	2	NA	87.614	516.505	1	65927100
TP8414	<nnxnp>	2	NA	88.804	429.226	NA	NA
TP91518	<nnxnp>	2	NA	91.153	559.55	1	68579810
TP24400	<nnxnp>	2	NA	92.716	466.578	2	60009674
TP21022	<nnxnp>	2	NA	94.348	570.143	NA	NA
TP11051	<nnxnp>	2	NA	96.171	596.879	1	69920187

Table A3 (cont.)

TP105272	<nnxnp>	2	NA	97.474	636.034	NA	NA
TP88148	<hkxhk>	2	80.833	98.377	644.135	1	71080829
TP51551	<nnxnp>	2	NA	99.124	606.327	1	70080914
X151	<nnxnp>	2	NA	100.086	646.102	9	1722376
TP16922	<nnxnp>	2	NA	101.212	628.455	1	71159594
TP55754	<nnxnp>	2	NA	103.209	617.803	1	70461933
TP8837	<nnxnp>	2	NA	104.627	582.155	1	69646572
X379	<nnxnp>	2	NA	110.543	655.894	1	73247705
TP51915	<nnxnp>	2	NA	115.528	662.362	NA	NA
TP65750	<hkxhk>	3	106.927	0	13.803	NA	NA
TP59249	<nnxnp>	3	NA	1.207	0	8	39443
TP58529	<nnxnp>	3	NA	4.132	51.27	NA	NA
TP38386	<nnxnp>	3	NA	5.441	9.871	NA	NA
TP40690	<nnxnp>	3	NA	5.894	65.315	2	2935293
TP110956	<nnxnp>	3	NA	6.492	27.055	NA	NA
TP43225	<hkxhk>	3	86.613	7.062	97.243	NA	NA
TP95904	<nnxnp>	3	NA	7.575	70.423	2	2647347
TP36242	<hkxhk>	3	82.988	7.849	58.816	2	2874313
TP112218	<nnxnp>	3	NA	8.311	92.83	2	3063599
TP109378	<nnxnp>	3	NA	8.758	75.032	2	1958586
TP119270	<nnxnp>	3	NA	9.323	44.907	2	2837643
TP22055	<nnxnp>	3	NA	9.875	78.773	2	3445013
TP25158	<nnxnp>	3	NA	10.591	86.791	2	3659319
TP20376	<nnxnp>	3	NA	11.111	81.873	NA	NA
TP27556	<nnxnp>	3	NA	11.777	109.559	NA	NA
TP27881	<hkxhk>	3	85.184	12.139	106.348	NA	NA
TP48989	<nnxnp>	3	NA	12.827	113.546	NA	NA
TP21848	<nnxnp>	3	NA	13.617	118.659	9	50063776
TP107185	<hkxhk>	3	77.357	14.104	142.224	2	8969070
TP7063	<nnxnp>	3	NA	14.382	349.888	2	9042290
TP23294	<hkxhk>	3	77.866	14.784	322.884	NA	NA
TP99704	<nnxnp>	3	NA	15.203	125.423	NA	NA
TP78227	<hkxhk>	3	79.244	15.409	135.172	2	9466570
TP82929	<hkxhk>	3	78.87	15.703	217.297	2	60385293
TP6717	<nnxnp>	3	NA	16.114	147.861	NA	NA
TP43327	<hkxhk>	3	76.074	16.349	159.506	2	12002881
TP74578	<nnxnp>	3	NA	16.674	131.149	2	8152789
X346	<hkxhk>	3	75.672	16.732	44.008	2	11583438
TP30900	<nnxnp>	3	NA	17.056	409.093	2	13927142

Table A3 (cont.)

TP28392	<hkxhk>	3	74.598	17.298	394.997	2	21885917
TP116516	<hkxhk>	3	74.368	17.787	389.692	NA	NA
TP93097	<nnxnp>	3	NA	17.991	336.417	NA	NA
TP10791	<hkxhk>	3	73.988	18.204	171.37	2	45447685
TP81558	<nnxnp>	3	NA	18.478	352.988	NA	NA
TP109373	<hkxhk>	3	72.941	18.675	363.937	2	56302424
TP20665	<hkxhk>	3	71.205	18.907	287.533	5	56039031
TP5353	<nnxnp>	3	NA	19.074	405.033	2	10620796
TP121442	<hkxhk>	3	72.357	19.38	401.071	NA	NA
TP81524	<nnxnp>	3	NA	19.541	416.417	NA	NA
TP5247	<hkxhk>	3	73.176	19.678	180.672	NA	NA
TP91574	<hkxhk>	3	72.06	19.906	356.147	2	39957618
TP97123	<nnxnp>	3	NA	20.041	413.5	NA	NA
TP20438	<hkxhk>	3	72.544	20.183	385.652	NA	NA
TP124295	<hkxhk>	3	71.481	20.378	420.144	NA	NA
TP85506	<nnxnp>	3	NA	20.436	154.082	NA	NA
X184	<hkxhk>	3	71.069	20.556	347.725	2	17325216
X244	<hkxhk>	3	71.069	20.556	419.736	2	17104859
TP50335	<hkxhk>	3	71.754	20.734	177.012	NA	NA
TP5618	<hkxhk>	3	73.516	21.147	382.3	2	57986940
TP115175	<nnxnp>	3	NA	21.248	308.106	NA	NA
TP95433	<hkxhk>	3	74.91	21.548	297.875	2	56218822
TP86180	<nnxnp>	3	NA	21.775	312.242	2	74084937
TP101331	<hkxhk>	3	70.238	22.17	424.078	2	59243697
TP70895	<nnxnp>	3	NA	22.281	183.712	2	57511875
TP32441	<hkxhk>	3	70.542	22.539	199.322	2	58418600
TP106651	<nnxnp>	3	NA	22.618	304.395	2	18628971
TP68023	<hkxhk>	3	69.539	22.878	427.7	2	58865019
TP97032	<nnxnp>	3	NA	23.09	360.574	2	51564367
TP59238	<hkxhk>	3	69.785	23.25	278.329	2	58877732
TP66208	<hkxhk>	3	69.007	23.578	435.941	NA	NA
TP90015	<nnxnp>	3	NA	23.774	316.763	NA	NA
TP56826	<hkxhk>	3	68.607	24.074	206.65	NA	NA
TP75257	<nnxnp>	3	NA	24.434	194.421	NA	NA
TP111295	<hkxhk>	3	68.104	24.739	229.414	2	59921456
TP46214	<nnxnp>	3	NA	24.882	282.013	NA	NA
TP65258	<hkxhk>	3	67.835	25.051	232.741	2	59948236
TP67440	<nnxnp>	3	NA	25.365	189.606	NA	NA
TP84297	<hkxhk>	3	67.175	25.645	224.523	2	60434673

Table A3 (cont.)

TP125431	<nnxnp>	3	NA	25.892	272.409	2	59065393
TP19266	<hkxhk>	3	66.621	26.263	238.934	2	60863940
TP85390	<hkxhk>	3	66.198	26.662	243.984	NA	NA
TP33898	<nnxnp>	3	NA	27.035	211.53	2	59737800
TP32246	<hkxhk>	3	65.436	27.443	249.038	NA	NA
TP25237	<hkxhk>	3	64.626	28.075	521.728	2	62121234
TP104896	<nnxnp>	3	NA	28.516	235.319	2	59753038
TP23050	<hkxhk>	3	62.325	28.755	515.092	2	62241917
TP90226	<hkxhk>	3	63.778	29.348	498.174	NA	NA
TP31579	<hkxhk>	3	63.295	29.689	490.561	2	62693001
TP98203	<nnxnp>	3	NA	29.838	480.615	NA	NA
TP91472	<hkxhk>	3	62.75	30.237	483.893	NA	NA
TP113905	<hkxhk>	3	61.971	30.534	530.125	2	63211022
TP122794	<nnxnp>	3	NA	30.601	262.091	2	62077030
TP1248	<nnxnp>	3	NA	30.832	449.66	2	61834324
TP79975	<hkxhk>	3	61.46	31.218	538.731	3	59504126
TP107270	<nnxnp>	3	NA	31.405	532.178	2	63371565
TP21139	<hkxhk>	3	60.673	31.584	535.322	2	63663489
TP91647	<nnxnp>	3	NA	31.996	471.607	NA	NA
TP115889	<hkxhk>	3	60.029	32.341	543.629	2	63630074
TP768	<nnxnp>	3	NA	33.049	255.351	NA	NA
TP93763	<nnxnp>	3	NA	33.512	460.36	2	62542815
TP102238	<hkxhk>	3	58.189	33.811	572.314	2	64564353
TP15397	<hkxhk>	3	57.702	34.656	584.669	NA	NA
TP1197	<hkxhk>	3	55.629	34.933	593.729	2	65426952
TP28811	<hkxhk>	3	56.671	35.747	612.484	2	65426411
TP114794	<nnxnp>	3	NA	36.056	575.533	2	64624756
TP16334	<hkxhk>	3	56.135	36.22	615.609	NA	NA
TP15724	<nnxnp>	3	NA	36.832	578.63	2	65386102
TP87208	<hkxhk>	3	54.824	37.039	606.116	2	65467837
TP14487	<nnxnp>	3	NA	37.239	621.198	2	65365768
TP38608	<nnxnp>	3	NA	37.714	600.471	2	65104955
TP122447	<nnxnp>	3	NA	38.139	617.654	2	65316777
TP81633	<hkxhk>	3	53.421	38.192	684.639	NA	NA
TP77327	<hkxhk>	3	52.705	38.735	667.195	9	57236059
TP15133	<nnxnp>	3	NA	39.09	558.988	NA	NA
TP55204	<nnxnp>	3	NA	39.65	633.055	NA	NA
TP100389	<hkxhk>	3	51.573	39.897	675.371	2	66396771
TP95014	<hkxhk>	3	51.152	40.428	678.876	2	66266840

Table A3 (cont.)

TP54553	<nnxnp>	3	NA	40.961	688.164	NA	NA
TP87621	<hkxhk>	3	49.882	41.481	693.314	NA	NA
TP50523	<hkxhk>	3	49.522	41.868	705.355	3	10078751
TP28470	<nnxnp>	3	NA	42.282	646.962	2	66429715
TP38077	<hkxhk>	3	48.846	42.607	651.847	2	66981484
TP64471	<hkxhk>	3	45.385	43.374	658.446	2	66713011
TP94811	<nnxnp>	3	NA	43.771	703.084	2	67064012
TP125125	<hkxhk>	3	47.389	44.006	709.255	2	67105808
TP109468	<hkxhk>	3	48.012	44.498	720.342	2	67372793
TP17557	<nnxnp>	3	NA	44.971	701.082	2	67280300
TP99177	<hkxhk>	3	46.746	45.273	714.223	2	67087382
TP93201	<nnxnp>	3	NA	45.804	697.175	2	66704022
TP71055	<nnxnp>	3	NA	46.365	728.524	NA	NA
TP67371	<hkxhk>	3	43.9	47.567	736.779	2	68295426
X26	<nnxnp>	3	NA	47.911	738.273	2	68655608
TP83935	<hkxhk>	3	42.019	48.583	757.998	2	69053555
TP44018	<nnxnp>	3	NA	49.146	743.409	2	70009018
TP115293	<nnxnp>	3	NA	49.88	747.562	2	69820182
TP26811	<hkxhk>	3	39.563	50.435	751.718	2	69793589
TP26812	<nnxnp>	3	NA	50.687	762.652	2	69793589
TP40151	<nnxnp>	3	NA	51.239	766.558	2	70278449
TP116945	<nnxnp>	3	NA	51.68	770.889	NA	NA
TP71070	<nnxnp>	3	NA	53.041	776.111	NA	NA
TP33536	<nnxnp>	3	NA	53.967	811.664	2	70813708
TP78025	<nnxnp>	3	NA	54.538	808.94	NA	NA
TP116242	<nnxnp>	3	NA	55.081	797.349	2	70768052
TP103093	<nnxnp>	3	NA	55.809	815.716	2	70992128
TP38740	<nnxnp>	3	NA	56.39	821.639	NA	NA
TP7454	<nnxnp>	3	NA	56.718	819.612	2	71340123
TP75158	<nnxnp>	3	NA	57.521	804.183	NA	NA
TP109863	<nnxnp>	3	NA	58.538	783.99	NA	NA
TP82945	<nnxnp>	3	NA	59.415	791.297	NA	NA
TP75971	<nnxnp>	3	NA	60.825	842.457	6	54264023
TP109359	<hkxhk>	3	36.535	61.227	825.42	NA	NA
TP57400	<nnxnp>	3	NA	61.989	848.128	2	72532310
TP40386	<nnxnp>	3	NA	62.862	830.007	2	72466310
TP39455	<nnxnp>	3	NA	63.605	835.479	NA	NA
TP108808	<nnxnp>	3	NA	65.093	854.026	NA	NA
TP84786	<nnxnp>	3	NA	66.066	858.702	NA	NA

Table A3 (cont.)

TP17634	<nnxnp>	3	NA	66.978	878.084	2	73521678
TP86496	<nnxnp>	3	NA	67.529	868.785	NA	NA
TP54186	<hkxhk>	3	22.435	69.421	915.78	NA	NA
TP48498	<nnxnp>	3	NA	69.883	885.819	2	73845737
TP69179	<nnxnp>	3	NA	71.564	894.935	6	49818683
TP119103	<nnxnp>	3	NA	72.855	924.347	2	74691754
TP80587	<nnxnp>	3	NA	73.951	931.493	NA	NA
TP53917	<nnxnp>	3	NA	74.909	907.071	2	74209270
TP13577	<hkxhk>	3	16.233	76.197	950.927	9	41367706
TP42656	<nnxnp>	3	NA	77.784	939.709	2	75419832
TP11861	<hkxhk>	3	6.119	79.783	1007.714	NA	NA
TP98523	<hkxhk>	3	8.121	81.025	991.428	NA	NA
TP794	<nnxnp>	3	NA	81.509	982.169	NA	NA
TP32326	<nnxnp>	3	NA	83.23	961.483	NA	NA
TP44324	<hkxhk>	3	11.345	83.998	973.531	NA	NA
TP120744	<nnxnp>	3	NA	85.483	957.187	NA	NA
TP57886	<nnxnp>	3	NA	86.955	967.398	2	76513547
TP69675	<nnxnp>	4	NA	0	5.482	2	49371829
TP111003	<hkxhk>	4	86.138	1.998	22.317	NA	NA
TP17320	<hkxhk>	4	84.364	4.266	16.264	NA	NA
TP105243	<nnxnp>	4	NA	5.204	27.979	NA	NA
X290	<nnxnp>	4	NA	6.591	NA	2	766164
TP18320	<hkxhk>	4	76.343	7.889	70.102	NA	NA
TP45713	<hkxhk>	4	78.663	9.308	38.283	2	1910904
X593	<nnxnp>	4	NA	10.273	NA	2	2833060
TP38166	<nnxnp>	4	NA	11.114	83.291	2	5237601
TP99504	<hkxhk>	4	73.595	13.436	53.767	NA	NA
TP104370	<nnxnp>	4	NA	14.437	192.666	NA	NA
TP24280	<hkxhk>	4	70.981	15.411	149.732	2	13585314
X589	<nnxnp>	4	NA	16.472	NA	2	62305422
TP5248	<hkxhk>	4	68.444	17.448	138.747	NA	NA
TP56423	<nnxnp>	4	NA	18.781	118.243	NA	NA
TP49060	<hkxhk>	4	67.481	19.913	130.652	5	11283264
TP71569	<nnxnp>	4	NA	22.614	101.718	NA	NA
TP48243	<hkxhk>	4	59.85	24.1	257.121	2	61433194
TP81026	<nnxnp>	4	NA	27.989	315.711	2	64740067
TP34324	<hkxhk>	4	41.459	42.305	438.723	2	69476363
TP57207	<nnxnp>	4	NA	42.937	446.702	2	69615179
TP110423	<hkxhk>	4	43.941	45.072	425.342	2	69317652

Table A3 (cont.)

TP97174	<nnxnp>	4	NA	47.909	432.867	NA	NA
TP29227	<hkxhk>	4	32.712	51.581	496.966	2	71634823
TP114311	<hkxhk>	4	35.392	53.365	466.994	2	71665039
TP123177	<hkxhk>	4	34.259	54.765	485.279	NA	NA
TP89969	<nnxnp>	4	NA	56.067	512.906	NA	NA
TP77955	<hkxhk>	4	29.773	57.624	522.713	2	72372971
TP33137	<hkxhk>	4	27.648	59.803	530.403	2	72932522
TP29890	<nnxnp>	4	NA	61.161	541.735	2	72848614
TP108600	<hkxhk>	4	25.946	62.327	567.576	NA	NA
TP118370	<hkxhk>	4	23.796	64.05	559.375	2	73535466
TP17574	<nnxnp>	4	NA	64.473	553.374	2	73525500
TP102280	<hkxhk>	4	21.558	66.389	583.61	NA	NA
TP116991	<hkxhk>	4	19.649	68.596	604.616	NA	NA
TP75964	<nnxnp>	4	NA	69.196	612.339	2	74384046
X305	<nnxnp>	4	NA	70.199	618.925	2	74081417
TP37607	<hkxhk>	4	17.122	71.528	594.382	NA	NA
TP24964	<nnxnp>	4	NA	71.96	621.993	2	74763909
TP110175	<nnxnp>	4	NA	74.254	627.463	2	75670926
TP53514	<nnxnp>	4	NA	77.394	634.101	2	76243114
TP86120	<nnxnp>	4	NA	79.297	641.105	NA	NA
TP98163	<nnxnp>	4	NA	82.695	662.05	NA	NA
TP24139	<nnxnp>	4	NA	84.592	671.584	NA	NA
TP85143	<nnxnp>	4	NA	87.388	654.17	2	77731079
TP32378	<hkxhk>	4	1.858	88.793	676.112	NA	NA
TP118850	<nnxnp>	4	NA	92.588	690.463	NA	NA
TP91491	<hkxhk>	5	83.316	0	92.231	NA	NA
TP42444	<nnxnp>	5	NA	3.581	136.504	NA	NA
TP25696	<nnxnp>	5	NA	5.734	106.669	NA	NA
TP28479	<nnxnp>	5	NA	6.883	125.676	4	3245691
TP72008	<nnxnp>	5	NA	8.082	116.565	3	1431361
X608	<nnxnp>	5	NA	9.29	88.297	3	219836
TP72956	<nnxnp>	5	NA	9.599	76.403	3	2391015
TP64593	<nnxnp>	5	NA	10.471	144.643	3	1850520
TP46517	<hkxhk>	5	66.995	11.242	169.986	3	3565963
TP2246	<nnxnp>	5	NA	11.654	157.729	3	2939504
TP67861	<nnxnp>	5	NA	12.744	66.696	3	3189585
TP50876	<nnxnp>	5	NA	13.233	151.409	3	2637841
TP41521	<hkxhk>	5	63.35	14.158	204.578	NA	NA
TP80561	<nnxnp>	5	NA	14.384	50.612	NA	NA

Table A3 (cont.)

TP26659	<nnxnp>	5	NA	14.893	164.049	3	3220061
TP101223	<hkxhk>	5	62.74	15.029	209.572	NA	NA
TP32325	<nnxnp>	5	NA	15.645	57.725	NA	NA
TP48739	<hkxhk>	5	61.503	16.191	188.213	3	55424433
TP47599	<nnxnp>	5	NA	16.59	178.356	NA	NA
TP76616	<nnxnp>	5	NA	16.962	196.941	3	5647729
TP80138	<hkxhk>	5	64.569	17.539	219.409	NA	NA
X277	<nnxnp>	5	NA	17.937	179.938	3	2814495
TP19054	<nnxnp>	5	NA	18.379	223.801	3	6133386
TP74491	<hkxhk>	5	59.492	18.792	255.512	NA	NA
TP75328	<hkxhk>	5	60.349	19.19	214.345	NA	NA
TP29303	<hkxhk>	5	58.197	20.113	240.788	3	9145992
TP32499	<nnxnp>	5	NA	20.511	259.778	3	8253723
X134	<nnxnp>	5	NA	20.824	253.535	3	7500246
TP18172	<nnxnp>	5	NA	21.393	346.741	3	10290990
TP66236	<hkxhk>	5	56.702	21.628	272.84	NA	NA
TP114236	<nnxnp>	5	NA	21.862	304.18	2	66299329
TP54576	<nnxnp>	5	NA	22.366	289.786	NA	NA
TP2243	<hkxhk>	5	55.55	22.542	277.11	NA	NA
TP46327	<hkxhk>	5	56.159	22.942	262.762	NA	NA
TP30254	<nnxnp>	5	NA	23.075	309.653	NA	NA
TP115991	<nnxnp>	5	NA	23.52	316.948	5	57760311
TP107339	<hkxhk>	5	54.321	23.833	284.704	3	10333769
TP105514	<nnxnp>	5	NA	23.96	232.03	3	9647675
TP77551	<nnxnp>	5	NA	24.392	297.344	3	10111227
X152	<nnxnp>	5	NA	24.699	448.876	3	49752585
TP24047	<nnxnp>	5	NA	25.24	338.985	NA	NA
TP82660	<hkxhk>	5	51.405	25.457	421.501	3	11960985
TP43240	<hkxhk>	5	52.733	26.004	324.136	3	11026572
TP21309	<nnxnp>	5	NA	26.289	404.837	3	13679402
TP11503	<hkxhk>	5	51.926	26.611	332.71	3	11626391
TP20454	<nnxnp>	5	NA	26.837	458.376	3	12952916
TP57338	<hkxhk>	5	50.665	27.313	411.73	10	14392046
TP34432	<nnxnp>	5	NA	27.788	471.082	3	51941314
TP111134	<nnxnp>	5	NA	28.18	465.541	3	27349983
TP93349	<nnxnp>	5	NA	28.594	452.575	NA	NA
TP79653	<nnxnp>	5	NA	28.856	475.577	3	52448091
TP76139	<nnxnp>	5	NA	29.188	400.384	3	51370392
TP93357	<nnxnp>	5	NA	29.562	354.224	3	52010322

Table A3 (cont.)

TP115352	<hkxhk>	5	48.533	29.669	448.32	3	53586293
TP112511	<nnxnp>	5	NA	30.337	478.742	NA	NA
TP29614	<hkxhk>	5	44.747	30.765	384.81	NA	NA
TP88354	<nnxnp>	5	NA	30.922	376.474	3	55461794
TP75224	<nnxnp>	5	NA	31.408	495.272	3	57219580
TP82958	<hkxhk>	5	47.379	31.721	395.349	3	54423298
TP70426	<nnxnp>	5	NA	32.03	361.911	7	52066357
TP33668	<nnxnp>	5	NA	32.529	369.589	3	55899666
TP110558	<nnxnp>	5	NA	32.954	482.52	3	57933249
TP76854	<hkxhk>	5	43.611	33.243	509.953	3	58437452
TP27847	<nnxnp>	5	NA	34.175	499.668	3	57700677
TP104437	<nnxnp>	5	NA	34.566	504.71	NA	NA
TP79214	<hkxhk>	5	45.913	35.189	488.609	3	57328579
TP13280	<nnxnp>	5	NA	35.57	546.932	3	59344146
TP24539	<nnxnp>	5	NA	35.997	515.919	NA	NA
TP12231	<hkxhk>	5	38.875	36.856	554.907	NA	NA
TP86119	<nnxnp>	5	NA	37.184	523.7	3	59344236
TP505	<nnxnp>	5	NA	37.751	531.638	3	59261038
TP85724	<nnxnp>	5	NA	38.394	539.008	3	60127991
TP35122	<nnxnp>	5	NA	39.125	553.36	NA	NA
TP112039	<hkxhk>	5	36.939	39.284	565.7	3	60807818
TP97381	<hkxhk>	5	35.477	39.923	560.644	3	60811992
TP99669	<nnxnp>	5	NA	41.191	588.822	3	61385774
TP50338	<hkxhk>	5	32.225	42.052	582.714	NA	NA
TP7134	<nnxnp>	5	NA	42.417	574.167	3	62433998
TP89053	<hkxhk>	5	30.926	43.043	578.65	3	61463409
TP48606	<nnxnp>	5	NA	43.861	613.678	3	61821109
TP111182	<hkxhk>	5	28.464	44.317	596.837	NA	NA
TP77851	<nnxnp>	5	NA	45.017	602.244	3	62657374
X98	<nnxnp>	5	NA	45.774	632.753	3	63773120
TP70184	<hkxhk>	5	26.289	46.072	607.966	3	62817126
TP9166	<nnxnp>	5	NA	46.875	636.423	1	65468586
TP69083	<nnxnp>	5	NA	47.425	633.9	3	65318044
TP56112	<hkxhk>	5	21.707	47.729	627.579	6	44931310
TP71065	<hkxhk>	5	22.901	48.307	623.03	3	63516505
TP85663	<nnxnp>	5	NA	49.182	684.379	3	65646191
TP80836	<hkxhk>	5	23.484	49.511	618.762	3	63526062
TP31842	<nnxnp>	5	NA	50.197	672.151	3	65672921
TP11992	<hkxhk>	5	24.503	50.836	631.962	3	63749598

Table A3 (cont.)

TP109063	<hkxhk>	5	19.549	51.174	641.652	3	64223575
TP56577	<nnxnp>	5	NA	52.257	691.803	3	66452817
TP110463	<nnxnp>	5	NA	52.736	715.629	3	66619495
TP109497	<hkxhk>	5	17.216	53.13	660.831	3	65259673
TP77724	<nnxnp>	5	NA	53.421	707.836	3	66862729
TP91993	<nnxnp>	5	NA	53.995	711.191	3	66434380
TP27956	<nnxnp>	5	NA	55.063	700.383	NA	NA
TP121477	<hkxhk>	5	13.314	55.534	667.87	3	65752255
TP72870	<hkxhk>	5	14.928	56.15	676.323	NA	NA
TP96294	<nnxnp>	5	NA	57.024	783.351	3	68081524
TP94861	<nnxnp>	5	NA	57.482	752.025	9	51377116
TP65982	<nnxnp>	5	NA	57.986	744.158	3	67679001
X6	<nnxnp>	5	NA	58.519	798.943	3	67658158
TP67656	<nnxnp>	5	NA	58.957	758.13	1	6338906
TP33671	<nnxnp>	5	NA	59.724	766.448	3	67971087
TP102831	<nnxnp>	5	NA	60.277	791.176	3	68068938
TP87631	<hkxhk>	5	9.075	60.634	721.73	3	67411652
TP15493	<nnxnp>	5	NA	61.358	845.35	NA	NA
TP8208	<nnxnp>	5	NA	62.287	775.228	3	68429377
TP38403	<nnxnp>	5	NA	62.934	826.995	3	69049735
TP2901	<hkxhk>	5	6.142	63.173	735.363	NA	NA
TP99491	<nnxnp>	5	NA	63.688	834.717	3	68997840
TP28007	<nnxnp>	5	NA	64.261	871.588	3	69070402
TP50954	<nnxnp>	5	NA	65.309	881.145	NA	NA
TP60861	<nnxnp>	5	NA	65.847	894.99	NA	NA
TP53614	<nnxnp>	5	NA	66.455	890.575	3	69724311
TP51324	<nnxnp>	5	NA	66.935	886.998	NA	NA
TP40961	<nnxnp>	5	NA	67.393	865.007	3	69638385
TP63049	<nnxnp>	5	NA	67.565	858.423	NA	NA
TP112969	<nnxnp>	5	NA	68.422	806.676	3	69049291
TP70753	<nnxnp>	5	NA	68.851	818.384	NA	NA
TP1912	<nnxnp>	5	NA	69.673	904.21	NA	NA
TP74455	<nnxnp>	5	NA	70.972	927.247	3	70616941
TP50066	<nnxnp>	5	NA	72.02	933.598	3	71107537
TP21315	<nnxnp>	5	NA	73.322	917.02	3	70598224
TP24299	<nnxnp>	5	NA	74.019	947.824	3	71630469
TP88459	<nnxnp>	5	NA	74.44	939.957	NA	NA
TP117302	<nnxnp>	5	NA	75.043	1068.526	NA	NA
TP12815	<nnxnp>	5	NA	76.238	1060.965	3	71816046

Table A3 (cont.)

TP114731	<nnxnp>	5	NA	76.762	1057.8	NA	NA
TP34458	<nnxnp>	5	NA	77.287	1051.773	NA	NA
X467	<nnxnp>	5	NA	79.06	1027.372	3	72353041
TP87122	<nnxnp>	5	NA	79.318	977.993	3	72205553
TP97462	<nnxnp>	5	NA	80.249	958.731	3	72152955
TP100964	<nnxnp>	5	NA	81.308	984.35	3	72592733
TP13687	<nnxnp>	5	NA	82.368	1001.235	3	73259136
TP89572	<nnxnp>	5	NA	83.191	1005.394	3	73111969
TP38035	<nnxnp>	5	NA	83.701	1033.173	NA	NA
TP33385	<nnxnp>	5	NA	84.773	1041.045	NA	NA
TP32442	<nnxnp>	5	NA	85.611	970.125	3	72197167
TP53019	<nnxnp>	5	NA	86.552	1024.944	7	52667767
TP105364	<nnxnp>	5	NA	88.817	994.824	3	73229444
TP17098	<nnxnp>	5	NA	91.159	1014.444	NA	NA
TP92140	<nnxnp>	6	NA	0	0	3	565021
TP107849	<hkxhk>	6	84.345	1.346	11.309	3	314979
TP96143	<nnxnp>	6	NA	1.948	7.524	NA	NA
TP100781	<nnxnp>	6	NA	4.82	31.762	3	1281815
TP98553	<nnxnp>	6	NA	6.246	36.861	3	2664477
TP43130	<nnxnp>	6	NA	7.265	88.683	3	1343828
TP59370	<hkxhk>	6	79.658	8.065	28.417	NA	NA
TP38935	<nnxnp>	6	NA	9.384	46.51	3	2534760
TP65846	<nnxnp>	6	NA	10.674	41.311	NA	NA
TP80751	<nnxnp>	6	NA	11.778	78.832	NA	NA
X319	<hkxhk>	6	72.744	12.091	85.116	3	1569586
TP71561	<nnxnp>	6	NA	13.026	122.397	3	3220835
TP6572	<nnxnp>	6	NA	14.124	69.342	3	2722235
TP15838	<hkxhk>	6	71.493	14.941	101.851	3	2778291
TP121077	<nnxnp>	6	NA	15.717	56.864	3	2940374
TP62722	<hkxhk>	6	73.497	16.688	96.83	NA	NA
TP9865	<nnxnp>	6	NA	17.37	173.585	3	4448068
TP29044	<hkxhk>	6	72.209	17.987	61.438	NA	NA
TP60736	<nnxnp>	6	NA	18.549	157.843	3	4159659
TP47849	<hkxhk>	6	75.501	19.293	53.52	NA	NA
TP52636	<nnxnp>	6	NA	19.878	182.49	3	4625231
TP119040	<nnxnp>	6	NA	20.653	164.141	3	4755788
TP67860	<hkxhk>	6	69.074	21.088	148.21	3	3189585
X643	<nnxnp>	6	NA	22.038	185.124	3	5530709
TP122344	<nnxnp>	6	NA	22.953	192.573	3	6160141

Table A3 (cont.)

TP118494	<nnxnp>	6	NA	24.676	240.89	3	8029882
TP95012	<nnxnp>	6	NA	25.721	218.838	3	8467450
TP107685	<nnxnp>	6	NA	26.516	232.497	3	8257005
TP68195	<nnxnp>	6	NA	26.955	226.709	3	8253713
TP116313	<nnxnp>	6	NA	27.635	203.858	3	8583142
TP13802	<nnxnp>	6	NA	28.337	210.626	3	7775546
X176	<nnxnp>	6	NA	28.439	212.544	3	6683212
TP21920	<hkxhk>	6	63.928	28.727	249.939	3	8314771
TP82618	<nnxnp>	6	NA	29.274	274.55	3	8500684
TP88593	<nnxnp>	6	NA	29.947	263.296	NA	NA
TP64986	<hkxhk>	6	61.745	30.503	267.728	3	8781041
TP27190	<nnxnp>	6	NA	30.964	258.886	3	10490166
TP119836	<nnxnp>	6	NA	31.946	254.768	NA	NA
TP74901	<nnxnp>	6	NA	32.497	288.886	3	11476585
TP11308	<hkxhk>	6	58.815	33.515	337.096	3	12806187
TP79775	<nnxnp>	6	NA	33.97	305.105	3	12486486
TP80446	<hkxhk>	6	55.61	34.444	323.224	NA	NA
X79	<nnxnp>	6	NA	34.559	349.118	3	52816333
TP42160	<nnxnp>	6	NA	34.805	371.665	3	12810253
TP8301	<hkxhk>	6	55.958	34.974	347.385	3	14894008
TP31941	<nnxnp>	6	NA	35.342	375.723	3	13553563
TP64494	<hkxhk>	6	55.137	35.468	316.314	3	13622745
X11	<hkxhk>	6	56.935	35.838	439.694	3	20393360
TP7851	<hkxhk>	6	54.511	36.077	417.925	3	53626637
TP59627	<hkxhk>	6	57.347	36.448	444.336	3	52300303
TP15256	<nnxnp>	6	NA	36.823	358.475	3	47910815
TP108289	<hkxhk>	6	58.053	37.231	408.693	3	50446284
TP52910	<hkxhk>	6	56.286	37.735	367.773	3	53136363
TP999	<nnxnp>	6	NA	37.87	459.57	3	54754381
TP93147	<nnxnp>	6	NA	38.333	467.948	9	49964719
TP9238	<hkxhk>	6	53.753	38.729	385.976	2	75517417
TP114756	<hkxhk>	6	56.559	39.262	475.47	3	56255046
X308	<nnxnp>	6	NA	39.287	403.67	3	59642734
TP97082	<nnxnp>	6	NA	39.576	396.928	3	58575533
X637	<hkxhk>	6	54.139	39.853	497.336	3	58594809
TP76291	<hkxhk>	6	52.95	40.105	493.284	NA	NA
TP85638	<nnxnp>	6	NA	40.487	483.136	NA	NA
TP3384	<hkxhk>	6	51.938	40.837	403.458	NA	NA
TP29527	<nnxnp>	6	NA	41.521	513.031	7	59494200

Table A3 (cont.)

TP16711	<hkxhk>	6	62.588	41.752	329.799	3	52179620
TP5254	<nnxnp>	6	NA	42.068	524.896	4	64329469
TP21338	<nnxnp>	6	NA	42.699	520.394	3	59562422
TP72920	<nnxnp>	6	NA	43.078	528.241	3	59413210
TP101499	<hkxhk>	6	50.24	43.45	509.035	3	59587457
TP52240	<nnxnp>	6	NA	44.095	502.045	NA	NA
TP67136	<hkxhk>	6	49.268	44.535	516.238	NA	NA
TP72912	<nnxnp>	6	NA	45.075	531.852	NA	NA
TP81183	<hkxhk>	6	47.44	45.827	568.044	NA	NA
TP86396	<nnxnp>	6	NA	46.249	542.724	3	60819650
TP116037	<hkxhk>	6	46.153	47.152	536.771	NA	NA
TP79881	<hkxhk>	6	48.172	48.276	550.847	NA	NA
TP104289	<hkxhk>	6	41.515	51.141	577.291	3	61805521
TP52419	<nnxnp>	6	NA	53.172	627.124	3	63781948
TP20609	<nnxnp>	6	NA	54.018	630.27	NA	NA
X485	<hkxhk>	6	38.294	54.927	632.181	3	63680821
TP38156	<nnxnp>	6	NA	55.76	639.344	3	64134033
TP102534	<hkxhk>	6	36.819	57.345	619.788	3	64771693
TP114732	<hkxhk>	6	33.768	58.494	660.609	3	66255310
TP110999	<nnxnp>	6	NA	59.128	652.409	3	65123247
TP102972	<hkxhk>	6	31.27	61.215	674.967	3	67554734
TP94873	<nnxnp>	6	NA	62.823	682.155	1	2414510
TP85722	<nnxnp>	6	NA	64.279	666.251	3	66862726
TP26451	<hkxhk>	6	28.398	64.852	669.951	3	67640867
TP84759	<nnxnp>	6	NA	65.646	694.028	3	67798476
X349	<hkxhk>	6	29.517	67.448	704.996	3	69100803
TP102101	<hkxhk>	6	24.676	68.943	765.456	NA	NA
TP9023	<hkxhk>	6	23.274	70.842	772.611	3	69918163
X195	<hkxhk>	6	25.274	71.863	792.497	3	69865284
TP27330	<hkxhk>	6	20.211	73.541	750.664	3	70561867
TP76778	<hkxhk>	6	17.684	75.725	812.713	3	71144271
TP113875	<nnxnp>	6	NA	78.06	829.765	NA	NA
TP31989	<nnxnp>	6	NA	79.922	836.393	3	71864021
TP8438	<hkxhk>	6	9.601	81.635	861.575	NA	NA
TP83064	<nnxnp>	6	NA	82.24	842.891	3	72205553
TP99345	<hkxhk>	6	0	83.61	904.834	3	73190448
TP593	<nnxnp>	6	NA	84.6	865.816	3	72732386
TP85309	<hkxhk>	6	2.031	85.571	898.258	3	73299993
TP118507	<hkxhk>	6	7.205	87.23	891.862	NA	NA

Table A3 (cont.)

TP94017	<hkxhk>	6	5.633	88.546	874.454	NA	NA
TP112986	<nnxnp>	6	NA	88.883	875.815	NA	NA
TP59638	<hkxhk>	6	4.456	90.168	883.384	3	74438364
TP48324	<hkxhk>	6	3.202	91.634	879.254	3	73992230
TP84733	<nnxnp>	6	NA	93.579	853.007	3	72752985
TP39760	<nnxnp>	7	NA	0	129.704	4	9421500
TP105993	<nnxnp>	7	NA	2.932	156.958	4	11683096
TP79248	<nnxnp>	7	NA	6.465	179.646	4	13923045
TP44131	<nnxnp>	7	NA	9.342	195.143	NA	NA
TP85628	<hkxhk>	7	54.351	10.824	192.071	4	14737043
TP56113	<nnxnp>	7	NA	12.268	201.385	7	14061664
TP19307	<nnxnp>	7	NA	18.514	359.727	NA	NA
TP7203	<nnxnp>	7	NA	19.642	226.597	7	5516132
TP16138	<nnxnp>	7	NA	21.166	215.371	4	56315951
TP60980	<nnxnp>	7	NA	22.82	221.747	7	5845008
TP2727	<nnxnp>	7	NA	25.025	233.563	7	4917191
TP87242	<nnxnp>	7	NA	28.993	333.815	2	71419325
TP64480	<nnxnp>	7	NA	32.127	371.339	NA	NA
TP76924	<nnxnp>	7	NA	33.321	315.633	4	40066402
TP47894	<hkxhk>	7	67.877	33.911	278.115	7	62838374
TP43727	<nnxnp>	7	NA	35.111	340.947	NA	NA
TP78983	<nnxnp>	7	NA	36.339	328.469	NA	NA
TP58240	<hkxhk>	7	72.8	36.609	307.219	7	61545104
TP32687	<nnxnp>	7	NA	37.657	325.502	NA	NA
TP54862	<hkxhk>	7	74.012	38.398	376.343	7	56974559
TP116208	<nnxnp>	7	NA	39.175	320.654	NA	NA
TP48334	<hkxhk>	7	65.203	39.678	245.372	7	64137662
TP119026	<hkxhk>	7	71.257	40.995	287.55	NA	NA
TP57806	<nnxnp>	7	NA	41.968	347.404	7	36467425
TP36567	<hkxhk>	7	70.316	42.864	300.12	7	59061884
X428	<hkxhk>	7	69.612	43.712	294.254	7	60132867
TP28957	<nnxnp>	7	NA	44.077	382.847	7	57870313
X83	<hkxhk>	7	66.244	45.191	250.96	7	63617802
TP107979	<nnxnp>	7	NA	52.183	395.09	NA	NA
TP1752	<nnxnp>	7	NA	53.117	399.3	4	62711161
X61	<nnxnp>	7	NA	53.495	396.643	4	63070853
TP99073	<nnxnp>	7	NA	55.785	405.145	4	62175362
TP26370	<nnxnp>	7	NA	57.474	409.316	4	61748646
TP52845	<nnxnp>	7	NA	59.416	413.446	4	61384768

Table A3 (cont.)

TP58267	<nnxnp>	7	NA	60.272	427.56	4	61209752
TP73334	<nnxnp>	7	NA	61.613	432.046	4	60792407
TP85188	<nnxnp>	7	NA	62.259	417.329	4	61451926
TP9078	<nnxnp>	7	NA	63.184	420.735	4	60829581
TP79662	<nnxnp>	7	NA	63.965	423.469	4	60209625
TP67597	<hkxhk>	7	79.841	64.667	462.356	4	58333549
TP95003	<nnxnp>	7	NA	65.623	438.485	4	60628843
TP41342	<hkxhk>	7	81.363	66.537	453.914	4	58482895
X190	<hkxhk>	7	80.039	67.005	449.929	6	52537823
TP42766	<nnxnp>	7	NA	67.36	448.203	4	59248476
TP94286	<nnxnp>	7	NA	67.888	445.118	4	59267836
TP22389	<hkxhk>	7	84.065	69.275	469.8	4	57787054
TP86177	<nnxnp>	7	NA	69.873	457.839	4	58003453
TP96905	<nnxnp>	7	NA	71.137	465.4	4	57698344
TP81204	<nnxnp>	7	NA	73.25	478.248	4	63951884
TP107527	<nnxnp>	7	NA	74.695	488.389	4	64291455
TP19463	<nnxnp>	7	NA	76.987	500.031	4	65177293
TP120972	<nnxnp>	7	NA	77.824	542.681	NA	NA
TP117210	<nnxnp>	7	NA	78.669	526.071	4	65430572
TP66618	<nnxnp>	7	NA	79.229	536.691	NA	NA
TP120595	<nnxnp>	7	NA	79.973	509.48	NA	NA
TP43156	<nnxnp>	7	NA	80.776	532.375	NA	NA
TP93224	<nnxnp>	7	NA	81.896	518.692	4	65455239
TP98958	<hkxhk>	7	117.989	82.723	NA	4	67870926
TP104154	<hkxhk>	7	97.624	83.407	567.892	NA	NA
TP22358	<nnxnp>	7	NA	84.67	556.286	4	66218431
TP40420	<nnxnp>	7	NA	86.553	577.285	4	66715900
TP30025	<nnxnp>	7	NA	87.97	582.97	4	66916884
TP31983	<nnxnp>	7	NA	88.547	585.726	4	66899834
TP111204	<hkxhk>	7	103.902	90.618	NA	4	66252666
TP76064	<nnxnp>	7	NA	91.4	593.152	4	67583309
TP53109	<nnxnp>	7	NA	93.666	598.88	9	47778279
TP50620	<nnxnp>	8	NA	0	0	4	1027662
TP35947	<nnxnp>	8	NA	1.825	15.295	4	90289
TP117139	<hkxhk>	8	72.16	2.701	24.958	4	442147
TP91178	<nnxnp>	8	NA	4.029	76.535	4	1682889
TP48421	<hkxhk>	8	74.269	4.63	19.782	NA	NA
TP78946	<nnxnp>	8	NA	6.218	10.324	4	84003
TP40812	<hkxhk>	8	70.116	6.873	31.93	4	1051451

Table A3 (cont.)

TP38365	<nnxnp>	8	NA	7.471	7.497	4	711541
TP9929	<hkxhk>	8	67.92	8.669	37.15	4	1472861
TP65721	<nnxnp>	8	NA	9.558	51.708	4	2775560
TP75487	<nnxnp>	8	NA	10.436	47.268	NA	NA
TP13236	<nnxnp>	8	NA	11.026	55.762	4	2306899
TP63176	<hkxhk>	8	65.07	11.46	44.487	2	615749
TP40456	<nnxnp>	8	NA	12.285	97.783	4	4361293
TP89361	<hkxhk>	8	63.629	12.53	58.836	NA	NA
TP117041	<hkxhk>	8	59.177	13.384	132.168	4	5465041
X269	<hkxhk>	8	64.733	13.861	73.201	4	2809730
X658	<hkxhk>	8	64.645	13.988	82.788	4	2809192
TP96759	<hkxhk>	8	66.106	14.528	67.027	4	3252336
TP105102	<nnxnp>	8	NA	14.864	87.069	4	4508745
TP66966	<nnxnp>	8	NA	15.701	107.105	4	4028015
TP75985	<hkxhk>	8	55.151	16.397	209.372	NA	NA
TP74939	<nnxnp>	8	NA	16.947	139.022	NA	NA
TP19121	<nnxnp>	8	NA	17.747	165.078	NA	NA
TP61531	<hkxhk>	8	58.234	18.213	117.973	NA	NA
TP117272	<hkxhk>	8	51.311	18.994	150.36	NA	NA
TP26719	<hkxhk>	8	57.297	19.441	113.592	4	5039160
TP86544	<nnxnp>	8	NA	19.931	144.91	5	59181489
TP25056	<nnxnp>	8	NA	20.344	147.289	4	6412738
TP22834	<hkxhk>	8	53.156	20.739	184.407	4	8362643
TP74543	<hkxhk>	8	60.337	21.258	170.735	4	7594395
TP28107	<nnxnp>	8	NA	21.877	288.642	NA	NA
X264	<hkxhk>	8	53.662	22.086	299.59	4	8350554
TP98446	<nnxnp>	8	NA	22.497	302.336	4	20600898
TP67586	<hkxhk>	8	54.048	22.751	159.733	4	7239179
TP3163	<nnxnp>	8	NA	23.06	295.284	NA	NA
TP40989	<nnxnp>	8	NA	23.525	186.765	NA	NA
X517	<hkxhk>	8	52.273	23.745	285.216	4	10118087
TP73228	<nnxnp>	8	NA	24.227	274.867	4	12125275
TP34575	<hkxhk>	8	50.396	24.406	279.339	4	9992651
TP111157	<nnxnp>	8	NA	24.889	190.363	NA	NA
TP38343	<hkxhk>	8	54.914	25.337	271.914	4	11612106
TP46250	<nnxnp>	8	NA	25.525	193.67	4	12341451
TP12062	<nnxnp>	8	NA	26.117	239.797	NA	NA
TP15134	<nnxnp>	8	NA	26.506	248.419	4	49803476
TP43931	<hkxhk>	8	51.829	26.689	216.42	10	54630844

Table A3 (cont.)

TP64270	<nnxnp>	8	NA	27.177	259.907	4	20737212
TP10721	<nnxnp>	8	NA	27.816	199.596	NA	NA
TP31906	<hkxhk>	8	49.228	28.482	317.926	NA	NA
TP24227	<nnxnp>	8	NA	28.774	227.819	4	49318834
TP109776	<nnxnp>	8	NA	29.603	310.716	NA	NA
TP10421	<hkxhk>	8	46.574	30.932	328.481	4	54064803
TP15537	<nnxnp>	8	NA	31.306	340.529	4	54080494
TP57309	<nnxnp>	8	NA	32.268	336.661	4	53773730
TP54196	<hkxhk>	8	44.862	32.647	345.134	4	54826427
TP57954	<nnxnp>	8	NA	33.315	366.969	4	54974789
TP8400	<nnxnp>	8	NA	34.039	353.388	NA	NA
TP122257	<nnxnp>	8	NA	34.49	361.418	NA	NA
TP51107	<hkxhk>	8	37.298	35.181	429.215	4	63012615
TP101856	<nnxnp>	8	NA	35.531	376.06	4	55760395
TP15001	<nnxnp>	8	NA	35.956	398.736	4	56480024
TP3118	<nnxnp>	8	NA	36.817	391.213	4	56658104
TP5931	<nnxnp>	8	NA	37.335	385.064	NA	NA
TP89888	<nnxnp>	8	NA	37.649	414.038	4	56871789
TP101892	<hkxhk>	8	38.958	37.848	418.384	NA	NA
TP19106	<nnxnp>	8	NA	38.264	438.387	4	63515183
TP28068	<hkxhk>	8	32.957	38.847	480.101	NA	NA
TP67506	<nnxnp>	8	NA	39.055	406.71	4	63509473
TP848	<nnxnp>	8	NA	39.708	486.539	NA	NA
TP26411	<hkxhk>	8	35.8	40.021	462.485	4	62376306
TP16753	<nnxnp>	8	NA	40.326	423.234	NA	NA
TP105324	<nnxnp>	8	NA	40.928	446.443	4	62273146
TP58630	<hkxhk>	8	33.817	41.115	498.329	4	61599237
TP33360	<nnxnp>	8	NA	41.55	477.578	5	46245409
TP112202	<nnxnp>	8	NA	42.029	455.864	4	61971584
TP99748	<hkxhk>	8	32.128	42.437	507.694	4	61229163
TP52180	<nnxnp>	8	NA	42.951	471.103	4	61520943
TP92927	<hkxhk>	8	29.239	43.591	513.118	6	56215355
TP93238	<nnxnp>	8	NA	43.909	504.02	4	61305566
TP83848	<hkxhk>	8	27.939	44.476	516.17	4	60629424
TP9079	<nnxnp>	8	NA	44.844	517.907	4	60829581
TP109906	<nnxnp>	8	NA	45.395	526.152	4	60461221
TP92731	<hkxhk>	8	28.484	45.941	536.478	NA	NA
TP125224	<nnxnp>	8	NA	46.604	521.787	NA	NA
TP92230	<hkxhk>	8	26.489	46.969	546.739	NA	NA

Table A3 (cont.)

TP8526	<nnxnp>	8	NA	47.414	529.374	NA	NA
TP107068	<hkxhk>	8	25.876	47.848	531.623	4	59865554
TP88116	<nnxnp>	8	NA	48.363	542.378	9	44884019
TP105581	<hkxhk>	8	23.936	48.671	577.08	4	59104031
TP877	<hkxhk>	8	22.949	49.013	570.242	4	59013422
TP65008	<hkxhk>	8	25.185	50.349	584.479	4	58866996
TP20721	<nnxnp>	8	NA	50.875	592.576	NA	NA
TP11494	<hkxhk>	8	21.545	51.872	600.236	4	58596316
TP122318	<nnxnp>	8	NA	52.107	628.791	4	58008710
TP52505	<nnxnp>	8	NA	52.857	613.769	NA	NA
TP86175	<hkxhk>	8	19.968	53.035	625.133	4	58003453
TP98841	<hkxhk>	8	15.765	53.878	634.38	NA	NA
TP7827	<nnxnp>	8	NA	54.503	643.052	NA	NA
TP100217	<hkxhk>	8	17.376	55.679	662.95	4	63771813
TP87748	<nnxnp>	8	NA	56.166	689.376	4	64307093
TP12699	<hkxhk>	8	16.52	56.605	652.209	NA	NA
TP45779	<hkxhk>	8	18.139	57.269	673.253	4	64094772
TP115288	<nnxnp>	8	NA	57.456	695.647	4	64313784
TP41425	<hkxhk>	8	13.983	58.45	692.831	NA	NA
TP42068	<nnxnp>	8	NA	59.033	700.732	NA	NA
TP115642	<hkxhk>	8	12.851	59.477	682.895	NA	NA
TP111259	<hkxhk>	8	11.643	61.046	729.544	NA	NA
TP88790	<nnxnp>	8	NA	61.64	716.15	4	65400765
TP74167	<hkxhk>	8	10.44	62.223	711.968	4	65178295
TP108475	<nnxnp>	8	NA	62.827	707.411	NA	NA
TP99997	<hkxhk>	8	8.329	63.3	719.688	4	65407645
X196	<hkxhk>	8	7.833	63.704	748.287	4	65210644
TP25151	<nnxnp>	8	NA	64.033	734.438	4	65679099
TP114429	<hkxhk>	8	9.374	64.489	737.298	NA	NA
TP316	<nnxnp>	8	NA	65.136	747.679	NA	NA
TP37950	<hkxhk>	8	7.057	65.731	742.705	4	65682351
TP110502	<hkxhk>	8	5.055	66.984	754.271	4	65966465
X187	<hkxhk>	8	4.319	67.376	773.888	NA	NA
TP53496	<nnxnp>	8	NA	67.566	765.205	NA	NA
TP110258	<hkxhk>	8	5.996	67.916	759.972	4	66249529
TP118400	<hkxhk>	8	2.921	69.013	767.222	NA	NA
TP70342	<nnxnp>	8	NA	69.804	790.073	4	66860542
TP12848	<hkxhk>	8	3.778	70.38	775.983	4	67135879
TP110439	<hkxhk>	8	1.243	70.751	782.257	4	67092087

Table A3 (cont.)

TP89535	<nnxnp>	8	NA	71.346	785.281	4	67376464
TP63484	<nnxnp>	8	NA	72.362	798.092	4	66537429
TP82569	<hkxhk>	8	0	73.529	802.872	4	66470400
TP104725	<nnxnp>	8	NA	74.174	812.781	4	66510076
X157	<nnxnp>	8	NA	76.392	794.105	4	67352063
TP62471	<hkxhk>	9	71.169	0	40.769	5	1329166
TP73017	<nnxnp>	9	NA	2.767	74.474	5	1737134
TP95624	<nnxnp>	9	NA	4.552	57.036	NA	NA
TP4585	<nnxnp>	9	NA	6.025	46.835	NA	NA
TP91917	<hkxhk>	9	63.188	7.337	61.984	5	1329210
TP31571	<nnxnp>	9	NA	8.741	52.932	NA	NA
TP48976	<hkxhk>	9	57.902	11.091	85.965	NA	NA
TP54141	<nnxnp>	9	NA	13.655	119.388	4	7165673
TP96583	<hkxhk>	9	50.356	14.991	113.474	9	12277971
TP75311	<nnxnp>	9	NA	15.659	124.034	5	2267856
TP76843	<nnxnp>	9	NA	17.739	126.964	NA	NA
TP3954	<nnxnp>	9	NA	19.649	130.86	5	2650538
TP106593	<nnxnp>	9	NA	22.036	139.027	NA	NA
TP14416	<nnxnp>	9	NA	23.521	135.004	NA	NA
TP51570	<nnxnp>	9	NA	23.867	142.439	NA	NA
TP90369	<nnxnp>	9	NA	24.383	136.095	5	3343843
TP106199	<nnxnp>	9	NA	26.446	147.621	NA	NA
TP37895	<nnxnp>	9	NA	27.847	179.668	5	5820162
TP84318	<nnxnp>	9	NA	28.474	152.309	1	2428396
TP69716	<nnxnp>	9	NA	29.283	160.36	8	4704286
TP97107	<nnxnp>	9	NA	30.114	156.215	NA	NA
TP3178	<nnxnp>	9	NA	30.89	162.833	NA	NA
TP62462	<nnxnp>	9	NA	31.486	174.41	NA	NA
TP115703	<nnxnp>	9	NA	32.098	168.822	5	5686329
TP80328	<nnxnp>	9	NA	32.54	164.822	5	5373507
TP92514	<nnxnp>	9	NA	32.799	166.686	NA	NA
TP38397	<nnxnp>	9	NA	33.185	171.28	NA	NA
TP52778	<nnxnp>	9	NA	33.936	186.16	5	7153993
TP94186	<nnxnp>	9	NA	34.387	220.805	NA	NA
TP67816	<nnxnp>	9	NA	34.887	246.621	NA	NA
TP29994	<nnxnp>	9	NA	35.669	226.217	NA	NA
TP101327	<nnxnp>	9	NA	36.31	214.868	NA	NA
TP8508	<nnxnp>	9	NA	36.72	193.764	NA	NA
TP33073	<nnxnp>	9	NA	36.985	189.575	5	7513669

Table A3 (cont.)

TP70746	<nnxnp>	9	NA	37.227	207.451	5	8252848
TP77585	<nnxnp>	9	NA	37.586	209.461	NA	NA
TP44690	<nnxnp>	9	NA	37.832	211.456	1	6548460
TP98262	<nnxnp>	9	NA	38.234	201.225	NA	NA
TP87411	<nnxnp>	9	NA	38.448	204.519	7	62707410
X411	<nnxnp>	9	NA	38.512	197.909	5	8108879
TP97790	<nnxnp>	9	NA	38.875	197.909	5	8617010
TP33716	<nnxnp>	9	NA	39.335	230.261	NA	NA
TP60596	<nnxnp>	9	NA	39.612	236.009	NA	NA
TP120011	<nnxnp>	9	NA	39.811	233.429	5	9753820
TP68981	<nnxnp>	9	NA	40.184	241.965	5	9838028
TP270	<nnxnp>	9	NA	40.498	238.495	4	64874968
TP91160	<nnxnp>	9	NA	40.983	252.178	NA	NA
TP15602	<nnxnp>	9	NA	41.425	256.144	5	11717354
TP124931	<nnxnp>	9	NA	41.727	258.647	NA	NA
TP48546	<nnxnp>	9	NA	42.255	292.504	NA	NA
TP107636	<nnxnp>	9	NA	42.58	260.419	NA	NA
TP7087	<nnxnp>	9	NA	42.923	261.825	NA	NA
TP26126	<nnxnp>	9	NA	43.201	263.778	NA	NA
TP102148	<nnxnp>	9	NA	43.527	284.358	9	1451505
TP90191	<nnxnp>	9	NA	43.781	285.9	NA	NA
TP76322	<nnxnp>	9	NA	43.98	281.896	NA	NA
TP15061	<nnxnp>	9	NA	44.098	280.127	5	15889875
TP76006	<nnxnp>	9	NA	44.326	276.959	5	14430497
TP48856	<nnxnp>	9	NA	44.627	272.68	NA	NA
TP103710	<nnxnp>	9	NA	44.938	269.962	NA	NA
TP8070	<nnxnp>	9	NA	45.145	267.183	5	25494308
TP21034	<nnxnp>	9	NA	45.494	296.016	5	42711245
TP15790	<nnxnp>	9	NA	45.834	306.493	5	43017729
TP18541	<nnxnp>	9	NA	46.12	298.091	5	42371893
TP55462	<nnxnp>	9	NA	46.318	300.396	5	42711751
TP3059	<nnxnp>	9	NA	46.669	288.361	3	67750321
TP80941	<nnxnp>	9	NA	47.057	303.326	5	44331026
TP4298	<nnxnp>	9	NA	47.705	311.65	5	46525147
TP29682	<nnxnp>	9	NA	48.092	313.416	NA	NA
TP78248	<nnxnp>	9	NA	48.442	309.074	NA	NA
TP34584	<nnxnp>	9	NA	49.148	316.11	NA	NA
TP11586	<nnxnp>	9	NA	49.558	320.256	5	48523710
TP13019	<nnxnp>	9	NA	50.185	325.072	NA	NA

Table A3 (cont.)

TP9788	<nnxnp>	9	NA	50.644	328.595	5	49498389
TP58152	<nnxnp>	9	NA	51.262	332.25	NA	NA
TP115766	<nnxnp>	9	NA	52.288	335.419	5	49860710
TP5125	<nnxnp>	9	NA	52.967	340.064	5	50331204
TP99836	<nnxnp>	9	NA	53.797	344.479	5	51304231
TP54269	<nnxnp>	9	NA	54.515	347.083	5	51032005
TP86750	<nnxnp>	9	NA	55.015	351.236	5	52258775
TP47639	<nnxnp>	9	NA	55.61	355.263	NA	NA
TP8641	<nnxnp>	9	NA	56.311	359.171	NA	NA
TP20195	<nnxnp>	9	NA	57.282	382.909	5	54388153
TP29206	<nnxnp>	9	NA	57.91	385.371	5	53182554
TP16947	<nnxnp>	9	NA	58.361	362.591	4	11265407
TP76712	<nnxnp>	9	NA	58.694	366.418	NA	NA
TP29309	<nnxnp>	9	NA	58.943	380.216	NA	NA
TP112083	<nnxnp>	9	NA	59.304	399.766	5	53208221
TP118405	<nnxnp>	9	NA	59.792	394.714	NA	NA
TP44558	<nnxnp>	9	NA	60.154	372.278	NA	NA
TP51856	<nnxnp>	9	NA	60.528	413.316	NA	NA
TP59289	<nnxnp>	9	NA	60.782	375.94	5	53190588
TP106520	<nnxnp>	9	NA	61.379	369.553	5	55124219
TP15424	<nnxnp>	9	NA	62.015	389.025	NA	NA
TP113821	<nnxnp>	9	NA	62.588	418.253	NA	NA
TP19474	<nnxnp>	9	NA	62.871	449.348	NA	NA
TP1489	<hkxhk>	9	26.279	63.223	408.311	NA	NA
TP64738	<nnxnp>	9	NA	63.5	422.484	NA	NA
TP51036	<nnxnp>	9	NA	63.985	432.558	5	56852240
TP106852	<nnxnp>	9	NA	64.451	405.04	5	56941368
TP78088	<nnxnp>	9	NA	65.132	444.62	NA	NA
TP72235	<nnxnp>	9	NA	65.622	438.977	5	57918172
TP53195	<nnxnp>	9	NA	66.123	426.339	5	56685389
TP27288	<hkxhk>	9	19.013	67.639	456.757	5	58963749
TP54855	<nnxnp>	9	NA	67.9	454.848	NA	NA
TP18171	<nnxnp>	9	NA	68.994	461.997	NA	NA
TP118832	<nnxnp>	9	NA	70.621	525.09	NA	NA
TP28874	<hkxhk>	9	8.922	71.893	490.324	NA	NA
TP29024	<nnxnp>	9	NA	72.553	484.302	5	60043436
X46	<nnxnp>	9	NA	73.108	502.31	5	61159244
TP55523	<nnxnp>	9	NA	74.676	497.647	NA	NA
TP78721	<hkxhk>	9	11.965	75.723	475.882	2	20879099

Table A3 (cont.)

TP42624	<hkxhk>	9	0.894	77.017	506.534	3	3805912
TP79286	<nnxnp>	10	NA	0	0	NA	NA
TP74459	<nnxnp>	10	NA	3.532	18.043	5	637031
TP65474	<hkxhk>	10	2.059	5.475	35.883	NA	NA
TP96082	<nnxnp>	10	NA	7.264	24.189	NA	NA
TP4584	<nnxnp>	10	NA	9.428	10.166	NA	NA
TP54975	<hkxhk>	10	8.584	12.333	59.996	10	49366493
TP13342	<nnxnp>	10	NA	13.444	44.413	5	1895724
X309	<hkxhk>	10	12.048	15.137	50.848	5	2202238
TP4939	<hkxhk>	10	14.095	16.817	52.311	NA	NA
TP54034	<nnxnp>	10	NA	17.157	54.213	1	7660041
TP87554	<nnxnp>	10	NA	21.624	73.377	5	2652616
TP40455	<nnxnp>	10	NA	26.858	89.144	5	5820267
TP53760	<hkxhk>	10	28.473	27.692	98.454	NA	NA
TP69717	<nnxnp>	10	NA	29.532	115.251	8	4704284
TP74387	<nnxnp>	10	NA	30.879	108.825	5	4981254
TP76637	<hkxhk>	10	25.818	31.43	105.899	5	5686283
TP103023	<nnxnp>	10	NA	32.853	122.082	NA	NA
TP93325	<nnxnp>	10	NA	34.17	127.708	NA	NA
TP13550	<nnxnp>	10	NA	36.226	131.916	1	63767069
TP46538	<nnxnp>	10	NA	38.721	138.808	NA	NA
TP84898	<nnxnp>	10	NA	40.312	148.03	3	49294432
TP100637	<hkxhk>	10	34.751	41.195	156.683	NA	NA
TP58261	<nnxnp>	10	NA	46.472	168.72	NA	NA
TP4741	<nnxnp>	10	NA	50.747	185.271	4	67226136
TP60139	<hkxhk>	10	51.917	51.922	258.653	NA	NA
TP14359	<nnxnp>	10	NA	54.668	208.722	NA	NA
TP41422	<nnxnp>	10	NA	55.9	216.313	NA	NA
TP7038	<nnxnp>	10	NA	57.076	224.02	NA	NA
TP124371	<hkxhk>	10	44.283	58.593	198.356	5	52942948
TP33282	<nnxnp>	10	NA	59.889	239.609	5	52136307
TP70969	<hkxhk>	10	48.924	61.171	280.843	5	56461891
TP27302	<nnxnp>	10	NA	61.901	265.023	5	53891216
TP3812	<nnxnp>	10	NA	65.742	274.542	5	55579685
TP15300	<nnxnp>	10	NA	68.134	291.115	NA	NA
TP16824	<nnxnp>	10	NA	70.504	312.115	NA	NA
TP71422	<nnxnp>	10	NA	71.861	299.89	NA	NA
TP78053	<nnxnp>	10	NA	73.958	306.434	9	54729767
TP98563	<nnxnp>	10	NA	77.508	319.54	5	59006856

Table A3 (cont.)

TP32989	<nnxnp>	10	NA	83.077	334.632	5	60213841
TP65858	<nnxnp>	11	NA	0	14.533	4	7145982
TP110571	<hkxhk>	11	3.578	0.453	44.175	NA	NA
TP57384	<nnxnp>	11	NA	1.149	124.698	6	2177365
TP68863	<hkxhk>	11	8.925	1.828	56.834	6	38382205
TP98716	<nnxnp>	11	NA	2.08	170.982	6	45299087
TP62823	<hkxhk>	11	6.442	2.562	51.013	6	40821355
TP72756	<nnxnp>	11	NA	3.103	62.507	6	30960859
TP118029	<hkxhk>	11	12.539	3.415	4.91	6	1521975
TP85263	<nnxnp>	11	NA	4.098	74.994	6	26680475
TP90606	<hkxhk>	11	10.539	4.355	70.117	NA	NA
TP9499	<hkxhk>	11	11.127	4.889	20.064	NA	NA
TP49960	<nnxnp>	11	NA	5.092	28.54	NA	NA
TP27313	<hkxhk>	11	7.029	5.453	35.594	6	40069291
TP121907	<nnxnp>	11	NA	5.729	119.783	NA	NA
TP4835	<nnxnp>	11	NA	6.17	115.487	6	37903176
TP121649	<hkxhk>	11	4.93	6.446	95.548	NA	NA
TP78729	<hkxhk>	11	9.827	6.814	82.069	NA	NA
TP4753	<nnxnp>	11	NA	7.114	9.823	NA	NA
TP96585	<nnxnp>	11	NA	7.509	79.392	NA	NA
TP107453	<hkxhk>	11	8.487	7.638	89.152	8	7733381
TP28407	<nnxnp>	11	NA	7.798	129.982	6	41427650
TP22027	<nnxnp>	11	NA	8.242	67.224	NA	NA
TP112139	<hkxhk>	11	11.902	8.36	131.766	NA	NA
TP37036	<nnxnp>	11	NA	8.513	135.592	4	10574190
TP40534	<nnxnp>	11	NA	8.894	111.859	6	25948247
TP64699	<hkxhk>	11	7.46	9.212	105.905	NA	NA
TP58984	<nnxnp>	11	NA	9.696	142.01	NA	NA
TP121928	<hkxhk>	11	13.93	10.169	195.902	6	46998341
TP90386	<nnxnp>	11	NA	10.442	148.749	6	46421652
TP125850	<hkxhk>	11	14.499	10.823	200.627	NA	NA
TP81270	<nnxnp>	11	NA	11.129	156.474	6	46421588
TP26654	<nnxnp>	11	NA	11.902	184.213	6	47452422
TP18328	<hkxhk>	11	16.782	12.58	215.678	6	48307640
TP119243	<hkxhk>	11	16.058	13.26	210.013	6	48147807
TP50584	<nnxnp>	11	NA	13.736	262.268	NA	NA
TP16477	<nnxnp>	11	NA	14.352	245.532	NA	NA
TP16176	<nnxnp>	11	NA	14.829	236.305	6	48508786
TP79198	<hkxhk>	11	18.922	15.244	233	NA	NA

Table A3 (cont.)

TP82316	<nnxnp>	11	NA	15.513	225.632	6	48702674
TP122861	<nnxnp>	11	NA	16.406	256.132	6	49299075
TP84707	<nnxnp>	11	NA	16.664	268.364	NA	NA
TP34583	<nnxnp>	11	NA	17.091	239.671	NA	NA
TP89885	<nnxnp>	11	NA	17.486	241.88	6	49323621
TP33000	<nnxnp>	11	NA	18.182	251.316	6	49135553
TP46813	<nnxnp>	11	NA	19.036	271.715	10	57161698
TP97309	<hkxhk>	11	25.209	19.602	307.202	6	50681896
TP50009	<nnxnp>	11	NA	19.895	286.589	6	50108394
TP57449	<hkxhk>	11	24.031	20.984	292.758	6	50549344
TP20046	<nnxnp>	11	NA	21.457	278.163	6	53957442
TP4644	<nnxnp>	11	NA	22.291	313.142	NA	NA
TP51230	<hkxhk>	11	27.444	22.723	343.278	NA	NA
TP85834	<nnxnp>	11	NA	23.57	328.565	6	51284121
TP74855	<hkxhk>	11	28.811	23.836	334.849	6	51205101
TP12740	<hkxhk>	11	31.574	24.683	363.315	4	66127143
TP24410	<nnxnp>	11	NA	25.161	321.154	6	51778130
TP27277	<hkxhk>	11	29.843	25.69	397.213	NA	NA
TP117148	<nnxnp>	11	NA	25.998	349.116	NA	NA
TP78231	<hkxhk>	11	30.608	26.413	355.838	NA	NA
TP823	<nnxnp>	11	NA	27.027	390.519	NA	NA
TP56157	<hkxhk>	11	33.094	27.684	407.543	NA	NA
TP94055	<nnxnp>	11	NA	28.09	352.577	6	51961016
TP92712	<nnxnp>	11	NA	28.403	414.448	6	52078132
TP84237	<hkxhk>	11	34.179	28.795	378.697	6	52091799
TP89290	<hkxhk>	11	34.8	29.529	383.416	NA	NA
TP79046	<nnxnp>	11	NA	30.62	437.317	6	52661686
TP13651	<hkxhk>	11	36.531	31.246	426.85	6	52475943
TP105380	<nnxnp>	11	NA	31.659	441.499	6	53172387
TP104277	<hkxhk>	11	37.518	32.248	433.077	7	37849905
TP11388	<nnxnp>	11	NA	32.941	450.505	6	52878651
TP39960	<nnxnp>	11	NA	33.421	455.078	6	53566510
TP42511	<hkxhk>	11	40.254	34.193	446.091	2	71605562
TP40307	<nnxnp>	11	NA	35.491	474.454	NA	NA
TP50831	<hkxhk>	11	41.988	36.042	469.541	NA	NA
TP82455	<nnxnp>	11	NA	36.738	462.99	NA	NA
TP50687	<hkxhk>	11	44.386	38.166	492.004	6	54171735
TP104186	<nnxnp>	11	NA	38.754	504.843	NA	NA
TP53118	<hkxhk>	11	45.351	39.463	498.653	6	54357368

Table A3 (cont.)

TP52144	<nnxnp>	11	NA	39.922	531.983	6	54573444
TP91994	<hkxhk>	11	46.455	40.632	509.585	6	54253601
TP32500	<nnxnp>	11	NA	41.486	528.057	NA	NA
TP115236	<nnxnp>	11	NA	42.097	536.445	6	54885087
TP72597	<hkxhk>	11	48.457	42.317	521.904	NA	NA
TP65724	<nnxnp>	11	NA	42.967	539.295	6	54948014
TP93974	<nnxnp>	11	NA	43.576	542.975	6	55201340
TP82367	<hkxhk>	11	49.677	43.965	545.558	6	55095381
TP90155	<nnxnp>	11	NA	44.742	516.183	6	54205397
TP66571	<hkxhk>	11	52.042	45.891	563.789	6	55310044
TP13284	<nnxnp>	11	NA	46.602	567.675	6	55606114
TP29843	<nnxnp>	11	NA	48.337	572.554	NA	NA
TP29320	<hkxhk>	11	54.242	48.804	576.758	NA	NA
X99	<nnxnp>	11	NA	49.232	525.332	6	55296845
X469	<nnxnp>	11	NA	49.794	NA	NA	NA
TP34839	<nnxnp>	11	NA	50.691	581.741	6	56145368
TP29424	<hkxhk>	11	57.816	52.174	588.632	NA	NA
X199	<nnxnp>	11	NA	52.276	588.081	6	56462968
TP26782	<hkxhk>	11	62.185	54.055	595.66	NA	NA
X76	<hkxhk>	11	NA	56.365	NA	6	57253680
TP119264	<nnxnp>	11	NA	57.587	612.978	6	57622514
TP66716	<hkxhk>	11	61.552	58.052	607.546	6	57131870
TP110656	<nnxnp>	11	NA	58.781	617.172	6	57585472
TP87561	<nnxnp>	11	NA	59.423	620.025	NA	NA
TP88947	<nnxnp>	11	NA	60.444	639.817	6	58119195
TP28963	<nnxnp>	11	NA	61.917	672.838	6	58309928
TP31185	<hkxhk>	11	69.799	62.546	625.591	NA	NA
TP20928	<nnxnp>	11	NA	63.179	656.634	NA	NA
TP71988	<nnxnp>	11	NA	64.058	664.066	6	58413854
TP97829	<nnxnp>	11	NA	64.829	677.881	6	58855270
TP7436	<nnxnp>	11	NA	65.511	682.622	NA	NA
TP44178	<nnxnp>	11	NA	66.156	649.644	6	58810918
TP112278	<nnxnp>	11	NA	66.923	689.147	NA	NA
TP74699	<nnxnp>	11	NA	68.209	694.321	6	59392957
TP85136	<nnxnp>	11	NA	69.823	702.723	6	59779109
TP22247	<nnxnp>	11	NA	70.721	708.104	6	60255011
TP65969	<nnxnp>	11	NA	72.706	714.443	NA	NA
TP77171	<nnxnp>	11	NA	73.637	733.99	6	60988538
TP83937	<nnxnp>	11	NA	74.401	739.018	2	69053555

Table A3 (cont.)

TP33318	<nnxnp>	11	NA	75.08	720.122	NA	NA
TP14575	<nnxnp>	11	NA	75.959	764.708	6	61836151
TP63864	<nnxnp>	11	NA	76.689	756.156	6	61816081
TP50090	<nnxnp>	11	NA	77.835	727.607	6	60857779
TP2851	<nnxnp>	11	NA	79.106	760.148	6	58364196
TP84073	<nnxnp>	11	NA	80.901	748.724	6	61929463
TP33107	<nnxnp>	11	NA	83.662	774.865	NA	NA
TP63705	<hkxhk>	12	72.558	0	56.816	6	2201431
TP44274	<hkxhk>	12	75.641	1.705	95.098	NA	NA
TP33241	<hkxhk>	12	69.688	3.125	50.878	6	3510624
X493	<hkxhk>	12	68.555	3.999	36.876	6	3509617
TP46119	<hkxhk>	12	70.803	4.879	78.788	6	40193762
TP36193	<hkxhk>	12	67.689	6.404	69.152	6	44557918
X662	<nnxnp>	12	NA	7.325	64.011	8	7737343
X137	<hkxhk>	12	66.092	7.799	109.644	6	49960123
TP44331	<hkxhk>	12	80.649	8.64	26.34	6	1553658
TP114670	<nnxnp>	12	NA	9.936	0	6	39528308
TP74270	<hkxhk>	12	73.743	10.783	62.27	NA	NA
TP11162	<hkxhk>	12	60.023	12.108	163.98	6	47984679
TP32985	<nnxnp>	12	NA	13.921	213.81	6	46044210
TP118194	<hkxhk>	12	56.753	14.886	169.273	NA	NA
TP100012	<hkxhk>	12	48.725	20.039	202.728	NA	NA
TP116644	<nnxnp>	12	NA	21.242	291.697	6	53157084
X87	<hkxhk>	12	51.644	22.163	227.886	6	49592234
X601	<hkxhk>	12	44.189	22.73	227.587	6	49212265
TP88434	<nnxnp>	12	NA	24.582	274.538	6	52842470
TP95961	<nnxnp>	12	NA	26.577	311.698	6	53646802
TP99866	<hkxhk>	12	25.291	27.627	267.989	6	52828050
TP86821	<nnxnp>	12	NA	28.581	281.906	6	53268370
X415	<hkxhk>	12	30.426	29.521	299.408	5	45152706
TP103071	<nnxnp>	12	NA	30.175	240.652	6	53329547
TP82360	<nnxnp>	12	NA	31.552	303.203	6	53961079
TP9557	<hkxhk>	12	18.779	32.567	317.249	NA	NA
TP59737	<nnxnp>	12	NA	35.358	331.969	6	55152525
TP65329	<nnxnp>	12	NA	36.212	349.987	6	55593033
TP115850	<nnxnp>	12	NA	38.185	366.634	6	55184161
TP55653	<nnxnp>	12	NA	39.534	373.416	6	55246040
TP44195	<nnxnp>	12	NA	40.565	360.841	6	55168044
TP31359	<nnxnp>	12	NA	41.348	380.837	NA	NA

Table A3 (cont.)

X45	<nnxnp>	12	NA	42.61	385.46	6	55594981
TP30194	<nnxnp>	12	NA	42.705	340.3	NA	NA
TP566	<nnxnp>	12	NA	44.258	387.728	NA	NA
TP90227	<nnxnp>	12	NA	46.186	395.162	6	56052544
TP82830	<nnxnp>	12	NA	47.193	422.219	NA	NA
TP17821	<nnxnp>	12	NA	48.698	433.554	NA	NA
TP20977	<nnxnp>	12	NA	49.463	444.634	NA	NA
TP54399	<nnxnp>	12	NA	50.136	439.822	NA	NA
TP101421	<nnxnp>	12	NA	50.742	414.195	NA	NA
TP115524	<nnxnp>	12	NA	51.044	405.352	6	56158679
TP79895	<nnxnp>	12	NA	52.61	463.077	6	56728310
TP89474	<nnxnp>	12	NA	53.312	454.043	NA	NA
TP110230	<nnxnp>	12	NA	54.596	482.297	NA	NA
TP68190	<nnxnp>	12	NA	55.255	489.917	NA	NA
TP90177	<nnxnp>	12	NA	55.884	473.816	NA	NA
X55	<nnxnp>	12	NA	56.437	493.872	6	57160241
TP49694	<nnxnp>	12	NA	58.612	561.003	6	57696622
TP64863	<nnxnp>	12	NA	59.717	578.231	6	57930469
TP74021	<nnxnp>	12	NA	60.351	587.462	NA	NA
TP61645	<nnxnp>	12	NA	61.228	596.237	6	58064321
TP52003	<nnxnp>	12	NA	61.784	571.948	NA	NA
TP81438	<nnxnp>	12	NA	62.623	600.225	NA	NA
TP69498	<nnxnp>	12	NA	62.922	602.584	NA	NA
TP75494	<nnxnp>	12	NA	63.797	608.865	6	58460285
TP75231	<nnxnp>	12	NA	64.725	534.995	6	59305048
TP79694	<nnxnp>	12	NA	65.405	503.806	NA	NA
X594	<nnxnp>	12	NA	65.687	505.945	6	59145596
TP74964	<nnxnp>	12	NA	66.405	620.306	6	59208299
TP77443	<nnxnp>	12	NA	66.856	629.415	6	59415167
TP112276	<nnxnp>	12	NA	67.51	516.883	6	59188999
TP34854	<nnxnp>	12	NA	68.319	510.593	6	59263401
TP21565	<nnxnp>	12	NA	69.432	525.112	6	59693386
TP9048	<nnxnp>	12	NA	70.444	644.051	NA	NA
TP119963	<nnxnp>	12	NA	70.879	648.651	6	60104301
TP82572	<nnxnp>	12	NA	71.42	637.755	NA	NA
TP69958	<nnxnp>	12	NA	72.159	545.449	6	59130009
X143	<nnxnp>	12	NA	73.087	682.836	6	60362521
TP61219	<nnxnp>	12	NA	74.097	654.59	6	60640621
TP27167	<nnxnp>	12	NA	75.104	724.595	NA	NA

Table A3 (cont.)

TP94336	<nnxnp>	12	NA	75.639	689.311	NA	NA
TP49992	<nnxnp>	12	NA	76.71	681.266	6	61348092
TP9605	<nnxnp>	12	NA	77.853	673.607	9	1286945
TP59203	<nnxnp>	12	NA	78.869	705.282	6	61375384
X544	<nnxnp>	12	NA	79.734	NA	6	62202181
TP2989	<nnxnp>	12	NA	80.361	732.44	6	60796725
TP122129	<nnxnp>	12	NA	81.411	664.115	6	60826678
TP82188	<nnxnp>	12	NA	82.374	697.183	6	61376055
TP44805	<nnxnp>	12	NA	83.894	715.232	1	8610381
TP34967	<nnxnp>	13	NA	0	17.565	NA	NA
TP76549	<nnxnp>	13	NA	2.2	11.237	7	70546
TP27014	<nnxnp>	13	NA	3.513	13.628	7	414414
TP64814	<nnxnp>	13	NA	4.648	0	5	60343266
TP68078	<nnxnp>	13	NA	6.211	7.441	NA	NA
TP68826	<nnxnp>	13	NA	6.644	22.138	NA	NA
TP64574	<hkxhk>	13	1.025	6.94	29.347	7	1606816
TP61741	<nnxnp>	13	NA	7.753	26.184	7	876783
TP29217	<hkxhk>	13	3.551	8.083	5.61	7	1941761
TP46769	<nnxnp>	13	NA	9.136	36.021	NA	NA
TP76505	<hkxhk>	13	4.923	9.696	56.868	NA	NA
TP56632	<nnxnp>	13	NA	10.105	44.164	7	2383749
TP86037	<hkxhk>	13	7.538	10.764	62.446	NA	NA
TP13644	<hkxhk>	13	6.063	11.773	53.417	7	2176636
TP43187	<nnxnp>	13	NA	12.72	78.35	7	2944810
TP65036	<hkxhk>	13	12.331	13.757	83.737	7	2916760
TP70187	<nnxnp>	13	NA	14.267	91.317	7	3903730
TP31709	<hkxhk>	13	9.89	14.701	69.025	NA	NA
TP47980	<hkxhk>	13	11.041	15.609	74.002	NA	NA
TP81065	<nnxnp>	13	NA	16.007	97.391	7	4384285
TP74335	<nnxnp>	13	NA	17.173	135.571	7	5342557
TP79169	<hkxhk>	13	14.72	18.015	102.465	NA	NA
TP113336	<nnxnp>	13	NA	19.001	113.204	10	57993353
TP119976	<nnxnp>	13	NA	19.583	121.743	7	5243624
TP16077	<nnxnp>	13	NA	20.839	187.641	7	6561765
TP53038	<nnxnp>	13	NA	21.697	150.198	7	6522248
TP32428	<hkxhk>	13	18.79	22.12	164.473	7	6002703
TP53314	<nnxnp>	13	NA	22.496	168.778	NA	NA
TP42478	<hkxhk>	13	19.737	23.007	173.3	NA	NA
TP110893	<nnxnp>	13	NA	23.239	160.59	NA	NA

Table A3 (cont.)

TP105160	<nnxnp>	13	NA	23.693	156.978	NA	NA
TP40257	<hkxhk>	13	21.07	24.294	266.42	7	8773064
TP53238	<nnxnp>	13	NA	24.681	260.378	NA	NA
TP82626	<nnxnp>	13	NA	25.169	280.361	7	6736332
TP28405	<hkxhk>	13	22.263	25.696	284.446	1	7182894
TP76647	<nnxnp>	13	NA	26.298	331.442	NA	NA
TP15118	<hkxhk>	13	24.153	26.532	276.871	7	47495693
TP25823	<nnxnp>	13	NA	26.899	264.879	7	8553945
TP54144	<hkxhk>	13	23.595	27.2	296.177	7	50325541
TP98910	<nnxnp>	13	NA	27.473	255.511	7	16070341
X247	<hkxhk>	13	26.82	27.801	232.86	3	55633219
TP42643	<nnxnp>	13	NA	28.048	343.338	NA	NA
TP86365	<hkxhk>	13	24.793	28.225	212.083	1	4714648
TP93012	<nnxnp>	13	NA	28.448	252.448	7	52984043
TP68246	<nnxnp>	13	NA	28.77	303.73	7	12583430
TP91267	<hkxhk>	13	26.658	28.995	326.095	NA	NA
TP6420	<nnxnp>	13	NA	29.198	271.23	NA	NA
TP57018	<nnxnp>	13	NA	29.486	248.156	1	6365439
TP2921	<hkxhk>	13	27.251	29.641	345.271	7	51832244
X105	<nnxnp>	13	NA	29.81	341.8	7	13309964
TP70526	<nnxnp>	13	NA	30.033	319.118	NA	NA
TP118867	<nnxnp>	13	NA	30.328	237.198	NA	NA
TP20105	<hkxhk>	13	25.945	30.627	225.59	2	49726103
TP2657	<nnxnp>	13	NA	30.906	242.331	NA	NA
TP121344	<nnxnp>	13	NA	31.269	217.531	NA	NA
TP70769	<nnxnp>	13	NA	31.788	205.059	7	8897161
TP108695	<hkxhk>	13	29.247	32.319	337.787	NA	NA
TP56343	<nnxnp>	13	NA	32.853	311.938	7	52989403
TP86046	<nnxnp>	13	NA	33.294	230.422	7	55221435
TP122052	<nnxnp>	13	NA	33.811	350.776	NA	NA
TP38626	<hkxhk>	13	31.315	34.322	360.04	7	57078563
TP109592	<nnxnp>	13	NA	35.618	387.601	NA	NA
TP46338	<hkxhk>	13	33.446	36.106	371.013	NA	NA
TP77993	<nnxnp>	13	NA	36.763	382.077	7	56695739
TP93689	<hkxhk>	13	32.738	37.026	379.014	7	57363399
TP42765	<nnxnp>	13	NA	37.863	375.473	1	7995736
TP7088	<hkxhk>	13	36.557	38.698	401.527	NA	NA
TP38016	<hkxhk>	13	37.071	39.662	412.458	7	57616600
TP102006	<nnxnp>	13	NA	40.155	366.804	7	57180956

Table A3 (cont.)

TP11306	<hkxhk>	13	35.491	40.8	433.256	7	58025243
TP123568	<nnxnp>	13	NA	41.505	395.166	7	57833578
TP97150	<hkxhk>	13	39.459	42.056	443.026	NA	NA
TP6879	<nnxnp>	13	NA	42.414	436.85	7	58029870
TP61657	<hkxhk>	13	38.341	42.792	451.01	7	58185257
TP43603	<nnxnp>	13	NA	43.081	398.447	7	57565604
TP87992	<hkxhk>	13	40.42	43.667	461.875	7	58591793
TP15689	<nnxnp>	13	NA	44.236	426.502	7	57963043
TP48416	<nnxnp>	13	NA	45.771	419.243	NA	NA
TP12853	<hkxhk>	13	45.107	48.381	487.418	7	60960931
TP11556	<hkxhk>	13	46.14	49.749	509.017	7	61305036
TP57728	<hkxhk>	13	50.327	51.135	501.247	7	61545104
TP10570	<hkxhk>	13	48.874	52.307	494.326	NA	NA
TP53689	<hkxhk>	13	47.48	53.712	515.881	7	61309247
TP69297	<nnxnp>	13	NA	55.558	525.59	7	61895323
TP55497	<nnxnp>	13	NA	57.42	531.304	10	56724800
TP97249	<hkxhk>	13	62.053	59.372	539.828	7	61790781
TP96074	<hkxhk>	13	56.609	60.378	564.517	7	62428311
TP30300	<nnxnp>	13	NA	61.642	570.904	7	62317994
TP119538	<hkxhk>	13	60.819	64.001	576.764	1	3094360
TP10437	<nnxnp>	13	NA	64.917	605.518	7	63010797
TP8378	<nnxnp>	13	NA	66.24	611.628	7	63010784
TP80556	<nnxnp>	13	NA	67.291	598.996	7	62993468
TP29362	<nnxnp>	13	NA	68.651	591.965	7	63027912
TP50035	<nnxnp>	13	NA	70.381	585.625	4	50093825
TP113611	<nnxnp>	13	NA	74.457	622.737	NA	NA
TP18081	<nnxnp>	13	NA	76.578	634.289	7	64247605
TP72333	<nnxnp>	13	NA	78.37	642.749	7	64137657
TP80160	<nnxnp>	13	NA	80.72	651.992	7	64186425
TP45746	<nnxnp>	14	NA	0	0	4	60983457
TP20129	<hkxhk>	14	72.665	2.532	22.079	3	71533048
TP97713	<nnxnp>	14	NA	4.55	15.324	NA	NA
TP56547	<hkxhk>	14	68.779	6.1	29.985	8	2032782
TP39889	<nnxnp>	14	NA	6.533	8.368	8	670304
TP76969	<hkxhk>	14	66.595	8.266	35.483	2	55331424
TP21854	<hkxhk>	14	63.155	10.28	49.401	8	1813252
TP15759	<hkxhk>	14	64.827	11.993	42.219	3	10685810
TP66266	<nnxnp>	14	NA	13.632	75.855	8	2265583
TP18220	<nnxnp>	14	NA	15.543	62.254	8	2727713

Table A3 (cont.)

TP60126	<hkxhk>	14	59.439	16.208	71.254	8	2448029
TP64052	<nnxnp>	14	NA	17.881	80.864	NA	NA
TP35057	<hkxhk>	14	57.586	18.288	82.786	8	2949637
TP67750	<nnxnp>	14	NA	21.845	93.815	8	3948796
TP61300	<hkxhk>	14	52.638	23.822	102.667	NA	NA
TP33900	<nnxnp>	14	NA	24.944	111.587	NA	NA
TP5818	<nnxnp>	14	NA	26.117	124.127	8	4757429
TP122550	<nnxnp>	14	NA	27.722	139.708	NA	NA
TP118350	<hkxhk>	14	48.922	28.424	133.6	8	5400283
TP7221	<hkxhk>	14	45.973	31.767	165.696	8	10833493
TP100798	<nnxnp>	14	NA	33.483	156.858	8	11550529
TP34580	<hkxhk>	14	41.429	33.675	175.528	8	26173910
TP13380	<nnxnp>	14	NA	34.581	170.355	8	12088752
TP9856	<hkxhk>	14	43.795	35.059	180.141	NA	NA
TP8536	<nnxnp>	14	NA	35.969	185.583	NA	NA
TP41144	<hkxhk>	14	40.458	36.038	150.527	NA	NA
TP52972	<nnxnp>	14	NA	36.888	161.107	8	11923823
TP34422	<nnxnp>	14	NA	37.976	191.105	8	39559035
TP34899	<nnxnp>	14	NA	39.201	195.278	NA	NA
TP49685	<hkxhk>	14	41.627	39.352	213.308	8	45698239
TP33486	<nnxnp>	14	NA	40.529	199.458	NA	NA
TP50855	<hkxhk>	14	37.546	41.478	227.705	NA	NA
TP37595	<nnxnp>	14	NA	42.567	205.942	NA	NA
TP57910	<hkxhk>	14	36.395	42.927	220.433	2	59703001
TP46009	<hkxhk>	14	31.896	46.004	261.17	8	49958931
TP41567	<nnxnp>	14	NA	47.279	243.477	NA	NA
TP64289	<hkxhk>	14	30.292	47.849	269.5	NA	NA
TP61623	<nnxnp>	14	NA	48.419	256.833	NA	NA
X131	<nnxnp>	14	NA	48.473	262.616	NA	NA
TP69707	<hkxhk>	14	32.695	49.109	276.353	8	50219719
TP70263	<nnxnp>	14	NA	52.357	300.546	NA	NA
TP10259	<nnxnp>	14	NA	53.45	295.223	NA	NA
TP1578	<nnxnp>	14	NA	54.65	287.901	8	50735258
TP95029	<nnxnp>	14	NA	56.466	321.781	8	51726492
TP3273	<nnxnp>	14	NA	57.958	309.889	8	51453000
TP84970	<nnxnp>	14	NA	61.422	334.268	NA	NA
TP85796	<hkxhk>	14	13.352	63.941	356.219	8	54041821
TP62090	<nnxnp>	14	NA	66.224	387.905	8	53865158
TP119793	<hkxhk>	14	9.765	67.445	362.847	8	54039067

Table A3 (cont.)

X506	<hkxhk>	14	11.477	68.07	346.674	8	54748793
TP61938	<nnxnp>	14	NA	69.612	401.456	NA	NA
TP41673	<hkxhk>	14	2.297	71.455	379.007	NA	NA
TP39501	<nnxnp>	14	NA	72.891	370.048	NA	NA
TP29170	<hkxhk>	14	5.261	74.203	373.489	8	55100685
X50	<nnxnp>	15	NA	0	NA	8	33994953
TP10760	<hkxhk>	15	NA	2.975	NA	NA	NA
TP53279	<hkxhk>	15	NA	6.261	NA	2	60348397
TP88339	<hkxhk>	15	NA	7.339	NA	NA	NA
TP96669	<hkxhk>	15	NA	8.979	NA	8	47512649
TP59958	<hkxhk>	15	NA	10.053	NA	8	6500830
X104	<nnxnp>	15	NA	10.198	NA	8	7977535
TP90088	<hkxhk>	15	NA	15.505	NA	NA	NA
X592	<hkxhk>	15	NA	19.925	NA	8	7977658
TP20329	<hkxhk>	15	NA	22.16	NA	1	9191434
TP81898	<hkxhk>	15	NA	23.83	NA	2	3896337
TP24781	<nnxnp>	15	NA	32.971	NA	NA	NA
TP8261	<hkxhk>	15	NA	40.909	NA	NA	NA
TP101332	<hkxhk>	15	NA	45.529	NA	8	2260546
TP34214	<nnxnp>	16	NA	0	21.883	NA	NA
TP18674	<hkxhk>	16	0	0.415	24.918	1	387849
TP103620	<nnxnp>	16	NA	1.366	2.618	1	745302
TP88506	<hkxhk>	16	4.152	1.958	45.109	9	1239247
TP53071	<nnxnp>	16	NA	2.419	10.925	1	1205575
TP35570	<hkxhk>	16	5.578	2.731	17.301	1	1043810
TP42646	<hkxhk>	16	7.59	3.929	37.679	NA	NA
TP75189	<nnxnp>	16	NA	4.61	32.04	9	1209046
TP3679	<nnxnp>	16	NA	5.332	123.345	9	2243763
X331	<nnxnp>	16	NA	5.796	51.118	9	1318926
TP96200	<hkxhk>	16	6.75	5.814	51.121	9	914667
TP42787	<nnxnp>	16	NA	6.416	90.537	9	1817713
TP43552	<nnxnp>	16	NA	7.067	76.213	NA	NA
TP55638	<hkxhk>	16	9.42	7.582	116.986	9	2270700
TP36095	<nnxnp>	16	NA	7.958	177.485	4	66539072
TP35530	<hkxhk>	16	10.645	8.761	137.152	NA	NA
TP111881	<nnxnp>	16	NA	9.33	103.045	NA	NA
TP17504	<nnxnp>	16	NA	10.336	168.058	9	5579506
TP18412	<hkxhk>	16	14.142	10.931	129.638	9	3514642
TP54434	<nnxnp>	16	NA	11.306	61.502	9	2276008

Table A3 (cont.)

TP19702	<nnxnp>	16	NA	11.966	110.925	9	3059983
TP38151	<hkxhk>	16	16.028	12.173	147.05	NA	NA
TP15309	<hkxhk>	16	12.841	12.736	159.38	9	4283369
TP95474	<nnxnp>	16	NA	13.164	190.939	9	4603472
TP88846	<nnxnp>	16	NA	13.544	183.908	NA	NA
TP49260	<nnxnp>	16	NA	14.188	187.767	9	6110931
X532	<nnxnp>	16	NA	14.745	129.62	9	2669340
TP19091	<hkxhk>	16	18.106	14.944	172.186	1	70874401
TP86363	<nnxnp>	16	NA	16.28	206.017	9	8363949
TP86872	<nnxnp>	16	NA	16.871	224.172	NA	NA
TP97071	<hkxhk>	16	19.711	17.169	307.68	NA	NA
TP1904	<nnxnp>	16	NA	17.797	214.196	NA	NA
TP2282	<hkxhk>	16	20.856	18.28	196.08	3	17007273
TP119050	<nnxnp>	16	NA	18.662	237.426	9	44660535
TP52356	<hkxhk>	16	21.677	19.162	251.995	9	38365920
TP42251	<nnxnp>	16	NA	19.566	247.481	9	42931024
TP74629	<hkxhk>	16	23.917	19.955	219.185	9	7573704
TP70855	<nnxnp>	16	NA	20.448	229.928	8	5692545
TP44970	<hkxhk>	16	22.732	20.647	228.133	NA	NA
TP7399	<nnxnp>	16	NA	20.746	266.104	NA	NA
TP100338	<nnxnp>	16	NA	21.052	273.435	9	44512446
TP81428	<hkxhk>	16	23.43	21.273	259.195	NA	NA
TP41687	<nnxnp>	16	NA	21.459	233.722	9	42899418
TP106160	<nnxnp>	16	NA	21.743	232.17	9	42427925
TP672	<hkxhk>	16	24.599	21.985	270.393	NA	NA
TP46238	<nnxnp>	16	NA	22.102	281.311	NA	NA
TP26555	<hkxhk>	16	25.006	22.43	242.706	9	49745201
TP61423	<nnxnp>	16	NA	23.008	277.552	9	43012236
TP120187	<hkxhk>	16	25.798	23.244	299.377	9	41348886
TP47576	<hkxhk>	16	26.356	23.863	313.971	9	47146884
TP118026	<nnxnp>	16	NA	24.162	323.912	NA	NA
TP69053	<hkxhk>	16	27.006	24.478	318.511	NA	NA
TP15723	<nnxnp>	16	NA	24.761	328.211	9	49065825
TP124819	<hkxhk>	16	27.64	25.235	285.672	NA	NA
TP46365	<nnxnp>	16	NA	25.653	330.504	9	49017649
TP90537	<hkxhk>	16	28.367	26.101	294.671	NA	NA
TP111661	<nnxnp>	16	NA	26.476	350.996	9	50216838
TP12366	<hkxhk>	16	29.356	26.948	335.488	NA	NA
TP74980	<hkxhk>	16	30.427	27.813	345.64	9	50217466

Table A3 (cont.)

TP114286	<nnxnp>	16	NA	28.565	358.823	9	51266919
TP10597	<hkxhk>	16	32.005	29.545	375.186	NA	NA
X496	<nnxnp>	16	NA	29.696	NA	9	50807789
X329	<nnxnp>	16	NA	30.235	374.719	9	52399520
X220	<hkxhk>	16	39.43	30.265	406.921	9	53272693
TP38195	<hkxhk>	16	36.893	30.939	365.022	9	51684423
TP107949	<nnxnp>	16	NA	31.062	419.722	NA	NA
TP26929	<hkxhk>	16	33.926	31.417	383.184	9	51838231
TP9705	<nnxnp>	16	NA	31.931	445.094	9	52117758
TP96260	<hkxhk>	16	35.831	32.149	432.109	9	51967286
TP30420	<hkxhk>	16	34.517	32.56	392.035	NA	NA
TP6551	<hkxhk>	16	35.18	32.98	398.055	NA	NA
TP71736	<nnxnp>	16	NA	33.411	402.331	9	52884124
TP57724	<hkxhk>	16	33.294	33.802	441.309	NA	NA
TP27994	<nnxnp>	16	NA	34.934	451.487	NA	NA
TP16445	<hkxhk>	16	38.585	35.268	414.875	9	53455999
TP72496	<hkxhk>	16	37.529	36.209	424.694	9	52586435
TP61859	<nnxnp>	16	NA	37.12	409.809	NA	NA
TP102848	<hkxhk>	16	41.294	38.91	492.345	9	53907108
TP40913	<nnxnp>	16	NA	39.461	502.367	9	55371528
TP37957	<nnxnp>	16	NA	40.482	459.915	9	54460210
TP66522	<hkxhk>	16	42.66	40.847	483.247	NA	NA
TP53291	<nnxnp>	16	NA	41.335	467.931	NA	NA
TP14298	<nnxnp>	16	NA	42.025	508.827	NA	NA
X177	<nnxnp>	16	NA	42.617	528.858	10	48867712
TP69923	<hkxhk>	16	44.737	42.708	512.674	9	55739481
TP58709	<nnxnp>	16	NA	43.064	522.888	NA	NA
TP108242	<nnxnp>	16	NA	43.837	516.738	9	55718119
TP4306	<nnxnp>	16	NA	44.649	463.342	9	54555904
TP75538	<nnxnp>	16	NA	45.667	472.793	NA	NA
TP91748	<nnxnp>	16	NA	46.978	478.788	9	56302935
TP3788	<hkxhk>	16	53.274	47.813	566.362	9	56794418
TP85654	<hkxhk>	16	50.935	49.557	549.666	9	57073290
TP41324	<hkxhk>	16	52.223	51.099	544.11	9	57219101
TP122635	<nnxnp>	16	NA	51.763	573.065	NA	NA
TP93130	<hkxhk>	16	57.494	53.185	617.368	9	57219737
TP53893	<nnxnp>	16	NA	53.676	621.69	9	57060035
TP87005	<nnxnp>	16	NA	54.374	577.516	NA	NA
TP32624	<hkxhk>	16	56.211	55.218	581.469	NA	NA

Table A3 (cont.)

TP25610	<hkxhk>	16	58.732	56.879	608.791	9	57503377
TP119266	<nnxnp>	16	NA	57.953	626.483	9	57510698
TP3065	<hkxhk>	16	61.382	58.588	592.404	9	57812548
TP100123	<nnxnp>	16	NA	59.734	631.098	9	57701498
TP68828	<nnxnp>	16	NA	60.996	638.297	9	57513995
X37	<nnxnp>	16	NA	64.008	645.818	9	59196167
TP50616	<nnxnp>	16	NA	64.827	651.052	9	8552668
TP51204	<nnxnp>	16	NA	68.956	661.46	NA	NA
TP99661	<hkxhk>	17	78.326	0	0	9	658466
TP67776	<nnxnp>	17	NA	3.18	20.088	NA	NA
TP30962	<hkxhk>	17	71.577	4.018	9.352	9	1043306
TP78989	<nnxnp>	17	NA	4.623	14.447	9	1207699
TP67613	<nnxnp>	17	NA	5.848	41.484	NA	NA
X582	<hkxhk>	17	NA	6.093	NA	NA	NA
X497	<hkxhk>	17	70.329	6.368	16.708	NA	NA
TP101209	<nnxnp>	17	NA	6.877	51.263	NA	NA
TP40139	<nnxnp>	17	NA	7.539	46.308	NA	NA
TP39402	<nnxnp>	17	NA	8.006	70.486	NA	NA
TP28040	<nnxnp>	17	NA	8.841	30.325	9	2255894
TP18813	<nnxnp>	17	NA	9.52	33.36	9	2159080
TP45641	<nnxnp>	17	NA	9.938	36.396	9	2159005
TP96640	<hkxhk>	17	67.369	10.526	60.117	9	2164551
TP3848	<nnxnp>	17	NA	11.096	26.482	NA	NA
TP45974	<nnxnp>	17	NA	11.686	64.061	9	2563980
TP114037	<nnxnp>	17	NA	12.405	75.714	9	2731807
TP89806	<nnxnp>	17	NA	12.747	97.725	9	3204814
TP69952	<hkxhk>	17	73.923	13.28	54.709	NA	NA
TP11196	<nnxnp>	17	NA	13.611	86.591	NA	NA
TP6828	<nnxnp>	17	NA	14.299	79.994	9	3231326
TP40595	<nnxnp>	17	NA	14.879	114.368	9	4430603
TP68065	<nnxnp>	17	NA	15.45	123.522	3	56257307
TP16986	<nnxnp>	17	NA	15.937	101.73	10	57968661
TP38418	<nnxnp>	17	NA	16.624	105.242	NA	NA
TP88471	<nnxnp>	17	NA	17.218	132.227	NA	NA
TP100897	<nnxnp>	17	NA	17.841	143.762	3	57351354
TP31197	<nnxnp>	17	NA	18.177	138.975	NA	NA
TP45030	<nnxnp>	17	NA	18.605	92.699	NA	NA
TP17723	<nnxnp>	17	NA	18.836	135.59	9	4354083
TP103539	<nnxnp>	17	NA	18.996	128.728	9	4170278

Table A3 (cont.)

TP108065	<nnxnp>	17	NA	19.483	118.861	10	48880673
TP74982	<nnxnp>	17	NA	19.952	109.082	NA	NA
TP38325	<nnxnp>	17	NA	20.606	148.267	NA	NA
TP51871	<nnxnp>	17	NA	21.136	156.582	7	7722240
TP34362	<nnxnp>	17	NA	21.761	163.358	NA	NA
TP64277	<nnxnp>	17	NA	22.064	160.342	NA	NA
TP94702	<nnxnp>	17	NA	22.383	151.28	NA	NA
X174	<nnxnp>	17	NA	22.614	164.444	4	60492701
TP29815	<nnxnp>	17	NA	22.801	153.81	9	5321312
TP111794	<nnxnp>	17	NA	23.141	166.582	NA	NA
TP15427	<nnxnp>	17	NA	23.294	168.867	9	5912416
TP108892	<nnxnp>	17	NA	23.678	222.48	NA	NA
TP13591	<nnxnp>	17	NA	23.994	214.402	NA	NA
TP103797	<nnxnp>	17	NA	24.457	178.67	9	14743761
TP53020	<nnxnp>	17	NA	24.705	209.349	NA	NA
TP13817	<nnxnp>	17	NA	25.01	205.677	NA	NA
TP91451	<nnxnp>	17	NA	25.177	203.31	9	7599165
TP55296	<nnxnp>	17	NA	25.367	218.627	9	6804654
TP52355	<nnxnp>	17	NA	25.658	171.876	NA	NA
TP58222	<nnxnp>	17	NA	25.961	175.008	NA	NA
TP33917	<nnxnp>	17	NA	26.267	281.289	9	11977261
TP30368	<nnxnp>	17	NA	26.659	226.472	9	48924906
TP46355	<nnxnp>	17	NA	26.802	198.715	9	49017700
TP61630	<nnxnp>	17	NA	26.931	279.324	2	58198442
TP123692	<nnxnp>	17	NA	27.068	246.153	9	49652048
TP42150	<nnxnp>	17	NA	27.461	239.295	NA	NA
TP115159	<nnxnp>	17	NA	27.584	241.585	1	149851
X327	<nnxnp>	17	NA	27.658	197.441	9	48738773
TP63420	<nnxnp>	17	NA	27.964	200.896	9	46424340
TP57303	<nnxnp>	17	NA	28.231	235.424	9	48534176
TP10889	<nnxnp>	17	NA	28.538	243.869	NA	NA
TP25673	<nnxnp>	17	NA	28.861	260.371	9	45848268
TP25659	<nnxnp>	17	NA	29.212	248.201	NA	NA
TP103701	<nnxnp>	17	NA	29.567	256.941	NA	NA
TP29513	<nnxnp>	17	NA	29.941	289.513	9	42985136
TP47726	<nnxnp>	17	NA	30.436	294.035	NA	NA
TP109531	<nnxnp>	17	NA	30.729	284.963	9	46496892
TP31253	<nnxnp>	17	NA	31.076	275.666	9	47301242
TP36261	<nnxnp>	17	NA	31.418	195.421	6	17502504

Table A3 (cont.)

TP70300	<nnxnp>	17	NA	31.807	183.158	NA	NA
TP59361	<nnxnp>	17	NA	32.177	299.602	NA	NA
TP39763	<nnxnp>	17	NA	32.67	230.897	9	49854438
TP39527	<nnxnp>	17	NA	33.3	264.517	9	50298933
TP100805	<nnxnp>	17	NA	33.543	189.669	9	6679118
TP40548	<nnxnp>	17	NA	34.195	252.168	NA	NA
TP85033	<nnxnp>	17	NA	34.757	305.039	NA	NA
TP6091	<hkxhk>	17	57.896	35.565	317.803	9	51371121
TP57286	<nnxnp>	17	NA	36.15	269.025	NA	NA
TP121332	<hkxhk>	17	56.437	37.195	330.494	9	51747518
TP66282	<nnxnp>	17	NA	37.779	311.366	1	13524858
TP57965	<hkxhk>	17	54.789	38.935	340.005	3	73615662
TP2671	<nnxnp>	17	NA	39.612	324.622	9	51704052
TP121176	<hkxhk>	17	52.27	40.398	361.885	NA	NA
TP2708	<hkxhk>	17	51.418	41.261	366.94	NA	NA
TP13568	<nnxnp>	17	NA	41.562	379.492	NA	NA
TP97982	<hkxhk>	17	50.514	42.207	372.234	NA	NA
TP85570	<hkxhk>	17	53.935	43.032	355.684	9	53105682
TP33899	<nnxnp>	17	NA	43.749	386.247	9	53298140
TP81552	<nnxnp>	17	NA	44.941	404.179	NA	NA
TP51988	<hkxhk>	17	47.724	45.623	399.525	NA	NA
TP82684	<nnxnp>	17	NA	46.064	392.19	NA	NA
TP69211	<hkxhk>	17	46.839	46.629	411.327	9	53971562
X635	<hkxhk>	17	48.611	47.413	381.469	9	53798708
TP111832	<hkxhk>	17	45.511	48.223	417.515	NA	NA
TP45656	<nnxnp>	17	NA	48.589	407.912	9	53821719
TP101384	<hkxhk>	17	44.539	49.45	441.782	NA	NA
TP122710	<hkxhk>	17	42.895	51.265	432.488	NA	NA
TP98285	<nnxnp>	17	NA	51.864	451.28	9	54928659
TP77149	<hkxhk>	17	41.378	52.332	425.529	9	54763630
TP65423	<hkxhk>	17	37.72	55.102	462.126	9	55390114
TP62130	<hkxhk>	17	37.032	57.134	471.516	9	55433298
TP67020	<hkxhk>	17	31.133	59.617	485.233	9	56329578
TP112104	<nnxnp>	17	NA	61.235	502.039	NA	NA
TP118562	<nnxnp>	17	NA	63.221	512.882	9	57055831
TP115051	<nnxnp>	17	NA	65.134	528.348	2	58685399
TP60890	<nnxnp>	17	NA	66.899	521.856	9	57166978
TP50400	<hkxhk>	17	11.925	73.753	557.426	NA	NA
TP69648	<nnxnp>	17	NA	75.832	561.472	9	58704139

Table A3 (cont.)

TP59137	<hkxhk>	17	14.954	77.831	548.809	NA	NA
TP62064	<nnxnp>	17	NA	78.96	566.396	9	59474160
TP103369	<nnxnp>	17	NA	81.093	574.662	NA	NA
TP37677	<hkxhk>	17	6.257	83.487	569.123	NA	NA
X92	<hkxhk>	18	4.937	0	30.359	10	658457
TP116668	<nnxnp>	18	NA	2.329	24.002	10	371537
TP31396	<hkxhk>	18	8.326	3.341	74.953	NA	NA
TP58130	<hkxhk>	18	11.77	6.118	65.035	10	1677080
TP19199	<hkxhk>	18	13.062	7.6	47.663	10	1608530
TP56078	<hkxhk>	18	16.336	10.162	83.43	NA	NA
TP36939	<hkxhk>	18	18	11.603	88.481	10	2179121
TP110894	<hkxhk>	18	15.216	13.289	96.854	NA	NA
TP108791	<hkxhk>	18	19.937	14.694	103.191	10	2538269
TP31388	<hkxhk>	18	23.423	16.992	121.26	NA	NA
TP37729	<hkxhk>	18	22.31	18.191	109.338	NA	NA
TP108478	<hkxhk>	18	25.489	19.84	127.672	10	3134937
TP68808	<hkxhk>	18	27.058	21.668	141.891	10	3593270
TP3109	<nnxnp>	18	NA	22.47	356.942	10	7528842
TP57706	<hkxhk>	18	29.195	23.714	160.29	10	4445426
TP53003	<nnxnp>	18	NA	24.837	168.62	10	4671514
TP17189	<hkxhk>	18	30.744	25.404	151.393	10	4907492
TP103441	<nnxnp>	18	NA	25.916	172.038	NA	NA
TP21167	<hkxhk>	18	32.591	26.938	164.995	NA	NA
TP60952	<nnxnp>	18	NA	28.199	219.51	10	14347689
TP71770	<nnxnp>	18	NA	29.084	175.222	10	5941593
TP45119	<nnxnp>	18	NA	29.619	178.949	10	6913053
TP16422	<nnxnp>	18	NA	30.156	341.292	NA	NA
TP26770	<hkxhk>	18	36.321	30.601	182.149	NA	NA
TP50484	<nnxnp>	18	NA	31.202	241.812	10	7157413
TP33039	<nnxnp>	18	NA	31.815	373.227	NA	NA
TP50539	<nnxnp>	18	NA	32.411	253.557	10	7004844
TP42891	<nnxnp>	18	NA	32.918	201.729	NA	NA
TP20258	<nnxnp>	18	NA	33.287	192.887	NA	NA
TP91842	<hkxhk>	18	41.187	33.537	264.518	10	9605996
TP31013	<nnxnp>	18	NA	33.928	334.779	2	67783807
TP88715	<nnxnp>	18	NA	34.297	277.501	10	8660371
TP105773	<hkxhk>	18	42.291	34.586	272.212	NA	NA
TP111846	<nnxnp>	18	NA	34.869	269.231	NA	NA
TP106222	<hkxhk>	18	39.73	35.331	379.541	10	10402647

Table A3 (cont.)

TP39442	<nnxnp>	18	NA	35.97	297.619	NA	NA
TP10850	<hkxhk>	18	43.31	36.407	288.601	10	11895318
TP24535	<nnxnp>	18	NA	36.722	386.435	1	52819331
X217	<nnxnp>	18	NA	36.884	388.179	10	20423246
TP20286	<hkxhk>	18	43.847	36.954	230.769	NA	NA
TP71717	<nnxnp>	18	NA	37.262	320.268	NA	NA
TP85797	<nnxnp>	18	NA	37.653	326.526	1	59599422
TP17631	<nnxnp>	18	NA	38.326	313.46	NA	NA
TP12644	<nnxnp>	18	NA	38.946	304.981	10	50151435
TP124712	<hkxhk>	18	55.294	39.682	391.54	10	51258208
TP21882	<nnxnp>	18	NA	40.023	421.16	NA	NA
TP12871	<nnxnp>	18	NA	41.234	453.351	NA	NA
TP119075	<nnxnp>	18	NA	41.591	393.798	NA	NA
TP55115	<hkxhk>	18	53.046	41.923	405.744	5	2629749
TP108666	<nnxnp>	18	NA	42.202	425.602	NA	NA
TP45803	<hkxhk>	18	47.607	42.583	447.163	10	52921788
TP80256	<nnxnp>	18	NA	43.077	430.043	NA	NA
TP48196	<hkxhk>	18	47.864	43.742	456.905	10	53557100
TP21374	<hkxhk>	18	49.146	44.224	441.138	10	52854169
TP6984	<nnxnp>	18	NA	44.792	399.236	NA	NA
TP61012	<hkxhk>	18	49.896	45.316	490.419	10	54749560
TP89052	<nnxnp>	18	NA	45.868	462.47	10	54701351
TP65457	<nnxnp>	18	NA	46.501	486	10	53999236
TP71800	<hkxhk>	18	52.01	46.887	497.413	10	55113396
TP26541	<nnxnp>	18	NA	47.482	468.179	NA	NA
TP7883	<hkxhk>	18	50.576	47.618	476.74	NA	NA
TP62326	<nnxnp>	18	NA	48.15	436.344	10	53189370
TP6831	<hkxhk>	18	54.715	48.843	416.05	10	51654068
TP10903	<nnxnp>	18	NA	49.392	519.203	NA	NA
TP99844	<nnxnp>	18	NA	50.81	507.083	10	54777605
TP84787	<nnxnp>	18	NA	52.973	528.674	10	56605555
TP13979	<nnxnp>	18	NA	54.393	537.204	10	56789694
TP54051	<nnxnp>	18	NA	55.537	548.281	NA	NA
TP122835	<nnxnp>	18	NA	56.548	542.892	10	56950156
TP62974	<hkxhk>	18	65.85	59.257	567.003	10	58077066
TP83276	<nnxnp>	18	NA	60.585	558.115	NA	NA
TP98147	<hkxhk>	18	67.694	61.911	615.276	10	58678111
TP41130	<nnxnp>	18	NA	62.516	623.909	10	58343075
TP62155	<nnxnp>	18	NA	63.833	606.365	10	58349975

Table A3 (cont.)

TP70587	<hkxhk>	18	63.761	65.12	576.884	3	3167377
TP12793	<nnxnp>	18	NA	66.235	585.209	NA	NA
TP29340	<nnxnp>	18	NA	70.283	595.307	10	58538438
X341	<nnxnp>	18	NA	73.536	642.669	10	60084282
TP82465	<hkxhk>	18	75.983	74.005	647.713	10	60820028
TP86027	<nnxnp>	18	NA	76.252	637.454	10	60024282
TP8663	<nnxnp>	18	NA	80.692	657.23	10	60615682
TP115211	<nnxnp>	19	NA	0	167.999	NA	NA
TP118684	<nnxnp>	19	NA	4.961	185.053	10	69463
TP113436	<hkxhk>	19	74.414	5.809	156.279	10	1509464
TP17190	<nnxnp>	19	NA	6.27	179.83	NA	NA
TP742	<nnxnp>	19	NA	7.491	190.978	10	1116895
TP83172	<nnxnp>	19	NA	10.773	201.931	10	1694062
TP118281	<nnxnp>	19	NA	12.648	138.986	10	1862546
TP21720	<hkxhk>	19	69.262	13.142	16.756	NA	NA
TP86273	<nnxnp>	19	NA	15.425	211.75	NA	NA
TP94863	<nnxnp>	19	NA	17.674	114.565	10	2705982
TP3382	<nnxnp>	19	NA	18.307	91.398	NA	NA
TP1336	<hkxhk>	19	56.537	20.039	223.486	10	3209383
TP40500	<nnxnp>	19	NA	20.603	234.473	10	3176967
X311	<hkxhk>	19	53.431	21.249	227.202	10	3193258
TP69434	<nnxnp>	19	NA	22.681	282.97	10	4436408
TP64460	<nnxnp>	19	NA	24.428	40.219	10	5542551
TP120677	<nnxnp>	19	NA	25.182	51.81	NA	NA
TP74230	<nnxnp>	19	NA	25.801	69.201	NA	NA
TP13180	<nnxnp>	19	NA	26.455	247.102	10	4747461
TP96659	<hkxhk>	19	43.675	26.831	276.408	10	4748474
TP13181	<hkxhk>	19	47.387	27.136	250.226	8	746872
TP27112	<nnxnp>	19	NA	27.617	261.698	NA	NA
TP72258	<nnxnp>	19	NA	28.612	292.712	10	6190892
TP97327	<hkxhk>	19	NA	29.124	NA	10	5602181
X355	<nnxnp>	19	NA	29.274	NA	10	5972378
TP11385	<nnxnp>	19	NA	29.851	298.666	10	6205953
TP2966	<nnxnp>	19	NA	30.42	23.976	NA	NA
TP41313	<nnxnp>	19	NA	30.764	317.633	NA	NA
TP124221	<hkxhk>	19	NA	31.122	NA	10	5683628
TP44375	<nnxnp>	19	NA	31.501	327.516	NA	NA
TP9952	<hkxhk>	19	38.292	31.689	337.568	NA	NA
TP60258	<nnxnp>	19	NA	32.35	349.211	10	8024846

Table A3 (cont.)

TP49161	<nnxnp>	19	NA	32.976	0	10	8758439
X165	<nnxnp>	19	NA	33.484	341.024	10	7176784
TP42892	<nnxnp>	19	NA	33.884	304.877	10	7948412
TP43639	<hkxhk>	19	36.529	33.989	310.23	1	8378320
TP53150	<nnxnp>	19	NA	34.169	359.475	2	59780017
TP123468	<hkxhk>	19	NA	34.567	NA	NA	NA
TP54776	<nnxnp>	19	NA	35.015	367.078	10	8758106
TP55504	<nnxnp>	19	NA	35.343	13.327	10	8959092
TP103764	<hkxhk>	19	NA	35.436	NA	10	6732701
TP966	<nnxnp>	19	NA	35.623	8.908	10	8741289
TP26072	<nnxnp>	19	NA	36.268	373.879	NA	NA
TP11432	<nnxnp>	19	NA	36.571	379.189	10	10086144
TP22888	<nnxnp>	19	NA	37.097	385.84	NA	NA
TP35386	<nnxnp>	19	NA	37.666	394.354	NA	NA
TP39432	<nnxnp>	19	NA	38.11	445.148	NA	NA
TP77370	<nnxnp>	19	NA	38.396	439.444	10	13835723
TP45204	<nnxnp>	19	NA	38.839	407.708	10	17949112
TP59844	<nnxnp>	19	NA	39.17	435.22	NA	NA
TP55679	<nnxnp>	19	NA	39.591	419.922	10	46065337
TP42352	<nnxnp>	19	NA	40.102	427.68	3	59562118
TP115052	<nnxnp>	19	NA	40.406	430.719	10	47940230
TP98914	<hkxhk>	19	28.897	40.574	414.472	8	30545127
TP92143	<nnxnp>	19	NA	40.815	423.954	NA	NA
TP113777	<nnxnp>	19	NA	41.202	401.523	NA	NA
X598	<nnxnp>	19	NA	41.483	432.615	NA	NA
TP104434	<nnxnp>	19	NA	41.825	505.027	NA	NA
TP113114	<nnxnp>	19	NA	42.124	476.012	NA	NA
TP30755	<nnxnp>	19	NA	42.742	480.048	10	50006194
TP97012	<hkxhk>	19	26.754	42.974	454.674	NA	NA
TP67385	<hkxhk>	19	31.99	43.232	502.031	10	50521165
TP13120	<nnxnp>	19	NA	43.636	498.544	NA	NA
TP110401	<nnxnp>	19	NA	44.202	484.078	1	3176653
TP32348	<hkxhk>	19	31.114	44.692	470.027	NA	NA
TP51996	<nnxnp>	19	NA	44.962	493.183	10	52241335
TP50353	<nnxnp>	19	NA	45.621	487.745	10	52007698
TP119574	<nnxnp>	19	NA	47.088	510.448	10	53323467
TP81771	<nnxnp>	19	NA	47.856	543.97	10	53742329
TP30808	<hkxhk>	19	23.102	48.807	516.705	10	52930679
TP89092	<nnxnp>	19	NA	49.518	531.817	NA	NA

Table A3 (cont.)

TP69065	<hkxhk>	19	19.268	50.073	551.773	10	54687633
TP100297	<nnxnp>	19	NA	50.904	558.698	NA	NA
TP58368	<nnxnp>	19	NA	51.518	563.698	NA	NA
TP39562	<nnxnp>	19	NA	51.973	554.711	NA	NA
TP64552	<nnxnp>	19	NA	52.367	572.352	10	55376838
TP86052	<nnxnp>	19	NA	53.248	567.893	10	55416227
TP39670	<nnxnp>	19	NA	53.635	579.444	NA	NA
TP95911	<nnxnp>	19	NA	54.198	581.591	10	55876423
TP49025	<nnxnp>	19	NA	54.971	576.546	NA	NA
TP45046	<nnxnp>	19	NA	55.852	589.437	10	56190966
TP19858	<nnxnp>	19	NA	56.56	611.38	10	56429831
TP48081	<nnxnp>	19	NA	56.905	600.533	10	56490706
TP90918	<nnxnp>	19	NA	57.466	608.675	NA	NA
TP92680	<nnxnp>	19	NA	58.068	585.9	NA	NA
TP109708	<nnxnp>	19	NA	58.509	596.861	6	55650820
TP12412	<nnxnp>	19	NA	59.034	593.043	10	56104503
TP93913	<nnxnp>	19	NA	59.87	604.473	10	56663437
TP70103	<nnxnp>	19	NA	60.907	614.76	NA	NA
TP15917	<nnxnp>	19	NA	61.559	628.163	10	57061514
TP30990	<nnxnp>	19	NA	62.599	619.391	10	57393184
TP99717	<hkxhk>	19	14.624	63.224	661.012	NA	NA
TP31433	<nnxnp>	19	NA	63.582	623.547	NA	NA
TP35539	<nnxnp>	19	NA	63.868	633.454	10	57294776
TP39598	<nnxnp>	19	NA	64.795	648.251	10	58025499
TP109360	<nnxnp>	19	NA	65.499	644.841	10	58015620
X86	<nnxnp>	19	NA	65.789	648.251	10	57906816
TP82440	<hkxhk>	19	12.194	66.508	666.833	10	58370618
TP87062	<nnxnp>	19	NA	67.102	638.979	10	57621860
TP981	<nnxnp>	19	NA	68.708	653.59	10	57771389
TP45006	<hkxhk>	19	9.442	70.174	677.335	NA	NA
TP53969	<nnxnp>	19	NA	72.545	671.136	10	58683827
TP63781	<hkxhk>	19	3.226	77.733	688.996	10	60079768
TP103857	<lmxll>	1	0	NA	124.255	1	7531646
TP53977	<lmxll>	1	1.395	NA	201.26	1	7608965
TP26698	<lmxll>	1	3.255	NA	148.606	1	6972841
TP94641	<lmxll>	1	5.99	NA	228.433	1	8027483
TP120250	<lmxll>	1	7.787	NA	136.311	1	7355092
TP30778	<lmxll>	1	9.451	NA	190.928	1	8373102
TP35558	<lmxll>	1	11.015	NA	218.876	NA	NA

Table A3 (cont.)

TP54160	<lmxll>	1	12.036	NA	211.2	1	8986497
TP91753	<lmxll>	1	13.035	NA	246.852	1	9113066
TP101395	<lmxll>	1	14.203	NA	262.219	NA	NA
TP56885	<lmxll>	1	17.064	NA	283.104	1	11028539
TP71906	<lmxll>	1	18.144	NA	289.211	NA	NA
TP96321	<lmxll>	1	19.413	NA	301.57	NA	NA
TP31922	<lmxll>	1	20.298	NA	296.967	1	11838724
TP48070	<lmxll>	1	21.681	NA	293.281	1	11673198
TP35916	<lmxll>	1	23.887	NA	315.378	1	12183348
X483	<lmxll>	1	24.515	NA	306.4	2	13073677
TP16433	<lmxll>	1	26.038	NA	329.323	2	69281722
TP117620	<lmxll>	1	27.641	NA	350.978	NA	NA
TP38519	<lmxll>	1	28.234	NA	346.722	NA	NA
TP21054	<lmxll>	1	28.917	NA	358.419	NA	NA
TP5484	<lmxll>	1	29.508	NA	363.558	NA	NA
TP108539	<lmxll>	1	30.532	NA	355.532	NA	NA
TP53028	<lmxll>	1	31.32	NA	374.672	1	14927017
TP107018	<lmxll>	1	32.088	NA	387.224	1	15187218
TP3604	<lmxll>	1	32.926	NA	396.964	NA	NA
TP118627	<lmxll>	1	33.407	NA	393.458	1	14999407
TP6624	<lmxll>	1	34.097	NA	467.564	1	17263707
TP77507	<lmxll>	1	34.807	NA	413.081	NA	NA
TP67762	<lmxll>	1	35.499	NA	578.486	NA	NA
TP52922	<lmxll>	1	35.783	NA	405.719	1	15858917
TP71674	<lmxll>	1	36.698	NA	426.802	1	16732425
TP69628	<lmxll>	1	37.338	NA	420.694	1	16470982
TP75226	<lmxll>	1	37.775	NA	447.701	NA	NA
TP4779	<lmxll>	1	38.224	NA	440.111	1	20084160
TP88485	<lmxll>	1	38.763	NA	565.415	1	46098137
TP34352	<lmxll>	1	39.458	NA	537.762	1	25514342
TP84960	<lmxll>	1	39.888	NA	552.437	1	23314965
TP84497	<lmxll>	1	40.173	NA	545.563	1	23162055
TP81503	<lmxll>	1	40.406	NA	590.42	NA	NA
TP86231	<lmxll>	1	40.671	NA	513.454	1	48783583
TP44744	<lmxll>	1	41.083	NA	520.238	1	20915723
TP5146	<lmxll>	1	41.298	NA	529.787	1	66934352
TP90809	<lmxll>	1	41.588	NA	460.087	1	22883568
TP58760	<lmxll>	1	41.886	NA	435.459	1	19340888
TP114602	<lmxll>	1	42.125	NA	604.345	NA	NA

Table A3 (cont.)

TP124685	<lmxll>	1	42.431	NA	493.02	1	50020560
TP110541	<lmxll>	1	42.756	NA	504.598	1	46097302
TP118174	<lmxll>	1	42.936	NA	673.545	NA	NA
TP95794	<lmxll>	1	43.131	NA	508.206	NA	NA
TP111656	<lmxll>	1	43.347	NA	600.589	NA	NA
TP17794	<lmxll>	1	43.622	NA	596.662	NA	NA
TP81309	<lmxll>	1	43.784	NA	557.952	NA	NA
TP84114	<lmxll>	1	44.137	NA	667.421	1	44970403
TP78616	<lmxll>	1	44.335	NA	682.501	NA	NA
TP35721	<lmxll>	1	44.472	NA	678.173	1	51726812
TP109945	<lmxll>	1	44.72	NA	737.356	NA	NA
TP10933	<lmxll>	1	45.071	NA	610.03	NA	NA
TP45210	<lmxll>	1	45.406	NA	652.316	NA	NA
TP14337	<lmxll>	1	45.652	NA	656.786	NA	NA
TP109339	<lmxll>	1	45.894	NA	647.686	1	54776152
TP94875	<lmxll>	1	46.095	NA	496.456	1	51929402
TP9540	<lmxll>	1	46.335	NA	743.21	1	52576331
TP121314	<lmxll>	1	46.791	NA	487.974	6	27257943
TP23041	<lmxll>	1	47.133	NA	661.339	1	52408883
TP6050	<lmxll>	1	47.814	NA	747.305	1	56594186
TP75784	<lmxll>	1	48.071	NA	752.991	1	56873619
TP117866	<lmxll>	1	48.714	NA	631.149	1	53346683
TP28993	<lmxll>	1	49.319	NA	640.346	1	54947726
TP81969	<lmxll>	1	49.995	NA	691.16	2	71144835
TP27368	<lmxll>	1	50.415	NA	478.76	NA	NA
TP115333	<lmxll>	1	50.741	NA	703.915	NA	NA
TP30912	<lmxll>	1	51.436	NA	713.35	3	52021574
TP105246	<lmxll>	1	51.985	NA	759.168	NA	NA
TP47638	<lmxll>	1	52.618	NA	765.267	1	58100727
TP81829	<lmxll>	1	53.498	NA	620.134	1	52409383
TP50445	<lmxll>	1	55.272	NA	896.208	1	58792697
TP112157	<lmxll>	1	56.685	NA	910.564	1	58986671
TP13783	<lmxll>	1	57.357	NA	919.44	NA	NA
TP72090	<lmxll>	1	57.657	NA	879.341	8	3848486
TP1640	<lmxll>	1	58.66	NA	783.69	1	60218969
TP66483	<lmxll>	1	59.461	NA	930.02	5	58650064
TP81670	<lmxll>	1	60.237	NA	775.553	1	60553796
TP90907	<lmxll>	1	61.327	NA	801.166	1	61421743
TP22362	<lmxll>	1	62.309	NA	837.773	1	62307934

Table A3 (cont.)

TP1435	<lmxll>	1	62.729	NA	949.354	NA	NA
TP91194	<lmxll>	1	63.437	NA	816.161	NA	NA
X130	<lmxll>	1	63.652	NA	816.161	NA	NA
TP73053	<lmxll>	1	64.144	NA	810.119	1	62744611
TP31201	<lmxll>	1	64.85	NA	821.265	NA	NA
TP20624	<lmxll>	1	65.764	NA	826.203	NA	NA
TP33821	<lmxll>	1	67.339	NA	998.847	8	54004073
TP111190	<lmxll>	1	68.382	NA	992.241	1	63923626
TP59717	<lmxll>	1	68.958	NA	973.352	1	64581021
TP39310	<lmxll>	1	70.042	NA	1004.556	10	5872615
TP77763	<lmxll>	1	70.484	NA	985.864	1	65478530
X633	<lmxll>	1	71.355	NA	1023.557	NA	NA
TP123368	<lmxll>	1	72.598	NA	1033.696	NA	NA
TP65702	<lmxll>	1	73.216	NA	1047.573	1	65926362
TP65766	<lmxll>	1	74.434	NA	1061.266	6	42682912
TP117175	<lmxll>	1	75.524	NA	1071.883	NA	NA
TP8747	<lmxll>	1	76.32	NA	1084.14	NA	NA
TP36794	<lmxll>	1	77.57	NA	1123.446	1	67346690
TP31312	<lmxll>	1	78.975	NA	1128.902	1	67527666
TP112746	<lmxll>	1	79.889	NA	1133.798	1	67886423
TP97044	<lmxll>	1	80.576	NA	1147.594	1	68302235
TP33046	<lmxll>	1	81.526	NA	1151.814	NA	NA
TP10629	<lmxll>	1	82.329	NA	1140.159	1	68595655
TP24062	<lmxll>	1	83.397	NA	1157.086	NA	NA
TP5329	<lmxll>	1	85.202	NA	1193.448	1	69731658
TP63496	<lmxll>	1	87	NA	1169.273	NA	NA
TP31334	<lmxll>	1	87.79	NA	1198.605	1	69403368
X527	<lmxll>	1	89.353	NA	1189.906	1	70053618
TP124512	<lmxll>	1	90.303	NA	1210.093	1	70240407
TP9005	<lmxll>	1	91.097	NA	1213.095	1	70334249
TP27815	<lmxll>	1	93.643	NA	1249.885	NA	NA
TP68905	<lmxll>	1	97.218	NA	1260.827	1	71474930
TP57972	<lmxll>	1	98.546	NA	1286.074	NA	NA
TP41374	<lmxll>	1	100.07	NA	1303.042	NA	NA
TP52446	<lmxll>	1	101.146	NA	1267.451	9	2695325
TP81402	<lmxll>	1	102.859	NA	1276.65	NA	NA
TP52517	<lmxll>	1	105.121	NA	1316.581	1	72712299
TP79457	<lmxll>	1	106.893	NA	1321.024	1	72691148
TP117788	<lmxll>	1	110.915	NA	1329.699	NA	NA

Table A3 (cont.)

TP69756	<lmxll>	2	0	NA	117.815	1	13285069
TP40880	<lmxll>	2	2.209	NA	128.78	1	13123736
TP16432	<lmxll>	2	3.004	NA	132.88	NA	NA
TP43122	<lmxll>	2	3.993	NA	124.794	3	62464939
TP47627	<lmxll>	2	5.297	NA	110.392	1	13845578
TP67277	<lmxll>	2	6.728	NA	136.447	6	58870436
TP34149	<lmxll>	2	8.801	NA	141.799	6	61047700
TP22738	<lmxll>	2	10.405	NA	102.248	1	14409034
TP88821	<lmxll>	2	11.277	NA	96.754	NA	NA
TP94624	<lmxll>	2	12.207	NA	145.758	1	15317082
TP47619	<lmxll>	2	13.614	NA	87.851	NA	NA
TP121559	<lmxll>	2	15.157	NA	152.038	NA	NA
TP116764	<lmxll>	2	16.889	NA	59.078	1	17587459
TP109894	<lmxll>	2	18.493	NA	71.366	1	17656522
TP48427	<lmxll>	2	19.01	NA	66.95	NA	NA
TP17387	<lmxll>	2	20.281	NA	75.98	NA	NA
TP95914	<lmxll>	2	21.551	NA	160.063	1	17880205
TP98480	<lmxll>	2	24.961	NA	171.162	1	19181816
TP74397	<lmxll>	2	27.131	NA	194.788	NA	NA
TP111288	<lmxll>	2	29.237	NA	180.352	1	20264678
TP37753	<lmxll>	2	30.059	NA	210.701	NA	NA
TP9927	<lmxll>	2	30.626	NA	176.462	1	20264617
TP25649	<lmxll>	2	31.169	NA	201.712	NA	NA
TP43660	<lmxll>	2	31.718	NA	204.982	1	21198093
TP88780	<lmxll>	2	32.652	NA	207.014	2	12226935
TP122148	<lmxll>	2	33.381	NA	216.514	1	21499816
TP110454	<lmxll>	2	34.212	NA	222.24	1	23117867
TP104550	<lmxll>	2	35.009	NA	226.737	1	22320583
TP61150	<lmxll>	2	35.352	NA	288.116	1	30798907
TP74486	<lmxll>	2	36.271	NA	265.274	1	27863809
TP23222	<lmxll>	2	36.685	NA	296.404	1	47240989
TP57075	<lmxll>	2	37.089	NA	236.467	1	45788229
TP99526	<lmxll>	2	37.497	NA	238.992	NA	NA
TP99812	<lmxll>	2	37.737	NA	241.516	1	44086265
TP88296	<lmxll>	2	37.956	NA	263.063	NA	NA
TP82187	<lmxll>	2	38.252	NA	261.312	NA	NA
TP111657	<lmxll>	2	38.645	NA	243.816	NA	NA
TP44618	<lmxll>	2	39.059	NA	267.367	9	12725086
X665	<lmxll>	2	39.258	NA	230.691	1	49673720

Table A3 (cont.)

TP87142	<lmxll>	2	39.589	NA	270.109	1	72370333
TP46296	<lmxll>	2	39.981	NA	273.879	6	782035
TP23664	<lmxll>	2	40.305	NA	277.406	3	3252564
TP105602	<lmxll>	2	40.913	NA	232.673	1	27217045
TP121270	<lmxll>	2	41.697	NA	312.226	1	50556310
TP18236	<lmxll>	2	42.317	NA	252.081	NA	NA
TP101706	<lmxll>	2	42.816	NA	247.006	1	49904081
TP31308	<lmxll>	2	43.673	NA	301.991	1	53199880
TP52894	<lmxll>	2	43.955	NA	256.834	1	52576745
TP88731	<lmxll>	2	44.547	NA	318.031	NA	NA
TP14126	<lmxll>	2	45.517	NA	324.029	1	54538009
TP63249	<lmxll>	2	47.313	NA	335.366	3	2220060
TP124668	<lmxll>	2	47.873	NA	330.278	NA	NA
TP22176	<lmxll>	2	48.718	NA	338.913	1	55592449
TP47259	<lmxll>	2	49.829	NA	343.087	1	56665263
TP78832	<lmxll>	2	50.97	NA	349.74	1	56918887
X372	<lmxll>	2	51.092	NA	349.74	1	56428774
TP90914	<lmxll>	2	52.218	NA	354.812	1	57389445
TP36030	<lmxll>	2	53.233	NA	369.65	1	58027314
TP88370	<lmxll>	2	53.867	NA	360.757	1	57955729
TP48341	<lmxll>	2	54.586	NA	365.998	1	57990892
TP52252	<lmxll>	2	56.255	NA	389.447	NA	NA
TP57535	<lmxll>	2	57.376	NA	374.844	5	7504311
TP99553	<lmxll>	2	58.344	NA	396.493	1	59430705
TP117506	<lmxll>	2	60.361	NA	382.236	1	59933860
TP106425	<lmxll>	2	62.366	NA	404.743	1	60542228
TP11580	<lmxll>	2	64.556	NA	412.268	1	61977153
TP85751	<lmxll>	2	65.619	NA	416.347	1	61994058
X209	<lmxll>	2	66.163	NA	NA	2	77647679
X97	<lmxll>	2	66.163	NA	NA	1	64057697
TP51820	<lmxll>	2	66.567	NA	428.278	1	62494780
TP2972	<lmxll>	2	66.974	NA	419.443	1	61916881
TP115280	<lmxll>	2	67.288	NA	423.53	1	62708826
TP25271	<lmxll>	2	68.081	NA	433.35	1	72200509
TP73510	<lmxll>	2	69.13	NA	437.755	NA	NA
TP75659	<lmxll>	2	70.002	NA	446.387	NA	NA
TP20657	<lmxll>	2	70.73	NA	459.919	1	64574950
TP98620	<lmxll>	2	71.269	NA	441.499	NA	NA
TP32383	<lmxll>	2	71.749	NA	467.101	1	65049766

Table A3 (cont.)

TP28988	<lmxll>	2	72.519	NA	453.626	1	65045009
TP8164	<lmxll>	2	74.037	NA	493.703	1	66516158
TP122374	<lmxll>	2	74.509	NA	501.917	NA	NA
TP96859	<lmxll>	2	75.144	NA	487.226	1	65936250
TP114546	<lmxll>	2	75.691	NA	473.908	1	65927145
TP66207	<lmxll>	2	76.615	NA	479.832	NA	NA
TP77252	<lmxll>	2	77.66	NA	530.706	1	67503106
TP91109	<lmxll>	2	78.57	NA	510.236	1	66625057
TP50805	<lmxll>	2	79.723	NA	522.34	1	66860325
TP48132	<lmxll>	2	81.537	NA	633.339	1	70588334
TP73244	<lmxll>	2	82.282	NA	628.07	1	70577046
TP90728	<lmxll>	2	83.044	NA	647.761	NA	NA
TP36012	<lmxll>	2	84.094	NA	639.537	4	65325809
TP60786	<lmxll>	2	84.727	NA	618.125	1	71515731
TP80947	<lmxll>	2	85.238	NA	621.625	1	71483690
TP64327	<lmxll>	2	86.325	NA	541.71	1	71377497
TP66288	<lmxll>	2	87.066	NA	592.927	NA	NA
TP46231	<lmxll>	2	87.952	NA	606.36	1	71744866
TP52314	<lmxll>	2	88.658	NA	548.11	1	71665017
TP65804	<lmxll>	2	89.682	NA	554.912	1	72371470
TP73503	<lmxll>	2	90.312	NA	580.199	1	72201718
TP82936	<lmxll>	2	91.12	NA	598.791	1	71879823
TP51743	<lmxll>	2	91.934	NA	613.136	1	71566565
TP86013	<lmxll>	2	92.735	NA	659.034	1	71024485
TP50563	<lmxll>	2	93.603	NA	586.888	NA	NA
TP97785	<lmxll>	2	94.655	NA	566.867	1	72625633
TP45917	<lmxll>	2	95.973	NA	560.411	2	76245712
TP14576	<lmxll>	2	97.104	NA	572.927	1	73689894
TP36204	<lmxll>	3	0	NA	1015.905	2	76935192
TP7530	<lmxll>	3	3.34	NA	999.185	NA	NA
TP122938	<lmxll>	3	4.769	NA	1002.218	NA	NA
TP52458	<lmxll>	3	6.732	NA	1005.082	NA	NA
TP100718	<lmxll>	3	9.038	NA	984.6	2	76790781
TP56148	<lmxll>	3	12.895	NA	963.005	NA	NA
TP92730	<lmxll>	3	14.355	NA	978.486	NA	NA
TP14787	<lmxll>	3	20.544	NA	940.594	NA	NA
TP72732	<lmxll>	3	22.931	NA	933.221	2	74590164
TP121118	<lmxll>	3	24.211	NA	924.442	2	74756483
TP43551	<lmxll>	3	25.135	NA	901.177	2	74085056

Table A3 (cont.)

TP11199	<lmxll>	3	26.708	NA	907.869	2	74074648
TP81388	<lmxll>	3	27.823	NA	892.974	8	169409
TP86222	<lmxll>	3	29.177	NA	879.343	10	6133914
TP112543	<lmxll>	3	30.538	NA	886.15	NA	NA
TP44866	<lmxll>	3	33.372	NA	868.773	2	72898847
TP48516	<lmxll>	3	34.885	NA	802.292	2	69968228
TP27310	<lmxll>	3	35.798	NA	848.861	NA	NA
TP49019	<lmxll>	3	37.513	NA	858.692	NA	NA
TP70626	<lmxll>	3	38.667	NA	830.809	2	72331110
TP51948	<lmxll>	3	40.125	NA	839.216	NA	NA
X298	<lmxll>	3	41.647	NA	760.107	2	68775145
TP26813	<lmxll>	3	42.752	NA	773.448	2	69793589
TP39776	<lmxll>	3	44.648	NA	744.394	2	68512471
TP116438	<lmxll>	3	46.029	NA	731.528	2	68177003
TP54908	<lmxll>	3	47.191	NA	725.379	2	68053901
TP15916	<lmxll>	3	48.476	NA	643.79	NA	NA
TP73823	<lmxll>	3	51.974	NA	637.244	2	65727711
TP29153	<lmxll>	3	52.306	NA	635.945	2	65787307
TP122484	<lmxll>	3	53.081	NA	671.674	NA	NA
X347	<lmxll>	3	53.832	NA	618.609	NA	NA
TP60424	<lmxll>	3	54.312	NA	629.446	2	65184002
TP28838	<lmxll>	3	55.342	NA	621.759	2	65438431
TP85281	<lmxll>	3	56.282	NA	588.368	2	65280606
TP82680	<lmxll>	3	57.067	NA	581.967	2	64774563
TP44659	<lmxll>	3	57.975	NA	565.996	NA	NA
TP8778	<lmxll>	3	58.924	NA	558.278	2	63869140
TP105250	<lmxll>	3	60.979	NA	553.347	2	63540083
TP55711	<lmxll>	3	61.72	NA	526.258	NA	NA
TP18940	<lmxll>	3	62.843	NA	548.475	2	63095642
TP16434	<lmxll>	3	63.448	NA	511.396	NA	NA
TP61524	<lmxll>	3	64.232	NA	504.546	2	61763955
TP85988	<lmxll>	3	64.766	NA	475.505	2	62528965
TP27517	<lmxll>	3	65.133	NA	509.214	NA	NA
TP56882	<lmxll>	3	65.562	NA	470.671	2	61720711
TP94317	<lmxll>	3	65.857	NA	507.459	NA	NA
TP72003	<lmxll>	3	66.405	NA	464.715	2	61124296
TP65524	<lmxll>	3	66.976	NA	457.987	2	61076151
TP56019	<lmxll>	3	67.566	NA	445.689	2	61161317
TP32273	<lmxll>	3	68.328	NA	451.763	2	61090317

Table A3 (cont.)

TP47777	<lmxll>	3	69.316	NA	202.468	2	14536576
TP44003	<lmxll>	3	69.959	NA	291.802	NA	NA
TP111164	<lmxll>	3	70.365	NA	173.657	2	52055272
TP83123	<lmxll>	3	70.635	NA	429.627	2	56016155
TP28097	<lmxll>	3	70.858	NA	432.607	2	59036229
TP38847	<lmxll>	3	71.06	NA	399.606	2	18596552
X166	<lmxll>	3	71.065	NA	432.607	2	59003882
TP17530	<lmxll>	3	71.31	NA	380.442	2	55673069
TP20170	<lmxll>	3	71.369	NA	438.513	2	13666459
TP27791	<lmxll>	3	71.636	NA	310.911	2	47012680
TP40745	<lmxll>	3	71.931	NA	296.17	NA	NA
TP24530	<lmxll>	3	72.216	NA	303.285	2	58678618
TP90206	<lmxll>	3	72.616	NA	440.857	NA	NA
TP4816	<lmxll>	3	72.842	NA	157.352	2	13790264
TP63097	<lmxll>	3	73.368	NA	266.3	2	59800846
TP78010	<lmxll>	3	74.099	NA	273.109	2	57606530
X225	<lmxll>	3	74.275	NA	159.554	2	8732472
TP49378	<lmxll>	3	74.759	NA	151.935	3	69721149
TP113333	<lmxll>	3	75.092	NA	168.444	2	8155647
TP54454	<lmxll>	3	75.472	NA	367.367	2	60098388
TP5095	<lmxll>	3	75.814	NA	257.966	2	56986331
TP98776	<lmxll>	3	76.47	NA	328.041	9	10809935
TP39982	<lmxll>	3	77.037	NA	163.469	2	8232029
TP65463	<lmxll>	3	77.62	NA	343.261	2	6946863
TP44877	<lmxll>	3	78.166	NA	189.63	2	59170325
TP29650	<lmxll>	3	79.654	NA	374.521	2	20576430
TP121191	<lmxll>	3	80.437	NA	119.767	NA	NA
TP113791	<lmxll>	3	80.826	NA	336.486	2	6825936
X256	<lmxll>	3	81.715	NA	121.892	2	3991673
TP23554	<lmxll>	3	82.053	NA	54.715	2	4603836
TP87830	<lmxll>	3	82.445	NA	50.557	NA	NA
TP18315	<lmxll>	3	83.542	NA	63.55	2	4782466
TP111988	<lmxll>	3	84.374	NA	100.883	2	5328148
TP79276	<lmxll>	3	87.39	NA	87.798	NA	NA
TP81640	<lmxll>	3	90.313	NA	76.267	2	615588
TP11456	<lmxll>	4	0	NA	689.467	NA	NA
TP38875	<lmxll>	4	6.576	NA	654.736	1	44153520
TP20664	<lmxll>	4	8.767	NA	663.247	NA	NA
TP9205	<lmxll>	4	10.913	NA	641.726	2	75994139

Table A3 (cont.)

TP24242	<lmxll>	4	12.222	NA	648.804	2	76292572
TP33681	<lmxll>	4	13.304	NA	629.03	2	75758847
TP78164	<lmxll>	4	15.301	NA	615.85	NA	NA
X271	<lmxll>	4	16.08	NA	NA	NA	NA
TP87617	<lmxll>	4	18.118	NA	600.811	NA	NA
TP102306	<lmxll>	4	20.89	NA	550.14	2	74189212
TP23493	<lmxll>	4	22.963	NA	539.601	2	73084599
TP115554	<lmxll>	4	24.977	NA	577.359	2	72899160
X2	<lmxll>	4	25.84	NA	562.393	2	73079176
TP32794	<lmxll>	4	26.286	NA	565.237	NA	NA
TP29718	<lmxll>	4	27.034	NA	533.445	NA	NA
TP38714	<lmxll>	4	28.113	NA	527.061	2	72466310
TP109954	<lmxll>	4	28.839	NA	572.601	2	72401666
TP17077	<lmxll>	4	29.235	NA	570.329	2	72243325
TP7963	<lmxll>	4	30.659	NA	516.445	2	71643971
TP105442	<lmxll>	4	31.618	NA	509.599	2	71670864
TP50785	<lmxll>	4	32.3	NA	479.373	2	70982556
TP80180	<lmxll>	4	33.168	NA	482.734	NA	NA
TP65500	<lmxll>	4	33.785	NA	502.911	NA	NA
TP96028	<lmxll>	4	34.644	NA	489.144	2	70688596
TP65830	<lmxll>	4	35.803	NA	470.344	2	70687679
TP83811	<lmxll>	4	36.672	NA	475.051	NA	NA
TP113542	<lmxll>	4	37.228	NA	493.331	2	70110576
TP83927	<lmxll>	4	38.105	NA	458.537	2	69992044
TP88358	<lmxll>	4	39.302	NA	446.804	NA	NA
TP83936	<lmxll>	4	40.173	NA	421.422	2	69053555
TP117503	<lmxll>	4	40.77	NA	416.754	2	69234389
TP45563	<lmxll>	4	42.395	NA	409.716	2	68852332
TP67635	<lmxll>	4	43.348	NA	404.142	NA	NA
TP107688	<lmxll>	4	44.563	NA	400.31	NA	NA
TP31175	<lmxll>	4	46.112	NA	388.12	2	67680830
X185	<lmxll>	4	46.619	NA	381.991	2	67072885
TP43275	<lmxll>	4	47.742	NA	380.644	2	66824166
TP52482	<lmxll>	4	48.559	NA	395.54	NA	NA
TP67349	<lmxll>	4	49.442	NA	374.915	NA	NA
TP49845	<lmxll>	4	50.075	NA	283.207	NA	NA
TP73385	<lmxll>	4	50.869	NA	369.662	2	65949134
TP54751	<lmxll>	4	51.48	NA	299.571	2	65747415
TP88243	<lmxll>	4	51.98	NA	288.258	NA	NA

Table A3 (cont.)

TP23684	<lmxll>	4	52.382	NA	364.597	2	65426953
X28	<lmxll>	4	52.751	NA	376.957	2	66101587
TP4287	<lmxll>	4	53.033	NA	294.902	2	64667708
TP61130	<lmxll>	4	53.78	NA	317.199	NA	NA
TP22912	<lmxll>	4	54.233	NA	358.765	2	62951956
TP53131	<lmxll>	4	54.443	NA	351.578	NA	NA
TP76824	<lmxll>	4	55.098	NA	304.233	2	63681933
TP102230	<lmxll>	4	55.381	NA	291.39	2	64267499
TP53590	<lmxll>	4	55.6	NA	276.145	2	64578348
TP23809	<lmxll>	4	55.993	NA	278.678	2	64167192
TP89452	<lmxll>	4	56.282	NA	272.632	2	63596763
TP12203	<lmxll>	4	56.825	NA	308.535	2	63289756
TP52426	<lmxll>	4	57.542	NA	268.364	3	4589747
TP78599	<lmxll>	4	58.29	NA	355.285	2	62917404
TP121936	<lmxll>	4	59.011	NA	200.366	2	50268650
TP83785	<lmxll>	4	59.656	NA	260.555	2	61208038
TP2312	<lmxll>	4	60.151	NA	345.021	2	61612826
TP64655	<lmxll>	4	60.528	NA	230.539	7	56694639
TP122729	<lmxll>	4	60.891	NA	253.811	5	41341175
TP90263	<lmxll>	4	61.357	NA	264.348	2	61480063
TP15772	<lmxll>	4	61.512	NA	250.033	2	61172701
TP97965	<lmxll>	4	61.891	NA	241.616	2	60095652
TP80465	<lmxll>	4	62.12	NA	243.605	2	61072119
TP113249	<lmxll>	4	62.54	NA	226.031	2	59228494
TP15929	<lmxll>	4	62.812	NA	247.14	2	60776656
TP36565	<lmxll>	4	63.217	NA	234.054	3	3992927
TP81117	<lmxll>	4	63.628	NA	237.691	NA	NA
X275	<lmxll>	4	63.876	NA	311.822	2	62336662
TP82888	<lmxll>	4	64.29	NA	223.113	2	58685333
TP66482	<lmxll>	4	64.73	NA	195.489	2	57500285
TP104455	<lmxll>	4	65.133	NA	216.311	2	45162440
TP2364	<lmxll>	4	65.457	NA	211.789	2	50029246
TP92367	<lmxll>	4	65.714	NA	207.001	NA	NA
TP21088	<lmxll>	4	66.013	NA	191.624	2	47212732
TP55694	<lmxll>	4	66.323	NA	187.477	2	20582946
TP100613	<lmxll>	4	66.576	NA	141.73	2	55333783
TP71994	<lmxll>	4	66.992	NA	219.836	NA	NA
TP19830	<lmxll>	4	67.286	NA	103.628	2	53975407
TP67752	<lmxll>	4	67.629	NA	135.667	NA	NA

Table A3 (cont.)

TP117582	<lmxll>	4	67.972	NA	112.902	2	15769038
TP30806	<lmxll>	4	68.196	NA	179.986	NA	NA
TP29118	<lmxll>	4	68.316	NA	145.328	2	9847880
TP44378	<lmxll>	4	68.608	NA	133.137	NA	NA
TP92134	<lmxll>	4	68.749	NA	146.951	2	13668989
TP75576	<lmxll>	4	68.94	NA	184.495	2	14324433
TP120195	<lmxll>	4	69.062	NA	177.144	2	14684533
TP85507	<lmxll>	4	69.285	NA	178.452	NA	NA
TP6278	<lmxll>	4	69.55	NA	182.206	2	14853776
TP69922	<lmxll>	4	69.811	NA	148.452	2	9096149
TP27149	<lmxll>	4	70.14	NA	156.846	NA	NA
TP69863	<lmxll>	4	70.479	NA	117.747	2	7796818
TP49466	<lmxll>	4	70.723	NA	108.44	2	16657731
TP68623	<lmxll>	4	71.14	NA	89.503	2	7865744
TP89404	<lmxll>	4	71.343	NA	128.338	2	7287023
TP50458	<lmxll>	4	71.436	NA	126.308	2	6789134
TP109287	<lmxll>	4	71.82	NA	122.796	10	15091243
TP99026	<lmxll>	4	72.174	NA	87.385	2	7965951
TP29625	<lmxll>	4	72.354	NA	84.055	NA	NA
TP30899	<lmxll>	4	72.742	NA	173.947	2	13927142
TP45066	<lmxll>	4	73.096	NA	152.597	2	10562530
TP125885	<lmxll>	4	73.736	NA	79.147	NA	NA
TP11134	<lmxll>	4	74.491	NA	60.221	NA	NA
TP6902	<lmxll>	4	74.716	NA	56.739	2	5257809
TP117254	<lmxll>	4	75.203	NA	168.026	2	13223261
TP95351	<lmxll>	4	75.764	NA	162.112	NA	NA
TP86688	<lmxll>	4	76.88	NA	50.243	2	4023750
TP80130	<lmxll>	4	77.562	NA	64.957	2	4719097
TP8329	<lmxll>	4	77.807	NA	45.622	NA	NA
TP123012	<lmxll>	4	78.448	NA	95.8	2	7857666
TP95572	<lmxll>	4	79.391	NA	336.89	2	56515872
TP19259	<lmxll>	4	80.338	NA	326.833	NA	NA
TP80392	<lmxll>	4	81.023	NA	40.125	NA	NA
TP9034	<lmxll>	4	81.879	NA	33.827	2	1779982
TP29388	<lmxll>	4	83.633	NA	18.695	NA	NA
TP101572	<lmxll>	4	86.892	NA	8.839	NA	NA
TP81639	<lmxll>	4	89.6	NA	0	2	615588
TP59666	<lmxll>	5	0	NA	729.037	2	70926274
TP9819	<lmxll>	5	3.013	NA	714.144	NA	NA

Table A3 (cont.)

TP29267	<lmxll>	5	4.283	NA	703.184	NA	NA
TP17402	<lmxll>	5	5.687	NA	724.106	3	67303896
TP86626	<lmxll>	5	7.213	NA	688.192	NA	NA
TP47986	<lmxll>	5	8.442	NA	695.135	1	22392648
TP41683	<lmxll>	5	9.956	NA	744.762	3	66536812
TP33245	<lmxll>	5	14.554	NA	654.625	3	65066638
TP3989	<lmxll>	5	16.218	NA	756.203	NA	NA
TP24285	<lmxll>	5	17.519	NA	649.578	3	65112106
TP91834	<lmxll>	5	18.701	NA	645.354	3	64808043
TP26754	<lmxll>	5	20.308	NA	766.144	3	63684208
TP65995	<lmxll>	5	21.08	NA	795.899	NA	NA
TP23969	<lmxll>	5	22.362	NA	788.025	3	7413221
TP71310	<lmxll>	5	23.922	NA	806.789	3	63743713
TP32507	<lmxll>	5	24.981	NA	613.262	3	63174157
TP123524	<lmxll>	5	25.899	NA	778.789	3	62979321
TP84044	<lmxll>	5	26.994	NA	772.249	3	63098688
X393	<lmxll>	5	30.711	NA	589.732	3	61682675
TP45845	<lmxll>	5	31.542	NA	588.476	3	61507949
TP121441	<lmxll>	5	33.218	NA	572.951	NA	NA
TP34910	<lmxll>	5	36.093	NA	563.302	3	60968907
TP50886	<lmxll>	5	38.593	NA	543.883	3	60252455
TP68305	<lmxll>	5	39.559	NA	535.447	3	59819172
TP100860	<lmxll>	5	40.29	NA	528.676	6	59208268
TP79349	<lmxll>	5	41.334	NA	429.71	3	51453767
TP19315	<lmxll>	5	42.17	NA	438.798	3	56025583
TP55785	<lmxll>	5	42.94	NA	522.446	NA	NA
TP44553	<lmxll>	5	43.254	NA	516.756	NA	NA
TP55770	<lmxll>	5	44.19	NA	373.564	3	54759326
TP30886	<lmxll>	5	45.154	NA	360.988	3	50399009
TP61515	<lmxll>	5	45.721	NA	499.975	3	56010790
TP112059	<lmxll>	5	46.277	NA	443.592	3	53396403
TP31804	<lmxll>	5	46.746	NA	392.704	3	54382804
TP82557	<lmxll>	5	47.112	NA	328.241	3	11476585
TP52480	<lmxll>	5	47.532	NA	388.83	3	54629958
TP100301	<lmxll>	5	47.798	NA	494.043	3	55068651
TP8009	<lmxll>	5	48.128	NA	403.175	NA	NA
TP30790	<lmxll>	5	48.713	NA	446.129	NA	NA
TP7257	<lmxll>	5	49.034	NA	456.098	3	52663638
X80	<lmxll>	5	49.206	NA	489.21	3	54629654

Table A3 (cont.)

TP11200	<lmxll>	5	49.326	NA	464.191	NA	NA
TP24899	<lmxll>	5	49.707	NA	347.509	3	19698699
TP16038	<lmxll>	5	50.041	NA	419.478	NA	NA
TP98538	<lmxll>	5	50.203	NA	471.514	NA	NA
TP65767	<lmxll>	5	50.525	NA	479.787	3	15473156
TP121806	<lmxll>	5	50.876	NA	434.937	3	51484417
TP116168	<lmxll>	5	51.14	NA	423.858	3	15352645
TP86117	<lmxll>	5	51.683	NA	415.187	NA	NA
TP54392	<lmxll>	5	52.154	NA	354.155	NA	NA
TP81258	<lmxll>	5	53.26	NA	339.578	3	11626432
TP75734	<lmxll>	5	53.753	NA	319.693	NA	NA
TP11886	<lmxll>	5	54.585	NA	313.395	NA	NA
TP57155	<lmxll>	5	55.215	NA	287.49	3	10047297
TP27659	<lmxll>	5	55.861	NA	290.684	3	9752815
TP96326	<lmxll>	5	56.521	NA	270.587	NA	NA
TP103876	<lmxll>	5	56.994	NA	296.077	3	9697407
TP108132	<lmxll>	5	57.467	NA	280.893	NA	NA
TP84721	<lmxll>	5	58.37	NA	244.314	3	8446421
TP81485	<lmxll>	5	58.828	NA	235.862	3	8842583
TP19960	<lmxll>	5	59.245	NA	265.122	NA	NA
TP109948	<lmxll>	5	59.952	NA	305.371	NA	NA
TP36710	<lmxll>	5	60.713	NA	249.953	3	8423514
TP115019	<lmxll>	5	61.908	NA	227.985	NA	NA
TP6876	<lmxll>	5	64.052	NA	198.29	3	4767179
TP65838	<lmxll>	5	65.037	NA	179.076	3	5069629
TP61589	<lmxll>	5	66.394	NA	12.504	3	3854632
TP114974	<lmxll>	5	67.36	NA	159.07	3	3754301
TP118409	<lmxll>	5	68.047	NA	153.828	NA	NA
TP15087	<lmxll>	5	68.915	NA	164.561	3	3147575
TP85275	<lmxll>	5	69.729	NA	0	3	4829825
TP56510	<lmxll>	5	71.368	NA	21.603	3	2793244
TP87953	<lmxll>	5	72.167	NA	134.249	NA	NA
TP91042	<lmxll>	5	73.18	NA	144.171	3	2633894
TP123001	<lmxll>	5	74.033	NA	139.504	3	2639081
X310	<lmxll>	5	74.807	NA	93.556	3	637355
TP70296	<lmxll>	5	75.746	NA	51.054	3	1850036
TP103921	<lmxll>	5	76.363	NA	45.541	3	1903044
TP26939	<lmxll>	5	77.095	NA	126.657	2	77779823
TP100603	<lmxll>	5	78.5	NA	57.321	3	1137096

Table A3 (cont.)

TP83646	<lmxll>	5	79.755	NA	65.185	NA	NA
TP14281	<lmxll>	5	80.686	NA	78.184	3	558841
TP64310	<lmxll>	5	81.25	NA	96.542	NA	NA
TP90858	<lmxll>	5	82.209	NA	88.845	3	309389
TP101005	<lmxll>	5	82.507	NA	73.749	NA	NA
TP33883	<lmxll>	5	84.134	NA	83.546	3	657864
TP45145	<lmxll>	5	85.833	NA	34.656	NA	NA
TP80936	<lmxll>	5	87.017	NA	111.511	NA	NA
TP27965	<lmxll>	6	2.473	NA	868.148	3	73271350
TP56691	<lmxll>	6	4.158	NA	886.132	NA	NA
TP51735	<lmxll>	6	5.87	NA	888.406	6	54662950
TP38301	<lmxll>	6	8.149	NA	841.488	3	72153622
TP98227	<lmxll>	6	9.152	NA	851.843	3	72457432
TP109193	<lmxll>	6	10.749	NA	828.971	NA	NA
TP33447	<lmxll>	6	11.479	NA	834.029	NA	NA
TP102602	<lmxll>	6	13.147	NA	819.078	3	71893512
TP20373	<lmxll>	6	13.999	NA	810.718	3	71704162
TP11836	<lmxll>	6	14.763	NA	806.215	3	71788679
TP71530	<lmxll>	6	15.706	NA	796.244	3	71573117
TP12816	<lmxll>	6	16.442	NA	801.39	3	71816044
TP123375	<lmxll>	6	18.415	NA	759.092	3	71022076
TP928	<lmxll>	6	19.355	NA	791.344	NA	NA
TP95369	<lmxll>	6	20.775	NA	779.267	NA	NA
TP24304	<lmxll>	6	22.114	NA	785.968	3	70880729
X360	<lmxll>	6	24.301	NA	747.463	3	70432267
TP102949	<lmxll>	6	25.527	NA	768.578	3	69936565
TP16297	<lmxll>	6	27.023	NA	685.166	NA	NA
TP102517	<lmxll>	6	29.188	NA	742.003	3	68881890
TP45374	<lmxll>	6	30.386	NA	737.448	3	67595913
TP86017	<lmxll>	6	32.517	NA	727.061	3	65223471
TP26973	<lmxll>	6	33.303	NA	699.118	NA	NA
TP79831	<lmxll>	6	34.087	NA	649.268	3	65771839
TP79469	<lmxll>	6	35.165	NA	655.024	3	66132201
TP34150	<lmxll>	6	37.765	NA	712.182	3	64263517
TP27129	<lmxll>	6	38.524	NA	636.871	3	63637419
TP116347	<lmxll>	6	39.325	NA	607.204	NA	NA
TP122332	<lmxll>	6	39.674	NA	603.226	3	63354563
TP10235	<lmxll>	6	40.666	NA	719.648	3	63544237
TP93595	<lmxll>	6	40.989	NA	612.822	3	62841485

Table A3 (cont.)

TP7135	<lmxll>	6	41.799	NA	599.246	3	62433998
TP112041	<lmxll>	6	42.119	NA	716.192	3	64244360
TP34021	<lmxll>	6	42.547	NA	707.958	3	63278522
TP18803	<lmxll>	6	43.041	NA	596.309	3	62237854
TP32856	<lmxll>	6	43.861	NA	588.072	NA	NA
TP43335	<lmxll>	6	44.657	NA	592.857	3	61858158
TP121953	<lmxll>	6	44.832	NA	583.551	NA	NA
TP121484	<lmxll>	6	45.667	NA	580.776	NA	NA
TP85719	<lmxll>	6	46.49	NA	566.096	3	60726977
TP77751	<lmxll>	6	46.729	NA	553.121	3	60906139
TP86435	<lmxll>	6	47.088	NA	558.394	3	61007791
TP75261	<lmxll>	6	47.781	NA	554.937	3	60642677
TP89939	<lmxll>	6	48.031	NA	546.6	NA	NA
TP76140	<lmxll>	6	48.786	NA	396.153	3	51370392
TP64578	<lmxll>	6	49.001	NA	562.704	4	62837338
TP75306	<lmxll>	6	49.545	NA	457.551	3	13707578
TP45920	<lmxll>	6	49.898	NA	356.404	3	51880856
TP64828	<lmxll>	6	50.484	NA	484.154	2	70617321
TP118688	<lmxll>	6	50.671	NA	429.094	NA	NA
TP16269	<lmxll>	6	50.964	NA	413.407	3	58392797
TP107395	<lmxll>	6	51.275	NA	434.144	3	55691773
TP73178	<lmxll>	6	51.509	NA	463.391	NA	NA
TP75903	<lmxll>	6	51.749	NA	421.407	3	51691446
TP40632	<lmxll>	6	52.2	NA	350.916	2	19536726
TP110931	<lmxll>	6	52.57	NA	425.125	3	57096187
TP115519	<lmxll>	6	52.749	NA	437.319	NA	NA
TP99902	<lmxll>	6	53.177	NA	303.791	3	15463664
TP55612	<lmxll>	6	53.316	NA	307.672	3	18259591
TP97802	<lmxll>	6	53.465	NA	377.788	5	18998868
TP82957	<lmxll>	6	53.626	NA	452.652	3	54423298
TP67400	<lmxll>	6	53.838	NA	382.748	3	58844312
TP63498	<lmxll>	6	53.941	NA	439.114	3	15473168
TP109304	<lmxll>	6	54.16	NA	479.567	3	51170498
TP72106	<lmxll>	6	54.313	NA	364.838	3	52366325
TP22618	<lmxll>	6	54.554	NA	496	3	56025577
TP13767	<lmxll>	6	54.731	NA	372.806	NA	NA
TP19748	<lmxll>	6	54.918	NA	489.57	3	17326112
TP109389	<lmxll>	6	55.06	NA	441.854	NA	NA
TP111818	<lmxll>	6	55.318	NA	389.404	NA	NA

Table A3 (cont.)

TP117076	<lmxll>	6	55.505	NA	500.606	NA	NA
TP87339	<lmxll>	6	55.808	NA	361.901	3	53606185
X57	<lmxll>	6	56.032	NA	465.464	3	58592304
TP80774	<lmxll>	6	56.17	NA	312.571	3	56751863
TP15604	<lmxll>	6	56.448	NA	345.135	3	12522657
TP67377	<lmxll>	6	56.79	NA	319.756	NA	NA
TP87104	<lmxll>	6	57.243	NA	447.37	3	12159867
TP7295	<lmxll>	6	57.621	NA	298.121	NA	NA
TP9897	<lmxll>	6	57.92	NA	341.449	NA	NA
TP59722	<lmxll>	6	58.292	NA	275.62	3	9428316
TP52767	<lmxll>	6	58.666	NA	293.241	NA	NA
TP95694	<lmxll>	6	58.999	NA	470.223	NA	NA
TP68015	<lmxll>	6	59.368	NA	272.158	8	52022275
TP21851	<lmxll>	6	59.633	NA	240.436	3	8528158
TP49061	<lmxll>	6	60.124	NA	230.007	3	7732669
TP80560	<lmxll>	6	60.336	NA	244.89	NA	NA
TP48487	<lmxll>	6	60.504	NA	235.903	NA	NA
TP86301	<lmxll>	6	60.779	NA	232.107	3	7457912
TP100214	<lmxll>	6	61.149	NA	227.088	NA	NA
TP37070	<lmxll>	6	61.555	NA	279.574	NA	NA
TP40208	<lmxll>	6	62.144	NA	287.654	NA	NA
TP79853	<lmxll>	6	63.013	NA	217.99	NA	NA
TP74641	<lmxll>	6	63.805	NA	221.927	3	5696498
TP119752	<lmxll>	6	64.378	NA	181.214	3	5121840
TP46019	<lmxll>	6	64.71	NA	211.891	NA	NA
TP91824	<lmxll>	6	65.373	NA	186.998	3	4531567
TP88519	<lmxll>	6	65.682	NA	127.699	NA	NA
TP69567	<lmxll>	6	66.141	NA	194.127	3	4522098
TP92726	<lmxll>	6	66.495	NA	136.338	7	51062035
TP80252	<lmxll>	6	66.878	NA	132.426	3	4211960
TP75902	<lmxll>	6	67.435	NA	202.606	3	4959528
TP6373	<lmxll>	6	68.096	NA	174.222	3	4469514
TP74592	<lmxll>	6	68.481	NA	140.952	3	15399740
TP1794	<lmxll>	6	69.361	NA	167.077	3	3430386
TP1300	<lmxll>	6	69.809	NA	122.063	NA	NA
TP24864	<lmxll>	6	70.276	NA	151.549	NA	NA
TP74101	<lmxll>	6	70.637	NA	159.074	3	3301594
TP45080	<lmxll>	6	71.11	NA	145.115	3	3035635
TP38204	<lmxll>	6	71.849	NA	105.543	NA	NA

Table A3 (cont.)

TP72007	<lmxll>	6	72.636	NA	110.566	3	1431378
TP105975	<lmxll>	6	73.228	NA	82.366	3	1724990
TP84782	<lmxll>	6	73.934	NA	116.189	3	1442818
TP67171	<lmxll>	6	75.029	NA	63.559	3	2234792
X70	<lmxll>	6	75.675	NA	53.285	3	2045071
TP41654	<lmxll>	6	76.182	NA	65.763	NA	NA
TP7296	<lmxll>	6	77.34	NA	73.56	NA	NA
TP34495	<lmxll>	6	78.507	NA	41.513	3	2651091
TP66703	<lmxll>	6	81.198	NA	24.196	NA	NA
X388	<lmxll>	6	82.725	NA	15.234	3	406901
TP75803	<lmxll>	6	83.687	NA	16.746	NA	NA
TP107399	<lmxll>	6	84.826	NA	19.387	3	701613
TP42854	<lmxll>	7	0	NA	0	1	27677019
TP105106	<lmxll>	7	2.92	NA	21.484	NA	NA
TP35943	<lmxll>	7	4.671	NA	7.164	4	90289
TP1380	<lmxll>	7	6.224	NA	12.585	NA	NA
TP102012	<lmxll>	7	8.107	NA	30.345	10	7968028
TP55390	<lmxll>	7	10.256	NA	38.354	4	1121672
TP24036	<lmxll>	7	14.501	NA	49.692	NA	NA
TP125051	<lmxll>	7	16.039	NA	59.32	4	1881239
TP81563	<lmxll>	7	17.01	NA	54.756	4	2010164
TP65934	<lmxll>	7	18.903	NA	67.923	NA	NA
TP82610	<lmxll>	7	19.993	NA	74.38	NA	NA
TP99329	<lmxll>	7	21.188	NA	80.55	NA	NA
TP24413	<lmxll>	7	22.884	NA	86.689	4	2976104
X62	<lmxll>	7	23.832	NA	96.095	NA	NA
TP117451	<lmxll>	7	24.98	NA	92.256	4	3621638
TP13046	<lmxll>	7	26.303	NA	104.175	4	4121673
TP120983	<lmxll>	7	28.625	NA	99.1	NA	NA
TP88585	<lmxll>	7	30.109	NA	111.653	4	4658764
TP39330	<lmxll>	7	32.774	NA	117.208	4	4986606
TP55175	<lmxll>	7	33.628	NA	138.067	4	5068374
TP64168	<lmxll>	7	34.493	NA	127.92	4	5399727
TP48387	<lmxll>	7	35.545	NA	135.137	NA	NA
TP53055	<lmxll>	7	36.806	NA	122.771	4	5088855
TP94688	<lmxll>	7	38.407	NA	132.2	4	5473022
TP45605	<lmxll>	7	39.745	NA	143.417	4	5673563
TP109586	<lmxll>	7	40.895	NA	147.238	4	6061303
X365	<lmxll>	7	41.962	NA	149.039	4	5961562

Table A3 (cont.)

TP41418	<lmxll>	7	42.809	NA	150.805	4	6456602
TP120555	<lmxll>	7	46.127	NA	159.418	NA	NA
TP96403	<lmxll>	7	48.007	NA	166.778	4	7328017
TP17213	<lmxll>	7	50.571	NA	171.009	4	9339969
TP79161	<lmxll>	7	52.278	NA	177.447	4	10027765
TP94894	<lmxll>	7	55.645	NA	187.464	4	12904717
TP3016	<lmxll>	7	56.455	NA	183.589	NA	NA
TP103720	<lmxll>	7	57.892	NA	227.554	NA	NA
TP14905	<lmxll>	7	58.667	NA	215.333	4	14971223
TP41064	<lmxll>	7	59.795	NA	200.244	4	16298511
TP88563	<lmxll>	7	61.037	NA	208.236	3	15896717
TP43154	<lmxll>	7	63.665	NA	255.269	7	863410
TP12081	<lmxll>	7	64.753	NA	266.03	7	64266464
TP21534	<lmxll>	7	65.87	NA	259.433	NA	NA
TP29196	<lmxll>	7	66.763	NA	249.141	7	64104278
TP64459	<lmxll>	7	67.737	NA	271.171	NA	NA
X202	<lmxll>	7	68.321	NA	274.275	7	63329978
TP71810	<lmxll>	7	68.867	NA	274.275	NA	NA
TP32288	<lmxll>	7	69.865	NA	416.005	7	57077472
TP32929	<lmxll>	7	70.76	NA	282.909	7	62607692
TP59114	<lmxll>	7	71.492	NA	285.561	NA	NA
TP79956	<lmxll>	7	72.083	NA	296.998	7	62615372
TP122816	<lmxll>	7	72.664	NA	304.295	7	58279668
X584	<lmxll>	7	72.906	NA	457.161	7	57312732
TP55456	<lmxll>	7	73.625	NA	325.522	NA	NA
TP69769	<lmxll>	7	74.27	NA	289.336	7	58185257
TP1785	<lmxll>	7	75.022	NA	293.242	7	62559793
TP20089	<lmxll>	7	76.151	NA	352.685	7	62595596
TP94722	<lmxll>	7	81.668	NA	475.822	4	63784817
TP90140	<lmxll>	7	82.324	NA	481.287	4	57525688
TP110019	<lmxll>	7	83.504	NA	490.904	4	63790465
TP83358	<lmxll>	7	84.981	NA	498.41	NA	NA
X421	<lmxll>	7	85.788	NA	474.378	4	63977438
TP34399	<lmxll>	7	86.501	NA	513.511	4	64563917
TP99012	<lmxll>	7	87.236	NA	516.854	6	60320278
TP54937	<lmxll>	7	87.87	NA	521.799	NA	NA
TP32330	<lmxll>	7	88.687	NA	506.956	NA	NA
TP29900	<lmxll>	7	90.133	NA	528.755	4	64563541
TP9282	<lmxll>	7	91.286	NA	535.708	4	65241562

Table A3 (cont.)

TP81106	<lmxll>	7	92.057	NA	538.773	NA	NA
TP94514	<lmxll>	7	93.504	NA	555.81	4	65522691
TP92075	<lmxll>	7	95.508	NA	545.894	4	65230639
TP76062	<lmxll>	7	96.53	NA	561.034	NA	NA
X226	<lmxll>	7	97.973	NA	566.185	4	65842476
TP19979	<lmxll>	7	99.485	NA	576.401	4	65997458
TP110259	<lmxll>	7	101.157	NA	581.234	4	66249532
TP59979	<lmxll>	7	102.962	NA	587.341	NA	NA
TP17421	<lmxll>	7	106.451	NA	595.863	4	66365851
TP38488	<lmxll>	7	110.282	NA	609.772	5	61110275
TP85161	<lmxll>	7	116.794	NA	648.807	NA	NA
TP112887	<lmxll>	7	119.097	NA	634.161	4	67770355
X52	<lmxll>	7	119.975	NA	631.734	4	67583451
TP14227	<lmxll>	7	121.791	NA	640.455	10	9694738
TP85921	<lmxll>	7	124.118	NA	624.348	NA	NA
TP67075	<lmxll>	8	2.295	NA	771.952	4	66474079
TP57984	<lmxll>	8	4.199	NA	778.35	NA	NA
TP115948	<lmxll>	8	10.034	NA	725.213	4	65227015
TP111659	<lmxll>	8	12.574	NA	702.467	4	64563845
TP59465	<lmxll>	8	13.533	NA	616.223	4	58297863
TP28484	<lmxll>	8	14.759	NA	648.223	4	57599035
TP50883	<lmxll>	8	15.488	NA	620.332	NA	NA
TP55633	<lmxll>	8	16.122	NA	666.692	4	57513870
TP65505	<lmxll>	8	16.759	NA	676.433	NA	NA
TP110018	<lmxll>	8	17.513	NA	660.955	4	63790468
TP2616	<lmxll>	8	17.854	NA	669.707	4	57493133
TP5347	<lmxll>	8	18.554	NA	642.645	4	57698327
TP34563	<lmxll>	8	19.17	NA	656.66	4	57435962
X664	<lmxll>	8	19.789	NA	573.586	4	58811382
TP67853	<lmxll>	8	20.19	NA	564.61	4	58988836
TP39741	<lmxll>	8	21.051	NA	552.791	4	58911159
TP118579	<lmxll>	8	22.08	NA	611.868	NA	NA
TP83576	<lmxll>	8	22.504	NA	608.282	4	58568845
TP41344	<lmxll>	8	23.626	NA	556.793	NA	NA
TP55820	<lmxll>	8	24.352	NA	561.28	4	59267441
TP29538	<lmxll>	8	29.915	NA	485.868	4	61702059
TP13657	<lmxll>	8	30.872	NA	473.113	4	62021079
TP12676	<lmxll>	8	31.823	NA	491.866	4	61564639
TP35280	<lmxll>	8	32.422	NA	467.134	NA	NA

Table A3 (cont.)

TP113775	<lmxll>	8	32.855	NA	494.425	4	61517121
TP14424	<lmxll>	8	33.409	NA	496.256	4	61599600
TP91997	<lmxll>	8	35.428	NA	448.967	4	62830626
TP15025	<lmxll>	8	36.404	NA	458.844	4	62706506
TP115241	<lmxll>	8	36.786	NA	454.738	4	62758307
TP116252	<lmxll>	8	37.883	NA	436.818	4	63012727
X540	<lmxll>	8	38.412	NA	399.245	4	62928686
TP19171	<lmxll>	8	38.633	NA	411.245	4	63112473
TP15188	<lmxll>	8	39.383	NA	403.022	NA	NA
TP20661	<lmxll>	8	40.019	NA	397.242	4	63110981
TP8306	<lmxll>	8	40.881	NA	393.46	4	63344383
TP79155	<lmxll>	8	41.257	NA	442.42	4	63070426
TP55068	<lmxll>	8	42.387	NA	373.521	4	56510045
TP97449	<lmxll>	8	43.181	NA	381.9	4	56833818
TP6305	<lmxll>	8	43.64	NA	388.923	4	56857893
TP97277	<lmxll>	8	44.355	NA	363.273	4	55119635
TP66831	<lmxll>	8	45.464	NA	349.751	4	54906410
TP11921	<lmxll>	8	45.858	NA	354.978	4	54830560
TP31855	<lmxll>	8	47.589	NA	322.764	4	54064351
TP74602	<lmxll>	8	48.305	NA	340.258	4	54397072
TP97273	<lmxll>	8	48.823	NA	332.636	4	54196490
TP96209	<lmxll>	8	49.454	NA	311.265	4	53226446
TP111053	<lmxll>	8	49.968	NA	336.01	4	53815092
TP77373	<lmxll>	8	50.632	NA	282.592	4	50512768
TP89283	<lmxll>	8	50.98	NA	232.525	NA	NA
TP15791	<lmxll>	8	51.434	NA	237.494	4	52078682
TP75791	<lmxll>	8	51.641	NA	242.365	4	52043187
TP80089	<lmxll>	8	52.004	NA	154.462	4	16826943
TP42476	<lmxll>	8	52.423	NA	287.638	NA	NA
TP76874	<lmxll>	8	52.728	NA	219.879	1	10990659
TP3693	<lmxll>	8	52.922	NA	217.48	NA	NA
TP48603	<lmxll>	8	53.012	NA	182.424	4	9138870
TP105994	<lmxll>	8	53.33	NA	205.622	NA	NA
X280	<lmxll>	8	53.457	NA	245.912	4	16571044
TP78785	<lmxll>	8	53.532	NA	292.649	4	13923042
TP18799	<lmxll>	8	53.866	NA	297.235	4	53128373
X343	<lmxll>	8	54.125	NA	247.253	4	7207664
TP3156	<lmxll>	8	54.265	NA	245.912	NA	NA
TP71091	<lmxll>	8	54.568	NA	180.038	NA	NA

Table A3 (cont.)

TP81664	<lmxll>	8	55.447	NA	176.127	NA	NA
TP27078	<lmxll>	8	56.044	NA	146.151	2	71065955
TP95453	<lmxll>	8	56.289	NA	139.123	4	5650355
TP81533	<lmxll>	8	56.853	NA	127.298	1	65166674
TP88657	<lmxll>	8	57.417	NA	111.718	4	5186904
TP33279	<lmxll>	8	57.737	NA	121.502	4	5055037
TP24713	<lmxll>	8	58.639	NA	195.252	NA	NA
TP24017	<lmxll>	8	59.639	NA	226.635	6	43248919
TP107174	<lmxll>	8	60.971	NA	265.257	NA	NA
TP7027	<lmxll>	8	62.151	NA	254.33	NA	NA
TP116977	<lmxll>	8	62.587	NA	102.619	4	5254419
TP84411	<lmxll>	8	62.983	NA	91.292	4	4776245
TP37452	<lmxll>	8	64.575	NA	81.794	NA	NA
TP36634	<lmxll>	8	65.5	NA	71.389	4	2778237
TP75230	<lmxll>	8	67.604	NA	41.477	4	1682809
TP28603	<lmxll>	8	73.562	NA	15.257	NA	NA
TP27592	<lmxll>	8	76.541	NA	7.095	NA	NA
TP45940	<lmxll>	9	0	NA	501.283	5	62328583
TP88676	<lmxll>	9	6.137	NA	493.268	NA	NA
TP13213	<lmxll>	9	8.35	NA	479.839	5	60177057
TP87767	<lmxll>	9	10.812	NA	485.887	NA	NA
TP37358	<lmxll>	9	15.025	NA	468.146	5	59552866
TP96814	<lmxll>	9	18.306	NA	443.971	5	59296294
TP89968	<lmxll>	9	22.336	NA	433.061	NA	NA
TP60810	<lmxll>	9	27.792	NA	418.926	5	57925283
TP75507	<lmxll>	9	38.365	NA	304.427	10	12110625
TP84753	<lmxll>	9	41.944	NA	271.477	5	2838311
TP67878	<lmxll>	9	45.87	NA	208.708	NA	NA
TP1473	<lmxll>	9	51.724	NA	152.988	5	2177961
TP121439	<lmxll>	9	54.03	NA	110.167	5	1994734
TP22374	<lmxll>	9	55.466	NA	106.02	5	1979284
TP87811	<lmxll>	9	59.575	NA	92.281	NA	NA
TP86470	<lmxll>	9	61.765	NA	98.291	6	58127795
TP77076	<lmxll>	9	64.134	NA	31.632	5	1324031
TP18526	<lmxll>	9	65.921	NA	66.484	1	16739440
TP95057	<lmxll>	9	66.883	NA	25.519	5	1371346
TP33999	<lmxll>	9	68.534	NA	20.474	NA	NA
TP123113	<lmxll>	9	70.024	NA	14.178	8	2929215
TP109302	<lmxll>	9	73.103	NA	74.131	NA	NA

Table A3 (cont.)

TP79849	<lmxll>	9	81.203	NA	0	5	203286
TP74817	<lmxll>	10	0	NA	26.626	5	1507354
TP10024	<lmxll>	10	6.231	NA	43.487	5	1866525
TP110611	<lmxll>	10	12.536	NA	69.301	5	2251935
TP88294	<lmxll>	10	15.092	NA	75.094	NA	NA
TP74392	<lmxll>	10	22.901	NA	86.315	NA	NA
TP77469	<lmxll>	10	29.279	NA	94.2	NA	NA
TP73803	<lmxll>	10	30.834	NA	120.27	NA	NA
TP38414	<lmxll>	10	31.857	NA	126.022	5	6890386
TP70466	<lmxll>	10	32.449	NA	136.886	5	8232590
TP1819	<lmxll>	10	33.352	NA	131.925	5	7182172
TP52351	<lmxll>	10	34.24	NA	144.758	NA	NA
TP105419	<lmxll>	10	35.348	NA	151.921	7	55847711
TP72866	<lmxll>	10	35.815	NA	170.031	5	15235717
TP118838	<lmxll>	10	36.488	NA	160.359	5	15238484
TP52723	<lmxll>	10	36.968	NA	175.424	5	13729370
TP55861	<lmxll>	10	37.909	NA	164.811	NA	NA
TP10652	<lmxll>	10	39.089	NA	226.624	NA	NA
TP50431	<lmxll>	10	39.68	NA	240.944	5	48523710
TP36000	<lmxll>	10	40.207	NA	180.791	NA	NA
TP63984	<lmxll>	10	40.532	NA	184.527	5	52136282
TP75946	<lmxll>	10	40.88	NA	232.709	5	43792415
TP92533	<lmxll>	10	41.178	NA	230.36	NA	NA
TP79454	<lmxll>	10	41.544	NA	305.119	NA	NA
TP44176	<lmxll>	10	41.689	NA	309.784	NA	NA
TP116348	<lmxll>	10	42.174	NA	317.64	10	6080174
TP4294	<lmxll>	10	42.504	NA	301.954	5	46525169
TP59287	<lmxll>	10	42.829	NA	313.168	5	53190588
TP50279	<lmxll>	10	43.176	NA	299.195	7	56380384
TP16605	<lmxll>	10	43.621	NA	244.939	5	53069616
TP43892	<lmxll>	10	43.913	NA	222.221	NA	NA
TP13015	<lmxll>	10	44.697	NA	236.605	5	51077700
TP52589	<lmxll>	10	45.169	NA	211.466	5	51133105
TP56313	<lmxll>	10	45.822	NA	217.335	8	48226728
TP94131	<lmxll>	10	46.267	NA	204.578	10	57121361
TP85199	<lmxll>	10	46.805	NA	190.825	5	46525087
TP95929	<lmxll>	10	47.452	NA	293.942	NA	NA
TP82620	<lmxll>	10	48.013	NA	286.955	NA	NA
TP115109	<lmxll>	10	48.59	NA	345.978	5	56979239

Table A3 (cont.)

TP74389	<lmxll>	10	49.357	NA	251.976	NA	NA
TP60653	<lmxll>	10	49.919	NA	325.662	NA	NA
TP88080	<lmxll>	10	51.059	NA	336.483	5	58064713
TP16216	<lmxll>	10	52.968	NA	368.868	6	1879973
TP108989	<lmxll>	10	54.194	NA	355.697	NA	NA
TP56554	<lmxll>	10	55.282	NA	382.685	NA	NA
TP27273	<lmxll>	10	56.348	NA	391.18	NA	NA
TP112153	<lmxll>	10	58.574	NA	411.818	5	60569096
TP4418	<lmxll>	10	59.698	NA	417.815	5	61131698
TP93364	<lmxll>	10	61.268	NA	401.147	NA	NA
TP56837	<lmxll>	10	64.131	NA	425.546	NA	NA
TP55901	<lmxll>	11	0	NA	166.866	10	6045098
TP69393	<lmxll>	11	1.056	NA	174.775	6	43161656
TP41299	<lmxll>	11	2.167	NA	27.634	NA	NA
TP27617	<lmxll>	11	3.274	NA	0	NA	NA
TP96405	<lmxll>	11	3.927	NA	143.192	6	45937924
TP84326	<lmxll>	11	4.735	NA	191.473	NA	NA
TP42502	<lmxll>	11	5.919	NA	148.158	10	6045066
TP48408	<lmxll>	11	6.246	NA	187.129	NA	NA
TP8780	<lmxll>	11	6.795	NA	85.151	NA	NA
TP18468	<lmxll>	11	7.262	NA	39.869	NA	NA
TP25793	<lmxll>	11	7.729	NA	137.91	6	39903268
TP64566	<lmxll>	11	8.657	NA	161.426	NA	NA
TP55725	<lmxll>	11	9.043	NA	182.024	6	41186952
TP87559	<lmxll>	11	9.276	NA	21.433	6	38142194
TP89531	<lmxll>	11	9.419	NA	115.715	NA	NA
X59	<lmxll>	11	9.716	NA	106.235	6	38333670
TP79403	<lmxll>	11	9.964	NA	76.978	NA	NA
TP106693	<lmxll>	11	10.232	NA	180.06	NA	NA
TP113056	<lmxll>	11	10.388	NA	66.435	NA	NA
TP67142	<lmxll>	11	10.704	NA	102.953	NA	NA
TP67962	<lmxll>	11	10.932	NA	183.99	NA	NA
TP101701	<lmxll>	11	11.496	NA	73.586	6	5555128
TP79961	<lmxll>	11	12.088	NA	204.871	6	635300
TP106720	<lmxll>	11	12.694	NA	151.291	NA	NA
TP82510	<lmxll>	11	14.612	NA	156.104	6	46172249
TP53343	<lmxll>	11	16.988	NA	222.271	6	48692442
TP2601	<lmxll>	11	18.445	NA	227.098	6	48916694
TP104661	<lmxll>	11	19.799	NA	250.231	6	49483649

Table A3 (cont.)

TP92735	<lmxll>	11	20.564	NA	280.444	6	49773984
TP3789	<lmxll>	11	22.001	NA	267.198	6	49881289
TP103807	<lmxll>	11	24.35	NA	296.166	NA	NA
TP99291	<lmxll>	11	24.639	NA	303.47	6	50666507
TP11670	<lmxll>	11	26.332	NA	299.477	6	50661946
TP46774	<lmxll>	11	26.972	NA	318.08	6	51153965
TP32060	<lmxll>	11	29.067	NA	329.123	NA	NA
TP49742	<lmxll>	11	31.107	NA	400.69	6	51476454
TP37044	<lmxll>	11	31.883	NA	368.44	6	51283607
TP25440	<lmxll>	11	32.961	NA	374.065	NA	NA
TP44908	<lmxll>	11	36.782	NA	421.198	6	52812729
TP32772	<lmxll>	11	38.368	NA	479.927	1	53704196
TP2979	<lmxll>	11	39.305	NA	482.895	6	53006607
TP45230	<lmxll>	11	40.098	NA	458.06	1	18288418
TP31810	<lmxll>	11	41.027	NA	475.813	1	212262
TP36393	<lmxll>	11	42.596	NA	488.568	6	53461515
TP95791	<lmxll>	11	43.055	NA	486.431	NA	NA
X118	<lmxll>	11	43.556	NA	447.756	6	53147886
TP44179	<lmxll>	11	48.873	NA	548.906	6	55168044
TP116182	<lmxll>	11	50.359	NA	554.584	6	54991802
TP19128	<lmxll>	11	51.717	NA	559.9	6	55389418
TP74717	<lmxll>	11	55.363	NA	666.637	6	56060129
X278	<lmxll>	11	55.74	NA	585.64	6	56933712
TP76454	<lmxll>	11	56.365	NA	581.863	6	56110655
TP119054	<lmxll>	11	57.475	NA	660.532	6	55985976
TP42475	<lmxll>	11	59.71	NA	675.062	NA	NA
TP15558	<lmxll>	11	60.941	NA	653.085	6	56303840
TP23199	<lmxll>	11	62.722	NA	646.339	6	56935539
TP13071	<lmxll>	11	64.623	NA	615.794	6	57102718
TP37681	<lmxll>	11	66.752	NA	637.738	NA	NA
TP116998	<lmxll>	11	68.704	NA	630.292	3	70750230
TP61793	<lmxll>	12	0	NA	360.713	6	55166083
TP4373	<lmxll>	12	2.127	NA	367.778	6	55104328
TP116090	<lmxll>	12	4.556	NA	355.43	NA	NA
TP71712	<lmxll>	12	6.113	NA	343.006	6	54513749
TP95912	<lmxll>	12	8.017	NA	349.334	6	54507832
X188	<lmxll>	12	8.957	NA	352.414	6	55049847
TP100908	<lmxll>	12	10.155	NA	336.192	NA	NA
TP93885	<lmxll>	12	12.868	NA	329.63	4	51906101

Table A3 (cont.)

TP8914	<lmxll>	12	16.155	NA	306.3	NA	NA
TP58	<lmxll>	12	21.225	NA	262.334	NA	NA
TP68657	<lmxll>	12	23.284	NA	254.893	6	52418520
TP70373	<lmxll>	12	26.612	NA	247.736	NA	NA
TP11281	<lmxll>	12	28.424	NA	284.974	NA	NA
X624	<lmxll>	12	31.162	NA	237.403	6	50812497
TP29504	<lmxll>	12	33.404	NA	240.534	6	51252581
TP60368	<lmxll>	12	35.192	NA	236.831	NA	NA
TP43329	<lmxll>	12	42.013	NA	218.529	6	49816500
TP36935	<lmxll>	12	43.219	NA	185.539	6	49819296
TP32213	<lmxll>	12	44.482	NA	228.62	6	50009820
TP122864	<lmxll>	12	45.893	NA	179.321	6	49814905
TP17335	<lmxll>	12	47.193	NA	189.732	6	49807402
TP79586	<lmxll>	12	49.924	NA	198.852	6	49363858
TP70540	<lmxll>	12	50.662	NA	195.647	6	49307305
X568	<lmxll>	12	51.261	NA	191.805	NA	NA
TP26838	<lmxll>	12	54.012	NA	155.676	NA	NA
X63	<lmxll>	12	54.754	NA	193.703	6	46044287
TP14502	<lmxll>	12	55.232	NA	142.839	6	48692502
TP39886	<lmxll>	12	56.07	NA	151.359	NA	NA
TP110964	<lmxll>	12	57.297	NA	160.603	6	48297428
TP28877	<lmxll>	12	58.307	NA	139.674	6	48493687
TP17446	<lmxll>	12	59.046	NA	147.389	6	48188517
TP32197	<lmxll>	12	61.208	NA	134.163	6	47011254
TP59867	<lmxll>	12	62.343	NA	130.993	NA	NA
TP84350	<lmxll>	12	62.901	NA	105.617	6	46904173
TP68113	<lmxll>	12	64.465	NA	127.14	6	46813910
TP63697	<lmxll>	12	65.399	NA	124.46	NA	NA
TP97338	<lmxll>	12	66.225	NA	73.291	6	46408692
TP37739	<lmxll>	12	67.482	NA	120.068	6	46221587
TP98718	<lmxll>	12	68.035	NA	116.675	6	45299095
TP3548	<lmxll>	12	68.487	NA	114.712	6	45861698
TP16460	<lmxll>	12	69.071	NA	112.316	6	45453923
X235	<lmxll>	12	70.825	NA	95.944	6	42610199
TP116453	<lmxll>	12	71.546	NA	66.276	NA	NA
TP38222	<lmxll>	12	72.876	NA	48.659	NA	NA
TP46844	<lmxll>	12	73.545	NA	11.982	NA	NA
TP76633	<lmxll>	12	74.041	NA	44.09	NA	NA
TP110560	<lmxll>	12	74.765	NA	36.109	6	7180943

Table A3 (cont.)

TP4442	<lmxll>	12	75.228	NA	31.66	NA	NA
TP43537	<lmxll>	12	76.015	NA	14.213	NA	NA
TP52627	<lmxll>	12	76.639	NA	39.187	NA	NA
TP36138	<lmxll>	12	77.311	NA	17.686	NA	NA
TP46771	<lmxll>	12	78.148	NA	20.787	1	65894372
TP65537	<lmxll>	12	79.632	NA	81.861	NA	NA
TP73246	<lmxll>	12	82.316	NA	88.644	NA	NA
TP30773	<lmxll>	13	0	NA	42.288	7	1198545
TP27598	<lmxll>	13	1.718	NA	38.33	7	1025652
TP64604	<lmxll>	13	6.798	NA	50.239	NA	NA
TP53390	<lmxll>	13	9.314	NA	111.979	7	4138298
TP50051	<lmxll>	13	11.686	NA	129.542	7	4528655
TP42777	<lmxll>	13	12.774	NA	136.095	NA	NA
TP102258	<lmxll>	13	13.943	NA	122.153	7	3953147
TP118806	<lmxll>	13	14.978	NA	92.553	NA	NA
TP56519	<lmxll>	13	16.316	NA	143.312	7	5191830
TP41685	<lmxll>	13	17.794	NA	180.987	NA	NA
TP29273	<lmxll>	13	18.414	NA	150.606	NA	NA
TP90208	<lmxll>	13	19.195	NA	157.217	7	5454278
TP68684	<lmxll>	13	20.672	NA	196.168	NA	NA
TP49814	<lmxll>	13	21.812	NA	252.824	NA	NA
TP33423	<lmxll>	13	22.566	NA	187.136	7	7675359
TP19844	<lmxll>	13	22.945	NA	190.774	7	8557538
TP55201	<lmxll>	13	23.182	NA	274.3	NA	NA
TP39555	<lmxll>	13	23.818	NA	243.378	7	13338942
TP81909	<lmxll>	13	24.491	NA	222.462	7	10445874
TP105497	<lmxll>	13	25.094	NA	217.154	NA	NA
TP75897	<lmxll>	13	25.566	NA	202.279	6	43936673
TP48135	<lmxll>	13	26.316	NA	207.669	NA	NA
X132	<lmxll>	13	26.872	NA	168.048	7	18758696
TP63008	<lmxll>	13	27.65	NA	235.527	7	51063007
TP43257	<lmxll>	13	28.209	NA	310.646	7	52056127
TP92194	<lmxll>	13	28.874	NA	303.405	NA	NA
TP51261	<lmxll>	13	29.73	NA	290.216	NA	NA
TP19173	<lmxll>	13	30.651	NA	313.402	NA	NA
TP99638	<lmxll>	13	31.713	NA	320.165	7	53286788
TP24514	<lmxll>	13	34.145	NA	353.817	NA	NA
TP70106	<lmxll>	13	35.221	NA	447.029	7	57432338
TP54221	<lmxll>	13	36.284	NA	407.595	7	57633215

Table A3 (cont.)

TP16960	<lmxll>	13	37.316	NA	419.964	NA	NA
X8	<lmxll>	13	37.735	NA	397.181	7	58207132
TP101571	<lmxll>	13	37.874	NA	437.766	NA	NA
TP78059	<lmxll>	13	38.85	NA	427.222	7	58060138
TP36888	<lmxll>	13	41.072	NA	463.424	7	58610966
TP84474	<lmxll>	13	42.027	NA	457.536	7	63734571
TP35699	<lmxll>	13	42.685	NA	465.75	7	59017172
TP30417	<lmxll>	13	43.391	NA	474.971	NA	NA
X596	<lmxll>	13	43.975	NA	484.929	7	60495814
TP4488	<lmxll>	13	44.449	NA	479.219	7	60279265
TP121848	<lmxll>	13	45.488	NA	469.375	7	59759328
TP100041	<lmxll>	13	46.592	NA	483.92	7	60850324
TP108847	<lmxll>	13	49.903	NA	523.779	7	61651183
TP55236	<lmxll>	13	51.475	NA	547.991	7	61738250
TP1167	<lmxll>	13	52.597	NA	545.624	NA	NA
TP56485	<lmxll>	13	53.808	NA	551.465	7	62032623
TP63973	<lmxll>	13	54.768	NA	554.653	7	62032757
TP87906	<lmxll>	13	55.916	NA	557.991	1	50564052
TP91170	<lmxll>	13	57.069	NA	567.77	7	62364226
TP44113	<lmxll>	13	57.879	NA	571.473	7	62473685
TP52730	<lmxll>	13	59.012	NA	561.043	7	62263421
X153	<lmxll>	13	60.219	NA	593.137	7	62997760
TP9175	<lmxll>	13	64.446	NA	586.203	7	62633707
X120	<lmxll>	13	66.487	NA	595.412	7	64135545
TP101119	<lmxll>	13	68.498	NA	602.709	7	63672883
TP76774	<lmxll>	13	73.075	NA	613.912	7	64125635
TP95740	<lmxll>	14	0	NA	387.839	8	54925125
TP5201	<lmxll>	14	6.876	NA	350.69	NA	NA
TP74766	<lmxll>	14	9.185	NA	353.945	NA	NA
TP77427	<lmxll>	14	11.615	NA	340.987	8	53828905
TP53263	<lmxll>	14	15.272	NA	334.55	NA	NA
TP81737	<lmxll>	14	20.174	NA	322.73	NA	NA
TP87162	<lmxll>	14	21.161	NA	327.86	8	52724839
TP104292	<lmxll>	14	22.437	NA	315.171	9	14718263
TP11012	<lmxll>	14	26.234	NA	307.72	8	51629622
TP5950	<lmxll>	14	27.449	NA	304.367	NA	NA
TP62187	<lmxll>	14	28.237	NA	292.558	8	51103751
TP40083	<lmxll>	14	29.39	NA	299.368	NA	NA
TP49788	<lmxll>	14	32.354	NA	273.962	NA	NA

Table A3 (cont.)

TP108670	<lmxll>	14	33.123	NA	278.242	8	50331019
TP101771	<lmxll>	14	33.611	NA	281.29	8	50313311
TP55776	<lmxll>	14	34.181	NA	265.009	NA	NA
TP115154	<lmxll>	14	34.869	NA	285.378	8	50219668
TP75912	<lmxll>	14	35.959	NA	255.512	8	49884278
TP63623	<lmxll>	14	37.155	NA	249.397	8	49407024
TP86741	<lmxll>	14	37.941	NA	238.423	8	54628426
TP117137	<lmxll>	14	38.609	NA	232.3	NA	NA
TP41636	<lmxll>	14	39.846	NA	244.398	NA	NA
TP27577	<lmxll>	14	40.94	NA	224.13	NA	NA
TP48287	<lmxll>	14	42.351	NA	195.248	8	44582395
TP63044	<lmxll>	14	42.57	NA	183.174	NA	NA
TP80557	<lmxll>	14	42.969	NA	145.091	NA	NA
TP35003	<lmxll>	14	43.62	NA	187.322	NA	NA
X214	<lmxll>	14	43.975	NA	178.74	NA	NA
TP66121	<lmxll>	14	44.368	NA	156.932	8	43251605
TP103882	<lmxll>	14	44.908	NA	208.496	8	19294447
TP121170	<lmxll>	14	45.346	NA	202.901	8	41831588
TP48683	<lmxll>	14	46.937	NA	128.823	NA	NA
TP64585	<lmxll>	14	47.411	NA	137.727	8	5476409
TP82777	<lmxll>	14	48.195	NA	125.36	NA	NA
TP3098	<lmxll>	14	50.655	NA	116.145	8	5029469
TP93328	<lmxll>	14	55.485	NA	94.502	NA	NA
TP123695	<lmxll>	14	58.058	NA	86.565	NA	NA
TP18658	<lmxll>	14	64.501	NA	58.398	NA	NA
TP40897	<lmxll>	14	66.272	NA	62.536	NA	NA
TP30674	<lmxll>	14	68.196	NA	53.865	8	1717868
TP28318	<lmxll>	14	69.684	NA	32.678	8	1490225
X201	<lmxll>	14	70.474	NA	44.047	8	3643181
X243	<lmxll>	14	71.868	NA	26.481	8	16168782
TP92838	<lmxll>	14	79.927	NA	13.306	8	38581
TP86357	<lmxll>	15	0	NA	371.772	8	55163152
TP96494	<lmxll>	15	4.308	NA	365.849	8	54874553
TP88845	<lmxll>	15	6.28	NA	360.613	NA	NA
TP22614	<lmxll>	15	8.318	NA	355.133	NA	NA
TP61475	<lmxll>	15	13.854	NA	342.563	NA	NA
TP39785	<lmxll>	15	17.997	NA	332.401	NA	NA
TP86645	<lmxll>	15	23.433	NA	315.286	NA	NA
TP121984	<lmxll>	15	24.386	NA	306.031	NA	NA

Table A3 (cont.)

TP78856	<lmxll>	15	25.211	NA	255.352	NA	NA
TP101446	<lmxll>	15	26.116	NA	295.715	8	51478063
TP123281	<lmxll>	15	27.122	NA	321.575	NA	NA
X119	<lmxll>	15	27.553	NA	327.084	8	53137669
TP58708	<lmxll>	15	28.453	NA	280.667	NA	NA
TP84967	<lmxll>	15	29.084	NA	287.404	NA	NA
TP68652	<lmxll>	15	29.667	NA	274.842	NA	NA
TP62012	<lmxll>	15	30.231	NA	237.296	NA	NA
TP85114	<lmxll>	15	31.044	NA	264.255	8	50762444
TP61622	<lmxll>	15	31.525	NA	245.626	NA	NA
TP37250	<lmxll>	15	32.296	NA	269.209	NA	NA
TP50179	<lmxll>	15	33.105	NA	230.717	8	49031278
TP77638	<lmxll>	15	33.761	NA	223.726	NA	NA
TP78744	<lmxll>	15	34.324	NA	164.244	8	40337474
TP28462	<lmxll>	15	35.005	NA	141.961	8	18027577
TP11809	<lmxll>	15	35.559	NA	196.978	NA	NA
TP15894	<lmxll>	15	36.123	NA	135.183	NA	NA
TP58671	<lmxll>	15	36.62	NA	218.049	8	9733362
TP61728	<lmxll>	15	36.904	NA	208.901	NA	NA
TP31641	<lmxll>	15	37.317	NA	213.22	8	17153840
TP98064	<lmxll>	15	37.643	NA	191.967	NA	NA
TP76889	<lmxll>	15	38.069	NA	202.882	8	3191111
TP114666	<lmxll>	15	38.428	NA	115.425	NA	NA
TP41510	<lmxll>	15	38.941	NA	157.263	8	42777391
TP84244	<lmxll>	15	39.605	NA	129.729	NA	NA
TP80321	<lmxll>	15	40.23	NA	185.175	8	15828256
TP26703	<lmxll>	15	40.833	NA	149.831	5	17280631
TP85714	<lmxll>	15	41.356	NA	112.897	NA	NA
TP22375	<lmxll>	15	42.416	NA	122.088	8	6755578
TP109660	<lmxll>	15	43.586	NA	174.293	8	9737451
TP27323	<lmxll>	15	46.729	NA	101.21	NA	NA
TP90205	<lmxll>	15	48.837	NA	90.795	8	3073264
TP108987	<lmxll>	15	49.841	NA	75.57	8	3182858
TP85219	<lmxll>	15	50.354	NA	69.501	NA	NA
TP66184	<lmxll>	15	51.18	NA	48.989	8	2105072
TP113085	<lmxll>	15	52.116	NA	54.577	NA	NA
TP43541	<lmxll>	15	52.947	NA	62.074	NA	NA
TP31463	<lmxll>	15	54.069	NA	82.855	8	3182105
TP124548	<lmxll>	15	59.474	NA	36.268	8	1892188

Table A3 (cont.)

TP78451	<lmxll>	15	62.827	NA	7.111	NA	NA
TP67445	<lmxll>	15	64.032	NA	16.111	8	1231322
TP41227	<lmxll>	15	65.252	NA	11.047	NA	NA
TP66248	<lmxll>	15	69.87	NA	0	8	1084708
TP2053	<lmxll>	16	1.679	NA	11.692	NA	NA
TP30685	<lmxll>	16	3.293	NA	0	9	1586728
TP71575	<lmxll>	16	8.357	NA	107.609	NA	NA
TP78478	<lmxll>	16	11.48	NA	57.135	NA	NA
TP37676	<lmxll>	16	12.081	NA	59.386	9	2520162
TP71240	<lmxll>	16	13.207	NA	79.475	9	3927177
TP78918	<lmxll>	16	14.836	NA	64.372	NA	NA
TP81031	<lmxll>	16	15.407	NA	98.536	NA	NA
TP86423	<lmxll>	16	16.401	NA	94.485	9	3255539
TP118917	<lmxll>	16	17.136	NA	73.128	NA	NA
TP64017	<lmxll>	16	17.5	NA	87.795	9	4421301
TP108479	<lmxll>	16	18.459	NA	151.606	9	4014508
TP42839	<lmxll>	16	18.912	NA	69.578	8	55327156
TP23616	<lmxll>	16	21.201	NA	206.583	NA	NA
TP97160	<lmxll>	16	22.322	NA	279.286	9	10655941
TP49755	<lmxll>	16	23.261	NA	267.511	NA	NA
TP53360	<lmxll>	16	23.745	NA	215.024	NA	NA
TP33918	<lmxll>	16	24.181	NA	256.48	9	11977261
TP20363	<lmxll>	16	24.694	NA	273.972	9	11703365
TP100008	<lmxll>	16	25.414	NA	262.412	9	40161789
TP29310	<lmxll>	16	26.722	NA	329.809	9	48711248
TP83949	<lmxll>	16	27.91	NA	339.938	9	49370890
TP5185	<lmxll>	16	28.694	NA	290.48	9	48983384
TP94143	<lmxll>	16	29.008	NA	323.747	NA	NA
TP46818	<lmxll>	16	31.123	NA	353.957	9	53108728
TP86487	<lmxll>	16	32.419	NA	380.369	9	52335100
TP52248	<lmxll>	16	32.837	NA	389.036	NA	NA
TP72251	<lmxll>	16	33.733	NA	385.428	9	51868471
TP4223	<lmxll>	16	34.394	NA	370.481	9	52085925
TP43315	<lmxll>	16	34.888	NA	395.925	9	52990634
TP86723	<lmxll>	16	36.381	NA	436.263	9	53180068
TP20255	<lmxll>	16	38.273	NA	484.788	9	54764368
TP123259	<lmxll>	16	39.812	NA	465.755	NA	NA
TP98782	<lmxll>	16	41.763	NA	499.77	1	69806636
TP91366	<lmxll>	16	43.975	NA	520.726	9	55670148

Table A3 (cont.)

TP52841	<lmxll>	16	45.318	NA	506.123	9	55799604
TP8373	<lmxll>	16	46.417	NA	535.147	NA	NA
TP98888	<lmxll>	16	47.189	NA	528.305	9	56003641
TP113216	<lmxll>	16	48.507	NA	657.642	9	56220997
TP83726	<lmxll>	16	49.091	NA	652.62	9	56097778
TP85236	<lmxll>	16	49.901	NA	540.53	NA	NA
TP55015	<lmxll>	16	50.305	NA	552.402	9	56419573
X414	<lmxll>	16	50.726	NA	550.555	9	56100690
TP54662	<lmxll>	16	51.127	NA	664.762	9	56097878
TP68435	<lmxll>	16	51.937	NA	632.513	1	15190185
TP59498	<lmxll>	16	52.742	NA	638.625	NA	NA
TP13202	<lmxll>	16	54.063	NA	645.392	9	56467309
TP101302	<lmxll>	16	55.28	NA	625.298	9	57194281
TP20061	<lmxll>	16	57.018	NA	676.366	9	56257303
TP125071	<lmxll>	16	58.435	NA	603.572	9	57812117
TP11284	<lmxll>	16	59.258	NA	606.351	9	57602741
TP3870	<lmxll>	16	60.281	NA	558.834	NA	NA
TP48589	<lmxll>	16	64.633	NA	598.96	9	58659143
TP75233	<lmxll>	17	0	NA	581.181	9	59333527
TP46631	<lmxll>	17	4.361	NA	574.61	9	59025652
TP95603	<lmxll>	17	11.021	NA	553.261	9	58521117
TP64616	<lmxll>	17	16.555	NA	534.362	9	57823420
TP120777	<lmxll>	17	18.88	NA	539.668	1	68318838
TP43662	<lmxll>	17	22.103	NA	527.51	9	57645319
X470	<lmxll>	17	23.279	NA	544.476	9	58044029
TP12763	<lmxll>	17	23.672	NA	522.36	9	57385338
TP16369	<lmxll>	17	25.161	NA	518.836	NA	NA
TP84885	<lmxll>	17	27.04	NA	511.308	6	48147858
TP97157	<lmxll>	17	28.261	NA	500.233	9	56963100
TP49013	<lmxll>	17	29.582	NA	493.887	9	56829074
TP9341	<lmxll>	17	30.663	NA	490.12	9	56768568
TP61860	<lmxll>	17	36.506	NA	481.335	9	55849541
TP86321	<lmxll>	17	38.254	NA	467.44	9	55402729
TP117650	<lmxll>	17	39.674	NA	475.75	NA	NA
TP96150	<lmxll>	17	42.095	NA	454.36	9	55264802
TP121402	<lmxll>	17	43.388	NA	436.157	NA	NA
TP13385	<lmxll>	17	46.398	NA	445.853	NA	NA
TP62447	<lmxll>	17	48.147	NA	394.41	NA	NA
TP59903	<lmxll>	17	48.622	NA	382.283	9	53680867

Table A3 (cont.)

TP102089	<lmxll>	17	49.149	NA	388.575	9	53860871
TP22642	<lmxll>	17	49.488	NA	346.477	9	53680923
TP16542	<lmxll>	17	50.846	NA	378.784	9	53638497
TP67153	<lmxll>	17	51.891	NA	352.585	9	53015553
TP4318	<lmxll>	17	52.647	NA	250.18	9	52903503
TP123338	<lmxll>	17	53.167	NA	376.311	NA	NA
TP21137	<lmxll>	17	53.515	NA	364.107	NA	NA
TP104209	<lmxll>	17	54.369	NA	334.895	9	53603274
TP3437	<lmxll>	17	56.135	NA	323.242	9	51970533
TP122989	<lmxll>	17	57.295	NA	283.027	9	53285327
TP118704	<lmxll>	17	58.143	NA	149.171	NA	NA
TP28459	<lmxll>	17	59.212	NA	221.014	9	57115286
X167	<lmxll>	17	59.939	NA	164.38	9	50579186
TP16656	<lmxll>	17	60.284	NA	125.053	NA	NA
TP112624	<lmxll>	17	60.888	NA	100.799	9	50215521
TP50646	<lmxll>	17	63.955	NA	188.336	NA	NA
TP106647	<lmxll>	17	66.232	NA	37.849	NA	NA
TP18618	<lmxll>	17	68.286	NA	5.285	9	728092
TP86068	<lmxll>	17	69.255	NA	20.349	NA	NA
TP92159	<lmxll>	18	0	NA	14.017	10	158077
TP33061	<lmxll>	18	1.92	NA	24.183	NA	NA
TP70217	<lmxll>	18	4.216	NA	0	10	549933
TP20769	<lmxll>	18	5.642	NA	7.007	NA	NA
TP102035	<lmxll>	18	7.09	NA	35.328	10	775077
TP86555	<lmxll>	18	9.868	NA	31.463	10	1080451
TP125292	<lmxll>	18	10.715	NA	43.624	NA	NA
TP88526	<lmxll>	18	12.34	NA	40.387	NA	NA
X65	<lmxll>	18	16.025	NA	48.618	10	1924546
TP96154	<lmxll>	18	17.082	NA	52.934	10	2226827
TP32470	<lmxll>	18	18.82	NA	59.349	10	2448171
TP6022	<lmxll>	18	21.855	NA	115.892	10	3209383
TP114605	<lmxll>	18	24.449	NA	136.673	NA	NA
TP69198	<lmxll>	18	25.715	NA	130.736	6	60106362
TP31129	<lmxll>	18	27.845	NA	146.345	NA	NA
TP120830	<lmxll>	18	30.134	NA	155.386	10	4978161
TP91686	<lmxll>	18	33.356	NA	185.769	NA	NA
TP91687	<lmxll>	18	33.595	NA	184.674	NA	NA
TP54605	<lmxll>	18	34.232	NA	193.874	4	11344761
TP45504	<lmxll>	18	34.831	NA	203.103	10	7005749

Table A3 (cont.)

TP68063	<lmxll>	18	35.396	NA	198.313	10	7438104
TP329	<lmxll>	18	35.799	NA	189.742	10	7426161
TP95309	<lmxll>	18	37.055	NA	316.756	10	16768894
TP9223	<lmxll>	18	37.641	NA	305.387	NA	NA
TP40269	<lmxll>	18	38.216	NA	210.443	10	8625486
TP49281	<lmxll>	18	38.939	NA	370.176	10	8758439
TP51438	<lmxll>	18	39.366	NA	221.916	10	49425135
TP124834	<lmxll>	18	40.128	NA	249.436	NA	NA
TP15164	<lmxll>	18	40.478	NA	243.039	10	38675435
TP8740	<lmxll>	18	40.839	NA	295.879	NA	NA
TP123605	<lmxll>	18	41.5	NA	255.204	10	47786772
TP85933	<lmxll>	18	41.798	NA	227.056	NA	NA
TP81855	<lmxll>	18	42.578	NA	360.235	NA	NA
TP9459	<lmxll>	18	42.762	NA	363.821	10	8014322
TP69170	<lmxll>	18	43.003	NA	232.671	10	12135967
TP29182	<lmxll>	18	43.493	NA	282.087	10	12311532
TP110955	<lmxll>	18	43.712	NA	214.907	NA	NA
TP54171	<lmxll>	18	44.09	NA	356.44	10	8758106
TP45175	<lmxll>	18	44.25	NA	353.899	1	4192
TP55680	<lmxll>	18	44.414	NA	275.605	10	46065333
TP67698	<lmxll>	18	44.615	NA	279.003	NA	NA
TP79063	<lmxll>	18	44.843	NA	285.638	10	43151200
TP98945	<lmxll>	18	45.023	NA	261.044	10	12274069
TP51799	<lmxll>	18	45.241	NA	258.951	NA	NA
TP74281	<lmxll>	18	45.429	NA	290.443	10	28470139
TP102810	<lmxll>	18	45.673	NA	325.265	10	17944282
TP40389	<lmxll>	18	45.925	NA	217.752	10	48944892
TP3319	<lmxll>	18	46.2	NA	351.814	NA	NA
X123	<lmxll>	18	46.386	NA	275.605	10	52518354
X502	<lmxll>	18	46.386	NA	275.605	1	1042529
TP15398	<lmxll>	18	46.433	NA	348.566	10	23908878
TP49172	<lmxll>	18	46.72	NA	235.144	NA	NA
TP16716	<lmxll>	18	47.094	NA	237.904	10	17946191
TP98114	<lmxll>	18	47.412	NA	345.319	10	49894131
TP41647	<lmxll>	18	48.043	NA	340.516	10	49907281
TP27682	<lmxll>	18	48.401	NA	331.103	10	51120664
TP88067	<lmxll>	18	48.718	NA	336.076	NA	NA
TP69479	<lmxll>	18	49.73	NA	451.389	10	53742253
TP99488	<lmxll>	18	50.104	NA	484.963	10	54295007

Table A3 (cont.)

TP5549	<lmxll>	18	50.696	NA	480.007	10	54224031
TP5069	<lmxll>	18	50.986	NA	460.425	NA	NA
TP117976	<lmxll>	18	51.224	NA	494.225	10	54224091
TP32036	<lmxll>	18	51.502	NA	473.353	10	54195039
TP52653	<lmxll>	18	51.842	NA	469.424	10	54853737
TP85840	<lmxll>	18	52.565	NA	465.118	10	55067700
TP9802	<lmxll>	18	53.412	NA	502.379	10	55412157
TP27468	<lmxll>	18	53.769	NA	512.536	10	55747545
TP114823	<lmxll>	18	54.131	NA	508.056	NA	NA
TP98623	<lmxll>	18	55.791	NA	527.006	10	56030729
TP87929	<lmxll>	18	56.356	NA	520.541	10	55906531
TP44836	<lmxll>	18	57.464	NA	550.176	3	73986714
TP65378	<lmxll>	18	58.143	NA	533.71	10	56370424
TP107118	<lmxll>	18	58.733	NA	541.094	10	56434536
TP18795	<lmxll>	18	59.759	NA	558.742	NA	NA
TP34636	<lmxll>	18	60.596	NA	588.962	NA	NA
TP10873	<lmxll>	18	60.978	NA	593.167	NA	NA
TP122185	<lmxll>	18	61.415	NA	572.486	NA	NA
X242	<lmxll>	18	62.137	NA	608.306	10	58642427
TP95828	<lmxll>	18	62.363	NA	596.408	NA	NA
TP2198	<lmxll>	18	63.123	NA	583.406	NA	NA
TP45831	<lmxll>	18	65.03	NA	602.59	10	58366734
TP3578	<lmxll>	18	66.777	NA	612.301	NA	NA
TP53557	<lmxll>	18	68.302	NA	620.914	10	59069486
TP66441	<lmxll>	18	70.982	NA	630.923	10	59812956
TP78761	<lmxll>	18	72.494	NA	637.004	10	60008286
TP37246	<lmxll>	18	73.779	NA	679.945	10	59599945
TP23920	<lmxll>	18	76.385	NA	644.876	10	60861760
TP31264	<lmxll>	18	77.529	NA	666.727	10	60303251
TP90482	<lmxll>	18	78.633	NA	659.532	NA	NA
TP99974	<lmxll>	18	81.136	NA	652.306	10	60970280
TP57216	<lmxll>	19	0	NA	717.029	7	41418733
TP81380	<lmxll>	19	2.061	NA	729.371	10	60560252
TP41105	<lmxll>	19	5.714	NA	694.215	9	1068287
TP79348	<lmxll>	19	6.749	NA	706.872	NA	NA
TP76749	<lmxll>	19	8.176	NA	699.889	NA	NA
TP99824	<lmxll>	19	10.655	NA	685.381	10	59764614
TP66551	<lmxll>	19	13.516	NA	641.933	10	58700730
X273	<lmxll>	19	14.468	NA	677.365	10	58642342

Table A3 (cont.)

TP89816	<lmxll>	19	15.454	NA	616.314	10	58462111
TP89188	<lmxll>	19	16.751	NA	588.085	10	54701351
TP42848	<lmxll>	19	18.122	NA	546.525	10	54687690
TP4872	<lmxll>	19	18.976	NA	564.624	10	55098329
TP63994	<lmxll>	19	21.09	NA	536.798	10	53702846
TP98235	<lmxll>	19	21.942	NA	524.468	10	53512454
TP43265	<lmxll>	19	22.572	NA	531.931	NA	NA
TP17900	<lmxll>	19	23.665	NA	459.703	10	51408727
TP31559	<lmxll>	19	24.699	NA	373.152	10	47105428
TP121981	<lmxll>	19	25.174	NA	445.263	10	49463042
TP80105	<lmxll>	19	25.837	NA	465.914	NA	NA
TP20190	<lmxll>	19	26.378	NA	381.805	10	47114060
TP84646	<lmxll>	19	27.117	NA	391.337	2	136117
TP102059	<lmxll>	19	27.564	NA	490.082	10	47756196
TP18309	<lmxll>	19	27.782	NA	494.612	NA	NA
TP69126	<lmxll>	19	28.373	NA	484.367	10	51744815
TP24621	<lmxll>	19	28.653	NA	478.649	10	50013912
X647	<lmxll>	19	28.836	NA	412.54	10	50564913
TP48456	<lmxll>	19	29.199	NA	386.984	10	9466193
TP7624	<lmxll>	19	29.4	NA	407.82	5	3220286
TP52141	<lmxll>	19	29.767	NA	421.551	10	49640501
TP29278	<lmxll>	19	30.151	NA	397.796	10	49564051
TP90491	<lmxll>	19	30.553	NA	428.507	NA	NA
TP58473	<lmxll>	19	30.981	NA	435.971	NA	NA
TP73264	<lmxll>	19	31.519	NA	404.127	6	42464981
TP120740	<lmxll>	19	32.561	NA	366.261	10	60371130
TP62427	<lmxll>	19	33.18	NA	355.77	10	11351785
TP59076	<lmxll>	19	33.977	NA	360.66	10	9137430
TP16722	<lmxll>	19	34.844	NA	343.874	10	8065062
TP12801	<lmxll>	19	35.311	NA	324.685	10	6934914
TP102291	<lmxll>	19	35.964	NA	350	10	7442757
TP18932	<lmxll>	19	36.813	NA	331.202	NA	NA
TP70095	<lmxll>	19	37.396	NA	318.567	NA	NA
TP47170	<lmxll>	19	38.625	NA	300.838	10	6481062
TP53945	<lmxll>	19	40.976	NA	288.887	NA	NA
TP66925	<lmxll>	19	41.795	NA	282.453	10	5340338
TP46375	<lmxll>	19	42.758	NA	273.478	10	4938477
TP51290	<lmxll>	19	44.737	NA	268.345	10	4445432
TP107400	<lmxll>	19	46.759	NA	261.892	10	4020092

Table A3 (cont.)

TP121155	<lmxll>	19	48.275	NA	255.813	5	1549802
TP95959	<lmxll>	19	49.335	NA	242.975	10	3630955
TP89523	<lmxll>	19	50.516	NA	239.341	NA	NA
TP70255	<lmxll>	19	52.841	NA	220.171	10	3437348
TP72930	<lmxll>	19	54.086	NA	215.98	10	3056936
TP10261	<lmxll>	19	55.256	NA	231.865	NA	NA
TP106202	<lmxll>	19	58.661	NA	207.724	NA	NA
TP56427	<lmxll>	19	59.95	NA	201.45	NA	NA
TP53381	<lmxll>	19	61.776	NA	191.261	10	1829933
TP98291	<lmxll>	19	62.709	NA	195.973	NA	NA
TP25639	<lmxll>	19	63.712	NA	186.548	10	2273092
TP102978	<lmxll>	19	66.073	NA	179.864	NA	NA
TP124025	<lmxll>	19	67.729	NA	172.264	NA	NA
TP17017	<lmxll>	19	70.678	NA	163.24	NA	NA
X73	<lmxll>	19	72.187	NA	140.998	10	723372
TP90066	<lmxll>	19	73.358	NA	149.736	10	1392613
TP28083	<lmxll>	19	77.883	NA	142.028	NA	NA
X116	<hkxhk>	11	17.649	NA	NA	6	49174455
X21	<hkxhk>	12	72.075	NA	34.842	NA	NA
X625	<hkxhk>	7	54.076	NA	NA	4	15759507
TP59971	<hkxhk>	7	44.19	NA	NA	4	7380085
TP77278	<hkxhk>	7	21.88	NA	64.684	4	3510254
TP87928	<hkxhk>	5	72.546	NA	10.054	NA	NA
TP92238	<hkxhk>	12	78.803	NA	6.07	NA	NA
TP94445	<hkxhk>	15	55.806	NA	22.303	8	4403215

[*] Marker type followed by the cross pollinator (CP) population type coding in JoinMap4.1. <nnxnp> indicates markers only polymorphic in the male parent (‘Kaskade’), <lmxll> indicates markers only polymorphic in the female parent (‘Strictus’), and <hkxhk> indicates markers polymorphic in both parents.

[†] Linkage group.

Table A4 Mapped but not cloned zebra stripe genes in maize and rice, and their corresponding orthologous regions in *Miscanthus*.

Gene name	Gene symbol	Species	Linkage group for the species in which gene was identified	Orthologous region(s) in sorghum based on marker positions on synteny maps in the Gramene database		DNA markers bracketing the maize or rice zebra stripe gene within the corresponding genomic region in sorghum and mapped to the expected *Miscanthus* linkage groups (physical distance of marker in Mb to the nearest flanking region in sorghum is shown in parentheses)					Markers within the corresponding genomic region in sorghum but mapped to unexpected linkage groups in *Miscanthus*	
				LG[*]	Range (Mb)	LG	Left flanking[†]		Right flanking[†]		LG	Marker
zebra crossbands1	*zb1*	*Zea*	5_long arm	4	58.624-63.717	7	TP41342[§]	(+0.141)	TP94722[§]	(+0.068)	14	TP45746
						8	TP11494	(+0.028)	TP100217	(+0.055)	17	X174
zebra crossbands2	*zb2*	*Zea*	Unknown									
zebra crossbands3	*zb3*	*Zea*	1_short arm	1	41.253-73.834	1	TP99150	(-2.606)	TP52517	(-1.122)	4	TP38875
						2	TP99812	(-2.833)	TP14576	(-0.144)	13	TP87906
											18	TP24535
											11	TP32722
											18	TP85797
											10	TP13550[‡‡]
											8	TP81533
											5	TP9166
											12	TP46771
											17	TP120777
											16	TP98782

Table A4 (cont.)

				8	0.010-0.057	14	TP92838	(-0.029)	TP39889	(+0.613)	3	TP59249[‡‡]
						15	TP66248	(-1.075/-1.028)‖			3	TP81388 [§§]
											19	TP13181
zebra crossbands4	*zb4*	*Zea*	1_short arm	1	62.174-62.764	1	TP22362	(-0.134)	TP73053	(-0.019)		
						2	TP85751	(+0.180)	TP115280	(-0.055)		
zebra crossbands5	*zb5*	*Zea*	10	6		11						
						12						
				7		7						
						13						
				8		14						
						15						
				9		16						
zebra crossbands6	*zb6*	*Zea*	4_long arm	4	50.986-57.122	7	TP16138[**]	(-5.330)	TP90140[**]	(+0.404)	12	TP93885
						8	TP77373	(+0.473)	TP89888	(-0.250)		
zebra crossbands8	*zb8*	*Zea*	9_short arm	10	3.595-4.076	18	TP68808	(+0.002)	TP57706	(+0.369)		
						19	TP95959	(-0.036)	TP107400	(-0.056)		
zebra necrotic1	*zn1*	*Zea*	10_long arm	7	8.782-12.035	7	TP60980[††]	(+2.937)	TP56113[††]	(+2.027)		
						13	TP40257	(+0.009)	TP68246	(+0.548)		
zebra necrotic2	*zn2*	*Zea*	Unknown									

Table A4 (cont.)

zebra necroticN571D	*zn*n571d*	*Zea*	5_long arm	1	1
					2
				4	7
					8
				10	18
					19
zebra1	*z1*	*Oryza*	11	5	9
					10
				8	14
					15
zebra3	*z3*	*Oryza*	3	1	1
					2
zebra4	*z4*	*Oryza*	8	7	7
					13
zebra5	*z5*	*Oryza*	4	6	11
					12
zebra6	*z6*	*Oryza*	7	2	3
					4
				10	18
					19
zebra7	*z7*	*Oryza*	5	9	16
					17

Table A4 (cont.)

zebra8	*z8*	*Oryza*	1	3		5						
						6						
zebra9	*z9*	*Oryza*	3	1		1						
						2						
zebra10	*z10*	*Oryza*	7	2		3						
						4						
				10		18						
						19						
zebra11	*z11*	*Oryza*	2	4		7						
						8						
zebra12	*z12*	*Oryza*	2	4		7						
						8						
zebra13	*z13*	*Oryza*	6	10		18						
						19						
				8		14						
						15						
zebra14	*z14*	*Oryza*	5	9		16						
						17						
						16						
						17						
zebra15	*z15*	*Oryza*	5_short arm	9	0.000-17.508	16	TP96200	(-0.915)	TP33918	(-5.531)		
						17	TP99661	(-0.658)	TP103797	(-2.764)		

[*] Linkage group.

[†] The “+” sign before the physical distance indicates marker outside of the region, and the “-” sign indicates marker within the region.

[§] Maize *zb1* gene region is outside of the QTL regions for *Miscanthus zb1*, *zb2*, and *zbi1*, and the distance from the QTL peak to the nearest flanking region of maize *zb1* is 15.5 cM, 30.5 cM, and 19.5 cM, respectively.

[**] Maize *zb6* gene region includes the QTL regions for *Miscanthus zb1*, *zb2*, and *zbi1*, and the distance from the QTL peak to the nearest flanking region of maize *zb6* is 29.8 cM, 14.8 cM, and 25.8 cM, respectively.

[††] Maize *zn1* gene region is outside of the QTL regions for *Miscanthus zb1*, *zb2*, and *zbi1*, and the distance from the QTL peak to the nearest flanking region of maize *zn1* is 28.2 cM, 13.2 cM, and 24.2 cM, respectively.

[‡‡] Markers are outside of their corresponding *Miscanthus* QTL region, and none of the markers are within 20 cM of its corresponding QTL peak.

[§§] Distance between the marker and its corresponding *Miscanthus* QTL cannot be calculated due to <lmxll> marker type, which indicates only polymorphic in the female parent (‘Strictus’), and therefore not mapped on the male parent (‘Kaskade’) map.

||Only one marker was found to be close to the corresponding genomic region in sorghum because the region was located towards the end of the linkage group. Physical distance was calculated between the marker position in sorghum and both flanking region in sorghum and separated by "/".

Table A5 Candidate genes for *Miscanthus* zebra stripe presence/absence and intensity identified from sorghum, maize, rice and *Arabidopsis* due to their function in chloroplast development and chlorophyll biosynthesis.

Miscanthus QTL			Putative orthologs					
Name	1.5-LOD support interval (cM)		Orthologous region(s) in sorghum based on sorghum physical map		Species	Gene	Function	Orthologous genes are indicated by the same number within section for each *Miscanthus* QTL
	LG[*]	Range (cM)	LG	Range(Mb)				
zb3 & *zbi2*	10	2.000-9.000	5	0.637-1.896	*Sorghum*	Sb05g000530	ferric iron binding	1
						Sb05g000870	putative uncharacterized protein	2
						Sb05g001270	cysteine desulfurase NFS1	3
						Sb05g001450	similar to serine/threonine-protein kinase NAK, putative, expressed	4
					Zea	GRMZM2G325575	ferritin-1, chloroplastic precursor/ferritin1/ferritin/ferritin-4	1
						GRMZM5G829928	putative uncharacterized protein	2
						GRMZM2G059700	cysteine desulfurylase	3
						AC212859.3_FG003	unknown	4
					Oryza	Os12g01530.2	ferritin-1, chloroplast precursor, putative, expressed	1
						Os11g01890.1	expressed protein	2
						Os12g18900.1	aminotransferase, putative, expressed	3

Table A5 (cont.)

						Os06g45280.1	protein kinase APK1B, chloroplast precursor, putative, expressed	4
					Arabidopsis	AT2G40300.1	ferritin 4	1
						AT1G21600.2	plastid transcriptionally active 6, involved in plastid gene expression	2
						AT1G08490.1	chloroplastic NIFS-like cysteine desulfurase	3
						AT5G01020.1	protein kinase superfamily protein	4
zb2	7	34.000-41.968	7	36.467-62.838	*Sorghum*	Sb07g024090	chlorophyllase-2 activity, chlorophyll catabolic process	1
						Sb07g025550	similar to CRS2-associated factor 1, chloroplast precursor	2
						Sb07g027430	similar to chloroplast 30S ribosomal protein S3	3
						Sb07g027500	PsbP, similar to thylakoid lumen protein, chloroplast-like	4
						Sb07g027700	oxidoreductase activity	5
						Sb07g027760	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, iron ion binding, protein binding	6
					Zea	GRMZM2G103197	electron carrier activity, oxidoreductase activity, chlorophyllase activity	1
						GRMZM2G173923	CRS2-associated factor 1, chloroplastic precursor (chloroplastic group IIA intron splicing facilitator CRS2-associated factor 1)	2
						GRMZM2G024079	unknown	3
						GRMZM2G172723	PsbP, calcium ion binding, oxygen evolving complex, photosynthesis, photosystem II, extrinsic to membrane	4

Table A5 (cont.)

						GRMZM2G115442	3-oxoacyl-[acyl-carrier protein] reductase	5
						GRMZM2G009479	lipoxygenase activity	6
					Oryza	Os10g28370.1	chlorophyllase-2, chloroplast precursor, putative, expressed	1
						Os01g31110.1	CRS2-associated factor 1, chloroplast precursor, putative, expressed	2
						Os04g16824.1	chloroplast 30S ribosomal protein S3, putative, expressed	3
						Os08g40160.1	thylakoid lumen protein, chloroplast precursor, putative, expressed	4
						Os08g39960.1	3-oxoacyl-reductase, chloroplast precursor, putative, expressed	5
						Os08g39850.1	lipoxygenase, chloroplast precursor, putative, expressed	6
					Arabidopsis	AT1G19670.1	chlorophyllase 1	1
						AT2G20020.1	RNA-binding CRS1 / YhbY (CRM) domain-containing protein	2
						ATCG00800.1	structural constituent of ribosome	3
						AT1G76450.1	photosystem II reaction center PsbP family protein	4
						AT3G55290.1	NAD(P)-binding rossmann-fold superfamily protein	5
						AT3G45140.1	lipoxygenase 2	6
zb1 & *zbi1*	7	46.000-52.000	4	40.066-62.711	*Sorghum*	Sb04g031830	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase activity, terpenoid biosynthetic process	1

Table A5 (cont.)

					Zea	AC209374.4_FG002	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase activity, terpenoid biosynthetic process	2
					Oryza	Os02g45660.1	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, ISPF chloroplast precursor, putative, expressed	3
					Arabidopsis	AT1G63970.1	isoprenoid F, encodes a protein with 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase activity. Plants defective in this gene display an albino lethal phenotype	4
zbi3	3	7.000-28.000	2	1.959-74.085	*Sorghum*	Sb02g002690	photosystem II oxygen-evolving enhancer protein 2, calcium ion binding, extrinsic to membrane, photosynthesis	1
						Sb02g002830	photosystem II 10 kDa polypeptide PsbR, oxygen evolving complex, thylakoid membrane, photosynthesis	2
						Sb02g002900	oxidoreductase activity, oxidation-reduction process	3
						Sb02g002960	photosystem I reaction center subunit psaK/psaG, chloroplast precursor, membrane, photosystem I	4
						Sb02g003230	9-cis-epoxycarotenoid dioxygenase	5
						Sb02g003310	RNA recognition motif	6
						Sb02g004380	chlorophyll A-B binding protein, early light-induced protein	7
						Sb02g004580	tryptophan synthase alpha chain, tryptophan metabolic process, tryptophan synthase activity	8
						Sb02g006100	enzymatic reaction of: carotene 7,8-desaturase (electron transport), in carotenoid biosynthesis pathway	9

Table A5 (cont.)

	Sb02g006430	NAD dependent epimerase/dehydratase	10
	Sb02g009540	thiolester hydrolase activity, fatty acid biosynthetic process	11
	Sb02g009570	aspartate kinase, cellular amino acid biosynthetic process	12
	Sb02g009575	aspartate kinase	13
	Sb02g010190	photosystem I reaction center subunit IV/PsaE, photosynthesis, chloroplast precursor	14
	Sb02g012201	chlorophyllase activity	15
	Sb02g012300	enzymatic reaction of: chlorophyllase-2, chloroplast precursor, putative	16
	Sb02g013390	sulfate/bicarbonate/oxalate exchanger SAT-1 and related transporters (SLC26 family), transmembrane transport, transporter activity, integral to membrane, transport	17
	Sb02g014000	similar to putative defective chloroplasts and leaves (DCL) protein, protein of unknown function (DUF3223)	18
	Sb02g018530	enoyl-[acyl-carrier protein] reductase	19
	Sb02g019450	similar to bifunctional aspartokinase/homoserine dehydrogenase 2, chloroplast precursor (AK-HD 2) (AK-HSDH 2)	20
	Sb02g020290	light-harvesting complex II chlorophyll a/b binding protein 7	21
	Sb02g020320	ferrochelatase activity, heme biosynthetic process	22

Table A5 (cont.)

	Sb02g020410	GDP-mannose pyrophosphorylase/mannose-1-phosphate guanylyltransferase, glucose-1-phosphate adenylyltransferase, nucleotidyltransferase activity, biosynthetic process	23
	Sb02g020430	anthranilate synthase component II, indole-3-glycerol-phosphate synthase activity	24
	Sb02g021480	polypeptide: retinal pigment epithelial membrane protein, expressed	25
	Sb02g021490	beta, beta-carotene 15,15'-dioxygenase and related enzymes	26
	Sb02g022910	porin/voltage-dependent anion-selective channel protein, transmembrane transport	27
	Sb02g022920	menaquinone-specific isochorismate synthase	28
	Sb02g022940	CRS1/YhbY (CRM) domain, RNA binding	29
	Sb02g024510	[ribulose-bisphosphate carboxylase]-lysine N-methyltransferase, protein binding	30
	Sb02g025740	light-harvesting complex I chlorophyll a/b binding protein 2	31
	Sb02g026930	zinc ion binding, predicted carbonic anhydrase involved in protection against oxidative damage	32
	Sb02g027070	phosphoribosylaminoimidazolesuccinocarboxamide synthase activity	33
Zea	GRMZM2G016677	photosynthesis, calcium ion binding, thylakoid membrane, oxygen evolving complex, extrinsic to membrane	1
	GRMZM2G174984	photosynthesis, integral to thylakoid membrane, oxygen evolving complex, thylakoid membrane38	2

Table A5 (cont.)

GRMZM2G011858	Oxidation-reduction pr39ocess, ferredoxin-NADP+ reduc40tase activity, oxidoreductase activity, favin adenine dinucleotide binding, NADP binding, thylakoid membrane	3
GRMZM2G012397	photosynthesis, integral to thylakoid membrane, photosystem I, membrane	4
AC205726.4_FG005	unknown	5
GRMZM2G026614	nucleic acid binding, RNA binding, plastid stroma	6
GRMZM2G355752	early light inducible protein 1 (elip 1)	7
GRMZM2G015436	tryptophan metabolic process, metabolic process, catalytic activity, tryptophan synthase activity	8
GRMZM2G454952	metabolic process, carotenoid biosynthetic process, oxidation-reduction process, oxidoreductase activity, carotene 7,8-desaturase activity, plastid	9
GRMZM2G111216	homoiothermy, cellular metabolic process, response to freezing, catalytic activity, UDP-glucose 4-epimerase activity, coenzyme binding, ice binding, plastid stroma	10
GRMZM2G007489	enzymatic reaction of: Oleoyl-[acyl-carrier-protein] hydrolase (Dodecanoyl-[acyl-carrier-protein] hydrolase)	11
GRMZM2G019314	unknown	12
GRMZM2G019314	unknown	13
GRMZM2G016066	photosynthesis, catalytic activity, thylakoid membrane, plastid, photosystem I reaction center	14

Table A5 (cont.)

GRMZM2G103197	electron carrier activity, oxidoreductase activity, chlorophyllase activity	15
GRMZM2G103197	electron carrier activity, oxidoreductase activity, chlorophyllase activity	16
GRMZM2G068212	sulfate transport, transmembrane transport, transporter activity, secondary active sulfate transmembrane transporter activity, integral to membrane	17
GRMZM2G037743	protein of unknown function (DUF3223)	18
GRMZM2G070422	metabolic process, oxidation-reduction process, oxidoreductase activity, plastid stroma	19
GRMZM2G104546	tRNA amonoacylation for protein translation, cellular amino acid metabolic process, cellular amino acid biosynthetic process, aspartate family amino acid biosynthetic process, oxidation-reduction process, nucleotide binding, aspartate kinase activity, homoserine dehydrogenase activity, aminoacyl-tRNA ligase activity, ATP binding, oxidoreductase activity, amino acid binding, NADP binding, cytoplasm	20
GRMZM2G131489	integral to thylakoid membrane	21
GRMZM2G047095	heme biosynthetic process, ferrochelatase activity	22
GRMZM2G061795	glucose-1-phosphate adenylytransferase activity, nucleotidyltransferase activity	23
GRMZM2G145870	tryptophan metabolic process, metabolic process, catalytic activity, indole-3-3glycerol-phosphate synthase activity, plastid stroma	24

Table A5 (cont.)

	AC197699.3_FG002	beta, beta-carotene 15,15'-dioxygenase and related enzymes, retinal pigment epithelial membrane protein, 9-cis-epoxycarotenoid dioxygenase	25
	AC194863.3_FG006	9-cis-epoxycarotenoid dioxygenase	26
	AC200234.3_FG002	unknown	27
	GRMZM2G022837	isochorismate synthase	28
	GRMZM2G142740	RNA binding	29
	GRMZM2G154767	unknown	30
	GRMZM2G117412	integral to thylakoid membrane	31
	GRMZM2G145101	carbon utilization, carbonate dehydratase activity, zinc ion binding	32
	GRMZM2G117268	phosphoribosylaminoimidazolesuccinocarboxamide synthase activity, purine nucleotide biosynthetic process	33
Oryza	Os07g04840.1	PsbP, putative, expressed	1
	Os07g05365.1	photosystem II 10 kDa polypeptide, chloroplast precursor, putative, expressed	2
	Os07g05400.1	ferredoxin--NADP reductase, chloroplast precursor, putative, expressed	3
	Os07g05480.1	photosystem I reaction center subunit, chloroplast precursor, putative, expressed	4
	Os07g05940.1	9-cis-epoxycarotenoid dioxygenase 1, chloroplast precursor, putative, expressed	5
	Os07g06450.1	RNA recognition motif containing protein, putative, expressed	6
	Os07g08160.1	early light-induced protein, chloroplast precursor, putative, expressed	7

Table A5 (cont.)

	Os07g08430.1	indole-3-glycerol phosphatelyase, chloroplast precursor, putative, expressed	8
	Os07g10490.1	zeta-carotene desaturase, chloroplast/chromoplast precursor, putative, expressed	9
	Os07g11110.1	NAD dependent epimerase/dehydratase family protein, putative, expressed	10
	Os11g43820.1	myristoyl-acyl carrier protein thioesterase, chloroplast precursor, putative, expressed	11
	Os07g20544.1	aspartokinase, chloroplast precursor, putative, expressed	12
	Os03g63330.1	aspartokinase, chloroplast precursor, putative, expressed	13
	Os07g25430.1	photosystem I reaction center subunit IV A, chloroplast precursor, putative, expressed	14
	Os10g28370.1	chlorophyllase-2, chloroplast precursor, putative, expressed	15
	Os10g28370.1	chlorophyllase-2, chloroplast precursor, putative, expressed	16
	Os09g06499.1	sulfate transporter 4.1, chloroplast precursor, putative, expressed	17
	Os08g21700.1	DCL, chloroplast precursor, putative, expressed	18
	Os09g10600.1	enoyl-acyl-carrier-protein reductase NADH, chloroplast precursor, expressed	19
	Os09g12290.1	bifunctional aspartokinase/homoserine dehydrogenase, chloroplast precursor, putative, expressed	20

Table A5 (cont.)

Os09g12540.1	chlorophyll A-B binding protein, putative, expressed	21
Os09g12560.1	ferrochelatase-2, chloroplast precursor, putative, expressed	22
Os09g12660.1	glucose-1-phosphate adenylyltransferase large subunit, chloroplast precursor, putative, expressed	23
Os09g08130.2	indole-3-glycerol phosphate synthase, chloroplast precursor, putative, expressed	24
Os08g28240.1	carotenoid cleavage dioxygenase, putative, expressed	25
Os09g15240.1	carotenoid cleavage dioxygenase, putative, expressed	26
Os09g19734.3	isochorismate synthase 1, chloroplast precursor, putative, expressed	27
Os09g19734.1	isochorismate synthase 1, chloroplast precursor, putative, expressed	28
Os09g19850.1	chloroplastic group IIA intron splicing facilitator CRS1, chloroplast precursor, putative, expressed	29
Os09g24530.1	ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase, chloroplast precursor, putative, expressed	30
Os09g26810.1	chlorophyll A-B binding protein, putative, expressed	31
Os09g28910.1	carbonic anhydrase, chloroplast precursor, putative, expressed	32

Table A5 (cont.)

	Os09g29190.1	phosphoribosylaminoimidazole-succinocarboxamide synthase, chloroplast precursor, putative, expressed	33
Arabidopsis	AT1G06680.1	photosystem II subunit P-1	1
	AT1G79040.1	photosystem II subunit R	2
	AT1G30510.1	root FNR 2	3
	AT1G30380.1	photosystem I subunit K	4
	AT1G78390.1	9-cis-epoxycarotenoid dioxygenase 9	5
	AT3G52380.1	chloroplast RNA-binding protein 33	6
	AT3G22840.1	chlorophyll A-B binding family protein	7
	AT4G02610.1	aldolase-type TIM barrel family protein	8
	AT3G04870.1	zeta-carotene desaturase	9
	AT3G63140.1	chloroplast stem-loop binding protein of 41 kDa	10
	AT1G08510.1	fatty acyl-ACP thioesterases B	11
	AT5G13280.1	aspartate kinase 1	12
	AT5G14060.2	aspartate kinase family protein	13
	AT2G20260.1	photosystem I subunit E-2	14
	AT1G19670.1	chlorophyllase 1	15
	AT5G43860.1	chlorophyllase 2	16
	AT5G13550.1	sulfate transporter 4.1	17
	AT3G46630.1	protein of unknown function (DUF3223)	18
	AT2G05990.1	NAD(P)-binding Rossmann-fold superfamily protein	19
	AT4G19710.2	aspartate kinase-homoserine dehydrogenase ii	20

Table A5 (cont.)

AT1G76570.1	chlorophyll A-B binding family protein	21
AT5G26030.1	ferrochelatase 1	22
AT5G48300.1	ADP glucose pyrophosphorylase 1	23
AT2G04400.1	aldolase-type TIM barrel family protein	24
AT3G63520.1	carotenoid cleavage dioxygenase 1	25
AT1G30100.1	9-cis-epoxycarotenoid dioxygenase 5	26
AT3G01280.1	voltage dependent anion channel 1	27
AT1G18870.1	isochorismate synthase 2	28
AT4G29750.1	CRS1 / YhbY (CRM) domain-containing protein	29
AT1G14030.1	rubisco methyltransferase family protein	30
AT1G19150.1	photosystem I light harvesting complex gene 6	31
AT4G33580.1	beta carbonic anhydrase 5	32
AT3G21110.1	purin 7	33

[*] Linkage group.

Supplementary materials and methods

Genomic DNA extraction

Young leaves from each progeny of the mapping population and the two parental genotypes were collected in 15 mL flip tubes (Nunc EZ) and stored in a -80 ˚C freezer. All the leaf samples were freeze dried as follows: samples were first frozen in the freeze drier at -34. 4 ˚C overnight, then vacuum was turned on and samples were freeze dried at -28.8 ˚C for 24 hours, -2.2 ˚C for 12-24 hours, 4.4 ˚C for 12-24 hours, 15.5 ˚C for 12-24 hours, 23.8 ˚F for 12-24 hours. After the samples were freeze dried, one 4 mm stainless steel ball and three 11 mm stainless steel balls were added it to the 15 mL tubes for grinding. All the dried leaf samples were pulverized at 1500 rpm for 3 minutes using a Geno/Grinder 2000 ball mill (SPEX SamplePrep, LLC; Metuchen, NJ). Lyophilized samples were stored at -20 ˚C before and after milling. Genomic DNA was extracted from lyophilized, powdered leaf tissue by using a CTAB method modified from Kabelka *et al.* (2002). DNA was quantified using a Quant-iT^{TM} dsDNA Picogreen® kit (Life Technologies) and DNA concentration was normalized to 100 ng/ul for GoldenGate™ and RAD-seq analysis.

RAD-seq libraries preparation

The protocol for generating RAD libraries for Illumina sequencing was developed by Dr. Lindsay Clark in Erik Sacks Lab at the University of Illinois (Clark *et al.*, 2014), based on a protocol used on sorghum, barley, and wheat (Poland *et al.*, 2012). Genome complexity reduction was achieved with a two-enzyme system, which includes one infrequent-cutter and one frequent-cutter. The combination of 6 bp rare-cutting enzyme *Pst*I (CTGCAG) and a 4 bp common-cutting enzyme *Msp*I (CCGG) produced a digest mainly composed of fragments with a rare cut-site and a common cut-site or fragments with two common cut-sites. Barcoded forward adapter (P1 adapter), contained a forward amplification primer site, an Illumina sequencing primer site, and a 4-10 bp barcode as unique identifiers for each DNA fragment. P1 adapters were designed with the *Pst*I restriction overhang whereas the P2 adapters (common reverse adapter) bind to the *Msp*I generated overhang. The P2 adapter was designed as a divergent "Y" adapter, containing the reverse complement of the reverse amplification primer site. This design prevented the amplification of genomic fragments lacking a P1 adapter and only amplified the

*Pst*I-*Msp*I fragments, which produced a uniform library, all consisting of the barcoded forward adapter and the common reverse adapter. The two-enzyme approach also allowed us to multiplex 95 samples into one sequencing library with one unused barcode as contamination control and library identifier and only tags adjacent to *Pst*I sites were sequenced. In this way, large numbers of SNPs can be both mined and genotyped inexpensively. Most individuals from this mapping population were duplicated in a second round of libraries in order to obtain at least 500,000 read counts per sample, except for 36 individuals with low concentrations (less than 50 ng/ul). These 36 individuals were diluted to 30 ng/ul and only included in library once for sequencing. Both parents were included in four libraries to obtain high read depth.

Adapters: A 96-well plate of *Pst*I adapters at 1 μM were provided by Dr. Pat Brown at the University of Illinois, Urbana-Champaign (Thurber *et al.*, 2013) and *Msp*I adapters were ordered from Integrated DNA Technologies (Coralville, Iowa, U.S.). *Pst*I adapters were adjusted to 0.1 μM whereas *Msp*I adapters were adjusted to 10 μM. The adapters were annealed by heating to 95°C and then slowly cooling to 25°C at a rate of -1°C /20 seconds.

*Pst*I adapters:

- Adapter 1 top:

  5'GATCTACACTCTTTCCCTACACGACGCTCTTCCGATCTxxxxTGCA3'

- Adapter 1 bottom:

  5'yyyyAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTAGATC3'

xxxx and yyyy were the barcode and its reverse complement, respectively. Barcodes and oligo sequences were obtained from Dr. Pat Brown's lab at the University of Illinois.

*Msp*I adapters:

- Adapter 2 top:
  5'CGCTCAGGCATCACTCGATTCCTCCGAGAACAA3'
- Adapter 2 bottom:
  5'CAAGCAGAAGACGGCATACGACGGAGGAATCGAGTGATGCCTGAG3'

*Msp*I adapters were ordered from the New England Biolabs.

Illumina PCR primers:

- PCR1:

  5'AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTC CGATCT3'

- PCR2:

  5'CAAGCAGAAGACGGCATACGA3'

DNA quantification and dilution: The genomic DNA was quantified using Quant-iT Picogreen kit (Life Technologies Corporation, Carlsbad, California, U.S.). Based on the Picogreen concentration estimates, the genomic DNA was diluted to a uniform concentration of 50 ng/µl in a buffer consisting of 10 mM Tris and 0.1 mM EDTA.

Restriction digestion: 250 ng of genomic DNA from each individual (50 ng/µl) was digested in 15 ul total restriction digestion master mix consisting of 1X NEB Buffer4 (New England Biolabs) with 5 U each of *Pst*I- HF(High-Fidelity) and *Msp*I ordered from New England Biolabs (Ipswich, Massachusetts, U.S.). Digestion reactions were incubated at 37 °C for 3 hours, followed by a 20-minute inactivation step at 80°C.

Ligation: Ligation reaction was completed in the same tube/plate as digestion. For 50 ng/ul genomic DNA, 0.15 pmol of barcoded *Pst*I adapters were first added to each well, followed by 5 pmol *Msp*I Y-adapter, 200 U T4 DNA ligase (New England Biolabs), and 8.5 µl of ligation master mix consisting of 1.18X T4 ligase buffer and 2.94 mM ATP. Ligation reactions were incubated at 25 °C for 2 hours and then at 65 °C for 20 minutes in order to inactivate the ligase.

Clean up and amplification: Ligated samples from all the columns were pooled together into a PCR 8-well strip tube and 5 µl from each well of the plate were added to the wells on the strip tube. 60 µl of each well on the strip tube were mixed into one 1.5 ml tube and kept on ice. 40 µl of the pooled library were combined with a loading dye and run on 2% agarose gel with ethidium bromide for 20 minutes at 100 V until the ladder bands below 500 bp were distinguishable. A clean razor blade was used for each library to cut out the library smear between 200-500 bp where DNA was visible in this range. The Qiagen Gel Extraction Kit (Qiagen, Venlo, Netherlands) was used to purify the DNA out of the gel slice. 3 ul of the gel-extracted purified library was amplified in a 50 µl PCR reaction (thermal cycling program at 98 °C for 30 seconds, then for 15 cycles consisting of 98 °C for 10 seconds, 65 °C for 30 seconds, 72 °C for 30 seconds and at 72 °C for 5 minutes.) using a high-fidelity polymerase Kapa Master Mix (New England Biolabs) and universal Illumina primers. The PCR product was run on a 2% agarose gel in order to remove primer-dimers.

Quality control: Each library was quantified using a Quant-iT Picogreen kit (Life Technologies) in order to determine concentration (with the expected concentration of 10's of ng/µl). A DNA chip was run on the Bioanalyzer (Agilent Technologies, Inc.), a chip-based capillary electrophoresis machine to analyze RNA, DNA, and protein. It was expected to show a smooth curve from around 200 to 500 bp. The Bioanalyzer (Agilent Technologies) software was used to calculate the average fragment size. The concentration of the PCR product in nM was calculated using the following equation:

$$z = \frac{10^6 * x}{649y}$$

x is the concentration in ng/µl, *y* is the average size in base pairs, and *z* is the concentration in nM. Each library was diluted to 10 nM in10 mM Tris. 20 µl of 10 nM library was sent to the University of Illinois Roy J. Carver Biotechnology Center DNA Sequencing Unit. A real-time PCR was used to confirm a concentration of 10 nM. Each library was sequenced on an Illumina HiSeq 2000 with 100 bp single-end reads. Fastq file sequencing data were obtained from the Keck Center at the University of Illinois for analysis.

Sequence analysis and RAD-seq SNPs genotype calling

The Universal Network-Enabled Analysis Kit (UNEAK) pipeline (Lu *et al.*, 2013) in TASSEL version 3.0 standalone was used for discovering SNPs and calling genotypes. The enzyme set *PstI-MspI* was selected for creating tag count files from FASTQ sequence files. The *UMergeTaxaTagCountPlugin* was used to merge all the tag count files across 299 taxa with a minimum tag count set at the default 5, which means only the tags with five or more reads across all individuals were retained for pairwise alignment. From the *MergeTaxaTagCountPlugin*

3,826,966 unique tags were produced. Then, the *UTagCountToTagPairPlugin* was used with error tolerance rate of default 0.03, and identified 126,055 reciprocal tag pairs, which only differ in one nucleotide (SNPs). The *UMapInfoToHapMapPlugin* was used to further filter the SNP data, with a minimum minor allele frequency (MAF) of 0.15 and a maximum minor allele frequency of 0.5. To reduce missing data, the minimum call rate (mnC) of 90% for *UMapInfoToHapMapPlugin* was chosen, yielding 10,398 SNPs. To give accurate genotype calls, we classified SNP genotypes using the read count information from the *hapmap.hmc* file via the UNEAK pipeline. For a given SNP, if only a single allele was detected for a given individual, a minimum of five reads was required to call a homozygote. If fewer than five reads were present, a missing genotype was assigned to that individual in order to avoid the error of calling a genotype a homozygote, when in fact it is a heterozygote; 3.9% of the overall data was converted to missing in this way. 119,974 missing genotypes were assigned across all the individuals and SNPs. Three confirmed *Miscanthus sinensis* doubled haploid (DH) lines (Głowacka *et al.*, 2012; Swaminathan *et al.*, 2012) were used to distinguish paralogous loci from heterozygous loci. Any SNPs appearing heterozygous in at least one of the three DH lines were removed from the data set. 2,229 SNPs were eliminated this way and 8,169 SNPs were retained.

RAD-seq SNP analysis

Due to missing genotypes in either of the parents, 263 SNPs were removed from 8,169 SNPs. The missing rate for each SNP increased due to the conversion of low confident SNP genotype calls into missing values. To maintain missing rate by SNP less than 10%, 1,892 SNPs were eliminated, with 6,014 SNPs retained for further filtering. Missing rate by individual is less than 30% across these 6,014 SNPs. The mean observed heterozygosity of these 6,014 SNPs was 51%.

Principal component analysis (PCA) was performed in R on 293 individuals with 2 parents across the selected 6,014 polymorphic SNPs. We were able to identify 19 individuals that clustered together with the female parent in the PCA plot (Fig. A6), 11 of which had appeared to be the product of self-fertilization of the female parent in GoldenGate SNPs analysis, whereas the remaining 8 had not been genotyped with GoldenGate markers. To further investigate these suspicious individuals, average heterozygosity was plotted against the proportion of missing data by individual, with 18 selfed individuals and 75 true F_1 cross individuals, both identified by

GoldenGate markers, and 201 tested F_1 individuals (Fig. A7). The average observed heterozygosity across each of the three groups was 38%, 54%, and 52 %, respectively. From the heterozygosity by missing data plot, 11 individuals with heterozygosity less than 0.4 were first eliminated. Then, 3 individuals with high missing data (greater than 14%) were removed. One outlier with average heterozygosity greater than 0.65 was removed. Thus, 15 individuals were identified from the heterozygosity by missing data plot and removed from the data set. The 8 individuals identified from RAD-seq SNP data but not from GoldenGate data were in the list of the eighteen individuals identified from the heterozygosity by missing data plot. Along with the 18 selfed individuals discovered from GoldenGate data, a total of 32 individuals were removed from the final data set due to high percentage of alleles from the female parent, high missing data, and low heterozygosity.

For a polymorphic SNP marker in linkage map construction, marker classes must be categorized beforehand. Because heterozygote under-calling was anticipated within parental genotypes, we categorized marker class based on the allele frequency distribution in 261 F_1 progeny (excluding the 32 suspicious individuals identified from the previous filtering step). Three peaks were observed (expected allele frequencies of 0.25, 0.5, and 0.75), which represented the crosses of AA×Aa with 1:1 segregation of AA and Aa genotypes, Aa ×Aa with 1:2:1 segregation of AA, Aa and aa genotypes, and aa × Aa with 1:1 segregation of Aa and aa genotypes. Then, Chi-square segregation distortion test (goodness-of-fit x^2 test with $P < 0.05$) was performed in each marker class (allele frequency ranging from 0.2~0.3, 0.45~0.55, and 0.7~0.8). Before running the test, if an unexpected homozygous genotype was observed among F_1 progeny (less than 10% of the total number of genotypes) for markers only segregating in one parent and not the other, the unexpected homozygous genotype was converted into heterozygote due to heterozygote miscalled from the SNP genotype calling procedure; 22 SNPs were excluded because the ratio of unexpected homozygotes among the total genotypes was greater than 10%. After converting unexpected homozygous genotypes into heterozygotes, Chi-square tests were performed in each marker class; 2,634 segregation distorted markers were eliminated ($P < 0.05$), and thus 3,371 non-distorted SNPs were retained. Next, the marker class of these 3,371 non-distorted SNPs was compared with two parental genotypes. Among these 3,371 SNPs, 86% matched their corresponding parental genotypes, and among the mismatched SNPs, 32% can be explained by heterozygote under-calling in the parental genotypes. A total of 315 SNPs were removed, and therefore a set of 3,056 SNPs were retained for genetic map construction.

References for supplementary methods

Clark LV, Brummer JE, Głowacka K *et al.* (2014) A footprint of past climate change on the diversity and population structure of *Miscanthus sinensis*. *Annals of Botany*, **114**, 97-107.

Głowacka K, Kaczmarek Z, Jezowski S (2012) Androgenesis in the bioenergy plant *Miscanthus sinensis*: from calli induction to plant regeneration. *Crop Science*, **52**, 2659-2673.

Lu F, Lipka AE, Glaubitz J *et al.* (2013) Switchgrass genomic diversity, ploidy, and evolution: novel insights from a network-based SNP discovery protocol. *PLoS Genetics,* **9**, e1003215.

Poland JA, Brown PJ, Sorrells ME, Jannink JL (2012) Development of high-density genetic maps for barley and wheat using a novel two-enzyme genotyping-by-sequencing approach. *Plos One*, **7**(2): e32253. doi:10.1371/journal.pone.0032253.

Swaminathan K, Chae WB, Mitros T *et al.* (2012) A framework genetic map for *Miscanthus sinensis* from RNAseq-based markers shows recent tetraploidy. *BMC Genomics,* **13**, 142.

Thurber CS, Ma JM, Higgins RH, Brown PJ (2013) Retrospective genomic analysis of sorghum adaptation to temperate-zone grain production. *Genome Biology,* **14**, R68.