Development and Application of Genic Simple Sequence Repeat Markers from the Transcriptome of Loquat

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ABSTRACT. Deep transcriptome sequencing allows for the acquisition of large-scale microsatellite information, and it is especially useful for genetic diversity analysis and mapping in plants without reference genome sequences. In this study, a total of 14,004 simple sequence repeats (SSRs) were mined from 10,511 unigenes screening of 63,608 nonredundant transcriptome unigenes in loquat (*Eriobotrya japonica*) with a frequency of 22 SSR loci distributed over 100 unigenes. Dinucleotide and trinucleotide repeat SSRs were dominant, accounting for 20.62%, and 42.1% of the total, respectively. Seventy primer pairs were designed from partial SSRs and used for polymerase chain reaction (PCR) amplification. Of these primer pairs, 54 exhibited amplification and 33 were polymorphic. The number of alleles at these loci ranged from two to 17, and the polymorphism information content values ranged from 0.24 to 0.89. We tested the transferability of 33 SSR polymorphic primer pairs in apple and pear, and the transferability rates in these two species were 90.9% and 87.9%, respectively. A high level of marker polymorphism was observed in apple [*Malus ×domestica* (66.7%)], whereas a low level was observed in pear [*Pyrus* sp. (51.5%)]. In addition, the PCR products from seven SSR primer pairs were selected for sequence analysis, and 89.2% of the fragments were found to contain SSRs. SSR motifs were conserved among loquat, apple, and pear. According to our sequencing results for real SSR loci, ≈12,490 SSR loci were present in these loquat unigenes. The cluster dendrogram showed a distinct separation into different groups for these three species, indicating that these SSR markers were useful in the evaluation of genetic relationships and diversity between and within the species of Maloideae in the Rosaceae. The results of our identified SSRs should be useful for genetic linkage map construction, quantitative trait locus mapping, and molecular marker-assisted breeding of loquat and related species.

Loquat belongs to the family Rosaceae and is an important evergreen fruit crop native to south-central China (Gisbert et al., 2009a, 2009b). It has become popular with consumers because of its sweet and edible fruit (Lin et al., 2004), which can be sorted into red- and white-fleshed cultivars (Fu et al., 2012). Over 300 cultivars have been recorded and preserved, most of which are landraces with high genetic diversity (Qiu and Zhang, 1996). To more efficiently use these abundant loquat germplasm resources in genetic breeding, they must be evaluated and identified using efficient molecular methods.

Microsatellites or SSR are 1- to 6-bp DNA regions repeated in tandem that are ubiquitous in both prokaryotes and eukaryotes (Gao et al., 2013). As a result, SSRs are simple and efficient markers useful in the analysis of codominance and highly polymorphic lines. SSRs have been used extensively in genetic

diversity assessments (Li et al., 2010a), cultivar fingerprinting (Wang et al., 2011), marker-assisted breeding (Gutiérrez et al., 2011), and diversity and linkage map construction studies (Chen et al., 2006; Pazos-Navarro et al., 2011). As a result of the lack of genomic information for most non-model plant species, it is expensive and labor-intensive to develop traditional SSRs from genomic DNA library screening (Temnykh et al., 2001). With the development of next-generation sequencing in transcriptomics, creating transcriptome-level sequence collections has become much more cost-effective. A wealth of genic SSRs, single nucleotide polymorphism, and other genetic markers have been identified and developed for non-model plant species (Li et al., 2013c, 2013d; Mardis, 2008; Zhang et al., 2012a). In comparison with genomic SSR markers, genic SSR markers are based on expressed sequences from coding regions and are potentially tightly linked with functional genes that control important phenotypic characteristics (Ramchiary et al., 2011). Genic SSRs derived from transcriptome or expressed sequence tag (EST) sequences have been widely mined and applied in molecular biology studies for numerous fruit tree species such as pomegranate [*Punica granatum* (Ono et al., 2011)], litchi [*Litchi chinensis* (Li et al., 2013a)], highbush blueberry [*Vaccinium corymbosum*

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(Rowland et al., 2012)], peach [*Prunus persica* (Wang et al., 2013)], pear [*Pyrus pyrifolia* (Yue et al., 2014)], and Nules clementine [*Citrus clementina* (Luro et al., 2008)], but they have not been developed from the loquat transcriptome.

Genic SSRs can also be developed from the data for ESTs (Bouck and Vision, 2006). However, only four loquat ESTs have been submitted to GenBank (as of 1 Jan. 2014), indicating a lack of development of EST-SSR markers in the species. Most of the EST-SSRs used in loquat genetic diversity studies have been derived from apple (Li et al., 2013b). To address this knowledge gap, we report the first development of genic SSR markers based on loquat transcriptome sequences obtained in our laboratory, which provides a valuable resource to complement SSR collections. The detailed information on the transcriptome will be described elsewhere. The aim of this study was to explore the SSR loci of transcriptome sequences in loquat, analyze their distribution regularity, and design primers to test the authenticity and identify the transferability of these SSR loci in other Maloideae species of the Rosaceae. These results will prove very useful for the evaluation of genetic diversity, cultivar identification, and marker-assisted selection in future research.

Materials and Methods

PLANT MATERIALS. A total of 33 accessions were used for the development and transferability testing of genic SSR markers in this study. Young leaf samples of 13 loquats and 10 pear cultivars (Table 1) were collected from the Loquat and Pear Germplasm Resources Garden (Yangdu Agricultural Research Station, Institute of Horticulture, Zhejiang Academy of Agricultural Sciences, Hangzhou, P.R. China). Young leaf samples of 10 apple cultivars were collected from the National Germplasm Resources Garden of Apple (Zhengzhou Academy of Agricultural Sciences, Zhengzhou, P.R. China). The names of the cultivars are listed in Table 1.

DNA ISOLATION. Genomic DNA for each cultivar was isolated from young leaves using the DNeasy Plant Mini Kit (Qiagen, Valencia, CA) according to the manufacturer's recommendations. DNA concentrations were quantified using a spectrophotometer (U-0080D; Hitachi High-Technologies

Corp., Tokyo, Japan), and subsamples were run on 1% agarose gels to test for sample integrity (data not shown). All samples were stored at -80°C until further use.

MINING OF SSR BASED ON THE TRANSCRIPTOME DATA SET. A total of 63,608 unigenes were obtained from the 'Ninghaibai' loquat fruit transcriptome acquired in our laboratory (unpublished data). The genic SSR loci in the loquat fruit transcriptome were searched from the unigenes using MISA (Thiel et al., 2003), a Perl script able to detect both perfect and compound microsatellites in nucleotide sequences. Compound microsatellites were defined as repeats interrupted by a nonrepetitive sequence of a maximum 50 nucleotides. MISA was set with the following minimum length criteria for the extraction of repeated units (unit size/minimum number of repeats): at least six dinucleotides (2/6), at least five trinucleotides (3/5), three tetranucleotides (4/3), three pentanucleotides (5/3), and three hexanucleotides (6/3). To reduce the errors caused by the parameter set, we reduced the necessary repetitions of the dinucleotide through pentanucleotide motifs, according to previous work conducted by Jung et al. (2005) and Poncet et al. (2006). Sequences containing corresponding repeat units were selected for marker development.

SSR PRIMER DESIGN. Primers for genic SSRs in the microsatellite sequences were designed using Primer3 (Rozen and Skaletsky, 2000) based on the following core criteria: a guanine-cytosine (GC) content between 40% and 60% with an optimum value of 50%; an annealing temperature between 54 and 63 $^{\circ}\text{C}$; a minimum product length of 100 bp; and a primer length of 18 to 24 nucleotides. Product sizes ranged between 150 and 350 bp. Primers were synthesized by Shanghai Jierui Co. (Shanghai, P.R. China). The sequences for SSR primer design were shown in supplementary file.

PCR AMPLIFICATION AND GEL ELECTROPHORESIS. PCR amplification reactions were performed using a Biometra Authorized Thermal Cycler (An Analytik Jena Co., Thuringia, Germany) and conducted in a total volume of 30 μL containing 30 ng template DNA, 30 μmol each primer, 15 μL 2 $\times$ Taq mix, and double-distilled (dd) H_2O to reach the total volume. PCR conditions were as follows: 94 $^{\circ}\text{C}$ for 5 min followed by 40 cycles of 94 $^{\circ}\text{C}$ for 30 s, 50 $^{\circ}\text{C}$ to 60 $^{\circ}\text{C}$ for 40 s, and 72 $^{\circ}\text{C}$ for

Table 1. Cultivars used for genic simple sequence repeat marker amplification and transferability in this study.

Code	Cultivar name	Genus and/or species	Code	Cultivar name	Genus and/or species
1	Ninghaibai	<i>Eriobotrya japonica</i>	18	Cuiguan	<i>Pyrus</i>
2	Oohusa	<i>E. japonica</i>	19	Laiyangli	<i>Pyrus</i>
3	Jiefangzhong	<i>E. japonica</i>	20	Sucui 1	<i>Pyrus</i>
4	Tangkebairou	<i>E. japonica</i>	21	Pingguoli	<i>Pyrus</i>
5	Guanyu	<i>E. japonica</i>	22	Huanghuali	<i>Pyrus</i>
6	Marc	<i>E. japonica</i>	23	Xiuyu	<i>Pyrus</i>
7	Gangbeihuangrou	<i>E. japonica</i>	24	Huashuai	<i>Malus $\times$ domestica</i>
8	Gangbeihongsha	<i>E. japonica</i>	25	Huaguan	<i>M. $\times$ domestica</i>
9	Changhong 3	<i>E. japonica</i>	26	Songbenjin	<i>M. $\times$ domestica</i>
10	Maomu	<i>E. japonica</i>	27	Enpai	<i>M. $\times$ domestica</i>
11	Senweizaosheng	<i>E. japonica</i>	28	Guoguang	<i>M. $\times$ domestica</i>
12	Zaozhong 6	<i>E. japonica</i>	29	Maiyan	<i>M. $\times$ domestica</i>
13	Tianzhong	<i>E. japonica</i>	30	Freedom	<i>M. $\times$ domestica</i>
14	Qingxiang	<i>Pyrus</i>	31	Hongjin	<i>M. $\times$ domestica</i>
15	Zaosuhong	<i>Pyrus</i>	32	Kelusi	<i>M. $\times$ domestica</i>
16	Zaojinsu	<i>Pyrus</i>	33	Kajia	<i>M. $\times$ domestica</i>
17	Changjin20shiji	<i>Pyrus</i>			

1 min and a final extension step at 72 °C for 10 min. To control the PCR product integrity, a 5-μL aliquot was visualized on a 1.5% agarose gel. The remaining reaction was run on a 6% polyacrylamide gel according to the specifications outlined in Li et al. (2013b) and then stained with 2% silver nitrate according to Bassam et al. (1991). The stained gels were photographed in white light.

CROSS-SPECIES AMPLIFICATION. To assess the transferability of our SSR markers, we tested their amplification in two other Rosaceae species: apple and pear. The PCR amplification reactions were performed like in the previously described protocols.

FRAGMENT RECOVERY AND SEQUENCING. The target fragments obtained from the acrylamide gels were cut, washed twice in 1 mL ddH₂O, and recovered according to Li et al. (2013b). The PCR conditions were performed as described previously, but only single-specific fragments detected on the agarose gels were cut. Further recovery was conducted using the DNA gel extraction kit produced by Shanghai Songon Biotech Co. (Shanghai, China), and sequencing was also conducted by Shanghai Songon Biotech Co.

DATA COLLECTION AND ANALYSIS. The following parameters were estimated from the microsatellite marker data: number of alleles per locus: expected heterozygosity [$He = 1 - \sum p_i^2$, where p_i is the frequency of the i^{th} allele (Nei, 1973)] and observed heterozygosity (Ho , calculated as the number of heterozygous genotypes divided by the total number of genotypes). According to the presence or absence of bands on the polyacrylamide gel, the same electrophoretic banding patterns were recorded as 1, whereas other patterns were recorded as 0. The polymorphism data were entered into Excel (Microsoft Inc., Redmond, WA) for cluster analysis using NYSYS-pc software (Rohlf, 2005), and a dendrogram was generated for the analysis of genetic relationships and diversity among the cultivars of loquat, apple, and pear. SSR loci recovered from the polyacrylamide gels were checked using SSRIT software (da Maia et al., 2008).

Results

DISTRIBUTION, FREQUENCY, AND CHARACTERISTICS OF SSR SEQUENCES. In this study, MISA was used to identify SSR markers in the unique sequences. From the 63,608 sequences examined in the present study, representing a total size of 48,295,300 bp, 14,004 SSRs were identified in 10,511 sequences for a frequency of 22 SSR loci distributed over 100 unigenes. The distribution density represents one SSR locus for every 3.45 kb (kb/SSR). A total of 6754 sequences contained only one SSR, whereas 2544 sequences contained more than one SSR locus; 1213 SSR loci were present in compound formation. This result indicated that SSRs were quite abundant in the loquat transcriptome sequences (Table 2).

The composition of SSRs was as follows: 2887 (20.62%) dinucleotides, 5896 (42.1%) trinucleotides, 2161 (15.43%) tetranucleotides, 622 (4.44%) pentanucleotides, and 850 (6.07%) hexanucleotides (Table 3). The most abundant motifs among the dinucleotides and trinucleotides were AG/CT and AAG/CTT with frequencies of 85.9% and 22.17%, respectively. The highest frequency tetranucleotide motif was AAAG/CTTT with a frequency of 13.98%. There were 93 kinds of pentanucleotide motif with AAAAG/CTTTT comprising 8.53%. The most predominant hexanucleotide motif was

Table 2. Total number and frequency distribution of each repeat type including mono-, di-, tri-, tetra-, penta-, and hexanucleotide in loquat.

Repeat type	SSRs (no.)	SSRs (%)	SSR frequency (%)	Avg length (kb)
Mononucleotide	1,588	11.33	2.5	30.41
Dinucleotide	2,887	20.62	4.53	16.73
Trinucleotide	5,896	42.1	9.26	8.19
Tetranucleotide	2,161	15.43	3.4	22.35
Pentanucleotide	622	4.44	0.98	77.65
Hexanucleotide	850	6.07	1.33	56.81
Total SSRs (no.)	14,004	100	22.02	3.45

SSRs = simple sequence repeats.

Table 3. The number of major SSR motifs of di-, tri-, tetra-, penta-, and hexanucleotide and their frequency in loquat.

Repeat type	SSR motif	SSRs (no.)	Total SSRs (no.)	SSRs (%)
Dinucleotide	AG/CT	2480	2887	85.9
	AC/GT	304		10.53
	AT/AT	97		3.36
	CG/CG	6		0.21
Trinucleotide	AAG/CTT	1307	5896	22.17
	AGG/CCT	1116		18.93
	ACC/GGT	713		12.1
	ACG/CTG	622		10.55
	AGC/CGT	621		10.53
	CCG/CGG	406		6.89
	AAC/GTT	398		6.75
	AGT/ATC	315		5.34
	ACT/ATG	298		5.05
Tetranucleotide	AAT/ATT	100	2161	1.69
	AAAG/CTTT	302		13.98
	AAAT/ATTT	229		10.59
	AAAC/GTTT	194		8.98
	AAGG/CCTT	148		6.85
	Others	1288		59.6
Pentanucleotide	AAAAG/CTTTT	53	622	8.52
	AAAAT/ATTTT	52		8.36
	AAAAC/GTTTT	45		7.23
	AAACC/GGTTT	22		3.54
	Others	450		72.35
Hexanucleotide	AGAGGG/CCCTCT	26	850	3.06
	AAGAGG/CCTTCT	23		2.71
	AAAAAG/CTTTTT	20		2.35
	ACCTCC/AGGTGG	20		2.35
	Others	761		89.53

SSR = simple sequence repeat.

AGAGGG/CCCTCT (3.06%) followed by AAGAGG/CCTTCT (2.71%).

LENGTH DISTRIBUTION AND LOCATION OF SSR MOTIFS. The length of the microsatellite sequences ranged from 10 to 25 bases. Significant variation occurred in the length of the sequences, which deviated from the normal distribution. The most frequent microsatellite repeat length range was between 10 and 15 bp (Fig. 1), whereas the second most frequent range was between 13 and 16 bp. Only nine (0.06%) of the sequences were longer than 30 bp. A negative correlation existed between abundance, variation, rate and microsatellite length (Fig. 1).

Fig. 1. Frequency distribution of simple sequence repeat (SSR) motif repeat size (loci length) in loquat. The x-axis indicates the length of SSRs motif. The y-axis indicates the number of SSRs with different lengths: (A) nucleotide repeats of different lengths, (B) dinucleotide repeats of different lengths, (C) trinucleotide repeats of different lengths, (D) tetranucleotide repeats of different lengths, (E) pentanucleotide repeats of different lengths, and (F) hexanucleotide repeats of different lengths.

Moreover, most dinucleotide and hexanucleotide motifs were found in noncoding regions, whereas trinucleotide, tetranucleotide, and pentanucleotide motifs occurred more frequently in the coding regions.

IDENTIFICATION AND POLYMORPHISM ANALYSIS OF SSR LOCI. Of the 70 SSR primer pairs, 54 (77.1%) generated clear DNA banding patterns with the expected size, and 33 SSR primers amplified polymorphic PCR products (Table 4). Figure 2 shows

Table 4. Details of 33 high polymorphism genic simple sequence repeat primer and statistical parameters including number of amplification bands, polymorphic bands, polymorphisms, polymorphism information content (PIC), heterozygosity observed (H_o), and expected heterozygosity (H_e) values among loquat cultivars.

Primer no.	Repeat motif	Primer type ²	Primer sequence (5' → 3')	Annealing temp (°C)	Product size (bp)	Bands (no.)	Polymorphic bands (no.)	Polymorphism (%)	PIC	H_o	H_e
62	(AGCTGG)3	F	GACTCCGAAAAATGCCTCTAT	55	252	4	4	100	0.27	0.12	0.88
		R	GTCCATGCAATTCCATTTC								
101	(TGAG)6	F	AGTTGAGGGTTTGAGGATTC	55	128	11	11	100	0.3	0.67	0.66
		R	ATAAGGAGCCCATTAACCAC								
137	(AGA)6	F	TTTCCCTTTAATCCCCAGG	55	164	8	8	100	0.73	0.61	0.27
		R	TAAAGCAGTCTCTCCAAAGAGTA								
160	(TCA)7	F	ATCCATGGCCAAATGAAAAC	56	174	14	13	92	0.36	0.88	0.7
		R	TGAGATTAAAGCCGGGCATC								
217	(TCCTTC)3	F	TTCAGCTTTTGTCTGTCCTT	55	242	12	11	91.6	0.8	0.42	0.61
		R	CTTGCTCGAACTTGGTCAT								
254	(CATG)5	F	CTACCTCACCGGAAGATGA	58	204	11	11	100	0.52	0.67	0.43
		R	GAGACACGTACATGATAAGACCA								
267	(AACC)5	F	CAATAAACACGATCAAGGCC	55	156	6	6	100	0.4	0.69	0.76
		R	TTTGAAGACGACGATGAACT								
328	(CT)10	F	ACCTTCTCTCATCATCA	55	180	2	1	50	0.89	0.3	0.88
		R	CCTAGGCAACTGAATATCC								
407	(CCCATC)4	F	CTTGACCTGTAAAGGCATA	55	205	7	7	100	0.57	0.35	0.11
		R	CAACTAAAACAAACCACACA								
436	(TTG)6	F	ACGGAAGATTGGGTGTAAAA	55	207	6	6	100	0.83	0.88	0.67
		R	CTCATTAAGTGTGTCAGCT								
458	(GAATGG)3	F	GACTCGTTGAACCAATTGTC	55	200	4	4	100	0.35	0.38	0.69
		R	TTCTTCTCCTCCTCACTCAT								
577	(AGT)7	F	TCAACAAGTAATCGAGCCTC	55	216	8	8	100	0.28	0.94	0.69
		R	GAAACCCATCAAAACAAGCA								
673	(GGCACC)3	F	ACAGTTGTAGCAAGCCTTG	55	246	8	8	100	0.46	0.7	0.37
		R	GAGTGTCCCTAAGAACGCC								
1461	(TTG)7	F	AGTACAAAATCGAGTGCAGT	55	159	8	7	87.5	0.77	0.94	0.71
		R	ACCAGAAATCACAAAGACACTC								
1726	(AAGC)5	F	GTGAAACAAAGAGGAAATCCG	55	207	5	5	100	0.37	0.43	0.74
		R	GAATCACTGATGCATGCTTC								
1812	(CGT)6	F	TAAAGAAATCTGAGCTCGTCG	55	235	7	7	100	0.35	0.67	0.71
		R	AATTCGACATGGAAGACGA								
2010	(GCA)6	F	TCTACTCTGCATTCTGTTCG	57	212	3	3	100	0.51	0.3	0.69
		R	GCAAGCAGAAGAAGTGAAATC								
2121	(GCTTGC)3	F	CCATTTCGACATCTTGATAG	55	211	2	1	50	0.5	0.3	0.88
		R	AAGTTCAATGAGGTGCAGAA								
3842	(TCGGT)3	F	TTCCAAATCCAAAGCCCTTC	57	227	12	12	100	0.63	0.52	0.5
		R	CGAAAAAAGTGGACCGAACAC								
4019	(CCAAT)3	F	GAGAGCAGCACCAACGTTTA	57	226	6	6	100	0.67	0.39	0.52
		R	AGAAAGCGCAGAGCTTGTAGC								
4181	(TTC)6	F	AAATCTCTGCGTTTCATCAT	55	172	12	12	100	0.62	0.61	0.58
		R	GGTTCTGGAAAGAGCATTGA								

Continued next page

Table 4. Continued.

Primer no.	Repeat motif	Primer type ^z	Primer sequence (5'→3')	Annealing temp (°C)	Product size (bp)	Bands (no.)	Polymorphic bands (no.)	Polymorphism (%)	PIC	Ho	He
4297	(AGAGAA)3	F	TCACAGCCTCGAAAGACAGA	58	240	11	11	100	0.67	0.82	0.51
		R	ATCACAGCAGGGAAGAATG								
5607	(AGGTCA)4	F	AGACTCCGTTCAACATCAAA	55	184	5	5	100	0.24	0.09	0.63
		R	GCTGTCTCTGTTAACTGA								
5855	(GAACA)4	F	AGAACCACTCAGCCAAAATC	55	166	3	3	100	0.34	0.03	0.88
		R	CTGTGAACACCAATTTTCGT								
6539	(GGT)6.(GTTGGA)3	F	CCATCCATGATTCTGGTCA	56	204	5	5	100	0.4	0.61	0.87
		R	GACCAAGCACCAAGAGATAA								
7028	(TGATT)4	F	AATGTATGCGGCAAGACTT	55	160	11	11	100	0.57	0.61	0.34
		R	TAATTTTGATGGACTGGGGT								
7950	(TTCAA)4	F	GATCTTTTGTGCAGAGGTG	55	221	2	2	100	0.69	0.15	0.88
		R	CTTTCGCATTCATTTCTG								
8037	(CTG)7	F	AACACTAGGCTGGATGATTC	57	179	3	3	100	0.62	0.61	0.69
		R	GGATTCAGATGACCCAGATG								
8106	(CCACCT)3.(TCCCTCG)3	F	GCAGCAGTTATACTCCACAT	56	230	17	17	100	0.46	0.85	0.25
		R	AAGAAGAGACGGGAAATGAC								
8119	(AAT)6	F	ACCCGTTAGTTGATGATGT	55	200	8	8	100	0.63	0.79	0.21
		R	GTTTATTGGGTTTGGTTCGG								
8296	(CAAA)5	F	ATTACGCCCTTGATTCTT	56	244	8	8	100	0.39	0.48	0.12
		R	GGAATGACGGAAAGTAGGTT								
9465	(TTCTGG)4	F	GATGCCAGATCTGACTTGAT	57	224	15	15	100	0.25	0.76	0.65
		R	GATTGACCAGTAGTACCAGC								
11454	(AGG)6	F	GTGTGAGAACCAATTTTGCA	56	214	4	4	100	0.73	0.61	0.69
		R	TACGTATTGGGGAACAGCTT								
Total/avg						248	243	97.9	0.52	0.55	0.59

^zF = forward; R = reverse.

Fig. 2. Representative polyacrylamide gel images of genic simple sequence repeat (SSR) marker amplified by primer pairs 4297 and 8296: Marker DL2000 (M), accession numbers of loquat (one to 13), accession numbers of pear (14 to 23), accession numbers of apple (24 to 33). Cultivar names are listed in Table 1. (A) Amplified result of primer 4297; (B) amplified result of primer 8296.

representative polyacrylamide gels amplified with primer pairs 4297 and 8296, respectively. A total of 248 alleles were obtained from the accessions, representing an average of 7.5 alleles per SSR marker and 243 (97.9%) of them were polymorphic bands. The number of alleles obtained for each primer ranged between two and 17. The polymorphic information content ranged from 0.24 to 0.89 with an average of 0.52, indicating that the SSRs developed in this study had high discriminatory power. The *Ho* value (heterozygosity) ranged from 0.03 to 0.94 with an average of 0.55, and the *He* value (expected heterozygosity) ranged from 0.11 to 0.88 with an average of 0.59 (Table 4).

TRANSFERABILITY OF SSR MARKERS. To test the interspecific transferability of these SSR markers in apple and pear, which belong to the same subfamily (Maloideae) as loquat, PCR amplification was conducted in 10 apple and 10 pear cultivars. Clear DNA fingerprints were obtained from the PCR amplification of apple and pear DNA using the loquat SSR primers as seen in the polyacrylamide gels of the SSR bands amplified by the primer pairs 4297 and 8296 (Fig. 2). Of the primer pairs, 30 produced the anticipated SSR bands in apple and 29 in pear, representing transferability rates of $\approx 90.9\%$ and 87.9% , respectively. A high level of marker polymorphism was observed in apple (66.7%), whereas a low rate was seen in pear (51.5%). This result indicated that the SSR primers derived from loquat had a high generality among Maloideae species.

SEQUENCE CHARACTERISTIC OF PCR PRODUCTS. Polyacrylamide fragments from seven primer pairs (254, 267, 3842, 4181, 5855, 7028, and 8296) were selected for further sequence analysis. Analysis of the 43 fragments indicated that 37 (88%) were successfully recovered and sequenced, of which four fragments contained no repeat motif and 33 expressed SSR loci, representing a rate of 89.2% (Table 5). According to our sequencing results for real SSR loci, $\approx 12,490$ SSR loci are found in the loquat unigenes, but the SSR motifs were only partly conserved between loquat, apple, and pear. The majority of SSR markers developed from transcription sequences in this study contained real SSR loci. More than 50% of the PCR products obtained from apple and pear had different sizes than were expected. Most of the repeat fragment motifs were different from those of the loquat cultivars. These observed differences may be the result of genetic divergence among the species (Table 5). The results also showed that different cultivars can share the same allele: sample Nos. 7, 8, and 9 were amplified from the three loquat cultivars Gangbeihongsha, Changhong 3, and Tianzhong, respectively. Compared with the original sequences, the identity values were more than 90%. Moreover, for the primer pair 5855, six sequences were recovered from three loquat and three pear cultivars; all cultivars shared the same allele, but the identity was lower in pear. Interestingly, different fragment sizes could be amplified from the same cultivar that contained the same repeating unit. For example, Nos. 22 and 23, the fragments

Table 5. Characteristics of fragments including amplification primer, expected and actual repeat motif, product size, and homology with original sequence recovered from polyacrylamide gel of different loquat, apple, and pear cultivars.

Code	Primer no.	Repeat motif in form sequence	Expected product (bp)	Fragment size (bp)	Fragment repeat motif	Homology with original sequence (%)	Original cultivar
1	254	(CATG)5	204	183	CATG	80.88	Sucui 1
2				203	CATG	70.18	Xiuyu
3				205	CATG	71.49	Huanghuali
4				213	(CATG)5	79.39	Huashuai
5				174	(CATG)2	79.41	Enpai
6				177	(CATG)2	80.98	Kajia
7	267	(AACC)5	156	156	(AACC)5	93.89	Gangbeihongsha
8				147	(AACC)5	93.95	Changhong 3
9				145	(AACC)5	90.38	Tianzhong
10				159	(AACC)8	83.65	Qingxiang
11				150	(AACC)3	79.49	Zaosuhong
12				111	—	34.62	Sucui 1
13				140	(AACC)4	89.1	Huashuai
14				143	(AACC)4	89.1	Maiyan
15	3842	(TCGGT)3	227	249	(TCGGT)3	70.68	Marc
16				251	TCGGT	78.09	Gangbeihongsha
17				255	(TCGGT)3	90.17	Songbenjin
18	4181	(TTC)6	172	181	(TTC)5	60.5	Huanghuali
19	5855	(GAACA)4	166	163	(GAACA)4	94.21	Jiefangzhong
20				160	(GAACA)4	91.87	Guanyu
21				160	(GAACA)4	92.46	Marc
22				160	(GAACA)4	80.7	Qingxiang
23				157	(GAACA)4	78.95	Qingxiang
24				159	(GAACA)4	83.63	Zaojinsu
25	7028	(TGATT)4	160	152	(TGATT)4	89.38	Changhong 3
26				147	(TGATT)4	87.5	Senweizaosheng
27				116	—	39.13	Zaosuhong
28				116	—	35.63	Changjin20shiji
29				116	—	34.38	Sucui 1
30	8296	(CAAA)5	244	227	(CAAA)5	93.39	Jiefangzhong
31				229	(CAAA)4	86.94	Gangbeihuangrou
32				239	(CAAA)4	95.92	Changhong 3
33				235	(CAAA)4	92.62	Zaosuhong
34				235	(CAAA)4	92.21	Huanghuali
35				234	(CAAA)4	84.49	Songbenjin
36				198	(CAAA)2	74.59	Guoguang
37				198	(CAAA)2	75.1	Freedom

derived from primer 5855 in the pear cultivar Qingxiang, shared the same locus.

CLUSTER ANALYSIS. In this study, an analysis of the genetic diversity among the 33 cultivars of loquat, apple, and pear was conducted using the polymorphic alleles obtained from the developed SSR primer pairs. A clustering diagram showed that the coefficients ranged from 0.58 to 0.96, and three major groups were identified at a similarity index of 0.67 (Fig. 3), which was consistent with the presence of three different species. In addition, a greater genetic relationship was observed between apple and loquat than between loquat and pear. In the loquat group, 13 cultivars were clustered into three subgroups with a high similarity coefficient (0.88). The first and the third loquat subgroups contained white-fleshed cultivars, whereas eight red-fleshed cultivars were clustered into the second subgroup. In the apple group, cultivars with the same geographical distribution such as Huashuai and Huaguan were clustered

together with a genetic similarity coefficient of 0.92. In the pear group, all 10 cultivars were clearly separated in Figure 3.

Discussion

SSR MARKER FREQUENCY AND DISTRIBUTION IN LOQUAT TRANSCRIPTOME. Genetic SSR markers are widely applied in diversity analysis, plant cultivar identification, and the construction of genetic linkage maps in population studies (Li et al., 2010b). As sequencing technology has developed, deep transcriptome sequencing has become a good resource for the development of SSRs because of the enormous amount of generated sequence data (Zheng et al., 2013). Markers based on transcriptome sequences are useful for the detection of functional variation and gene-associated genetic analysis. Based on the 63,608 nonredundant unigene sequences used in this study, a total of 12,416 SSRs were identified, excluding mononucleotide repeat

Fig. 3. Dendrogram constructed from 33 cultivars including loquat, apple, pear using polymorphic genic simple sequence repeat (SSR) marker developed in this study. All the cultivars were obviously separated into three groups: cultivars on the top belonged to the loquat group (one to 13), cultivars in the middle belonged to the apple group (24 to 33), and cultivars at the bottom belonged to the pear group (14 to 23).

motifs. Approximately 19.52% of the transcriptomic sequences possess SSR loci, representing a greater proportion than those found in highbush blueberry [18.24% (Rowland et al., 2012)], field pea [*Pisum sativum*, 17% (Kaur et al., 2012)], tea [*Camellia sinensis*, 16.67% (Tan et al., 2013)], citrus [13% (Luro et al., 2008)], *Amorphophallus* [11.8% (Zheng et al., 2013)], and *Epimedium* [3.67% (Zeng et al., 2010)]. Our results indicate that the number of SSRs was sufficiently large to identify markers. The distribution density in loquat was one SSR locus per 3.45 kb, which exceeded the distribution densities observed in rubber tree [*Hevea brasiliensis*, 0.28 kb (Li et al., 2012)], *Cryptomeria* [0.92 to 1.72 kb (Ueno et al., 2012)], and peach [3.2 kb (Wang et al., 2013)] but were lower than those of *Epimedium* [6.69 kb (Zeng et al., 2010)], sesame [*Sesamum indicum*, 4.08 kb (Zhang et al., 2012a)], and peanut [*Arachis hypogaea*, 6.22 kb (Zhang et al., 2012b)]. These differences of SSR density may depend on the minimum length of the SSR repeat motif.

According to a previous report by Zeng et al. (2010), the frequency of nucleotide repeats theoretically decreases with increasing length, and dinucleotide repeat motifs are the most frequent repeat type followed by trinucleotides, tetranucleotides, pentanucleotides, and hexanucleotides. However, in this study, trinucleotide repeats [5896 (42.1%)] were the most dominant SSRs in loquat followed by dinucleotides [2887 (20.62%)] and tetranucleotides [2161 (15.43%)]. Hexanucleotide

and pentanucleotide repeat units comprised only 4.44% and 6.07% of the total, respectively (Table 2). This trend is consistent with the results reported for other plant species (Li et al., 2010b; Liang et al., 2009; Luro et al., 2008; Moccia et al., 2009). In addition, the most abundant dinucleotide and trinucleotide repeat motifs were AG/CT and AGG/CCT, respectively. Similar results have been found in other plant species (An et al., 2009; Jiang et al., 2013; Li et al., 2012; Triwitayakorn et al., 2011).

Because genic SSR markers belong to gene-rich genome regions, they can be exploited for use in the marker-assisted breeding of loquat. Therefore, the set of genic SSR markers developed in this study represents a promising genomic resource. In addition, the length variation of the SSR motifs in this study showed deviation from the normal distribution, which may be the result of the strong convergence of selection pressures. This hypothesis is consistent with the conclusions drawn from previous microsatellite studies on tea plant (Li et al., 2010a; Wang, 2011) and seabuckthorn [*Hippophae rhamnoides* (Jain et al., 2014)]. Furthermore, most dinucleotide and hexanucleotide motifs occurred more frequently in noncoding regions, whereas other

motifs were found in the coding regions. This phenomenon was also observed in *Cymbidium ensifolium* (Li et al., 2013c).

POLYMORPHISM AND TRANSFERABILITY OF SSR MARKERS. As a result of the sequence conservation of transcribed regions of the genome, a significant portion of the genic SSR primer pairs designed from the transcriptome of a given species is expected to show a high degree of transferability in distantly related species (Moccia et al., 2009). The transferability of genic SSR markers over different taxonomic levels has been demonstrated previously (Bory et al., 2008; Zheng et al., 2013). In our study, SSR primer amplification of the target loquat genomic DNA was comparable to the 60% to 92.2% success rate found in previous studies (Cloutier et al., 2009; Dutta et al., 2011; Rowland et al., 2012; Wei et al., 2011; Zhang et al., 2011). A total of 33 polymorphic SSR markers were obtained, which was higher than the total in mei [*Prunus mume* (Li et al., 2010b)] and significantly lower than that in *Amorphophallus* (Zheng et al., 2013). The transferability of EST-SSRs among different related genera has been reported in many crop plants (Luro et al., 2008; Wang et al., 2011). The high transferability rate of loquat markers to apple and pear indicate that species in the Maloideae may be more closely related than was previously believed. In this study, the markers from loquat had high transferability rates, 90.9% and 87.9% in apple and pear, respectively, which indicated that the different species in the Maloideae may be

evolutionarily closely related; the homologous comparison results also confirmed this point.

CHARACTERISTICS OF RECOVERED PCR PRODUCTS. In this study, 37 polyacrylamide fragments representing seven primer pairs were successfully recovered, and 89.2% (Table 5) of them contained real SSR loci, which was higher than the results obtained in mei (73.08%) and loquat (80%) by Li et al. (2013b) and Shangguan et al. (2010, 2011). It is worthwhile to note that the size ranges of most of sequenced PCR products in apple and pear were different from those observed in loquat, and showing lower identity between this three species, these observed differences may reflect genetic divergence among the genera, which will provide representative information for understanding the characteristics of genetic evolution of the three comparative genomics and phylogenetic relationship among these three species.

CHARACTERISTIC OF ASSESSMENT OF GENETIC RELATIONSHIPS AMONG DIFFERENT SPECIES. Until now, little research has considered the genetic evolution of and diversity among the three Rosaceae species of loquat, apple, and pear using SSR markers. In the loquat group, the similarity values ranged between 0.87 and 0.96, implying that loquat has a rich genetic diversity. It should be noted that ‘Zaozhong 6’, ‘Sengweizaosheng’, and ‘Jiefangzhong’ were clustered in the same subgroup as was consistent with a previous report by He et al. (2011). ‘Sengweizaosheng’ and ‘Zaozhong 6’ were grouped together with a high similarity coefficient of 0.96, which was consistent with the origin of ‘Zaozhong 6’ as a hybrid between ‘Jiefangzhong’ and ‘Senweizaosheng’. The similarity coefficients of apple ranged from 0.89 to 0.94, whereas those of pear ranged from 0.80 to 0.90. The cultivar classifications between apple and pear groups were generally consistent with the genetic background and original geographic distribution data. It is noteworthy that the cultivar Pingguoli in the pear group, which was introduced from Jilin province of China, had a lower coefficient than the others. These results also indicated that the loquat SSR markers were useful in the evaluation of genetic relationships between and within the *Malus* or *Pyrus* species.

Conclusion

To the best of our knowledge, this study represents the first development of SSR markers from RNA-seq in loquat. A total of 14,004 SSR loci was obtained and 70 primer pairs were successfully designed based on the transcriptome sequences, 33 of which were validated and showed high polymorphism in loquat. As a result of the conservation of genic sequences, these markers had a higher transferability across species, indicating higher than expected genetic similarities among apple, pear, and loquat. The developed SSR markers represent a valuable resource for conducting marker-assisted selection, linkage mapping, and germplasm characterization analysis in loquat.

Literature Cited

- An, Z., Y. Zhao, H. Cheng, W. Li, and H. Huang. 2009. Development and application of EST-SSR markers in *Hevea brasiliensis* Muell. Arg. *Hereditas* 31:311–319 [in Chinese].
- Bassam, B., G. Caetano-A, and P.M. Gresshoff. 1991. Fast and sensitive silver staining of DNA in polyacrylamide gels. *Anal. Biochem.* 196:80–83.
- Bory, S., D. Da Silva, A.M. Risterucci, M. Grisoni, P. Besse, and M.F. Duval. 2008. Development of microsatellite markers in cultivated vanilla: Polymorphism and transferability to other vanilla species. *Sci. Hort.* 115:420–425.
- Bouck, A., and T. Vision. 2006. The molecular ecologist’s guide to expressed sequence tags. *Mol. Ecol.* 16:907–924.
- Chen, C., K.D. Bowman, Y.A. Choi, P.M. Dang, M.N. Rao, S. Huang, J.R. Soneji, T.G. McCollum, and F.G. Gmitter, Jr. 2006. EST-SSR genetic maps for *Citrus sinensis* and *Poncirus trifoliata*. *Tree Genet. Genomes* 112:1248–1257.
- Cloutier, S., Z. Niu, R. Datla, and S. Duguid. 2009. Development and analysis of EST-SSRs for flax (*Linum usitatissimum* L.). *Theor. Appl. Genet.* 119:53–63.
- da Maia, L.C., D.A. Palmieri, V.Q. de Souza, M.M. Kopp, F.I. de Carvalho, and A. Costa de Oliveira. 2008. SSR Locator: Tool for simple sequence repeat discovery integrated with primer design and PCR simulation. *Intl. J. Plant Genomics* 412696:1–9.
- Dutta, S., G. Kumawat, B.P. Singh, D.K. Gupta, S. Singh, V. Dogra, K. Gaikwad, T.R. Sharma, R.S. Raje, T.K. Bandhopadhyaya, S. Datta, M.N. Singh, F. Bashasab, P. Kulwal, K.B. Wanjari, R. Varshney, D.R. Cook, and N.K. Singh. 2011. Development of genic-SSR markers by deep transcriptome sequencing in pigeonpea [*Cajanus cajan* (L.) Millspah]. *BMC Plant Biol.* 11:17.
- Fu, X., W. Kong, G. Peng, J. Zhou, M. Azam, C. Xu, D. Grierson, and K. Chen. 2012. Plastid structure and carotenogenic gene expression in red- and white-fleshed loquat (*Eriobotrya japonica*) fruits. *J. Expt. Bot.* 63:341–354.
- Gao, Z., J. Wu, Z. Liu, L. Wang, H. Ren, and Q. Shu. 2013. Rapid microsatellite development for tree peony and its implications. *BMC Genomics* 14:886.
- Gisbert, A.D., I. Lo’pez-Capuz, J.M. Soriano, G. Lla’cer, C. Romero, and M.L. Badenes. 2009a. Development of microsatellite markers from loquat [*Eriobotrya japonica* (Thunb.) Lindl.]. *Mol. Ecol. Res.* 9:803–805.
- Gisbert, A.D., J. Martinez-Calvo, G. Lla’cer, M.L. Badenes, and C. Romero. 2009b. Development of two loquat [*Eriobotrya japonica* (Thunb.) Lindl.] linkage maps based on AFLPs and SSR markers from different Rosaceae species. *Mol. Breed.* 23:523–538.
- Gutiérrez, O.A., A.F. Robinson, J.N. Jenkins, J.C. McCarty, M.J. Wubben, F.E. Callahan, and R.L. Nichols. 2011. Identification of QTL regions and SSR markers associated with resistance to reniform nematode in *Gossypium barbadense* L. accession GB713. *Theor. Appl. Genet.* 122:271–280.
- He, Q., X. Li, G. Liang, K. Ji, Q. Guo, W. Yuan, G. Zhou, K. Chen, W. van de Weg, and Z. Gao. 2011. Genetic diversity and identity of Chinese loquat cultivars/accessions (*Eriobotrya japonica*) using apple SSR markers. *Plant Mol. Biol. Rpt.* 29:197–208.
- Jain, A., S. Chaudhary, and C.S. Prakash. 2014. Mining of microsatellites using next generation sequencing of seabuckthorn (*Hippophae rhamnoides* L.) transcriptome. *Physiol. Mol. Biol. Plants* 20:115–123.
- Jiang, B., D.S. Xie, W.R. Liu, Q.W. Peng, and X.M. He. 2013. De novo assembly and characterization of the transcriptome, and development of SSR markers in wax gourd (*Benicasa hispida*). *PLoS One* 8:e71054.
- Jung, S., T.A. Abbot, R.C. Jesudu, J. Tomkins, and D. Main. 2005. Frequency, type, distribution and annotation of simple sequence repeats in Rosaceae ESTs. *Funct. Integr. Genomics* 5:136–143.
- Kaur, S., L.W. Pembleton, N.O. Cogan, K.W. Savin, T. Leonforte, J. Paull, M. Materne, and J.W. Forster. 2012. Transcriptome sequencing of field pea and faba bean for discovery and validation of SSR genetic markers. *BMC Genomics* 13:104.
- Li, C.Q., Y. Wang, X.M. Huang, J. Li, H.C. Wang, and J.G. Li. 2013a. De novo assembly and characterization of fruit transcriptome in *Litchi chinensis* Sonn and analysis of differentially regulated genes in fruit in response to shading. *BMC Genomics* 14:552.
- Li, X., H. Xu, and J. Chen. 2013b. Genetic diversity and relationships among 47 loquat cultivars revealed by EST-SSR markers. *Sci. Hort.* 160:375–382.
- Li, X., J. Luo, T. Yan, L. Xiang, F. Jin, C. Sun, and M. Xie. 2013c. Deep sequencing-based analysis of the *Cymbidium ensifolium* floral transcriptome. *PLoS One* 8:e85480.
- Li, X., L. Xiang, J. Luo, B. Hu, S. Tian, M. Xie, and C. Sunday. 2013d. The strategy of RNA-seq, application and development of molecular marker derived from RNA-seq. *Chinese J. Cell Biol.* 35:1–8 [in Chinese].

- Li, D., Z. Deng, B. Qin, X. Liu, and Z. Men. 2012. De novo assembly and characterization of bark transcriptome using illumina sequencing and development of EST-SSR markers in rubber tree (*Hevea brasiliensis* Muell. Arg.). BMC Genomics 13:192.
- Li, S.X., X.Y. Zhan, Y.Y. Wang, and T.M. Yin. 2010a. Content and characteristics of microsatellites detected in expressed sequence tag sequences in *Eucalyptus*. Chinese Bul. Bot. 45:363–371 [in Chinese].
- Li, X., L. Shangguan, C. Song, C. Wang, Z. Gao, and J. Fang. 2010b. Analysis of expressed sequence tags from *Prunus mume* flower and fruit and development of simple sequence repeat markers. BMC Genet. 11:66.
- Liang, X., X. Chen, Y. Hong, H. Liu, G. Zhou, S. Li, and B. Guo. 2009. Utility of EST derived SSR in cultivated peanut (*Arachis hypogaea* L.) and *Arachis* wild species. BMC Plant Biol. 9:35.
- Lin, S.Q., X.H. Yang, C.M. Liu, Y.L. Hu, Y.H. He, G.B. Hu, H.L. Zhang, X. He, and Y.X. Liu. 2004. Natural geographical distribution of genus *Eriobotrya* plants in China. Acta Hort. Sinica 31:569–573 [in Chinese].
- Luro, F.L., G. Costantino, J. Terol, X. Argout, T. Allario, P. Wincker, M. Talon, P. Ollitrault, and R. Morillon. 2008. Transferability of the EST-SSRs developed on Nules clementine (*Citrus clementina* Hort ex Tan) to other *Citrus* species and their effectiveness for genetic mapping. BMC Genomics 9:287.
- Mardis, E.R. 2008. The impact of next-generation sequencing technology on genetics. Trends Genet. 24:133–141.
- Moccia, M., C. Oger-Desfeux, G. Marais, and A. Widmer. 2009. A white campion (*Silene latifolia*) floral expressed sequence tag (EST) library: Annotation, EST-SSR characterization, transferability, and utility for comparative mapping. BMC Genomics 10:243.
- Nei, M. 1973. Analysis of gene diversity in subdivided populations. Proc. Natl. Acad. Sci. USA 70:3321–3323.
- Ono, N.N., M.T. Britton, J.N. Fass, C.M. Nicolet, D.W. Lin, and L. Tian. 2011. Exploring the transcriptome landscape of pomegranate fruit peel for natural product biosynthetic gene and SSR marker discovery. J. Integr. Plant Biol. 53:800–813.
- Pazos-Navarro, M., M. Dabauza, E. Correal, K. Hanson, N. Teakle, N. Real, D. Real, and M.N. Nelson. 2011. Next generation DNA sequencing technology delivers valuable genetic markers for the genomic orphan legume species, *Bituminaria bituminosa*. BMC Genet. 12:104.
- Poncet, V., M. Rondeau, C. Tranchant, A. Cayrel, S. Hamon, A. Dekochko, and P. Hamon. 2006. SSR mining in coffee tree EST databases: Potential use of EST-SSRs as markers for the *Coffea* genus. Mol. Genet. Genomics 276:436–449.
- Qiu, W.L. and H.Z. Zhang. 1996. China fruit records—Longan and loquat. China Forestry Press, Beijing, China. p. 91–239 [in Chinese].
- Ramchiary, N., V.D. Nguyen, X. Li, C.P. Hong, V. Dhandapani, S.R. Choi, G. Yu, Z. Piao, and Y. Lim. 2011. Genic microsatellite markers in *Brassica rapa*: Development, characterization, mapping, and their utility in other cultivated and wild *Brassica* relatives. DNA Res. 18:305–320.
- Rohlf, F. 2005. NTSYS-pc, Numerical taxonomy and multivariate analysis system. Version 2.2. Exeter Publ., Setauket, NY.
- Rowland, L.J., N. Alkharouf, O. Darwish, E.L. Ogden, J.J. Polashock, N.V. Bassil, and D. Main. 2012. Generation and analysis of blueberry transcriptome sequences from leaves, developing fruit, and flower buds from cold acclimation through deacclimation. BMC Plant Biol. 12:46.
- Rozen, S. and H.J. Skaletsky. 2000. Primer3 on the www for general users and for biologist programmers, p. 365–386. In: Krawetz, S. and S. Misener (eds.). Bioinformatics methods and protocols: Methods in molecular biology. Humana Press, Totowa, NJ.
- Shangguan, L., X. Li, N. Ning, Y. Wang, Z. Zhang, and J. Fang. 2011. Development of EST-SSR markers in apricot. Acta Hort. Sinica 38:43–54 [in Chinese].
- Shangguan, L., X. Li, C. Song, X. Wang, Y. Wang, Z. Zhang, and J. Fang. 2010. Development of EST-SSR markers in *Prunus mume* and its application. Acta Bot. Boreali-Occidentalia Sinica 30:1766–1772 [in Chinese].
- Tan, L.Q., L.Y. Wang, K. Wei, C.C. Zhang, L.Y. Wu, G.N. Qi, H. Cheng, Q. Zhang, Q.M. Cui, and J.B. Liang. 2013. Floral transcriptome sequencing for SSR marker development and linkage map construction in the tea plant (*Camellia sinensis*). PLoS One 8:e81611.
- Temnykh, S., G. DeClerk, A. Lukashova, L. Lipovich, S. Cartinhour, and S. McCouch. 2001. Computational and experimental analysis of microsatellites in rice (*Oryza sativa* L.): Frequency, length variation, transposon associations, and genetic marker potential. Genome Res. 11:1441–1452.
- Thiel, T., W. Michalek, R.K. Varshney, and A. Graner. 2003. Exploiting EST databases for the development and characterization of gene-derived SSR-markers in barley (*Hordeum vulgare* L.). Theor. Appl. Genet. 106:411–422.
- Triwitayakorn, K., P. Chatkulkawin, S. Kanjanawattanawong, S. Sraphet, T. Yoocha, D. Sangrakru, J. Chanprasert, C. Ngamphiw, N. Jomchai, K. Therawattanasuk, and S. Tangphatsornruang. 2011. Transcriptome sequencing of *Hevea brasiliensis* for development of microsatellite markers and construction of a genetic linkage map. DNA Res. 18:471–482.
- Ueno, S., Y. Moriguchi, K. Uchiyama, T. Ujino-Ihara, N. Futamura, T. Sakurai, K. Shinohara, and Y. Tsumura. 2012. A second generation framework for the analysis of microsatellites in expressed sequence tags and the development of EST-SSR markers for a conifer, *Cryptomeria japonica*. BMC Genomics 13:136.
- Wang, L., S. Zhao, C. Gu, Y. Zhou, H. Zhou, J. Ma, J. Cheng, and Y. Han. 2013. Deep RNA-Seq uncovers the peach transcriptome landscape. Plant Mol. Biol. 83:365–377.
- Wang, L.Y. 2011. Mining and application of molecular markers from EST database and transcriptome sequencing in tea plant. Chinese Acad. Agr. Sci. Press, Beijing, China.
- Wang, Y.J., X.Y. Li, J. Han, W.M. Fang, X.D. Li, S.S. Wang, and J.G. Fang. 2011. Analysis of genetic relationships and identification of flowering-mei cultivars using EST-SSR markers developed from apricot and fruiting-mei. Sci. Hort. 132:12–17.
- Wei, W., X. Qi, L. Wang, Y. Zhang, W. Hua, D. Li, H. Lv, and X. Zhang. 2011. Characterization of the sesame (*Sesamum indicum* L.) global transcriptome using Illumina paired-end sequencing and development of EST-SSR markers. BMC Genomics 12:451.
- Yue, X.Y., G.Q. Liu, Y. Zong, Y.W. Teng, and D.Y. Cai. 2014. Development of genic SSR markers from transcriptome sequencing of pear buds. J. Zhejiang Univ. Sci. 15:303–312.
- Zeng, S., G. Xiao, J. Guo, Z. Fei, Y. Xu, B.A. Roe, and Y. Wang. 2010. Development of a EST dataset and characterization of EST-SSRs in a traditional Chinese medicinal plant, *Epimedium sagittatum* (Sieb. Et Zucc.) Maxim. BMC Genomics 11:94.
- Zhang, H., L. Wei, H. Miao, T. Zhang, and C. Wang. 2012a. Development and validation of genic-SSR markers in sesame by RNA-seq. BMC Genomics 13:316.
- Zhang, J., S. Liang, J. Duan, J. Wang, S. Chen, Z. Cheng, Q. Zhang, X. Liang, and Y. Li. 2012b. De novo assembly and characterisation of the transcriptome during seed development, and generation of genic-SSR markers in peanut (*Arachis hypogaea* L.). BMC Genomics 13:90.
- Zhang, Y., L. Jun, X. Zhong, F. Li, P. Bo, J. Yu, Y.C. Jing, and J.Z. Xiong. 2011. Characterization and development of EST-derived SSR markers in cultivated sweetpotato (*Ipomoea batatas*). BMC Plant Biol. 11:139.
- Zheng, X., C. Pan, Y. Diao, Y. You, C. Yang, and Z. Hu. 2013. Development of microsatellite markers by transcriptome sequencing in two species of *Amorphophallus* (Araceae). BMC Genomics 14:490.

Supplemental file

Seventy unigenes derived from loquat transcriptome used for genic SSR primer design in this study. The details in bold were listed in sequence of unigene code, motif type, repeat motif, repeat size, SSR start position, SSR end position; p2: dinucleotide repeats; p3: trinucleotide repeats; p4: tetranucleotide repeats; p5: pentanucleotide repeats; p6: hexanucleotide repeats. The nucleotides of the unigene sequences in pink were repeat motifs, and the ones in yellow were the position of the primers. The left and right primers and the product size designed by Primer 3 were listed below the unigene sequences.

1. G1_Unigene_BMK.62 p6 (AGCTGG)3 18 996 1013

GAAATATATTCCATATATGCCTAAGTTTACAG
ATATGTTACTGAAGTAGTACGTTCCCTCGTCATG
ACAGCACATATATGTACGTATATGCTTG
CTTTTATCTTGATTATATCTTTGGATTTTGAAAGAAG
AAGACGCTCGGCCGTAGATATTTGCAGCTGTATGAG
TTACAAAATTACAATATACAGAATGACATGAG
CTACTGTAATGAATGAGTATTACAGCTATGGTG
ACTGTAACCCTCCAAAAATGATCTTTTCAGACGG
TAAGTTTATAATGATGACCCAGTCTTGATG
CTTAAAGCGAACTTTTCATGTGATCTCTCTAATATG
AAGATGTTGCCTTTATCATCCCTCCCTAATCTCAGGG
TATCATCAACATATCTGAAGAAATTGAATTAAG
AAAAAATATAATCTCTACCATTCGAAAAATCAG
AAAATCTCAAGCAGGATTACTACTACGTCAAAGTGG
TAACTATTAGGATACGTGATCTCAAGCCATC
CTTCCGGGTTGAAGATCCCAAGCAGAATATCA
TAATTTTTCCGGAACACGTTTCATTAAGTACTCGG
AGTGATTGTGGAGTTGTCTAGTTGATGTCA
ACTCTTGAATTGGATGCTTTCTTGAAGGAGG
CCTCAATTGTCAGCCGTCCATTAACAGATT
CAATCCTCTCACGTGCAACTTGATCACATTAAGT
CTTTACCCCTTAGCAATGTTAATATTCTGGAAGAAG
TCACCCAAGGAGATGAAGTCCCTCAATCCCAG
CTTTGTTTCGTTTGAACCTAAATAGTAATTGTACTG
TACACAAGTTTCCAGCATCCACCCACCCTTTGTAG
ATTAAGAAGAGGATCTGGAGTAGGATTCCGAG
ACTCGAGCTGGTTGACGAGAGCTTCAATCTGAG
ATTTCTTCGCAGACGGGACTCCGAAAAATG
CCTCTATTGATTCTTTGATTGCTTCCAAAAGCTGTG
TCTTAATAACCTCATCATCACCAACGTCCAAGCTGG
AGCTGGAGCTGGAACCTTTCTTCTGCAACTG
ACCTCACTGTGCAAGTGTGTGCGCCATAACCCAA
CAAATCTCGTGCTTTGATGTGCGGTGAGACCAAA
CAGCGAGCAGGTGCCGCCATGTTTCTGGGTCTCAG
TCTAGGCACTGGCGGAAATGGAATTGCATGG
ACAAGCACGCTGGCCATCAATCTTCCAATGACTCG
ACGGCACCCAGAGATGTTCACTGCTTGCTAG
TAATCCCCAAGCTCATGTCCATGCCAGTGAGAGGG
ATGGGGGAAACCTTACAGCTGCTGTGTGACGAGAG
CTTTTAGGCTGTCCTTGTGTTGTGCTGTTTTCTCA
TAGCAGCATGTGTTTG

LEFT PRIMER GACTCCGAAAAATGCCTCTAT
RIGHT PRIMER GTCCATGCAATTCCATTTC
PRODUCT SIZE: 252

2. G1_Unigene_BMK.64 p4 (TTCT)6 24974 997

AAGAAGTTTTAGGATCAAACATTTTCATAAATGCAG
TTGAATTTTATCGCACATATTTTACAATAAATG

TTTAGTCGAGTCTCCTGTACAAATAGATTATAG
CACAGGCAGGCACACCTAAGAGTGTTTTTACA
CAAATGGAAGCAGTAGACAGACGTTCCAG
TATATCTCTGTTGCCACGACGGAATGGATTCATCGG
TCCAGCATCTCTTTGTTTCTAAGAGGCGGACAG
ATTGGATATGTGTTCCGTAATGCTAGCTTTGTTTCG
AATTACAGGCATGAAGCGCAGTGCATACGTCGGTTG
TTTCGAGGAATTGCTCTGCATTGGTAAG
AATGGGGGGGCCATACTCGAAAACGTACCTCTTG
CACTTTTTGGGTATAGTTCTCCACCGAATTGCATG
CCTTCAGAAGCAACTCAATAATCTCCAGCTTCGTG
TCGGGATCCTTCAACTTAACCAACACCTCTGAAACAG
CACGGTGACATAATCCACAGCTATCCTCTTTGAATTG
TGAAGAAAACAAAGCTACTTGCTGACAGAGATTG
ACCTTCCGACAGAACTCAGAAGGTTGTAGAGAGG
TGGCCTCTAAGAAGAAGAGAGGAGCATAATAG
TCCACCAAAGTGACACACTGCTGGCTGAATGAGCG
CAAATGATGGCAGGCCTGATGTAGGTATTCAATG
ATCTCCGCTCTGGGTCTTGTTTTCACTAATGTAAT
CAAGTGCTTGGTCAGCAAACCTCCTCACACAATGTG
CACAGTTATCATTTCGACAACACTTCTTCAACTTGG
AAAGTTTGAGTTTCCAACTGGTGGTCTGACTTTG
AAACTGACAGATCAAGGTTTGTGAGTTGTCTAGCAT
CACAAGCCCAACCAGCCGCCAGCGCAAAAAGAAA
CAAAACCCCAACTCTCACGTCCATGGTACCTGCG
TTTGTGAGGAGAGAGAAAGAAAGAAAGTGG
AAAACCTTGATGTCTAGGAATTCTTCTTTCTTT
CTTTCTTTCTTTCTTTGTTTTCGAAGGGTTGGGGG
TGGGCGTTTGGGGGAGCGTTGAATTGTCTG

LEFT PRIMER CGTTTGTGAGGAGAGAGAAA
RIGHT PRIMER GACAATTCAACGCTCCCC
PRODUCT SIZE: 126

3. G1_Unigene_BMK.101 p4 (TGAG)6 241863 1886

GCATTTTATTACATCAGGAACACACCACTCGCAATG
CAAGTACTTACATGGTGCCATTTTCGAATCATTCA
CATCCGAATTACCTGTAAATCCAGCATCTTG
TTTATCGATAGAAAAGTACAAGACATTCTACTCAG
CTTTTTCCAAATTACACAAAAGCATCAAGGACG
AACTACTACAGGATTTAACTTTTGGGAGTGACG
ATTTTGCGCTTGATAACTGATAAGCAAAAGCCATAT
CACCAGAAGAGTAACCTATCCCTCGGAAGCATA
TTAGTTACTGCACCCCACTCCATCTAGCCCAG
TCTACGAAGTGCATCCCCCATAAACATTGTTTG
AAAATCGTACTCCGACAGTGAAAGCCATTGCAA
CAAGCGGTTCTGTTTCGCCAAAGGCGATGCCTCTAC
CAAGCGTTCAAGTCCATTGATGATTTGATAGCGGG
TATTGGAAGAGACAGCAAGGAAACACCCCAAAG
AGCTGCACTCTTTATTAGAGGTGGAACAGGTATG
TCCTCTTCTGACTTCTTTATGCTCCGCTTGGCAG
TCATGATCAAGTTTGCAATTCCTTGGCCTATAATAC
CACATCCAAAGCCTACTGCTCCATACAAAATG
CCCTTAAAAAAGTAAGTGGAATTCTCTGCTTTACAG
AATATCTACATCCTGGCCTTTCCGCTTCAAATA
CACTGCTAGGAAGAGCTCCATAAGAATGTTGCAAG
CGTCCAAGCAACCCTTTAGATAATGATGGTTTCCCAA
TACGAGCATAGGGGGCCAACATCCCAACTAAAGCAA
CATTAAACCACCACCCCAACCAAAAGATCTGCAACA
TACAGCTCAAATTTCTGCCAGAAATCTTTTG
CCCCTCTTTGAACTTCCGCAAATGTAGCACAAACAG
AATCAATGACTATCTCTGTTCCAATTTTGAAGAG

AAATGATGGATCAGCAAGCATTTCGATCGCGAAG
 CATAGAGCATGACCTCATTAAGAAACCTAGAGG
 CCAGGCTGACCCCTGCAAATCCAGATATCTAAGGAG
 AAGCACTTTGCGAATTCCCACGCTCTTGGCAG
 CCTCAATCATATCAGAGGGAAGCCTAGCCCCTCGAG
 CCTTAGTCTCTTTCATAATCTCTTCAAATTTCA
 TAATTGGCCCAAACCTCTTCTTCTTCTTATCACCCC
 CACCACCGTCACCACCACCACCACCTCCTCCTC
 CACCTCTACTGCTCGTATATTTACCATTACCACCAC
 TACCATCAATCATATCCTTATCACTACCAC
 CACTCTCGGTTTTTTGATCCACACTCATTCTCCG
 AAATCCTCATTTCCTTTTTCTACAATAACATCCCG
 TCCCTCATTCGAAACAGCTATTGTGCCTAACTCGG
 ATTGTGATTTCAGCCCGAGCCTCGGACATAGACATG
 ACCGTAAATTTCCGGTCTTTCTTCACCGAAAACG
 AATTCAGCCTATCTCTAAAGCTACTATTCTATAGAG
 CACTGGAAAAGCAACCTCCTTTGCATCATTCC
 TAAACCTTATTCCATAAGAAATCAAATTCTGACTCCA
 CATCTTCTCCGAACGACCTCGTTCGCGAAAGTTG
 CAACATTTCGATATCCCAAAGCTCGAAGAACAAGCCG
 CCATATTGCCTTGAGAGATCTCAAAAATGTCTAAG
 TCGATAATGCACGCCGAGAGAAGTCGACGAATTAT
 TACGCAAGTGCCACAAACACAATCTTTAAAGTCAGG
 CAAGAGGTGATTGCGCGGAGATAACGGAGGAAAGTG
 AGAGGGAAAGTGGGTGGAAGGTAAAATTGGTG
 TTTGGCTGCCGAGAAAGTTGAGGGTTTGAGGATTG
 ATTCCGAAAGCGATAGCTGGGATTGGTAGGTGG
 TTGAGTGAGTGAGTGAGTGAGTGAGGGAAGCGG
 AAACCTCGAAAGAGAGACGACGTGGTTAATGGG
 CTCCTTATATCCTTT

LEFT PRIMER AGTTGAGGGTTTGAGGATTC
 RIGHT PRIMER ATAAGGAGCCCATTAACCAC
 PRODUCT SIZE: 128

4. G1_Unigene_BMK.137 p3 (AGA)6 18 81 98

AAGGAACCCACCGTCGCTTTTTTATCCCTC
 CTTCTTTTTCCCTTTAATCCCCAGGAATTCGACTCTG
 TTCCCTCAGAAATCAGAAGAAGAAGAAGAAAA
 TAAAAACCAAACAGAGAGAAATGGGGCTG
 CTCTCCAACAGGGTGGATAAGGGGAGCTTGAAG
 CCAGGGGATCAGATCTACTCTTGAGGACTGCTTATA
 TATATGCCCATCACGGCATCTATGTTGGGAATGACA
 CAGTCATTCAATTTACCAGACATGGACAAGAAG
 TAGGAACGGGGACAATGCTGGATCTTCTTTGGTTAG
 CTCAGGGCCAGCCCAACCTCGACAACCCTG
 CCAAATTTGCACTCCACGGGAAGAGGGCAGTGGTG
 TTCTCTCCTCATGCCTGAAGTCTTTCTTGCAAGGTGG
 CATCTTGATCGTTTTGAATATGCTGTAAACCTG
 CTCTTTTTATTGCAAAGCACGCGCGGAACCTG
 TACCCTTGCACTCTCAGACCCAGACGATGTTGTGG
 TCCATCGAGCAAAATACCTGTTTGAGAATGGCTTTGG
 TTGCTACAACGTGTTCAAGAACAACGTGAAG
 ACTTTGCTATCTACTGCAAACGGGACTGCTTG
 TTCTGGATCAAGGAACAATCGGGCAAAGTGCCAAG
 CAGTATCCATCATAGGGGGACCTCTTGCAAGCTG
 TTTTGTCCACGCCATTGCGTCTTGTCACAACCAATG
 TTTATGGGATGGCGGCAACTGCCATTGGAGTCTACTG
 TGCTAGTAGGTATGCTGCTGACATTGGCATGAGG
 AGGGATGTAGTGAAGGTGTCGGTCGAGGATATG
 ACAAGGAGAGTGGCAGCTGGCCTGCTCCAGGTGG
 CCGAGGCCCAAATCACAGCGGCCCAATCACGG

CCCTTGCAGGAGGTTCTTCGAACCTTGTCTCTTG
 ATAGTATGATTGTTTTTATCACATTAATAAGTACTTG
 TGCAATGACATCTGCTGTTTAAGCTGGCTTGTATG
 ATGAGATGTTTGTGTTTTCTTCATGTTGTCCACCGG
 CATTGTGGAGTTTATAAAGGCCAAGATTGGTGG
 CATCTGCCTTATTCAAAAACCTTCTTTGTAAAATG
 ATCGGTGTGGGATATTTTTTTTTTACTTTATTTCATG
 ATCATACTTACTAAGGTACCGAAGTATAACACCTC
 TAGATTTGTACCACACATTTCTTTTTTGTGGATA
 CAAATGATGTTGGGGGAGGGGAAATCGAACTCGTG
 TTGGATACAAATG

LEFT PRIMER TTTTCCCTTTAATCCCCAGG
 RIGHT PRIMER TAAGCAGTCCTCCAAGAGTA
 PRODUCT SIZE: 164

5. G1_Unigene_BMK.160 p3 (TCA)7 21 242 262

GCACGCATTTTTTTTTTTTTTTTTTTGTAATGTATAAA
 TACTCAAATATCATATAATCTTGAACCTATGTACCAT
 CATCATCACCACCATCATCATCAAGTCACATATCG
 AACCAAATAAGAAAAGAACGAAAAATAAAATA
 AAAACAGAAAGATTTGTAAAAACTCTCTCTC
 TTTTTCCCTAGCGATGAATTAATCCATGGCCAAATG
 AAAACCAATAATAACAATCATCTCTTCTCATT
 TCATCATCATCATCATCATCTTCTTCTTCTT
 TATCTCTCATCTTCATTATAATCTAAGCCTGAAGCG
 AGTTAAACGCGTCGCACCTGCGCCTCACCTCTCCCTG
 ATGCCCGGTCTTAATCTCATGATGTCCAAG
 CTCTCTCATTTGCATGAGAAAAAGCCTTGA
 AAAACTCCGCTGGTCAGTAAAGTACAACCTCCA
 CAAAAGGCTTCGTCCTCGGGTCTTGTAGCAAG
 TGCATGGTCCGATGCCAGCAGCCCCAAG
 CCCCTCTTTAGAATCTGAAAGTACATGT

LEFT PRIMER ATCCATGGCCAAATGAAAAC
 RIGHT PRIMER TGAGATTAAGACCGGGCATC
 PRODUCT SIZE: 174

6. G1_Unigene_BMK.217 p6 (TCCTTC)3 18 94 111

TAAAGCCCTCCTTGAAACCTCAGACATTCAGCTTTTG
 TCTGTCTTCTTCTTACACAATGTCTCTGACACCAA
 TATCTTTGCTCACTCTCTGTATCCTTCTCTC
 TTCTCCTTCTTCTTCCACCGCCACCTTAACCCTCCA
 CAACCTCCTCCAAAGCCAAGGCCTCCCTGCCGGG
 CTCTTCCCGGCCAATGTGAAGTCCTACAATCTCAAC
 CAGATGGGCGCCTGGAGGTGCATCTGGACCG
 TTCTTGCAATGACCAAGTTCGAGACAAGAG
 TCTACTTTGAGAGCATAGTCAGAGCTAATCTCAG
 CTATGGCATGCTCAGAGGCTTGGAGGGTTGACT
 CAGGAGGAGCTTTTTCTTTGGCTGCCGGTGAAGGG
 AATCTCAGTGAGCGATCCGTCTTCTGGGTTGATTTTG
 TTTGACATTGGTGTTGCCCATAAAGCAGCTTT
 CTCTCTCTCTATTTGAAGATCCCCTTGTCTGCAAG
 CCTCAATCTCAAGGCATTTTCATTGAAGAGTGAAGG
 AGAAAGGAAGATTGGATTTTCAGGCCAGAGATGAAG
 ATTTGATCTTTTGTCACTTGGAATAATTTTCTCATG
 TTTTGCTTTTTGGGTATTTTTCTCTTTTAATTTTGAG
 CAAAAAAGATTGAATGTTTCATGGAAGCTTGTTAGG
 ATTTGAAAAACAAAGGAAAGCAAAAGTGTGTGAAG
 ATTTTGAATGAAATAGTGCAATTTTGGAAGCTTG
 CTCAATTGGAAATTTTCGGGTTTTATATATTTTTG
 TCTTAG

LEFT PRIMER TTCAGCTTTTGTCTGTCCTT
RIGHT PRIMER CTTGTCTCGAACTTGGTCAT
PRODUCT SIZE: 242

7. G1_Unigene_BMK.254 p4 (CATG)5 20352 371

GGCGGAGTACAGGCCGAGCGGTGGCTGGAGAG
AGGAGAGGAGAGAGGGGACTCACAAGAAGTGAAG
TTCGTTGGTAGGGACACATATAGCTATCCGG
TTTTTCAGGCGGGGCCGAGGATCTGTTTGGGGAAGG
AGATGGCGTTTTTGCAGATGAAGAGGGGTGGTGAG
CGGGGTTCTGAAGAGGTTTAAAGCTGGTCCCGCGGG
AGAGGGAGGGGTGGGGATGAGCCGGAGCTGCTGG
CCTACCTCACCGGGAAGATGAAAGGCGGCCTTCCGG
TCACCGTTTTGGAGAGGGCTTAATTAAGTATATATTG
TCAATGTGTGTATCGTAATGATTACGTAGGTAAT
CACATACATGCATGCATGCATGCATGTAGATGCTTAT
TATTTTGTGAATTTTACCTTTTAACTTTGTAA
TATTTGGTCTTATCATGTACGTGTCTCTAAAGAG
TTTGTACTCTCCATAGTTATATGGATGGATGTTTTG
ATGTTTTGGGCACTTGGT

LEFT PRIMER CTACCTCACCGGGAAGATGA
RIGHT PRIMER GAGACACGTACATGATAAGACCAA
PRODUCT SIZE: 204

8. G1_Unigene_BMK.267 p4 (AACC)5 20205 224

TCGGTCACTTAACGCTGCAATTCACAAGACAAATC
CAGATCTGAGACTAGCCATTGTAATTGTGTGATG
TTATCTTCTTTTCCATATATTAGCAAATGTAA
AAAAGGCATCAAAAAGAAGATTACAGAAGAAAAA
TATGGATTAATTACCCAATAAACACGATCAAGGCCG
CTACGACACACAATCATATATTGTAAAATTTACAAAC
CAACCAACCAACCAACCTGGAGGGGTGGATTGTG
TTCATTAGGATCAATCATCAATCCCTAATGCCAAG
CTCAACCTCGAGTTCATCGTCTCTTCAAAGAG
CTTAAGAGAGACGGGCGTGTTGCTCTT
CTCTCTTCTTCTTCTGCCATATCTTGAACATG
AAAACGCAGAAGCCGATGACAGCCGCCACCCCCAG
CAGCACAACTACTGCTTGAGCGCCGCCGCG
ACCCACTTGAAGCTTTGTCTCCTTTCTTGGGAG
TGGGAGTTGAGGGCTCTTCTGCCGAACCTAAATCG
AAGAGGAGGCTAATGGACAAGAGGAGGAG
ACCCATTTGCAGCAGTTGCAGACATCTTTGG
CAATGGCGGCTCCGAAGTCCATTCATGTCGTCTG
TCGTGTTTCTCGCGGAACCCAAATAAATCAACG
ACGGTGAAGATGTCGTACAAGTACAAATACAAATA
CAACGTTGAATTTTCAACTGCAATTTGGAAGTGG
ACGGGGAATGCTCTCCGTTGTTTCTTCCAACCTAC
TAAACGTCAAACACTCACTCCAACCTAACGAATG
TACGGGTCACTGCTGTCGTACAAATTTCTTTTA
CAATTCGGAAGTCTA

LEFT PRIMER CAATAAACACGATCAAGGCC
RIGHT PRIMER TTTGAAGACGACGATGAACT
PRODUCT SIZE: 156

9. G1_Unigene_BMK.328 p2 (GA)10 201997 2016

AGAAAAGAAGAAGCAAAGGCCAAAGAAGATTCTTG
ATGTCATTGTTTCTTGTTACAATCACAAATTTCTTTA
TACCAAAATCCACGGCTGAGATCTTACAACCTTTC
CAGTAGACCCCAACCATCATTTATTACAAC
CCTCCTCCCCCATGTTTCCAGATCTACACCTTATG
TCCCCTTCCCCCATATTTTTCTTAAACATTTT

TATCTTCTTTTTCTTCTTCTATATGAAATTATATATG
ATACATCAAGAACAGCTGCAACATTTTGGATCCAAT
TACATCCAGGACCACACACCCAAATTACT
TAAAAAAAAAAAAAGTAAAAACGGAATTTAATTCAA
CAAAAAATTTAGACAAAAGGCCATGTGATCGGTG
ACTTGATGATTTTATCAACCGGACTCGTCGGTATG
CTGACCGCCCTTCTTCCCCTGTCCATTTCTTTTTT
TACCCTCGTCTCGATCCCCTAATAACTGACGTAC
CACTTGACGAACTTCTCAGCCCCACTGG
CCAAATCCGTGGTGGGTTTGTACCCGAAGTCCTTG
TACGCCAGGGTCACATTGGCGTGCCTGTAGGGCAGC
TCCCCGTTTCTCGGCATCTTGATCACGTGCTTCTCG
CCTTCGTGCTTAGAAGCCCTTCCAGTATCGACAC
CAGTTTCCCCACCGGCACCGGCGACGTGTTGCCG
AGGTTGTAAATTCGCACTGGGCGGGG
CCTTTCTTTTTGCCCCACTTCCCCTGCTTTTTTTCGG
CTGTGTCCAACGCTCCCAGGCACCTTTTACTACG
TCGTCAATGTACGTGAAGTCACGTGCCACTTCT
TATCGTCCACTGTTTTGTAGACGTGATCGG
TTTACCCTGCAGTATGTCCTTGGTGAAAAAGAAA
TACGCCATGTGCGGGTCTCCCCCAAGTCCG
TACACGGTAAAAAATCTTAAGCCGCTGAGGGAAAG
TCCGTAAATATGATTGTAAGTGTGGGCGATTTCT
CACCGGCTTTTTTTTGTGCGCGTAGAGACTGG
CCGGTTGGTCAGTCTGTGTCAGCTCGGAAAACGGG
TTGTGCGGTGTTGAGCCCGTAGACCGAGCTGGACG
ATGCCAGACAATGGAGGGCTGAGGATTTG
CTCTTTTGGCACTTCGAGGAGATTGACGAACCCG
CAATGTTGGAGCTCACGTACGACTGCGGGTTCTG
CATAGCGTACCGGACGCCAGCTTGGGCGGCCAGG
TGCAGGATGTGCGTGAACGGCACCATCGAACAG
CTTCGTGAGCAGCGGCTCGTCGTTCAAGTCC
CCCTCCACGACGAACACCTCATGCTTCTTCAG
CAGGGCTGCTCGACCGCTTAGCGAAGGGTCTG
TAGTAGGAGTTGAAGTTGTGCGAGTCCGAGAATC
CATCGCCCCGCTTTTTTAAGGCGAGGGAGCAGTG
AGACCCGACAAAGCCGGCCGCGCCGGTGACCAG
CACCGACATGCCGTTGGGGCGTCTAGGAGTGGCAG
ACTTGCGGACCTGTTTTTCCCAAGCAGTCC
CTCCCACTCCCCACCGTAGAAGGCGGAGGAGAG
AAAGTTGTGAGTGGTGTGGACGTGGTTGG
CCCCACCGCCGACGTGATCGGAGAGCGGAGGG
TAGTTGAGGGTGAAGAATAAGATGAGGACAAGGG
CGACGAGGAGGGTGGCACGGAAGAGGAGCTTGG
AGGAGGCGTTGAGAAGCTTGGTGCTGTTGACCCTG
CGGAGGTAGCTGTTGTAGCGCTCCAGCTTTATGG
TCTTGCTTGTATCTGGCGGAGAAGCCATTG
CCAAAACTTACACCAAAATATACAGAGAACC
CAAAATCCAAAGTATATATGAATCAAAATACG
AAAATATATGTACCCAAATTGTGTA AAAACAAAAG
AAAGGGTTTTGTGCTTCGGGACAGAAGAGACGG
ATCTAAAGACAAACGAAGGGACTCAGAGCTG
AAATGTGAATGAGCCCTGAATTTGGGGGGAGTG
CAGAAAGATGAATATAAAGATGATGAGAGAGAG
AGAGAGAGAGATGCAATAACAAATTAATAACAA
CAACGAGCTTTGCTGTGTATTTTCTGTTGTTG
CTATTGTGCCAGTAACCTTCTCTCATCATCAT
CATGGATCCATATCTATCCATCCCCTTCT
CTTCTCTTCTTCTTCTCCTTCTCTCTCTCTCTC
TCTCTTGGTTAACTCAGAACAACTCTGTTT
TGGGGGTAGAGCGAGAAAGTTCAAGCCCTAGAGG
TAGAGAGAGAGGATATTACGTTGCCCTAGG

LEFT PRIMER ATGTGAATGAGCCCTGAATT
RIGHT PRIMER GCACAATAGCAACAACAGAA
PRODUCT SIZE: 138

G1_Unigene_BMK.328 p2 (CT)10 20 2157 2176

LEFT PRIMER ACCCTTCTCTCTCATCATCA
RIGHT PRIMER CCTAGGGCAACTGAATATCC
PRODUCT SIZE: 180

10. G1_Unigene_BMK.407 p6 (CCCATC)4 24 56 79

TCCCGCTTTCTTGGACCTGTAAAGGCATATCC
TCTCCCCTCCTTTGTTCCATGCTCCCATCCCCATCCC
CATCCCCATCCAAATTAATAATTTTCATTTAAATTTG
ATTTATTCATTTTATGATTGTTTTGGTAGTTTATTATG
CATCTGGATCAGATGAGATGAGATGAGAGAGGATA
TAGTTAAAATTGGATATGTGGTGGTTGTTTTAGTTG
AATTTCTTTTCATATATCTCGTGCTACATTTCTTATTG
CATGTCACCTTTGAATGAATGATATATTACTTTTGG
TATCTTGATTGATGTGGACGATTGAGTTGCTGCTTGG
TAGTTTAGCTGTAAACATGTATGTATATCACCTTG
CTTTTTTCGTTTTTTGTTAGTGTACCTTTTGTTA
TATGGTATCGTTGTTGGGTTTTGAATGATGTTTAAT
CAGCTTCGGATTACGGCATGACGTACACCAGCCCTG
CTGCCAGCGCCAGCACCAGCACCAGCAGGGGACAG
ATGAAAATCTTTAGGGCTTAGGGTTTAGTTGATTG
CATTGTCTTGTGGGCTGTATGCAATTAATGAATT
CAAAGTGTAGAAAGATTACAATTTGTAATGAACAAG
AATTCTTTTAATGTAAACCAGCTGTAACCTTTGATAG
TTTGACAAATGGAATGGAATGGAAGGGCGATAG
CCAAAACCTGATTCATGCTCTATTTTACTAGGTG
CAAATGAATTGGATCTTTG

LEFT PRIMER CTTGGACCTGTAAAGGCATA
RIGHT PRIMER CAACTAAAACAACCACCACA
PRODUCT SIZE: 205

G1_Unigene_BMK.407 p6 (CCAGCA)3 18476 493

LEFT PRIMER CGTTGTTGGGTTTTGAATGA
RIGHT PRIMER CCACAAGACAATGCAATCAA
PRODUCT SIZE: 146

11. G1_Unigene_BMK.436 p3 (TTG)6 18 1076 1093

GGAGAAAAGAAAACAAAAGGGCTCTGGAGCAGTGG
CTTTTGGGAAGCAGAAAGAATGGTAGAGGAGAAG
CCTGAGGAAGAAACCATGGTAGAGGAGAATATGG
AATTATCAGAAGTACCCTGAAGACTACTCATTTTG
TGCTGGTTTCATGGCATAAGTCATGGAGCATGGTG
CTGGTACAAAATCCGGTGTCTCATGGAGAATTCCGG
CTACAAGGTATCGTGTGTCGATCTCAAGAGTGCCGG
CATCGATCAATCTGATGCGAACTCAGTCCTT
TCTTTTGATGATTACAACAAGCCACTCCTGGACTTG
CTGTCTACTCTCCCTGAGAAATGAACAGG
TAATTCTGGTGGGACACAGTGCTGGAGGGCTGAATG
TAACTCAGGCCACTCTCAAGTTCCCAAAG
AAAATTCTCTTAGCAGTATATGTTGCAGCAACAATG
CTCAAACATGGGTTCTCCACTGATCAAGATTT
CAAAGATGGTGTGCCAGATTTATCAGAGTTTGGTG
ATGTATATGAGTTTGGGTTTGGATTGGGAGCTG
ATAAACCTCCAACAAGCGCCATTGTCAAGAAAG
AATTCCAACGCAAAATCTCATACCAATTGAG
TCCTCAAGAGGATTGACGCTAGCTGCCATGCTTTTG
AGGCCAGGGCCGCTCTTGGCAATCACGTCAG
CCCATTTGCAAGGGGACGGCGTCATCGACCAAGTG

CCACGAGTTTACGTTAAAACGCTGCATGACCATG
TCGTGAAACCAGAGCAACAAGGTTTCGATGGTAAAG
AGGTGGCCGCCATCGGAGGTCTATGTTTTGCATAG
TGATCACAGCCCTATGTTCTCCACCCCATTTCTG
CTATTTGGCTTCCTTGTAAGAAGCAGCGGCTTC
TTTTGGTGGACTTAAATAGTAGCTAGGACCAGGAG
CCTAGGATTTTTCTACTTTCATTGGAAAAAAATT
CAAATAATATTGGGGAATAAGAACATATGGAG
CACTTTGAGCTAACGGAAGATTGGGTGTAAAATCG
AGCGCATTGGCGTTATAGGATTTATATCGACCACACA
TAGTGGTGTGGGATACGGCTTGATTGTTGTTGTTG
TTGTTGTAAATAGGGGAATAAGAATAATCAAATG
TTCATCAATTGGATATGTGAGACGCTAAAACGACCG
TAATGGCATTATATGATTTATATAGCTGACCACACT
TAATGAGATAAGGTTTGGTGGTTGTTG

LEFT PRIMER ACGGAAGATTGGGTGTAAAA
RIGHT PRIMER CTCATTAAGTGTGGTCAGCT
PRODUCT SIZE: 207

12. G1_Unigene_BMK.458 p6 (GAATGG)3 18303 320

CAAGCAATATCCATCACACAATCAGACAAGATG
ACTAGGACTGAGCGAAACATCTCCCCTGCGGCTTTG
ATCAAGGATCGATCCGTCTCCAAATCCGGTCTTG
ACAAGTCCCTCAAGAAACAAGGTGCCGGTCCCCA
CAACTGGGGCTCCATCACCCAAGAAACCGCCGGCTA
CATCCACAACCCCGACTCGTTGAACCAATTGTCCG
CTGACGAGAGGATCGGTGTTGACGATGCTGATGCCG
ACGACGCCGATGCCGATGCCGAGGAAGAGCAG
AAGGAGGGTGAAGACAAGGTTGAGGAGAATGGG
AATGGGAATGGGATCGATATCAAGAGGAATGG
ACCGGTTCCGAGGAGGATGAGCTCGATTGAGTGAGG
AGGAGAAGAAGGAGGCTGCTGCTTGGAGGAAGGG
AGCGATGGGGAGGGGTGATGTGCGACCTCAAG
AACATCGCCCGAACCTCCGGCGCCTTCAGCCAAAG
CCCTCCTGAGAACGGTGCCTTGTCACCTCCCCGG
TCAGGAACATGAACACCTCGCTCAAAAGCTCGGG
AAATACTAAACCCCTCAATCCATGAACCCACCA
CATCGCGCCAACACTTTTGAGCGCCTTTCCG
TCCCGGTTACGATCGAAGTCGACCTGGATCGGACA
CAATTAACACGTATTCACACATTTGAAAGCATA
TTTACATATTCATAGGGTAGATGGGGGTTGAGCAG
TTGAGTGAAATGGTTGTTGAACTTTGAGAAGAAAA
CAACGTTGTATCACTTAATGAAACAGAAG

LEFT PRIMER GACTCGTTGAACCAATTGTC
RIGHT PRIMER TTCTTCTCCTCCTCACTCAT
PRODUCT SIZE: 200

13. G1_Unigene_BMK.577 p3 (AGT)7 211911 1931

AGTGCTCCCACTCTTTCCACTTCGTTTGCATTGCCAA
CAATGTCAAACATGGAAATATTTGCTGCCCATCTG
CCGTTCCAAGTGGAATGATGTACCTTTCCAAG
CTCCACCAACGTCGCAGATGCTCAACAAAAC
CACTTGGGTACATCCATAACAGTTTTAACCATCG
TTACCAGTCTCACCTCCCATTTGCTGCCGCAGG
TCCATCCCGAACCACTTAGCTTCTCAGATGATGAG
CCTCTCCCGTCCACCTCGCCTAGTCGATTCTCTGG
CCCCAAAATGTTGCAATCAGGACTTATACAGAG
TATTCTGCTATCCCTGTTGCAAGATCTCGCCCAA
CATTTCTCTGTTCTTGTGAGCGTTTCGAGCAC
CACCCCTTCAAGGAGGTTCAAACAGCCATGGCCG

TACCCCCATTGACCTTGTAAACAGTTCTGGATGTAAG
 TGGCAGCATGTTTGGCACAAAACCTTGGCCTTCTCAAG
 CGCGCTGTCAGATTTGTCATACAAAACCTTGGGG
 CCTTATGACCGACTTGCCATAGTTTTCATTCTCAAC
 TACTGCTAAAAGGGTCTTTCCTCTCCGAAGAATG
 ACTATTGATGGTTGTGAAAGCGCCCTTCTAGCAG
 TCGAGTCGCTTAGAGCACATGGTGGAAACCGACATTG
 TTGGAGGACTCAAGAAAGGAGTTCAGGTCCTTGAAG
 AACGCCGGGCAAGGAATCCAGTTTCTAGCAT
 CATCCTCTTATCTGATGGAAGAGACAATTGCACC
 TATGACTCACAGAATACTTCAAGTCCAAACCGGG
 TCTCTGAGTTCTTGAACCAATTGCCAGCTTCGG
 TACATTGTAGCAATGTACCCGTCCACACATTTGGG
 TTTGGCACTGACCATGATGCCACTACTATGCATGCTA
 TATCTGATTCATCCAGTGGCACCTTTTCCTTCATTG
 AGTCAGTTGCTATGATACAAGATGCCTTTGCTATG
 TGCATTGGTGGTCTTCTCAGTGTGTTGGCTCAGG
 AACTTCGACTCACAGTTAGGTCAGCATCG
 CACGGGGTGCAGATTGTATCAATACCATCAGGGAG
 CCATGTGAGTGAGATTTCTGACGAGTGTCAA
 AAAGGTGCTGTTGATGTTTGGAAATATGTACGCAG
 AAGGAGGAAACGGTTTCTGGTGTACCTTTTAG
 TTCCAACATCATCAGCAACTGGAAACAGGGAAGG
 CGTAAGGAAGACATCACTGTTAGATGTGTCATGCG
 TGTACAAGGATCTAGGCTCAAATGAGTCAACC
 CATGTGCAAGGTGAGAGAGTAGAGATACTAAG
 ACCTGACGTTTGGTCCCCTGCAGATGAGGCAGTGTG
 TTTGGAGGTGGACCGTCAGAGGAATAGAATTCTGG
 TGGCTGAAGGTATTGCAGAGGCACAAGTAATGG
 CTGAAATGGGAAATCTAGAAGGGGGCACAGG
 CTATTTTGGCACAACGAATAGCAACCATCTTAACAT
 CACCGGCAGCACAAAGCTGGGGATGGTCTTTG
 TAATTGGCTGGAAGCTGAGCTTCGAGAAATCAGGG
 ATAGAATGGCTAGTATGGAATCATACACACAG
 ACCGGGCGTGCTTATGTTCTTTCAGGGTTGAGCTCA
 CATTCATGGCAGAGAGCCACAACCTAGGGGTG
 ACATGACAACCCAGATTATGACTATGAATGAAGG
 TGGAAACTCACGCAGCAGGGCAGTTGGCTATGAAA
 CACCTACTATGGTTAACATGGTAAGGATGTCGCAG
 AATCTTGGGGTTAATCGCACGGCTTAACTTCAA
 CAAGTAATCGAGCCTCATAGCCTGACTT
 CATTTTTCGGTAAGGTGTGAATACGGATATACAACG
 TTCATCCTCGGATTAATTCATACTAGGCTGATAG
 TATTAGTAACTGGTACTTTCAAAAGAAACCTTTTA
 TAAATTCTGACAGCAGTAGTAGTAGTAGTAGTAG
 TCGTCGTCTTCATACTTAATCCTGCTGCTTGTGTTG
 ATGGGTTTCCACATGATTTTCCTTCATAATTG
 ATGGATATTCGAGTAGTTGAGATTCTTATGGGAAG
 TTAATATTCG

LEFT PRIMER TCAACAAGTAATCGAGCCTC
 RIGHT PRIMER GAAACCCATCAAAACAAGCA
 PRODUCT SIZE: 216

14. G1_Unigene_BMK.673 p6 (GGCACC)3 18342 359

GTTTATTTAAGCGAAGAGAGTTGTGGTCGTACAG
 CGTTTACGTAATGTACAGATAATTTGTGGAGACTCG
 CGCACATCATTCTCCATCCTCCCAGCTTCACTCAT
 CAGCAGACACTCACTCCAGTGTCTTCTTAGTTGG
 ACACCTCACAGTCTTTGGAGATGTGGCCGGTCTTG
 CCACAGTTGTAGCAAGCCTTGGCAACCTTGTGCGGTG
 CCTGGTCACACTCCTTGGAAATGTGGCCGTTCTTG

CCACACGAGTAGCACTTGACGGCGTTGGCCTGGCAG
 TCCTTGGCAAAGTGGTTAGGGCCACCGCACTTGAAG
 CACATTGGTCCCTTGGCACTGGCACCGGCACCGG
 CACCAGTAGCACGTGGCTTTCTGGCGGCTGGAG
 CTGGGGCGTCTCGCGGGCGGGCGTTCTTAGG
 ACACCTCGCGGGAAATGTGGCCGAACCTCGGCACAG
 TTGTAGCACTTGGCACCTTGGGCGCTGTTTGGGCAG
 TCACCCTGCACGTGACCAACGTACCGCAAGAGTAG
 CACTGCTTGGTGGCGGCAGTCTTTGGCTCTGGGCAGG
 CGGAAGACTCGTGGCCAGCTGGCGACAGTTGTAG
 CACAATCTCTCGGTCTGCTGGCAGTCGTCAGCGATG
 TGGCCGGCCTCGCCGCACTTGTAAACAGGATCTTGGG
 AACATTTCTATGGTTTTTATGTGTGTG

LEFT PRIMER ACAGTTGTAGCAAGCCTTG
 RIGHT PRIMER GAGTGCCTAAGAACGCC
 PRODUCT SIZE: 246

15. G1_Unigene_BMK.683 p5 (ATCCA)4 20 771 790

GTTGAAATGATTAAGAGACGACGTACTGATCAAA
 TATTGACTGTTTCATTCAAATACAGACACATCG
 ATAAATCCCGAAGAGATGATCATTATACACGGTG
 ATTCATAGTCGGGCTATTGTACCTCAGATTTAGG
 ATTCCCTGACATTTTTATTTTGGTACACAAAAGTTCA
 CATCACAACATTATCAAACCAGCCTAACATT
 TATTTTGCTAATCCTTCAATCCTACCTTCAGCTCA
 CAACACACACATAAACGGAGTGAAGATCCGG
 AAAATCTTCAAGAGTCGGTGGGGACTTGACAATG
 AAATTCTGACGGCTAATGGGATTCATGACCACCGG
 TGGACCGGCAGTCCGAGGCCATGCTTG
 AAACCTCTTGTGAGTTTCTTCCCACCATTTGTTTG
 CAACGGTTAACGGAGTACTTCTCTCAA
 TATTTTCTTGTGACGGAATAATGGTCAGCTG
 CCCATGCCACTGCAAATGATCCCAAAACAGCAGG
 AATGATGTATTTTGCAGGCATCTTCAAATTT
 CAAACTGCCAATGACATAACCCAGTTTCGTGAGAG
 AATATGCAATGACAACAAAATACGAAGGCATT
 CAAAATATCCCCTAAGGTCACGTTTGGTCCCTTAGG
 ATTGGTAGATGGGATAACTTACTAGATTCAAGG
 TATGCTGAAGTAAGAGATGAAGACCG
 TTCCTTCAACTTGGGCAGAAATTTGGAAGTCAG
 CCTTCATATCTTACTTCAAGATACTTTGAATCTAGTG
 AGGTGTCATATCCAATCCAATCCAATC
 CAAACCCGGGCACCAAACATGGCCTAAAACGAAC
 TAGATAGTTCCCTATCTGTTTGAATTGCCAATTAAG
 AACGACTAGCCTAGTTCCTATTTGGTGGCTGGG
 ACTACAGAGGGCAGGAACAATTAAAATGG
 AATAACTGTCGTGGCCTATGCTTGATGAGCTTAACAA
 TAGCGGGACTAAGACTCAGTTAAATTAG
 ATAACCTTCCCACCTTATCAAAGACAACATG
 TCTCCTCCCCAAGGGTTCAGGAGAATCTAACATG
 CAACCAAAGGTATATCCCCCTACTATCAGTATCTA
 TATCATCGTGTGAGCTATTACTATCTTCTCATCATG
 TGGATTTACATGATGAGAGAGA

LEFT PRIMER AACTTGGGCAGAAATTTGGAA
 RIGHT PRIMER GCTAGTCGTTCTTAATTGGC
 PRODUCT SIZE: 169

16. G1_Unigene_BMK.704 p6 (TTTTGT)3 18 702 719

TCCCTCCAATCTCCCCAATTTCCACCGTCTCTTCG
 CCTTCCTCTTCTTCTGCACTCTTCTGTCGTCAACCTT

CAACTCCCTCCCAACAGTCAAAAAGTCAAAG
 CCCTAACACCGTCCGATGACCACCTACGGCAG
 ATCCCGACCTCCTCCTCGTCTCCCAAGG
 CCCCTCCGGCGAGTACATCTCACGCGCCAAGGACCG
 CATCAGGGCCGGCCTCGGAGCCCGCCGGCCATGG
 AAGCTGATGTTCAACTTCCGGTCTTCAACTT
 CCCCTCCTCTTCTCCGACGCCTTCGGGCGGGTCCG
 ATCGAACTATGCCTACTTCCGGATGAACATATG
 CCATCGTGGTGCTCCTGATCCTGTTCTCAGCCTG
 CTCTGGCACCCGATCTCGCTCATCGTCTTCGTCAT
 CATGATGGCCGCCTGGCTCTTCTCTACTTCTCCG
 CGACGAGCCGCTGGTGCTGTTCCGAAAAACGGTAG
 ACGACCGCGTCGTTTTGATCGTGCTGGCGGTGGTG
 ACGATCGTGCTGCTGTTCTTGACCCACGCGACGGTG
 AATATTCTGGTGGCGCGGTGATTGGGGTTGTGTTGG
 TGATTGCGCACGCGGCGTTGAGGAAGACGGATG
 ACTTGCCGGTGACGAAGAGAACTCTGCGTTGTTG
 ACTACGCCTGCATCTTCTCTGCTTAAATACTCCG
 ATTCGATTCTCTGTTTTGTTTTGTTTTGTTTTTTG
 TAATTTATGGGTTTTGGTGATCGAAGTTGTTGATTG
 TATCTGCCAGTCTGCTGCTGCGCCCAATTGTTGG
 TTTGCGATGAATCTAGTGTTTTTCTTATGGTGG
 AAAAGTGTTGTGCATATTTGTTCCCATTTTG
 TTTCTCCGCTCTGGTGTGTCTGTGTAATTTGGTCTG
 CCTAGTCAAATGGTATTTTACTTGTCCCGTCTCG
 CTCAGGCTGATGAACATCCGATGAGCCGACCCTCG
 AGGAAGGATACTTGCAATACTTATATTGACTCG
 TTTCAATTTGATAATTTTTGCTTCAGGAAAG
 TTCTCCGGTGGGGAAAGAATACCGGTTTCAG
 CTAATACTAAAGCGTGCTGGTCTTCACTGGAAGCAT
 AGGTTGGTTGTTTTTCTGACAAATATGGAACG
 TTTAGAAGAAGTCATGGTAAAGTTGGGATTCT
 CAACTGATTCTTCTGAGCAGTTTATTTGAGAGGAG
 CCTGAGGAGGAAGCATCCTAGTGAATGAAGTATTG
 CTTCTATATAATGGTGGGAGAGATTGGATCTTG
 ATTGTGGGTGGTAGGGGAGCTGCAAGTAGCGTTG
 CTGGGTGGTTGGGGAAGGGGCGAAGACCATTAGGG
 TGGATGTTTGAGTGATACAAGGGAGAACGCAAAGG
 ACACGACGAAGCAACGAGTAGTGCTGGGGACTCGAG
 TTTTCGGATCTGAAGTTCGCGCTCTCTGCTCTATT
 CACCTGTTTTTGGTAATTTTTCAAAGCTAGG
 TCAAATTGCGGTGAAGATGAATTGAAGCAAATTC
 CATCTCAGTGAGTAGCTGTTATTCTTCTCATCTCCA
 TATTGCGTTCCGTCGTTTAGAATCAACGCTCGGCCG
 AGCATTTCAATTTGCCCGAAAAACATGGGCATGG
 CTAACGGAACACGATTGAAGA

LEFT PRIMER CCTCTGCTTAAATACTCCGA
 RIGHT PRIMER CAGACTGGCAGATACAATCA
 PRODUCT SIZE: 108

17. G1_Unigene_BMK.782 p6 (GGCGGT)3 18 417 434

GGACTCAGTGCTCTCGGACTCAGATCTGAAG
 TCAAACGACGCAAACGCTCTCACGGTATCCACT
 CATTCGAGGAGAGGAACATGGGTCGTGGAGTCAG
 CAGCGGAGGGGGAGAAAGCTCTTTGGGCTATCTG
 TTTGGAGGTGGAGAAGAACTCAGAATCCCGTGGCG
 AAAAGGGGTACGGCTCCTCAGAACCAGGCGCCGG
 TTCCAACCTGCTGAACCACTGCTCAGAGGGCTACTG
 TCCCCGACCACCTGCAGAACTCAATAGTGGAG
 ATTCCCGCTGGCGTACCTGGGAACACTTCAAACAAC
 TATTTCCGAGCTGATGGCCAGAACTGCGG

CAACTTCCTCACAGATCGACCATCAACGAAAGTG
 CACTCAGCCCCCGGTGGTGGATCATCCCTAG
 ACTACCTGTTTGGAGGGCGGTGGCGGTGGCGGTGG
 CAAGTGAAAGCCTCACGCCGCTGAAGTTGGAATCG
 TCAGTTTGGCCCTCGCGCACCTTTGTAACCTTGG
 ACCCTCTGTAGATGACTTCTCCTCTGTAACATTC
 TAGCACTTCTGCGGCGGGGATTTGTTGGGTTTAAAG
 CTTTACGCTGCTGAAACTTTTCGAGTTAAGTTGG
 CCGATGATATAATCGTTTACAAATTGCACTACATG
 TTCTACAAGGATTTTTCTGTTTTTAATCGAAATTTG
 TACAAGTTTTTTAGATTCTGTTCGGAAGGAAAG
 AAGCACACGAGAAGCGTTTCTCCATGAAGTCG
 CTTAAAAAATCAATTGATGTTATCGAAACCCCG

LEFT PRIMER AACTATTTCCGAGCTGATGG
 RIGHT PRIMER AACTGACGATTCCAACCTCA
 PRODUCT SIZE: 172

18. G1_Unigene_BMK.949 p6 (AGGGCA)3 18 200 217

AAGCACAACGTGGAGATGAAGAACGGCAAGATCGTG
 TTCAAGGACATGGTGCAGCGAAACGACGATCCATTG
 CAAGGCCAGGGATCCGGTATCGATGCTTACTTGG
 ACGCCGTCAAGCAGGCTCCAGTGAGAGGCCAGAAG
 AACAAGTTGAAGTTTAAAGAAGACCAAGGACGACG
 AAGAGTGGTCTGACTCTGAGGACGAGGGCAAGGG
 CAAGGGCAAGAAGGCCCTTCCAGCGCAAAAGGG
 CAAGTTCTCGAAGAGTGGTGGCGTGGGTAAAG
 CCAAAGCAGAAGTTCAAGGCGAGAAAGAAGCTTTG
 AGGATGATGAAGGTGAGAAGAAGCTTTGAGAAGG
 ATGTTCAAGGCGAGAAGACGCTTTGAGAAGGATG
 ATCAAAGGCTTGAGCAGGGCCGCGCCTGAAGTG
 TATATTAATG

LEFT PRIMER TATCGATGCTTACTTGGACG
 RIGHT PRIMER GCTTCTTCTCACCTTCATCA
 PRODUCT SIZE: 243

19. G1_Unigene_BMK.1448 p2 (AG)11 22 950 971

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 TTTGCAGGAAAATATTGCGTTCTTCTATTCTGTTTTAG
 TATAGTTAGATTGTTGAAATGATGCAGCAGCAGCAG
 CATAGGAGCAATCATGCCTGGCCAAAAGTGTAAG
 AAGCATGAAGGAAATTTGCAACAAATTAATACTAAA
 CACACGTTTTGGCTACATATCAAAGAAAGAATACCG
 AGGTGCAAGTTGCAACAGACAGCAGTTGCAACATG
 CCAACATATACATTCAAAGTAAACAGAACACAGTTA
 CAGACAGGTTACAAGAATCATGACCCAGAAG
 CCTGGAACATCCATCAGTGTGATGTTTACCAACG
 AGGGGGCCCCACCACCGCCACCAGGTCCACCACCAC
 CCCACCACCACCAGGTCCACCCATCCACCAGGGCCAC
 CAGGTCTCCACCAGGTCCGCCGCCGCCCATCCAC
 CAGGTCCACCACCAGGTCTCGGCCGAACATTGG
 CCCACAGCAGCGCTCAAACAGGCAGCAGCAG
 CACAGGAAATAAGCACAAGATGATATAAGGTTGCAT
 ACACCGCCACATAGGAAACCTAAGCAATCAAAA
 CACGGTGGAACCTCCTCCCGGTCTCCCGG
 CCTCCTCCTGGTGGCATGGCTCTCTGATGACGATG
 ATGATCTGATCAATCTCTCTCACTCTCTCTTG
 ATCAAAAAAAGCCCTGAGGATATTTCTGCAG
 CTTCTTTCTTAATGAACCTTGCAACGCAGCTATTG
 AAGTTTGTCCGCTATATATACATGAAATCTTGATG
 AGAGAGAGCGAGAGAGAGCGAGAGAGAGACG

CTTAATGGCTAAGTATATATGCCTGAACTAATG
TCGGCTGTATAGTTTCATGTGCGCTGTATAATTAAG
TTAACACTTACAGAGACACAGAGAGAGAGAGAGAG
AGAGAGATGGAGGTGCTGCAAATACTTCACATG
A A C A A A G G G A A C G G C G A G A C T A G T T A T G
CTCAAACTCTAAATTTTCAGGAAAAAATATTATC
CATCGTAAAGCCAATCGTTGATGAAACTG
TACAAAAATTGTTGTGCTCAAATATAGCAC
CAATTGGGAGCATGGGAATAGCGGATTGCGGTG
CTCATCTGGACCAAACGCCTTCTAGTTATCTCTGAG
ATAATTGATGCCATACATGCCACACATAGCGGCTCAT
CATCATCCACAGAGTTTAGAGTGTCTTCTAAACG
ACCTCTTTAGCAACGACTTCAACACCATTTTTATG
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CCACGCCTGGCTCGTTTTACGGCAGGTTGTTTCCAG
CCAAGAGTTTGCACCTTCGTGCACTCTTCTTCTAG
TCTCCATTGGCTCTCTCAGGTCCCTCATGGCCTGG
ATTTCCAGGCAGCTGGCAAAGCTTTGAACAAAGG
AAAGATTTGGATTTCTAAGACCAGCCCTCAATGCG
TTTTGGATGCATATTCAATTTCAATTTACAAAGG
ATTTTTCGTTATTTCTAATGTCCCGGCTGAAGAAA
TAATTGGTGGAGGACGGATGGTGTGTCACCTCA
TAGGCAGGTCATCCTCTGACCCATCAACTCCAGAG
AGCTGCTACCAATGGGATCTCCTTGCTCATGCAT
TAATGACCATGGTTTCAGAGGGTCTTATTGAAGAGG
AAAAGGTTGATTTCCTTCAACCTTCCGTACTATG
CCCCAAGTGAAGAGGAAGTGAAGCTGGTGTAG
AAAAAGAAGGATCATTTATAATAGACCGCCTTG
AAGCCTTTGAAATTGATTGGGATGGTGGTGCGG
AAACAACCGTCGTAGCCAGTGGTCAGCAAGCGG
CCAAGACCATAAGAGCTGTGGTTGAGTCGATG
ATAGAATCTCATTTTGAAGAAAAATATCATGGATG
ATCTATTTTCGTGCTACGCCGAGCTCGTCCGCCG
ACTACTTATCAAATCTAGAACCAAGTTCTCTCA
ATTTGTGTTATTTCAGTCATTAGAAAGGACTGAG
TTTTCTTAACTTCCCAATCAAATTTTTCGTCAACAG
ATTAAAGATCTGGTCTCATTGTGCATATTTTTAG
TTATGTTGTTGGATTTTGTGTTTGAAGAAATG
TTAAGGGGAGATCATATTTAATAAATTATGTTTG
TACTACTTTTCTAATAAATGTGAAACCTACTTG
AACAACTTACTTGTATCGGAGGTTCTACTTCTAT
TAAAAACATAGACGTGAAATCTACTTGAAGAACCC
TACTTGATTTGTTTTACATGTAATATAATTACGGG
CTTGCCCCATTACTCATCCAGA

LEFT PRIMER TGAACTAATGTCGGCTGTA
RIGHT PRIMER CATGTGAAGTATTTGCAGCA
PRODUCT SIZE: 115

20. G1_Unigene_BMK.1461 p3 (TTG)7 21 2000 2020

TCTCTCTCTCTCTCTCTCTATACCAAGAGGAG
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TTCCAAACCATAACGTAATTGAAGGACGATG
ACTCTCGGCACCCTCCCTGTAATATAACTTG
TTCTTTCTGCACCCAAATTCTCTCTCTACTCTG
TTTTCTCTCTCTGTCTCTCTGTGTAGACCAATAGG
AGTTGATTTTGCTGGCATTGCTCGCCACCTTTGAAG
TTCCAAACCTGACGCAATTGAAGGGAAATGACTCG
CGGCATCTACCGTTGGCAGCTTCGGATCTTCATAT
CATGGATGGAACCTCGAAGAAATTCCCACTG
ATATGTGCGCGGTAGTGGCGGATTCAGTTGATCAG
ATGCTGGTCCAAATGGGGAAGGCAAAGGAAGTTGG

CGCTGACCTCGTTGAACTTCGGGTCGATTTTTTG
AAGAACTTCAGTCCAAGACAAGACCTCAGTG
TATTGATCAAACAAAGTCCTTTGCCTACCCTTG
TCACTTACAGGCCAGCATGGGAAGGCGGTCAATA
TAAGGGTGACGACAAGCAGCGACAAGATGCACTG
CGTGTAGCCATGGATTGGGAGCAGATTTTATTG
ACGTTGAACTTAAGGTAGCCGACGAGTTCTA
CAATTCCATTCAAGGGAGGAAGCCAGAAAAGG
TCAAAATCATTGTTTCTTACACAACCTATGAG
AAAACCTCCGTCTGCCGAGGAAATTGGTGATCTTG
TTGCAAGGATACAAGCTACGGGAGCTGACATAGTG
AAGATCGCAACAACCTGGCTTAGACATCACCG
ACTCTGCACGTGTATTTCAAGTATTAGCGCATTCT
CAAGTCCCAATGATAGGGCTTGTATGGGCGAG
AAGGGTTTGATCTCACGCGTACTTAGTGCAAAA
TATGGTGCATTCTCACTTTTGGTACTATAGAGG
CGGGAGTAGTATCGGCTCCTGGGCAGCCCACCG
TAAGAGATCTATTGGACTTGTACAACCTCAGACTTA
TAGGGGCCGATACCAAAGTACATGGTGTGATAGG
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CAATGCAGCATTCAGATCTATCAATTTCAATGG
AATTTATTTGCCTTTGTTGGTTGATAACGTTGCG
AATTTTATTGACACCTATAACTCCCCCGACTTTG
TTGGATACAGTTATACAATTCCTCACAACGACG
CTGGGATTAAATGCTGTGATGAAATCGATC
CAAATGCCAAGGAAATAGGAGCTATTAGTTGCATG
ATCAGGAACCCGGCTGATGGGAGATTAAAAGG
CTACAATGTGGATTGTCTAGGAGCAATTGCAG
CAATTGAGGAAGGACTTCAAGCATTAATGG
TTCAAGTAATGGATCTGGTTCCAGTTAGCCGG
TAAACTATTTGTGTCGTATGGGAGCTGGTCTG
TACTGGAAAGGCACTTGCACATGGTGGAAAACAG
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TATGACAAAGCCAAGGCACTTGCAACAAAG
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CAAACGCCACATCGGTTGGAATGAAGCCGAG
AATTGATCAAACACTCTTATCCAAGAACGCTTTG
AAGAACTATTCTTTGGTGTGTTGATGCCATTCTA
CACCTAAATGGACAAGACTCTTACAAGAAG
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ACGGAAATGTTCTCAATCAAGCATTGTGTACAGG
TTGAAAAGTTTTCTGGTTTACCTGCACCAAAG
CAACTGATCAGGGATGTGTTGGCAAGAAATG
CATGAGGAATGTGTCTCAAATCTCCCGTTCCAG
CCAATCCTGTGCTTTTCCAGTTGTGGTTAACGGG
AAGATTTAGTACAAAATCGAGTGCAGTGGCG
TTTCAAGATTCATAGAGTCGACTTCACATAATG
AGATACGGCTTTGTTGTTGTTGTTGTTGTTGTTG
CTATTAACCTTACCATGTTGTACCAATAAAATTTT
CAGTTTTCACATATGGAGTGTCTTGTGATTCTGG
TGAACATGAATTTTCGAAACGTTTTGTACTTAGG
TCATAAACAATTCATTAGACAAAAGGCGTGAATTG
ATACAATTTCAAATTTTGGGTGCCAATAAGAG
CAAATTGAAACCTCGTGGCCTATTTTGAAGAACCC
CAAACAGGGAGGTGTGCAATGTAAGAGGCAACTGGG
ATTAGGCTAAGCTACATAATGTGTGTCAGCCATAA
CAATTTGGTTGACCCTTTTGGCGAG

LEFT PRIMER AGTACAAAATCGAGTGCAGT
RIGHT PRIMER ACCAGAATCACAAGACACTC
PRODUCT SIZE: 159

GTGGTGGTGGTGGTGTATGGTGTATGGTGAATCACA
CAACCGGTGGGTGGCAGAGGAGTCACCGGATGCG
ATGGCTCAGTTGGTGGAGGAGGAGGAGATGGATG
ATTTGGTGGTGGACTACTTATACCTGTGCTTGTGAG
TGGTGGTGGGGTTTTTGTATGAATAATGCTTGTGTG
TGGGTGAAGGAGGTGGTGTGTATAATGTTTCGTG
TGTTGGTGGGGGTGGAGATGCATATGGTGTATGG
CAGTGGAGGTGGCGGAGGTGGTGAAGAAGATGG
AGATTGTGGGAAGGTGGAGGCGGTGATGAAGG
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TGGACTTGTGTAACATGATAGCTTGGAGGTTGG
TGGGACGTTGGTTGAGTGCTGTTGAGGTGGGGG
AGGCGTGTGGGGCTGATAATCGGGAGCTGCTGCG
TGCTGTGGTGGCGGCGGCGGCGGCGCAAGCATA
ATTGTAATGATAGCCTGGAGGCAACGGCGGCAC
CATATCATGTTTCAGAGTGAGGTGGTGGGGG
CGGGGGTGGTCTTAGATGGGTACTTGGTG
ACACCTCTTGGGAGGGTGGTGGTGGTGGTGGCGG
CGTCAGAGTCCAATGACCATGACTACTGGATGG
AGGGGGAGAGGGTGGAAGATGAGTCCTGGGCG
ATACTCTTTGATTAGGTGGTGGCGGAGGTGAAGG
TGGTGAATGGTAAGTGGGCCTTGATTGGGAATGGG
AATTGGAGTGAGGAGGAGGTGTTGTATGAGGCG
CTACAGGCGAAGGAGGAGGAGGAGAAGAAGAAGG
CTGTGATGGTGGCGGCGGAGGATGTGATCTAGTCG
AAGGCGATGACTCTGAAGTCGGGGGTGGGGG
TGGGGGTGTTGAAACCCGAGGCCTTCTTTGAGAAGG
CGGCTTATTCCGAACAGGCGGAGAGGGTGTTGAG
ACCCGTGGAGGCCTTTTATTAGAGCCGTCGCGG
CCTCCTGGACTGCTGCCTCCGCCTCCACCGGGATTG
CCGCCGCCGCCCTCCTCCAGGACTGCTGCTGCTG
CATTTGAGCTTGGTGCAGTCGACGGGACGTGCAG
CTGGGGAAGTACATTCCCTTGCGAGATCTCTGATCCGG
CTTGCCACGAATGCAGTTCTTGCAGCATTGGAATTA
CATTATTTTGTAGAGATGGCAGCACAAAGCAGGAG
CCTCTCCGGTGAAATAGTTGAAGGAATAGGTAAAG
TTCTGCAGCTGAGGCAGCTGGCAAACACTCGCCAG
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CTGCTCCAAGCTCTTCATGTTTTTGCCGACGGTGG
AGGGAAGAGGACCCCTGAAGCTGTTGAAGCTGACG
TCCAAGACGGTGAGATTGGTGAGGAGGCCG
ATCTGGGGCGGCAAGCAGCCGGTGAGGTTGTCTGTG
AGGAGGATGATCTCGTTGAGGGTGTGGCCATCTTTC
CAATGCTGGCGGGGATGCAACCGCCGAGTTTG
TTATTGGCCAACACCAGCACAGAAACCGGGGAGTTG
CCGAGATTGTGGGGGATGCCGAATCGGAACCTGCTTG
TCGTTCAGGAAAAACAGCTCGAGATCCTTGTGCAAG
AGCTGGGAGGGGACGGAGCCCTCGAACTCGTTGAAG
CGGAGATCCAAGTACTTGAGGGAAGGCAGAGACAG
CACTACTTTGGGGAAATCTCCGACAAAGCGGTTGTTG
CTGAGGTGAGCTCATGGAGCAGCTGCAGGCGGGCG
CAGGGTGCTTGGGACAACGCCACAGAAGCGATTGG
AGTTGATGTGGAAGAGTGCAAGGTCCGAGAGGAGG
CCAAGCTCCGGAGGGAGGTAGCCGGCAATGTCAGCG
TGGTTGAGGTCAATGCCAGCCACCACGCGTCTCCG
CGGCCTCCAATTGAATTAGGAGCAGGAGCGCGAG
TATACGCCCATGTAGGAGCAGACGTCCGAGCCATTTC
CAGGTGGCGGTTGAAGTTGAAGGGGTCGGAGAAG
ATGGAGGACTTCCAAGCTTGGAGGGCAACGTAGG
CTTGGCGAAGCCTTGGGTTCTCAAAGTGGAGGAGG
CTTGGATCTACTGCTTTGACAAGTTCATCAGTATCAG

AGAAAATGAAGATACACAAAGTGGAACTTTAG
TTATCTGATGATTTTAAAATATGTCTAACCAA
CATTTTAAGCTAACTTTTCTTGAAAAGCATTCTAAG
AAGAAAGCAAATATGTAAAGTACTTTCAAGTCG
CTTGTTGATTTACCAACAAATGCCTGCAATCCAG
ATTTGTGTTGGTTTAAACCACCTTTGTCTG
CTCTAAAACCTTCTTCGACATTCATTGATAAATTA
CAATATTTGAAGTACCATCTAACCTAGATTGTAG
AGCATTTTCATCTGCCCCCAACATAGGACAATAG
TGGTTACGAATGTTCTCTAAACGCTCTCCACATCTG
TAGCAGAAAGCAGTTCTGCACCTGCACATCATG
AACATGCAACCCACCGATTTTTCCACATAGAACCTA

CATTTGGGGCATCTTCTCCATTGTTGCTTCTGCG
CAAGGTTCTTCAACATGATATCCTCCCTTTCCCTCT
CATCCTTATTCAACTTTAGAACTCCTCGCATTCG
ATCCCCTCGTGCCAAGGAGCCTTACACTGAGCACAG
AACATTCTCCAACAATTTGGACACGCTGATTG
CCTCACAACCTCTTTCCCATCATTAATCAACATTG
CAGAGCAATCCTTATAGGGGCAGTAAATTTCTCTG
ACCCAAGAATCACAGCCTCGCACATAGCAG
TTCCCCAGCGATCAAACACCTCCGGAGGCGAG
AATCGGCCGGAATACTCGGGCTCCAGCAGCCCTA
TACAATCAGGAACAGGGCACCTAATGCTGGTAATG
TTCTCTTGGAGCTTGGAGGCCACGTACTTAACCATA
CACTCAGTACAATAACCATGGCTGCAGTTTTTCG
ATCCGAAACAACCTCGATTCCCAGACTTGTGATCGACG
CAGATTTCACAAACGAAATCTGGGACACTTTTAG
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AAGGGAGTGTTGGATGGTTTAAACCTAAG
AATTCTGAGCTCGTCGTCACCGTCGTAGAAG
TCTAGGGTTTCTTCAGAGAGGTCGATAAAGTTG
CTTGCTGCGGTGGGCTTGAAGTTGATTGAGCAG
AGAAGCCGTGATCGATCGAAGGTCTCCGTCGCCG
CCGTCGTCGTCGTCGTCGTCATCGACGTTGATGGGG
ATGGTTGAGGGATTCCGCGAACTGGGTGTGAAG
CTGACAGCGTCGTCCTTCCATGTGCGAAATTGGGGATG
TGGGAGTGAGACGACAGTGGGTTCTCCATCTTTAG
CTTTCTTTCTTCTTCTCATTGGCTGTCAGCGTCACTG
ACAGAGACTGACGCTTTTGGATGCTCCG
CCTCTCTCAATTTCACTTTCTCCCTTCGTACTG
TACACGCTATTTCCG

LEFT PRIMER TAAGAATTCTGAGCTCGTCG
RIGHT PRIMER AATTCGACATGGAAGACGA
PRODUCT SIZE: 235

24. G1_Unigene_BMK.2010 p3 (GCA)6 18783 800

TTAAACCCCATATTCCGAATAGCCGGCCAAAGAG
CCACGGCGGCGACGCCCCACAAGTATACTTTATCCTG
ACCCACTTACCGAATTTCGAGAACCTGCAAGAG
ACCCAGAAGTTCAGGGCTGAGCATTCCAGGAGGCTG
TTGAAGGAGAGGAGACTTTTGGGCCCTG
ACCTCCACCGTGTGATAGGCGTCTGTGCAGAGG
TAATCAGTGACTTCTTGCAAAAGGAGTATGGAGG
ACCTGAGCCTTGCACTGATATATTGGTTGCTCTG
AAAGAGAAGGAACCTACCAGGAGCACCTTTGGCTG
CAAGAACATCTCTGTTATGGGCTCAAAGCTACCTCG
ATCGAGACTGGGAAGTTTGAAGCTGAAAACACC
CAAATGATGTATCATTTTGTAAATCCACACAAATT
TAATTTTTGGTTTTGTATTTCTCCAGATCATTTA
TATTTCAAACACACAAAAATGGGGAAGAG
ACCCATTGGCTACCAGGAACTCACACTTCTAATA
CAATGTCAGATTCAAGTCTTTTTTCTGTGTGTTG
CTGTACAGATGGATTATTGCTTTCAACATGGGATG
AATTTTTGGGGGTTGGGGGGTGATGTGATTG
ACATTGGATTAGAAAATTTGGTACCCGACTCCATG
AATTTCCGGGGTTTCGATCCATTTTGCACCTCCATTG
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AAACCGCTGATCAGTTTACGCCCTCGGAGATG
CTCTGCAACGAGGGGGCGCCAAGACTTGGACCTCAG
TGCGGCAGCAGCAGCAGCAGCATTGCTGATGATG
TCCTTGATCGGTGCCTTTTCGCGTTTGGAGGCATG
CTTGCTATTCTCTCTCTCATCAGATTT

CACCTTCTTCTGCTGCCTCTTTCGCAACCCGAG
CAACCCGAATTCTCTTTCCCTTGCCCCGTTTG
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TTTCTTCTTTTTTCGCCTTCAAAACCTTCATAACC
TCTTGAGTAGTGACCAGCCGGTAGGCATGGCCGAG
AGCGAGAGTTTCGTTTGGCCGAAGAAGCTTGACG
CGAGTGAGCGCACCCGCTTTGCCGTG
CTCCTCCTTGTGATTCTCTGCTACTTGTTCGTG
ATCTTGTTTCGGAACCCGGCAACGGAATGATG
AGGGAAACGTAGTGACCGGGGTTCAACCTCAT
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CATCCTCTCTAGCTTCCCACTCGGATGCTGTATCAC
CAGAGCTGCTGCATCAATGGCTTGACAG
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AAGAAAGAAGTCACTTTCTGTACAGCTCTCC
TCCCATTGTTCACAACCCACAACCCAAAGATA
TAAGCAAAGGTTTACCATATT

LEFT PRIMER TCTACTCTGCATTCTGTTTCG
RIGHT PRIMER GCAGCAGAAGAAGTGAAATC
PRODUCT SIZE: 212

25. G1_Unigene_BMK.2117 p6 (TGCTGA)3 18465 482

AGCGAGTCGAGGCCCGAGGGTTTATTGACTCGAGAG
AGAATCGGGAGACACCGTGGAGACCAAAATTAGGG
TTTTAATTTGGGTGTGAGCAGGACCAACGAAGAAGG
AAGAAGCAATGGAGGGTCTCGCAGAAGGAGTG
AACAACTTGCGAATAACAGACGCATCACACAACAAG
AAGAAGAATCGCATCCAAGTCTCCAACACCAAAAAG
CCCCTCTTCTTCTACGTCAATCTCGCCAAGAGG
TACATGCAGCACACAATGAGGTGGAGCTCTCCG
CTCTTGGAATGGCTATTGCCACAGTTGTTACCGTTG
CTGAGATTCTGAAGAACAGTGGATTGGCTTTGGAG
AAGAGAATCATGACTTCTACAATTGACATGAGGG
AAGGTGCAGGAGGGCGGCCATTCAAAGGCAAG
ATTGAAATACTGCTTGGAAGTCAGAGAAGTTTCGACG
AGATAATGGCTGCTGATGCTGATGCTGATGCTGCTG
CTGCGGCTGAGGAAGGCATTGAGTATGAGTAGAGTTG
AAATGTGTTGTTTCTGATATCTAGCTTGGTGCATG
CTCTAGTAGGTTTCTTTAAACAGTGGATGTCTTG
ACTTTTGTTACTAGATTTCGTCCTCTAGTGGCATTTTG
TTTAGCTGCGGTAAAATTTCTTTTAGGGATTGTTG
TAGGAAAGCGTTATCTCTGCAACCAAAAAG
ATTAAAAGTTATTCCTATGTTAATTATCTAAGCCAA
CATGTGTGTTAGGATGTTATGAATTTATTG
CTTCTTTCTGCCGGAGCATGGAATTAATTTAGCTTTG
CGATTTCATGTAATGCACTGATAACACGCTATTGG
TCGGGAACATAAATGATATAATCAATTTACA

LEFT PRIMER TGGAAAGTCAGAGAAGTTTCG
RIGHT PRIMER AAAATGCCACTAGAGAGACG
PRODUCT SIZE: 204

26. G1_Unigene_BMK.2121 p6 (GCTTGC)3 18506 523

GAGGCCAAGTATATGAGTGTTGAATGACCTGAAT
TTCATCGAAACAGAGAATTTGATCGTGCAA
CAAAATCCGTTCCAATTTGGTAAACAATAACTTGTG
CTTGAAATGGATAGTGCACCAAGGTGGCAAGTTTCG
ATCTAAAACCTCATTCGATTTCCAATTAGATAAAAAAG
CATTACAATGGGATGGGGTTGAGTAGAGCGTTG

ACAAGTTCTCTCATAAGCTAGACACAAGTAATC
TACTCTAGCATTCATCCACTGAAGCTTCGGGGGTGG
CGGCAGCAGCAGCAGCAGCCGCCTTAGAAG
ATTTCCCTTTCTTCTTACCTTTGCCTTTAGTTGTTG
ATCTTGAGACTCTTCTTCTCATGGGAACTTTGAAG
AACAAGTCTTGGTGTCTTTAGATTCTTCTCCATCAG
CATCGGCAGCAGCCATTTGACATCTTGCATAGTTA
TAAGTCCCTTCTTACAGCCTCGTTCTGATCTCGGCG
CCATTTTTCAAGAGCTTGCGCTTGCGCTTGCCGGAG
ATGGAGAGGGGTTGAGGCTTGTTGTGGAG
CTTCCCGGTGGTTGGGTGCGCGTGAACCG
ATCTCTTCTTCTCCGCTTTCTGCGCTCTCTTCTC
TTCTGCACCTCATTGAACTTCGCCATCTCTCC
TCTCTCTCACTAAACCTAGCCACCGCCAACTG
CTTCAACTTGAAAGGAAATTATTGTCATGGTTG
TTTTACGAGTTACGAG

LEFT PRIMER CCATTTGACATCTTGCATAG
RIGHT PRIMER AAGTTCAATGAGGTGCAGAA
PRODUCT SIZE: 211

27. G1_Unigene_BMK.2184 p3 (GAG)6 18 340 357

TGCCAGCATCTTCATCCTCTCTTCTATATCGTCACGG
ACGGATAAGAGCCATGTGGGTTTCCGATTTCATGG
TGGACTTGTTGCTGCTGATAAACTACTTGGACTTGG
AGGAGCCGACGACACAACCTGAAGAAGGAGGATTG
ATGAAGCTGCTGATGTTGTTGTTTCTTCCACCG
CTGTCGATCCCATCGATATGTCTCAACCCTCCTAC
TAGGCTACAATATACTTGTATCTAATCCCTCTG
ACTCGTGTCTTGAGAGAAGAGAGCAGAAGCAGCAG
CACCACACAACTTAATCTTTGCCTTGTAAG
TACAAGACATTAAGCGCAGATCTCGAGGAGGAGG
AGGAGGAGCAATGAATTCGAAAAATAATAATG
TTCAACGAGCATCAACACTGTTCAATTCACATATGTG
TATGTATGCATGTGGGTTTGGCTTTGGAA

LEFT PRIMER TGTCTCAACCCTCCTACTAG
RIGHT PRIMER GTTGATGCTCGTTGAACATT
PRODUCT SIZE: 200

28. G1_Unigene_BMK.2519 p3 (GAG)6 18 228 245

ACATCACCCAAGATTGGTCTATGCCTCTGTACTTCT
CACCAAAAAGAAAACACAAGCTGAACCTAACAAGATG
AACAACAAAAAGACATGAACAGAAAGAGGAGAAG
AAGCCTCGGAGGCATAAAAGTAGTAGTAAGGATGTG
AATTGTTATTCGCCACTCCTGCTCCTGTTGTTGCTG
TTGTTGGCACTGGACCTGCAGGAGGCATGCCGTAG
AGTACGTAAACCGAGGAGGAGGAGGAGGAGCG
CCTTTCGAAGGATATGATGGGGGGCATTGTTTTGG
CCGTGAGGGAGGTGGCGAAGGTGATTGTTTTGGTGG
CGAGGGAGGTGGAGAAATGTAGTAATATTGAGG
TGGAGAGTGGTGTGCTGGTGGCGGTGATTGTAG
AGGTGATGGCGGTGGACCTGAAGGCTCGAGTTG
AGGAGGAGGAGGTGGTGAACATATGACTGG
ACATGTAGTGCAGTCACTGATGCATATTAAACCAG
TCTCAGGATCCACCGTTTGATCTCCATATGTG
AACCTGGAACACGATCATCCGAAAATCGCTG
CCATCAAGGACCGGGGAATCCATTTCCCTACCATG
AATCTCAAAGCTCTGGAGTTAGCCATCTGACAG
AAGCATAACCTTGAACCTGACCAAGTTGTGAGG
TAGCCTTCAGAAAATTTGTTCTTCTTATCCG
CCTTTTATACAAACGTA

LEFT PRIMER AATTGTTATTCGCCACTCCT
RIGHT PRIMER CCACCAAAACAATCACCTTC
PRODUCT SIZE: 175

29. G1_Unigene_BMK.2540 p3 (CGA)6 18 57 74

CTCCTTCTTTCCCTCTCTCTGCACAAAGACGACGACG
ACAAAAAACAGACAGAGTCCGACGACGACGACGACG
ATGATCAAAGGGCTTGTTCACTTCGTGTTTCGCAG
TCTACTTGGTTTCTCTACCGTCGGGTATCCAACTG
CCCGTGGACGGGCGGGTCTCTTGCTGAAGAAACCCG
ACCCGGAATAATGCTGCCGCCACTGCTCGTTGGTTGG
TCGCTCAGAATTCTTGGGGCGTCTTGAATACTATCT
CAAGTGAATTGGGAGGAGCACCTTCGGGAATGTGG
TTTCATTTAGCGATGGAGAACCTGGAAAAGGCAGTGG
TATCCCTTACTTCTACTTGACAACCTTGATCCGACTG
CAAGAAATGCACTGGAAGATCCAAGAGCTTCGTTG
ACAATTAGTGAGCATCCTGTTGGAACCTGTGGCAA
TAGAGACCCCGAGAATCCCGCTTGTCGAAAGCTTA
CACTTAATGGGAAGCTGAAGCTGCGGATCCCAAAG
AAACAGAGTTTGCTATAAGTGCCTTGTTACAAAA
CATCCGGAGATGAAGGACTGGCCCAAGGATCA
CAACTTCCAGTTCTTCAAATTAGACATCGAGAATATC
TTTCTGATCGATTGGTTTGGCGGTCCAAAACCTCTTA
CAGTCGATCAGTACCTTCATCCCAAAACGACAAAG
AACGCCTTGATTGAGGATTACTCGCGATCTCACTG
TAATTCCTCTTGATGTTTCATGAGCTGGATGGATCCG
CATTTCGAATTGTGCATAATAACTCTGTTGTAATCA
CAGGAGACAATTGTAATTATATATAATCATCCCAATG
TAAGTTCTGGAAGTCGTTACGCAAATGCGCAG
ACCAATTATCCGATTGAACGTTTGGAGATAA
TAATTTGTCTGTACAAGGAAGTATTTTTCTTTCTG
CTTCTGTGTTTTAAGCTTAAAATGTAACCTCG
CCCTTTGTAATGATGATTGTGGTTGATTAAAATGAG
TTGTCCCGATTCTCG

LEFT PRIMER CTCCTTCTTTCCCTCTCTCT
RIGHT PRIMER GATAGTATTCAAGACGCCCC
PRODUCT SIZE: 250

30. G1_Unigene_BMK.3842 p5 (TCGGT)3 15 515 529

GGTTAGAGTTGAGGAACCATTGCTCAAATTGAG
TTAAAGTTGAGGAACCATTCTCCAGTTGGATTAAAG
TTGAGGGACCAATGGTAATAGATTTTTAGTTGAGGG
ATCATAGCTGCACATTTTGATGAGTTGAGGAAT
TAATGGTAATGAAATTTAGTTGAGACACCATTGATC
CAATTGAGTTAAAGTTAAGGAAGTATTGCTACAATT
TACTCAATAAGAAAAATAGAGAAAGTGGGAAGATGG
TCATTTACAAGATCATATAAACCAATCTTATGCTAT
TAACAACCTCAATTGCAAAGAAAAATGATGACCA
TATCCATTCAAAAAGCAAAACAAAAAGAGAAAG
CTCTTCCAAATTCCAAAGCCTTCCAAACCTTCTC
TATAACCAATGAAATATCCTCCCTAATTGAACCAAG
TATGCTTCTTGAAAAAGTTCTTAAGCTTAG
TTTCAAACCTTGGAACCAAGCTTCACAAAAATGAG
TATACATTCAATAAGGTGTAAGGATTTCGAGTCGG
TTTCGGTTTCGGTTTTTTTTTCAATCTTTCAATTTTCG
TTAGGTGTTTCGGTCCACTTTTTTCGGTTTTTTTAACC
CACCCCTAGCTCTCTTGAAGTACGTTACACGTGTG
CAGGCTGCTGCTACTTGGCGCT

LEFT PRIMER TTCCAAATTCCAAAGCCTTC
RIGHT PRIMER CGAAAAAGTGACCGAACAC
PRODUCT SIZE: 227

31. G1_Unigene_BMK.4019 p5 (CCAAT)3 15 148 162

GAGAACCTTCCCGGCCTTTCGCGTCTGCCACCCATT
CAAAAACCTAGCAAAAACCTTAGAGAGCAGCAC
CAACGTTTATGTATCCGTTAGTATGCCCTAGATT
CAAAACACTCGATAAAAACCTCGTGAGAACCCC
CAAATCACC AATCCAATCCAATCCAGTCGAATC
CATCTATACTCTCAATGGAGCTGGTGGTGGCCTCG
TCGTCTGTCTGAAGCCGGCATCGGCTGTTGGG
ACCTCCTCAACGGCGCCGAGCAGCTCCGCTACAAG
CTCTGCGCTTCTCCGCCTCATGGCCTCATTTGCG
TCGGCGAGCGATTCTCGCCTCCTCTCAGCTCCGTG
AGCCTTCCGCCTCCTCTGGCTCTGTCCAGTACTGG
TCTTGGTCCAAGCCGCAGGTTGATGTGAAGAG
CTTCCCAGAAGAACC GATCAATCCGCTCGCTGCG
AACAGCGAAGGGACCTACATTGCTGGCGGTGG
CTCATCGGGGAATATCTACTTGTGGGAGGTTAA
TACTGGTAGACTGCTTAAGAAATGGCATGCTCAC
TACAGAGGTGTTAGTTGCTTGGCATTTCGGATG
ATGGCTCCCTGCTGATTTCCGGGGTCAGAGGATGG
AGGCATTAGAGTTTGGTCTCTTATAGGATTATTCG
ATGATTATCAAAAGTCAACAGGAAAGCCATCTG
TACATGCATAATTTTACGGAGCACACTCTTTGTG
TAACGGATGTTGTACAGGATATGGTGGATG
CAAAGCCATTATCGTGTACAGCATCACAGGATCG
CACATGTAAGGTTTGGAG

LEFT PRIMER GAGAGCAGCACCAACGTTTA
RIGHT PRIMER AGAAGCGCAGAGCTTGTAGC
PRODUCT SIZE: 226

32. G1_Unigene_BMK.4067 p6 (CGGAGG)4 24 436 459

AAAGAAAAACCAAAGCAAAAGAATAATCAAACG
TCAGAGAAATCAAGGTCTACCAATATAAACAGCAA
CAATAACATTAATCATACGCAACCTCGTCGCTCTAG
ATCGCGAGCTGTATTGTCTGGCATCGCCGTCCACGGCG
TCGTATTGTCTAGATTATCAGGCAATGGATGCGG
ATAAGCGGAAGCGCGACGACGGAGGAGAATTGG
AGGGGAAGAGAGCGAAAGCAGTCGAGGAAGATCG
TAACAGAGATCAGGAGACGGTAACGGAGGAGGAGG
TGGAGGAGTTCTTTGCGTACTCAGGCGGATACATG
TGGCAGCCAAGCACTTGGGCGAAGCGGCTCCATGG
AATGGAGGCCCTCATTCCAAGTTGAAGATTTTGAGG
AAGATAACGAGTCCCGTATGACAAAAGACCCAAA
AAAGCAGGAGAAACAAACGGAGGCGGAGGCGGAGG
CGGAGGAGGAAGAAGAGCCGTACTTGAGCTTGAGGG
CCTTGAGCCTGGCATCGACGTCGGCGACGGAGG
ACTCTAGGGTTTTGGACTTGGGGTTCGAAGAAGCGG
TTTGCGGTGGCTTGTAGTTGTCTCTGCGTCGTCG
TATTGGTCTTCTGTCCTCCGATTGCTGTTCTG
TCCTCCTCCTCCGACTCGTAGTTGTCTGGAGTCGATG
ATGTGATCCTCCCGGCTCTGAGCGGTTCCCATGG
ATTTTTGTCTGGAGAGATGGAGAAATCGAGAAATG
CGAAAGCTTTTAGAGGTTATGATTTGTACGAGTG?

LEFT PRIMER CCCTCATTCCAAGTTGAAGA
RIGHT PRIMER CCAAGTCCAAAACCTAGAG
PRODUCT SIZE: 187

33. G1_Unigene_BMK.4181 p3 (TTC)6 18 358 375

GCAGATTCTCATTTC AATAATTGAATCAAATTCTA
TAGTATGTACAAGATAAATAATCTGTTACATG
ACAATTTAACAATCTGCTCAAATCCTCAAACCTTCT
TGAAC TAATTACTTGATATCGAAATTCGTTTAAAG

TTTAGTAACTACGAGTTACTGAGGCTGCTGCCATGTG
CTTTTATGGACGATGAGGATTGAATACTGACG
CCACGGAATTGGCTAATCTCGCCACTATTCTCTTCTT
CACCTGACCCCTCTTGGGAATCGGGCCGGCCAG
AAAATCTCCTCGAGAAATCTCTGCCGTTTCATCATCG
CTCTCCCGGCGGAAGAATTGGATGTGGAACCTTC
CATCTCTCTAGTTCTTCTTCTTCTTCTTCTCTG
TAAAACCTTCTGAATTCTGTATGTGGTTTTCTGAAG
TTTTGATGCAAAATACAAGTTGGTTTTGCTCAATG
CTCTTTCCAGAACCCACTGCTTTCTTATATACCAC
TCAG

LEFT PRIMER AAATCTCTGCCGTTTCATCAT
RIGHT PRIMER GGTTCTGGAAAGAGCATTGA
PRODUCT SIZE: 172

34. G1_Unigene_BMK.4297 p6 (AGAGAA)3 18 101 118

CGAATTCGTTGCTGTCTGCTTCTCTCTGTTCTACA
TAGAATAGCCGTCAATCCGTTGCTCATAAGTCA
CAGCCTCGAAAGACAGAGAGACAGACAGTGAGAG
AAAGAGAAAGAGAAAGATATAAAATTCAG
AACTTGGCATTTTAACGGTCAAACATTAGCTTAAA
CAGCTCATTAAAGGCAGAAAGAGGAGAGAGGGAG
AGAGAGCTTTGGTGAGAGCTTTGGTGATTTCATAG
TAGCTGGACATATATTCCGGCAATGTCTGTTCCCGG
TTGCTGGAGGCTTCTGCATTCTTCCCTGCTGGTG
ATTCTGGTCTGTTTCGGCGTTACAGATTTGGGTCTG
CTGCGAATTGCAGGGCAGGGGCAATACGGGTATTCC
CAGGAAATACAGATAATGTCTATCAAAAGGTG
CAGGTGGAAGCAGAGAGGAACACGATGGAGAAG
AAGAGCAAGATAAGCACAGAAAGCCCTG
TTCCAAAAGTACTTCCGGCGGAAGCACTTCCAG
TTCCAACTTCAACAAAACAGAAAAAGGATATGAAG
AATCCAAAAGAGAGTGCCCGAGTTGCCCGAG
ATAAACTCCACAACCTAGTCAAATTATTCAAATTG
CCTTTTTTCTTAGGAAATATTTCTTGAATTAAAC
CAAATAACCCACGTTTTTCTCATATCGTTTGTCAAG
TTCTATTTCATTATGTTTTGGTAATTCATGAAGTGAG
AAAACCGGGGGTATTTTGGATTAATGGGTAAATTAATC
TAGTTTATAATTTCTTGAGATTGATGGATCATGAAT
CAAGATTTGTACAGAAAAGTTGAGAAATTTGTACGAG
CA T T T C T T T G A T A C A T A G T G A T G T G A T A G
AATCTCCTTA

LEFT PRIMER TCACAGCCTCGAAAGACAGA
RIGHT PRIMER ATCACCAGCAGGGAAGAATG
PRODUCT SIZE: 240

35. G1_Unigene_BMK.4719 p3 (TCG)6 1899 116

GGAACCGCTTCATTCAATTTTGTCTCGCTAATTA
CATGGGCGTTCTTTGCCGATCTGCAATACCATAATC
CAAGGTATTTCTACATCTTCCGTTTCATCGTCGTCG
TCGTCTGTCGTCATCACCATCAGTAGTATG
TCTCCTCTACTATTGTAGCTAGACTAGATAGCACTAG
AACCTCCCTTTTATGTTGTTGTTTCCATCGTATATAT
TATTTTCTTGCTAATTAATTATGAGTCTTATAAG
CCTGTACCAAGCTAACTTGGCTTTTTTAAAG
TTCAAATCGCTTTTCTCATATTTCATGTATGATG
AATAATATGATGTATTAGAGTATGTTAGGCTCAAG

LEFT PRIMER CCCGATCTGCAATACCATAA
RIGHT PRIMER TGAGGAAAGCGATTTGAAC
PRODUCT SIZE: 241

36. G1_Unigene_BMK.5242 c (ACATCT)3(ACATCA)3 36 203 238
 GGAAGAGATATCAAGTTTACGTGAGGAATTAGATAC
 CATTTCTAAATCACTGTCTGTTTCTGACATTGGG
 CATCTATCTTCTCACGGGTCCTTGGAAGTGGACGAAG
 AGAGTAATAATCATAAGAAGGGCGAGTCACACCA
 CAAGTTTTTGAACAATCTTAAATCATCGCCGTCAT
 TATCGTTGATATCTTCATCAAACTCAACATCTACATCT
 ACATCTACATCAACATCAACATCATCATCTCTTTGGG
 AAGTGGATGTCAACCGGCTTATGCATATGTCAACAG
 ATGAATTGAAAAGCTATTTCACTAAATTGAAGAG
 AAGTCATGAGTCTGAAGTGCAAGTTTTGACTGAG
 CAAATTTTTCAGCCTGAGGAGAGAATTTTTTAGAG
 AAAGGGGTTCTCTTTGCCATCGAAGAAAATCAAGG
 AGTTTGACATGTGGCGTAGGAGAATCTCCGAGG
 TTATTACCAAATTAGATGAAGTTCTTGTTGAAAAGG
 AGGAAGTTGCTACATGTGGTAATAATGAAGAAAG
 TCTTAGCAGTTTGA

LEFT PRIMER TCTTAAATCATCGCCGTCAT
 RIGHT PRIMER AACTTGCACCTCAGACTCAT
 PRODUCT SIZE: 190

37. G1_Unigene_BMK.5607 p6 (AGGTCA)4 241349 1372
 GAGAGAGCACTGAGCGAGCGCGCTGTTTGGCAACG
 ACGCGACGGCCATTCCACCTGTATTTACCGCTCTAA
 CACGGGGAGGGGCGTCCAGATGTCTTTGCATATTGG
 CAATCTATCAGCTCACACTCGCGGAGATGATCTTAAA
 CATGTCTTTTGGAGGTTTGGACGATGTAACCTTGCGG
 CTGAGGGACAGATATGGGTTTGTGAATATGATTTTG
 TGCAGGATGCTAAGAAAAGCGTTGAGAGCATTA
 CAGGGTAGGAAGATCTGTGGGGAGCCTTTAACAC
 TAACATGGTCAAGAAAACAGCCTAAACCTTTT
 CACGGAAATCCAAGAGGTGTGAGCTCCTATGTGCTA
 CAACATGAGAGAAGAATGAATGAAAATGATTGGCG
 AGATTACGAATTGGACAATGAGCAACCAGATAGTG
 ATGGTAAAATGCTTAATTCTGTGAACATGCGTGATG
 ATGACAGAGGTGATCATCGAGGAGATATTCAAG
 ATTATAATGGAGATCGTCATGATTTTAGGGAAGG
 TCTTCCAGATGATATTGGTGGAGCTGTGCCCAAG
 CTGGTGGACACTGGCAGGTGGGGTGAACAAG
 TTCATGACCCATCAAACGCCAATGGGGTGGAATTTG
 ACCGATATGAACCTCACCAAGATCATGATAGGAAA
 TATGAAGATGAAAACCTGTGCGATGGCATATTCTGG
 TGGTGGTTTTGCTCCACGAAGTTCCCAAGAGAATG
 TGAGGAATCAGAGAATGAATTATACTACTTTGAAC
 CATTCCAGTGATATGCGGAGTACTTGCTTTAGTTG
 TGGGGCATCAGGTCAACAAGATCCGAAATTTG
 TCCCAGGAAATATTCTTCTAGAAGAAAGCTCA
 CAAGGTTTGATAATAGGCAAGATGATGCCGCAT
 ATGAAAGAAGTAGGGGTGAAGCTGAGCTAGAAAGG
 ATGGGATCTAGGTCCATGGGAGAAATGCAGTTG
 ACTGAGGGTACTGCATCAAGGTACATGAATGGTGG
 AATGGCAAGTGGTTCAGGAAAGCATAAAATGGTG
 ACAGACAATGTGAGCTGCCCTACAGGAAATGAAAA
 CAATATTACAGAAATAAAGGACCGTGAAGGAAA
 TAAGAGAAAGTAGAAGGGGAAGGTGAATCG
 CCAAAAAGGCACAGTGGTAAGAAAGCAAGGAGG
 TCAGTTTCATCATCACCTCATTCTCGTTATGCTG
 CATCCAGACTCAGATCATGCTCAACTTCTCAATCG
 TCAAAGTCTGTGACAAGGTCTGGTTCCCACTAGG
 TCAAACCTCAGCATCTAGGGGAGAACACCACTCTG
 TATCTTCTGATTCAAGACTCCGTTCAACATCA

AAAAGTTTGAAGTTTAGGTCAAGGTCAAGG
 TCAAGGTCAAGCTCCTCTATATCCTTGTCTGTAT
 CACTTAGTCCGTCAACATCCTCTTCAAATAAGGCG
 CATACCAATCTTAAAGCCTCTGCTGGTACTCC
 CAAATCCAAGGAGATTCAGGTAAACAGAGACAG
 CAAGTTGAAGGTGATGCCTGCATCGAGAAGGCTG
 ATGATGAAAATACAATGGATGCGATAAAGAGCAG
 TCATGCAGTATCAAGTTTTGACGCAGAAGATG
 ACATGAAAAATGATCATCATTTTCAGATGAATGGTG
 ATGGTGAAAACCATACTATGTCCAGGTCAATTCATG
 AAGTAACAAATCCGGGCACACCTCTGCCAGAGG
 TAGGCTCTCATACTACTGGGAGTTTGTCCCCAG
 AGGGTTTGAGTGATTTTCAGGATCAACAAAACCTC
 TAATGCACTGGTGATTGGACATGTACCATCTCAAT
 CAAAGGAGCCAGCTTCAGAAACCCCTATCTACCG
 CACCCTGGTTCGTTCAACAAGCATATCCTCAGATG
 AGTTGTGTATGGTTTTGAAGCACTATGACCTGGAAC
 TACCAGAAGAAAGTGAAAGGCATTTACCCTTCG
 AGGGCTACTTTGGTTCTGCTCGCTTGTGGCCATGGG
 AGGTTATTAATTACAGGAGGCTGAAAAAAGG
 CCTAATTTCTGTTGAGAATTATGCCAGGCGAGTCG
 TTCAGAACCAAGAATTTGGCATCGTTGATAAG
 TACATCCGAAGCAGCAGTGGGTGGGGAG
 AAATTGGTGTTGACAACCCTTGAAAGGTTTTTCTA
 CATCAATGTGCCAAGTTTTTGTTCACCTGGTTATCG
 AATCGTATTTTGCCTTAGGTAATTTGAATCGCAAG
 CAGTAGCTCTAGCAGGTGTTGGAAGAAGTTTTG
 AACAGATTGGATTACGGTGCAGTGACTCCTTTG
 CATTGTTATAAAGTTGCATAATGGACTCAAG
 TCTCAGGTATATGTAGTGGATTCACAGGATG
 CTTCAGGTCACTCATGAAGAACTTGAAGGATTGG
 TTGCATTTGCAGCCTAAAACATTGGATGCCATTG
 TGATCCCACATGTCTGCTTTTGCTGTATCTG
 TTTTCTGATGTCATCTCTTTTCAAACACTAACAA
 TATTGGAACCTCAGGAAATCGGTCTATGACGACAT
 CAGCACTTATATGGAACAGGAAAACAGTGGGG
 TCTTGCAGAGGCATCGACCTTGGCTTTTCACTCGCTG
 AGCTGCTTGAACAAAACCCAGTCAGGATTAGAAGG
 AAGAAATCCGGAGGAGTTCTATTTGCCTTTTCAA
 CATTCCACGTAAAGGGTCTCAATCCACTGTTA
 CAGACTAACCAGGGGACCACCGTACGCAAG
 ACAAGGCGCACTCCACGTGTCAGTCATTTATC
 CAAAGCAGGTGGCGTTTAAATTTATCAGCCTTTGG
 ATTAGACTGACGGCTGAGTTTTTCGTTTTGCTGCG
 TCGCATCGCGCTAAAGAGGATTGTCGAAACCCCTT
 CAGAACTCTCACTTTCAAGTCTGCGCGCAG
 TCCACTCTCTCTCTCTCTCTCTCT

LEFT PRIMER AGACTCCGTTCAACATCAA
 RIGHT PRIMER GCTGTCTCTGTTTAACTGA
 PRODUCT SIZE: 184

38. G1_Unigene_BMK.5644 p5 (GAGAC)4 20 1192 1211
 CGAGTACTCTCACTGAAAAACAGACAATTTTCG
 ACAAGAAGTTCCGAAATTATAATCATTAGTTAAA
 CAGCACAAGCTGTATGAACGCAGTCAGTCTGG
 ACATGATTACTAATAGATATTCGATACTGTCACCATT
 TAAAACTACAATACAGGGGAAATTAACCTAAAC
 TAGAGGTCAATGTCAAATACTTATTGCGGCCAGTGG
 CTGGCATATAAGCTTCTCCTGCTCCTGAACTT
 CACGGGGAAAAACAACACAGACCTTCCTTCAC
 TAATGAGCTAGGGTAACACTTGATTTTCTTGTACAG

AGAATAGTATGATGCCCCCTTCTCCATAGCCGATAATG
CTGCTTCTCTTGTGCTGAATTCCAGATACCCATAA
CATTTATCTTCATGGTTGTGCACCATTACTTCTATAA
CATCTCCAATTCCAACATCAGGTAATAAAATCACGG
AAATGACGATAGAGATCAATTTAGTAACCTGTGG
AGCTAGATTGGCCACAAAAAATGAATAACGAAACCG
TTGGAATTCTGTATTTGCCTTCTCATTATCAT
CACCTGACCATTATTGCCATCGCCAGCATTCTTAG
TTCTATGACAGCTAGAAGATCCTTCACCCGAG
AAGGGCAAATGTGAGGATAGTGTCCGTTTTTCGT
CAATATAGACAGTCTTTAACTGAGCAAATGTATG
ATGATCACGTTTTATGTTGCAATACTGCGACT
CAATGGAGCACATGTAAGTATGACAGACGCTACA
CATTATTTAGCACCAGGTTCTACTTTTGTGCCAGG
AGGGCACGATCGAGCCAATGGGCACCATGCAATG
TGGTGGTCATTTTTACCACAAATGCTGCAAAAG
TAACCTTCTTTCACAAGAGGGGCGAGCAACCCAAG
TCTCTCTGGGCTTCAGATAATTGGGGCACTCCCAAG
AGGTGTGCTCACCAACGTAGTCACAATAAACA
CAAATCTCGCTGCTGCTGACACTATCATCAGAACTA
TAGTAATCAGAAATCGAGAACCATTGTATCCTCTG
ATTGCTCCTCCCAAGGACAGACTTGATTGACTTCTG
TTTTTTCTCTTTAACACGGAATCTTGATTAATT
TCTCTCTCCCTTTTGCGAATCTCCTTATCCTTGAC
GGGCTTGACGAGAGAGAGTTGCTTTCCATGG
CACCGGCTTGACAAGAGCAGAGACGAGACGAGACG
AGACCAGACGTGTGTAGATGCAGAGGAGATAA
TACGGTGCCCAACCTTCAAACAACCGTCATCTG
CACTTGTACAGGTAAAAAAGGAGTTGCTGTTA
TAAAGAGTTGAAACATGAAATGACCCAG

LEFT PRIMER CGAATCTCCTTATCCTTGCA
RIGHT PRIMER CAGATGACGGTTGTTTGAAG
PRODUCT SIZE: 152

39. G1_Unigene_BMK.5855 p5 (GAACA)4 20 140 159

GTTGAGTATGAGACGACTCCAACAGTAAAAAGTAAG
ACAGAGCGGTCAAAATTGAGAACCCTCAG
CCAAAATCCGTCATTTGTTTTACAGAAATCAAATT
TTGAGTCCCAATTGCCCACTTTCAACAAAAATAAG
ACGAACAGAACAGAACAGAACAGAGTCCCGTTACCA
TACGCACGCCAAGGCCACAGAGGAGGCAACG
AAAATGGTGTTCACAGCCTGATGGTGGAGACGG
TGGCGCACCTGTGCGCCGAGATGTGGCAGTACTTGG
CATGCTTACCGGAGCGCTTGAGCAGCCACCGGTTG
TTGGATCTCATCTTCTGCCTCCCTCTGCGGCAG
TTGGGTGCGCTGGCTTTCTGCCTCTGGACCTTCC
TCTGCGTCCCTCCGCCCCGACTCCTACCACTAC
TACTCTTCCCTCCGACTCCAATGACTCGTCCAC
CACCGTCGATTACGATGACTATTACTACGATCCC
CACTCTGATTGATCCCCTTCTGCTTCTTCGATTG
TCTTCTCCTTCGCCGGCTCCCCTCTACAGAAGATG
CAGGATGGAAGATGGATTCTTCGATAAACTCTTTCG
TTGCAATACATTGTACGGTTTGTCTGGGAGGGGG
ACATATAATTGAGGAGCAGGCTTAACTTTGTGG
TAGTTAGATTACTGGTTGCTGGTGGATGAAAAGG
AGAATTACTTTCTGAATACAATTAAGTTGAGATCC
CATTCCTGTGTTTATATGAAAGCTTCAAACAG
TCTTAGATCCTTTGAGTTGTTGATATTACGTGGAAG
CATCGATATTTGATCATATGCTGGTGATGTTGATT
TACAAATTGTACGAAAATACTGGATGATATGG
TTAATAAATAGTAACACTCAACGTTTTACAGCAA

LEFT PRIMER AGAACCCTCAGCCAAAATC
RIGHT PRIMER CTGTTGAACACCATTTCGT
PRODUCT SIZE: 166

40. G1_Unigene_BMK.6116 c (GGAATT)4ga(GATTGG)3 44 227 270

GAAGTGATGTAGAAAATTGCTGACCCATAAGTACCG
CGAACATGTTGAAGTTCGTACCGCAAGTCAATGGG
CGCCTTAAGGATGTAGTTTGAGGGCCCCGGTGGG
TTTATTGGGGCGTTGTTTCTCCCGACGACGATGG
TCCGCGTGACTCGGCTCTGGGATGTGAAAGGAAG
AAACTTTATTTGTGTTTGGGATTGAAGCAGTTAGGG
TTAGGGTTTGGGTCGTTTCGGAATTGGAATTGG
AATTGGAATTGAGATTGGGATTGGGATTGGACA
CAAATAAAAGGAAGCTTGTGCGATTCCAAAT
CAACTGTGCGAGCAAAAATCCCTAATTTTCTCG
TCATTTTAAATAACT

LEFT PRIMER CTGGGATGTGAAAGGAAGAA
RIGHT PRIMER TTTGCTCGACAGTTGATTG
PRODUCT SIZE: 166

41. G1_Unigene_BMK.6539 c (GGT)6agtgggtgactgcccggagca ggaactttggccagcatttctactatctgtgtgaaattgtgatacaaaagtgaagtgc aagtc(GTTGGA)3 124 2256 2379

CCCCGGGCCAGCGTTGTACTTCACTTGATGTTGAAG
AACTTTTGTGAGAGAAAAATATAAGGTGTTAG
TTCTTGTGGCAATTCTAACTCAGGTTTACAAGCAGG
CAAAAACCCGTTAATACAGAAGCTCATACGCAG
CTGGTACATCATGCACCGGGTCACCTTTTTCGG
TTTCTTTCCATTATCTTCCGGCAAGGGAGACTTG
TTTCCCCACCCCAAAGATGAATGCCTTCCCTAT
TCCTCCAGCACCTCTGGCTGTTCTTCTACACGTCA
CACACACTTACTTGATGGCAAGGGAAGTCGAAG
AGTATAACATGATCCACACCCGAAAAATCAATTC
CACGCGATGCTCTGACAGATATTTTATAAACGG
CAACTTGCTGATTACTGTATGTAAGCAAAGTTTCA
TACAGGAAACGATGCAGAAAGCAAAGAGTAC
TACCTATCAGTGCAAACCAAAAACTGTTAG
ACCTCCTTTGAATTAGAGTTGGTGAACCTCCTCA
TATTTGCGAGTCTTGATCCTTGGGCCAAGGCAGAG
TGGAATGGTAGAACCCGAACGCGAGTTCC
ACTTCTGTCAAAACGTGTTAATATATTCTCAACT
TTTCTGCACGTCTCAATCTTGTGTCAGAAAAT
TATCGATTTGGGAAGTGGACTTCCCTCCACAAG
CTGTAGAAGAGCAGATTTCTTATTTGAGAATG
CCTTCTCTGGAGATCTTCACTTCCATCATCTC
CACTGCAATCTACAAGCACCTCTTCAAGGCCAGAG
CTTATACGGTGATTCCAGGTGCCATGACTACTTTA
CAATCAGGAAAGGATTCAACCAATTTGTTA
TAAATTCCAAGGGTAATGTTGCAGTCACAAAAAG
ATATTGCGTGGTAACAGGTGCAGAAATTG
ATTAAACTTTCCAGTGCTGCTTCAAATCCTCAT
CATTAAAGAGTATATCTACCTCATCCAGTACAGCG
CATCTTAGATTTGATAAGTGCACGAAGCCCTCTT
TAATCAGATACATAAACCGACCAGGTGTTGCTAT
TAGGATATCCACACCTTGTCTAAACTTTCCATCTG
AGTTTTCTGCCGATGACCACCAGTTACAACCATAG
ACCTTACTGGAACCCCAAATTTTGACATTGAACGG
CAAACACCCAAAACCTGAGAAGCTAACTCAGCAG
TTGGTACCAGTATAACAACCTCGAGGACTCATTG
ACGAGGACTTGCTCAGCCCTTGAAAGTTCTT

CTTCCCTTAAACGCTGAATTACTGGAGCAAG
ATAAGCTAATGTCTTGCCAGATCCACTTTGGTCTG
CTATAATAGACGTTTTTCGCCTCAACAACAGG
ACCAAATGCCATGGCCTGAATATGCGATGGGCG
CTGGAAAAGCTGCCTCTTCAGACATTCAATCATA
TATTCAGTGAACCCACATCCCTAAAGGATTTTCG
ACTGAAAAAGTCATTGTCTGGTGGAAAATTTTC
CTTCGCTGATTTAGGTTCGGGCAACTCAGCCAAG
TCATACACTGACCCTCCTCCATTGCCCA
TCCTTTTGTGAGTGAGAAGAAGAACCTCTTGAGCTG
AATCCTTTTGTCTGGCTATGTTGGTGTGACACCTA
TAAGGCTTATGTTGTTTGTGTTTGTGATTGTGAGAG
ATTGGCTCAAACCATTTTCCGTCCTTTTCACAGG
AGAAATGGTCCATGTTGTTTGTCTGTCCC
CTTCCTCCGCCTCATGTCCCTAAATTCTTTCGAG
TGGGAATCCCTTGAGCGTCTTCCACCAAGACCG
CGGGCATCTGCTCTGTTCTTTTTCCCATCAAATT
CAAGTCTTGAAGGCGAATTGACAAATGGTGGTG
CATCTTGACATTTTCTTCATCATCACTTTTCATC
TATTTCTTGCTTAATCCGAGAAGGTTTCTCCGCTA
TAGATTTCACTCATGTACCTTCAACCTCCCG
AAACTTTGAGCAACTCTCCTAGTAGTAGGTG
CCGTTTGACGGCCACTGCCTGTAAATGGTGG
CACATGCTCAATTCCCACCCAACTCGATGGG
TGGTAGTGCTTCTGGTGGTGGGAGTGGGAGGGG
CATTGTTGTCTTGTCCGAGGACGATGAAATCG
TCCATGAGGTCATAAGAAGCTTCTGCTGCAGCTG
CAGGGTTATCGGTGGGTCTCTGACTGAAACTG
CAACTAATCCCCCATTTTCTCGTCTGATGAAG
ACAGAGACACTTGCAGCTGTGGGTTCCCGCCATC
CATGATTCTGGTTCAAGGCGTTTTGGCCGCAGG
AGGTGGTGGTGGTGGTGGTAGTGGTTGACTGCCG
CCGGAGCAGGAACCTTTGGCCAGCATTCTAC
TATCTGTGTGTGAATTTGTGATACAAAGTGAAG
TGCAAGTCGTTGGAGTTGGAGTTGGATGAGGTG
ACAAGTAACAACGGTTATCTCTTTGGTGCTGG
TCTGCTCCTG

LEFT PRIMER CCATCCATGATTCTGGTTCA
RIGHT PRIMER GACCAGCACCAAGAGATAA
PRODUCT SIZE: 204

42. G1_Unigene_BMK.7028 p5 (TGATT)4 20 5877

GGGCAATGTATGCGGCAAGACTTTATTTATGATGTG
AGATTAGGTAAGATAGGCAGCTGATTTGATTTG
ATTTGATTTGAAGACTTAAAGAACAACAAGTAA
CAAATTTGGACAATCAAAGAGGGAGAATACAATG
ATCACCAACCCAGTCCATCAAAATTATAACAACA
CAAAGAAACAAGCAGCCCTCTAGGCCCTGGGTG
CTAGCTTAGACTTGATTTTGTCAACCTGCTTGG
TTCCACCTGGAATGTCTTGGTCAGCACATTATCCGG
CACCTCCGGCGTGGCAGCGAACAACGTGAGGGCG
ATGTTCTGGGTGCCCTGCAGCTGAGAGTTAAATG
CGGCAATCACCGAAGCCGGACTCTTCCATTGTTG
TTCTGGAAGTGAACCAACCTTTGGGGAACGCAAAG
ACTTCACCTTGCTTAATAGTTTTGCCGATGAACTTG
TTTGCTGTGGTAATAAATCCAACCTCCAATACTCCT
CAAGAACGTAGACAATTTCTGTGGCTCTGGGGTG
AGTGTGCGGTGGGTAAATCCGCCGGGGGCATAG
TCTATTCTGGCAAGCGAACGCCGAGGGTGTG
AGGCCGGGGATTTTTTCGACATTGGCTAAAGTCAC
CAGGGAGCCGAATGTGTTGTTGGTGAGGCCTGG

TTTGGCTAGTCCGGCGAAGAAAAAGTCCTCTGCTG
TTGCATTTGCTGCGTCCTTGACAGACGAATCCATTG
ACTTTCACCGCGGCGGTGAGGTTCGGCGACG
CAAATGTCCTGAAGCATGTCTGGGATCAGCGGCAG
AGCTGCCGAAGACGGTGGCAAAAGCCACAAG
AAAGAGAGCAAAGACGGCCGCCATTGGTGGTGG
TGGTGCTAATTAGAAAAGAAAACGCAGGGTAGTG
CCAGAAAGGAAGAGAAAAGTCTGGATGTGTGAATG
ACTAGGAAATGATTGGTAGGATGAGTATTTATAG
CAAAGGAGTAGGTGAATGTTGAAGCCTTTGGTACG
TATTGTGGTAAAT

LEFT PRIMER AATGTATGCGGCAAGACTT
RIGHT PRIMER TAATTTTGATGGACTGGGGT
PRODUCT SIZE: 160

43. G1_Unigene_BMK.7859 p6 (TCAAGA)4 24 1651 1674

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CTCTCCATACTAAGGAAAGGAGAGCGGTTTTATTAG
AACGTTAGGATGGAGCAGGAGCTCTTCTTTTCGTGG
CTTAAATTTGTTTCCATATCTTAAATGGTGTG
TTTTTCTATGAGGATGGCGGTGTTCTCTGGTGGAG
CCCAGAAAAATTGAACAACATTTTGGGAAGCAAGGG
ATCAGAGGACCCCTTACCGTTTCTTCATTGGAAATTA
CAAAGAACTTGCTGGCATGATGATCAAGG
CCTCCTCTCAAACCTTCTCTTCTCTCACC
TATTCTCCCTAGAGTTCTTCTTTTACCATCACTGGAG
AAAAATCTATGGTGCAACATTTCTTGTGTGGTTTGG
ACCTACAGTTCGACTCACAGTTGCTGATCCTGATC
TAATTAGGGAAATATTTACCTCGAAGTCAGAATTT
TATGAGAAAAACGAGGCTCACCCACTTATTAACAG
CTGGAAGGTAATGGCCTCCTAAGTCTCAAAGGTG
AAAAATGGGCTCGCCATAGAAAAATTATTACCC
TACCTTCCATATGGAGAATGTCAAGTTGTTGATACCGG
TGATGGCAACAAGTATAGTAGACATGATGG
ACAAATGGACAGCAATGTCCAGCTCCGGTGAGGTAG
AGATTGAAGTTTCCGAGTGGTTCCAAAACCTAACAG
AAGACATAATTACCCGGAAGGCGTTTCGGAAGCAG
CTACGAAGATGGAAAGGCCGTTTTCCATCTACAAG
CTCAGCAAATGGCGTATGTCACCGATGCTTTTC
AAAAAGTTGCTTCCCTGGTTACAGATTCTTGCCCA
CAAGAAGGAACATAAATTCTTGGAATTGGACAAG
CAAATTAGGAAGTCATTGATAAAGCTGATCGATCG
ACGGGTAGAGAATTCGAACTCGGGCGACAATGTG
CATGAAAAATGTCCAAAAGATTTGCTAGGTCTTATG
ATTCAGGCCTCAAATTCTTCCCTTGTTCCAATAT
CACTGTCAATGACATTGTTGAAGATGCAAGAG
CTTCTTCTTTCGGGAAAACATACCACATCCAATTTG
CTGACATGGACAACGGTTCTCTAGCAATGCACCCA
CAGTGGCAGCTACAGGCACGTGACGAGGTGCTGAGGG
TGTGCCGATCACGTGACATACCCACAAAAGATGATG
TTGTAAAGCTTAAGACGCTGAATATGATCCTCAATG
AATCACTACGATTGTACCCACCTGTGATCGCGACG
ATCCGGCGGTTCGAGAACAGATGTGGAGCTCGGGGG
ATACAAGGTCCACGTGGGACCGAGCTTCTGATTCCG
ATCATAGCCGTCCATCATGATCAGAGCATATGGGG
CAATGATGCGAAGGAGTTCAACCCGGGACGGTTTCG
CGGAGGGTGTGGCACGGGCCGCAAGCACCCGGCGG
CGTTCATTCCATTTCGGGCTTGGGGTCCGCACATG
CATCGGGCAGAATCTAGCGCTGTTCCAGGCCAAAAC
TAGCCCTTGCCATCATGCTTCAACGCTTCTCTTCAGG
CTGGCCCCCACCTATCAACATGCACCTACGGTACTG

ATGCTACTTCACCCACAATATGGGGTACCCAT
CATTTTCCAACGCCTGCCACAGCATGATCAGGG
TCAAGATCAAGATCAAGATCAAGATCGAAAT
CAAGGGCCATGATCTCGTATTGTCACTATGCAACAC
CAGTCATTTGCGTGTGAGTGTGCCGTATGATTGG
AATTGAATTGACCGAAATACCCCTTTCGG
CCTTTTTTCGTTTTGTTTTGTTTTCTTTTTCTTTTTGTG
CTGGGTTTCCTTATAACCATAGAAGCTAAGCTTAT
TAAGGTCAAAGGTAATATCTTAAAGAAAGATGTTG
CACTCCCTTTCATCTAGCTTTTTACTGACCCTCATG
ACCATGGTTTTCTTACCAAAGGGGAAAAG
AAAAAACTAACCCTG

LEFT PRIMER GTACTGATGCTACTTCACCC
RIGHT PRIMER TCAATTCCAATCATACGGCA
PRODUCT SIZE: 178

44. G1_Unigene_BMK.7950 p5 (TTCAA)4 20496 515
GTCGAAACACGGTTCCTACTACATTTAATACAATG
CATGGTATCACTCAAACCTCCATGTGTTCCAACAA
CAAGGTAATATAATTTCTCTGACAGGGAGATGGG
ATTCCTATTAATAAGAGCTTCAGTCGACAAAGTG
CTGGAGTAAAGCTTGTAAGCCATGATATGATTCCAA
CATTTGGTCTCCAAATTATTCAAGTAGGGCTTCTCA
TATGAATTTCTGGTCTCTAAATTTCTGCAATGGCG
CTTCTTATCATCTCGGCAGCATGGGGCTG
CACAAAAAGGTGAGTGCTATCCAAGACATGTAT
TATGAACCTCTGTGAAGCTGGCAGTGAATTGTGCG
TAATTGATGATGAATTGCGCCATAGGTATGTCA
CAAGAGATGAACAGTCTTTTAACAGCATTTCAC
CATCTTGTATCAGAAACCTCAAGATCTTTTGTTCAG
AGGTGGTTCGGAGATTTTGTCCGTCTCCGTCTGCAT
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CAATTCAATTCTATTTGCCTTCTTGTAAGTGGAGG
CCCCTGATTAATTCAATCCAAACCTGCATCAAAATCC
CAAATCAAAGAACGAGATAATATCCAGATTGTG
TAAAAATTAACAGGAAATGGAATGCGAAAGG
ACATTTTCCTACAGTTTTCACGGTCTGAGATGGGGGTG
TTGATTTCCATGTGCGCAGCAGCGAGCTCCACAG
TCTGAGACGTGCTAACAGAGGCGCACGGTGCGAAG
TCCGCGCGGCTGGCTGGGTCTGTGGCTGGGTTTGTG
ATGAAAAGACCAAAGAGCCTTTGAAACGCTTG
CAAAATTAATACCCCTTTCAACCTAGTTCA
CAAATCCATTTGTAAGGGAACATGAATCACCTTTA
CATGAAATAAATTTTAGAAAAATCAAATGTGGG
AATAAGTGAA

LEFT PRIMER GATCTTTTGTTCAGAGGTG
RIGHT PRIMER CTTTCGATTCCATTTCCTG
PRODUCT SIZE: 221

45. G1_Unigene_BMK.7991 p3 (ACC)7 21243 263
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ACAAAGCAGTTGGAGAAAGACTATGATGTTTTGAAG
AAAAAATTTGATGCTCTTAAGGCTGACAATGATG
CTCTTCAGGCTCAAAATAAGAAGCTTCAAGCTGAG
TTATTGGCTCTAAAAAGCAAAGATTCATCAAAATG
AAGTGGGGTTTAACTTCAAGAAAGAAAATG
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TTCAGACCAACCAACCAACCAACCACTCTCAACC
TAGAAATTTCAAGAACACCGCAACCAACGAGCAG
CCCGCCTTCTGATTCTCCTCACGAGATGAATGG
AAAAAACCTCTTCCACCGTCTCCTCCTCCTCAGG

TCTGCAAGCACAAACCAACTCCTCCAAGGATCAT
CACGGTCAGATCTTCAGTGCCTTAAAGTTGATCAG
ATGATTTCAGGATGAAGGCTTGTGCAGCATG
TTCAATGGGATTGATCAAGAGCATCAAGGGTTTTGG
CCATGGCCTGAGCAGCACCATTTTCATTAATAAATTG
ATCTTCCAATTATTTCCAAACCTGAAGATTAATTA
CATTATTCTGAAGCAAGTTTGGCCAAGGCTCTGTG
ATCAGACAAGTAATGAATTAATAAATTAGGAAA
TTTTTTT

LEFT PRIMER AGTGGGGTTTAACTTCAAGA
RIGHT PRIMER GTGAGGAGAATCAGAAGGC
PRODUCT SIZE: 154

46. G1_Unigene_BMK.8037 p3 (CTG)7 21 708 728
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CCGAGGTATAAGGAGTACCAGAGTAGGTAGAGG
AAGGTCTCGATGACTGGGGAGTAAAGTCGGCGAAG
CTGCCCTTGTACTGTGGCTGGAAAGGAGAACGCG
AGGCGCGTGGTGACTGGCGCTGGACGTTTCGTG
CTCAGTGGGGACAAGCGAGTGGTGCGCGCACGGCTG
ACGGCCTGGGCATCATATTCATTCCAAGCACGCAAC
CAGGTAGCCAGACCAGCAGGGTCAGTAGGATCACAG
TGCAAATCGAAGGAGATGAGGGCAAGCCATTC
CATCTCGAGGTTATTTCAGCTCAGACACCTTGATG
CCAGTGACGTCGGACCAGGAGCGGTTGATGAAGGTG
TTGTCGTCGAGGAACTTACTGCCAGAATCAGGGCG
ACGGCGAGCAGGCGGTAGATGTGATTCTCGGACG
AAGAGGTAGTCCTGGGGGGATAGTCTCGCAGACG
AACGGTCAAGTAGTGCAGACTGAGGAGGATGGTTG
CCGAGGGCAGTCTGGTGGCCGACAGGACTTGCGAG
ACCCACTTGCGGAACGAGGGCTGGATTGGAACAC
TAGGCTGGATGATTCCCGACGCCGATTTCGGCCA
CAAAGTTGGTCATGCGTTCCATGTCTGATGTCGAG
CTTGGCCGATACTCCACCTGTTGTTTTGTCTTC
CTTCTGTGTCGATTGCTGTGCCTGCTGCTGCTGCTG
CTGCTGCCTGACCTTGCCCATCTGGGTTCATCTG
AATCCCCTTGCAAAGTTGCGG

LEFT PRIMER AACACTAGGCTGGATGATTC
RIGHT PRIMER GGATTTCAGATGACCCAGATG
PRODUCT SIZE: 179

47. G1_Unigene_BMK.8106 c (CCACCT)3cctctttctcctcgtaacc(TCCTCG)3 56392 447
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TACCAAATACCAAAAACAAAAAACAATAAT
CAAATAACAAAGATTTCTACTAATAACTCCAAT
TAAAAGAAAATGCATAAATCGAATTTGCTTGCAG
TAACCTTTTCTTTTACTTTTTACTTTTACTTTAACTT
TATCTGGTTTCAGAAAATATCCAGAATTTCCAAGATG
AAATTGTTGCAGAGGGGACAATTGCCCGCTGG
ACCCACAGCTCTCGGGAGCACATCCTGCAGAACGTG
TGCCCGCAGGGAATAAACGCCGCCCTTTATG
CCTCACCATGCACACGCAGCAGTTATACTCCA
CATTCCCTTCTTCCGCCGCCACCTCCACCTC
CACCTCCTCTTTCTCCTCGTACACCTCCTCGTCTCG
TCCTCGTCCATGGTGTACGTGCACTCCACCCC
CATCTGCCTGTCCGTCTCCTCCAAACAAGTCCAT
CAACGACATCCTCACCGCTCCGCCGTCCCGACG
CCGCACCTGTCTCTCCCGACGACACGTATTTCCCG
TCTCTTCTTCCGCAGACAATGCCGCCGCGGAAG

CTTCGGCAGCCTCTTGCGCCGCCACGGCTTCCCTGG
 CCGACAGCGATCTCTCATCGTCCAGCGCCGCCG
 ACAATCGCCGTCTTGGAGAGTCCGCCGCGACCTCG
 TCGGCCGCGAACC GCACGGAGCCCTGGCGCGAG
 AACATCGAGGCGCGGGGTTGTTTATATCCACCTCG
 TCGGGCGGAATCGAGGGGTTGGCGCTGAAGCGGG
 TGGAGCCCCGCCGCGAAATTTGCCTCTCGACCTGCTG
 AGTCATGTCTGAGATCGGACTCGGAGTGCAGTAG
 CGGACCGAGCTGCGACGCGAGTTGAGAGACCGCGGG
 TGGTGGTGGTGATTGGAACCGTAGTTAGCAG
 TATTCCGGATGGGGATATCGGAGGTGGGGACACGG
 ACGGAGGAGGTCCAGGCGGAGCCGGCGCGTTTGA
 TAGGAGGCGGTCTTTGAACGACTTCCAGGCTTTC
 TTATCCTTCTTGCCAATCAGGGCCCCGGTAGG
 ACTTGGGCTCCTCGTCGCGGATTATATCGAGCAGGG
 TCCGACCCGAGATTGTGGCGGGAAGTGCGGGGCGG
 TGGAGGGGGCTGTTTGGCGGCTGCAGGGGCCAGCG
 ACACGTCGTGTAGGCTCAATCCGGCAAAG
 TCTCTCCCGTTGCTACTTGCTGACATCTGATCGAG
 AAGCGTTAGCCTCCGGCGACCTTCCATTTCA
 TAAAATCCACACACAAAAAAAT

LEFT PRIMER GCAGCAGTTATACTCCACAT
 RIGHT PRIMER AAGAAGAGACGGGAAATGAC
 PRODUCT SIZE: 230

48. G1_Unigene_BMK.8119 p3 (AAT)6 18 97114

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 TAATAATAATTGTTAACGGATGAAACGGGTCTGGG
 TTCGGGTGATCTATTAGCTTAACAAGTTGGGTCTGGG
 TGACCCGTTAACTTAACGGGTCTGGGTTCACCCG
 AACCACCCCAATAAACCCGACCCGTCAGCTCCA
 TAATCATGACACAAGAGTATCAATCGTCTAA
 CATTTCCCAACATCATTTAGATATAGGATATATAT
 TATTATCAAATCTAAAACTGGGAAACACACAAAA
 CACCTAATTCACAATGCCACCTAATTGCATTATCCG
 ACTAAAATTAGTAACCCAGTCTCAACAATAG
 ATCATGCATATGATAATTTCAATTTTATCAGACTGGG
 CTAAAAAATCATTGCAGTCTCTTGGACTGTG
 ATTTCTCGTGGCCACTACATATTAGAACAATAGGTG
 TAGGTGCTACTTAGCCTTAAATTAGCAGAAGCAG
 CTGAGCTCGCAGCTAACCAAGTAAACATGGATCAG
 TAAACCAGCCAAGTCACGCTCATTAAGGTGGGTG
 CATTAGGCATCTTCCAACAAAACAAGTCATATTG
 TAACGCGGTTAAGGACAGACAGAGAGCTTGTTTCA
 TAATAATTTTCAATGAAGGACTTGAAATGAG
 TACTTCTTTGGGTGAGTTGAGTAACACAGAAGAGTG
 TAGTAGTGGCACCGACGACATACGAAGTGTGAAAG
 TCTTGGAGAGACGGGTATAGCATGGCTCA
 CAAACCTTTTCAATAAGATTTTGAAAACCAAAAAG
 ATGCCAAATGAGTGGTGGAAAAGCACATTGGTG
 CCAATCTACAAGAATAAGGGAGACATAAAATGTAT
 TAACTATAAGGGTATTAAGTTAATGAGACATA
 CAATGAAGCTTTGGGAGAGAGATTGAGTATAG
 AAAATCAATTCCGGGTTCATGCCAGGTAGTTG
 ACTAAGGAGACATACAAAATTGCATCAACACGTG
 CAAAAAAGAGTGTAGCAGAGATGGGAATGCTTTG
 TTGAGTTGTGGCCACATGAGAAATGACAGATTG
 AGAACTAGGATATTCGAAGTAAAGTAGGAGTGCCCA
 CAATTAAAGATAAGATGAGAGAAAAGAAATTAAG

TGGTTTGGACATGTAAGCACAAGACCTATAGATG
 CTCTGGTTTGAAAATTTGACTATGAGACAAAGG
 CTGGGGTAAAAGGGGTAAAGGAAAAACCTAAG
 AAAACTTGAAAAGAGACTCTAAAAGAGACATGGAG
 TACTTAAAGCTAATGAAAGAATGGATGCAAAAC
 TAGGCAGAATGGCATACTAAGATTCTTACAGCCG
 ACCCCACTTAGTGGAATAAGGCTTTGTT

LEFT PRIMER ACCCGTTAGTTGATGATGTT
 RIGHT PRIMER GTTTATTGGGTTTGGTTCGG
 PRODUCT SIZE: 200

49. G1_Unigene_BMK.8296 p4 (CAA)520 132 151

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 ACTTATTCAAAAACCGAAGGGTGTGCGAAAATTG
 CTTTCATAAAATTTGATTTTTATTCTAAGAAAAG
 CAATTGCGATGGCTCATTAGCCTAAACCAAACAAA
 CAAACAAACAAAATGGAAGGCTTCAATTGATTTA
 CAGCATGCTAACTTCACACGCTGAGTGTCTAATTTCA
 TAGCAAGTCAGTGTTGTAGGCCTGAACCTACTTTCCG
 TCATTCCAAAGTACTCGCTTGTTCTGCAGCCAGTG
 TAGGCAAGATGGCCATAGCCTCACCGTCAATGGCAG
 TAGCACCATTCTTGAAGCATGCCGTCTTGAATTTAC
 TAGATATCTGTTCTTCTGTTCTCTTATGTTAGTTG
 CTTGTACCTCACCAACTATCTCTTCTCCAATATAG
 ACAGGCAACCTGAAATGCAAGCTTTGGGAAACATA
 TATAGCCCCAGGAAAATGAGAAGATATGATCT
 TGGGGAACAGGGCAGCTACAAGCATCCCGTGAAC
 CAGTCGATCTTCAAATCCAGCATTTTCGAGCAG
 CCTCGGAATCTAAATGCAGAAGGTTAGAGTCATG
 ACTCACTTTTGAGTACTCCAAAACATCTTCATTGGTG
 AATACTCTATTTTGCTTCAATGTATCTCCACTTC
 TAAGAAAACCAGCTGCTGCTGACGAAAAACCTCT
 CAAAGAAGGTAGGTTGACCGAGAGTAAGTTCCGG
 CCAAGCATAACTGTAACCGTTTCTAAACGCTGTCCAG
 CAGAGTAGCAGCCCGCCAAAACCTACGTTGATT

LEFT PRIMER ATTTACGCCCTTGATTCTT
 RIGHT PRIMER GGAATGACGGAAAGTAGGTT
 PRODUCT SIZE: 244

50. G1_Unigene_BMK.8884 p2 (AG)11 22739 760

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 CAACACAAACCAACTTATATACAAACAAAACCT
 CAAAGCACAACGTGGCATAGATCGATCATAGTCCG
 CATAACAATAATTTACTAACAGTAGTCTAATC
 TAATTAAGCCAGTGAATTTCAACCCTTCTTAATTACT
 TATAAATCACTTCACATGATAGAACAAGCATGTGG
 ATTTTCGTCGCTAAACATAGAGGTATACTTGTCG
 TCCGGCGCATTCGGGCCCGGAAGTGCCTGAGTCACG
 TTCCTCACGTAGCCGGAGGGAGCCTTCTTGTCATAAG
 CTCCGGCGACATAAGGATATGCCACCAAGTTG
 TAAGGCACGTACGGCCAAATCTCTGCCTTCTTCCCTG
 TGCTCTTCACTTTCTTTAACACCTTGTTTGGCTCCACG
 TATCCCGTCAACGTCACCTTGCTCTGCTTTCTG
 TTCACCTCCACTTGCTTAGCCCCCTTTCATGTTAGAAA
 CAGCATTTTGAATCTCCTTTTCAACGACCATCACAG
 TCCATTTTCACTTGATTTCACCGTCTGCATTGG
 CTTCCGTTTCTTTCTTGTTTTGAGATTGTGAAATAG
 TCTGAAAGAGCATCCAGAGCACCCATTTCTCTC

CACTCTGATAATTCTGATCTGAGTTTTTTTTTTTGTG
 TTAGAGAGAGAGAGAGAGAGAGAGAGGGGGAGAGAG
 CATTGTTGAAGGAAAGAAGAGGGGATGAGGAAGTTCG
 ATCCATGGCCGATTTTCTTCAAGCGAGAATGG
 AACCGGAACCTGATCACCAAGTTCTCTCTCGG
 CCTCACCGAGGAAGATGCCAAGAAGTCTGCCCTTCG
 TTCAGAGGCACAAGAGGTGATTTATGTTCCGGTGAT
 TAGCCACCTTTGTGCTAGCATTGTGGAGAAGACGG
 CCCTCGTGCTATTCTCAAGGACCATAATAACGAAAG
 AGAGATGTTCTAGATACTCTTTTTTTGAATTTTCTG
 TTATGTTTTGGATGACTTGAATAACATGAGAAGAAA
 TACTTGATTCAATTGGTTTTGAATTTTGTGCGTTTGG
 CCAGACATTCTTCAAAACATTAAACAAAGTTGTG
 TTAGAGTTTCACGTTTTTGTGAAAGTGCTTT

LEFT PRIMER ATTGGCTTCCGTTTCTTTCT
 RIGHT PRIMER TCCTTCAACAATGCTCTCTC
 PRODUCT SIZE: 157

51. G1_Unigene_BMK.8968 p6(ATTTCG)4 24163 186

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 CACCATTGGATTTTAATTATTATAACTCTATCCAAT
 CCAAACCGACTTCTTTATCTGATTGCCTCGATTCTAG
 CAAAAATTGGCCCAAATTTTCGATTTTCGATTTTCG
 ATTTTCGAGGATTTAGGTTTTTTTAAGAGTTGTTG
 ACCTCAATTTTCTAGTTTTCCCGAGAAAATAAGAAAG
 AAAGATGATGCGGAGGCAGCAGGAACAAGACCAG
 CAATCTAGGGTTTTCTACGAGCTATCGGCTCTGG
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 CAATTGTCGATAACTCCACGGTGATGCCGCCGTCG
 TCGTCTTCGTCGTCTGTTGAGGCGGCCCGCGCGCG
 TCGACGGCGCAGATCTCGCGGCTGGGTTCTCGCTCG
 TTGATGCTGGGGATTTTCGATGGCTCTGATGCTGTG
 CGGATCGGTGACTTTCTTCATTGGGTTCTTATTGATG
 CCGTGGGTGCTGGGATTGGTGATGGTGTTGTATG
 TGGGGGGGATCCTGTCGATCCTCTCCGTTTGGGG
 AAGTCGATTCTTTGCTACGCCTCTGCTCCGTCGACG
 CCGCGGAAGGACATTCTGCGTGGAAGCTATTGTG
 AAGGAGAGGGAGGAGGTGGTTCAAGAGAGTTG
 ATATGTCTTGCAGAAGGACGGAGCAGCAGCAGCAG
 CACAGATGTTGTTCTTGTGAGAGTGATGCTGCATA
 TAGGTAAAGGAATGTTGTATAGGCAGCTGGGGCGG
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 CATGAACAGTGGATAAATGTTTTATTAATACTC
 TACTGAATATGAGGAAATGGCTTCTGAAATAG
 TATATTGTTGAAGGATGATGAAATTCCTAGTTTTG
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 TATATATCTCTTGTCTCAAATCTGTAAAAGTTTA
 TAGCTCAGCTCAACATTTCTTCATTTTCTGG
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 TTGGTAGTAACTTGTGTGGGCAGGGAAGGGAAGGG
 ATGAGAAAATTGTAGGGGAATTTAAAGTCGTTCACT
 TAAATGTACGCAATCCATCCGGTGGGAAATGAAG
 AGGCACGGGATGTG

LEFT PRIMER TCTATCCAATCCAAACCGAC
 RIGHT PRIMER CCTAGATTGCTGGTCTTGT
 PRODUCT SIZE: 195

52. G1_Unigene_BMK.8995 p2 (CT)10 2091 110

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 TAAAGACGCTGAAAATTTGGACTCTCTCTTTCTCT
 CTCTACTCTGCTTTCGCAGTCCCTCTCTCTCTC
 TCTCTCTCTTTTCTCCGTTGCCGGCGTTTCAGCAAG
 TGAAGTCGAACTCAGTGAGTGATGGGTGGCGAG
 TTACGTTACGAGATCGCACAAAATGCCTACGTAAAG
 CTAGTGCTACACGCTCTCAAGCACAAAGACCTCCG
 CCGTCAACGGCATCCTCCTCGGTGCGGTCTCCCCCA
 CAACGACGTCTTGGAGATCACCGATTCCG
 TCCCTCTCTTCCACTCCCACATCGGCCTCCTCC
 CCCAGCTCGAGATCTCCCTCATCCTGATAGAGGAG
 CACTTTGCTGCTAAGGGAGTGAGCATTGTGGGG
 TATTTCCATGCTAACGAAAGGTTTGACGATCACGAG
 CTCGGCGGCATTGCCAAGAACGTGCGGCGATCACATT
 TATCGCTACCTTCCTCAAGCCGCAATTCTTTTGCTTG
 ATAACAGAAAGCTTGAAGCTTTATCGAAGACTAAGG
 ACCGCAGCCCCGTAGTGCAGCTCTACACGAAGGATG
 CATCCAGGACTTGGAAAGTTAGTTGGATCAGATGG
 AAACCAAGTTGACCATCAAGGAGCCATCAGCAAATG
 TTGTTTTATTGGATTACATCTCCACTGAAAAATGG
 CAGGATGTTGTAGATTTTCGATGATCACCTCGATG
 ACATTAGCAAGGACTGGCTGAACCCAGAAGTATT
 CAAGTAAACCGGCCATCCCTTTCGGTATTGCAAATG
 CCTCCATGCTTAACTCAGTTTCTCGTGCTGGGTATAG
 AGGACAAGGGGGGCATACATTGACGTCAAGCTCAT
 CACTTTCTTTTTTTGTAAGGAATTTTCGAGATG
 TAAAAAACTGGATATCAATTATCTTCTCATACTTT
 TACGTTGACGCCATAGGGTTTCAGCATCTTCTTTTG
 TGGACCACTTCAAATGAGGTTTATGGTTTGGTTGTAG
 AATTGGAACAAAAATGTCAATTTCAGTTTGG
 ACCTCAAGTTATCTTTCCTTTCGATCATGTTTTCTTG
 TTGACTGGGTTTACAATGTTATGTTGTGTTAG
 AATACTGGGTTGAAGAGTTTGTGTGACGTATTG
 TTTTCGTATAATATCCATTACCTCAATGTGTTGTGTTG
 TGGCAAACCTCGTTATCTTAATAGGTGATATG
 ATACTGGCCTGATTTGTTAGCGGGTCGTGTCATTTTCG
 TTTTGTGTTGGGTAAACGGTTCATGCAAG

LEFT PRIMER CGCTGAAAATTTGGACTCTC
 RIGHT PRIMER CACTAGCTTTACGTAGGCAT
 PRODUCT SIZE: 173

53. G1_Unigene_BMK.9351 c (CTCTTT)3gag(ACCTAC)3 39 435 473

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 TAACATTACAATTCAACGTTTA
 AGTTGGTATTTGCCAACAGTGGCGCCCTTGATATAA
 CAAATCACTTGTTTAAAGAGCCTCATGCCTACT
 TAAAGTGTTACAAGCATTTTAAACCGATAAGAG
 TAAAAAACACTAGCAAGGAGAATTGTATCACCAA
 CATCCACTTTGATAGCATAATGTAGTGATGCCGCAG
 CATATGATCCAATCGCAATGCTTGATTTCTCCGG
 CAGGTTTATTGAAGTTTACTTTGCTGTATGAGTGG
 CTGTTGGGGCTCAATTTCTCCGGCAGTCACAGCCG
 CAGCCGCACCTGTAGAAGTAGTGTCATGACGTTGG
 AGAGAAGATCCCTCCTTGTGTTTCCAACCTTTAG
 TTTTGTAGCCAATTCAAGTGTCATGAAGCCTCTT
 TCTCTTCTCTTTGAGACCTACACCTACACCTACTTG
 AGTAGAACAGCACCAGCACCAGAACCCAGAAC
 CATTCGCATTAGCTGCGTTTCTCAACGCCTTATT
 CTTTTTGGCCGACCGAGCCCAACCAACAAG

CCCCTCTTGTATATGTTCTTCAAATATAGCCTTCTTG
AACGAACTTCCCATCTGTGTGACAATTGCGTACAG
TGGCAAGGTACTGTAAGTGCAGACGAACTGAACG
AATACTCCAATTACAAGCCTTGGGATAACATAAC
CAAGTTCCCCCATCATGCAGGAATGAAATTTATACTG
AACCAATATCCAGAAGAAAAATGCGAGTTCAAACG
AATTTTGGAAACAAGATGATATGAACAAGTAAGAG
AACGAGTCTGGGACGGTGGAACCAAAAAATG
ATCATCTGAAGGCTGAACAACCAAGTCACCTTCG
ATTGCAATGTGTTTCTCAGCAACCTCATGGGCCAG
TTGACTTATTACATGCTCCAATTTAGTCCCAACAG
CAAGTAAAAGTATGAATGGAATGAATGCTATCCAG
AAATAGGCATGCCAACCCGACACATTCAGCAACAAG
AAGATGACCACAAAGATCCAAAGATACCAACT
TATCCCAACGACTCTTTTAAAGTCTGCTTCAAGGG
CACGAATCATGTACTTGTGGAATTTAAATTTTG
ATTTGTCTTGCAATGGGTGCTGATGAAGCCTAGTCG
CATTGTCATATAATCTGTTTTGGTCACAGAGCCA
TAAAATTGCTTGAAAAATGCATGCAACCAGCCAAG
AATAACTGAATTTCTTTCCAATACCACGAAAGCGG
CCCCTAATAAAATCATGATCGTGGACGTGGGTG
AACTTCATTGTCAAAACTTCTTGTGGGTG
TACTCCTTTTTTGGTGATAGAATCCTCCCAATG
TTTCCATTGACGTATCTTTGCTCCTCCAAAAAG
AATGGTTAGAACACAGAAAGTCACATGCACCACAG
CCAGCACAAAAATGAAGATGTGAAGATGATG
CAATGCCGTGGTGGATAACAGAGGGACCTTC
CCCTCTGAACAGGAGCCGGACGTGGTGGAAGCAG
AGTCTTCAGCAAGAAGGCGACGGGCAGCACTG
CTCCAGGGAAAGAACACGGTCTGGAAATGGGCAC
TAGTACTAGTACTGGTGGTCTCTTTCTTGCAAGG
CAGCCATTGACCGGCATGTTTTTCGGTTATACAG
ATTTTGGCTATACGTCTCTTGAACACCGTCAGCAG
CAGTGATATAAACCCCAAAAGCATCAACTCTTC
TTTGATCTTCTGCAAGGCCTGAAAGAGAGG
TTTCTGGTTGTGTTTCTTGAGATACTTGCCAGTGATG
TGAAGGGTCTCTCGAGGAAAAGTGAAAGGATG
ACTATGACACTAGACACCAAGCCACCACCCAAG
TCGGAGTGTACTCCAAGGTTGTTCTCCTTCTG
CCATGACGGATTGGAAG

LEFT PRIMER CATGACGTTGGAGAGAAGAT
RIGHT PRIMER TAATGCGAATGGTTCTGGTT
PRODUCT SIZE: 158

54. G1_Unigene_BMK.9401 p6 (CCAAAC)4 24 126 149

TCCCTCCCCCTAACCATCTCCCTTATTTCTT
CTCCCTTCCCTTAATTCTTTCTTTATAAATTGAAC
TACCATCCAATTTACTTCTCCCACTCATTAATTAAT
TAATTTCCCCCAAAACCAGAACCAAAACCCAAACC
CAAACCCAAACTCAATATATATTATCATGCCATCACC
CACCACAATCATAACCATAAACACCCCG
TCCACCTCCTGCCCTGCTCCAATTTTCCCAC
CAAATCGCCCTCATTTCCCGCCAAGAAATCTGTTTAC
TACAAAACCATCCTCCACAACCTTAGACCAA
CAATGGCAAATCTTTCTGGGTTCGGTTTTCAG
TATTGGGTCCCAGTGGTGGCTTCTTCCGGTACTAG
TGGCAGTGTTGCCGATGATGAGGTGCGCACCCCTG
ATTGAGTATGCCTCCGGCGAGGGAGGTGCCACTG
TAGGAGATGATCTGGTGCTTTTGTTCACCACTTA
CAGTAGCGCTGCAAGAGAATCGCAGCTCTTGATG
CTTCTCCTTTCAATTCCAGCCTTGGAAGCACAAAGG

TCTCGCTGGCGGCGGCGCTTCGGCTGCTGGGTCAGG
CCGGGATGCACCGAAGCCTCTCGATATCGTTTTCG
AATGAAATCATCTTGTATCTCTTAAAAAATTCTGG
AAAAGTAGCCGTCATGGCTTCAGAAGAAGATG
ATACTCCAATTTGGATAACTGATGATGGCCCATTTG
TGGTGGTAACGGATCCTCTAGATGGTTCTCGAAA
TATTGATGCATCCATTCCCACTGGAACCATTTTTGGG
ATTTATAAACGCCTTCCGGAGCTGGATCATCTAC
CAAAGGAGGAGAAGGCTTTGCTGAATTCACCTCCAG
AAGGGAACCTAATCTTGTGCTGCCGGCTATG
TTCTTTATTCATCTGCCACAATATTCTGCACCAG
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TATTCTGTAAATGATGCTCGATATTTTGACTGG
CCCAACGGATTAAGGCAATACATAGACACTGTGAG
ACAAGGGAAAGGCAGATACCCCAAGAAGTACTCTG
CACGTTATATCTGTTCTCTGGTAGCAGATTTT
CATCGAACTCTACTGTATGGTGGAGTGACAATG
AATCCAAGGGACCACCTTCGTCTGGTTTACGAAG
CCAACCTCTTAGTTTTCTGGTGGAGCAAAG
CCGGGGGCAAAGGTTCTGATGGTAAAGGTAG
AATTCTATCGATTCAGCCAGTCAAGCTGCAC
CAAAGGCTGCCTCTGTTCTGGGGAGTTTGGAGG
ACATGGAAGAGTTAGAGAGTTACGGAGATGTGCAA
CAGAAAGTGAACCCGGGATACGAGGTTTGACAA
CATCAATAGGCTGATCTCACAAAATCCAGTGGATA
TATCGTCTGAGTAAAACCTGGGAATGGCTTAT
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AAGCTGTGTGTGATTCTCCTCGTTTCTCGGAAAC
TAAATGTCATGAAGAGTGTGCTGTTAAAAAC
CAGGTGACATGAATATCTTCTGTATGTGATTTAT
CATGTAAAGAAGACTAGTTTGTATGATATG
TTCTTGTAATTAAGAAGTCTGTTTGGACAAAAAG
TTGCTAGAAATTGATGACTCTTTCTTTTACTTATTG
AAGTGCAGCAGGTAAATGATATTTGGCTAAAGTAT
TAGTGAATGAAATAAATTCATGAGGAA

LEFT PRIMER TTCTTCTCCCCTTCCCTTAA
RIGHT PRIMER GTAAACAGATTTCTTGGCGG
PRODUCT SIZE: 245

55. G1_Unigene_BMK.9465 p6 (TTCTGG)4 24 488 511

TGAAGTTCGTAAGTCTCGCCGCTACTTCCCTCTTCG
CCGCCTCTTCTTACGCTATCGAAGTCGCTTGTCTGTG
TCAACGGCGTCCAGCAATCTGTTGTTGACTTGG
ACACCGGTAACCTGTCCATTCCCAATCCAG
CTAAGTTCGCTGTGGTCTTTGACTTCGTCTCCGCTG
ACAACCTATATCGTTGACGCATACTACGCTCTTGTGCG
ACGGACAGAAGCACTGGAATGACATTGGCAATG
CTGGCAGAACCATTGAAATTCCTGCTCTTTACTTG
TCGACCTATGGTGACGCGCCACTCTACCAATCG
CTTTGAGCCAGACTCCTGCCATCAACTCTACCTCTG
CCTTGAGAGCCAGATTCAACTCTAAGCTTG
TCTCCAAGAGAGATGCCAGATCTGACTTGATTGCTTA
CATTGAGTCTTTGACCGGTACTGCAGTTGCCGTCG
CTTCCGTTGGTACTCCAGATGCTGCTTCTTCTAGTG
CTTCTTCTGGTTCTGGTTCTGGTTCTGGCGCTGCTGG
TTCTCTCACTGCTGGCTCTGGTCTGCTGCTGCTGG
TTCTTCCACTGCTGCTGGTGCCACTCTGAGTCCG
CCGCTGCTGGTACTACTGGTCAATCTACCTC
CACCTCCACTTACGTGTCGACCAAGCTCATCACCAT

CACGTCTTGCTCCGACAACAAGTGCTCCGCCACCG
CTGTTTCTGCAACTGAGGGCTTGACTACTGCCACCG
TCAACGGAGAGACCACCGTGTACAGCACCTGGTG
CCCAGTTACCTCGACCTCTGCTGCCGCCGCCTCTAC
CACCCTGCGGTGACCACCAAGATCATCACCCT
CACTTCTTGCTCCGACAACAAGTGCTCTGCCACCG
CCGTTCCAGCTACTGAGGCCCACTACTGTAC
CACCACGGTCAGACCACTGTCTACAC

LEFT PRIMER GATGCCAGATCTGACTTGAT
RIGHT PRIMER GATTGACCAGTAGTACCAGC
PRODUCT SIZE: 224

56. G1_Unigene_BMK.9873 p5 (GAATT)4 20 500 519

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TATCCATCATATGTTGTTGGCTTGTAATTTAG
TTCATGTACGTGGCGCATATATGTTTCTAAATGTG
CATGTTGTTGAGTTGATTTATCATTTAAGACAAAG
AACTATTGTCAAAATCTGATGCGCCTGTCTGATAT
TAGATTTGGCTATCTGATATGAGTTCTAGACACTTC
CATTCCAGTTGTACTTTTAATTCGTTTGCCATG
TATCGTATGGGGGGTGGGGTGGGGGTTAACTTT
TATTTCTTTTTTTGTATGCTGCCCTTAATGTGTTTG
AATGTAGAAAAGTAATTTGTCAAAGACGGCTCCG
AGTTCAAATGGAATGGAATGCCGCTGCACCTTG
ACGACCGGACCGGATGAAGTGGTACTTATGCCAT
CAGCAGCCGACGCCCTTTCTTTCTTTGCCAC
CTTCTCTCGTGTGCATGTAGGAGCCAGCCAGCCGG
CCGCAGACCAAAACATGGAATTGAATTGAATTG
AATTGGGAGTCTCATATTTCCCTTGCTTTATTATT
TATTGAAATTAATTCAAACCAACTGAAAAGTAAC
GATGTGATATTCCACATGGGGTATTTTATTTGACCG
CGAGTCGGCAGTGGAATTATTCCCGAAACAAA
TAAGGACCTTTGTTGTATTCTACAGTTGATATATT
GGCATATTTTCG

LEFT PRIMER TTTCTCTCGTGTGCATGTAG
RIGHT PRIMER AATAATCCACTGCCGACTC
PRODUCT SIZE: 196

57. G1_Unigene_BMK.11082 p4 (AAAT)5 20102 121

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TATTGGAATTAAGAGTCTTCCCTCTCAGAAAATAAA
TAAATAAATAAATGTAGTGATCAAATGAGTAATC
TTCTGTGTTTTAAAGTCCCTTAAGCTGGTCAATGAG
CCCGGTTAATGTTGTCCATTTCTCAATTGCACTGG
CAGAAGACACAAATGCAAGCTTGGAGGACTCTACAT
CATTCCGCGTAAGTATGATATCAATGAAGCTAGTG
AGGAGTTGAATGTATCCACCTCAGTCTTCTC
TTCAGGGCTAGAGCTTAGCTTATTCAAAGCGAGG
TTCGCCTTCTGAACCAATCTGTGTGCTGCTGACTC
CAAGAACCCTGAGCTGCTGAGGCAAAATCG
TTACTTTTCGATGGCCTGGCCTGCTTTGCTTAGCCGG
TACACAAGTTCTGAGATATCCTGTTTCTT
TCTTTGATGAGCTGAGAACTCCTTGCTTTCAAG
CCTCTTCTTCTGCTTCTTAACCTTCTCCAACAG
TTCCTCATCATCATCAGCTTCCAGAATTGCTGCAT
TAGAACTGTTGAAATCTTTGCCGACCAATGAG
AAGGCAAAGCTGGTGAGAAAGCAGATGGACAGG
CTTCTTTTGGTGAGGATTGGAGCAGGTGAGTGTGG
CTCTTCATTAGGGCCTTACAAAAGTCAATCC
TCTCCTTGTAATGTTTTTTGGACATGAAGTAATG

TCGGTGGTGTGTCAGTGAAGAAGACGTAACAG
AAGATGCCGAGGAGGAAAGGGTTGAAGGGAGG
AAGGATTTTGCAGTGGAGAGAATGGCTGTGG
CCATTTTCTTTGATTGTTTTTTTTTACCTTATTTTTT
TCTGATGATTTTTTTTGGTTCGAAAATTTCAGAGG
TATTGAATTGACATGTTAGAACTTTTGAGGATAAG

LEFT PRIMER CGGAAATCAATGGAGACTCT
RIGHT PRIMER AAGCTTGCATTTGTGTCTTC
PRODUCT SIZE: 215

58. G1_Unigene_BMK.11093 p3 (CTC)7 21 1198 1218

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ATGATGTACATTTGGTAACAAATCCTTGGCCAAA
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TACAAATCATTGAAAGGAATATAAAAGAACG
CTTCTTTAGTAAATATATAAAATATACCAGATAACG
AAATTCCTCCACACGAAATAACGGAATTCCTCCA
CACGAAATCACAAAACCAATCTCATATCCTCAG
CAGCTAACACAAAATGAAGCTCTAAATCTCAAACAC
TATTAGATTTAGGGTTGGCTGTGCAACCTTCATGG
CTCTCGTTACACCAGCGTAATGCTTCGTTTCTTG
AATTATCTATCAGATCTTCGGTGCAGAATTTCAAG
AGTCCACAGCAACTCTTCCATGAAGTCGGCTG
CAGGGGGCGTCCGGCGACAGGTACAATGGACGG
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ATCTTGTCGGCATCAGCTGATTCGACTGCAGG
AACCTCTTCTTGTAAGCAGTACCCGATGACTCCC
CAGTTTGCTCTTCGAAACCAGTAACCTTTGTTTCTCG
ATCCCCCTTTGACACAATATCTGCAACAGCAGCAGG
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CTTCTTCAGTTTCTTTCGACACCAGATCGGTTTCG
ACTAGAGAAACCCCATTAATCTCTTCCACATATG
ACAATGTTTTTCTTCTGTCTGTTTCGACACCTCCT
CCGTGATAGCTGGCGAAGATTACACGGTCTCATC
CAAAGACACCGCAACTTTCTCCTCCACCTCCTC
CACCTCCTCCACCTTGGTTTCCACTACAACAC
CACCTTGATCCAAATGATTGTACACAGATTCAACCG
TCTCAACAACCGAGACAACAACCTTCTTCGG
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CACCTTCCGCCTCTTCATCCGAACCTATTACTTG
AACTCGAACTTGAATAATCAGCATCATCGCGGG
TTTCCTTTGCCGGCTTGGAACAGTCATCGATGGCTA
TATCCCTCACAGATTCAACCACAGGTTTTGAGTCG
CCAACATCCTCCGGTTGAACATTTTCTGCG
CCCTCCAACCTCCCATTCAAAGAATCCGCCATTTCC
TTAAGATCTGCAGAACTTTCTGCTCCTCCTCC
TCTCCTCCTCTGCAACTCTCTCTCTCTCCCCTCT
CAAGCAACACAGACAGCCACCAGCTCTCTCT
TTCTCTCTCTGTGGAAGTTTTGACAGGGACAATG
ACGGCGGTCTCCGCTGACGTACGAAGCTAACGAAG
CGTGAGAATATTAGTGACATGGATGCTTCTTTGCCCG
CCAATGGGGCTTTTAACTGCGAGAGCTTCTCAGCG
CTCTCGATTTCCCAATGGAAGACATTGATGACAGCG
TCGAAGATAACGATTGGGATACCAAGTTCCAAGACA
TAGAGCCACCGCCTAACATTGATCAGTTGCTTGG
TTCAGGGATTTTCAGCTATGATGACAAAAGAAACA
TACGAACCTCTCCACTCCGTATGGACATATGTATCAG
CGACCGCAATTCCCAAGTGTTACTTGTGAAAC
CATCCGACGACAGGTTAGCCTTCGCAAAGATG
ACCTTGAAAGCATTGGCTCTTGTGCTGCGCAATTTG
AGCCCAAATTTGAAAAGCGCACCCGAAGCAAG

CTTTCACGAAGCAGGCGTGCAAACCCAATTATTT
 CAGTACACAGTTTCATCCTCAGTACCTCATC
 CAATTCCTCTGCCTCTGAAAATTTATGTCGTTGGG
 ATGCTTGTGAATTTAACTTAGAAGCCTCTCGCACAG
 AGGACACATCAAACACTGCCAAAAGAAAACAGAAG
 AAGAAAATGGGAAAGCTCTCCATGGACGAAGCAGG
 TGAGAGTCGGGAGACTAAAAGATGCACACATTG
 TCAAGTGATGAAGACCCCTCAGTGGAGGGAAGGG
 CCACTAGGACCGAAGACCCTCTGCAATGCATG
 TGGGGTTTCGGTACAGGTCTGGCCGCCCTCCTCCAGAG
 TACCGCCCTGCAGCAAGCCCTACATTCATCGCATCAG
 TGCATTCAAACCTCGCACAAGAAGGTGATCGAGCTG
 AGAAGCAAGTCTTGCCAGGGGGCGAGCATGGGG
 ATTTTGTCTGTCGGGACAGTAGGAAATTCAGATGG
 CAGTAGTAGTGGCAGGGGTAGTCATTTATTTTCATTA
 TATCTGGAATAATGAGAAGAGTCTTCGATGTTGAG
 ATAACCTTTCTTTTTGTCTCTGTTTTATTGCTTTCTG
 TTCTAATTTATTTGATGTGTTCTTTGTGTACATGATGG
 AATAAGATCGTAGAAAGCAGTCGTTACCTCTG
 TCAAGGAAAAAACTAGAAGAGCAAAAGAAA
 CAAACGAACTAGCTCTTGATCTCCGAGTTCGTTCTGTG
 AGGGTCGACTTGTGATGTCCAG

LEFT PRIMER CTCACAGATTCAACCACAGG
 RIGHT PRIMER TTGTCCTGTCAAACTTCC
 PRODUCT SIZE: 227

59. G1_Unigene_BMK.11099 p5 (TAGAC)5 25 1831 1855

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 CTCGCAAAATCCCTACAACCCTAAACCCTAGGG
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 TATCTTAATCTTCCCAATGGGCAAAATCAAGCAAG
 AAATCCGCCACCAAGGTTGAGGCTCCCGCTGTGG
 TTGTTCCAGCTCCTAAGTCTGGAAAGAAAGGTAAG
 AGAGATGCCGAGAACGAAATAGAGAAAGGTTGTG
 AGCGCAAAGAAGCAGAAGATTGACGAGGGTGTAG
 CGCAGGCCATTGAGAAGAAGAAAGTTGAAGCAAAG
 ACCCAGAAGAAGAAAGTGGAAACTAGTAGTTCCG
 AGGAGTCTGATGTGTCTTCTGACTCTGACGTGAAGG
 CTCCTAAATCTAAGGTAGCTGCTAAGAATGG
 CCAACTGCTGCTATAAAGAAGAAAGATGTCTCAA
 CTGAAAGCTCAGATGAGAGTAGCGATGATTCGG
 AAGATGATGCTAAAACCCCTGCAAAGGTTACTG
 CCCAAAAGCCAGCTGCAGCTGCTAAGAAAGG
 CCCATCAGTGCCTGTTAAGAAGGCAGACACTAG
 CAGCTCTGAGTCTGAAGAGAGCTCTGAATCTGAAG
 AAGAGGAAGTTGTGAAAAAAGTATCTGCTG
 TAATCCCTAAAGGAAAGGACGTTTTCAAG
 CTCCTCTGATGATAGTTTCAAGAGGAGGATTCTGATG
 ATAGTTTCAGAGGAAGTGAAAGGGTACCA
 CAAAAACTGTTGCCCTGCTGCTAAGAGTGTTTCAAG
 CCATCCAAAAAGGATGAGGATTCAAGTGACTCTG
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 TTCAGAGGAGGAACCTCCAAAGACAGAGAAAG
 TAAAGCCTTCTCAAGTTTCAAAGCAAGATAGCAG
 TGAGTCAGAGGAGGAATCCAGTTCTGACGAAGAAG
 AGGAAGATGAACCTGCAAAGACTCCCAAG
 AAAAAGGACACTGATGTGAAGATGGTAGATGCCG
 AGTCTGAGAAAGAAAGCTCCCAATACCCAG
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 CTGGAAACCTGAACTTCCGTATTGAGGAACACG

ATTTGAGGAATTTCTTCAAAGATGCTGGTGAAGTTG
 TTGATATCCGTTTTGCCTCAGATCCAGAAGGGAAG
 TTCAAGGGCTTTGGACATGTTGAGTTCGCCACAG
 CTGAAGCAGCAAGGAAGGCTCTTGAACCTAATGG
 TTTAGATTTGCTTGGTCGTGATATCAGACTTG
 ATCTGGCTCGTGAAAGGGGTGAAAGGGGTGCTTA
 TACTCCCACCGGAAGAGAGAGCAACTCATATCAG
 AAGGGACCACGCGGTGCGTCCAAAACAATATTTG
 TTCGAGGTTTTGACAGATCCCTCGGGGAGGATGAG
 ATCAGGAGCTCCTTAAAGAAGCTTTTAGTTCTTG
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 CTTTAGAATTTAATGGACATGAATTTGGAGACGG
 TTAAGTGCAGGTGGAAGAGGCAAAACCAAAAGGTG
 ATTTCCGGTACTCCAGGAGTAATGACGGGGG
 TTATTCCAATAATCGTGGTAGAGGACGTTTTAGCAG
 CAGCAGCAGGGGGGGTAGGGATGGTGGTGGACG
 TGGTTTCAGGGATGGTGTACGAGGCAGAGGACG
 TGGAACAAACCAACCTAGCTGCTCCTGG
 AACAGGGAAGAAACCCTTCGACGACGAGTAG
 ACTAGACTAGACTAGACTAGACTTGTGTAG
 TAATCGGTTCGGCGGCCAAGGGAAATTGTGGAAG
 ACTTATGTTTGGCTCTTTTTAATTTTATCATATTT
 TATTATTTTAAATTTTGAAGGCATGTCTGGTTTTG
 AGCTTTACTTGGACATGAAGTCAACGCAAGAGTG
 AGTGAACCTACTATGGAGTTTTTGGATTTATG
 TCTTTAATTAATTTTGAAGCGTTAATATGGTATTT
 TATTACTCAAATTATTTCCGATCTCCGGC

LEFT PRIMER GTGGTAGAGGACGTTTTAGC
 RIGHT PRIMER GTAGGTTCACTCACTCTTGC
 PRODUCT SIZE: 330

60. G1_Unigene_BMK.11165 p6 (AACCT)3 181231 1248

GACCCTTTCTCAAATAAAATGTTCTTAATTTCAATT
 CAAATGCAAAGGATCATGTTATCAATATCCAGTGTG
 AGACTTGTTTAAATTTCAACCGTTCACTTGG
 AAAAAAAAAAACCGGGGAGAAATTTTCAATATAG
 ATAACCTACAATGATCCTTAAAAAGATGAATATG
 AGGGGCGGGGGGACTAGGAGTGCAGCTTGACAA
 CACGACATAACCTTTCAAAGAAGATAGGGCACATG
 TTTGTGCTTAAACTATGTATCCTTCATCCATTCT
 GGTGCTTCCCTCTCAAGCGTCCCCAAGGATGCGGTG
 CGATACAGAAGTTCTACTTTCGTTACCAGCAGCCCTG
 TTCATCCATGTAAGATTGAAGGCATAACCACCTTG
 ATTGATGCACAGCTGAGATGCATATTTCTTCAGCTTG
 ACTAACAGTAGAGAACTTTAAATCCACCATATACT
 CAACAAGCACTTGAAACACGCAGTTAACCTGG
 CCAATTGGTTTTGCACAACCTGGTCTTTCAATAG
 TTCTACACCATTTGTGGCTCTTGAACAGTTACAAGAG
 CCCCCTAGAAGGCATAACTAAATCCTCTGCCTCAG
 ACTGGGAATTTCTTCTACGCTTACTTG
 TCCTTTTTTTCTTTGAGAGATTTCTGCTGCTCCTG
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 TCCATTCTCTGTGTTGCTACCTTTTCGATGTG
 CTAATAATTTCCCTCCTGTTGCAGCTTTTGGAG
 CCTCTCTACTTCATCAGAAAGTTTTTCATTTTTCTG
 TTCTCTTCCAACAAATGATTCTGGTACTCGGTG
 CATTGTCAGCTTTGGTGGACCTGCAATTAATTTG
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 TAAAAATTGACTAATCGGAATTCCAATGGATCCG

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CAACCTCTCATTTTCTTTTCGCAAATGCTGAATA
TACTCCTCCGCAACAGATACATAATGCTTG
AACTTTCTTTCTTGATCTTTACCAATATCTTC
CAACTCCGACCATTCTTTGTCTTGATTTTCGAGTACT
TATCGTAGAGTTTGGAGTAGAGAGCTTCTGTGGTCG
ACATTTGTGAGAAGCCCTGACCAATTCTTCTTTTCG
ATGACCAGTACGATCGCTGAGCCCTCAGG
CCTCCCCCAGGCGAAAACCCCTAACCCCTAACCC
TAATCGCCCTGCTACTTGTAAGTACTGAGGAGGACG
ACGACTCTGTGAGAGTCGGAGACTGAGGGGAG
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ACACGGAGGGGAAGAACGCCAGCTACTCGGCTGATG
TTTTTAAAATTACATAAACATCCGCTGATG
TTCTTAAATTGTCTCGCAAGTTGATGAACG

LEFT PRIMER TCTTCTTTTCGATGACCAGT
RIGHT PRIMER GTTCATCAACTTGCGAGACA
PRODUCT SIZE: 265

61. G1_Unigene_BMK.11242 p6 (CTTCTG)4 24 2455 2478

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CTGTTCTTCCCATATCCCTTTACCTAGCTAGCCCACC
TCAGGAATCTCCCTTCTCTCTGTTTCTTCTTC
TCTTGAAACAGAGAGATTTTACCATTTTAATTTTCGG
TTTCCATTTGGGTTTTGTGGGGTTCAATTCATGAAA
CAAAGATTAATTGCAGAGATATTGTAGAGAGAGATA
CACACTCACTGTACGCAGAAAGAGAAAGGAG
ATAAAGGTAGTTAATACTTTCTGAGATCATGAAACA
TAAGGATGGAAAACCAGGGCCCCAAGGTACCAGGG
TTTTCCCATGACAATATTGTTTGTGTTTGTATGCGGG
TTTTTATTCTATCTTGGTGGAAATGTTCTGTTCTG
AAAAGAACAATAATTGAGCCTGTAAGGTGCAAGATG
TCACAGAGGCGATTCAATCATCTCTCCAG
TTAAACCCGTTACCTTTGCTGAATGCAGCAGTG
ACTATCAAGACTACCCCCATGCACGGATCCAAGG
AGGTGGAGAAAGTATGGTGTTCATCGGCTTACTTT
CATGGAACGGCACTGCCCTCCGGTATTGGAGAGG
AAAGAATGCTTAGTTCCACCTCCAGATGGCTACAAG
CCACCAATCAGATGGCCAAATAGCAGGGACGAATG
TTGGTACAGGAATGTGCCATATGATTGGATTAACAAA
CAGAAGTCCAATCAGAATTGGCTGAGAAAAAG
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CTGGGGAGGTGATTTGTTAGATCGTGGGATTT
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CTCAGGTTCAGTTTGCTTTGGAACGTGGAATTCCAG
CAATTCTTGGCATCATTTCTACACAGAGACTTCC
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CTCAAGATGCCTCATCCCATGGACGGAATTTGGTGG
AATTTACCTCCTTGAAGTTCATCGTATACTCCG
TCCTGGAGGTTTTTGGGTCTGTCTGGTCCACCTG
TCAACTACGAAAACCGCTGGCGTGGGTGGAACAC
CACCGTAGAAGAGCAGAAATCAGATTATGAAAAG
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TACAACAAAAAGGATGATATTGCTGTTTGGCAG
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LEFT PRIMER CCCTGTTTCCCGATTTTCAT
 RIGHT PRIMER CTTGTTACATCTCTCCGTC
 PRODUCT SIZE: 256

62. G1_Unigene_BMK.11339 1 p6 (AGCCGG)3 18 542 559

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LEFT PRIMER AATTTTCATGCACGTCAAGCT
 RIGHT PRIMER TCGTACCTGTCCTTGCTC
 PRODUCT SIZE: 206

63. G1_Unigene_BMK.11347 p3 (ATT)6 18711 728

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LEFT PRIMER AACTCAACTTGTAACCC
 RIGHT PRIMER CATGTCACACGGATAAGCC
 PRODUCT SIZE: 237

64. G1_Unigene_BMK.11454 p3 (AGG)6 18 143 160

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LEFT PRIMER GTGTGAGAACCAATTTTGCA
 RIGHT PRIMER TACGATTGGGAACAGCTT
 PRODUCT SIZE: 214

65. G1_Unigene_BMK.11485 p3 (CGT)6 18 2399 2416

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 TGGTCTGTTGACGCAGCGGCTAGCCTCCGCGACGG
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 TCAAGTATTGAAATTA

LEFT PRIMER GGAGCTGATGAAATCCTTG
 RIGHT PRIMER CGTCATCGTCATCATCC
 PRODUCT SIZE: 287

66. G1_Unigene_BMK.11513 p3 (GGA)8 24 145 168

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LEFT PRIMER ATGGCGAACAAATACGAACA
 RIGHT PRIMER TGTAGGAGTAGCAGCAGTAC
 PRODUCT SIZE: 201

67. G1_Unigene_BMK.11522 p6 (ATGGCA)3 18 1018 1035

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LEFT PRIMER TGTAAC TGGTTTCTGGAGGT
 RIGHT PRIMER GGACCCTACCATCTACCAA
 PRODUCT SIZE: 207

68. G1_Unigene_BMK.11609 p6 (TTTTTA)3 18 746 763

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LEFT PRIMER TGAAAAGGAGCAGGGTAGGG
RIGHT PRIMER ACAACAACATGAACGGAGCT
PRODUCT SIZE: 217

69. G1_Unigene_BMK.11759 p3 (GGA)7 21 1852 1872

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LEFT PRIMER GTTGTTTCCAAGAGTGCCGT
RIGHT PRIMER TCGGCGGTGTCTAAGAGTTT
PRODUCT SIZE: 194

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LEFT PRIMER TCGAACGACCATCTAAGACA
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PRODUCT SIZE: 194