



US007638275B2

(12) **United States Patent**
Lewin et al.

(10) **Patent No.:** US 7,638,275 B2
(45) **Date of Patent:** Dec. 29, 2009

(54) **GENE EXPRESSION PROFILES THAT IDENTIFY GENETICALLY ELITE CATTLE**

(75) Inventors: **Harris A. Lewin**, Urbana, IL (US); **Zonglin Liu**, Peoria, IL (US); **Sandra Rodriguez-Zas**, Savoy, IL (US); **Robin E. Everts**, Champaign, IL (US)

(73) Assignee: **The Board of Trustees of the University of Illinois**, Urbana, IL (US)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 355 days.

(21) Appl. No.: **10/857,294**

(22) Filed: **May 27, 2004**

(65) **Prior Publication Data**

US 2005/0137805 A1 Jun. 23, 2005

Related U.S. Application Data

(60) Provisional application No. 60/474,577, filed on May 30, 2003.

(51) **Int. Cl.**

C12Q 1/68 (2006.01)
C07H 21/02 (2006.01)
C07H 21/04 (2006.01)

(52) **U.S. Cl.** **435/6**; 435/7.1; 536/23.1;
536/23.5

(58) **Field of Classification Search** None
See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

- 5,041,371 A 8/1991 Cowan et al.
5,374,523 A 12/1994 Collier et al.
5,614,364 A 3/1997 Tuggle et al.
5,645,834 A 7/1997 Cockrum et al.
5,767,080 A 6/1998 Beck et al.
5,850,804 A 12/1998 Hill et al.
5,939,264 A 8/1999 Rothschild et al.
5,981,187 A * 11/1999 Cook et al. 435/6
6,013,857 A 1/2000 Deboer et al.
6,017,563 A 1/2000 Knight et al.
6,183,786 B1 2/2001 Knight et al.
6,319,525 B1 11/2001 Knight et al.
6,492,142 B2 12/2002 Renaville et al.
6,548,740 B1 4/2003 Bremel et al.
2001/0053849 A1 12/2001 Kreek et al.
2002/0058085 A1 5/2002 Knight et al.
2002/0124803 A1 9/2002 Chen et al.
2002/0169302 A1 11/2002 Havukkala et al.

FOREIGN PATENT DOCUMENTS

- WO WO 01/49879 7/2001
WO WO 02/36824 5/2002

OTHER PUBLICATIONS

- Coleman et al. Drug Discovery Today. 2003. 8: 233-235.*
Liu et al. Clinical Immunology. 2004. 112: 225-230.*

Singh et al. Proceedings of the New Zealand Society of Animal Production. 2004. 64: 8-10.*

Ashburner et al. (2000) Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. *Nature Genetics* 25(1):25-9.

Band et al., (2002) A 3800 gene microarray for cattle functional genomics: comparison of gene expression in spleen, placenta, and brain. *Anim Biotechnol.* 13(1):163-72.

Benjamini, Y. and Hochberg, Y. (1995), "Controlling the False Discovery Rate: a practical and powerful approach to multiple testing," *Journal of the Royal Statistical Society. B*, 57, 289 -300.

Brown and Botstein (1999) Exploring the new world of the genome with DNA microarrays. *Nature Genetics* 21, 33-37.

Diehl et al., (2000) Manufacturing DNA microarrays of high spot homogeneity and reduced background signal. *Nucleic Acids Research* 29(7).

Eisen et al. (1998) Cluster analysis and display of genome-wide expression patterns. *PNAS (USA)* 95: 14863-14868.

Hegde et al. (2000) A concise guide to cDNA microarray analysis. *Biotechniques* 29(3):548-50.

Huang and Madan (1999) CAP3: A DNA sequence assembly program. *Genome Research* 9(9):868-77.

Rosenwald A. et al. (2002) The use of molecular profiling to predict survival after chemotherapy for diffuse large-B-cell lymphoma. *N Engl J Med.* 346(25):1937-47.

Rosenwald and Staudt (2002) Clinical translation of gene expression profiling in lymphomas and leukemias. *Semin Oncol.* 29(3):258-63.

Smith and Green (1999) (*Unpublished*) Repeatmasker, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>.

Cox et al., (2002) Identification of candidate genes regulating HDL cholesterol using a chromosomal region expression array. *Genome Res.* 12(11):1693-702.

Yao, J. et al. (2001) Generation of EST and cDNA microarray resources for the study of bovine immunobiology. *Acta Vet. Scand.* 42(3): 391-405.

Wayne et al., (2002) Combining mapping and arraying: An approach to candidate gene identification. *Proc Natl Acad Sci U S A.* 99(23):14903-6.

Burton et al., "An Immunogenomics Approach to Understanding Periparturient Immunosuppression and Mastitis Susceptibility in Dairy Cows," *Acta vet. scand. (suppl.)*, 98: 71-88 (2003).

Ishiwata et al., "Characterization of Gene Expression Profiles in Early Bovine Pregnancy Using a Custom cDNA Microarray," *Mol. Reprod. and Dev.*, 65: 9-18 (2003).

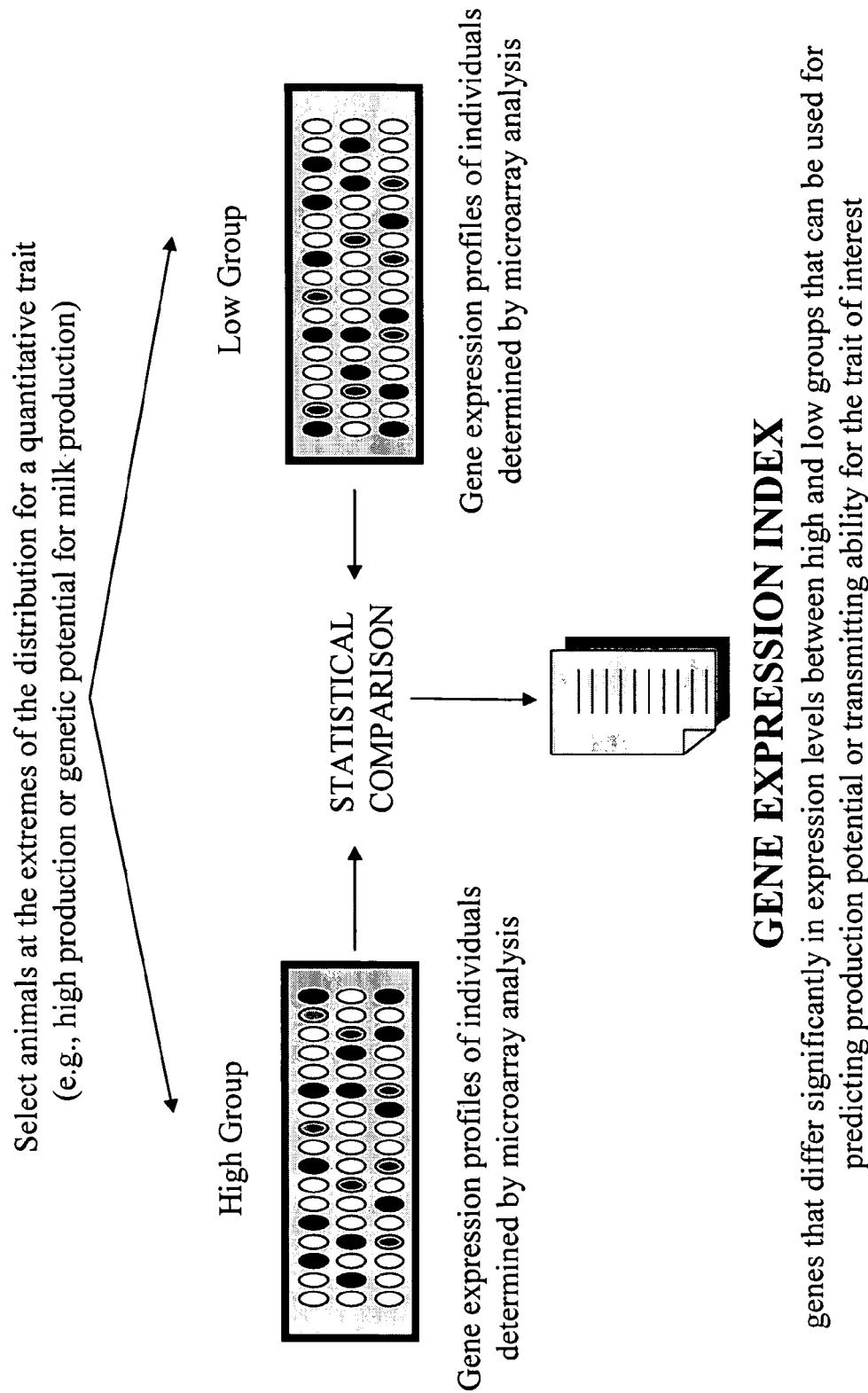
* cited by examiner

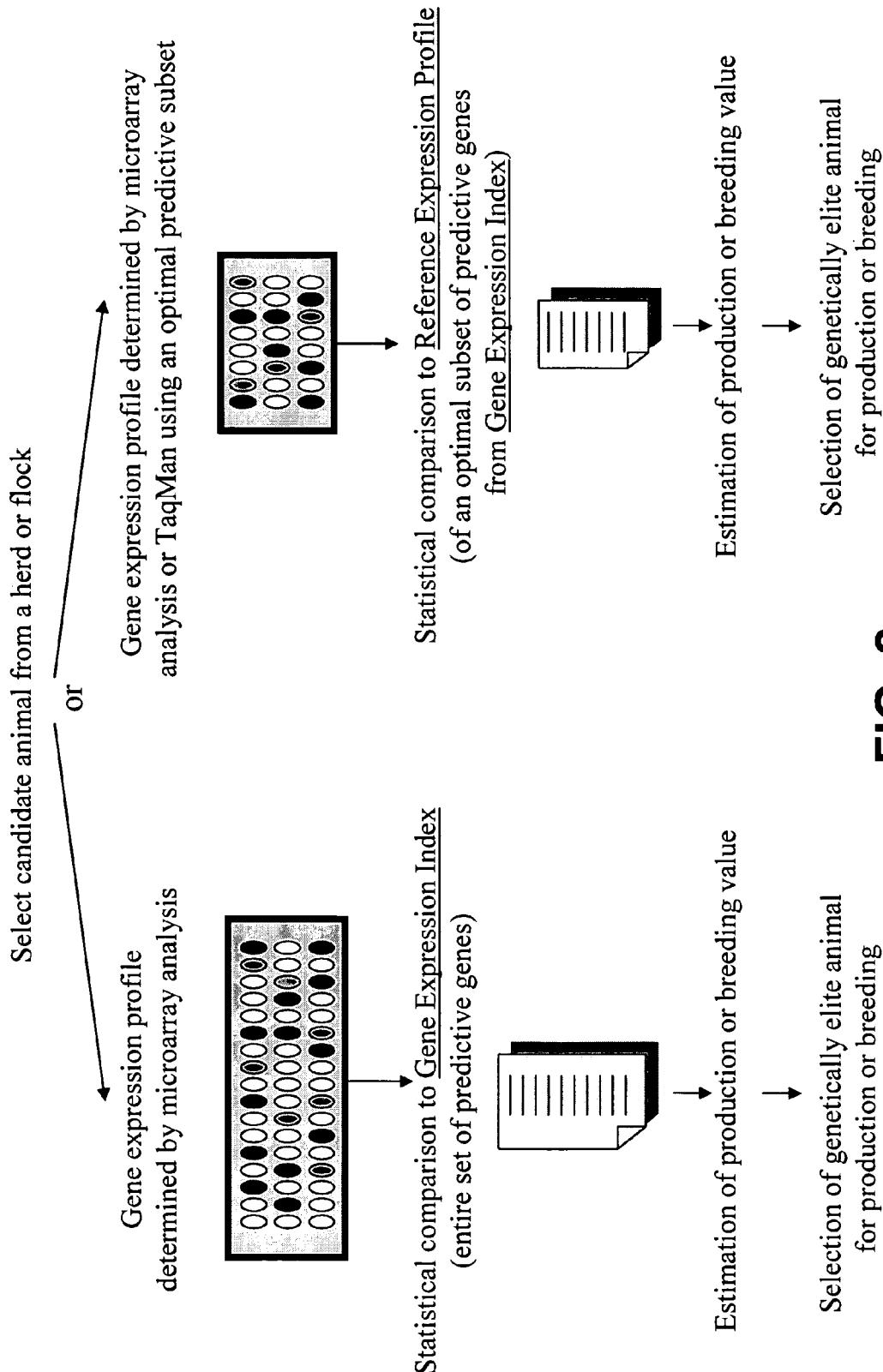
Primary Examiner—Carla Myers

(74) **Attorney, Agent, or Firm**—Barnes & Thornburg LLP;
Alice O. Martin

(57) **ABSTRACT**

Genetically elite ungulate mammals are identified on the basis of gene expression profiles from biological samples such as liver and blood. Methods and compositions are presented to select genetically elite animals with a desired phenotype such as high milk production for breeding to improve production levels. A method to select an animal with a specific phenotype, e.g. milk production and health traits, includes creating a Gene Expression Index for a specific phenotype and using the index to identify candidate animals for breeding by comparing the index to gene expression profiles of the animals.



**FIG. 2**

Canonical Discriminant Analysis of Cows and PTA

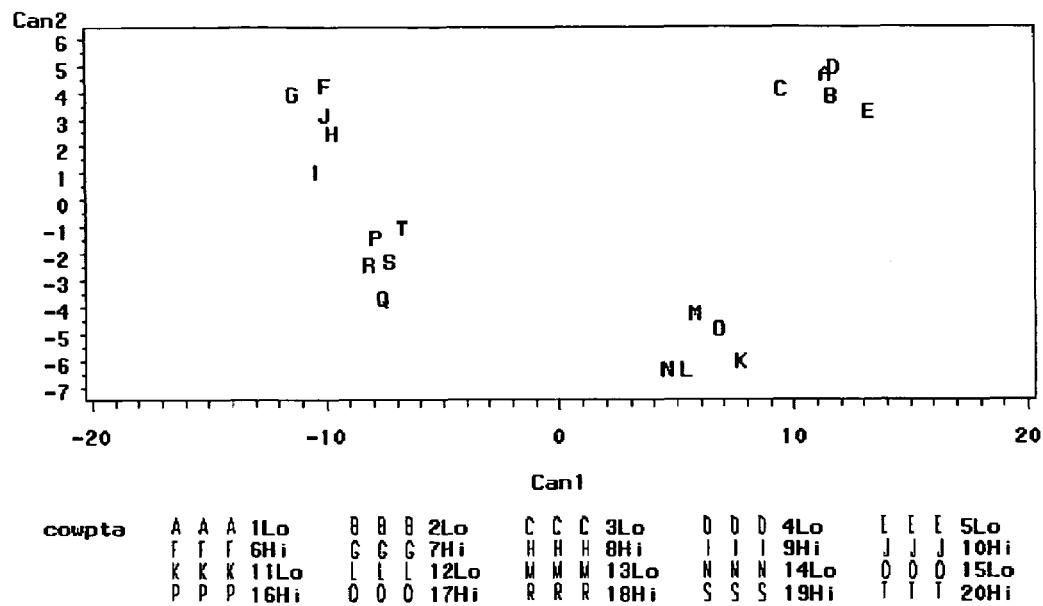


FIG. 3

1

GENE EXPRESSION PROFILES THAT IDENTIFY GENETICALLY ELITE CATTLE

This application claims priority from U.S. Ser. No. 60/474, 577, filed May 30, 2003.

BACKGROUND OF DISCLOSURE

Animal improvement has been achieved through selective breeding since the beginning of animal agriculture. In recent times, animal breeding employs a quantitative genetics approach, where improvement is based on evaluation of production records of progeny and relatives, e.g. records of milk production and carcass quality, followed by breeding pedigree animals whose phenotypes are closest to a desired phenotype. Most improvement in dairy cattle, for example, is made through use of sire lines selected in this manner.

Marker-assisted selection using genetic markers that identify chromosomal regions containing genes (genetic loci) that affect quantitative traits (QTL) is an approach that is currently being developed by the animal breeding industry, e.g. for cattle traits. For example, a polymorphism in the somatotropin gene causing a change at amino acid position 126 provides a marker that can be correlated to the trait of superior milk production, but does not necessarily identify the polymorphism as the cause of the trait. The actual cause of the increased milk production may be due to some other closely linked (i.e. in close proximity) genetic factor or gene in the cattle genome, and not to the existence of the somatotropin polymorphism. Consequently, these statistics-based animal breeding methods are generally slow, expensive and inaccurate because the genes themselves underlying the traits of interest have not been identified, so selection does not achieve completely successful or predictable outcomes.

Further, complex gene action and interactions among genes serve to complicate objectives of traditional breeding programs. Selection based purely on phenotypic characteristics does not efficiently take into account such genetic variability, and is therefore not optimal.

For example, these traditional approaches are used for the purpose of selecting and breeding dairy cows capable of superior milk production. Although such programs have improved milk production, there are disadvantages because of the significant costs and time involved before the success of the program can be determined. For example, a traditional breeding program requires the breeding of many cows with a particular bull and subsequent analysis of the milk production of the female-progeny of these cows to determine whether the bull is of superior genetic value. A particularly successful breeding family of cattle is the Holstein line derived from the bull Carlin-M Ivanhoe Bell.

Female progeny must be raised, become pregnant, allowed to give birth and milked for a minimum length of time before milk production capabilities can be analyzed. Although this type of improvement program has improved milk production, there are disadvantages because of the significant costs and time involved before the success of the program can be determined. A breeding program relying on traditional techniques and selection criteria typically requires the investment of 4 or more years in a group of cattle before significant analysis of the program can be undertaken. It would, therefore, be advantageous if additional methods or criteria were available that were quicker and cheaper to determine whether a bull, heifer or cow should be included in a breeding program designed for superior milk production.

Boosting the level of growth hormones via introduction of additional hormones can improve cattle performance. An

2

example is the use of bovine growth hormone or somatotropin. This has been made possible by the cloning and isolation of genes that express such proteins and then adding the resulting products of these commercially produced proteins to animals via feeds, injections, drugs, and the like. This method of boosting production of essential proteins however is inherently limited by the underlying genetics of the animal and because the effects are not heritable, does not offer anything in the way of selection of genetically superior animals for optimum genetic capabilities.

Furthermore, qualified administration of multiple injections of growth hormone keep costs high, and sick animals cannot be given growth hormone injections. There is also a concern that animals that are treated with growth hormone are more susceptible to mastitis. In addition, public acceptance of growth hormone is still uncertain. The results of bovine growth hormone injection include an increase in overall milk production, with no change in milk composition. This is a significant disadvantage because a dairy producer is paid on the basis of three milk characteristics, total volume of milk, total pounds of fat in the milk, and total pounds of protein in the milk, thus quality is as important as quantity. Producers may be paid more for protein than fat. Thus it can be seen that there is a continuing need for means of efficiently selecting and breeding cattle for improved milk production without concomitant decrease in milk composition, particularly protein content. In general, better methods of identifying animals with desirable predicted transmitting ability (PTA) for desirable phenotypes, such as high milk production and yield of protein and fat, are needed for long term benefits.

Microarrays are being developed for many research applications in animals, e.g. to study responses of genes to external stimuli. Microarray technology is revolutionizing biology by permitting the simultaneous analysis of transcript levels of thousands of genes in different physiological states of an organism, tissue or cell. Construction of microarrays is most efficient when information is utilized from annotated genome or EST sequencing projects. Evaluation of transcript levels using microarray technology has led to new insights into animal development, cancer, infectious diseases and aging. Microarrays have recently been produced for studying the functions of cattle genes and gene expression changes in different physiological states, although results to date have been quite limited.

In summary, a need exists in the art for a method of genetically evaluating animals such as ungulate (hoofed) mammals to enable breeders to more accurately select those animals which not only phenotypically express desirable traits, but those which express favorable underlying genetic criteria leading to the desired phenotypes. Therefore, it would be advantageous to find ways to more accurately predict quantitative traits from genomic information.

SUMMARY OF DISCLOSURE

Methods and compositions to identify and select genetically elite animals, e.g. ungulate (hoofed) mammals, with a desired phenotype for breeding, in particular, a quantitative trait such as high milk production, carcass quality and resistance to disease, include creating gene expression profiles from individual animals, developing a Gene Expression Index for phenomic selection by comparing gene expression profiles of animals whose phenotypes are at the extreme ends of a continuous distribution of the phenotype, and using the index to identify and select elite animals for breeding to improve economically important traits.

A method of making a gene expression index for phenomic selection of elite ungulate mammals, e.g. cattle, sheep, goats, horses, and deer, includes the steps of defining and selecting a phenotype that has multiple levels, for example, quantitative complex traits, especially those that are economically important, such as milk production levels, and other traits such as high protein values, carcass quality, fertility and resistance to disease. A plurality of genes is selected for which gene expression can be determined to create gene expression profiles of individual animals. In an embodiment, the first group of animals differs from the second group of animals in predicted transmitting ability (PTA) for the desired phenotype, e.g. high milk production, fertility, disease, resistance. cDNA is prepared from RNA isolated from biological samples such as blood or liver from a first group of animals that has a first level of a defined phenotype (e.g., high genetic potential for milk production or fertility). The cDNAs are hybridized to the plurality of nucleic acids representing the genes. Hybridization can take place on a microarray which may be designated a DNA microchip or biochip. cDNAs from RNA isolated from biological samples from a second group of animals that has a second level of the phenotype (such as low genetic potential for milk production or fertility), are also hybridized to the plurality of nucleic acids, either on the same or a different array. The expression profiles of the two groups of animals are compared statistically and the genes that differ significantly between the two groups form the Gene Expression Index (FIG. 1) This index can be used for phenomic selection, a method that involves comparing gene expression profiles of candidate animals for animal breeding to the Gene Expression Index or to a Reference Expression Profile created from an optimal subset of genes in the Gene Expression Index.

The method of creating a Gene Expression Index that can be used to identify genetically elite ungulate mammals then includes the steps of:

- (a) comparing expression levels of genes in tissues (e.g., blood) of ungulate mammals classified according to multiple levels of a selected phenotype (e.g. genetic potential for milk production);
- (b) determining a set of genes that differ significantly in expression levels at different levels of the selected phenotype; and
- (c) using statistical criteria, creating a list of genes that are differentially expressed (Gene Expression Index) in animals classified according to the different level(s) of the phenotype (e.g., high and low genetic potential for milk production).

A Gene Expression Index that includes genes whose GenBank accession numbers are listed in Table I, Table II, Table III or a combination or a subset thereof is disclosed. In the Gene Expression Index, an optimal subset to create a Reference Expression Profile includes 1 to about 100 nucleic acid sequences, whose GenBank accession numbers are selected from Table I, Table II, or Table III.

A method of determining whether an ungulate mammal (candidate animal) is genetically elite for a phenotype/trait of interest includes the steps of:

- (a) determining a gene expression profile for the animal using RNA collected from one or more tissues;
- (b) comparing the expression profile with the gene expression index or a Reference Expression Profile for that tissue(s); and
- (c) identifying the animal as an elite animal if the gene expression profile is similar to expression levels of genes the Gene Expression Index.

For example, a method for predicting milk production or genetic potential for milk production in a cow (candidate animal) prior to her first lactation includes the steps of:

- 5 (a) obtaining a gene expression profile of the candidate cow as a heifer; and
- (b) comparing the profile to a Gene Expression Index created from heifers or cows with known milk production levels, or known genetic potential for milk production; and
- 10 (c) predicting milk production or genetic potential for milk production of the candidate animal by ranking similarity to the Gene Expression Index.

For example, a method for phenomic selection of a breeding bull predicted to transmit high genetic potential for milk production to his offspring includes the steps of:

- 15 (a) selecting an optimal subset of nucleic acids from the Gene Expression Index representing genes whose sequences are designated by GenBank accession numbers listed in TABLE I, II, and III, to create a Reference Expression Profile, wherein the Reference Expression Profile accounts for a significant fraction of the variation in the phenotype of interest;
- (b) creating a gene expression profile of the subset of nucleic acids for the the candidate bull;
- (c) designating the candidate bull as genetically elite if the gene expression profile is similar to the Reference Expression Profile for the phenotype of interest, e.g., genetic potential for milk production (measured as predicted transmitting ability, or PTA).
- 20 (d) selecting a bull for a breeding program if the Candidate Expression Profile shows has a high similarity to the Reference Expression Profile (FIG. 2).

A microarray that includes nucleic acids derived from cattle RNA, whose nucleic acid sequences are designated by GenBank accession numbers listed in TABLES I or II or III or a combination thereof is within the scope of this disclosure. Any other suitable gene expression detection methods such as PCR and Northern blots can also be used to test the expression levels of genes in the Gene Expression Index and is in the scope of the disclosure.

An optimal subset of nucleic acids whose expression levels in blood leukocytes are useful for predicting genetic potential for milk yield includes genes encoding for a factor upregulated during skeletal muscle growth (SEQ ID NO: 1), Sjogren syndrome antigen B (SEQ ID NO: 2), ribosomal protein L22 (SEQ ID NO: 4), pre-mRNA branch site protein p14 (SEQ ID NO: 5) and other genes represented by for example, SEQ ID NOS: 1-10 in TABLE I. New functions related to lactation are provided for these genes by this disclosure.

An optimal subset of nucleic acids whose expression levels in liver are useful for predicting genetic potential for milk yield includes genes encoding for histone 1 (SEQ ID NO: 359), epithelial v-like antigen 1 (SEQ ID NO: 360), poly (A) binding protein (SEQ ID NO: 361), and any other genes represented by SEQ ID NOS: 358-367 in TABLE II.

An optimal subset of nucleic acids whose expression levels in both liver and blood are useful for predicting genetic potential (TABLE III) includes genes encoding for a core promoter element binding protein (SEQ. ID. NO: 368), a low density lipo protein receptor-related protein (SEQ. ID. NO: 369), a ubiquitin conjugating enzyme E2L3 (SEQ. ID. NO: 370) and any other genes designated by SEQ ID NOS: 371-408.

A kit for detecting gene expression profile differences includes in discrete compartments:

- 60 (a) at least one microchip comprising nucleic acids whose sequences are designated by genes having GenBank accession numbers listed in TABLE I, II or III;

5

- (b) reagents to perform a microarray analysis; and optionally
- (c) a computer program that can compare expression profiles and identify genetically elite ungulate mammals for breeding or for production traits

Kits may also include a subset of oligonucleotides, whose sequences represent a part of the sequences designated by GenBank accession numbers listed in TABLE I, II or III.

Reagents to perform quantitative PCR and other methods of detecting differences in Gene expression profiles, are also suitable in kits. A kit that utilizes any suitable method for detecting gene expression is within the scope of this disclosure. Such methods also include conventional reverse transcriptase (RT)-PCR, and Northern hybridizations.

The Gene Expression Index is created by statistical comparison of gene expression patterns in tissues collected from animals differing in a particular phenotype or trait, e.g., genetic potential for milk production (FIG. 1). A summary of the approach is given here, with details given in the Detailed Description of the Disclosure. Microarray gene expression data are processed for spot quality, and intensity values are normalized. Gene expression in the tissue (e.g. liver or blood) is measured relative to a standard reference control (pool of RNA from different sources) for all samples and all genes. The gene expression intensity values relative to the intensity values in the standard reference (the gene expression ratios) are calculated for all samples for all genes on the array. Ratios are compared for animals in each group, e.g., high and low for a trait, using ANOVA. The relative difference in gene expression between the two groups of samples is measured as a “ratio-of-ratios” (see Definitions) for each gene. The probabilities of the differences being due to chance are corrected for the number of comparisons made using the false discovery rate (FDR). The genes with the highest significance value falling below a certain FDR threshold are considered “significant” and used to create the Gene Expression Index (FIG. 1). A Gene Expression Index can be created for more than one trait, or a weighted index can be created for multiple traits simultaneously. More than two groups of animals may be compared. An optimal subset of genes can then be selected to streamline the testing of candidate animals for breeding or retention in a herd (FIG. 2). The optimal subset is created by selecting those genes with the highest significance for predicting the trait, i.e., those genes whose expression level account for a large amount of phenotypic variation in the trait among the animals tested. A gene expression pattern created using an optimal subset of genes is called the Reference Expression Profile (FIG. 2).

A method of determining whether an animal is a genetically elite ungulate mammal, suitable for phenomic selection of any trait, includes the steps of determining a candidate expression profile (see Definitions) for a candidate ungulate mammal and comparing the candidate expression profile to a Reference Expression Profile. The animal is designated an elite animal for purposes of breeding or production, if its gene expression profile is similar to the Reference Expression Profile. Similarity is determined by comparing the expression profile values using statistical methods. Phenomic selection may be for high milk production or other economically important traits, such as health traits, fertility, or carcass quality.

In an embodiment, a method for selecting a genetically elite animal predicted to have high genetic potential for milk production, includes the steps of selecting an optimal subset of nucleic acids from TABLE I-III, to create a Reference Expression Profile. Genes included are those encoding for a factor upregulated during skeletal muscle growth (SEQ ID

6

NO: 1), Sjogren syndrome antigen B (SEQ ID NO: 2), ribosomal protein L22 (SEQ ID NO: 4), pre-mRNA branch site protein p14 (SEQ ID NO: 5). The Reference Expression Profile accounts for the greatest amount of variation in the phenotype or a predetermined amount of variation in the phenotype, for example in TABLE I, genetic potential for milk production. cDNA from RNA obtained from a biological sample from the animal is used to create a gene expression profile. For a specific phenotype, a trait for which gene expression profiles are derived from RNA from various tissues, the predictive set of genes for the phenotype may overlap among the tissues or be unique. For example, for genetic potential for milk production in cattle, TABLE I shows predictive genes identified from leukocytes, TABLE II shows predictive genes from liver. TABLE III shows predictive genes from blood and liver. The expression levels ranked by significant differences between high and low genetic potential for milk production (or PTA), may not be identical when RNA is derived from leukocytes versus liver.

The GenBank accession numbers of cattle DNA sequences whose expression profiles are predictive of cattle milk production, are listed as genes in TABLE I and include both unannotated e.g. BF040830 (SEQ ID NO: 139), BF041863 (SEQ ID NO: 127) and known genes e.g. BF040826 (SEQ ID NO: 10), BM366099 (SEQ ID NO: 22) in cattle and in other species. That is, the list in TABLE I includes those genes whose expression level in peripheral blood leukocytes is different between the high and low PTA groups of cattle at a significance level of less than or equal to an FDR adjusted p-value of 0.29 (see Materials and Methods). Significance level cut-offs vary, and that will alter the number of genes used for selection.

Nucleic acids whose GenBank accession numbers of cattle DNA are listed as genes in TABLE II, whose expression profiles in liver are predictive of genetic potential for milk production include both unannotated e.g. SEQ ID NO: 358 (AW464111) and known e.g. SEQ ID NO: 359 (AW464166) genes. The unannotated genes are of unknown specific function, but their utility is that their gene expression profile is predictive of milk production. “Gene” used herein refers to sequences which are derived from sequencing cattle cDNAs and/or ESTs. Gene quantity was determined by comparing sequences with the human and mouse UniGene databases and other GenBank resources.

A Gene Expression Index may include nucleic acids selected from the group consisting of genes in TABLE I, genes in TABLE II, genes in TABLE III, or a unique combination or a subset thereof.

A method of increasing milk production in cattle also includes selecting a gene or genes from TABLE I or TABLE II or TABLE III and modulating expression of the gene in the target cow, heifer or bull to increase milk production. Modulation indicates the variation in the level of the protein in the cattle or the level of gene expression of other genes that affect lactation as a result of transgenic and non-transgenic manipulation, e.g. somatotropin injection.

A gene expression profile-based phenotypic selection is not limited by the number of phenotypic markers, such as enzyme levels or blood groups. Gene expression data can be correlated with the expression of complex phenotypes. Also, gene expression profiling can be applied to any sex (e.g. identify elite bulls for milk production), life stage, including embryos, and targeted at specific tissues that determine particular phenotypes. In addition, correlations between expression profiles and phenotypes selected provide insights into metabolic and signaling pathways that affect complex traits.

Gene expression profile-based selection is useful to lower the high cost of progeny testing currently used to prove a sire's genetic merit, because young sires that are determined by genetic testing to have undesirable Gene Expression Index values would not have to be progeny tested, thus saving the seedstock industry millions of dollars and increasing the rate of genetic improvement for targeted traits. In addition to identification of genetically elite bulls, the gene expression profile of individual females can identify those animals that will have the highest lactation levels and also those that can serve as bull dams for the production of the next generation of elite dairy cows.

Thus, methods of the present disclosure for identifying genetically elite animals based on gene expression profiles using any tissue as a source of RNA greatly reduces the time and expense for identifying breeding animals and improves the accuracy of selection.

DEFINITIONS

Array, microarray: molecules connected to a matrix or support in a specific arrangement relative to each other.

Accession numbers: relate to sequences that represent cattle genes in GenBank. The UniGene database provides unique identification numbers of the corresponding genes in human or mouse databases. Cattle gene sequences are aligned to human or mouse sequences to determine "gene" identification and or similarity.

Biochip: also known as a chip, DNA chip, DNA microarray, DNA array, peptide chip or peptide array; includes array of biological molecules such as DNA fragments, peptides, proteins, lipids, and tissues connected to a matrix.

Biological sample: a biological material obtained from blood, liver, skin, tissues, saliva, tears, bodily fluids or bodily secretions.

Candidate animal: an animal that is screened for a desired molecular phenotype, e.g. expression profile, to determine if it is a genetically elite animal.

Candidate Expression Profile: an expression profile obtained from a biological sample of a candidate animal whose phenotype is to be predicted.

cDNA expression array: also known as cDNA array or gene expression array or gene expression microarray. The ordered alignment of different complementary DNAs (cDNAs), or fragments of cDNAs, or oligonucleotides immobilized on a support (e.g. a nylon-based membrane or a glass slide). Such arrays may contain tens of thousands of different cDNAs on a small space (e.g. 1x1 cm, or less), and are used to determine differential gene expression patterns. cDNA arrays can be produced by different techniques. For example, one method uses PCR amplified partial sequences of cDNAs.

Elite: an animal with desired or improved characteristics (traits).

Expression profile (gene expression profile): a gene expression dataset generated by simultaneous detection in a sample from an animal of expression of a plurality of genes, whose genomic DNA, cDNA or oligonucleotide fragments thereof are determined by methods including microarrays wherein the DNA is immobilized onto a matrix or support, to which labeled cDNA from a target sample(s) are hybridized.

Expression ratio: ratio of expression value of a gene from at least two biological sources or at least two different time points.

False Discovery Rate (FDR): an approach to statistically analyze false positives in multiple samples. Instead of controlling the chance of any false positives, FDR controls the expected percent of false predictions in a set of predictions. A FDR threshold is determined from the observed p-value distribution.

Gene: a specific sequence of nucleic acids that generally includes introns and exons and regulatory regions. A "gene" referred to herein also includes ESTs cDNAs or fragments thereof, which include exons.

Gene index: (Gene Expression Index): a selective list of genes based on their differential expression profiles that correlate to the genetic potential for a desired phenotype. A Gene Expression Index represents expression values arranged or ranked using a specific classifying scheme such as hierarchical clustering or p-value (probability level) sorting.

Genotype: the complete genetic complement at a locus or of an organism.

High PTA ratio: normalized fluorescence intensity level of a single DNA sequence on the microarray for an individual or group of high genetic potential animals divided by the normalized fluorescence intensity value for the same DNA sequence expressed in the reference standard control. Fluorescence intensity is directly related to the level of sequence-specific mRNA in a cell, cells or tissues (other measures of relative expression are within the scope of the disclosure).

Hybridization: the formation of duplex molecules from complementary single strands (e.g., DNA-DNA, DNA-RNA, RNA-RNA). A single stranded nucleic acid molecule is generally labeled, e.g. with a detectable dye (radioactive or fluorescent) and used as a probe that may anneal to molecules with similar sequences that are single stranded. Conditions are varied to detect degrees of similarity, i.e. the more stringent the conditions, the greater the similarity needed for hybridization to occur.

Low PTA ratio: normalized gene expression ratio from a biological source with low predicted transmitting ability for a particular phenotype. (See also, High PTA Ratio.)

Marker: any specific DNA segment whose base sequence is polymorphic and is used as a diagnostic tool to identify a particular phenotype or a method of detecting the presence of a linked gene. Markers used herein refer to molecular markers and markers determined by expression profile analysis.

Matrix: a support such as glass slide, silicon, gold slide, gel pad, nylon membrane or other similar structures on which an array or microarray of molecules is formed. A matrix or support may contain functional groups to attach biomolecules.

Modulating: refers to a controlled increase or decrease of transcript or protein levels of any specific gene through genetic or non-genetic methods.

Nucleic acids: DNA, cDNA, mRNA and any other modified nucleic acids. Nucleic acids also include single stranded DNA, double stranded DNA, RNA-DNA hybrids, complements and reverse complements.

Optimal subset: a selective list of genes whose expression profiles account for the greatest amount of variation in a desired phenotype, or a predetermined amount of variation. An optimal subset may include as few as one gene.

P-value: represents the probability that a deviation as great as, or greater than, that obtained from the experiment will occur by chance alone. In other words, p-value is the prob-

ability of observing a test statistic that is as extreme or more extreme than currently observed, assuming that the null hypothesis (H_0) is true.

Phenomic selection: selection of animals for breeding or production on the basis of one or more phenotypic markers that directly contribute through molecular processes to a particular phenotype. Phenotypic markers can include profiles of RNA transcripts (transcriptome), protein profile (proteome) and metabolites (metabolome).

Phenotype: the observable structural and functional properties of an organism which results from interactions of both genotype and environment. The phenotype can be exhibited in multiple levels or degrees. The term phenotype also includes improved phenotype, desired phenotype, favorable phenotype, preferred phenotype and target phenotype.

Pleiotropy: multiple effects of a gene which can result in distinct, apparently unrelated phenotypes.

Polynucleotide: any single stranded or double stranded molecule with a sequence of more than ten nucleic acids. The cDNA spots on a microarray are all double stranded, but are denatured during the process of hybridization.

Predictive genes: a subset of genes from a gene index selected to account for a predetermined amount of variation in a phenotype, based on gene expression profiles.

Printing: a process by which a biomolecule such as DNA, RNA or peptides are immobilized or attached to a matrix.

Proteome: the complete set of proteins in a cell at a given time.

PTA: predicted transmitting ability of an animal in reference to phenotypic traits; a measure of genetic merit.

Quantitative trait locus (QTL): a genomic region controlling expression of a quantitative trait, the locus may have several alleles; or two or more separate genetic loci that contribute cooperatively to the establishment of a specific phenotype or trait.

Ratio-of-ratios: ratio of normalized gene expression ratio from a biological source with high predicted transmitting ability for a particular phenotype to the normalized gene expression ratio from a biological source with low predicted transmitting ability for the particular phenotype. The ratio-of-ratios gives the absolute difference in expression for a particular gene among the two sources or groups.

Reference Expression Profile: a gene expression profile obtained from an optimal subset of predictive genes from a Gene Expression Index. Variation in expression of genes in the Reference Expression Profile accounts for all, some or a predetermined amount of variation of a trait.

Similar: a measure is similar if the correlation between it and another measure is statistically significant.

Statistical significance: statistical methods allow an estimate to be made of the probability of the observed degree of association between variables, and from this statistical significance can be expressed, commonly in terms of the p value.

Target animal (candidate animal): an animal that is potentially an elite animal.

Traits: phenotypes, e.g., genetic potential for milk production.

Transcriptome: an entire set of mRNAs and non-coding RNAs expressed by a given cell, tissue or organism.

Weighted Gene Expression Index: a list of genes organized according to a weighting factor. A weighted index can be used for phenomic selection on the basis of its ability to predict a phenotype(s). One method to create a weighted index is to multiply the p-value for a given gene (in the comparison of two phenotype classes) by the percentage of correct predic-

tions when the gene is used to identify high or low PTA animals at the population level.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows a schematic illustration of creation of a Gene Expression Index for phenomic selection of an ungulate mammal.

FIG. 2 shows a schematic illustration of phenomic selection of genetically elite ungulate mammals for production or breeding using a Gene Expression Index or Reference Expression Profile.

FIG. 3 shows that a scatter plot of the first two canonical discriminant functions (Can1 and Can2) of gene expression separates cows into high (Hi) and low (Lo) PTA groups number represent individual cow identification. Table IV shows the data for the cows.

DETAILED DESCRIPTION OF THE DISCLOSURE

Methods of the present disclosure ("phenomic selection") will enhance or replace progeny testing, significantly increasing the rate and efficiency of genetic improvement in animals.

Multiple phenotypic traits may also simultaneously be improved by these methods. Quantitative traits may be controlled either by the action of a major gene, or by many genes interacting with environmental factors. Construction of a Gene Expression Index for a specific trait permits use of that index for selective breeding. The gene expression profile for a particular trait may be linked to a single gene with a major effect or associated with a number of genes with additive effects. Premises of the disclosure are that 1) the genes whose expression levels are under artificial selection include genes that directly affect the quantitative trait of interest, and/or 2) genes that might not physically be associated with a mapped quantitative trait locus (QTL; trans effects) can be used as a reliable predictor of the trait. In other words, using "polymorphism" in gene expression levels as a correlated indicator(s), alleles that control a particular trait, despite being present at a chromosomally distinct locus or loci, will also be selected. This represents an effective approach for "marker assisted selection," because of the possible roles of pleiotropy and epistasis in determining complex phenotypes. For example, an important predictor of a complex phenotype may be the expression level of a transcription factor that is regulated by five polymorphic QTL. Monitoring the expression level of the transcription factor directly controls for many favorable alleles at the QTL level. Because individual animals will have different expression patterns for the QTL identified by expression profiling, the Gene Expression Index can be used to identify genetically elite individuals. Using this scheme, the animals with the maximum number of QTL positively affecting a trait and the minimum number of QTL negatively affecting the trait would be selected for breeding. Values might range from +100, which would represent 100 percent positively associated expression levels of all genes positively affecting a trait, to -100, which would represent 100 percent negatively associated expression levels of all genes negatively affecting a trait. This is an example of a weighted index. Selection can be performed on either sex using indices that are common to the sexes or be sex-specific. Selection can be performed at any stage of development, depending on the trait. Even embryos may be tested.

Gene expression patterns that are associated with phenotypic variation in a quantitative trait may be part of upstream or downstream regulatory pathways and are thus potential

11

candidates for drug targets or genetic modification. Expression patterns may vary both quantitatively or qualitatively to have value in predicting a specific phenotype.

The present methods can reduce the number of animals needed to achieve a production goal and reduce breeding costs. Gene expression profiles from young male calves can be tested before entry into sire evaluation programs. Young bulls whose expression profiles most closely match the "ideal" phenotype predicted by the gene index are advanced in breeding programs while those that have lower overall index values are culled from the program. The bulls' expression index value allows ranking of that bull for genetic merit, thus permitting prediction of milk yield (and other traits) among his daughters. For young female calves (heifers) the expression profile is used to predict milk production (and other traits) during the animal's individual future lactation or lifetime. Heifers that have a low expression index value are then culled from the herd. Animals may be tested in any life stage assuming tissues are available, but the index used may need to be matched to each specific life stage.

The Gene Expression Index provides information as a supplement to other traditional tools for selection. However, in cases of equal pedigree merit, the Gene Expression Index or Reference Expression Profile will help distinguish among the lines and thus lead to substantial improvements at much lower cost, and much more quickly. It is contemplated gene expression profiles could replace current statistical methods for animal breeding.

Extension of comparisons to more than two phenotypic levels is straightforward under the ANOVA approach or any other equivalent statistical method. Phenotypes for which these methods are useful are the basis of three milk characteristics, total volume of milk, total pounds and percentage of fat in the milk, and total pounds and percentage of protein in the milk. Thus, quality is as important as quantity. Producers may be paid more for protein than fat.

A suitable starting number of genes for an expression index is 10-300. The more stringent the p-value [or false discovery rate (FDR) adjusted p-value] used as a cut-off, the less number of genes that are included in the index. Sufficient number of genes need to be included to account for a large proportion of variation in each phenotype. The various factors that determine the number of genes included in the Gene Expression Index for trait analysis may depend on the technical and practical feasibility (e.g., handling of multiple genes in an array or multiple samples in a quantitative PCR), the robustness of the statistical significance of the expression data for a subset of genes that correlates with a particular trait, and nature of the trait (e.g., monogenic vs polygenic).

A method of making a Gene Expression Index for phenomic selection of elite animals such as ungulates, in an embodiment, cattle, includes the following steps: First, a phenotype to be improved is selected, such as high milk production, high milk protein levels, high milk fat, fertility, disease resistance, carcass quality. PTAs are available for these traits in many breeds of cattle and pigs. Next, a plurality of nucleic acids with measurable expression levels is selected, and hybridized to cDNAs created from RNAs of biological samples from a first group of animals expressing the phenotype at a first level, and compared to a reference standard or to other samples, directly (e.g., in a loop design). The same is done for a second group of animals expressing the phenotype at a second level. Expression ratios are then calculated for nucleic acids from each group. It is then determined whether there is a statistically significant difference between the expression ratios of the two groups (FIG. 1). A Gene Expression Index is created in which the nucleic acids (genes) are

12

ranked according to their statistical significance. Multiple groups and multiple levels are within the scope of the disclosure. The methods are extendable to more than two groups using ANOVA.

An optimal subset of nucleic acids from a Gene Expression Index is used to create a Reference Expression Profile that accounts for the greatest amount of variation in the phenotype, or for a predetermined amount of variation (FIG. 2). The Reference Expression Profile is compared to a gene expression profile created from a biological sample, such as blood or liver tissue, from a candidate (target) animal. Comparison is made by microarrays or relatively inexpensive assays such as quantitative real-time RT (reverse transcriptase) PCR, e.g. TaqMan®. An animal is selected for breeding if the two expression profiles are correlated.

A cDNA library was created using mRNA from bovine placenta. Approximately 17,000 clones were partially sequenced and are termed expressed sequence tags (ESTs). Using standard normalization and computational techniques,

10 a collection of 12,620 ESTs was selected after eliminating redundant clones. Further refinement was performed by

15 eliminating repeats, clones with bad sequence reads, clones having sequence length of less than 300 bp, and multiple ESTs representing the same gene by BLAST analysis against

20 the human UniGene databases. This reduced the collection to 7,653 ESTs representing approximately 6,000 unique genes. These 7,653 ESTs, represent ~6,000 genes were printed in

25 duplicate on a glass slide (microarray). The microarray was used in hybridization analysis of blood and liver RNA

30 samples from cattle. Based on the microarray results from cattle blood samples, genes whose expression levels were significantly different among heifers grouped by PTA for milk production were included in TABLE I. Similarly, based

35 on the microarray results from liver samples, genes whose expression levels were significantly different among the same heifers grouped by PTA for milk production were included in

30 TABLE II. Based on the microarray results from liver and blood samples, genes whose expression levels were significantly different among the same heifers grouped by PTA for

40 milk production were included in TABLE III. Thus, TABLES I-III do not contain all the genes present on the microarray. The tables contain genes whose expression levels have predictive values for the trait of interest.

An embodiment of the disclosure is a method for selecting 45 genetically elite cattle predicted to have a phenotype of interest. This is accomplished by selecting an optimal subset of nucleic acids from TABLE I or TABLE II or TABLE III (a Reference Expression Profile) and comparing against a gene expression profile created from a biological sample of a candidate animal using a microarray, or quantitative PCR or another method for determining mRNA levels in a cell, tissue or organ. Afterward, the candidate cow or bull is designated as

50 elite if the two expression profiles are statistically similar. The degree of similarity to the expression pattern obtained with

55 Reference Expression Profile provides a relative measure of genetic merit of the candidate animal.

An embodiment of the disclosure is increasing milk production in target cattle or genetic potential for milk production (in bulls and cows). This method includes selecting a gene from TABLE I or TABLE II or TABLE III or a unique combination or subset thereof, for a Gene Expression Index.

60 Furthermore, modulating expression of specific genes in the target animal is contemplated. Subsets of genes whose GenBank accession numbers listed in TABLE I or II or III are also aspects of the disclosure. TABLES I-III show genes that differ significantly in expression levels for milk production in cattle. Another aspect is a

13

group of polynucleotides (polydideoxynucleotides) selected from a group designated by GenBank accession numbers listed in TABLES I-III, for which there are no known functions. These include novel cattle genes, that is, genes with no existing human or mouse equivalent, or whose ortholog cannot yet be identified by sequence comparison.

A subset of approximately 1 to about 100 genes from the gene expression indices (TABLES I-III) can be used to predict a desired phenotype. The number in the subset is related to the contribution of any gene to the variations in the trait of interest. The greater the contribution, the fewer genes are needed.

EXAMPLES**Example 1****Development of Microarrays for Predicting Milk Production**

A microarray printed with about 7,500 cattle genes was used to profile gene expression in liver and peripheral blood leukocyte samples collected from two groups of heifers selected for significant differences in predicted transmitting ability (PTA) for milk production. The equations ("animal model") for predictive PTAs are published and used by DHIA as part of their routine summaries. The PTAs of 20 heifers selected from the extremes of the PTA distributors were obtained from the DHIA records of milk yield (also correlated with fat and protein yields). The two groups of animals were age-matched (all heifers) and of the same breed (Holstein Friesian).

The microarray for gene expression profiling included a plurality of approximately 7,500 cDNAs spotted in duplicate representing a unique gene (cDNA) set of approximately 6,000 genes (see Materials and Methods). Creation of the arrays was performed essentially as described by Brown and Botstein (1999), although any microarray production method for expressing profiles is suitable for practice of the disclosure. The genes represent amplified inserts from a cattle placenta cDNA library referenced in Band et al. (2002) as disclosed herein. A cDNA library from which approximately 17,000 ESTs were sequenced and screened to reduce redundant gene sets through computational methods. The resulting unique gene set was amplified for printing on the microarray. Not all the genes that are on the array are shown in TABLE I. Only those genes that are significant between PTA groups in blood are shown in TABLE I. TABLE II shows genes expressed in liver that exhibit significant differences between PTA groups. Table III lists genes whose expression patterns differ in both blood leukocytes and liver.

Microarray Construction

A 7,653 gene cDNA microarray was created, representing an expansion of the 3,800 element microarray described by Band et al. (2002). The microarray was created according to the methods in Band et al. (2002). Briefly, a collection of 12,620 ESTs from a normalized and subtracted cattle placenta cDNA library were used as to select all new cDNA inserts that were added to the 3800 element array. Normalization equalizes the representation of the cDNAs in a cDNA library, thus reducing the over representation of genes, whose mRNAs are expressed to higher levels. Subtraction involves the reduction in the number of new cDNA clones to be sequenced by hybridizing the previously sequenced cDNA molecules against the cDNA library to eliminate duplicates. The placenta cDNA inserts were unidirectionally cloned and sequenced from the 5' end using the M13 reverse-48 primer

14

(AGCGGATAACAATTCACAC). Sequences were trimmed of vector, low-quality reads and minimum length of >300 bp using a local script and filtered for repeats using RepeatMasker (Smith and Green, 1999). Clusters of ESTs were then created using CAP3, (Huang and Madan, 1999) using default parameters, except that 40 bp was set as the minimum size of the overlap between clones. Sequences entering CAP3 had an average Phred score of 20. After CAP3 assembly, all clusters and singlets containing sequences present on the 3,800 gene array were removed from the data set. New sequences were selected for the array using an approach that combined BLAST with evaluation of clone position in the transcript. First, all sequences were analyzed by BLASTN against human UniGene database (build 155- Oct. 25, 2002) and mouse UniGene database (build 116-October 2002) and checked for duplicates on the basis of human UniGene identification numbers of the best BLAST hits. Second, a representative clone was picked from each cluster with a UniGene identification number not represented on the 3,800 gene array (clusters without UniGene hits were also used). Clones were selected from clusters with the longest and most 3' high quality read that were available. Third, singletons with and without a human UniGene hit were selected. With the few remaining places in the rear ranged grid of clones, a low level of redundancy (for intended control) was introduced by selecting clones with stronger similarity scores to human UniGene clusters than original clones used for the 3,800 set. The total number of selected sequences for the microarray was 7,653.

Amplification of clone inserts, clean-up of PCR products and spotting of the microarray were performed as described by Band et al. (2002) with some modifications. Amplification of inserts employed M13-FWD (GTTTCCCAGTCAC-GACGTTG) and M13-REV (TGAGCGGATAA-CAATTACACAG) oligonucleotide primers (Hegde et al., 2000). After purification, PCR products were redissolved in 3×SSC supplemented with 1M betaine (Diehl et al., 2001). A row of 32 control spots was placed in every grid of the array. Controls include the endogenous housekeeping genes encoding beta actin (ACTB), glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and hypoxanthine phosphoribosyltransferase (HPRT), BLV genes env and tax, exogenous soybean control genes chlorophyll ab binding protein (CAB), Rubisco small chain 1 (RBS1) and major latex protein (MSG). Negative controls are Cot1 DNA, genomic DNA, spotting buffer, poly-A and H₂O. Duplicate spots were placed in different blocks instead of adjacent to each other as in the 3,800 gene array. This layout permits identification of the true experimental variation over the entire slide, thus facilitating interpretation of statistical analyses. Spot and printing quality were assessed on one slide by hybridizing a Cy3-labeled random nonamer (Operon, Alameda, Ca). The accuracy of the reracking, spotting and clone annotation was evaluated by resequencing the entire set of clones of the original 3,800 gene microarray and sample sequencing 8 clones per plate of the new clone set. Analysis of the sequence data revealed an error rate of 2% for the first set and 0% for the second set. Mislabeled clones were reannotated on the basis of the sequences obtained.

Functional Annotation of Microarray Sequences

All sequences were masked for repeats using RepeatMasker prior to BLAST analysis. Similarity searches were conducted for all sequences against the human UniGene database (build 166) using BLASTN. The remaining sequences with no significant similarity to human UniGene sequences (E-value threshold of e⁻⁵) were analyzed by TBLASTX against the human UniGene database followed by BLASTN

15

against the human genome draft sequence (build 34.2, Jan. 12, 2004). In all searches, best hits were used to annotate the cattle sequences as putative orthologs. Previous comparative mapping studies have shown that such predictions are at least 95% accurate (Band et al., 2000). The GO annotations associated with human UniGene numbers were parsed from LocusLink (Mar. 1, 2004 release). GeneOntology (GO) terms (March, 2004 release) were downloaded (Ashburner et al., 2000) and used for GO annotation of the sequences. Many of the steps of the process, including BLAST and GO annotation, were automated with Perl computer programs.

Example 2

Hybridization Analysis for Predicting Milk Production

cDNA samples from 10 heifers (see Materials and Methods) that were predicted to have high predicted transmitting ability for milk production based on breeding values of their parents, were tested 2 times (once with Cy3 dye and once with Cy5 dye) using a microarray slide printed with ~15,000 spots, or approximate 7500 cDNA molecules in duplicate. Cy3 and Cy5 dyes are used to label cDNAs. Similarly, cDNA samples from 10 heifers, that were predicted to have low predicted transmitting ability for milk production based on breeding values of their parents were tested 2 times (once with Cy3 dye and once with Cy5 dye) using microarray printed with 7,500 genes in duplicate. Therefore, every low PTA ratio (normalized gene expression ratio for heifers with low PTAs) or high PTAs (normalized gene expression ratio for heifers with high PTAs) shown in TABLE I or TABLE II (see Sequences for clones in Tables I and II) refers to an average of up to 40 data points. For example, every experiment involves isolating RNA from cow blood, synthesizing and labeling the cDNAs with a fluorescent dye (Cy3), and co-hybridizing on a microarray with Cy5-labeled cDNA prepared from the reference standard RNA. The experiment is replicated by dye-swapping (labeling sample with Cy5 and the reference standard with Cy3). The reference standard is produced by pooling RNA from brain tissue and three different bovine cell lines. Thus, the reference standard is the same for all comparisons. Following labeling, the cDNA samples (blood and reference standard) are hybridized to the same microarray containing approximately 7,500 gene spots in duplicates. Likewise, the experiments are repeated for other cows whose predicted transmitting ability (PTA) for milk production is known.

A “reference standard” RNA pool was created to enable comparison of expression profiles obtained using the 7,653 gene array. RNA collected from brain tissue of three cows (two Angus x Hereford and one Hereford) and the following cell lines were used to create the reference standard: B-lymphocyte cell line BL3⁰ (ATCC: CRL-8037), bovine tracheal epithelial cell line EBTr (ATCC: CCL-44; provided by Dr. M. Abrahamsen, University of Minnesota, St. Paul, Minn.) and bovine kidney cell line MDBK (ATCC: CCL-22). EBTr was grown in MEM whereas MDBK and BL3⁰ were grown in L-15. Both culture media were supplemented with 10% FBS, 100 U/ml penicillin and 0.1 mg/ml streptomycin (Sigma, St. Louis, Mo.). After checking the quality and quantity of RNA, 8 mg of total RNA from each source were mixed to create the pool and frozen at -80°C. until use. Labeling of the reference RNA with Cy3 and Cy5 and subsequent co-hybridization revealed 70% (Cy3) to 75% (Cy5) of spots were 3 standard deviations above background signal.

16

Analysis of the Data

Fluorescence intensity data were available in a total of 40 microarrays, 20 pertaining to 10 high PTA animals (including dye-swap) and 20 pertaining to 10 low PTA animals with dye-swap. Dye-swap refers to switching of the dyes used to label the cDNAs derived from mRNAs representing the high PTA and the low PTA groups. Dye-swap accounts and corrects for differences in the fluorescence intensity due to dye instability or labelling efficiency. The fluorescence intensities from half of the animals within each PTA level were obtained at the first stages of the experiment by one person and the remaining half were obtained at a later stage by another person. This potential variation was considered a sub-experiment effect and was accounted for in the model. Each sequence was available in duplicated spots within the microarray. The intensity record was the median of all pixels in the foreground subtracted from the associated median background intensity. A filtering process was implemented to remove suspicious observations and use only data that were reproducible. When the foreground minus background intensity was lower than one, the difference was set equal to one. All background-subtracted spot intensities lower than the mean plus 3 standard deviations of the corresponding slide-dye background intensities in both dye systems were removed from the analysis. The logarithmic transformation (base 2) of the background-subtracted intensities was used in the follow-up analysis. A spot intensity was removed from the data if the corresponding sample:reference ratio was extreme with respect to the rest of the ratios available for an animal, i.e. an outlier.

The Cook’s Distance (a metric for deciding whether a particular point alone affects regression estimates), a well-known influence statistic that measures the change to the estimates that results from deleting each observation (Cook, 1977) was used to identify suspicious ratios. Sequences with less than 10 sample:universal control ratios per PTA-sub-experiment group (from a maximum of 20 ratios) and with less than two high or low PTA animals per sub-experiment were removed from the analysis. A global Loess normalization based on 20% of the data in the neighborhood of each spot average fluorescence intensity was applied within slide to the remaining sequences. In addition to the within-array normalization for fluorescence intensity effects, an across-array scaling of the normalized ratios for dye effects was implemented. The resulting normalized ratios were analyzed using a linear mixed effects models and an analysis of variance (ANOVA) approach for each sequence. The model included the fixed effects of sub-experiment and PTA group nested within sub-experiment and the random effect of cow. False-discovery-rate (FDR, Benjamini and Hochberg, 1995) adjusted significance p-values of the PTA effect were obtained for each sequence and the contrast between PTA estimates represented the adjusted ratio-of-ratios due to the logarithmic transformation of the fluorescence intensities. “Ratio-of-ratios” was used to estimate the absolute differences in gene expression between the two groups.

The statistical model used was conservative and powerful for detecting differences in gene expression levels between the highPTA and lowPTA groups. LOESS transformation of the data for normalization was used. The FDR was used to reduce the number of false positives. An FDR of $\leq 10\%$ is reasonable, although higher FDR can also be used. Raw probabilities for the ANOVA are also given in TABLES I-III, in addition to FDR adjusted p-value. In TABLE I, the number of genes with effects at each FDR p-value cutoff is: <0.1 (number of genes ~50); <0.2 (number of genes ~200); and <0.3 (number of genes ~357).

The model used in calculating the difference in expression level of each gene on the array was $y_{ijk} = m + P_i + \text{PTA}(P)_{ij} + C(\text{PTA})_{ijk} + e_{ijkl}$, where y_{ijk} = log₂ transformed and LOESS normalized ratio of cow/reference intensities "I" for data set i (e.g., experiment 1 or experiment 2), PTA level "j" (high or low) nested within data set, and cow "k" nested within a PTA group and data set. m equals overall mean; P_i equals fixed effect of data set i; PTA(P) equals fixed effect of PTA level j nested within data set; C(PTA) equals random effect of cow k nested within PTA level; e_{ijkl} = random residual associated with observations y_{ijk} .

TABLE I provides gene expression data from blood for approximately 357 DNA fragments representing approximately 357 genes that have varying levels of significance in predicting a desirable phenotype (e.g., milk production).

The "GenBank ID" column in TABLE I refers to GenBank accession numbers of cattle ESTs/DNA fragments representing a cDNA clone on the microarray. In TABLE I, the data set was generated from two sets of separate experiments (e.g., first set of 10; animals; and a second set of 10 animals) and the data from the two experiments were combined to generate the gene expression profile from blood. ANOVA was performed on LOESS transformed fluorescence intensity values for the combined gene expression data (fluorescence intensity equates to expression level of a gene). The standard errors were calculated for expression data of each gene on the microarray. The "fold-change" ratio-of-ratios column in TABLE I shows the change of gene expression level of highPTA group relative to lowPTA group. The differences were transformed to a linear scale for easy comparison (a value of 1.5 means that expression level was 1.5 fold-greater in highPTA vs. lowPTA group). Comparisons are always for highPTA-to-lowPTA ratio-of-ratios. The "ratio-of-ratios" is calculated by dividing the "high-PTA-ratio" by "low-PTA-ratio". This quotient, referred to as the "ratio-of-ratios," represents the ratio of high-PTA-ratio to the low-PTA-ratio values. The normalized ratio is calculated as follows:

- 1) compute the log 2 (tissue/reference) (after background subtraction and removal of spots<3SD)
- 2) normalize the log 2 ratio using Ab binding gene
- 3) find the average of normalized log 2 ratio for all spots pertaining to the sequence

The "raw_pvalue" column shows the probability estimate of ANOVA for difference between high and low PTA groups. The "FDR adjusted p value" column shows the FDR for ANOVA as disclosed herein. The FDR was calculated for the combined data (from experiment 1 and 2), unless a gene's expression data was absent in either experiment 1 or experiment 2.

In TABLE I, the "Gene Name" column provides a descriptive name of the gene associated with that particular GenBank accession number. Other details of the gene can be obtained from the GenBank database by using the appropriate GenBank accession numbers. The "gene symbol" column provides relevant gene symbols if available. The gene identification was determined by BLAST analysis of the cattle sequence on the microarray against the public domain DNA sequence databases. If a human gene was identified, the human gene name was given. If there was no similarity to a human gene, but significant similarity to a gene from another species (e.g., mouse), then gene name was given from the species with the highest significant BLAST score. The "GenBank ID best hit" column provides GenBank accession numbers of nucleic acid sequences that returned the best similarity when compared against the cattle sequences. A GenBank ID representing a cattle sequence will appear only if there was no hit in the human or mouse genomes. The "UniGene" column

provides identification numbers for the best hit of cattle sequence on the microarray against human unigene databases. Human UniGene release 166 (Jan. 12, 2004); Mouse UniGene release 135 (Feb. 27, 2004); human genome Build #34.2 (January 2004); Cow UniGene Build 55 (Mar. 9, 2004); TIGR9 (Sep. 3, 2003); LocusLink of Mar. 1, 2004 were used to update the "UniGene" column.

In TABLE I, for genes differentiated expressed in blood samples, the list was sorted based on the FDR adjusted p-value. Presumably, the genes appearing on the top of the list have a higher predictive value compared to those appearing at the bottom of the list. The order of the genes in the list may vary depending upon the trait tested and tissue analyzed. However, the genes in the list provide a statistically robust method for milk yield using gene expression data.

TABLE II shows the data and calculations, based on liver samples, using similar column headings as used for TABLE I. Testing and analysis of gene expression ratios as described for blood samples in TABLE I were performed using liver samples. TABLE II provides a list of 10 genes, whose expression profile in liver is predictive of high milk production and associated traits in cattle.

TABLE III contains a list of genes expressed in both liver and blood that have significant effects on PTA. The analysis was done as described for the blood data in TABLE I. The gene expression levels from both blood and liver predict PTA across various tissue types. This provides confirming evidence that these genes are involved in regulating the traits of interest.

In TABLE III, the "contrast blood" and "contrast" test statistics column provides a comparison between two levels (i.e. transformed and normalized estimated ratio of cow:reference intensities) of an independent variable (PTA high and low) for blood and liver samples only. ANOVA was performed on LOESS transformed fluorescence intensity values. Standard errors were calculated. The "raw p-value blood" column represents an unadjusted p-value for ANOVA of blood data. The "contrast liver" column represents a comparison between two levels (transformed and normalized estimated ratio of cow:reference intensities) of an independent variable (PTA high and low) for liver samples. ANOVA was performed on LOESS transformed fluorescence intensity values. The "raw p-value liver" column provides an unadjusted p-value for ANOVA of liver data. The "Gene Name", "Gene Symbol", "GenBank Best hit" and the "UniGene" columns are as described for TABLE I.

The genes in the list provided in TABLE III are arranged based on the raw p-value for both blood and liver. For example, a listing in TABLE III was generated by comparing genes with raw p-values of ≤ 0.10 for both blood and liver. The genes appearing on the top of the list have a higher predictive value compared to those appearing at the bottom of the list. The order of the genes in the list may vary depending upon the trait tested and tissue analyzed. However, the genes in the list provide a statistically robust method (see peripheral blood).

Results from the analysis of fluorescence intensities collected from high and low PTA animals were used to identify the sequences with the highest potential as biomarker predictors of PTA level (FIG. 3). Only genes significant at FDR-adjusted p-value<0.1 (50 genes) and with information on all 20 animals (14 genes) were considered repeatable and highly likely to be true positives. The predicted values for the 20 animals from the linear mixed effects model corresponding to genes represented by the 14 sequences (AW461980, AW464526, AW465165, AW465571, AW466043, BF039168, BF044446, BF044893, BF046007, BF046202,

19

BF440243, BF440261, AW466044, BF039212) were used in a discriminant analysis to identify the sequences that can most accurately classify animals into high and low PTA groups. These 14 genes define an optimal subset to create a Reference Expression Profile for a candidate mammal. A stepwise discriminant analysis (Klecka, 1980) further reduced the number of genes used to distinguish PTA groups to five represented by Gen Bank (AW466043, BF044446, BF039168, BF046202, AW461980). Stepwise selection started with no genes in the model and in an iterative process, the variable that contributed most to the discriminatory ability of the model was entered and the ones that contributed least and did not meet the statistical criterion (*p*-value<0.15) were removed. Disjoint cluster analysis using Euclidean distances, also known as k-means model, divided the animals into clusters with centers based on least-squares estimation. Canonical variables were used to depict the cluster of animals based on the selected sequences (FIG. 3). Canonical discriminant analysis was used for the purpose of graphical representation of the cluster of cows by PTA group. Canonical discriminant analysis is a dimension-reduction technique that finds the linear combinations of the quantitative variables that provide maximal separation between the classes or groups (SAS online manual 2002, The SAS Institute Inc.). This approach successfully discriminated animals by PTA.

Example 3

Developing a Gene Expression Index for Phenomic Selection

The expression profiles of the genes in high PTA cows and low PTA cows (TABLES I-III) were ranked according to their *p*-values or FDR-adjusted *p*-value, i.e. gene expression profiles represented in TABLES I-III were classified based on statistical significance. For example, in blood samples from cows with predicted transmitting ability for high and low milk production, a total of 357 genes (or partial DNA fragments representing those 357 genes) were found to differ significantly between the groups at <FDR adjusted *p*-value of 0.29 and approximately 25 genes at <0.051 FDR-adjusted *p*-value (TABLE I). Any other relevant statistical method can be used to rank the genes.

In liver samples from cows with predicted transmitting ability for high and low milk production, a total of 10 genes were found to differ significantly between the groups at ≤ 0.4 FDR-adjusted *p*-value (TABLE II). The genes listed in TABLES I-III are part of a Gene Expression Index useful for identifying a candidate animal as predicted to be elite, that is, to have increased (high) milk production.

These results demonstrate that genetically elite cows can be identified prior to their first lactation on the basis of gene expression profiles of liver or peripheral blood leukocyte RNA. When applied to bulls, this method may enhance or replace progeny testing, significantly increasing the rate and efficiency of genetic improvement by breeding. Multiple phenotype traits may be improved simultaneously using this method. This method is generally referred to as phenomic selection.

Example 4

Developing a Weighted Gene Expression Index for Phenomic Selection

Based on the expression profiles of all the genes in the microarray, a Gene Expression Index is developed, where the

20

genes ranked higher in the index according to statistical significance between high and low PTA for milk production (or any 2 levels of a different trait) account for a greater fraction of the phenotypic variation in the trait. More levels could also be added. One method to further refine the Gene Expression Index is to create a weighted Gene Expression Index. This is accomplished by comparing actual milk production records from the high and low PTA cows from genetically distinct backgrounds and in different herds to their gene expression profiles for the genes in non-weighted index. Weighting of the index is accomplished by ranking the actual production values or PTAs of cows or bulls in the population and adjusting the *p*-value-based ranking of individual genes by a defined multiple. The weighted index can then be used to rank candidate animals in a breeding program. The genes with a greater weighted average will have the most predictive power for the trait, such as high milk production.

Example 5

Identifying a Candidate Animal for Selective Breeding

Expression profiles of genes selected from a gene index are evaluated in the cattle population for their ability to predict high milk production. The RNA isolation, synthesis of cDNA and labeling are performed as described in MATERIALS AND METHODS. Hybridization can be carried out with a microarray containing genes selected from the disclosed gene index. Alternatively, particularly useful at field level, quantitative PCR analysis for measuring gene expression or an equivalently sensitive method can be performed for a limited number of genes selected from the gene index. For example, quantitative real-time RT (reverse transcription) PCR analysis is less expensive for a limited number of genes and diagnosis is portable.

Following microarray hybridization or quantitative PCR, the expression profiles of tested genes are compared to the expression profiles of genes in the Gene Expression Index or Reference Expression Profile (FIG. 2). Similarity of the expression profile of a sample from the candidate animal to the Gene Expression Index indicates higher probability for increased milk production.

The Gene Expression Index and the weighted Gene Expression Index disclosed herein can also be used to identify bulls for predicted transmitting ability for high milk production. This is based on the premise that a strong selection pressure for increased milk production must have influenced the fundamental gene expression pattern, and this gene expression pattern that correlates with increased milk production must be present in bulls as well. Consequently, the gene expression indices disclosed herein can provide a basis to correlate expression profiles from cows at the population level, as well as a specific bull's daughters for increased milk production. Therefore, the need for expensive progeny testing can be minimized. An aspect of the disclosure is that blood, indeed any tissue for which expression profiles can be obtained, at any stage of development, can be used for creating the index. With complex traits such as lactation that involve hundreds of genes, many of which will be involved in intermediary metabolism, RNA levels of such genes are expected to be consistently different in animals of different PTA levels. That is, an animal with a high potential for milk

21

production would have a different "metabolic set point" that is reflected in leukocytes as well as in other tissues.

Example 6

Identification of Novel Genes Involved in Milk Production

Several genes with differential expression levels in high milk producing cows and low milk producing cows were identified through a microarray analysis. Based on the sequence information of these genes, several genes do not have counterparts or functional annotations in humans and may represent genes unique to milk production in cattle. The data provided in this disclosure presents an insight to analyzing functions of several unannotated genes.

Example 7

Genetic Manipulation of a Desired Gene

A method to manipulate gene expression in a ungulate mammals is through in vitro fertilization of a genetically altered egg followed by an embryo transfer. Methods to generate transgenic ungulate mammals include microinjection of DNA into the oocyte under conditions which permit the transfection of the oocyte, and contacting the transfected oocyte with sperm under conditions which permit the fertilization of the transfected oocyte to produce an embryo. Following the fertilization of the transfected oocyte, the embryo is transferred into a hormonally synchronized non-human recipient animal generally of the same species (i.e., a female animal hormonally synchronized to stimulate early pregnancy). The transferred embryo is allowed to develop to term. A transgenic offspring is then identified based on the expression of the desired gene or by detecting the presence of a recombinant protein. An altered gene expression or a difference in the amount of protein indicates a successful gene transfer to generate a transgenic offspring expressing a desired characteristic such as increased milk production. Genes suitable for manipulation through transgenesis are those disclosed herein.

Example 8

Selecting for Traits in Dairy Cattle and Beef Cattle Using a Gene Expression Index

The following are traits other than milk production that are suitable for developing gene indices for cattle selection:

A. Dairy Cattle

1. Health Traits in Dairy Cattle

The primary problems are mastitis, digestive and reproductive disorders. Use of antibiotics and drugs is already limited for lactating cows. Therefore the ability to predict better health traits in breeding cows is valuable for the dairy industry to minimize economic losses due to diseases. Adequate evidence indicates that the variability in disease incidences and health disorders is under some degree of genetic control.

(a) Somatic Cell Score:

Somatic cell concentration is a quantitative trait in cattle with moderate heritability and is apparently affected by many different loci. Somatic cells in milk consist primarily of leukocytes and neutrophils secreted in response to invasion by an infectious pathogen. Somatic cell counts in milk serve as an indicator of udder health and are elevated during mastitis infections. Research has indicated that somatic cells in milk are elevated when heifers give birth to their first offspring,

22

although clinical symptoms may or may not be present. The relative roles of pre-calving infections, or even calfhood infections, environmental stressors, or onset of lactation in causing elevated cells counts is not clear. Correlations between somatic cell score and mastitis infection and QTL are available. The methods to create gene expression indices disclosed herein can be used to predict somatic cell counts in cattle and to predict disease resistance for mastitis infections.

(b) Immunity:

Overall immunity is a measure of healthier and longer productive life for cattle. The methods for creating gene expression indices disclosed herein can be used to estimate the predictive transmitting ability for disease resistance in cattle.

(c) Fertility and Longevity:

Reproductive traits such as fertility can also be predicted using the methods of the present disclosure. Longevity of dairy cattle is a result of overall fitness and a Gene Expression Index can be used to predict longevity of the animal in a herd.

Correlations between somatic cell score and fertility in dairy cattle have been detected and can be used with a gene according to the present discussion to predict longevity.

2. Type Traits in Dairy Cattle:

The standard type traits that can be used in methods for creating the gene expression indices disclosed herein include stature, chest, width, body depth, angularity, rump angle, rump width, rear legs set, rear legs rear view, foot angle, fore udder attachment, rear udder height, central ligament, and teat length.

B. Beef Cattle

In addition to some of the traits such as health, disease resistance, and reproductive fitness, beef cattle are selected for higher carcass and meat quality and growth traits. Beef cattle traits may also include customer satisfaction traits, such as marbling, tenderness and composition. These beef traits can also be predicted using methods of the present disclosure.

Example 9

Phenomic Selection for Traits in Swine Using a Gene Expression Index

Health traits including immunity or disease resistance (e.g., resistance to intestinal *E. coli* associated diarrhea), reproductive traits such as fertility, and meat quality (tenderness and intramuscular fat content) in swine (an ungulate mammal) can be predicted using the Gene Expression Index methods disclosed herein. The methods described herein for analyzing PTA for milk production in cattle can also be used

to evaluate PTA for the above-mentioned traits in swine. These methods include isolating a suitable tissue sample such as blood from swine and comparing the expression profiles of genes from the swine samples with reference to a Gene Expression Index created by methods disclosed herein. Boars and sows with superior genetic merit as assessed by comparison to the relevant expression index, can be used for selective breeding.

Example 10

Analyzing Phenotypic Traits in Sheep/Goats Using a Gene Expression Index

Analyzing traits in sheep or goats (ungulate mammals) includes predicting traits for better meat quality, increased milk production, wool quantity and quality and other health traits such as immunity or disease resistance and fertility. The

methods disclosed herein for analyzing PTA for milk production in cattle can also be used to evaluate PTAs or phenotypes of the above-mentioned traits in sheep or goats. These methods include isolating a suitable tissue sample such as blood from sheep or goats and comparing the expression profiles of genes from the sheep or goats samples with reference to a Gene Expression Index created by methods disclosed herein for a specific trait. A high correlation of the trait with the expression of genes present in a Gene Expression Index created by methods disclosed herein indicates superior genetic merit for the chosen trait. Sheep, goats, deer, horses and other ungulate mammals can be selected for breeding according to the methods of the disclosure to improve production efficiency, health and profitability.

Example 11

Race Horses

Racing ability in horses can be predicted by creating a Gene Expression Index and comparing gene expression levels in horses that have known racing ability, or phenotypes that are correlated with racing ability. Gene expression profiling is performed on RNA collected from muscle tissue collected from foals. When the horses reach racing age, the patterns established when they are foals is correlated with racing ability or racing-related traits (e.g., speed). An index associated with speed can therefore be established. Candidate foals are then tested at birth and the patterns most closely matching the patterns of horses with greater speed can be identified.

Materials and Methods

Experimental Animals. A total of 20 Holstein Friesian dairy heifers were selected for study, 10 with extreme low breeding values for milk production and/or composition traits and 10 with extreme high breeding values. All animals were housed at the University of Illinois Dairy Farm, operated by the Department of Animal Sciences. A cow's genetic merit is determined from the predicted transmitting ability (PTA) of her dam, and the daughter yield deviation (DYD) of the sire. Only offspring of sires and dams with high accuracy predictions (>0.80) were used. Blood and tissue (liver punch biopsy) samples were collected in pairs (one high potential, one low genetic potential). All samples were collected at the same time of day, in the same season, all prior to the heifer's first lactation. Animals were fed identical diet and housed under identical conditions.

Total RNA purification for gene expression analysis. Two tissues were sampled from each animal: peripheral blood leukocytes and liver. Liver tissue was collected using a standard approved biopsy procedure. Total RNA isolation was performed using optimized protocols developed for this project. Briefly, blood samples were collected in a 250 ml bottle containing 100 ml of 0.5M EDTA and mixed well. The sample was thoroughly mixed with an equal amount of a lysis buffer (8.9 g NH₄Cl, 0.1 g KHCO₃ in one liter of H₂O) and centrifuged at 3,500 rpm for 10 min at 4° C. to separate blood leukocytes. The procedure was repeated with one-third the amount of the lysis buffer until clean leukocytes were obtained. Liver biopsies were collected and stored in liquid nitrogen and/or RNALater (Ambion, Inc., Austin, Tex.). Frozen liver tissue was ground into fine powder in liquid nitrogen using a mortar and pestle. Tissue preserved in RNALater was cut into small pieces before being used for RNA isolation. Total RNA was extracted using TRIzol reagent (Life Technologies, Carlsbad, Calif.). Briefly, each sample of leuko-

cytes or liver was homogenized in TRIzol using a mechanical homogenizer, debris was precipitated by centrifugation and discarded. The RNA was further purified by extractions using chloroform, acid phenol:chloroform, precipitated by adding isopropanol, and incubated at -20° C. The isolated RNA was cleaned using 75% ethanol, resuspended in RNA storage buffer, aliquoted and stored at -80° C. until use. The integrity of total RNA was examined by denaturing agarose gel electrophoresis. RNA concentrations and purity were measured by spectrophotometry.

RNA probe labeling. RNA labeling procedures were adapted from Hegde et al. (2000) with modifications. Based on the optimized protocol disclosed herein, 10 µg of total RNA for each sample were used for each labeling reaction. In a typical 30 µl reverse transcription reaction, 10 µg of total RNA in 7.5 µl is mixed with 1 µl of oligo (dT)s (2 µg/µl) and 1 µl of exogenous control gene mix, and incubated at 70° C. for 10 min. After cooling on ice, 15 µl of labeling buffer is added followed by 3 Ill of Cy3-dUTP or Cy5-dUTP, separately, 2 µl of SuperScriptII (200 U/µl) and 0.5 µl of RNasin (40 U/l). The mix is then incubated in the dark at 42° C. for 2 h. Each of the labeled Cy3- and Cy5-dUTP reactions are purified separately using a column purification system (QIAGEN, Valencia, Calif.).

The length of labeled cDNA and the quality of the paired probes was examined by electrophoresis. The probes incorporated with Cy3 and Cy5 are measured using spectrophotometry. Total dye incorporations are calculated using the following formula: Cy3-dUTP (pmol)=(OD₅₅₀× volume)/(E₅₅₀×10⁻⁶); and Cy5-dUTP (pmol)=(OD₆₅₀× volume)/(E₆₅₀×10⁻⁶), where E₅₅₀ is the molar extinction coefficient of Cy3 (150,000 cm⁻¹ M⁻¹) and E₆₅₀ is molar extinction coefficient of Cy5 (250,000 cm⁻¹ M⁻¹).

Hybridization to microarrays. Prior to hybridization, the arrays were treated with prehybridization buffer (5×SSC, 0.1% SDS and 0.1% BSA) by immersing into the prehybridization solution at 42° C. for 45 min. The prehybridized slide was then washed five times by sequential dipping in MilliQ water at room temperature with a final dip wash once in isopropanol. The washed slide was spun dry at 500 rpm for 1 min and used immediately for hybridization. The purified labeled probe was combined with 20 µg of bovine Hyblock DNA (Applied Genetics Laboratories Inc., Melbourne, Fla.) and 1 µg of poly (A) in µl volume. This hybridization mix was denatured in a water bath at 95° C. for 3 min and subsequently mixed with an equal amount of 2× hybridization buffer (50% formamide, 10×SSC and 0.2% SDS) and hybridized at 42° C. overnight in a CMT-hybridization chamber (Corning, Inc. Corning, N.Y.) using a LifterSlip (Erie Scientific Company, Portsmouth, N.H.) for each array slide. The hybridization chamber contained a small piece of moist filter paper next to the array to maintain proper moisture. The chamber was sealed and incubated at 42° C. in a water bath in the dark overnight. The hybridized slide was washed in a buffer containing 1×SSC and 0.2% SDS at 42° C. for 5 min with agitation. Then it was washed in a second buffer containing 0.1× SSC and 0.2% SDS at room temperature for 5 min with agitation, followed by a third wash in 0.1×SSC at room temperature for 5 min with agitation. The slides were spun dry at 2,000 rpm for one min after final wash before they were scanned. All samples were hybridized to duplicate slides and repeated with reverse labeling for a total of 2 slides, or 4 spots per gene per experiment. Slides were scanned for both dye channels using an Axon 4,000B Scanner (Axon Instruments, Inc., Union City, Calif.) and data acquisition was done using Gene Pix 3.5 and raw data saved in files of gpr format.

25

Spiking control using exogenous nucleic acids. Exogenous nucleic acids were spiked into labeling and hybridization reactions for use as a reference for normalization and validation. The spiking control consists of three soybean (*Glycine max*) genes, photo system I chlorophyll ab binding protein (Cab), major latex protein (MSG), and ribulose bisphosphate carboxylase small chain I precursor (RBS1). The polyadenylated RNA of the exogenous nucleic acids was prepared by in vitro transcription using MAXIscript (Ambion, Inc. Austin, Tex.) and quantified by spectrophotometry and gel electrophoresis. One microliter of spiking control contains 10, 100 and 1,000 µg of mRNA from MSG, Cab and RBS1, respectively.

TaqMan® Analysis. One microgram of total RNA from each sample was denatured at 70° C. for 10 min and reverse transcribed in 20 µL reactions containing 500 ng oligo-dT primer, 500 KM dNTP, 100 µM DTT, 40 U RNasin, 1× first strand buffer and 200 U reverse transcriptase (SuperScript II, GIBCO BRL, Rockville, Md.) at 42° C. for 1 hour. Quantitative PCR was carried out on an ABI7700 PRISM sequence detector in 25 µL reactions containing 1× Quantitative PCR Universal PCR Master Mix (Applied Biosystems, Foster City, Calif.) 1 µL cDNA, 200 nM each primer and 100 nM probe. The PCR protocol consisted of denaturation at 95° C. for 9 min followed by 40 cycles of 95° C. for 15 s and 60° C. for 1 min. All reactions were carried out in triplicate. Standard curves for both target and reference genes were constructed using 2-fold serial dilutions of adult spleen cDNA. Relative amounts of transcripts are calculated.

26

p-values. p-values represent the probability that a deviation as great as, or greater than, that obtained from the experiment will occur by chance alone. In other words, p-value is the probability of observing a test statistic that is as extreme or more extreme than currently observed, assuming that the null hypothesis (H_0) is true. This can be expressed as the conditional probability $P(\text{data}/H_0 \text{ true})$, where "P" is read "the probability of" and "/" is read as "given" or "conditional upon." If the p-value is small, it is concluded that the deviations are not entirely due to chance, and the null hypothesis is rejected. If the p-value is greater than the predetermined value (e.g., 0.05), the data confirm reasonably well with the predictions of the hypothesis, and the null hypothesis is accepted.

15 False Discovery Rate: This method is used to adjust for multiple comparisons by setting an acceptable proportion of false positives for an experiment (Benjamini and Hochberg, 1995). In this case the p-values are ranked in increasing order of p_i ($p_1 < p_2 < p_3 \dots < p_m$, $m = \text{total number of comparisons}$). The p-values for each comparison are then sequentially compared to an adjusted cutoff for each p_k equals to $(\text{FDR})^*(i/m)$, where FDR=the false discovery rate. The null hypothesis is rejected for any comparison in which $p_k < (\text{FDR})^*(i/m)$, until a comparison is made in which the observed p-value is greater than the adjusted cut-off. All larger p-values ($p_k \dots p_m$) are not statistically significant. If the smallest p-value yields a false discovery rate higher than the selected FDR, the null hypothesis cannot be rejected for any test.

SEQ. ID. NO:1 BM362588
GCACGAGGGGGATCGAGGGGAGCAGCGTACGGTGAAGGACACAGGGCGTGGAGTTGAACCCCT

TGAAAGATTGAAATCATGGCAGGTGCAGAACGTCGATGCCAGTTCACTGGTATCAAAAAAATTTCA
ACTCTTACACTCTCACAGGGAGAATGAATTGTGTGCTGGCACATACGGAAGTATTGCTTGATAGTCTTATA
CTTCAAGTTAACGGTCTAAAAAAACTCCAGCTGTGAAAGCAACATAACAGATTCTGAGCTGTACATTCTGT
TAAGTTCCCATGCCTGAAGAAGCTAATGTCAACTCATGTGATACTCAATTGTACAATAATTATGAACC
TGGAAAAAAAAAAAAAAAAAAAAAAA

SEQ. ID. NO:2 BF440243
TTTTTTTTTTTTTTGACTATCTACAAAATTATTGTCTATTACAGAAGAAAAGCATGCGTATCA

TTAAACAAATAAAATGTGTTTCTCACAGCGCAGTACATTTNNNNAAAAAAATTTTAAAGCTGTATCA
CAGAAACAAGACACAAGGTTTAAAGAGCTAACACTCATTCAGGGTCAACTCATGGACATG
AGTCCTGAAACACAGTTGCACGCATAAGGCATTGCAACCAAAGAGATCTGGTTTATTCGGCAGCCCC
TGCATTCTGATGTATGGTCTCTGNNNGTTCGAATTGCCATTATCCACAAAGATTGCAAACGTGAACCTGATA
CGGATCTGACGCCCTAAACAAACCTCCCTNNAAACTGGCTGCTCATGCGCAGTCACTGACAGTCGTTCC
ATCTCTCAAACGCAAGGCCACCATCACGAGATCTACCTCCATCGCTGNNTATTAGAATCTGAATAGGTC
CCCGAGCACGAGAATCTTATCATCCACCATGCTCAAACGCTGGTAGTAAGTA

SEQ. ID. NO:3 BM361928
GCACGAGAGCCGGCGTCAGAGGAGTGCAGACGCTGCTGGTGACCCGTGGCGCTCTGTGGGG

CCAGGAACGTAAAGAGAGC AAAATGGCTGAAAATGGTATAATGAAAAAATGGCTGCTCTGGAGGCCAAA
ATCTGTGATCAAATTGAGTATTATTTGGAGACTTCATTTGCCACGGGACAATTTAAAGGAACAGATCA
AACTGGATGAAGGCTGGGTACCTTGGAGATAATGATAAGTTAATAGGTTAACCGTTAACGACAGACT
TTAATGTAATAGTAGAGGCCCTGAGCAAATCAAAGCAGAACTCATGGAAATAAGTGAAGATAAAACTAAA

-continued

ATTAGAAGATCTCCAAGCAAACCTCTCCCTGAAGTGACTGATGAGTATAAAATGATGTAAAAAACAGATCT
GTTTATTAAGGCTTCCCACAGATGCAGCTCTGATGACATAAAAGAAT

SEQ. ID. NO:4 BM364471
GCACGAGCGGGAGAGCGGCACCCACACCGTGTGTCGGCGGTGAGTCCCGCCAGCCGAGCTGC

ACGTCCCAGCCCCGGGAGACCGGAAAAACCGAAGGACCTGGATTCCAGAGCAGTCGCCGCTGACTG
CTGCTCTCCTGCCGTTGCCGCGGGCTCCGACTCGCCGCTGAAGACCGGCCCTGACAGGCCTAGA
GCCCTAGGCGGCCCTCCGAGCCGACGTGTGCCGCGGTGCACTGTGAGTAATCGAGCGCTCTCC
ACGGCCGTTACAGATTAAATGGAGGAATTCCCTGGCTAACCTGGATACTAACAGCTGGAGGCCATCG
CTCAGGAGATACGTAGACCTGATAGAGGATTCTGTTGGCTCTGCTTGAGGTGCACCGGGCAGTC
GTGCGCTACTCTCACCTGGAAATCGCAGAGACTGGTAACGTGAAGGATTGGCATTAGCCAGTTGAAGAT
AAAGGAGCGTGTGCCCTCCGCTTGCTCCCTCCGGAGAATCTGGGAATGGCCTGATCAGCAGC

SEQ. ID. NO:5 BM365159
GCACGAGATGGCGCTGTGAAAAAGCTTGTGGCGAAGGGGGCAAAAAAAAAGCAAGTC
AAATTCACTCTGAACTGTACCCACCTGTAGAAGATGGAATCATGGATGCTGCCAATTTGAGCAGTTCTC
AGGAGAGGATCAAGGTGAATGGAAAAGCTGGCACACCTGGCGCGGTGTTGTAACAATTGAAAGAAGCAAG
AGCAAGATTACTGTAACCCGAGGTGCCCTTCCAAAAGGTATTTGAAATATCTTACCAAAATATTGA
AGAAGAATAATCTACGAGATTGGTACCGTAGTCGCTAACAGCAAAGAAAGTTACGAATTGCGTTACTCC
AGATTAATCAAGATGAAGAAGAGGAGGAAGATGAGGATTAACACTCAATCTGGAAATTGATAAGTTCTT
AAATAAAATTATCAACTGAAAAAAAAAAAAAA

SEQ. ID. NO:6 BM365446
GCACGAGGTTGATGCTCTGTATCTGATGCCCTGCGCGTCGAAAGTAAGCGAGCTCCAGAGGAGTG
CGGAGAAATTCAAGTCTTCTGCTGTAACCTCATCAGCCGCCAAGATGGCGATGCAAGCGGCCAAGAGGG
CGAACATTGACTTCCACCAGAAAGTAAATGGATTGTATATAAGAAATTGCTTACAAATCACAGCTGA
AGAAATGTATGATATATTGGAAATATGGACCTATTGTCGAAATCAGAGTGGGAACACACTGAAACTAG
AGGAACAGCTTATGTTGAGGACATCTTGATGCCAAGAATGCATGTGATCACCTGTCAGGATTCAAT
GTTTGTAACAGATACCTT

SEQ. ID. NO:7 BM365732
GCACGAGGGACGCCATGGCGACCAACATCGAGCAGATTAGGTCTTCGTGGTCAGTAAATTCCG
GGAATTCAACAGGAACATCAAGTGGAAAGGAGTGAAGGACAGCTCAATGGTAAACAAACACCTATTG
AAGGAAACAGGCAGGTGATGCAGCTGCCCTGCCAGGAACCTACCAATGAAGACATAGTTCAAGATA
GAGGAAGTACTTCTGGGTCTTAGATACAGAATTACGATATAAGCCAGACTGAGGAGGCATCCAGAAAA
AGTAGATGTGTCGTCCAAACAGATCCTACTGATGAAATTCTACNNNAAGTCGAAGAAGCATAAAAG
CACAAAAAA

SEQ. ID. NO:8 BF046007
TCTCTGCTGCAGTGGCCACACCCATCCCGCCATACCGGCCCTAGCCTGGCTGCCACGGCGCC
GCACCTGCCGGGCTGCCCTAGAGGCGGAAGATGTTGAGCGGGCACGGAGGATCCAGGCCTACTGGCCT
AGTCGGGCGAGAGCGGAAGGCCACGTGGTTCTCAGGCGCAGTGGAGAAGACGCCAGGATCCAGGCT
CGCCCTGCTGCAGCGCAGGCCCTCGGGCCCTGTGCTGCCAGTGGTTCCAGAATGTCAGTAGATG
AGTCCTGACACACAGGATTAGTTAGTGTGCCAGAAGATTCCAGGATGACTGAAGCTAACCTCTGGTGA
AGAGGACATGACAGGGATGGAACGAAAGCCTCAGGACCCGGTTGCCCTTTAACTGGCAGTGCCTG

-continued

ACACTGAAGTAACTGAAAATACCACCTTGTCACTGGAGCCGTCCTTAGAATAAGACCTGTTGCCAGTAAAG
CTGTCTTCATCTGTGCGGATCTACAGAGTTGGAGAGAACAAAAAA

SEQ. ID. NO:9 BF044446
TTTTTTTTTTCTTCTTGTCCCCGTCCTCTTCTCCTCTCATCTGAGCCAACATCTCTA
TCCTCGGGCTTGTCAAAACTCCTTTCTTCTCCTCTCTTCTCTTGTNTTCCTCTGCTTCATC
ATCACTAACTCTTATCACGTCTTCCACCTCAAAGGAGGACAAATCTGTCACCTCTCCATCACAAA
CCGGGGGAAAAAGCTAAAGGAGACTGCAGCACTTACACCAACGCCACCTG

SEQ. ID. NO:10 BF040826
TTTTTTTTTTTAAGGCAACAAAAGCTICAATCTCTCTCAAGTAAACAGAACTAGTACAGTAT
ATTATTTCTGGAACATGTACCCCCGGAGAAGTAACACAAGAGTTAAGGGGGCTCTGAACACACTCA
CACACTCCCCCTACCCCAATGAACCAAGTCTCTCTCACACCCACGACACACAGAGCTATTACAGGCGCA
AATGTATACTATGTACAAACACACAGATCCGGTTTCCCCTCAAGTCTCTGGCAGACTGCCACCAGAGAG
GAGGGATGGGCTAAGGAAGGGAAAGAACAAAGAACAGTCTCTGAAGGAACCAAGCTGAGCCGTGAGT
TGTGAGGTGCTTAGGGCGTGTCTTCTCGTATTCCAAGATGCGCATTGTAGAGTTGGGGTTGGCGGTT
GGAATCAACAAAAGGAAACAAAAGAACCCGAGGAGAATGGTGGGATGGATACGAGTGACAGGTTGG
GCCAGNGACAGAGATGCTGAGCGTTCACACAGAGACTAGGGCAGGAGGAAAGTGCAAATCGAGGCAA
CGTGTGAGCTTCTTGTTGATTGGGTGC

SEQ. ID. NO:11 BF039212
GCATTTGTTTTTTTTTTTTAAGAGGCAAGTCTGTTCCATGAACCGTGTCTCCTTAAAG
CTCTGGGGTTGGGGGACGATCATGGCTGAGCGCTGGACAAACCGAGGGTACAAACACATCTCGGA
TGTGGTATCTGTCCAGAACATCCAGGTTAAGAATCGTCCAAGCCAGGCCATAGCCGCATGTGGACACGTGC
CATATTTCTCTGATCCGTGACAGTAAATAGGGAGTGGGATCAATCCCTCTCTTTGTAACCTGCCAGGATC
TCTTCATTATCCCAGATAKGATGGAGCCACCCACGATCTCACCAACATTGGGCATCAACACGTGACAGATT
CGGTGAGCCGGGGTGTGACGGAGCGCGCCTTCANNATTGGACATGTTCTCCCGCGGATCATCATGTGT
CTGTTGAGCTGGACG

SEQ. ID. NO:12 AW461477
TTTTTTTTTTTTTTTGAGGGAAACATAAGCAGAGTGGCGTCACTGGTTATTGTATTCTGAA
GTGTCATGGGGGGCCGGGGAGGGGTGTGAAAACAAGCCTGCTTATCAGCAGTCTAAAGCCTTATCACCT
GAGATTTGCATTCTGAAACAAAATCATGATTGAGTATCAGCACATATGTCCTGTGAGATCTGGGTTCCAGC
CCTGGTGGATGGCTGGACTAACCTGACGTGAGGTAC

SEQ. ID. NO:13 AW464361
ATCCGACCACTGAGGACTGGCATCTCGCTCAAGCCCCAGAGTCTGGCGGGACACCGGACTGG
CCAGGCCAGCTGGGGCCCCGCTGTAGCTGCCAAAGGAGAAGGAAACACGNNCCTGGAGCTNNCACCA
AGCGGGTGCNNNCCGCCACCGAACCGCAGAGTCTGCTTCTNNCCAGTGAGGAGCAGCGTGTGAG
GTGCAGCCAAACGGGGACAAAGTGAACAAACGCCGCTGCCCGAGTCACACTCAGNCCGTAGTACACCTCCG
AGAACAGGAGCTCCCAGGGACAGACGAGCAGCCTGTGCCGAAGCTCGTGGCA

SEQ. ID. NO:14 AW466044
GTTACAGAATAATATGAGAAATGCCACTATCTAGTTAGTGGCTCTACATAAGCAAAGACTATCCT
GTCTTGTGGTACTGAACCTTGAAGATGTCCTCTGGAAATGGAAAAGTACCTGTATTAGGAGCTAAGTGC
AGAAGGAGTTATCAAACCTGACTCCATATAGATAATGAACAGTTAGGGAAAGCATTTCCTGGAACTAAG
AAGGACTTACCTGACATTGGCCTCATTCTGGCCTTCACTTGTCTATAAGAATCATGGAACCAAGAGTTGAGTT

-continued

AAGAAAATTGGAAAAAGCAGCTGAAAACATCTCNGNNNCCACTTAACAATTAAAAATTCCACTTAAGATGC
TAAATAATCCATTGCTTATGTAGCAACTCAACGATGTTCTCAA

SEQ. ID. NO:15 BF039490
TTTATGAGCAGCTAGAATGTGCTGCAACAGAAGCTGCGACACGCCAGTGGGCCAACATCACT
AACGCAGCCACTGCTGCTACCCACAGCGGCCACGGCCACTGCCACCACCCAGCACCGAGGGCAGCAACAG
CGAGAGCGAGGCTGAGAGCACCAGAGAACAGCCCTACCCGTCCTCTGCAGAGAAGGGTACTGAGGATTT
GTCCAAAACCTCTTGATGTACACTGTCCCTGCTGTCCAGGGCTTCTCCGTTCCATCTCCTGTCACGAGGCA
ACAACCTCCAGGACACGCTCAGACTCCTCACCTTATGGTTGATTATGGTACTGCCAGATGTAATGAAGC
CTTAGTGGAAAGGGGTGAAAGCAATCCAGATTGACACTGGTTACAGGTTACCCACAGCTCATGCAAGAAT
TGATACGCCAAGGCCCTGGTGGGACGTCTTACCCACAGCTCAGACATTGGTCGGTACCCACCCAG
GCCCTCATCTACCCACTGACAG

SEQ. ID. NO:16 BF042320
GGGGTTCAAGGATCACCAAGGGCCGGTCTGACTTCAACCCCATGTGTCGGTGGGATCTCTGCAGTG
TGTGTCCTGGCATCTCCTACCAGGGAGCAGGCTTGACTTCTCCCTCTGTGGGCTTCGTGACAGTCGAGG
TCACGGCCAGGGCAGGGCCTGGGCCCCCTCTCTGGAAGCCGAGCTGTGGCGTCACGTTACTCGCCTCCCCCT
GCCTCCAGGACGGAGAGTCTGTTTCCCTGCTCAGGGTGGGATACAAAGGTCAAGGCTGTAGGCCGAC
CGCTGGCCCACGAACCTCTGGGAGGCTTCTAAAGACGTTGAAACAGCTGCCCGAGCCGCAGGCCCGCT
CTGGGACACCCTGGGCCCTGAAGCT

SEQ. ID. NO:17 BF043074
CGCTCGGAAGGTCCCCGGTGTGCACTCCTCAGCAGGCCCTGGGAAAGATGGCGGCCCTGGGGAC
GGTCAGGAGCCCCCATGTCTGTCCCCGGTCAGTTCGAGTCACCCGGGACACCTGGGAGGCCACCATG
AAGCCAACCTCACCCACCTCATGGTCATCAACATGCAAGCAGCCCTGAGGTGCCCTCCAGCCCCACAG
GAGCCGTCAAGACTGGACTTCAAGAGGTGGCAGAGGTCCAGATCTGCAAGACACCTGCTGGTCAGGTTCT
GAGTCGGAGCCGGAGCAGGCCCGTGTCTCCAGCCGCACGGCTCTAAGACGAGGTGCACGCCGG
GGCGTGCTGAGGACCTGCTGAGGAGCCTTCCCGCAGACCCGGGGTGGGACCGCTTGGCAGGAGCCC
AGCCTGGAGCGGTCAAGAGGCCAGACCCGAGGGCTGGCCCCGTTCCAGAAGAGAGACACTGGCTCG
GTCGCAGGGGGC

SEQ. ID. NO:18 BF044776
GCCCGGTCTACTCTGGGTGGTCTAAGCCGGGCCAGATCGACCCCTGACTGAGGAGAGGAGTG
CGGTTCTCTAGGCGCTTCTCCGTTGGTCTCCCGCTTCCCTCAGCCTCCACCAACCCGGGGACCCGAGA
GCTCGGTGTATGCCACCCCTGACCCCGTAGAGACATGTCCACCCGGCTGGCGCGTCATGAGGGA
CTTCAAGAGGTTGCAAGAGGATCCTCCAGCCGAGTCAGCGGGGCTCCGTCAGAACAACATCATGGTTG
GAACCGGTCTTGGGCTGAAGGGACCCCGTTGAGGATGGAACCTTAAGCTTACAATAGAATTCACT
GAGGAATATCCAAAATAGCCACCAACGGTTAGATTGTCTCTAAGATGTTCCATCAAATGTCTATGCA
GTAGCATATGTCGGACATACTTCAGAACCGTTGGAGTCCAACCTATGATGTCCTCCATTAAACATCCAT
ACAGTCTCTACTGGATGAAACCCAACTCCAAATAGTCAGCAAATGCCAGGCTGCTCAGCTGTACCGAGGAA
CAAGCGGGAGTATGAAAACGTGTTCTGCGATAGTAGAACAGAGCTGGCGTACTGTTG

SEQ. ID. NO:19 BF046287
GGAGGGAGTAGGACGGGAAACACTTCTCCCCACAAATTCAACAAAGAGCATTAAACGTCGA
GTAAATTCCACAAAACAACCTCTGAATGCCGGCAGAGGACATCAGGCACCGAGAAAAGCAACCCAACTCTC
GAAAGGAGTTTACCAACGCTCAGACCCGAGTTCTGGTGAGAAATGGCTCATGATGCGTCATCTCTG
CCGTGTGCAAAAGTGTGGCACAGCACCCAACTCCGAGACAGTGGAGCCAAGTGGCTGTGCGCAGTGGC

-continued

GGTATAAACAGCAGCTACAGGTGGCTTCTTAAGCAATCGTGGAAAGCATGTTCGCGTGTCACCAGT
 CTGTCAACTGAAGTTATGTTCAAGAATTCCAACCTAGGGAGAATAATCACACAAGTTCTACCTACCTAA
 AGACGACTGTGAGATTTGAGAGGTACTGAAGATGAAAGCACTCCAAATGTGTGAGGAGTTAAAAAAATGTT
 ACTCATCATTATGATAAAAATAACCATAATGATGAAGATGTTGGTAAC TGCTCTAATTGGTTCTTTGTT
 TATCTCACACAGACCATATGCAATTAAAGCTTTATTAAATC

SEQ. ID. NO:20 BM362351
 GCACGAGCCAATCCTCCTCCACCCTAGTGCCAATGACCACACGGCTGTTACAGGTAAATGACC

TTAATCCAGCCCCCTGCCTGCCCAAGGCTCGGGGTGACAGCCAGGCCAGGGACAGGCCGGCA
 GGGCCGGGGACCCCTAGCGGCACGATCCCCAGCGCGCTAGGTGTTGCGTACGACCAGGGACTGCTCCAGC
 TCCTGCCTGCGCTGCTGGATCTGTAAGGAAAGGAGAGCAGGCGCAGGTGACCAGTTGCTGCCGCCCCGGAGG
 CCCCTCACCTGAGGTCGGACTCTGGAGCTTGAGCTGGTGTGGACTCAATCGTCGTGGATCTGCAGTGCAG
 GCTCCAGCCCCACCTACTGTCCAGAGCGTGATCTCTGCTGGTGGCCGTNGACAGCAGGAAGCTGCTCAT
 CTGTCCTTCAGGGCTCTCACTTCCACGTCAATGTCGTAGCACGCCGTTCTCTGGTCCGACGGGT

SEQ. ID. NO:21 BM366715
 GCACGAGGTGCAATGGTGAAGCTGAGCAAAGAGGCCAAGCAGGGCTGCAGCAGCTTCAAGGG
 AGGACAATTGCCCACCGCTGGGTTTATTCCCTCGTGTGATTTACCTGGGTTAAAGAGGGTGCAGATCCT
 GGAATGCCTGAACCAACTGTTGAGCTTGGGATAAAGGACTGTTGGTCATCTGGTTGGAAAGCA
 GTCAATGCAGAGGAACAACATGGAAGGTGCTCTCTGGTGGATAAGAGATGGGACATCGTCAGACGGT
 CACCAAGTTGGATGGCACAGGGCTTACTTCTCAGATGCATCTGTCAGAGTGGAACCTCTACTGACTTATT
 TATGATAGACTGTATTAATAATGTTAACATGTTAAAAAAAAAAAAAAAAAAACT

SEQ. ID. NO:22 BM366099
 GCACGAGGTGCGCTGGCCCGCCGTGGTGTAAACGGATTCTGGCTCATCTACGAGGAGACCC
 CGGGGGTGTGAAGGTGTCCTGGAGAACGTGATCGGGACCGCGTCACCTACACCGAGCACGCCAAGCGCA
 AACTGTCACCGCCATGGACGTGGCTACCGGGTGAAGGCCAGGGACGCACTCTACGGCTCGGCGGTT
 AAAGTTCAGGCAGCCATTGGCATAGTCTAATAAAACCAAAGGCCCTTTCAGGGCCACACAA

SEQ. ID. NO:23 AW464526
 TGTAACTTGACCCAGTCTGACTTGTTGTTCTGTTCTGTTCTTTCCCCCTGGAATACAGGACGG
 GACCAGGGCCCTGTACTCGGAGCCAAGGCTGCTCTCAGGCATTGTAAGCCTTTGTGTTGCTCTTT
 AGGTAGGATAATTGCGGACTGAACCCCTGGCTGCGGTATATATGAGAACTGCTCCGCGGGTCCCTTG
 CGGGATGTTCCATTGCTCATGTTCAAGAACAAAGGAGTTGTGACCAACTATGTTCTTCTTAATT
 AATTCTCTACATTCACTTTCTCCTCTGGTACTAGTCTCTGTAAGCCTTCTGTTCTCGTCCAGCCT
 CTGAGCAGCCCTAGGTAGGATTATGTTGGCTCCCTTCTCTGTAGAGGGGATCCCTTATCTGTTT

SEQ. ID. NO:24 BF046202
 ATGATGCTCTCAATGATGGCACCTTCAGGTGAATTCTACCATGATCATACAAAATAATCATCTG
 TAGCCAAAATGAAGAATACCTTCTCACCTACATCAATGAGGACAGGATATCTACAACCTTTAGACTGACAAG
 TCTTCTGATGTCGGCTGTTGTTAGAATTAAAAAAATCGAATGGAATACGCTCTGAACATGCTCTACAGAGG
 TGTAACTAGGAGATTCTGAAACGGA

SEQ. ID. NO:25 AW466043
 TTGATCACCTGCCATTGCTACGGATTTGATTGCTGTATGACGAGGAGGTGATCTGAG
 GATGCGCTTCTACAGTGGAGAGCAGCAAGGACCCGGCAGAGCAGAAATGGGAGGGTGTGGCCCTGAAGTC
 TGTCACGGCGTTCTTACATGGCTCGGGAAAGCAGAAAGAGGGAGTCTGAGGATAACTAAAATCCTAACAC
 AAAACGAAAGAAAAGAAACAATTAAAGTATTTTAAAAAGTTACGTCTCGCCAATCACAGTCAGCA

-continued

AGGCCAATTCTCGCAGAAACCCCCACGTGTGCACGAGTGGAAAGGGAAAGAGAAAAAAAAGGTGATCA
TGGAGGAAAAAGGTACTGGAAAAAAAGTAAACTTCAAACCTGAGGGCGGGAGCACTAAAACCAAATACAT
GTATTATTTATAGAAAATTTCTGTTTAATCTTCTTTAAATGAGGACTCATACTTAAAAAAAACA
CATCTGTTAGCAAAAAAAAAAA

SEQ. ID. NO:26 BF040403

AGGGTCCTTCCACCCTAGGCCCTGGGTGGGTCTGGTCTGGCACCCATGCACGTCTGCTT
CCTATGAGGCTGAGCAGGGACAGGGCTGAGAGGGAGGCGTGGCCAGGTGAGAGGTGAGGCCTGCTCA
GGGCGCTGGGCTCAGTTCCCCTGTGAAATGGGTGATGCAGGTCTGCAGGGCCGGCAGGGTTGGAGCT
TCTGTTGGAGCTGCCACCCCTCACGCCAGGGATGACAGGGTGGCAGTCTCACCTCCGGCTC
CCCAGCCAACCTGGGGGCCATCTGTACCCCTCTCGTTCTGGTCTGGTCTGACCGTGAGGTCAA
GCTACCTGATCTGACTGGATGTCAGGGCTTTATGTCACCTCTGACCCCTGAACCCCTCAGTCCCTCATGG
TCTGGGGAGGGGCCACTGCTTACACCCGCTTGTGACAGGCCAGCAGCTAGATGCGTATCAGCCAAT
AAAGGCCCGCCTGA

SEQ. ID. NO:27 BF039168

TGTGGTGTGGCGAGGTGACCTGAGGTGCGGTGACCATGGCCGAGTTGGGATCTGACA
GGGGTGCAGGATGTGATCACCTACAGCTTGTGCCCTCGAGCAGCGCCTCCGACTACTCAGCAAGG
GCATCCCCAACGTTCTGCGCGAACCTGGCGTGCATCCTCGCGTCGCGCCGCGTGAAGTGCCTGGCGGG
GGAGAGGCTAGACTCCATCCACAGAGGGTATTGCGGGTCCCTCAGTGAGCACTCTGCAGCTGCCATAAA
CACGCTTCTCTTCAGTAGTCTGAACTGGCATGTGCTCCGCATCTTACAGATAAAGGAGTT
GGGTACAGAGAAAATGACTGGCTCAAGGTCACTTGTGATTCCAGGGTCTCCCTGAGCTCACCTTACCC
ACTTCTTCCTAGCAGTGAACGTGTTGTAAAGGTGCAGCAGATTGTGATGAGTTGACATTTGACATT
TGCTAAAACCCACAGAAGTGTAGATTTC

SEQ. ID. NO:28 BM3 62530

GCACGAGCTTGGTTGGGGCGTCCCGCATCTAACGGCAGGAAGATGGTGGCCGAAAGAACGAAA
AACTGACTGGAGTCGATCAACTCTAGGCTCAGCTGGTATGAAAAGTGGAAAGTACGTGCTGGGTACAAA
CAGACTCTGAAAATGATCAGACAAGGCAAAGGAAACTGGTCAATTCTGCCAACAACTGCCAGCCTGGAGG
AAATCTGAAATAGAGTATTACGCCATGTTGCCAAAATGGTGTCCATCACTACAGTGGCAATAATTGAA
TTGGGCACAGGATGTGAAAATACTACAGAGTATGCACACTGGCTATCTGATCCAGGTGATTCTGATATTA
TTAGAAGCATGCCAGAACAGACTGGTAAAAGTAAATCATGTACAATTCTTAAATAAACTGGCAGAG
CTTGTAAAAA

SEQ. ID. NO:29 AW461980

TTGAAGTTGCTGAAGAGTCTCAATCACTATGTCAAGCGACACAGATATTCTCTTCTCATATGA
TGAAGATCAGGGATCTAAACTTATCGAAAAGCTAGAGAGGCACCTTGTCCCATTGAATGGCAGGTT
TGCAGCAATTGTCATATGGATTATAGATTGAAGAGCAGGGACATACTAAATGTCTGTCACCTGATC
CACATGCGTGTGGCAGCCAAGGCTTGTGAGGAGCAATGACTCTGGTATGGCTATTCCCTGTATCAAG
AATTCTGGGGAAACCTAAACCTAGAAGAGGAGATGCTGTCTGGTGTCTGGTGGCTGCTTGTAA
GACATCTCATATTGA

SEQ. ID. NO:30 BM3 64411

GCACGAGAGTGGAGGCCGTGGGCCAGCGGGAAAGCTTAGATGTGGAGGCCGTGAGACTTAGGAG
ACACCTGGGCCGTTAGGGAGACTCAGGTGGGGACACTGGTGGATCCGACCTGACCCCTGGCCAGTCT
CGTTCTCGCGGCCGCCTCCTCACCCGCCCACTGGGCTGAAGTGGCTCCGCCTCTGATCTGAGCCTG
GTCCCTCTCAGGCAGCTGACCCCTGACCTCGGGCGCTCCCCCATCTTGGCGCGATGGCTACAGGCGGG
ATGTCCGGGACATTCTAGAACCTGGGGTCCAGAGGGAGACGCAGCCTCTGGGACCATCAGCAAGAAGGAC

-continued

ATTATCAATCCGGACAAGAAAAAGTCCAAGAAGTCCTCGGAGACACTGACCTCAAGAGGCCGAGGGCAT
 GCACCGGGAGGTCTATGCACTGCTACTCTGACAAGAAGGACGCGCCCCACTGCTACCCAGTGACACT
 SEQ. ID. NO:31 BF039456
 TGATTCAGAAATAGAACATCGCTCTGATGCTGAAGGTCCTCGTCTCAAACACTAAAAGTTCTTATT
 GAACCGTCTCTCCAGGAAGCAAATGGCTTGGAAAGTCCTCCACCCAGGCCAAGCCAATGTTCCAAGGA
 AAAGCTTGGTAACCTATTGCTAAGAAGTTCAAGGCTGACGCCAAGACGTTGTCACCTCGGCTTCCACACT
 CACTTCGGTGGCAGAAGTACTGGATTCTGCTTGGTATACGACAACCGTGAECTACTTGTGAAGTACGAAC
 CCAAATACAGACTCAGAAGACTGAAAGCTTGAACAAACAGAAAGGCCAGAAAGGAATTG
 AGAACCAAGAGAAAGAAGGTCAAGGAAAGGAAAGTCCAAGATCCAAGCCGAAAGAACAGAAGTAAAGTA
 TCATATGCTCCCTTATATGGCTGGTCGACTCGGAATTTCTGCGTATTGTTCTTTCTATGTGCGCGTAT
 AGTTCATGCATGAATCTGAAAATGAAACCATAATTAGCAAACAAAAAG

SEQ. ID. NO:32 BF042632
 GCCGTCCAGACAGCAAGACAGAAAACCGCGCATCACACACATCTGCGGAGCAGAACAGGCCT
 TCAACATCAAGCTGGCTTGACACGCTGCACGGCTGGTGAGCACACTCAGCACCCAGGCCAACCTCAAGA
 TGAGCAAGGCCACCAGCTGAGAACAGCGCCGAGTACATTGCCATGCTGCAGCAGGAGCGCGGCCAG
 CAGGAGGAGGCCAGCAGCTCCGGACCAGATCGAGGAGCTCAATGCTGCCATTAACTGTGCCAGCAGCA
 GCTGCCTGCTACCGGGGTGCCATCACACACCAGCGGTTGACCAATGCGAGACATGTTGATGACTATGT
 CCGGACCCGCACGCTGCACAACGTTCAAGGTTGGTATTCAAGCATTCTCATCCGGCCCTGTTGAGTCCTC
 AACGGGATGGTGTCTACAGCAAGCCTGC

SEQ. ID. NO:33 BF044457
 TTGGGAGCAGATCATAGCTGCTAGGTTAAGAAATTGATTCTCCGCAGAAACATGGATTTCGGTGT
 AGCGGAACTGTTACGGAGATGCTAAGATGCAAAGGTACATTCAAAACAGGCCGACAATTGGCTGGA
 AAATGACTTGGTTAAACCTGATGATCTTACAGCATTCTGAGGTTGATGAATACTAATGAAGCTGTGGATG
 TCACTGAGCAGCTCATTAAATGAGGGTTGCTGCTGCCCTGCTGTCTGCCCTGGTGTGACATTG
 AGGTGGAACATTCTGGCTAGTGCGAGATTACTTGTCTGTCTTATGAAAATCTGGTATTGGAAAAC
 CTCCAATGGATGTGGAGAAAGATTCAAGATGAATTACATTGGTTGAAATAGATTCTGAACCA
 GCATCGAGTCAAGATAATGCAT

SEQ. ID. NO:34 BF040573
 GAGACCATGGCTTAAACCTCTTATTAAACCCAGAACATGGCTTAAGCAGTACCATATTACTTC
 TTGATAATAGTGTAAATCTTTATGCTTCACTGAGGAAAGGAAAGTCTGGATCAATGAAACCCATGTG
 TGACTTGTCTTATCATCTTCTCCAGGGCCCTTCTTGTGAGCTATGCCCTTGAATTGGAAAGTGCT
 TTGGGATCAAGCAGCATCATAAGATCACTGAGCTAACCTCCCTGAGGAGCTGAAACGGTTCTCCACAT
 TTAATGTCAGCGAATGGCAGACAGAACAGACAAATGTTATTGAGTGTGAGACCACTGGATT
 CAAGTTAAAGTCAGGTTATAGAGTTCAGCTAAAGTTGGTGTGAGCTGAGACGTTTATGAGCTTCG
 TAGGTTCTTGTGCTGTTGGGGTATGAAAATTATCTCCCTGCCCTGGAGGGTGGCTANGAT
 ATCCATGGTGTGAATCTACCCAGCACTGAGCTGGAACCCCTTATGCTTGTCTAATTAGTCCCAC
 TCTT

SEQ. ID. NO:35 BM364731
 GGCCTCGGGTGCCTACCCGGCGGTGTCGGGTGAAGATCCCGCGGCCCTGCCGTGGCCGCC
 GCCCCCTTCTGGCTGGCGAGGCCGGCTGGCGACTCTAGGTGGCGAGCCGCTCTGGGTCAAGGC
 TTCTGGAGCTGGTCTGTCGGGGACCCGGGGAGTCGGACTGTCAGCCGGAGGCCGCTGCCCG
 GTGGCTGGTGTGCCGCCGCCGCCGGAGCCGGGGAGATGGCTTCCGCAAGGGGACCACTTCG
 CCTACTGAGACCTTGGGGCGGCCGGATTCCCTCTGCCCGGCCCTCCCTCAGTTGCCACTTGG

-continued

GGCCTGGCTGGAACAGTGGACGAAGGTGACTCTCTGGATGGACCAGNATACGAGGAGGAAGAGGTGGCC
 ATCCCGCTGACCCTCCTCCGACTAACAGTAAGTCAGAACGCCGGTTGGGGAAAGCTGACTCGTCGGAA
AAAAAAAAAAAAAAA

SEQ. ID. NO:36 BF042198
 GTTGGCTCAGGGTTTGCTCATGGTTCTCAGTGGCTGTCCGAGAAGTATTCAAGTGGGAC
 ATCACTGGTATGAGTTCTCAGCAGGGTAGGGCATATCTTGATGGACTTCGGTGAATCATTACTGATTA
 GGAGGACAGTTGGGGCCATCTGCCCTGCACAGGAAGAGATCTGGACTCATGAAATGAGATA
 ACCCCGAAGGGACCAAATGGAAACTGACATCAGAAAATCTGATAACAAATCATTAAATTGATCAAATGG
 CCTTAATTCTGAGTTGGTAGGCTTATCAATATGTTGCTTACAGTGGGGTAGGGAAAGTAGAGGGAGAGAA
 AGCAAGACATTTACTAACGACCTCTAGGTGCCAGACGCTAGGCTAACGACTTACGTGAGCTGGTCA
 TATAAGGCGTGTGAGAACCTGTAAGGAATGTTACTAGTATTACACTTGACAGATGAA

SEQ. ID. NO:37 BF045424
 ATGTGGCAGACTGCCACAGTCTCAATAGAATGGCCCTTGTCTCCGACAGTCTGAAGGCCACCA
 GTCAGAACTGTAACGTACTCGAGAAAAGCAAGAGGAAGACTGTGAAAGCTGTCATCTATAGTT
 CTTCGACTTCATAGCGGCCTGTGGCTAAGGAGGAAGGCTGGTATAAGAAAAAATTATGGAAAAAGACGGTT
 GCAAGAAAAGACGCTTGAGGGATTGTCTCTGCAATAAGACCCAGAGTAAGCTTCTAGATAAAATGACA
 ACGTCTTCTGGAAGAGGGCAGGACTGGTATGCTGATGATCCTTACAGATGTATCATGATCGAACAAACTGA
 AAGTATAGATCAGAAGATCCATGATTCTCAGTTAACTGTATATCTGTGTGTATGGTGTCTTGCAAA
 GATGAAGTGGTATAAGACATGATGTAATTGTACCAACTGATACTGGACATGGGTACCAACATTAAACT
 TAACAATGTTTAAACTTAATGGA

SEQ. ID. NO:38 BF039771
 TGGGTCGGCATAGCCATGGCGCTCGTGTCTTGGCCCTGTGTCGCCGACTTCCCACGGCCTCGC
 GCCGCTGCCAGGCCTCCACGCTAGCCGCGCCGGCGCTCAGCACTACCCCTTCGCCGGAGACCG
 GACGAGGCGCTGGGCTCCGCTGCCGCTTGGTGTGCGCAGGTTCCAGGAGTTACACAGCTGTGCCG
 CCAGTATAGCGATGACACACCTTGACATTGGAGGGAAATCAAGGACCGTGTCTTACGTCTGAAACTCTAT
 GACAAGATTGACCCAGAAAAGCTTCAAGTAAATTCCATTATGAAAGACCTGGCTTAGACAGTTGGAC
 CAAGTGGAGATTATCATGGCCATGGAGGACGAATTGGTTGAAATTCTGATATAGATNCGGAGAAGTTA
 ATGTGTCACAAGAAATTGTAGATTACATTGACAGATAAGAAGGATGTATATGAAATAAAATATCAGACCCCTT
 TTCTCATTGAGAGAAGGCTNNNAGATGCTGGAGTGTCTGGCGTGAGAACGCAATTCTGCATCATTGCT
 GACTTTGCGAGTAATTCTGTTAGACTT

SEQ. ID. NO:39 BF041569
 ATACTGGTGTGGTCAGGCCCTTCTTGAAGAGGTAAAGGTGAATCTGGCTTATTGAGGCTTCA
 GGTTTCAGTTTTGATCTTAAAGTATCCTCAACCTGTGGTGCAGGAAAGCAGAAACTATGGCTGGATTAGN
 TNATGAATATTACGNNNNTGAAATTAACTTTACATTGAGAACAGCACTGATTAGGGAGATGATCAGAT
 TCTTTTAAATACACTGAAATGACCTAGTGAACATAGGCATGTAGTGGTTGTGAGGGTAACCAGACAC
 AGATTTACTTTGCCTNAAGACAAAGGGAGATAAAAGCAACAAG

SEQ. ID. NO:40 BM366529
 GCACGAGGTGAAGCTGAGCGTACTGGATTACGCCAAGGCTGTGGACTCTGGACCGCTGGTC
 ATCTGTCTGCTGTATGGGGTCAAAGCGCAGCTGCTATTGGGCCAACGTGTGGCTCAGTGCCTGGACTGATG
 AGGCTGCGGTGGACAGCCAGCAGAACAGCACCTCCTACAGACTAGGTGTACGCCGCTTGGGAATTCTGC
 AAGTGACTCCCTGACCCGCCCTAGCAGTCTACCTGCCCTGGACCTGTCTGGCTCATCCTAGCTATGCCCTGC
 CTTGAGTGAATGCCAAGGTCAATTGCTAAATGAGGCAGAGCCAGACTAGTCCCCGGTCTTGTGATTCC
 CAATGTGGCGATATTCCACACTGTACTGCTTATAATCATTCAAGGGATGACCTCCCTACCCCCATGATTTT

-continued

TGTATTTCTAGTCTGAAGTGTTCGTTTGTAAATAAAGCTTCCCTTTGAAACAGAAGACTGNN
AGGTCAAGGCCATCCCTAGGAACTGAGTCCAATACTCATTAAAATGGAGCACTGATGAA

SEQ. ID. NO:41 AW465571
GGCGCTAACGCCTTTTTAAGTTTCAGGTACCCCTCACTAAAGGCACCAAGGCTAAAGTAG
GACAACCATGGAGCTTCCTGTGGCAAGAGAGACAACAAAGCGCTATTAACTAAGGTCAATCAAATGGTGT
CGCGTACAGCCCCATCTCTGTTAGAAATGAGGACTTGACTCAACCCCTGACAATGTGATTGAGGCTC
TCTGGGGAGCGAGCATTAAGGAATGCTTGAGTACCTGTATATATATCCCCTGTGCTGCTTAATATTA
ATTGGCTGTTTCATAGCAGCTGTTAATGAAGCCTGAACTTCAGTGTATGCTTGAGGGAGGGAAAGGG
GAAAGCGGGCAACCACCTTCCCTAGCTTCCAGAAGCCTGTTAAAGCAAGGTCTCCCACAAGTGA
CTCTGCCACATGCCACCCGTGCTTGGCTAGCGCAGNCCTCACCCCTCACCTCGATGCTGCTGGTAG
CTTGGATCCTGTGGCATGATCCATAATCGCTT

SEQ. ID. NO:42 BF043043
GGCGACTATCCCTACTTGAAACGAGTGCAAAAGATGCCACGAATGTCGCTGCAGCCTTGAGGAAG
CAGTCGAAGAGTGCTCGTACCGAGGATAGGTGGATCCCTGATTGACAGACACGGTCCGTCGACC
GGAAGCCAAGCCCAGCTCGTCTGCTGTGGAGTTAGAGAGGTAGCCAGTGCAACCTGACCAGCTCACCA
CATGCCAGATGGCTCTGGGGAGAAGAGGGTACCGTGTGCAACCGATCACATACTCAACCATTAA
CCGTGCTGCTGCCTGTCAGTGGTGGGGAGCGACACATCCCTCATGGGAGAATCCATTACTCAGTAAT
GGCGCCTGACACGTACCCATTGTAACGGCTGCTAATAATGTTAATTAAATATGTATGTTACAGAGCTAAT
AAGTGAATGACCAAGACTTATAATTAAACACTTAAGTATCCTAGAAGTTACTGCTTTCCCTGGAAATA
TGGAGAACTACTTTCTATGTTATTTATGTAATTAGCATTGTTCTGGTTAGGGAAAGCATGT

SEQ. ID. NO:43 BF043765
GCAAAACCCCTTTCACTGGCGATCTGGATAGCAACACTGAGCCAGGACTACATTGGGAGGCT
ATTCTGCCCAAGTGTGGCTGAGTAACTGTGAGCTTCTGCGATGTTCTGTTGAGTAACTGTGTTCTTGGT
GTCTGCTCCCCACTTAGCACGATCTTACCATCATTATTCCTGGATGTTCAAGAAATTCCCTAGAAG
AACATAATGGAGAAAGGTTGTTATGCCGTGAGGGGAATTGAAAGACCAACATGTCTATGTTGAGTG
TGTGCCAGAATGTGTTCTGTTGACTGTGATGTTTGTGACTCTCTTCAATTGTTGCTGGGTGATTG
ATAAGATTCCAGTTCTTCAGGTATTTGATTCCAGCATGTAATACACATTGAAATGTATTAAAAAGAAATTG
AACTGTAAATAAAATGATTCTTAGTAGAAACTCCAGTTAAACACGAAGAACAGTTGAAAGGGANAAAA
AAAAAAAAAAAAAAAAAAAAAAAA

SEQ. ID. NO:44 BF044823
TTGTACCATCTCTCATTAGTTGATCTGACTGACTGTCTCTCAATATTTGCTGGTT
ACACTTAAGCTGCAATGCACTGATGTTGGCAGACAATAACTCAGCTAGCTTCCAAATATTTATTTCTG
CTCCCTGCGCTTTCACTGCTGATGGAGGTGTCACATGGTACCCCTTCTTATGTGAGTCTGGT
TAGCAGGGTCAGATGAACTGCCCCAGGGCACTCATGTTGAAACACTTCACACCTGGGAGACTCTTGT
ATAATGAGTCCTCAAAACAGATATGGTCAAATATGGTCTCCGTAGGGTAGTTCCAGTGGAAATGGGGAAAC
ACTCTTCCAGAGATGGCTCTAGTAAGTCTTCACCTACCTCATTTAAGGCCAGTTATGCAAACAACTTG
AATACCTTAGAGTAAGTAGAAGTTATAATGTCGGTCTTCATTGGAAGCAAAATTCTACTGCCTGATG
TTGCTGGTGGTCCGTGATTTATCATCAGAGTCG

SEQ. ID. NO:45 BF044893
AGGCCTGAGAAAGTGAAGATTGAGGTGAATGAGAGCGGCACGCTGGCTCCTCCACAGCCC
TTGTAGTCTCAGCCGAATGGCCCGAGGAGATCATCATGGACAGACCCCTCCTCTCGTGGTGGCGAACAA
TCCCACAGGAACGTCTGTTGATGGCCAAGTGATGGAACCTGACCAGGGGAAGGCAGCCCTCATCTGG

-continued

GACAGAATGGAGATGTCCAAGAGGAAGAAAGTCGGAGCAAAGAATTCTTATTAAATTCACTTTCTGGAAAA
 AGAGAAGATGTTATTTATTTCCATGTAATTCTTTGAATCTGCCTCTAGACCTAACTCTGGGCT
 CTCTCAGGAGGGCAAAGAGGACCTTGAGTTAACCTCCAATGGAGACCTGGAAAGACTGGGAGGCA
 TAACACCCAGCGGGCTCCAACTGGACTGTAGGACTCCCAGGACCGCTGGCCAGCTGCTCTGCCATCGT
 TCTGCCCTGGTTGGGTTGGGCTGGATCCCACCGANNCCCTGGTAGGATGGCACCACAAGGCCATCATGAA
 GGAGCTTTGTGTTCA

SEQ. ID. NO:46 BF046610
 CGTGGCCCCAACGTGGCCCTGGCCCGAGCCAGCACAGCAGTGAAGCAGCCCACCCGTGCC
 ACGGTCGTCTCCCGGGCCCTGAGCCCTCCCCGCTGCATCCAGCCCCGGAAGCGGAAGCTGCCTGCGGAC
 ACCCCTGGAGCCCCGGAGACACCAGCACCCGGCCTGCCCCGAGGAGGACAAGGACTCGGAGGCCGAGGT
 GGAGGTGGAGAGCCGAGAGGAGTCACCTCCCTGTCCTCGCTGCCTCCATCTTACCTCATCCAGC
 TCCGCCAAGGACCTGAGCTCCCAGGCCTGC

SEQ. ID. NO:47 BF440261
 TTTTTTTTTTTTTAAAGAGTCATACCATGTTTATTGGACATCTAACATGGGTGTGGTGGGA
 CCTATGGGTTGGACAGGGCACCAATGACAGCCTCAGTGAAGTCTTGGCAGNNNGCATAACCAACCATGTCAG
 AAAGTCGAACCTGTAGGGAGAATTGTTATCATCTGTGGCCTGGCCCATCCCTAACCCCCACCACTA
 ACTGTTCCCTAAGGAAGCCAGCTCCAACAACTAGGCTCTGCCAGAAGGTAATTATGGTCTAAAGTATA
 GGGCTCTCTGGTCCACAGTACTGAAGGGAGGTGTATGGTGTGGTGGAGGAAATAAGGGCTC
 TAGCCCCATAGGGTGCAAGTGGCGATGACAGACTTGATGAAGTCGGTTGTTGCTGTAGCCCCATG
 TCTCGAGTCCTGACCTTGCACCTTAATCACCTTCACTGCCTCTGCAATCATGTTGGAGTGTGCTCG

SEQ. ID. NO:48 BM362515
 AGGCCCCATCTGAGTCGGCAGGAGAAGAGCCCTGCTGCCCTGGAGAC
 AAGAAGGCGCGCATGCGTGCATAATTGAGAAAGGAGAAGAGCAATGTTGACACCTAATTGAAGCCCACAA
 GGAGTGCATGAGAGCCCTGGGATTTAAGATATGAAATGGTGGCATGGTGTGCTCTGGAGTGAATAGT
 TCCTGAAAAATGAAGAAGATTCACTTGGAGTTCTTGCTGAAATTGATAAATAAAAATTATTTAT
 AATTATTAACCCCCCCCC

SEQ. ID. NO:49 AW465165
 TTTTTTTTTTTTTTTGAAATTCTACAACTCTTATTACAACACTGTTAACAACTGTACACT
 TTTCAGCCTGAAACATTGGTACTTGATGGAAAATATGTTGACCAATTCTAACATTCTTCA
 TATACATATACATATATTATGCATACATATAACATATAACATATAATTAAACCTAACAGTTGGCAGTC
 ATAAAATTAATGAATAAGTGCACATCAAAGGAAATACAATATAAGTTCAAAAATTAAAATCTGTCT
 TCTGGGATTCTGGACTTCATGTTTT

SEQ. ID. NO:50 AW464987
 CTTTAGCCTAACGCTCTGTATTACATTTGCCTGAATTATTCTATTAAACCATTCAAGTGTCC
 AAGAGCGGAAATGGAGGATGGAGATGACATTAAGTGCTATTTGCTCTAACATGGCAGGTCCCCACTC
 TCTCAGGTAAGCCACTTGATGATATTCTGCTCTGTCTCAGGGAGATGTAGGATGGAGGTACTTATG
 AAAACAATATCTTTCATGACAGATGGGAAAGTGGAGGATGGGACACTGTAAGCAGTATTATAAAA
 ACAAGAACACAGAGGATGCTGGTTGTTACTTATTCTTC

SEQ. ID. NO:51 AW462906
 TCTTCCCTAACGACGTACCCGGACATGTCTTGGTGTGGTGGAGGAGTGAAGACGTGCCCTGTCC
 TTGGGTGCACGCCGCTCTGTCACCTGTTGATCGTGGTTCATAGTGGAACTCTAGCTAGCTGGGAG
 AAAGAGAATCTCTGCAGCAGGAATCCCGTGTCTCAGATGCAGGTCAAACCGTTAAGGAATTCCGGAATTC

-continued

CCATCTAAATACTGAGACAGGAAGGAAGGCCAGATGGCTAACGCACAGTCACTTGTTAGTTAGGGCAGCATT
AGAAATCGAGCTCCTAAAGTGTTCCTTCGTAGC

SEQ. ID. NO:52 AW463449
GAGCAGCGTCAACGTAGGCAGCGGCTGTGCAGAAAAAGGGCCCGAGGAATTGTCTCAGGAACCTGC
GGCCCCGGCACTAACATTCGAGGGTGAAGCTTTGACACCAGGGTGACACTTCCAGAAGITGGTC
GCTGCCGGAGCTTCAGAGGTCAGTGCAGCTTACAAGCGCTTACCCAGTGCAGCCTGAGATGACCCAGC
GCATCTATGACAAGTTGTAACCTCAGTTGCAGACTCTATCCAGGAGGAATCTGAAATGAAAGCTGAGG
GAAACCTGGAAGCTGTCTGATTGACCTGGACCGATTGTGAAAGAAAGCAAAGACCGCAAGGAGCAAGCC
TGGCGCCCCAGTGGATCCGGAGAAGGACCTGCGCAGCGCCATGGGCCACTTGCTGCAGCAGCGGGAT
GCCCTGCAGCGTGTGCAG

SEQ. ID. NO:53 BF040406
AGGGTGTGGTCCGCAGCCCCCTGGGGCGAGCGCAGCAGGCCATGGGCCACTTGCTGCAGCAGCGGGAT
CGCGGCCTNNNGGTGGTGGGGAGGCTTGCACGAAAGATGTCCAGACTCTGCCCTGTCCCACCGCC
CTCCCCGCCCCCGCCCAAACAACTCAGCGACATATCCAGGCCAGTGTGGGTGGGGAGGCCTCGTTAA
CTTGAGCACTGTGGGAGGGCCCC

SEQ. ID. NO:54 BF042130
ACAAAATTTTATTGAGGGTGCCTTATGGTTATTGAAATTACAAAATAAATGAAGCATGCTT
GTATCACCAAGGTTATTGACTTTAGTAAGGGTGTATACACGTAAGGAAATTACAGTCAGTAATCTGC
TATAATAGAGGTTATGACACAGCACTGTTGAAATTGAAAAGGTGTGACTTAATTGCAGGGTCCCTGAG
GAAGGTTTCGAAAGTAAACATACCTGGCCCAAANNNTCTTCTCTCTTCAAATGAAACCTTTT
AAGTTGGAAAATGGCACCTAAGGCAATTCTGGAGTCTAGGAAGGACCGATTGCAGTCAGCCACTGTTGG
CTAAGCCACTCC

SEQ. ID. NO:55 BF043536
GAAGTGTGACCCGGGTTCTCAAGCCCCCAGGTGCCCCGGCTCCACCCGCCCTCACCAGGA
CTCGGGCCCCCTGGGGCCCCCAGCTCCAGTCCCACAACCTCAGGCAGGCTGGTCCAGGCCCTGGCTGCC
AGTCACCAGCCCCCAGGGAGGAACCGCCCTCCAGGGGCCACTTCCAGGTTAGAAAAGTTATC
TCCCATTCTTCAGCCAAGATGTTCAAGTAAATTTTAGTACAGCACTTAGGGACCACCTCTAACTGTG
CTTCTGCCACACAAGTGTCTGGCAAGGCCCTCTTTAAGACATCAGGAAGGCCAGACCCCTTT
GGGTCAAGGAGCGCTNTGCAGCCCCAATAGCAAGGCTGTCTGAGCTGCCGGCCCCCGAAGCCAG
GACCCCCAGAGGAAGGAGGCCAGGAGAGCACAAGTCTCTGGAGCTGCAGCCCCACCCATGGTT

SEQ. ID. NO:56 AW464569
GTTCTAGAATTAAATTGAAACATTAGTCAGTTAATTGGACATATGTTGAAATTCTTCAC
ATACACATTTGCTCATATATGAAGTGGGGCTAAATATCAGTATTCTCAGAATATCATTAAATG
AAATTAAATTGATTAATTGGATTGTGTACCTATTGTCATGCAAAATTCCTCAGGTCTCAGAATT
TCAACTACCTATGATTTTTTACTGTCAACTCTTTGACAGCAACTGGTAAAGAAATTGATCCAAGAC
TTAAGAGGCAACTCTTCCTGGTTATGAGTCAGCTTCATTACACAGAATAAGCATGTACATATAGGCA
CTATTAAAGGTATTAGCAGGTAGTAAATCTAGCTGGACCTTAGTTCTGACAGAGTAGGTTCTGCATGT
CAGGTGTTCTGTAGTTTGAGAGCATGAAATATAAAACTCTGACACCTCGGCTAGTACATATTG
GAAGTTAACTCACTTCAGNTGTTGAGAGTTAAATAACATGTTGAAAG

SEQ. ID. NO:57 BF040351
AGATTTCAAAAGGAACCTGCTCGAGTCTGAAGGTGAGCCAGCCTTCTAAACCTCTCAGAAAA
GGGAAACTGACACTTGAATTGTCACCCCTTCCTCATGGAAAGGGAGGAGCCTTAGAAAGATTCTT
CTAAACTCTGGCTTAGGTAATATATTCTAATAAAACATAGGCTACTCTAACACATAGAATTAGATGCCTC

-continued

```

ACGTACGTGAGAAAATCTGAATATAGGACAAGGGCCTGCTTTAAAAACAGACTCAACTGAGCTGATTA
GATGACGTGAGGCCGCTTGCCTCAATAACATGAAGTTGGACAGTCCTACTCCTATTGAGAAGGAAA
TTGGCTGAAACATACCTAACCTCAAAGAAGGAAAATTGGACCTTAAAGGTATCAAGAAGCCAGCAT
GGTACTTAATTACAACATAACATTGACCTTAATGGGAAGTCATTTATTGCACTAAAGGCCTGCTTGCTG
AAGTCTCTTAACCTCTTCTGTAGAACCTTATTCTTCCACTAGTACAAGGAGAGAAGAGTTCTTATAATT
GAATGTTATCATAAAGAGGGAAATGGA

```

SEQ. ID. NO:58 BF440195
TTTTTTTTTTTTTTAACTCAAAGACTAAGAACAAAGTCAGGAGCTAAGTGACTTCTGAGTTCAATG

```

ACTGACCCATCAGAGATTAGCCAAGGCCTCTCAGATGGCTGCCAAGCCTGGCTGTAACACTGATCTTATA
ATGTGGCACACTGTCTTCTCACAGAAATATAGGTATGGGAAGTGGATCATATGGCAGTATCCAGCC
CAGAAGTAACTCAACAAAGACATTGAAACTCTTACTTATGTTAATGAGAACCATATGTATCTGAGTA
GAACCTACCAAATAAGAGCACCTTGTCTTCTTAGAGAGGTAACTGGGGATCTGACGGTGGAACT
GCACACATGACCAATGTAGAAAGATCTAGACAAGTACCCCTAGGGGTACGTGGCCCAAGAGTCGGTCTGAA
GAGCCTCAGGTGACCCCTCTACTTGAATGTGTAATTCTACTCCTCAGTCCTAGGGGTGGAGCAATCA

```

SEQ. ID. NO:59 BM3 62654
GCACGAGGCCGATGCTCTAACAGATCAACAAATGCCAAGAGAGGCCAGGTCTTA
TTAGGCCGTCTCCAAAGTCATCGTAGGGTTCTAACAGTGTGAGCATGGTACATTGGCGAATTG
AATGATTGATGATCACAGGGCTGGAAAATTGTTGTGAACTCACAGGAGGTAAAGTGTGGAGTGAT
CAGGCCTAGATTGATGTCACAAAGATCTAGAAAATGGCAGAATAACCTGCTCCATCCCCTCAGTT
GGTTTCATTGTACTGACAACCTCAGCTGGCATCATGGACCAGTAAGAAGCAAGACGAAACATACAGGAGGG
AAAAATCCTGGATTCTTTCTAGGGATGTAATACATACAAATAAAATGCCCTAGAGGACTCTGATGCTTC

SEQ. ID. NO:60 AW462632
TGTCTCCGTTGGGAGCCTCACAGACATATCTAGGTAAAGATCGTTAAATAACGCCAGCCA
TCGCAATGCAAAATAAAATCAATCCTCCGCCACAGGCCAGCTGCGCTGCCCAAGTCCCCTGGCC
GCCCTAACAAATTAAAAAGTGTTCAGCGAGAGTGGCTGGCGTAGTGTGAAACGGGTGTGCCGCCGGGGT

SEQ. ID. NO:61 BF040216
AGTGTCTTGCCTAGGAAATCCCATGGACAGAGGAGTCTGCTGGCTACAGTCATGGGTACAAA
AAGATCAGAGACAACTAAGTACTAACATAACATTAAGATGACAGAGAAGTCATCAGACTCCTCATAAT
GTTGGCCTGGAGTACTGAGCTCTGGCTTAAGCACTGAGCTGTGGTGTACAGCCAGAGACTAAGTGGAAC
CTTAAGACCTGAAAGTGGCCCTCTAACACTAGCTAATTAGTCAGCAGGCACATCTAGAGTGTGG
AGAGAATGCAAGCCATTATAAGTGAAGAGCTTGCTGCCCTNGAGGGAAATAAGTTAAAGAGATTCCATC
AAATGAATTGCTCAACTGCAGCAAGNNNTCCATTATAAAATCTAGGCTAAATGTNGCTGAAT
TGCTCTGAAATAACCGTGCCACCAACAGCAATACCTTATCAGTGTGAGGAATAGCTACTGCACATAA
GTAGAATAAATGCACATATAAGTAGAATAA

SEQ. ID. NO:62 BF045874
AATTACTTCTAGAAGTTGGAAATTACCTTCCATCAATTCAAGCTAACAGGAATGGATTCTGGTA
CAAGACGATATAATTCTCTCAGTTGCAGCCANNNCTAACACAGTTACAGCAGCAACCTGA
AAAGATGAAGAATCATTNNNTAAAACCAAGAACTATTAGCTCTGGTTAATTATGATCTAATTG
GACATGCTCTGAATCTTAAACTGGTATTCACCTCTCATTCAAGCTTCACTTAGCATACCGTTCA
GTTTGAGATCTGTTAATAACACGGCACCTGTAAGTCACAGCCTTCAAT

SEQ. ID. NO:63 AW461973
ATGCACCTCTTAATACCATCAGTGTGTGTGTGTGTAAGGACGCGCACACGCACGCATG
TGTATGCTCAGTCATGTCCAACCTCTGCACTGGACTGTAGCCCACCCAGGTTCTGTTAATGGAATT

-continued

TTCCAGGCAATACTGAGTGGGTGCCATTCTACGCCAGGGTATCTTCTGACCCNNAAATCGAGCCTGCAT
CTCCTGTGTCCTGCATTAGNGGCAGATTCTTACCACTGAGCCACCTGGGAAGCCCCATTTTGGAAATTAA
GAATTCCCACATAGGA TTAAAGGGACACAAATATTCAAATCATGGACCCCT

SEQ. ID. NO:64 AW461973
ATGCACCTCTAACTACCATCACTTGTGTGTGTGTGTGTAAAGCACGCCACACGACGGATG
TGTATGCTCAGTGATGTCCAATCTCTGCAGTCCTATGGACTGTAGCCCACCAGGCTTCTGTTAATGGAATT
TTCCAGGCAATACTGAGTGGGTGCCATTCTCACGCCAGGGTATCTCTGACCCNNNAATCGAGCCTGCAT
CTCCTGTGTCTCCTGCATTAGNGGCAGATTCTTACCACTGAGCCACCTGGAAAGCCCCATTTGGAAATT
GAATTCCACATAGGAATTAAAGGGACACAAATATTCAAATCATGGACCC

SEQ. ID. NO:65 AW461973
ATGCACCTCTAACCATCACTTGTGTTGTTGTTGTAAGCACGCCACCGCAGCATG
TGTATGCTCAGTCATGTCCAACCTCTGCAGTCCTATGGACTGTAGCCCACCAGGCTTGTTAATGGAATT
TTCCAGGCAACTAGTGGGTGCCATTCTCACGCCAGGGTATCTCTGACCCNNNAATCGAGCCTGCAT
CTCCTGTGTCCTGCATTAGNGGCAGATTCTTACCACTGAGCCACCTGGAAAGCCCCATTTGGAAATT
GAATTCCACATAGGAATTAAAGGGACACAAATATTCAAATCATGGACCC

SEQ. ID. NO:66 AW462202
CAGTGTCCGCGCAGCTGAAGTGTGGATGGATGAATTAAAGAGCTACTACCATCGCAATCCCCAG

GCCCGCCTGGAGCCTTTGGGACGTGACAGAGAGGAGACAACCTCGTGCAAGGCTTGGTGTAAAGGACTTC

AAGTGGTTCTTGAATACCGTGTATCCAGAGCTGCACGTGCGCTGAGGACAGGCGCTGGCTTCTTGGGATGCTCC

AGAACAAAGGACTGAGAGATTACTGCTTGACTACAATCCTCCAATGAGCACGAGATCACAGGACACCCAGG

TCATTCTGTACCGCTGTGACCGGATGGGTCAAGAACCGAGTTTCAATACACATCCCAGAATGAAATACGCTA

CAACACCCACCAGCCAGAAGGCTGCGTGGCAGTGGTGGAGGAACAGACGTCCTCATCATGCATCTGTGTGA

GAACACCAACCCCC

SEQ. ID. NO:67 AW465524
AGCAGAGACCCACATCAGACAGCTCTACACGTGCCGATGAAACAGGGTCTTCCTCGGGCTGGAG
GTTTGACTGCTGACCTGTCCTCTCAGNGTAGCCCCACCCCCATCTCTCCAGTGGAAAGTCTGTTGCAACA
AGCTTCCGCTCCACTCAGGGATGCAAATGCCACGGAGATCAAGCTGCTGGGGAAAGTGTTCAGTCTCT
AACACATACTCTGTTAGTGTAACTGTTAGGCAAATGGAAGAAAGACCAGGTCGAATTCT
GAAATAATTATTCTAGGCCTCCCTCCTGTCCTACCTCATACACCACCATGTCGAGATGTTCTTATTCTTAA
GGATGAGTGTGCTGTTGAATACAAATGTAAGTGTGCTGCTGCTTAACGGAGATGCATGGCTATGTTACCGT
GCTGGGGCANTGTCGTTCTAAATGCCATCGTAAATACCATG

SEQ. ID. NO:68 AW465958
ACAAACCTAGACAGCGTATTAAGGAGACAGACTTGGCAACAAAGAGTCACCCACCCCCAC
CTCTGGCCTGGACGACCCCTCTGCCAGCCTGGAACCTTCGGTGAGCCAGAGTGTGGGCAGGGTCC
TGCAGTATCAGAGAGCTGCCTGAATCCGGGGCAGCCCTGGGCCCCCTGGCCCTTCTCGTGA
TGGAGGCGGACTGGGCAGAGGCCAAGGCTCGCTGGGTCTGGCCTGGGAGGCCACGTGTACGGGTAGGC
GCGCTCTCGGCTGGCCTGCTGGCCTGCTGGCCTGCTGGCCTAGGCCCTGGCCCTGGCCTGCCGCCGGCG
CTCCCTGCCTGGCCTGGACATGCTCTGCTCTGGCTGGACCACGCCCTCCGCTTTCTACGA
CGGCTACGGGGACCGCGACCGGCTGGGGCGCTGGCTGGCTGGCCTGGCTGGCTGGCA

SEQ. ID. NO:69 BF041193
TGGTTCTCGGTGCTTGAAGACTGAGAAGTTACAGATGGAGAACAGCAGCAGCTGCAGCAACG

GCAGATACTTCTAGGGCTAAATACAGGGCTGTCAAGGAGGAATGCCGGGGCTTACCTTCACTTCCTGGAAA

AATCTAGATGTGACTGCTATATTGACCTGTCTGGTGAAAGATTTGAAAATTCAATAGTGTTGAACTGC

-continued

TGATTATTGGATTTTTTTTTAAACTTGGCACATGGCTATAAACCTGGTGCAGGAATTCTCCCCA
 CATTGGCTCATGGAGAGACTCCTCACTTGCAGCTGTGCCCTCACTGTCCTGACTTATTCTCTCCTCAAT
 GCTGATACCAGAGAGCAGCAACGCAGACGGTTACTCCAGCTGGCACCCACCCCCCTCACTAAATTACT
 CCTG

SEQ. ID. NO:70 BF042630
 GTAATTCATGGGACTGGAGCATTTGGAGCAACAAAGTGCCCCGGTGCTACGTTCTCACCTTGTTAT
 GAGATTCAAGTTATTTATCCCTTTCAGTGGCAATAAGAACCTTGTGGACTTCTGTTAATCGTACA
 TAATGTGTAACACACTTCTTGAAAGCAAATTCAAGGCAGTGAATCTGTATGTGTGGTGCTGTGTC
 ATGTGGCTGTCCATTGGCAGGCAGTTGATCCCTGACGCCGTACACCACACTGCATGAGTCAGGCCCTG
 ATCGGGTGTCTCTGCTGGATGGTAGGAACACAGAGCTATGAAAGAACACTTGTACCTGCTCCATCGG
 TACAGTGCTAGCTGAGGAAAACAGTCCACATGTATTCTTTAACAGGACTCGTGTCTAGTTCTGTAAT
 TTATGTTCTTTAATTTAATAAAAGCTGAACGTGAAAAA

SEQ. ID. NO:71 BF043059
 AGCNNAATGAAAGTTAAGTCTGTGATCCCTGGTGCCCCAGCCCCTGAGTGTGCCTCCAGGCTCAG
 AGCCTTGGTTCGAAGCTGGTCTCTGACAAGGCCAGTGTCTCCACCCAGGTGGAGAGCAGGTGCTTG
 GCGGAAGGCCAGGGTTGAAAAGTTAATGTGAAAGACCCCTCCCAGGCCCTGGCTTGCTGGAGGGC
 CGTCAGTCCATGGCTATGTTGAGACCCCGAAACCCCTCCCTGTTCTCTAAGTGAGGAGCTGGTCTGTGCA
 GGATTTGTGTGTGTAAAGAGGATCTGATGTGTTGTCTTACTGTCGAGCCCTGTGAGAAGAGNCTGG
 AAGGGCAGGGGTGGGCTTGGAAAGGGACACCCCTCTAGGGAGAGCCCAGGGCCATGAGGTGTAGAG
 CTGGAGACTGGGCTGGCCTGGCGGGTCTGAGTGCAGGCTCCGTCACCCGTTGGGCTGACTGGTC
 TTA

SEQ. ID. NO:72 BF043236
 GGGGAATGAGCAGCGCTACAGAGGGAGGCAGCCGGACTGCTGGCCCTCCTCCATGCT
 GAACCCAGGACCAGCCACTGCAACTACGGCTTAACCTCATGATAACACCTCCCTCATC
 CGATGTGCTGTTATCTACCAACTGCTCATCTGCTCTGCTTGTGCTCTCAGTACTCTGCTGCTG
 TTTCCCTGGCTGCGTTATTGCGACGATGCTCCCTGACTAAACGTGGTACTGACAAC
 TGACGTTAACTCTG
 CACCYTTGTTGGCACCTGGAGTTGAGCCACTGGCTCACAGACCGCAGCTGGCTGAGGACCC
 CATCCCCAGG
 GATGCTTCTGATCCTGTGCATTCCCTCATG

SEQ. ID. NO:73 BF043635
 GAGGTTACTTCACAGGAACCAAGGGCAACAGGGCCACATCTTTTGATAAGAATTGACTTCCAGCTTAAG
 GCAAAGTAGGGCACACAGAATGTTGCAACTACCGGGAGTTTTTGATAAGAATTGACTTCCAGCTTAAG
 CTCTAAATTCTGATTTAGTTGAATCTTGGTGAGAACCGAGAGGCCAGACTCAGCTGCCAGGACTGTCCA
 AGGAGCAGGAGCAAGTGGTGGCCCTGAACGTGCGGTGCCGGAAAGCATGTTGAGCCAGCGTGGGG
 TTAACAAGACCTGGTACCCACCGAGGAAGCAGGAAGTTCCAAAACAAGGAGGAAAAATAGATG
 CTGAAGAATCAGAAGCTACAGCTGTGCAGCACAGGCTGCCCTAGACCTGGATGGACATAGCC
 AGACGAAAAGCTCTGTGATACACTGACATGTTATAACTGTCGCGTATGGGGCAGGGACCAGAATTCC
 TCTGTCGTTGGAGAAAATAGGCATAGAG

SEQ. ID. NO:74 BF043736
 TGTGTGATTCTTAAACACAAAAAGAAGCCTTAGGAAGAGACAGGTAGAGGGTCCCTCA
 CTTTGAACCTGGTGGAAAGCAGTGAGGGACTCCGGTGGCAGCTCTGGGGTGGCTTGGGGCTGGTCTG
 TCGGGCCGGAGAGGAAGACCCGAGCCCTTCTGCTCCAAGAAGNCCTGGACGTTCTTCCAGTGCA

-continued

TTGGACCAGAACAGCGACAAGGGGTGCCCTCGAACCCAAGAAGCGTCCCAGATCCAGCATCGCTGAAG
GGGGGCCGTCGAAACCATCCCGCTCACGAGACCAATGCCCTTGTGAGACTCGT

SEQ. ID. NO:75 BF044851
GGGATCTCAAAGAGTTAGGGTCCCTGAGGAGGTAGAGTGCCTACCAACCAGTAGGATATTCTAA
TGGGGGCTCCTGGTGCCAGAGCTCTGGTGGCTGCCCTCAGCATCCCATCATCCTCCCCAGGTGGCTC
CCCCATCCCCGGGGATGGTCCCTGAGCGACTGCCACCATGGCTCAGCGCTACGTGGAGAAAGTGTGAC
CTCAGCCTTTGGGGCTCCAGCCAACCACGTCTGTAAACCAGTATCTGCCTGGGAGGGCATCATGC
CCCCAGGGATGGGCACTGTACTACCCGACCGTCAGCACTATCAGCTTGGCTCACCACATGCTGGACCT
CTACGAGCCTCGGCAGCCAGAGGATGATAACCCGACAGAGCAGCCCCGGCCCCGGCCGGCACCTC
TCTGCTGCTTAACCGCGCAGCTGGTGTCCGTGGCACCGCTACCGCCTCCTCCATGGCATCGCG
GCAGCCAGCGT

SEQ. ID. NO:76 BF045170
GGCGAGCTCTGACGCAAATAGGTCTTGAAATTGAGGGCTGCCCTGAGGTGTGCAAGGGTCA
GCACCCCCGATCCCCCGCTGCCCTTCCCTGTCCAGGGCGGTGCTCCACCACAGTCAAAGGCTGCTG
TCAGCAGACACCTGGCTGAGCGGTGCTCCCTCAGGAGCCGGAGGAGGGACCCCTCTGCTCTGCTCC
CACCCCTCACTAGCATCATCTGTAAACCAGGTGAGCCAGGGTGGAGAGGGACTTGGAGAGTCCAGGCATC
TGCTTCCAGTCTGCTTGAGGGCTCAGCTCCCTGAGCGGCCAGGGCTGCGAGTTCTGGCATTGGGTGAC
AGGCCAGTAGACTGCCTTCAGCCTTGTGCTACTGTGTCCTCCTCTGCTCCGGCCCTCCACCAAGA
GATCCTGTTGGACTTGCCGCTGGACCGGGCTATGAGCTTCCCTCTGCTGCTCCGGCCCTCCACCAAGA
GGTCCCTGCCTGCCCTGTTGCTATCATTGAGGAAGGGAGTGGAGAACTTCCCA

SEQ. ID. NO:77 BF045305
CCTCAAACCGCAGGCCGATTGCTCCAGCGGGGCTCCACTCTGGTTGGGTCAACCGTCCC
CTCTGGGAGGGCTGGAGCTTGTTCATTAAATGACCTTGAGCCTTGAGGAAACTGAGGAGGGAA
GAAGTCTTGACTGCCTAAACGGTCAACTCCTCTAAACTTGAAGGTGGCACCCCTCTTCTGTTAAGTTG
GTGTGTGTGTGTGTGTCTGCGTGCAGACAGTCGGTCACTTTGTCCACTGTTGGACCCCTGCTGCCCT
GGGCTGTGGTTTCCGGTCCAGGGCGGCCCTTCTCCAGGAGCTGGCATTGAAGACTTGTCACTTCTG
GAAGGGCTCTGACCCCTCTGCCCAGTATTGGTTATGTCCAGAGGGAACTAGGTATCATGGTTTC
CTTGGACTTGTAAGCTTCAGGATTGCTCAGTAATGAATGAAAACATCACGGAGACATGGGAAGAGCAGTG

SEQ. ID. NO:78 BM3 62735
GCACGAGCGAGCCGCGAGGCGGGCTCGGAGGTGTAATGGACGTTAATACTGCTCTGCAAGAGGTACTG
ACCGCCATGGCCGAGGAAGGCATTGCTGCTGGAGGTGTAATGGACGTTAATACTGCTCTGCAAGAGGTACTG
AAAGACGCCCTCATCCACGATGGCTTAGCAGTGGAAATCGCGAAGCTGCGAAAGCTTGAACAGCGCAA
GCCCATCTGTGTGCTCGCATCCAAGTGTGATGAGCCTATGTATGTCAGTTGGTGGAGGCCCTTGTGCTG
AGCATCAAATCAACCTGATTAAGGTGATGACAACAAGAAACTAGGGAAATGGTAGGCCTCTGTAATTG
ACAGAGAGGGAAACCTCGTAAAGTGGTTGCAAGTTGTGTTGGNNAAAGGACTATGGCAAAGAATCTC
AGGCCAAGGGATGTCATCGAGGAGTACTTCAAATGCAAGAAATGATGAAATAACTGATTCTGTTTCAA
AAAAAAAAAAAAAA

SEQ. ID. NO:79 BM3 66522
GCACGAGCCGTGGCGAACAGGTGAAAGGCCGCCCTGCCGGCGGGAGGTGGTCAAGGCGAAG
GCCGGAGCGGGCTCTGCCACCCGTCCATGGCATAACGCTGGAGCCGTTGTCTTCTCCCTGTTGACGCGA
TGAATGGAAAGGAAGGAGTCGTCGAATGTTCTCGTTAAGTCCAAAGAAACGGACTGTCCGTATTCTCCAC
ACCGTTGCTGCTGGGAAAAAGGGATCGAGAAGAATCTAGGCATCGGAAGGTCTCCCTTCGAAGAGAA

-continued

GATGATTGCTGAGGCCATCCCTGAGCTGAAAGCCTCATCAAGAAAGGAGAGGAGTTGTCAAGAACATGAA
 ATGAGAAGGCCTTACCGAGCTCGGCTCCCTAACCTATTAAAGGCATCATGTCAGTGAAAGCCGTTCAAG
 ATACTTTGTCGTTCAATTGCTCGTTGAGGGAGTTGTATTAAACGAACCACCCCTTGCAATCTGGTCAG
 TCTGTCGGTGCATCAATAAAGCAGGCTTGTATTCAAAAAAAA

SEQ. ID. NO:80 AW461513
 TTTTTTTTTTTTTAATGGATGCGTGTACCATGCTAGGGCTGTCATCCTCACAAAGCTGGAA
 TTCTGGCCACAGTGCCTCGCGAGNNACAGACCCCTCAGGCACACACGCAGCNGGAGAACAGGA
 AGGGACAGGCCCTCCCGAGCGAGCAAAGGACAAACTCCATTAAAGATAAAAGTCATTGCAGAAGA
 AAAAAAAAAGTCTTTAAGAGACAATCCTCACAAAGGGGAAACGAGCACC

SEQ. ID. NO:81 AW462120
 TTCATTGGAAAAAAAGATTTTATTTACCATAAAAATGCAAACGTGAAATAAACCCATCTCCTAA
 GGTGGACGTTACAGCTATTAAAGTATTCCAAGCTCCCTGGAGAACGCTGACAATTATAAAATTAAACAA
 GTTGCGCCCTTAAACTGAAACGTTCCAAGTAAAAATAATTAGCAAACGGCTCTTAAAAAACACAC
 AGGCTAACCTGACTAGAAACCAAAGCTAATTAAACAGCCTGTTTGTATGTAATGACTTGA
 GTTGTAAGGAGATGTGTGGACCCCTGTGTACCGACCTGACGCTCTCTGTGTATGCTGAATGACTTGA
 ATTGTCACAAAGTGAATGTTGGACTCTCTGTATCCCCTGACCCAGCCCCGTAAAGAG

SEQ. ID. NO:82 AW463593
 AGGAGTCCTACCCCTGGGATCATTCCACAATCCCCATGGCTCCAGCTCCAGCTCCGTGGACACCA
 GTGGACTTACAACCCCTGTCCGAGGGCTGCTGCTGCTGCTCATGCTCATCTGCTCTGTGCCAA
 GGCAAACTCATGCCGCTCTGCGCTCTGACGTGTTGTTCCATCGAAATCCTTACAGACAGGTTATGA
 ATGCCGCCAGCCTCTCCATGACTTCTATAACCTTCCACAATAATGTTCAATGAGTTGATGAAAAATATGC
 CCAGGGAAACTATACTATATCAATGTCACCAAGAGCTGCCACCCAATTCCATGCTCCGAAGAAAG
 AGATATAGTCCAGCAGACGAACATTGAAGACCTTAGTAAGTGGACACTCGTGTGTACTCCTGAAATA
 TCCCTGTCATCATCTAGTCACGGAGCTGCAGCATATGAAAGAACTGTCAAACGCCCTCATCAAGGCCACAA

SEQ. ID. NO:83 AW465056
 GGGACCAACGGATCCCTCATCCCCACCAACCCGGAGGACGAGTTGGGTGGAGTTGGGTGG
 CTAGCTTCCCTGGCTCTCCCCACAGAGCTGACGTGTCCTGGGTCCAGGCATGGCATTTCACGGGCG
 GGAGGGTTCGGTGGGGTACAGGACAGCTGCGCTGGCCTTCCCTCCCTGTCCCTGCTGCTCTCGCTGG
 GATGCAGATGTATAGTGCAGCTGGCGTCCACCGAGTGGCTCACCATCCAGGGCGGCTGCTGGTCCGG
 CTTCTGCTTCTCTCACTGCCTCAATAATCTGGAGAATCTTGCTTGGCAAAGGATTCAAGCAAAGAT
 CCTCCCTGAGATTCTCTCTGCCTCTGGCTCTGTTGCATAGGCCTCATCACAGAGTCTGTGTCACCA
 CTTGCTTCATCTCTCCATGGTGGCTGTACTACATCAACAAGATCTCT

SEQ. ID. NO:84 BF046404
 ATTTTTCTTTTTAAATTTCACACTACTGGGAAATTATTCTGTCCAATAATTATAAAAGTC
 TTTTCGACTTGAGCACATGGACAAAGTAACTTGATTTGAAACTAGAGGCATAGGCCATGCATGTTAGTACTTT
 ATTATTTGGCTTCTGCCATGTTAGGAAAACAAATATGAAAAGGTCAATTCTTAAACCATGGAATT
 CTCAACTAAAGTGAATCAAATTCTTATGTATGTAATTCACTACATTAACACAAAGTTTATATCATGCCA
 GTTCACATAGCATAGTGGAGTCACCATCTCTAGAATGTTGCTGCAAACCTTAACCTGCTTGTAGAATT
 AAATTAAACCTGCGCAGANNCCAGCTCCGAAAGCTATGAAAATCCTAGGTGGCTGATGTGGAAACCTC
 TTTCCACTGCTGCCAGCCCTCAGGATGTGCAACTTAGTGAAGGAGAGAATCTTTCTAGGAAAATGAGCC

SEQ. ID. NO:85 BM366368
 GCACGAGCAGCCGAGCTCCAGACCCAGATGCCAAGCAGTCTGTGCTGGACTGCTCCATCGCT
 GACTGCCTGAGGTTCCGCTGTGACATCCCCCTTCGGCGTCCAGGAGGAACCTGACTTCATCTGAAGGGCA

- continued

ACCTCAGCTTCGGCTGGGCCAGCCAGTTGCTGCAGAAGAAGACATTGGTCGTGAGTATGGCTGAAGTCACAT
TCAACAGATCTGTACACCCAGATTTCAAGGACAGGAGGCATTTGAGAGGCCAGGTAGAGATGGTAG
AAGAGTATGAGGTCTACAGCCCCATGCCCTCCTGTGAGCAGCTCCATGGGAGGACTGCTGCTCTGGCCCT
CATCACAGCCTTAAGTGTGGCTTCTCAAACGTCAATAACAAAGAAATGATGGATAACAAGCCTGA
AACACACTGCACCTCAATGGGGAAAGATATCCACCATGAGACCCCAGACTACCTTGTCGAATAATCCACTTC
TCATTTATGTCTATTCCCATGGCTGACCTTGCGCTCACCTAC

SEQ. ID. NO:86 AW462010
ACAAGAAAATGTTACACACACGGACGAGAAAGGATTACCCCTCTGATGTGGCTGCAGCACAC
GGGCAAATAGCTGTGGTAGAGTTCTACTTCAGAATGGCGCTGATCCTCAGCTTTAGGAAAAGGTCGAGAA
AGTGCTCTGTCTTGGCTGTAGCAAGGGTACACAGATATTGTCAAATGCTGCTGGATTGGAGTTGATG
TAAATGAATATGATTGGAATGGAGGG

SEQ. ID. NO:87 AW465551
TTCTAGCAGTGGGACCAGGCAGCAGGACGAGGAGATGCTGAACCTCCAGCTCCTGCTGCAGTGGCT
CGAAGAGTCAGGCCCTAGAGGACGATGCAACAAATGAGGGCTGCAGACCTGGCGAGAAGAGAGGGCCCTC
TTCCAGCCCCGAGAACCCCAGAAAAGAGACCTCGGGAGACTCTGATGTGGAAATGGTGGAGGATGCATCCCG
AAAGGAGATGACAGCCGTTGTACCCCCCGAGAAGGATCATCACCTTACAGTGTCTGAGTCTCCAGGA
GGAGATCACAGCGGGGCATGAGAGTACCTCTCGGGAGATGCTGCATAACCACCTTGTGGCTGCG
TGAATCCTCAGTGGCCTTGGCACAGCATCAGACCAAGTTACCTCTCACACACCAGACTAGTGAAG

SEQ. ID. NO:88 AW465274
TGCCCAATTCCAAATGTCAGAACTCTCCATTCCACAAAGCTCCCTGAACCAAGTGAAGCCAGTG
AGGCAGCTGCAAAGAACCCCAGCCAAGGCCAGACTGACAGATCCCATTCCACTACAGAGACGTCAATT
GCACCCCGCCAGAGGCCTAAAGCTGGCAGACTCAGCCCAACCCAGGAATCTCCCATCAAACCCAGGCCCTG
ACCCCTCGGAAGAGGCCACAGTTAGCCCTCAGGCCCTCAGGCCAGGATCCAGCAATCAGCTGGCTTTA
GCCAGTGTCTCAACCAAAAAACCCAGCCCCACCCAGTCAACCCCTACACAGTCTCAGCCCAAGCAGCC
TCAGGGCTCCGCCACCTCACAGCAGCCCTTCCGCCGCCAGGCTCTGCCACCCAGGCCAGGCC
GCCCCAGCACAGCAGCAACTCTCCTCAAGCAGCAGCAGCAGCACAGCGCCGCCACAGCAGC
CAGCGGGCACGTTCTACCAAG

SEQ. ID. NO:89 AW462049
GGTATCGCCCCCAGATCATGAACGGCCCTGCACCCCGCCCCCTGGTGGCGCTGCTCGACGGCA
GAGACTGCACCGTAGAGATGCCATCCTGAAGGACCTGGCACCGTGGCTCTGCGACGCACAGTCCACCC
AGGAGATCCACGAGAAGGTTAAACGAGGAGTCGGTGCCATGATGTATCACACCATCAGCTCACCAGGG
AGGACCTGGAGAAGTTCAAGGCCCTGAGAGTGATGTCGGTAGGCAGCGCTATGACAACG

SEQ. ID. NO:90 AW463986
GTCTGGCTGAGCCTGACACCCCCAGGGGAAAGCAGTGCAAGAAACACTGGTTCCAGCCGGAG
GGATCTGCACTTTGTGTTGACCAAAAAAAAAAGGTTAGCAGTGAGGGCTAAGGAGACATCCAGCC
TCTGATAACCTAACAGAGGAGAAGTCCCTGGACTTGGACCCCTCTATTGTCGACCTCAGCCCAGGGGGACT
GCTACCGTGAGTACCTGGGGAGGGAGGGATGGGAGTT

SEQ. ID. NO:91 AW462385
TGGAGAGTGGAACCCGCCATTTGCCTCCGGATCATCATGGACTCCAGCATCTGAAGCAGGC
CTTGAGTGAGATTGAGACACGCCAGAGCGAGATCATCAAGCTGGAGAACAGCATCCGGAGCTGCACGACA
TGTTCATGGACATGGCATGCTCGTGGAGAGGCCAGGCCTGCTTCCAAAATCCCTCTGGGCCCTCGC
CGCCTGGAGGGGGCCCTCTGGAGCTGGGGTCCCCCTGGCCCTGCAGGGGGAGATGATTGACAGGATTGAGT
ACACAGTGGAACATTGGACTACGTGGAGAGGGCGTGTGACACCAAGAAGGCCGTCAAGTACCAAG

- continued

AGCAAGGCTGCCCGAAGAAGATCATGATCGTCATCTGCTGTGGTCTGGCATTGTGATGCCCTCACCT

TCGGGGGCATCTCGGATAGAAACCACCCCGCTGCCACTCTGCTCTGGAC

SEQ. ID. NO:92 AW462546

TTTTTTTTTTTTTTGGCAGGAGACAAAGCAGGTTTATTGGCTCTGGGCAAGGGATGCC

TAAGGTGTGAGTTAAGGCAACTCAGCTGGTTCAATGCCAAAGGGCAGGCCAGGGAGGGAGAAGGGT

GACTCNNNATTGAAGCAAATCTCGCATTCAAGTCCCTGGCCGGAGACCTGGGAGTCAGTTCTGGGAGG

GCATGGGTTCTAGTGTCCCTGGGTCTGTGCTTTGCTAGGATTGGGAATGGTCTGGGGCAGGAGC

CTTGAATGCACAGCCTTCATTCAGTAACGACCATTTAATTGTTCTTGCAACTGANNNACTGGCAC

ACTGTGTCCGTCAAGCGCTGTCACTCGCCCTAAATTCACTTCTGGATCACTGCTGGGTCACTTTC

SEQ. ID. NO:93 AW463148

ACTGCGCCCTCAAGCCTACATCATCAAGATTCAAACAGCTGCCAGCGTCTTCAAGGAGGCACA

GAAAATAGCTCTAAACACCTGGATCCTGGTGAATCTTCCTGAGGCAGTACTTCGTTTTGATCGTA

AAAAATAGAAGGATTGGCCTGGCTCCGGCAGTGAAATGCTGGACTATCAGCAAGCATTGACTAAATCAGTC

SEQ. ID. NO:94 AW464583

TGCCGCGCCGGTCGCCAGGCCCTGCCCTCCCCACGCCCTCCGGCGTCGGGCTTCTCCGCCCG

TCCCCCACCCCCACGCCCTCCCGCCGCTGTCCGGTTCTCCGCCCTGTTCTGCCCTCTCCGTACCTCTG

ACCGGTGTCCCCCTGCCCGCTTGGGCCAGCTCCCGTCGGAGCCCCCTCCCTCCGCCCTGGTGGTGTG

TGGGGGGGGG

SEQ. ID. NO:95 AW465767

CCGGCCCTCGGGCGGGAGGGAGAGAGCATAGGAGGCAGGCTGAAGGCGCAGCTGTGCTGGACG

ATGGCGGGGACGGCACTCAAGAGGCTGATGGCGAGTACAAACAACTAACGCTGAATCCTCCAGAAGGAAT

TGTGGCAGGCCCATGAATGAAGAGAATTGGATGGAGGCATTGATCATGGGCCAGAACACACTG

TTTGAGTTGGGTGTTCTGCCATCCTGAGTTCTCACTGATTACCGTTAAGTCCCCAAAGATGAGAT

TTACCTCGAGATGTTCACCCAAACATCTACCCAGATGGCAGAGTCTGCATCTCCATCCTGCACGCTCCTGG

CGACGACCCATGGCTACGAGAGCAGCGCGAGCGCTGGAGCCCCGTGCAGAGCGTGGAGA

SEQ. ID. NO:96 AW466125

CTCGCGCAGTCGTCTGGCGAGCGAAGATGGCGGCCAGAGGGAGCCTCCGCTAGGGGACGG

AAGCCCACCGACTTGAAGAGCTGGAGGACGGAGAGGACCTGTCACCAGCACTGTCACCCACCTGGAGTC

AGTCCATCATCTCGGATCCAGCTAGCTTCTGCAGAAAGATATTAGTACAAACTCCAATGGTCAAACCTG

CAGAAGTTGCGCTAGATGATGACAGAGAAGATTTTGAGCTACAGAGGAAGTTCTGGACAGTC

CAGAAAGGGAAACCTATACTCTCCCGAACCTCTCTGCAGTCACACCTGTGACCCCCAACACACTCATTGC

TCCCAGAATTGAATCAAAGAGTATGTCGCTCTGTGATTTGATAGATCCAGGGATGAGATTGAAGAAGA

AGCAAATGGAGATGTTTGATATAGAAATTG

SEQ. ID. NO:97 AW466146

CGGTCCCTCGCACCCCTTCCGAAAGCGTGGATAGTGGCCGTGGATTGTGGCGTAGTTAGGA

ACTCACATCCGGACAATGGTGTGCATTCCCTGCATCGTCATCCAGTTCTGCTCTGGCTACAAAAAGTC

CTGGAGCCATATATACCCCTGATCTCCCCCTTGTAGCCGTATGTGGCCTCGAAAGCTATACGAGAAA

CCAATGATAAAACAAAGGAAAGTAGACTATAAGGGTGCAGACATAATGGATTACCAACAGGACCA

ACAGAAATGTGTGATAAAAAGAAAAGACTAAACTGATTGTCGGAGAGGATCTCATTGTTATAAAATGGACCT

GATACTATGAAGCACCTCTTGTAAATTGTCGATCTGATTTCCAAGACCAGAATTGGGTTAGATATTAACA

GTTCAGACATTACCTATGCTAATCAGGAATACCT

SEQ. ID. NO:98 BF042961

GTGGTCTCAAGGCAGGGGGCAGGCAGGGGTGGCTGTTAGCCCTCACAGATCAGTGGCTTGGC

AGGTCTGAGAGCTGCCCACTGGCCAGACTCCCTCCAGCAGCAGAGCCAGGCTGGGCTTGCATGTCCAGC

-continued

CTGAGCAAGCTAACAGGATGAAGCTGAGGCTTCTCCCCACTGTGACTGGAGTCATGTTACACCAGCACC
 TTTTCTGCACATGTATCTCAATCCCACAGGGAGCTCGTCACCCCTGCACAATGACATTCCAACCACAC
 CAGCCAGAAGTTACAGCCAACCTTGCTGACTGTACAAGCAGCACCTGGTCCATTGGCACGGTCAGTGAT
 GTAAGC

SEQ. ID. NO:99 BF043647
 GAACTTGAGGGCCCAAGCCTTATCTGAGCCTTCCTCAATACGGGTTGGACTGGGCTCCTC
 CATGCCTAGTGAGAATTCCATGTGGCTCAGAAGACTTGGCATGCAGGTGCCGTGCTGATGTGCTGCCTGT
 GTGTCGGACACACAGTGGAAAGCTGGAATTGATGGTCCATGAAGGCTTACCCCACACACACTGCAGCCTCCC
 CAGATCAAGTAGGTGTATTCCCCCTGGCAGTCTGGCAACGGAGCCAACAAGAAAATTTAGGTTGTTTA
 AATTCCCTTTTTAAACTTGAGTATTGCGTACTGAGAGTTGATCACAACCTCCATGCTTCATAAGCGGACG
 CCATGTTAGGTCAAACGTGGCACCATGAGTCCTCCGTGGCTCCTGGACAGAGACCCACCTCAAGATCAGA
 AGCCCTTGGATGGCGTGCAGATCTCATTGCTCAATTAGCCTCGAAGNNCTAATTCTCATCCCAGTCTCAGT
 TGGATTTCGGCACTCTCTGCATCGAGTCCTGGACTGAACCAAGCTCTGTGGTT

SEQ. ID. NO:100 AW462175
 GTACTCGGGCGGCCATGGGGGGTTGGCAGGGCAGGTTGCCAGGCCTGGTTCTGTGGGCTCTCGG
 CAGCCCCCTGCAGGTCCAGCCTTGGTTACACGTGCCGCCGCCATGCTAGCCAGCAAGGACTT
 TAACAACGCGGTGAGCCAGGTGAAGGCTCTGAAGGAGGATCCGGCAATGAGGTGAAGGCTGAAACTCTACG
 CGCTCTACAAGCAGGCCACTGAAGGACCTTGTAAACGTGCCAAACCAGGTATGCTGGACTTATCAATAAGA
 CCAAATGGGATGCATGGAACGCTCTGGCAGTCTGTCCAAGGAAGCTGCCGACAGAACTACGTGGACTTGG
 TGTCAGGCTGAGTGCTCCTCTGAGTCCCCAGCCC

SEQ. ID. NO:101 AW464554
 ACGCCTTCCTTCCTACCCAGAAGTAGAAGCCCAGTGGCAGGGCAGCAGCCTGCATAGACTCAAGT
 CTGCCCACTGGTCACTGGCGCTTGGTGGCTCTGGGTCATGCTACCTCTTCCCAAGTTAATTAGA
 TAAATTACACTGGCTGAAGTNGGGACCCCTTCTTCCCTGAGGAGCCCCAAGACCAGAGACAAGGCCAG
 GACAGCTGGGACACACTCCTGGAGAGGTGCACTCCCTCCCTGTTGGGGGAAGCCCAGACCCATGCGA
 ATCAGCTCGCAGCCAGGCTTGACAATCTCGCAGCCTCACGATTGGTCCACTGCCACTTGGTTCTC
 CTGGGCAGGC

SEQ. ID. NO:102 AW464010
 CACCAACGCTGTGGCGCCGGAACGCCAACGGGACCCCGTGTGCAACGCCCTGCCCTACTACAAG
 CTTCACAACGTGAACAGGCCGTGACCATGAAGAAGGAAGGCATCCAGACCCGAACCGGAAGATGTCCAG
 CAAGTCCAAGAAGAGCAAGAAGGGTCCGAGTGTGCTCGAGGAGCTGTGAGGTGTGAGGACAAGGCCT
 CCCCATTCAGGCCGCCGCCCTGGGGGACATGGGCCGTGGGCCACCTGCCGCCCTCAGCCACTCCG
 GTCACATCCTGCCACCCGACGCCATCC

SEQ. ID. NO:103 BF045005
 GATGCGAATACCTGCCCTAACGCCATACATGAAGCACCTCCTCAGCCTGCCATCTGGTGCTGATG
 GACGAGGACGTTGCACTTCTCTACCAAGTGTGCTTACGACGCCAGCAGGTGCTCAAGCCTCCGGCG
 TCGCCCGCGACCCGGAGTAAAAGCGAGTCCCCACAAGCTGCTGGCATTGACCGCATGGCAGCTCCAC
 GAGCAGAGGCCCTGTTGATTTCACTGGAACAGCAAACATGAGCTGAATTCAAAGTTGGAGATGTGATCT
 TCCCTCTCAGTGGATCAATAAGACTGGCTGGAGGGACTGTCCGGGAACACAGGCATCTCCAGTGT
 CCTTGTGAAGATCCTCAAGGACTTCCAGAGGAGGAAGACCCACCAACTGGCTACGCTGCTATTACTATG
 AGGACACCATCAGCACCATCAAGGACATTCAGTGGAGGAGGACCTCAGCAGCACCCACTTCAAGGACT

-continued

TGCTGGAGCTCATGAGGCCTAAAGGCTGCTGGACCTTCCGAACTCTGATCTCTCCCACCCAGGCGGGAGTT

CCAGAGAGAGGACATGCCCTCAACTACCGACGCTG

SEQ. ID. NO:104 BF045561
GGATCCCGGAAGTGGAGACCGGGGTCCCGCAGCGGGCGGCCACGCCGGGATGCG

ACCGTCGTGGGTGGGAGCTGGCGCATCGCCAAGAAGAACGCTTGCCGAGGCCAAGTACAAGGAGCGAGGG

ACTGTCTGGCTGAGGACCAGCTGGCCAGATGTCAGACAGTTGAGATGTCAGACACCTGGAAGAA

TTGCCAGCAAACACAAGCAGGAGATCCGGAAGAACCTGAGTTCCGGTGCAGTTCAAGACATGTGTGCC

ACCATTGGCGTGGAT

SEQ. ID. NO:105 BF046270
AGCCCTTAGATTCCTGGAGTGGACCGGACCACTCTGACTTCCCTGAGAGACCTGGAATCTGAGC

TCTTACAGCCAAGGATCTTGGTGGCTCAAGCTGGGAGGGACCAGGGATGGAAGATAGAAACTGGTATC

AGTGGGACATTCCTGGAATCTGCCGAAGAGGGACCACAGAGAACATCTCAGTCTCTCCTGTGTCCTTA

CCCTTCCCAGAGATAGTTCACCCCGAGTTCTAACCCCTCTTCAGAGGCATCCAGAACGTGATAGCCTA

GGCTGGATGTGCCCTAAGGAAGTGGATTCAAGTCTATACTTGACTCTGACTGTGTAATCCCTGCCCTT

CCATAACCTGTGGAGGTTCTTCCCTTCATAGAGGAGGAAGTGCAGGTGAAAGGTGAAAAATGAC

CATACAGCCAAGCAAACCCAGGATCTACAGAGGAATGCCACTGGTTGAGGCCTCCATACTCCTCATT

CAAATTCCCTCCATTGGATC

SEQ. ID. NO:106 BF043456
GAATTCACCTTATGCCATCATGAATCCTGATGGGTATGAAAAGGCCAGGAAGGAGATCTAGTAAG

TGTAATCGGCAGAAACAACAGCAACAACTTGACCTGAACCGGAATTCCCGGACCAGTTCGTTAGATCAC

AGAGCCCACCCAACCAGAAACTATTGCTGTGATGAGCTGGATGAAGACCTATCCATTGCTGTCAGCAAA

CTGCGATGGAGGACTTTGGTGTAACTACCCCTTTGATGATGATGAAACAGGATTGCCACATATAGTAAA

TCACCAAGATGATGCTGTGTTCAACAAATAGCACTTCTTATTCCAAGGAAACTCACAGATGTTCAAGGTA

GACCTTGTAAAGAACATGTACCTAATGAGTATTTCTCATGGAATAACAAATGGAGCCAGTTGGTACAATGT

CCAGGTGGTATGCAGGACTGAACTATTTGCAAAGAAATTGCTTGAAAGTGAATGACTATTGAACTANNTGTGTG

AAATACCCATTGAGAAAGACCTGCCAAATTGGGACAGAACATGAAAGATCCCTAATCCAGTTATGAA

CAGGTGACTA

SEQ. ID. NO:107 BF040324
GGAGTGAGTCGGCCCCGCTCCCTGCCCGCCGAGTCACCCAGGCCCTAGTGACACTTGCAGCT

CTGCAGCTGGCCAGGGCCAGGAGCTCCCGCCCTGGAGGGCCGCCAGTCGCTGCCACCCAGCGCA

ACCCACGGCGTCCGACTCCCGGATACCAAGCCCTGGAGGGCCGCCAGTCGCTGCCACCCAGCGCC

ACAGTTCCAGACTGGGACCGCGGGCTCGCCACCCCTCCGAGTGGCAGAGGAACCGCCTGGAGGAGCCTG

GCTCGGCCGTTCTGAGGCTCAGTCCTTGAGCTGAAATGAAAATTGCTGCCCTGCGCAAGGA

CACTGCAGCCCCAAGGGACACCCCCAGAACGGAGGACTGACTACTGAACCCCTAGCCACTGCGGA

CACTCCCAACCGTGACCCCTGAGGTGCCTCCGGATGGGATAGAATAAGATACTGGCCTTGGACAGCTANGGT

TCATAGCAAAGGAATGATATTAGTGAGCCGGACTCTTATGACTTCCATGAGAAAGCTAAATTCTT

GATGTG

SEQ. ID. NO:108 AW462307
GGTCCTTATCATCTGTCATCAACATGACTTTGCTGTTATGTCAGGATGAGGGCATATGG

TATTGTTATGTGGTGGCTGCAGTGGCTAGCGTAGCTTATCTGAGCTTGTTATGTCAGGATGAGGGCATATGG

ATTCGACTGGGACATGCTCTGGACTCTGGACACACACGCTTATGAAACCTATCTCTGATGGATGGAGGT

GTCAGTGCCATTGAAGGATACGAGAAGAGATTGTTCCACGTTGCTCTTTCCGTACTCCACATGACTACAA

-continued

TTTGATTATTGAAAGAGTTGTTCAAGGATTCCTCAAAACTACGACTCTGGTTCAAAGCATTGTGCAA
GTTTAGTGTGAAATCTACT

SEQ. ID. NO:109 BF043382
GGGTTCTTGAAGACCTGGCACCTGGAGCGCAGTGGCCTAATCCAGGACTGGAAACATCTGGC

TTGTTTACCTGGACTACATTAGGGTATTGAAATGCTCCGTATACAGCAGGTGGATTGCTCAGGTTATGA
ACTCGAGCAGTGCACACCAAAAGTGCACCTACTGTGCAACAGGATAGAGCAAATCCAGTGTACAATGCCA
GGACCGCCTGGCTCAGTCAGACATGCCAACCTGCTGCGGGTGGTACTGAGCCTTCAGCA
TGCCTCTGATAAACCTCCGACTCAACGCCAGACCCCTCAGCGAGTCCCTTGCCTGTTGGCTCCCCACATT
GGCGGGCCCCCATGCCCTGAGGACTATGCCCTGGAGGAACCTGCGCAGCCTCACACAGTCTACCTGCGGGAA
CTGACTGTCGGAGGCCAGTGAGCCCTNNCTCCACCACACTCACATGCTGTTCACACTCACCACACAG
AGGGCTCTGCATCAAGTGTGATTGCCCTGTTGCCCTCTGGCATGGAATCTCCCTCCC

SEQ. ID. NO:110 BF043624
TTTCTTCCCCCTACAAGGCTCCAGAAGCCCTAGTTGCCCTGACACTTCCCTTTATTAGG
CGTCCCTGTTGGGTGAGAATCATGAAAACAGATCCTCTGCTAGCCTCATGATGAAAGTTGTTAGACAC
CAGCTTCTGGAAACTCGTGTGATTAAATGGCATGTGACCCCTCTGTTCTGGGACTCAATCAGAA
AGGTAAAAGCCATTAACAAAAGTTAGTAAGAGTTTATTCATCTCATATCTCCCTGCCTGGGTTACGGCCT
ACTGACTGAAATAAAATCATTCTGATTGGACGCAGACCTGCTGTTCTGGACTCTGAATCCATGTTCATAT
TTCTCTGGCCACTGAACACCTGGAGATTCCGTTAGGGAGT

SEQ. ID. NO:111 BF440494
AGTTCTTGGAAATCTGACAGCTCAAATTTAGACCCATTAGTTCTAATACAAGTTCATCTTAT
TGTCAAAGTAAAGCAATATTCTGTAATACTTAACTATGAAATGCAAATGAGAACCTTCTCAGAGTAC
TTCTCACGCTCTAGGATTTACTAATTCTCCTCCTTCTAAATAGGGTTAATGTTCAAGGCCAACAAAG
AGCAGTTCTTGATTTGATAAGAGAAAATTGGGATACATTAGCAAGTGTGCCTGATGTAAGCAGCTA
AACACAATAGCCAGCATAGTCATTAACACTGCCTGACATATTCAAGAAAGAACGGCATAGCTAAATGTGAT
TGATGTTGTTATTGTCAGAATCAAAACTCTTAGAGTCCACGGTTGTGTGAAACACACTGGATGTTTCA
CATCAGCTCAATTAAATGGGTTACTGTAGAAAGGAAAAAGCCAATGAAAGGTATCTACAGGCAGACCT
ATTTTACT

SEQ. ID. NO:112 AW461523
GAAAAAAATGGCGCCGACGTGAGCGCAGGCCACCGAAGGAGTCGCCAGCCTAGTTGG
AGCCGCTGAAGCCGCGGAACAAGAGGCTGAACCAAGCTGAGGATGGATGAGGAACCCCTGGGCCAGCC
TGGACATGCCGCTACTGCAGAGCCAGCTCCAGTGAGACCGACAAGGGGTGCCCCAGTTCTGGCTGCTA
TAGACAAATCTCTTCTATGGAGGAGGAGGCCCTGACCGGGCAAGCACACCCCCAGTGTGGGACGTG
GAGGGGCCACCGGAGGGACCCAGCAGGGTGCCTCCCCAGCCCCAGACAGTGGCATTCCGGACCTGGACAC
ACCCTGGCCAACCAGCACTGTCCTGGGACCAAGTGAGGACCTGCGCGTCCAGACGACGCCACCA
GGGAAGCA

SEQ. ID. NO:113 AW461688
TTTTTTTAGAAAGACAAACTGCTTATTAAACACTGGAAAAACATTAAAGGCAAATGTCCA
TTATATAACCAAGAATGTTAACGATTTGAAATGTTAATCTTCTAAATTGTTAGGCACCTCCAGAGAGCT
AAATATTGCAAATTATCCTACCAAGATGTCCTGTAATACCAAAACTTGATATGAAACACACA
ATTACCCAAAGTCACCATGTTAGGTTCAATTAAATTACAAGTAAAGTTGTTCAAGATGTTCTGACACA
TGAAGCGTCCAGTTGAATTCAAGAAATGTTAACAAAGTATCTCCTTTTGCTGTGAATGTTGGTATTG
CTGTATTGTTGGCTTATATCCACTACAGATACTGGTTCTAGGCCAGCCAAAGGGCTTCAAGCATTGAAGGCT

-continued

TGAAATAACTCTCCAACTCATTAGACATTCTCTTCTCTACCACGCCCTGATCCAAATGGTAGATGTCCTT
GGAGAACCTGGGGTGGGTCTGCTGCTG

SEQ. ID. NO:114 BM362465
GCACGAGGCCAGGGTCACCCCTGAGCAGGGAAAGCACCGCGATGCTGACCAGGTTCTGGCCCGCG
CTATGCCAGCTGGCAGAAAATGGTCCCCACGGCGAGCCTGTTGGGCGCTGTGGGTGCCGTGGGCTGG
ATGGGCCACTGACTGGCGCTGATTCTGGACTGGTGCCCTACATCAACGGCAAGTTCAAGAAGGATGACTA
GAECTACAACCTCAGGCCCTCTGATGTCGTGCTGCCCTGCCATCTGCATCTGAACTGCCAGGCT
CTCTGGATGGACTCTAGGAAGTCCCCTGGCAGTCATTTCTTTGGTGGAAATAACTTTGTGTGG
ACACACAGCATTAAACCTCACTCTGAAACCTGAAAAAAAAAAAAAA

SEQ. ID. NO:115 BF440206
ACATTTAACATATTTACGTGCAACGTTAGAAGCTTAAGTTGGTAAAAACTTTCATTCAG
TGGCTGTTAGTACATAAAAGTCTCAGAGTTAAAGGTATACTTGTATTCGATTAGTAATCTCAAGA
ACTCATAGGGAAAGTCAGTATCAGCAGGAAAGTGGTAGCTGGCTGAAACATACCCACAAAAACCCAGAGG
TGAGGGAAAGGCATTTAATGCTTA

SEQ. ID. NO:116 AW464711
ATTTTTTCAGGCCTTCTCCAGGAGCATGTTCCAGTGTACCGCAAAGTACTAACAGTATATAAC
TGACATCGTGTACAGTTGCAAGGCACTCGGATGGCAAACAGTCTTATTCTATACACCTAACGTCAGTAT
GGTGCCTGGCACATTGGCACCTCAAAATATGTTATGGTAAAGGTAGGCTGTATGTTGTCAGCTAG
AAAAACAGTACATCAGCACTTATACTGGTCCCTTCTGGTCAGTGGCACATCTCGTGTAGACTTGA
CTTAAATGGATAAGCACTCCCCAGTGGTCAGAACACTGCGAAAACAGAAGTATGGGAGGTGCAACCTG
GCAGGCAAATGCTGCCTGACAAATACCCCTGGTAGCAAAGGCCCTGACTTGGATGATCCTGATCCCTGGT
TGTCACGAAAGAATAGGATGGATAAATAGACCATATTGACATTAACCT

SEQ. ID. NO:117 AW465606
ACCATTGTTTTGGTTTTAAATTAGACAAAACCGCTTGGAAAGGGAAAGTCTCATGCAG
GTTATAGGTCTTCTGTCTAGGTTCAAGGCTTGCAACTGGACTGCAGACTCTTACCAATACGGGATT
TACCTTTCTGAACACTGCAGTTAGGCTAGAGCTGAAGTTGGAGGAGCCTGAGTGTCTTCAACAGTGA
TGCAATGGATAAAATAGCTGGTTCTATTAACTGTATAGACAGTAAACAAAAATCTTAACT
TAACTAGCTTCTTCAAGATGCGTTTATTTGTCAGTTACAGTCAGTACAGTAACTTACTGCTGGTACAGTT
GTACTCTAACAGATTGATTTGATATCCACGTTACTCCCT

SEQ. ID. NO:118 BF042255
AATATATTACAATCTTCAAAAGTCGTACACTCCTCAGTTCTATTGTGTGATCAGTTGTGTTATT
TGTATTTGTCCTCCCTCTTCAAGAAACCTATCTCTCTTTGCCATCTCAAATTGAGAATCT
CAACTCTGGTTGCTGAACCTGCCTGGCCAGCTCCCACAAGCAATACCTCCCTGTTCCAGCAGGACCAAGGGA
GCCGGCCTTCAGTGAGTGAACCTGTGCAACTGCCTCTCCCTCAAGGGTGGGACCTGGCTGGAGTCCT
GACCCCTGGCTCCAGACAGAGATCTCGCCTCTGCTGTGAGGCAATCTTGGCACACCTGGATTTC
CCCATGACCCAGGTATTTTTGGTCAACGGACTCTGGACTCTCAAAAGGATCTGATCTTGAATT
GCACAGCCCT

SEQ. ID. NO:119 BF042909
GCACGCCCTAACAGTGTGCTGACTATTCTCTAGGACTTGAATTGGAGCTTGAGGGAAAC
GCACCTGGCCTCAGTTACAGAGTGGGCCTGGTAGGATAAAATCAAATTATTGAGTTACTGAGGGAAAC
AAGCATCTGGCTCTTCATCTAGCATCTTAAATCTGAGAATGCTAGCTGAGGGTAAAAGCCTGGGATA
GGCCTGCCCTGAACACTCCTCTGCTGTTATTACAATCTTAGCTGAGCACCTCAACCCCTGGCTGTATATG
CAAATAGTCCAAATAAGCATTATCTTATAAGACTTGACAGGAAGCTAAATTATGAAGCATCTCGCCAG

-continued

GTCCTGACACCTGGGAGGTGCTGAATACTGGTCAAGCTTCTCCGTAGGTACCGCCAGAAAAGGTGGCAGGG

GAAGTGAACCATATATCTGACCTCTGAGCCTTCAGTTAGATTATGGGGTCAGTGGTATAATTAGG

TTTGTAAACAGCAGTAGCCAGTATTGGAGTTATTACACATAATCGAG

SEQ. ID. NO:120 BF042997

TTTTGTGAATTGATTTAAATAATTAAAGGAATATTCTGAAGACTATAGTTCAATTATTAGG

AAAAAATATAAACATACATGTTAAAGATCATTGTAGTGACATTAGAAATAGATTCTCAAATAACA

TAATTAGTTTGTAGTGCTACCAGTGGAAATGCATTCTGCAGAAAACATGGTTACCTTCAGATCTGAGCACAC

TGCCCTTACATCAAAAAAAGAAAAAAGATAATAAAAAAAAAACACAACTTGATTAGTTAAATTTTA

GTAGACGACATCTGATTGTTGAAGAGCAAGTTCTTATTACCTCTCAAGGAAGTGCTTATTTCACC

TCTTCTGAGCATCTTATCCTTTGTAATAAGAACACCCGCAAATTACAGAACTTCATAGCAC

GTGCGATTTGATTAAGATCGGCATAACACTGGCCATGAACATGTAATTGGACTTAGAAAACCCAGGCTGTA

GTTCCTCAACCTTAAGGAATTTCGAAAGCTTGTAC

SEQ. ID. NO:121 AW461908

GGCTCTGGGCTGGGGCCACGTCAGTGGATCCAGCGCTGAGGAGGCGGCACGAGGCCAAGA

AATAAGAAGCGAGGCTGGAGGGCGCTCGCTCAAGAGCGTCTGGACTGAAAGTCATCAGTTCTGGAGGAC

GTGCGGCTGCAGGAGCGCACAGTGGCCCCCTCGATCTATGGCTGACATTCTGCATTTCATCTCCAGTGG

CTTGATATCAGAGGCCCGATGAGAAACTTTCTCGTGGACACTGGCTCAAGGATAAAAGAACTGAACAA

GAAGAGGACCAAGGCCAGAAGAGGTCACTGCTCTCAAGAAGCCCTCCGGAGGCACCTCATCTAGAGA

ACACCTCAAGGTCCTGTTCCAAAGACGTCTCGCCA

SEQ. ID. NO:122 AW462811

TGGACGGCCAGTGGAGCTGATCAAGGCCCTCTGGCCCTGCCATTGGCTCAGACACGTGGTG

GAGGAACCGATCCCTTCCCCGAGACGTTGACGGCAGACCCGACCGGGCTCCGGAGTTATCGTGCAGAC

GGGCGCTACATGCTAGTGGAGAGAACCTGTTACCAACGATGCCCTGAAGGTGACGTTCTCATCACCCG

CATGACCGGGCCAGCTGCACTGGGTGATCCCACATCAGGAAGCAGAGCCCCCTCTCAACGATTACCG

GGGCTTCCCTGGCGAGATGAAGCGGGTTGGATGGTGGAAAGCAGGAGCTTAGGCGGGAGCGCCTC

GGGTCTGGGGGGGGGGTGCTCGGGGGAGGGTCCGCC

SEQ. ID. NO:123 AW461534

CATTTTTTCAGCGGATCAATTTCAGATCCTCAACTCCTGTTGAGTCTATCAAAGATTCACTCAGTG

TGAGAAAATGCCCTTTCTCCCTTACAGAAGGAAGTAGTCTTCTCCCCACATTCACTGTTACTCTAGAGCA

GGACTCAAGATAACAATTGAGTATAGTGTCTGGAAAGTGCAAGCCTTAAACAGGATACGGGTCTCCTCCAG

TGCTGGTGGTTCCAGTTCTGTTCAACAAAATGAAGGAATACCCAGATTCTGAGTATCCTGAGATTA

CCCTGCTACCAACTCCTCTGTTCTATTGCTGTGAAAAAAGGATCATTGCAATTCCATTGTAAA

ACTGAAAATGGAGAACAGAACGACTGTATCGCTGCCGTTCTGC

SEQ. ID. NO:124 AW461574

TTTTTTTTTTCTGATAACGTGTTAATTACGTCCATTCAAAGATACTCCTTCCAGTTAA

AGACGACGCGTGGTGGAGGCCTGGCTGTGTCAGAGGGGGCGGCAGCTCACAGGGGCCAGCTCCT

CCCAGGCCTCACTGGCGTCACGCCACAGCGGCTGGCCTGGGGCGCTGCTCCCTGCTGGCAGCCCCAGGCC

TCTGGGGCCCGACCCCTTGCCCC

SEQ. ID. NO:125 AW465706

GAAAGAACAAATGCTCGGAAGAAAAAACATCACAGTGAAGGAAGTACTACTACTATGAAAGGCAT

AGATCAAGGAGCCTATCTAGTAATAGATCAAAGACTGCATCTACAGGGCCTGACCGGGTGAGAAATGAAAA

-continued

GCCTGGTGGAAACGAAAATACAAAACACGGCATTGGAGGGACTAATGATGTTGCTAACCATGTCATGA
ATTTGCTTCAAAGTAAA

SEQ. ID. NO:126 BF041813
TACAGATGAGGAAATTAAGGCAGAGAGAACTAGGGATTGCGCTGAGGTAGGTCTCGTGC
AAAACCAGTTATATAAACCCTATTTCATTTAATGATGATAGGGGAAAAAAACAGTCCTA
GTAACATCATTAGCTCAGAGAGGAGTGGCAGTGTCCCTGAAATGGATTTCACATAATGGCATTAGAA
GGTATTAAATCATAACAGATCTGACCCGTTCTGGTATGGTTATGCAAAGAACTTAATGAAGTTTCAA
CATGGCTCTAAATTGGGGCATTCTGGTCAAAATTGGTCCCTGGAACCTCAAGGTGCTTCAAATT
AACAAATAACTTGAACACTGACTCCTGCAGTATGGTATGCCTCCCTGCCAGGTGGCTTCTGGATACTC
ATGGCACTCTACGTGCCGCAACCAAGACAAGCAGAGGTTCAACACTGTATTCCCAGNNAGGTATGGCAT
TGATTAAAACCTCAACATTTCAGGTTGAGAAACTGGAAACATCGGAGCAAGTAAGCCTAAAATAG
CCTTGTGTTTCTGGTACTATATCTTCATATAGAACTCAAATTGTGAAAAG

SEQ. ID. NO:127 BF041863
TTTTTTTTTTTGAGCAGCGCTTGATTATTAGCATTAAAAACCCAGTTCAATATACAAAA
CAAGCTGATTTGTTGTCAGTGTAAAAGCACTCCTTAAATTAACATTTAACGATGGATTAATG
AGTGATTCCTGGAAAGCACTCAGTGAATGAATTTGCAATGAAACATCAGATGCACACCACGGGG
CACCAAGGGGNNNNGGGATCCACAGGGCTGCTCATCACAGCGTCTGACCCAGACACTGTAGGTGCCACACA
CGTCCCCGGTGGGTATTGCCGCTAACGACCCAGGGCGGGGACGACTGTGAAAATTCACTGCACGTTAGA
ATAACGAGCAACTCAGCTGCAACTAACCTGCCAGGCCACCGCAGCTGCAGCGATGAGCCGTGACA
CTCGGGCGNNCACTGAAAGTCGCTGGACAATGTTGTGAACGTCATGCTCGCTGTGGCCCCG

SEQ. ID. NO:128 BF044557
ATTCAATGAAGCTACAGAGGTTCTGGACTGTTAGTGGTTAGGAACCAAGCCATCAACGTCAGT
CAGCCCTCTGAGGATGGCGTATGGCGGAAGTGTCCATTCTCACTGTGGCTGGTGTGGTGAAGTGGCTG
GTCTACGGTGAACGTGCTGTAAGGCATCTGCTGAGGAGAAAGGGCTGTAGTACATTAATTAAAGA
TAATTAGAAAATGGAGTAACTGGCAGAGAAAGAGGAAGCGTAATTACTACTATATGGGATCTAAA
AACAGACCCAACAGAAAGTCATTATTGCCAGGAGCCAGTGTGAGGAGCTCCGCCGTGGAAAGGTCA
GGAAGGAGGCTGGCAGACGCAAGGGGATCAAGCCTCAGGAGTCCCTGGAAATTCTGAGCTTCTAC
CCCCAAACCAGAGTCTGCCTACTTCTGCTTGTGCTCACCTACACCTCTGACTTACGGGGCTGTCCCC
TACCAACCTCTCTGAAAAGAGTTAAATTACAG

SEQ. ID. NO:129 BF046723
TATTTTGCCAGGTTCCCGTCTCAAATGCACAGGCTGGATTGTTACATCATGGTATCTCCATCC
TGGGTGGACAAACGGCAATGAGTTAAGATTACAGCCCTTAATCCTACCCAGCAGTCAACTGGAGAC
CTTGGGGTCACCAACTCAATCTGGGATCCAGAAGGTGACCTGCCTCAACCTGCCTAGGGATCTGGTCC
CTTGGAGGTTGTGACGCTCAGCCTGCTGGAGATCTGCCAGTCCAGGGTCCAGGAGGTTGACGTGCCTC
GACCTGCCTGAGGATCTGACCCCTGACCCAGGGAAAGCCAGCTCTCAGGTTGCAACAGTACTGGTAGGATA
AGCTTCAGAAAGACTCACCCCTAACGTAAGTCCACCCATGGAAATAGAAGGAAGCCTATTAGTTGTGGACTG
TGCCCCAGTTCAACAATAACTCANGTCCAACAAGAACCCATTGCCCTCTGGAAGTCTAAAAGAGGCC
CTCCCAAAGTTGCCATCTGGACTTAGACTCTTACGAGGGACAGGTGATTTAAAGGAC

SEQ. ID. NO:130 BF440382
TTTTTTTTTTTTAAATATGAAGGAGAAACATAAGGTTGGGAGGGATAGCAGGAAAGAAATG
ACATCAATTATCTTACATATCCCCTCTAGGCAGTTCTCAGACATCAGATCTTAACTTGGGTGT
GGATCAGCTTCATACTCATAAAGGGACCAGTTAAACATGCATAAGCCTGGAGACTCCAGGATGGTC

-continued

TCCCTCCCTCTTTAAATGCTGTGGACTAGAAAGGCGCCACTTGCTAAAAACTCTACATCAGTGTCCCTGG
 AGCCCCGAGGCTCCTCAGGTTCCCTGAAGACCTAAAGGATAGCACAGAAAAACTTCTCCCTAAATGG
 GTTTCTGAAGCCGGAACAGGTGTCAGGAGGGATCTCCTGGCATGCGTTCACAGTAGGCCATCAAATCT
 GCAGCTGCCTGGACACCTTATCCTATCGATGTTGGCTTCATCTCAGCTGTTCTACCAGTTCTGGCTTG
 TGCTATGCTGGGGTGTGCTGGCATTGGAATGCTGGTAGGTTTC

SEQ. ID. NO:131 AW463169
 AAGAGTACCACTCGGGAGCAGCTCGAGCCGCTCCCTGCAGGGCTGGCTGCTACGTACACCTT

TATCTGAAACATTTGACTACCTGAGGGTAACAACATGCCATGATGCCCTGGTGAACCTGTCTACGAC
 TGCCTCTCCGGCTGGCCAGCCCAGCCTGAGCAAGGAGGAGGAGTGGACTGCCTGGGCTGCAGCTG
 CATCGGGTCGGGAGCAGCTGGAGAAGATGAATGGG

SEQ. ID. NO:132 AW463234
 GGCACCAAACCCAAACCGCAGTGCCCAAGTCACAAGCCACGGAGGAGTCTATGAAGCNNNATGTA
 AAGGAGAAAACATCGCAGAAGATATCTAGATCAAACAATAGACAAAGAAAGCCAAGCCACTTGAAGT
 TAAAAAAAGTCTTGACTGACCGTACACCGTGGGATTGTCCACACATCCTGCTGGGGTCTGGCGCCACCCCA
 TCAACAGGAACCAAGAGCCGGGGGAGCCTCCAGCCCCCTCCCTGAGGCCAGAGGGAGCCTTTGGAGAAA
 CAAGTACCAAGCAGATGGGAGCTGGCTTCCCTGTTCAAAACAGAAAAATTGAAAAGCAGGCAGC
 AGNNGGAATCTTAAAGGCTGAGGAAGAGATTGGAAAGATCAGCTGCCATGCAAAATTGAAGCCAGCCCCT

SEQ. ID. NO:133 BF039617
 TGAATTGCTACACCCCTCTCAGGTGATCTCCGAACCCAGGGATCAAACCCACGGCTCCTGCAGCTC
 CTGCACTGCAGGCAGATTCTTACTGCTGAGCCACCAGGGAGCCCTAGAGTACATAGGCTGAGTATAATG
 TCATAGATCAGAAGGGCCTGCTTGTGACATTCCCTAGATCCTGCTTGAACGCCATTGGTCATTAATC
 CACATTCTAGTCATCACAAATCTTAAAGGTATCACATCTCTGTGTTTAAAGCGACCAGTGAAGA
 CTATAAGCTCTGGAAAATATGAATAAAACTAACCGCCTGAAGTATCTGAAATGAAAGATATTGCTATAAA
 CATTAGTAGAAACTTAAAGGACTTAAACCAGAAGTGTAAAGTAAATTTACAATTAAACATATTGTTGTA
 TTAAATGTTCAATTGCTTGTGCTTG

SEQ. ID. NO:134 BF039493
 GGAAATGGCGATTCCCTGGGGGGGGCTGGGAAGCCTCCTGCAGTGGGCCAGTACTGCTA
 GGGGTGCTAGGAGCAAAGGAAGAACACAAGGTGGAAGAATAGTGGAGTCGGTACTTGCAGTATGAAAAG
 AAAGCCCCAGAGGCTCCTGCAGCAGATGCATTAAAGGCCGGTGGGACATGCCCTGCAGGTGGAACAAA
 ATCCAGCCAGCTCAAAGAGCAAAGATGGCAGTGGCTTGACAAAGGCAACCTGCAGTCACTTGCTGGA
 GGGGCATGACACTGCCTGTGACCTGGATCTCAGGCATTGATAAAAGTGTGGTCCGAAAGACTCCA
 CAACTAAAAAAAAAGTCAAAGAAAGCCGAGTTGTATCCTCTGTGAGTGAAGAGGCCAGATCTG
 TTACAAGCAATGGAATGATGGAGTCCCAGACTCTCCTTGACCCCTGCTGACCGTGAAGATGGAGAATGGC
 CTGTCTGCATTGAAAGAACAGGCAGAAAAGAACCTAGAAATATTGTGAAAGAGA

SEQ. ID. NO:135 AW461726
 TTTATTGAGTCAGCTCATGATCAGAGTCACTCATACCTGATCATGGCAAGGAAGTACGCCCTG
 TCCCTTATCTCTCCCTTCTGTAAGCTCCAGGCCCTGGCATGCAATTGTCCTCATCCTCTCTAGTCCAGTT
 AGTGAAGCACTCTCACATAACCATAGCCTCCGCTTGCTGGCTTTTTGTTCTGCCATGGAGTATGTG
 CAAGGCCAGTGCATGGATGTGAAAACCTGTCATTGCCAGGTACAAAAAGGAGTCATCACTACCCTACTG

-continued

TCCGAAGCCCTGAGCTGTATTCTGGCCTCACTCTAAAATGGCCTGCTTAGAGCTGATGGCCAAGCAGTAAG
 CTGCAGGTGTGGGTGCCACAGGTAACTCTGGAAGGAGCACAGGGGATGGTCAGGCCAGCTGGACCACCAT
 CTA

SEQ. ID. NO:136 AW463524
 ATGTTCCCTACCATGTTGGGAGAAGCTGAACGGCACAGACCTGAGGACGTGATCCGTAACGCC
 TCGCCTGCTCGACGAGGAGGCCTCAGGTTCATCCATGAGGACCACCTCGGGAGCTGCTACCACCATGG
 TGACGGCTTCACAGACGAGGAGGTGGACGAGATGTACCGAGAGGCGCCATTGATAAGAAAGGCAACTTCA
 ACTATGTGGAGTTCACCCGATCCTCAAACACGGGCCAAGGACAAGGATGACTAGGCCATCCCAGCGGCC
 CTGCCCGNNNCTGTCCCAGCCACCTGCTCCACATATACCGTATGCACCAGCTCCATGCCATGAGGCCAGA
 GCCCCCTCTCAGAGGACTIONCCTGAGGGCCGGGGCCAGCTCCAGTGAAGGAAACGGGCTGAGAA
 AGCACAGCACCAAGGCCAGGGCAGAGCCAGCGGGAGGCCGGTGACCCCTCCAAGGAAACCCATCTTCG
 GAGCTGGGCCAGGGGGCTGGACCGGG

SEQ. ID. NO:137 AW465396
 AAGCCCATCACCTTCCTGATGGACGCTCTTACCTGCAGGAATCTTAGTCTCCCTCCTTTATGGA
 CTTCATCACAAACCGAACAGTGTGGCGAATCCAGAGGTGTTGACCCAACCCGGTCTCACCAGGTTACTC
 AACACAGCTATGCCCTCCTGCCCTCTCAGGAGGATCCAGGAACCTGCATCGGAAGCAGTTGCCATGAATG
 AGTTGAAGGTGGCGTGGCCCTGACCTGCTTCGAGCTGTCAACAGATCCCTCAGGGTCCCTGTGCC
 CACTCCAATCATGGTGTGAGATCCAAAATGGGATCCACTTGCAGCTCAGGAAACTGTCTGATCCAGGACT
 TTGTGATTAGATGAACAACATCATATAAGACAGACTTGTCTCTGTCTGGTGATTAGGATGAGGACACCTGG
 GCAGCCATTGCTGGACATGTTAAGTCTTGTGTGACCACTCAGCCTGTCCTCGGCTCTCCAGTGCCTACC
 CATGTGTCAGTCATGTGGCTTCCCTCTCTGCTCTCCCTTAATAAGTTGCATG

SEQ. ID. NO:138 AW465666
 GCTCAAAATATGCGCATGCCCTTGTCAAGCAGGCTGGCCTGACTCCATCAGTTACCTAACAA
 AATAACAATTCTCCTTGATTATTGCAATTCTAAATTCTGATAATGATCTTACATTCCACTTTCCCCAGT
 TATACTTCCACATGATAACACCAGAGAAGAAGATCCTTCTACTGAAGAACACAAGAAATTGAATAGT
 TCCTTCTCCTGCACANNNCAGAAACAAACTTCCAATGACAAAAAATGTCAGACTTTTCAGTTCCAA
 TACGTTCATAGAAAATAAGTAAGAACTATTTAAATACTAAAAAATAAAATAAAACCAAAATCCAGT
 GTCATGTGGCCTGGGTTCTAAAAACAAAAACAAAAACGAAAGCTGTACATAAAACATCCTNNCCG
 GTCCATTCAGCATGCTTTCAACAGAAGTCCCAATTATGATGGCGCTGGAAAGGGATTGGCATT
 TATATCCTCC

SEQ. ID. NO:139 BF040830
 GTTATCTGTACCTGGACTTGTCTGCTATGGAACAGCTGTTGTTGACAAACACCTTGAAAACCTTG
 AACACCTGACCCCTTGAAACCTTACCCCTTACACCTTACCGCGTGCCAGGCCCTTCTGACTTTCACTGGTT
 GACTCTGCCCTTCCCTCCAGAGCTGGCTGGACCATCGCTCTGGTACCCGTGGAAGTTAGGCGCACAG
 CAGCTTCCAGCTGCCATGCAGAGACCTCCAGCTCAGAACAGGCTCGTCTGCCAGGCCAGACCCCTCTG
 TTCCCTCAACCAGTTCTCTGCGACTCGGAAGCGATGCAACCCAGGGAAAGAAACCTTTATCAACATGGGCC
 TTGTCCACATGTCTGGCTTAAGACTCAAAGGGCCTTGAAAGCCACATTTGATGAGTTGGTAAATG
 AGTTGGGCACACAGGGATTAAATTCTGAAAAGCAGCTTAAAGAAATTAGCAGAGTAAATTAAT
 GGTGAAATGGGTGCTTAATCCTCGTCAACCCCTAAGTTTATTGAAAATGGCAAGATTGTTAATTCAAG

-continued

TGCTCTTGGCTTGCTTGAGCAAAAGGATGGACTCTCTCCAAGTCTCCATTAACTGGTGGAAAGATGGG

GCTTTG

SEQ. ID. NO:140 BF040980
 TTTTTTTTTTTTGAGCAATGACATTAACTTCTGGAAATGATTGGGTATCTGAGAACACGCTGT
 GGGCGGCTATGCTGGCTCCCGATGTGGAGCTGGGCCCGCTCCGAAGGGGTCCTGCCCGGGTGGAA
 GGAGCGGGCGGCCGCGGGCCCTGACCGGCAGGGCGGGCAGCCCGGGCGNCGGAGCTCCAGAATGGC
 ACAGCANNNGGCCATGGAGAGGCTCAAGGACCGGAGGGTCGACACGCTCGGCCGGGCAAACCTCCATG
 CCCTCGACGTCCACTTCTGCTCCAGTCGTCGGAGACGGCNGAGCCGTGCTGTCGGTGCACGCGCT
 CCAGGCTCTGCCCGACA

SEQ. ID. NO:141 BM364711
 GCACGAGCCCAGTTGAGCGTGGGAAGGGATGAACAGCGTTACAGGAGTTACTCAGGAACAAG
 GAACCCCTCTGAGATCTCAGAACCTGCACTGTGAGAAGACAGACAGACAAACAACTAAGGATTAAGGC
 ACACTGCTTATCATCAGGCTTACAACACTCACACAGGAATGCCAAGACTTGGTATGGATCAGCTGCCATGTT
 TGCCCATGCAGGAAGAGAGGGTTGGTACACCAATGTACGCATTCTCAACAGGCCAACCATCTGCTTG
 GGATGTGTTCTCACTGTATGCAAATGCTCAGAAGAAACAGGGCTACAAACACACACTGTACTCTAGTTA
 AGGACTGGCCAGCTGGAGGGTCACTGGTACGTGAACCTGGAACCTCTGCAATGCATCTCCAAAATAA
 GATGGGCTGGTGGACGGACAGGGCAGAGACAGCTGTGTATGTCGGTACAAAAGGCCACGGTAGGTGTT
 CAGGCCTTCATGGCTTTGACTTCTGTGCAT

SEQ. ID. NO:142 BF039094
 GCTGATGGACCTGGTGGAGCGCCAGCTCGGGCCTGGCCTCACGGAGCCTGAGCCTGAGCTGC
 GGTGGACCGCCTGCAGGCCGTGCTTGTCCGCGGTGGCAATGAGGATGTGGTCCAGTGCATGGAGCTGGACGG
 GGGCTGGCAGTTGCTCAGGACCTCGCCTGGCACGGAGGAAGGTGTACCCGGCTGGCCAGTGGCATGGAAA
 GTTCGCAGGCCCGGGCTGCCCTGGTGTGAAGCTGCTTCAACCACAGAGTAGCATGTATGAGGTCCA
 GAGGGTCACCTCCACAGCCTCCTGGCTGAGCTGCTCAGCAGCAATGTGGTGAACGACCTGATGCTCC
 GTCACGTGCTACAACCTGATGGCACGGCAGAGGACACGAGCGCCCGGTGCGGAGGCTGGTGTCCACGG
 CCTGGCAACATCACCTGGCTCCAGATAAGGTACAGACCCACAGCCCCAACTCCTGACAGCCATGAT
 CGGTGGCTGGACGGACAGGGGACGACCCACACAGCCTGGTGGCGCT

SEQ. ID. NO:143 BM366975
 GCACGAGCCACCCCTGCCTTCTCCTGGGAGCTAGCATGATGGGACTGAGGCCGA
 GGGGAGACAGGCCCGTCCAAAGCTGCTGCTCCCTTGGCTTGGGAGTTGAAGCCTGGACACC
 GTTCTTAGGGCTCCGGCTTCTCCCTCCCTGCCCTCTCTTGCTGTGATGCCAGGCTGTACAGC
 CCAGCCTCTCCAAGCAGCAGGAGGCCACTGCTCTAGGCAGCTTGTGCTGCAAGCCTGGAAACGA
 GTTGTCCACGCCAGTGGCAGAGACAAAACCCGGTTTAGGCCGGTGTGGAGGACAGACTGGCAAAG
 CGGGGGATAGACGAGGGGCCGGTGTCTCAGGATAGCAGGCTGTGCAAGGACCCGGGTCTGGGCAC
 AGGGAAATGCAACCCGCTGGCAGCCCTGGGCAC

SEQ. ID. NO:144 BF044410
 ACCTGAGGTTCTCCAGATGAGGCCCTACAATGAAAAGGCGGACGTGTTCTTATGGTATCATCCTCT
 GTGAGATCATGCCCGCATCCAGGCTGATCCAGACTATCTTCCCGAACAGAGAATTCTGGCTAGACTATG
 ATGCTTCCAGCACATGGTGGAGACTGTCCCCAGACTTCTGAGCTCACCTCAACTGCTGTAATATGGA
 CCCCAAACACGCCATCCTTGTGGAGATTGGAAGACCTGGAGGAATTCTGAGCCGGTACAGGAGGA
 AGAGCTGGAGAGAGACAGGAAGCTGAGGCCACAGCCAAGGGACTTGGAGAAAGGACCTGGGGTGAAGC
 GACTGAGCTTACTGGATGACAAGATAACGCCAAGTCCCCACGCCAAGACGTACCATCTGGCTGTCGAA

-continued

GCCAGTCAGACATTTCTCCAATAAGCCCCACGTACAGTGAACGTCTTCTGATTAACTCCCTGAGTAAACT
GTTATAATAATGAAAAATGTGTAECTCATGGCAGTAGTAGGTACAGAGATGCCCTTCTGTGATGTTACTGG
CTCTGATTCTCATTCACTATT

SEQ. ID. NO:145 AW465824
GGAGGGGGCCTCAGGGTGGAAAGAGCAAGAGCGGGACCACACCTGCCTCCTCACTCACTGCCCTCTC
CCTGTCCTCATGCAGGGCAGTCCCACAAGCTTGAACGACGCTCTGCCCTGCCCTCCGGGCCCTA
TGGGGCCCTGCCCTGGCAGGAGCTCTCCACCCGGCCGCCCTCTCACTGCACTGGTGGCGTCCAT
GCTGCAGCCAACCCCTTCACGGCAGCTCCGGGCCATGGACCTTCTGAGTCCCAGCACCCACATTGATC
CCTTGCGTCCCACAAGCTCGCCTCTGGCTGCCCTCCAACGGGCCCTTGGAGGCCTGGCAGCCC
CACATTCAACTCCGGCGCGTCTTGCCCAGAAAAGAAAGTCCAGGGCCACCAGCCTCGCCTCCCCCA
GACCCATGGGGCGCCTGCACCGCAGTCCTCGCCTTGCCTGGGACGCTGCCTCCGGGCCCT

SEQ. ID. NO:146 BF045830
CGGGGTGGTGTACGCCCTGGACTACAGTGCAGGGAGCTGGTGGGACGCTGCCTCCGGAGAGGC
GATTGGTCACCGTGTGGAGGGACGGAAGAGGAGACGGACTGGTGGGAGCTGGCATGGCA
GGAGGGTTACGTGCCCTGTAACACTTACGGCTCTTCCCCAGGGTAAGCCTCAGAGGAGTAAGGTGTAGCT
GGAGAGAAGGACGTTCCAAGGGAGACAGGATGAAGCAGCAGTCCTCGCTCCAGACCTCCTCCTCT
TCCGCTGCATATCTGTACCCCCAACGCCCTGCAGCGTGGGTCTTGCCAACAGCTCTCGAAACCTG
GGGAGAACGAGAACCCGAGCTAAACTTAGAACGCTGCCT

SEQ. ID. NO:147 BF046712
GCTTCCTGAATGGAGGCAGATGAAGGTAGAACAGCTATTCAGAACAGAACAGACTG
ACAACCTTCAGTCGGATGGTCAACGAGTCTGAAAAATGCTCTCCACCGCTTCAGGAGCTCCGGAGATC
ATCCTGGGAAGCCGCTACAGCACACCCATCGACATATGGAGTTGGCTGCATCCTTGCAAGAACTTTAACAG
GACAGCCGCTCTCCCTGGAGAGGTGAAGGGAGCACAGCTGGCCTGTATGATGAACTTCTGGGATGCCAC
CAGCAAACACTCTGGAACAAATCCAAACGTGCCAAGTACTTTATTAACCTCCAAGGGCTGCCTCGTACTGTT
TGTGACCACGCAGGCCGATGGGAGGGCTGTGCTTGTGGAGGTGCTCGCGAGGGTAAGAACGGGTC
CCCCAGGCAGCAAAGATTGGGTGACGGCANTGAAAGGGTGTGAGGACTACTTATTAT

SEQ. ID. NO:148 BF039623
ATTTCCTGTTTATCTTAAGGTCTTTGGTTCATCACGGTACAGTATGTTGTAGATCATGCAATGAA
ATTGTCTTCTCCACCGATCCCTCATTGTCATGACACTGTCAGGCTGCACACTGTTCAAGGTCTGACTCTGTG
CTCTCCGGAGAGTCACACAGAGGTAAGGGTAAGGCAAGTCACTCTTAACAGAGAACAGATAGTTAATAC
GAAAACCTGCATATTTTTTTGGTACTCATTAAAATTATTTAAAATTGTTATTTTAATTGNNN
GATAATTGCTTACAGTATTCTTGGTTCTGCCATACATCAATATGAATCAGCCATAGGTATACATATG
CCTCCCCCTGAAGCT

SEQ. ID. NO:149 AW465584
ACAGCCAGGTGCCGTGAGAGAGGTGAAGAACCCNNAGACAGCAGGAGAGACAGTGGGATCTC
GGAGCAGGAGTGTGGTGGCCAGGGAGCCTGGGCCGCCAGGGACGTGCTTACATGGGATACTGTCTGTGA
GGCGCTTGGAACCGTACCTGATGGTGGGAAGCAATCAGTAAAGACCGTTAGGCCACCTGCTGAAGTCTTGC
CTTTCCAGTCCCCACTGCTAGGGTCTCCGCCCGGCCAGGCTTCAAGGCTGGACATCGCTCTCTGCTCCG
TCTCACCCCTACATCTCTCCACGTGCTGCCGATGGAGCCTT

SEQ. ID. NO:150 AW462929
AGATTAACACATTTATATAATGACTCTTAAAGCTTACACCTTGGGCCANNGTACTCCTTGGCAG
AATACATTTAGATATAAAAGACGTTATTAATACATTGCACAGTTGTCAAACACGAAACCGAACGC

-continued

TGCTCGCGGCAGCTGCCGC GGTTGCTGCTACATGGACGNNNCCAGCCGAGGCCGAGCGCTCCTCTCCTGTCC
ACTGCCAACGGGCTCCGTCAAGGGCTTTGAGCAGGAGGCT

SEQ. ID. NO:151 BM366972
GCACGAGGTAAAAGCAACAATCAACTAGCCGAAACGAGCCTCTAAATTCCGTCTACTCCAGTGC

CGCTTCTCTAAAGTTGCTCCACGGTCCAGTCACAGTTCTCAGGGCTCTGGCGGTCTCCAAACGCTGTGTT
CACAGGAAAACAGGGTCCACAGGAAGGGAGGTATGCGGACGCCCTGGTAAGCACCTGTACAGCGCGA
TACCGCGGGGTCTCAGTTCTCCGGCTTGTGGCTGGCGCAAGGCTGCAAGCATCTCTCCATCAAG
TTGAAGCGGACTCGCGTTGCTCTCATTCTCGGAATGGGAAGTAGTTGAGAAGATCGAAGTGCCCCATGT
AGGAGCAGTAGGAGTCGCGGTGCTGGTTACCAGCATTCCCACCTCGTGGTGTCCCGTGGCCGGTGGGA
TGTACTTGGACTGCAGATGCTAGCTGGCTGTAATGGGTAGCGGTCCGTATCTCACCGCTTTCCCTTG
CTCCCAGGTGAAAGGCAGCCACTACAGGCACTCGCTCTGAACTTCA

SEQ. ID. NO:152 BF041965
TTGATGAGGGCAGAACCCAGGGCTGGCGTACCCCTGGGCCACCTGCTTCGCCCCACCCAGGG

CTGGAGCGACCCATAGAGGTGCCACCTCCCTCTGATGGCAGCCCCAGCCACGCTCCCCAGCCAAGTGCT
CTCCCTCAGACAGCCAGAGACACCTGGAAGCCCTCCCTGCTCCACCATTCCTGCTGGGAACCTGAAGGTCTC
TCAGAGGCTTGACCCCTGTGGCTTGCTCCCTCGGTCTGGGACCCCCAGTGTGCTGCTGACGTCTGTCTG
GGGCTCACCTGCGAGGAGCCGTTCTGAGCTGCCCCATTACCCCTCCCCCAACTACCCAGGTGGTGGTCC
TCCCTGCTCAAGGCTTGAGGGCTGGCACAGGTAGGCAGGGCAGATCCTGCTGCTGCTGCAACCGCCCCGCT
GGCACCTAGTGGTGTAGCTGCTGGTTGAATGTCAGCACCCCTGCAAGGCACTTTAAAGGAGTGTAT
GTTGCTG

SEQ. ID. NO:153 BM365835
GCACGAGGAAGAAGATCCTTGCAGAGAGCATGTTCTGGTGAGGATCTCTCATCCCTCCAGAA

GAGGAGAAGAGGAAACACAAGAGAAGCGCTGGTGAGGCCAACATNNNTATTCATGGATGTAAAATG
CCCAGGATGCTATAAAATCACCAACCGCTTTAGCCATGCACAAACAGTAGTCTTGTTGAGGATCTACT
GTCCTCTGCCAGCCTACAGGAGGAAAGCGAGGCTTACAGAAGGATGCTTTCAGACGGAAGCAGCACTAA
AAGTACCCCTGTATCAAGATGAAGGGAAACCATCCAAATAAACACGTTTGGATAAAAAAAAAAAAAAA

SEQ. ID. NO:154 BF045124
TGTAAGATGCCAAGACAGGACGTGATGCCGTGACGCTTGAAACAGTGCTCAATCCTGAGAGATG

AGCATCAGTTACACAAGGACTTCTTATCCGAGCAGTGATTGTGAGAAGAGAAGGATGCCGATAGAA
ATGTACTGAAGAATATCAAATGCAGGAAGTATGCTTCAACATGCTACAGCTGATGGCTTCCCAAGTACTA
CAGACCTCCAGAGGGACTTATGGAAAGGTGACACCTAACGTTACCAACATGAAATAAACAGGAACACA
AATAACGCTTCCGTTGAAAATCTCCACCGTTTGTGTTCTGATGAATT

SEQ. ID. NO:155 BF040256
GATGAATCATCTGACCGAAGATGGCTGCTACCTGACATTCTTGTGAAACAGGACACAGAA

TTGACTCAAGTTATAGCAACACCAAGCAAGCACAGTCAGACATCCTGGTTGGAGGAGCCTGACCAATT
GAACCCCGATCCTTACTCATCACCGTGTACCTGGCAGGCCAGAGGCCGACTTCTATGTAAGGACTC
ATTGGAAAAGTCCCTGATGCTGGAAAGATTGACGGCAGGGAGAAGAGGGCGTCAGAGGACAAGATGGC
TGGATAGCATCTGGTCAATGGATATGAACTTGGCAAACCTCAGGAGATGGTGGAGGACAGAGAGGC
GGCGTGTGAAGTCCATGGGTGATCACAGAGCATCAAGCCGAGTCCCTGTGTTATAGCAGCTTCCAGT

-continued

GGCTATCTATTACACAAGAAGCCGAAGCCTGCTCCTCCACCCCTGCAGTAGAGGCTCTTGAAGACGGGT

AAGCAGATTGTTCCAGTGTAAACTACGCTCCTGATCCCGTGA

SEQ. ID. NO:156 BM364415
GCACGAGCGGGATGGGGGGCTGGCAGCCTTGACAAGGCTCGGGTCGAGAGAGCCTGG

CCCCAGGGCTCTCCCACAGCCTCAGCAGTGGAAAGCAGCTCAGGGCAGCATCTCAGCTCCAGGAGA

CCCCATGGGTACCCCATGGCCCATCGAGCAGCTGGCCAGGTTCAACCCCTCCTCAGCAGTGCCTTGCT

GGCAGGGAGTGGCTCTCTGAGGAAACAGGGTCCCCCTTGCCTACCAGTTAATGCCGGCACCC

AGGAACCCGGAATAGAGGCAGGGCTGTGGCCAAGTAGATCAGAAGGANAAGACAGGGGGAGCGTGGG

GGTCCTGGTCCAGGGCACTTCCATGACCACCCCTGCTCCATGAAGGCCCCCTGGATGTCACTGCAGCAG

GGAGAGCCAAGGGCGTGTGGTGGCTGGCTCCACAGAAGGAGACTAGGGATAACAACCAGA

CAGGCCTGATAAGAGGCACTCAAC

SEQ. ID. NO:157 BM365799
GCACGAGGGTTACTCCGTGGAGTTGGAGCTTGGCCTCCAGGCGCTGAGGGCCGGTCAAATG

GAGTCTCCGTGGTGCCTCTATGGGTCTGGAGGTACTCGCCGGAACGTGCGCGTTGCCCTCCCGGGTGG

TGTTCTACTGTAGAAGAGCAGGGACTGGCTAGAGAGGGAGGTATGCTGGCTGCTCGAACGGACAGG

ACCCATACAATATACTTGCCCCAAAGGCAACCTCAGGTACCAAGGAGGACCTAATTAGTCCCCTCATCAC

CAACAAGCGGATAGTGGCTGCATCTGTGAAGNAGNAAACAGTACTGTATCTGGTCTGGCTGCACAAAGG

CGAGGCCAGCGATGCCAGCTGTGGAACCCATTACAAGCTGGTGCACACCA

SEQ. ID. NO:158 AW462329
GTGACCGGCCGATGCGTGTGGCCCTGGCCGCGCTTCCACCCGGACCACCTGCACCTCTG

CCTGCGCCGCTACCAAGGGCTCTTCCAGGAGCGCGGGCAAGCCCTACTGCCAGCCCTGCTTCAA

GCTCTTGGCTGACCGCTGCCGGCTGCCCTCGGGAAAGCGGAGCCACAAAGACCTGCCCTTCCCC

ACCCCTCAAAGATCGGGCTCTAGACCCCAAGGCTTGTGGAGCTTGGCTCCACGAGCCGGCT

TCTTGAGGCCTACCCACTGCAGGGACTGGCCCTGAAGATACTGTACGTTCCGTGGCGAGTCAGAAA

AGGCTCCGTGAACCTTAAGGCCACACGCCCTCCGAAGTGGTCCGTACACTGACCGATCCCACGTGAGCCC

TTCACTTTGTTCC

SEQ. ID. NO:159 AW462136
AGGCTGAGAGGAAGGACGGTAGGCCACCCGTCCACGTGGACAACTGCATCCTGAATGCCGAGGCC

TCGTGTGCATCAAGGAGCCCTGCTACACTTCCGGACTTCAGGCCATTCTTATCTGAACGAAGACTT

TGATGGAGGAAACTTTATTCAGTAAGATGCCAAGACCGTATGGCAGAGGTGCAGCCCAGTGC

AGGGCTGTGGATTCTTCCGGCACGGAAACCCGATGGAGTAAAGGCCGTACCAAGAGGGCAGCGCTG

TGCCATGCCCTCTGGTCACCTTGATGCTGACACAGCGAGAGGGAGCGAGTGCAGGGAGCACCTGGT

AAAGATGCTTTAGCCAGA

SEQ. ID. NO:160 BF041338
TGAATAAGGAAACTGTGGAAAGTTTCCAAACAGACATTGCAGAAAATGCTTGAAAATGCCTT

AGAAACAGAAATTCTACTGTCAGTGTAGCTGACGAAGAATTCTCCCTCAGAGAAAATCGTTGAC

CTGGTGGTAGCAGTTAACGTTGCACTGGGTGAATGACCTCCTAGAGCACCTTGAACTCCGGTGTCTTACA

TAAAACAGATGGCGTGTTCATTGGCAATGTTGGAGGTGACACGCTTTGAACCTCCGGTGTCTTACA

GTAGCGGAAACAGAGAGGGAGGGCTTTCTCCGACGCTCCCTTCACTGCTGTCATGACTTAGGA

CATCTGCTGGAGAGCTGGCTTAATACTCTGACTGTGGACACTGATGAAATTCAAGTTAACTATCCTGGG

-continued

TGTTTGAAATTGATGGAAGATTACAAGAAGAAAGTCCAGAACATTGACCTAATTGCAAAAACGCGTATCAG
CTGAGGAACACATGAGAAGTTGGAGGCTTCACAGTAGTTAAGGGATGGGTGAGAG

SEQ. ID. NO:161 BF041765
GCCCGAGGGAGGCAGAGGCTCCACCTCGGCCAACGGCTCGGGGGAGGCTGCCAGGCCGGCG
GACATCGTGTTCATGAAGACGCACAAGACGCCAGCACGACCGCTGCTCAACATCCTGTTCCGCTCGGCCAG
AAGCACGGCTCAAGTTCGCTCCCCAACGGCGAACGACTTCGACTATCCCGCTTCTCGCGCAGCC
TGGTGCAGGACTACCGCCGGGCTGCTCAACATCATCTGCAACCACATGCGCTTCAACTACGACGAGG
TNCGGGGCCCTGGTGGCGCCAACGCCACCTTCATCACCGTGTGCGCACCCGCCCTTCGAGTCC
CCTTCCACTACTTCGNCTCCGTGGTCCCTCACGTGGAAAGCTCTGGGCCGACAAGCTGGCGAGTTCT
GCAGGACCCCAGCGCTACTACGACCCCGCGCTACACGCCACTACCTCCGGAACCTGCTCTTCGAC
CTGGGCTACGACAGCGACCTGGACCCAGCAGCCC

SEQ. ID. NO:162 BF045167
GGTGAGAAGTGACGATTGGAACACAAGTACAGCTCACGCCGCTGGACTGGTCATGCTGGACAC
AACATCGCTTACTGGCTGGACCCAGGACCAGTGCAGATCCACCTGCTTGGAACGTCGTGATCTGGC
CTCCGCCAGCCTGCCACCTGGTACGCCCTGCTGTTACATGGTACCTGCTCAGACGAGAGAGTC
TCCGACCTCCCTGAAGACCGCTGGCTGCCTGGCTGGCTGGCCGGGCTCTGGCCCGGGGCTGGCTGTG
AACTACCTGCCTTCTTCCTGATGGAGAAGACGCTTCCCTACCAACTACCTGCCGGCCTCACCTCCAGAT
CCTGCTGCTGCCGTGGCCTGGAGCACATCAGCGACCACCTGTCAGGTCCAGCTCAAAGGAGCCTTC
ACGGCCCTGGTGTGCGATGGTCACCTCTGCCCTGTCACGTGTCACATGCTGCCCGCTGACCTATGGGT
ACAGGTCGCTGTCACCCAGTGAGCTC

SEQ. ID. NO:163 BM362349
GCACGAGGACTAGCGAGATGGCGGGCTGCAGCGATTGGTGGGTCCGAGGCAAATTGGTCTT
CGTGAATTGCTATCCATTGCGCAGCGCTGCCCGCAGCGAGGGCGTCAGGACTTCATTGAGAACGC
TATGTGGAGCTGAAGAAAGCGAATCCGACCTGCCATCCTAATCGCGAGTGTGCTGGATGTGAGCCAAAG
CTCTGGGCCGCTACGCAATTGCCAAGAGAAGAATGTCTCTGAAACAATTTCAGTGCTGATCAGGTAAC
GAGCCCTGGAGAACGTGCTAAGTAGCAAAGCCTGAAAGTCTCACTGAGGATTTAAACACAGCCGAGAG
TCTGGGCTCTGTTGACTGAGAACATGTGGAAATGTATTGTTCTGTATAAGATTGTGCTGAAATGC
TGTCTAAAAATGATCTGATTGGATCCCACCAACTACCCATTATTGTGCAACCACATGAGGGAAAGCAGTTGA
ATATAAAAATAAAACCTTATTCTGT

SEQ. ID. NO:164 AW462081
CTCTTTGTTAACGAGAGATTAACTCTGTGGTATTGTGACAAATGGGAAGAAGAGACATAGTGT
TAAGGCCAAGTTGGTGGCTTAGCTAAACTGAGAAAGAAATTTCACAGTGGAAAGGCTGGGGCTGGTCACA
ACTCAGACCCAGGCCACACAGCTGCCCTGTGGAGACCTTGCCTGGACTTTGCTTGGCTCTCGCTTA
AAGCCAAGGCAGCACTGTGGATTCTGTAAAGCCACAAAGAGCAATTCACTGAGTGGGGAGCACACAA
ATTATGGGAAAGGGGGCAGTCTACAGCAGGATTATATCAGGGTTATGTTATTAGGAACCTCTCTGTGCA
ATCATGTTGATAAGATGTGAGAGAGATGGACATAGATCCTTGCAACTCAATCTGTTACTCTCCCTAAATT
ATACCTTTGAGGAAGTTTATCTAATTA

SEQ. ID. NO:165 BF042546
CAACCCCTCAACGCCATGCAGATCCTGTGGATCAACATCATCATGGACGGGCCGCGCAGAGC
CTGGGTGTGGAGGCCGGTGGAGAAGGACACACTCCGGCAGCCGCCGGAACGTCAGGACAGATCCTGAG
CCGAGCCCTGTCTGCCGATCCTCTCGGCCACCACCATCATCAGCGGGACCCCTTCATCTCTGTGAAAG
GAGATGCCGAGGGACAGGGCAAGCACCCTCGCACCAACCATGGCCTCACCTGCTTGTGTTCTCGACC

-continued

TCTTCACGCCTTGACCTGCCGCTCCAGACCAAGCTGATCTCGAGATCGGCTTCCCTCGGAACCGCACGTT
 CCTCTACTCTGTGCTCGGCTCCATCCTGGGACAGCTGGCTGTCAATTACACGCCGCCCTGCAGAGGGTCTTC
 CAGACAGAGAGCTGGGGCGCTGGATTATTGCTTTAACCGATTGGCCTCGTGTGTTCATCTGTCAG
 AGCTCTCAAGCTGTGAAAGTTCTGCTGCAGAGCCCAGAAAAGCCC

SEQ. ID. NO:166 BF043129
 GCTCTCTCAACCTAAAGAAGACTGGCGCCACGACCTCCTGGTCCCTCCGCCCTATTAGGTC
 GCTGCAGATCTGTGAAACGGTGCAGGGCGAAAAGTCAGACTCTTCAGGGAGTTCCGGCAGTTGAGGAT
 GCACCGGGGAGGGCTGTCGGGCGCTGGAAACAGAGATTGAAAGCAGCAGGAAACCGGAACGACCTGACC
 GCAGAAGGAATGCAGAGTAGGGCAGTAAATAGAGTGTGTTT

SEQ. ID. NO:167 BF043441
 ATTTGTTCTGTCTTACCTGCCTTCAATTAAAGCCCTGACTCAATTGGTGTGAGAAGGAACAAAA
 CCCAGGCCATCCCAGTGCTCTGCCCTCAGCACCAAGGGCCAGCATGGACCTGGTAAGGAGGGCACAGTG
 GATATCCACCCAAGACAGGGAAATGAGGATTATGAGGAACATGAAATGTAGTGGATAAAACTAGACCCCTCTG
 ATGCCTCAGCTCCAGCATGTCTCAAAAGCAGTTCAATGTCTGGGAGGAACAGGGCTGTCATAGCTCAAA
 ACCACCAACCTTACCCATTATTCCTGGTCCCTCAGAACAGCAGTGCTGGGAGAAACATGAATATTGATTG
 GTTGAGATTACCAAAAAATGCAAGGCAAGTGTGTTGTGGGGAGCTGGTTGTGATTGAGGCGGTGGA
 TTAATTCTGAGTTGAGTCCACAGGGTCGGAACGGATACAACGTGAGCAGTAACGCTTCACTGAGCTCTGT
 GGAGCTCAGATGGTAAAGAATCTGCCTGAGTGCAAGAGACCAAGGTTCAATCCCTGAGTTGGAGGATCC
 CCTGGAGAAGATAATGGCAACCTATCCAGTATTCTGCCTGGAAATNCCATGGAGCTGTAGTCTGATGGC

TACA

SEQ. ID. NO:167 BF043441
 ATTTGTTCTGTCTTACCTGCCTTCAATTAAAGCCCTGACTCAATTGGTGTGAGAAGGAACAAAA
 CCCAGGCCATCCCAGTGCTCTGCCCTCAGCACCAAGGGCCAGCATGGACCTGGTAAGGAGGGCACAGTG
 GATATCCACCCAAGACAGGGAAATGAGGATTATGAGGAACATGAAATGTAGTGGATAAAACTAGACCCCTCTG
 ATGCCTCAGCTCCAGCATGTCTCAAAAGCAGTTCAATGTCTGGGAGGAACAGGGCTGTCATAGCTCAAA
 ACCACCAACCTTACCCATTATTCCTGGTCCCTCAGAACAGCAGTGCTGGGAGAAACATGAATATTGATTG
 GTTGAGATTACCAAAAAATGCAAGGCAAGTGTGTTGTGGGGAGCTGGTTGTGATTGAGGCGGTGGA
 TTAATTCTGAGTTGAGTCCACAGGGTCGGAACGGATACAACGTGAGCAGTAACGCTTCACTGAGCTCTGT
 GGAGCTCAGATGGTAAAGAATCTGCCTGAGTGCAAGAGACCAAGGTTCAATCCCTGAGTTGGAGGATCC
 CCTGGAGAAGATAATGGCAACCTATCCAGTATTCTGCCTGGAAATNCCATGGAGCTGTAGTCTGATGGC

TACA

SEQ. ID. NO:167 BF043441
 ATTTGTTCTGTCTTACCTGCCTTCAATTAAAGCCCTGACTCAATTGGTGTGAGAAGGAACAAAA
 CCCAGGCCATCCCAGTGCTCTGCCCTCAGCACCAAGGGCCAGCATGGACCTGGTAAGGAGGGCACAGTG
 GATATCCACCCAAGACAGGGAAATGAGGATTATGAGGAACATGAAATGTAGTGGATAAAACTAGACCCCTCTG
 ATGCCTCAGCTCCAGCATGTCTCAAAAGCAGTTCAATGTCTGGGAGGAACAGGGCTGTCATAGCTCAAA
 ACCACCAACCTTACCCATTATTCCTGGTCCCTCAGAACAGCAGTGCTGGGAGAAACATGAATATTGATTG
 GTTGAGATTACCAAAAAATGCAAGGCAAGTGTGTTGTGGGGAGCTGGTTGTGATTGAGGCGGTGGA
 TTAATTCTGAGTTGAGTCCACAGGGTCGGAACGGATACAACGTGAGCAGTAACGCTTCACTGAGCTCTGT

-continued

GGTAGCTCAGATGGTAAAGAATCTGCCTGCAGTGGAAGAGACCANGTTCAATCCCTGAGTTGGAGGATCC

CCTGGAGAAGATAATGCCAACCTATCCAGTATTCTGCCTGGAAATNCATGGAGCTGTAGTCTGATGGC

TACA

SEQ. ID. NO:168 BF043441
ATTGTCTGCTTCACCTGCCTCATTAAGCCCTGACTCAATTGGTGTGAGAAGGAACAAAA

CCCAGGCCATCCAGTGCTCTGCCCTCAGCACCAAGGGCCAGCATGGACCTGTAAGGAGGGCACAGTG

GATATCCACCAAGACAGGGAAATGAGGATTATGAGGAACATGAATGTAGTGGATAAACTAGACCCCTG

ATGCCTCAGCTCCAGCATGCTCTCAAAGCAGTTCAATGTCTGGGGAGGAACAGGGCTGTCAAGCTCAA

ACCACCAACCTTACCCATTATTCTGGTCTCCAGAACAGCAGTGCTGGGGAGAAACATGAATATTG

GTTGAGATTACCAAAAAATGCAAGGCAAGTGTGTTGGGGAGCTGGTTGTGATTGAGGCGGTGGA

TTAATTCTGAGTTGAGTCCACAGGGCGGAACGGATAACTGAGCGACTAACCGTTCACTGAGCTCTGT

GGTAGCTCAGATGGTAAAGAATCTGCCTGCAGTGCAAGAGACCANGTTCAATCCCTGAGTTGGAGGATCC

CCTGGAGAAGATAATGCCAACCTATCCAGTATTCTGCCTGGAAATNCATGGAGCTGTAGTCTGATGGC

TACA

SEQ. ID. NO:168 BF043441
ATTGTCTGCTTCACCTGCCTCATTAAGCCCTGACTCAATTGGTGTGAGAAGGAACAAAA

CCCAGGCCATCCAGTGCTCTGCCCTCAGCACCAAGGGCCAGCATGGACCTGTAAGGAGGGCACAGTG

GATATCCACCAAGACAGGGAAATGAGGATTATGAGGAACATGAATGTAGTGGATAAACTAGACCCCTG

ATGCCTCAGCTCCAGCATGCTCTCAAAGCAGTTCAATGTCTGGGGAGGAACAGGGCTGTCAAGCTCAA

ACCACCAACCTTACCCATTATTCTGGTCTCCAGAACAGCAGTGCTGGGGAGAAACATGAATATTG

GTTGAGATTACCAAAAAATGCAAGGCAAGTGTGTTGGGGAGCTGGTTGTGATTGAGGCGGTGGA

TTAATTCTGAGTTGAGTCCACAGGGCGGAACGGATAACTGAGCGACTAACCGTTCACTGAGCTCTGT

GGTAGCTCAGATGGTAAAGAATCTGCCTGCAGTGCAAGAGACCANGTTCAATCCCTGAGTTGGAGGATCC

CCTGGAGAAGATAATGCCAACCTATCCAGTATTCTGCCTGGAAATNCATGGAGCTGTAGTCTGATGGC

TACA

SEQ. ID. NO:168 BF043441
ATTGTCTGCTTCACCTGCCTCATTAAGCCCTGACTCAATTGGTGTGAGAAGGAACAAAA

CCCAGGCCATCCAGTGCTCTGCCCTCAGCACCAAGGGCCAGCATGGACCTGTAAGGAGGGCACAGTG

GATATCCACCAAGACAGGGAAATGAGGATTATGAGGAACATGAATGTAGTGGATAAACTAGACCCCTG

ATGCCTCAGCTCCAGCATGCTCTCAAAGCAGTTCAATGTCTGGGGAGGAACAGGGCTGTCAAGCTCAA

ACCACCAACCTTACCCATTATTCTGGTCTCCAGAACAGCAGTGCTGGGGAGNAACATGAATATTG

GTTGAGATTACCAAAAAATGCAAGGCAAGTGTGTTGGGGAGCTGGTTGTGATTGAGGCGGTGGA

TTAATTCTGAGTTGAGTCCACAGGGCGGAACGGATAACTGAGCGACTAACCGTTCACTGAGCTCTGT

GGTAGCTCAGATGGTAAAGAATCTGCCTGCAGTGCAAGAGACCANGTTCAATCCCTGAGTTGGAGGATCC

CCTGGAGAAGATAATGCCAACCTATCCAGTATTCTGCCTGGAAATNCATGGAGCTGTAGTCTGATGGC

TACA

SEQ. ID. NO:169 BF043441
ATTGTCTGCTTCACCTGCCTCATTAAGCCCTGACTCAATTGGTGTGAGAAGGAACAAAA

CCCAGGCCATCCAGTGCTCTGCCCTCAGCACCAAGGGCCAGCATGGACCTGTAAGGAGGGCACAGTG

GATATCCACCAAGACAGGGAAATGAGGATTATGAGGAACATGAATGTAGTGGATAAACTAGACCCCTG

ATGCCTCAGCTCCAGCATGCTCTCAAAGCAGTTCAATGTCTGGGGAGGAACAGGGCTGTCAAGCTCAA

ACCACCAACCTTACCCATTATTCTGGTCTCCAGAACAGCAGTGCTGGGGAGAAACATGAATATTG

-continued

GTTTGAGATTACCAAAAAAATGCAAGGCAAGTGTGGGGAAAGCTGGTTGTGATTGAGGCAGTGG

TTAATTCTGAGTTGAGTCAGAGGGCGGAACCTGGATAACAACGTGAGCAGACTAACCGTTCACTGAGCTCCTGT

GGTAGCTCAGATGGTAAAGAATCTGCCTGCAGTGCAAGAGACCANGGTCATCCCTGAGTTGGAGGATCC

CCTGGAGAAGATAATGGCAACCTATCCAGTATTCTGCCTGGAAATNCATGGAGCTGTAGTCTGATGGC

TACA

SEQ. ID. NO:169 BF043441

ATTGTGTTCTGCTTCACCTGCCTTCATTAAGCCCTGACTCAATTGGTGTGAGAAGGAACAAA

CCCAGGCCATCCAGTGTCTGCCCTCAGCACCCAGGGCCAGCATGGACCTGGTAAGGAGGGCACAGTG

GATATCCACCCAAGACAGGGAAATGAGGATTATGAGGAACATGAATGTAGTGGATAAAACTAGACCCCTCTG

ATGCCCTGAGCTCCAGCATGTCTCAAAGCAGTTCAATGTCAGGGAGAACAGGGCTGTCACTGCTCAA

ACCACCAACCTCTACCCATTATTCTGGTCTCCAGAACAGCAGTGCTGGGGAGAACATGAATATTCTTG

GTTTGAGATTACCAAAAAAATGCAAGGCAAGTGTGGGGAAAGCTGGTTGTGATTGAGGCAGTGG

TTAATTCTGAGTTGAGTCACAGGGCGGAACCTGGATAACAACGTGAGCAGACTAACCGTTCACTGAGCTCCTGT

GGTAGCTCAGATGGTAAAGAATCTGCCTGCAGTGCAAGAGACCANGGTCATCCCTGAGTTGGAGGATCC

CCTGGAGAAGATAATGGCAACCTATCCAGTATTCTGCCTGGAAATNCATGGAGCTGTAGTCTGATGGC

TACA

SEQ. ID. NO:169 BF043441

ATTGTGTTCTGCTTCACCTGCCTTCATTAAGCCCTGACTCAATTGGTGTGAGAAGGAACAAA

CCCAGGCCATCCAGTGTCTGCCCTCAGCACCCAGGGCCAGCATGGACCTGGTAAGGAGGGCACAGTG

GATATCCACCCAAGACAGGGAAATGAGGATTATGAGGAACATGAATGTAGTGGATAAAACTAGACCCCTCTG

ATGCCCTGAGCTCCAGCATGTCTCAAAGCAGTTCAATGTCAGGGAGAACAGGGCTGTCACTGCTCAA

ACCACCAACCTCTACCCATTATTCTGGTCTCCAGAACAGCAGTGCTGGGGAGAACATGAATATTCTTG

GTTTGAGATTACCAAAAAAATGCAAGGCAAGTGTGGGGAAAGCTGGTTGTGATTGAGGCAGTGG

TTAATTCTGAGTTGAGTCACAGGGCGGAACCTGGATAACAACGTGAGCAGACTAACCGTTCACTGAGCTCCTGT

GGTAGCTCAGATGGTAAAGAATCTGCCTGCAGTGCAAGAGACCANGGTCATCCCTGAGTTGGAGGATCC

CCTGGAGAAGATAATGGCAACCTATCCAGTATTCTGCCTGGAAATNCATGGAGCTGTAGTCTGATGGC

TACA

SEQ. ID. NO:170 BM361957

GCACGAGGAGGCCTTCAGGATGGTCAGCGTCTGACGTACCGTGTAGGCTGTCTACAATAGAGCC

TCTAACAAAACAGGCTGTCCCCGACCCCTGGTAACAGAATTGTTACCTTATACCAAGAAGGTTGGAAA

GCACCAAAATCTGCATGTGGTGTGTGCCAGGCCACTGAGAGGGCTTCGTGAGACCAAAAGTTCTC

ATGAGGTTGTCTAAACGAAGAACACGTCAAGCCGAGCCTATGGGGTCCATGTGTGCTAAATGTGTCCGC

GACAGGATCAAGCGCGTTCTTATTGAAGAGCAGAAGATCGTTGTGAAAGTATTGAAAGCACAAGCACAG

AGTCAGAAAGCTAAATAAAATGAACCGTTTGAGTAATAATCAAAAAAAAAAAACTCGAGG

GGGGC

SEQ. ID. NO:171 BM362618

GCACGAGCCTGGCTGGGGCGGGAGCAGGTGGCTGGAGGGACCCGTGCCCTGGTGTGGCG

CCAGGGCCGACTCCCGTGGATCTTCTGTGAAAAACCTCGGGTGGCAGCGTGTGCTGGTGGCTCAGCC

TCTGACAGTGTGTTACAGACAAGGCCGTACCCCTGGGAAGGGTGCCTCCAGCGTCCCTGGCTCTTG

AACCGCTACTTGAATTAACCGTAGGCCTGCTGTAGAGTCCACTGTGTTATTGAAACAAGGCATGTTCAAT

-continued

CCAAAGTGTATCGTCAAAGGTACTAACTTGAGTAGAAGAATTACAGATGACTCTTTAATAAAATT
CTCCCTTTCCAAAAAAAAAAAAAA

SEQ. ID. NO:172 AW461418
AGTATATGGTATGTCATCGAGTGAAGATAATGTTAATAAGAAAGAAAATGCATTGTTCAGATG
GCAGATGCAAATCAAGCTCAACTAGCAATGAATCATCTGAGCGGTCAAAGACTTATGGAAAGTGCCTCGT
GCTACACTGTCCAAGCATCAAGCGGTTAGCTCCTCGAGAGGGACAAGAACAGCAAGGTCTGACTAAGGAT
TTAGCAATAGTCCTTGACATCGCTTAAAAACCTGGCTCTAAAACCTCCAGAATATTTCCCCGTCAGC
TACTCTGCATCTTCAACATCCCCCTCTGTTACAGTAGATGACTGAAGAACATTTTCAACANAGCTGGA
TGTTCAAGTGAAGGCTTTAAATTCTCCAGAAAGATCGCAAATGGCACTCATTCA

SEQ. ID. NO:173 AW461640
GGAGATGATGAATTTTGACCTTGACTACTAGGTAGTCGACATGGTCCGGCAAAACGTGCCT
CACCCCTCCAGCATCCAACCCAAGGAGCATCCCGTGGATCCAAACAGATCCCTGCCTTACAATTGGAA
CATTTCGGAACTTAATCCATGAGCATTGGATATTGAAAAGAAAACCAGAAACAAACAGACCCAACCCCTAC
ACTTGGTTGTATGGTGTAGCGCAGCAGCCTACAACTAGTTCTAAATGCCACTTGGACTAATTAAAA
AAGAATCCCAGTTTACTTTACTCGATGGTAAATTGGTGTCTGTATTATGGGAAAAAACAAAAA
GATTTTTAACCTCATACATAGAACAAAAACTTAACGTGTAAACCTTCAA

SEQ. ID. NO:174 AW461984
GGAAGGGTGTGGTCAGGAGCTCTGGCGGTGGCTCTCCCTGGGGTCCGCACAGCATCCGGT
CCAGGAAGTCTCGCAGCACCGGGGAGACCTGTAGGAGTTCTCGACTTGGGGTGGGGCTGTCCGAAGCC
TCTTCATGGCTTGACAGGGAGTCACTGAAGTAAGGTGGTCTCCATCCACCATCTCAATCACCATGATGCC
CAGAGACCAGATATCTACCTCAGTTGCATACAGAGACCTGGAGATCACTCTGGAGCCATCCAGTATGGGGT
TCCCACC

SEQ. ID. NO:175 BF041453
GAGTTGACACGACTGAGTGAATGACTGAACTGAATGAGTGGACTGTGTTGGGG
ATCTGATTGAACTTCCATGGAACTTATAACTGAGGGAGGAGGGAACTGGGGCTGGAGAGCAACAGT
GGGAAGGCTGATAAACACCACCACTACAACAGTGTGCTTCTGCGCAGGATGGAAAACACATGCATCCG
CACTGTGCAAATCACCACCTCTTCACACCCAGACAGGTGGTGGTACTGCAAATACCTGGGGCCACTGA
GGACACTGGAGGGACACTACTTGCAGGAATGTTACTCATAGAACTGTTCAACTGTGATGAAACAGTC
ATTGGGAGTGAACCTCACACCAATTGAGATGTGTAAAATGAATTATGAAATTGGATCCAGTTT
CTTTGCATATATAAGGAAGCTTTCCCTCCCTGAAATAGTCCTGGCATGTGGTAGGCACCTCAAATATT
TATTGAATGAATCAATGAAAGAATATTGTCTTAAAAAAAAAAAAAA

SEQ. ID. NO:176 BF042148
GAATGACAGCAGTGTCTTCTGTTTTTTTTAAATTAAACAGACCAGCCTTAACGTGGGTT
GAATCCTAAAGGACATTGCCACAGTGTGACTCAAGGAAGTATTGGTGGCAGGTGAGCACCAGTGACAG
CCAAATGGAGGGACATACTTGACATGGTCAAGTATTCTCTAAATTCCAGGAAGTTCTTGCAGATGAAG
AAAAACATTTCCTCCCCCTTCCCCACCCACCGTTTTTTTTTTTTA

SEQ. ID. NO:177 BF042689
ATCAGGAGAAGGAAGTGTGGTCAATAAGCCCTACGGTCTCCCTGTGACGGTGGCC
CAAGCTCTGCATCAGTGTACTGCCTGTGGCAAAGATACTCCATGGCCCAAGGCAAAGCCGCTGCA
CCTGTGCCATGGCTGGACAAGGAAACCACAGGTGAAATGGTGTGGCTGGGAAAAGAAGTGGCGCATCA
AGTCCAAGAGCTGTTAGAACCCGTAGGTGACAAGAAGTACTGGGCCATCACCGTGCAGCAGCAGCAT
TGAAGCGGGAGTCGTGGACATCCCCATCGAGNNNGAGGCGCAGGGCAGCAGCATCACCACAAAGATGA
CGCTGTCCCCGAGCTACCGCATGGACGACGGGAAAGATGGTGGGGTGCAGCAGCCGGAACGCACAGCTG

-continued

GCAGTGACTCAGTACCGGGTGCTGAGCAGCAGCCTGTCCGCCCTCTGGAGCTCCAGCTATCACGGGA

ATAAAACATCAG

SEQ. ID. NO:178 BF045165
AAGATTAAAATTTCTACATTTAAACAAACTCGAAAGAATTTTTGGAATGTTGAGGAGGAC

TTCACACCTGTTCCAGAGTGTGGATACCAAGCGAAGGAAATAGAACAGATAAAATGGAATCCGATACTGAT
GAAAATGGACACATTCTGGTGGGCCAGTGGAGAAAAACAGCAAACAGCACTGCTGGCATCGTCCGTA
GTCGATTACGAGCTGAGATGCCCTGGCCTGAGGCATCATCCTGACGACCCGGGTTTGGAAATCAGTG
CAGTGGCGCTCTCAGATCTCTAGAACAAACACTGGAGCTTATAGGAAGCAATATTAATGGAATCCTTATGG
GTTAGGAAGCAAAAGCATCCATTACATCTCTTATACCACATGGAGCGTTCAAATAAGAAATCTACCTACC
TTGAAGCACAGTGTCTGTTGCTGGTTGATGGTTGCAGAGAGGGTAAATTGAAGGAATAGTATGGGAT
TGCAATGATGGTTGTTAATCAAGGCCATGGCACCCTGGTTATGTTGGCGATCCCAGATACTTATAT
GAATTCAAAACCAAGTTATTATCAACATGAATCTGAACAAATATGAGTA

SEQ. ID. NO:179 AW461802
GACAGACATTATGGCCACCTTCCAAGAGCAGCCAGCCAGCCGTCAGGCAGCCCCAGGCCAGAGGA

TGAAGATGCCGCTTAGACGAGTACGACCTCTACAGCCTGGCTCATCTTACCCGGAGTGGAGGCCGAA
AGTCGGACCAAGAGAGAACGCCATCAACACCAACCGCCACAGCCCTGGGGCATGAGAGGAAGCTGG
TGACCAAGCTCAGAACACGGCGGGAAAGCGAGGGCACGGCCCTGAGACAGGACTGGAGATGAGGCC
AGAGGACGGACACCCACAGCAATGGAATAGGACTGAGGAAGAGCCAGCCCTGGGGCGGGATCCAGGCC
TGCTTGGCCACCCACCCACCCAGGACTTACCTGACTGAGACTCTGGGGCACCGAGGAAGCAC
CCCCGGCCCCAGAGAAAGGACAAGATGAGAAGCA

SEQ. ID. NO:180 AW464520
ATGAAAGTATCTGCTGAATTGGTTGGTGTACATTACATTCAATGATCCAGTGAAGAAAGGAATTGAC

TTGGGGCCTTACGAAATACAGAACAGGGCACCCTTAAGACCCCTATAGCATTATCAAGGAAGGAATCCAG
GCCCCATTCTGGGCTGTTTACACATCAGCACTTAGTGTCAATTGACCTGATGAATAGCATATCCATAG
AGATCGAGATGATAAGGGTAAAAACTAAATTCAAGTCCACCCCTTGCTGGCATGTCCAAACCA
GAACCTGTTGCTATTCTCCCTAGCTACCAAGTGAACATGTTATGTTAATGCTGAGAAAAGCTGTG
TCCTTAAGTCTAAGTATCCTGAAAGAGTTGGTAACTACTCACATGAACTTGCTTGTGACCATAGGGT
GATCAACACGCTTCTGGCATCTC

SEQ. ID. NO:181 AW465157
GGCAGCCCGCGCTACCGAGGTGTCCCCGGAGCTGAAGGATCGAAAGAGGATGCAAAGGGATG

GAGGACGAAGGCCAGACAAATCAAGCAGAGCGAAGTCGGACCAATTCAACCTGGAAACAACCTCAACGA
GCTGGAAAGGCTTTGATGAGACTCACTACCCGGACGCCCTATGCGTGAAGAAGCTGAGCCAAACGGCTGG
GCTGTCGAGGGCGGAGTGCAGGTTGGTTCAAAATCGAAGAGCTAAATGAGAAAGCAAGAAAATCAACT
TCATAAAGGCGTCTCATAGGAGCTGCCAGCCAATTGAAAGCTTGTAGAGTAGCACCCTATGTCATGTAGGT
GCTTTAAGGATGCCATTCAAGCAGGTCAGGCCAGCTGCAGGTGGACAGCGCCGTGGCGAGGCCAC
CACCTGCACCCGACCTGGCGCGACGCCCTACATGATGTT

SEQ. ID. NO:182 BF039056
ATGGCTGGAGGCAGTCTTCAAGCCCCAACAAATCCACTCCAGCCTGCGTGGAGTCCACTCAGAC

AGACAGATTCTGTGGCTAAACAGCCAGGATATAGAAAGCCAGTCCATCCCCAGCATCCTGAGGAGCC
CTCCTGAAGGCCACGAAGATGAGCGGGCTCTGGCTCTGCAGCCCTCTCCTCTGGC

SEQ. ID. NO:183 BF040869
GTCATTGGCATGAGATCTTCATTAAGCTGAAACACGACTCACGCTACGTCCATCAAATCCTTG
CTGTGCGGACTGCCGTGATGGGTGTATCTGTTCTCATTGGCCTTGGCATCTAAAGTACCGAGGGAGTAT

-continued

CAGAAGTACGCGCTGCTGTGGATGGAGAGCTTGCAGTGCGCCTCCGGCTTCCTGGCCATGCTGTCCACTG
AGGTCTCTGTCCTCTGCTCACATACTTGACCCCTGGAGAAGTCCCTGGCCGTGCTTTCCCTTC

SEQ. ID. NO:184 BF043917
TGTGTGGTGTCAAGATGCCAGCCTCAGGAAGCCAGTCAAAGAGGGATGTGGCCACAGAAAAAGA

ACACCGAAAACAAGCACAAAGCAAGCAAAGAATAAAAATCAGAGAAAAGTAGTAGTTCTGAGAG
TACAGACAGCAGCAGGCCAGACTGAAGAAGGGCCCACAGACCTGTCACCCAGGAGTTGCTGAGACGGC
TGAAGCGCTTCCAGTAAGGGAGCAGTAATTGAAATTCTGCCCTGCCGTCACCCAGGAGTTGCTGAGACGGC
ATGGAAGTTCAATTGATCACTCAGTTACATTGATAGATTGATTTATGTAATTCATGCTGTGAAATA
ATTTTTTTAAACCTTGACATTCAAAGCCTGCTGGAAAGTTGCTGAAATTGATTCTATTTAACTTCT
GTTAGTGTCAAGGAAAGAAATTCAAGACTGTACAGTTAATTAAAGGCATTTGTAAA

SEQ. ID. NO:185 BF045154
TGTAAGCTATAGTTCATAGAACAGGGCTTATTGCTGAATCCTCCCTCCCTGAGTTCATAA
TTGGTGTGGCACATAGTAGGTTAGCTGGAGAAATTGTAAGTAAAGAAAAGGTCAAGTCTAGGCAA
GGTTTCCATCAGNATGCACTCCGCCTGCTGTGTTCAACAACCCAAAGGGCTATAAGCTGTATTCTGTTCC
CTGCCCTCAGAGGTTCAATGCTGAATAATCAGCACCTCCAAGGCCTGACCTCACCCATTGGTCGTT
TAGAACCCCTGCTCCTCTCTAAAGGAATAGCCATTGCTATAGGACTGTTCCATGCTCCTCAACACTGCT
AATTAGTAACCATAATTCTATAACAAGTCATGGCACTAAATAGCCTCTACAGAGAAATGAAATGTT
GAACCCCTGAAGCACTTAACCAAAGGATCAATCTACTGTGGAGTT

SEQ. ID. NO:186 AW461470
GGGCTTCGCACTGTTCATCCAAACACATCACTTCCCTTAAGACCTGTGGAAGCAGTCCTGGACACA
TCCGCCATGGTCTTACCAACACCTGCCGCCATCCGGCTGTTCTGGTGGCTCTCAATTGCTTGGCC
TGTCTGTCAATTGCACTAAAGCCAGAGGAACGAGATACTACGAGCCCCACCCAGCTGAAACTCGCCTCATC
GCTTTACCCCTCAGTAAGAAATAATCAACTGCTGCTGAAACACTGAGGATCCNNCACTGAAAAATGGAC
AGAAGCCCCAGCCTTCAGGGAGTTATTCTAGGACAGGGAGAACAAACCGCTGACAGAATAAGTAAGCAGAAT
ATCTAGTACATGGAAGCACTATG

SEQ. ID. NO:187 AW464274
GCTATTCTGACCTGTGGGGCGTGTGGCTTCTGGGTGGCTAGGCATGCTGCCCAGGGCTGTGGC
AAGACTCCTGATGCTCTGGACCACCCGTACTGGGTGATACTGGCCCTGTACCCGTGGCTGAGGCGCCACT
GGCTTGGTGGCCCTGACTATGGCCTACGGCTCACATCAGGGCCCTGACCCAGTGGCTTCTCCGTGCTGC
CTGAACTGGTGGGACTGGAAAGATATACTGTGGCTGGACTGGTACAGATGGTAGAAAGCATGGGGGG
CTGCTGGGGCTCTGTCAAGTTACCTCCGGATGTGACAGGCAACTACACAGCTTCTTGTGGTAGCTG
GGCCTTCCCTGCGAGGAAGTGGAGTTCTCATCACTTGGCCACTTCTCTGCTCAGCTCCTACCTCC
AAGCCCCAGGATCTGTAAACA

SEQ. ID. NO:188 BF044013
GTGGCCATGGCTTACGTTGACTCGCTGCTGCAGGCGGCCCTCTCGCGTCAATGCCATGCCGT
GCTTCACGAGGAGCGTTCCCTCAAGAACATTGGCTGGGAACAGACCAGGAATTGGAGGATCGGAGAAG
AGCCAGGAATTAAATCTCAGCTAATGAACCTTATTGATCTGTAAGAACCGTGTGAGAGTGCCTATTGATAA
TAGTAAACTCAATTGCAATTGATTACTTTACTGTTGGTGAAGATCAGTGGGGAAACGGAGACTCCAAA
GAAGAGCTGCCAGCAGAAGTTATTACTCAGTCTTATTGAAGTACATATCTAGCTGGCTCTCCCTGGAC
TTGACAAAAATGTAACCTGACAATAAAACCAAGAGTCCCTATTCTGATTAAAAATGTTGACTTAC

-continued

AGTTTATTGTAAAAAGATCGTATCATCAGAGGCCATAACTGTCGAGGATTGAAATACATTGGATTGCTGACT
GCTGATAAAAGTCATGCTATGAAAAGATTGTTAAAAGG

SEQ. ID. NO:189 AW461516
GGCCCTGCTGCTCCACACAGTGGAGGTACCATGACCTAACGGTCAGGACACCAGACGTGCCAGA
AGCCCTGCAGCACTGGCTGGACAACCTCCGACACTCGGAGGGAGGCCAGGCTGGCAAGGCCACATCTGT
CACCTACAGTCATTCCCAGGAAAGGCGGGTTGCTAGCTGCTAGCCTGGTGGGACGTCAAGTTATGGGCTG
GAAGTCCTACCCGGAGGCTGCTCACTGAAGTGTAAACAGGCCAACAGCGGATGGAAGGCATGCCGCTGCTG
CTCCAGGTCTCCCCGTCCCCAGGCCAACATGACATCCAACAGCACCAGGAGGTGCCAGCCCCGTTCT
GCAGGGGCCCTGGGCTCTCGTGGCCCTGGCAAGCCTCATCGTCGCTGCCAACCTGCTCTGGCGTGGGTA
TCGCCGGGGACCGCCGCTGCCAGGGCGCCGCT

SEQ. ID. NO:190 AW462075
TGAAACAGTCAGTCCTTGCAATTCTCTCCCTACCTTCCTCAGCAGAGCCTGCCTATTCCCT
TCCCTATGATGCTGAGAGACTCCCTGGTGGCACAGATGGTAAAGCGTCTGACTACAATGTTGGGAGACCC
GGGTTCAATCCCTGGTCAGGAAGATCTCCTGGAGAAGGAATAGCAACCCACTCCAGTGTCTTGCGCTGGA
AAATCCCATGGACAGAGGGAGCTGGTAGGCTACAGTCCATGGGTGCAAAGAGTAGGAGACTACTGAGCA
ACTTCACTTCACTTATGATGCTGGGAAGATTGAGAGCAGGAGGAAGGGGACAGCAGAACAGTAAAGACAGGGAA
GTTGGTGGCATACCAACTTAATNNNCATGAGTTGAGCAAGCTCTGAAACACAGTAAAGACAGGGAA
TGGCATGCTGAAGGCCATT

SEQ. ID. NO:191 AW462448
TGCAGGCCTGCAAAATCAGGCAGCAAGCCAGACCGGGCACAGACGAAGTTGCCAACCCCTGTC
TAGATGACCGCAAAGGGCTAACCTCAAGAGAAATGCTAGCCAATCACCAAGGCTCTTGTGTTCGCGC
TGATCACGTGACCAGGCCTGGCACACAGATCCAAGGATGGGTCTGCCCAGCGAGAGGCTGCTGGC
GTAAACCACTGACCCGAGTCCTGCTCTAGACCTCTGAAAAGTCAGTGGCGAGCAGGTCTGTTAGGTGG
GGCTGAGCTGAGAGGTCAGACCGGTGTTGAGGCTAGTTCACGAGGTGAGGATAGTCAGGTGTCAGAGTG
AACAGCCCGTGAGTGAAGCCGAGACGGGAGCCGCTGCCGTAGTCAGTCGCTGTCCCGGAGCAGCCGG
GTGCTGGTGACAGGCATGCCGTGGGGTCGTGCAGCGCTGACTTGAGTCCA

SEQ. ID. NO:192 AW462519
ACAGCTTGAGGATGAGATGGCAACCTCAGGTGGGGCAGACAGGACAAGGTAGGGCAGGGT
CCGGGAGGGGGCGGACAGAGCACAGGAAGTGTGGGTGTGGGCACCTAGTGGGTCTCCCCCAGGATTG
CTGAGGGCTGGAATCAAGGTCTAGCCCAGGGATCCTCTGACCCCTCTTGTCACTCTGGCTCAGGACCA
TGCCTCTTCTACAGGAAGCTGCTAGACACTACCCATCACAGTGGCTTTGCCAACATGATATCCA
AGAAGGGAACATCTACTGCTCTCAGAGCCTAAACACCCGACAGCCTCATGCTGGGACTTCGAGTACAG
CAGTTATAACTACAGGGCTTGACATGGAACCATTTGTGAGTGGTTACGATTACTCACGAGGAG
TGGCTTCTACAAAGCGCAGCGTCAAAACTACCCACTGAGGGACAGCAGCTCCATTCTGCCACTACCT

SEQ. ID. NO:193 AW464128
GCATAACAACTGACCAAGCTGAGACCGTATTGCCTGTCATCAATAGTGGAAAGCAGAGTGTGAC
ACAATTCTCCTGTCCTTCTGATTTTATATAAGAACACTGGAACAGTAGAGAACAGCACAGCGTAATA
CAAATGGCTGCCCTTCTTAACCAGTGGACATAAGAAGTACTACGATGGCTGGTCTGGTGGTTGAAGGTGC
ATTTACAGAAGCAAAGTAGTCTGGTTACTGGCAGCCTCGAATAACTCTGATACTGATTAATGGCTCA
GTCAGGATATCAGCAGGAACCTCAGTAGTCTCTCAAAAGCATTTCAAAAGCAACAATTCTGGATTGCTCC

-continued

ATTGCTTCTTGTAGTCCTGCAGTAGTAAGACGCCATCATTGATAACTCCCTGGAATCTGCTAATAAG
TCCATCAATCTGAAACACCCATGGGACTGACTAAAAATAATTGCTGAAACCT

SEQ. ID. NO:194 AW465040
GAGGGGGTTGGCTGTCAGGGCCCAGGAGGCCGTTCTGAAGGGTCTGGTGAAGGGTCCCAGGTCC

AGGATCGGGTGAGGTATAGCCTCCCGTCTCGGAGGGTCTGCCCTGGGCCTGAGGCACGGACATCTC
GGCTCCAGCCACAGCCTCGGGCACCAAGGGCTCGGGCCGGAGACCTGCGCCCTGGGGCATGGTGAGG
CCTCCAGAGTCAGTCCCACCTCCGTCTGGCTGTGACCGTCGGGCGGGACCGAGTCTGAGGTCTGGTCA
GACCCGGTACCCATGCGGGCCGCGCCTCCCCGGGGCCACCAGGGTGAACGGGGCGAAGTGGCGTAGTCA
CTGGCGGCCCCGGAGCCACCAGGACGGGCCCGGCCGAGAGCCGCGGGCGCGCGANNNGGCCGCG
GGGCGCCATGACGGCGCGCGGGCCACCAGGGCGCCGGCCGCTCCATGTCCCGGGCGCCCTCA
CATCCCCCGCAGCG

SEQ. ID. NO:195 AW465639
AAACCTCAGNGAACAGCAGACAGAGATGTCAGAGGTATCAATTCTCTCCAGTGACCCCTCAGTTG
AGTTGGGTCACTAGGAAAGGATGACTGGACAGTATCTCATGCTCTGCTCAAGGAATCCTCCCTAGTC
CCAGCTTGCTGTCATTAGAACACTCTCATCAGCATCTAATTGCAATTCTCTGATAACATAGCCAAG
AACTGCAGACTTCATCTGTGTTGGAATGTCGATTGTCATGGTAATAACACTAACGTGGTTTCAGGATA
ATAAGTGGCTTAATTGCTAATTAGAGAAGATTGGTTGGTGTATCTGTAAAGAGATGATAGCCTGAA
ACTATCATTAGATAATTCCCATTAACATTATGCAGACATTATCAGACTGATAAGCTCCAAGCTGGCTG

SEQ. ID. NO:196 AW465776
GAAATTGACAGCTGAGAGCTCCTCAGTAATTAAACGTTAACCTCGGAGTTAGCTGTGGAG

AGAGGTCGATCCTGAGCGATGCTAGTTAGCCACCTGAAATCTCTGGTGGTTCTGTTATATGGTGA
CCAGAAGGGGAGGAACAACCTGTGCTGAAGGAAGATGGAGGTGGCTCTGAAGATGGCTGTTGGTTGG
AAGCATGCTTGTATTTCAGGCTGGTCAGTAAATTTACTGAGTATATAGTATGCTTACACCTT
AGGCAAAGACAAGCCATCTAACCTCAGTGTCTCTTGTGAAAGTTATCTGGTACGAAAGAGCATT
GAGAGTAAATTAGTTGCAAAAGTGTAACTGTAAAGCATGCTGGTAGCTGCTATCTCCACATGG
CTAAAATGAGACTGGTCAGTAGTCGGAGGTC

SEQ. ID. NO:197 AW466079
TCAAGGAACTAAACCTTATTAACGAGATGTGTTACAGTCATTGACATCTCATACAAACAG
CTATGGGAAAGACTATGGCCTGAAATTGGGATACAACTCAACTGGGAATATCTAGTCACACAGGTATA
TAACAGAAACCTTGGCGGATTGTCACTATAGCAGAGCCATTCAACACTGAACACTACACTGG
GAGCTTTTCGAAAGATATCCTGAAGCTGGAGCGGGACAGAAACCTAGGGAGCAAGTACTGGAAACAGTGA
AAAACAATATCGAGTGGCTAAACAAAACAGGGACACCATAAGAAACTGGTTCTGATTGAAT

SEQ. ID. NO:198 BF039189
CAGCCGCCAGGAAGCGCAGGCCCTCAGGCTCGAACAGTCGGACAACGAATCCCTGCAGTCTGG
CGGAGCCGCTCCGCAGGCTCTGAGATGGACTCCGGCCCGCGTCCCCAAGTGCAGTCGGACCACGACTCC
GAAAGAGCATCTGACAATGAGGGCTCCGGCCAGGTTCCGAAATGAATCTGAACCCGAGGGATCCAACAA
CGAGGCCTCGGATAGGGCTCAGAACGTGGTCAGATGATAGCGACTAGGCTTATTCATGAATATGCTCA
TCTCTGCAGGAAACTTTTTTACATATGAAAGCTGTGATAAAACATTCAAGGTGGTAGTGGTGA
ATTTTGCTAAGGCAATTTCCTATCCATTGTCACATTACTATGACCGCAAGAGATATTCCCGTGTAG

-continued

AGTCTAATATTGAGTCTTGGAGAAAAGGTGACTATTCTTCATTATGGTACAATTCCACCTATTACATGTGA

AAACC

SEQ. ID. NO:199 BF042267
GGAATAAACACAGAACCGTGGCTCTAAAGAGCAGGAAGACTTCTTCTGCAACCAGGTACCC

ATAAAATTATCGTCCCACCGGGCATTTCTGGCGTGAAAAGGAATGGTATTGACAAACACCCGAGACA
AAAGGCATCACTGGACGTCTCGGTGAACCAGGAGCACGCTACCCCTAACAGGGACCCGACATCTGACTG
TGCTTGCACTAAAGGGTGAGGCGCACGGTAGGGACGCCACCGCAGCGCAGGGAGAGGCGTGGCTGCGGC
TCNNNACCCGCCACCTCTTCAAATCCCTCACTGGTGTCCGGCCGCGCCGTGCGGTGATGGGATCACAG
CCCCCGGCCAGGGCTGAAGCTGGGCCGCAGGGACAGCGCAGCCTACTACCTGCTGGCTGCCAGGGACC
CGTCGGCTCTCTGAGTCACGGAGATGCCAAGCAAAGTGTGAACACCCACAGCCTCAGTGCAAGAAGGA
CTGGTATTATTCACAGGGCTGTGCTGAGGACTGAACAGTTCATATATGTGAAACAGCTAACACAGTGC
GGCATAAACAAATAATAA

SEQ. ID. NO:200 BF043458
GGTTCTTGCTGGAGATATCTGGGAGAAATTGATACAAGATTCTTTGTGCAGTGGCAACTT

GCACTATTGGGAAGTGGATGCTATTATGTGGAAAAGCAATCGAATTGTTTATCATGTATGAACATT
GATGGTGGATTTGGTGCAGACCCAGGTTCTGAATCCATGCTGGCAGATCTATTGTTGCACAGGATTCTGG
CTATTACTAGTCAGTGCACCAAGTAAATTCTGATTTACTCGGTTGGCTTGTGAACGACAGCTTCATC
AGGTGGACTCAATGGAAGGCCAGAGAAGTTACCAAGATGTATGCTATTGTTGGTGGCTCCCTAAA
GATAATTGGAAGGCTTCATTGGATTGATAGAGAAAAACTCCGCAGTTCATCCTAGCATGTCAAGATGAATA
AACAGGAGGATTGAGATAGGCCAGGAGATATGGTAGATCCTTCTACTCTGTTGAAATTGCTGGATTG
TCACTTTGGGAGAAGAACAGATTAACCTGTTAGCCCTGTTTGATGCTGAAGAAGTACTTCGGAGAG
TGAATGTTCAAGCTGAA

SEQ. ID. NO:201 BF043688
TCATTCAATGCCGGGGTCCAGCGACCCATCCCAGGGAGCCAAGAGGTGGCAGCTGTAGCACCAGG

GACTTAGTCGAAAGTCAGCGGACTTCCTCAGACTTCCCTCTCCGTGAAGGGAGGGGCCAGTGC
GAGGCCGGGATGCACCCGAAGAAGCCCACCCCTGTCAGTGATCAGAACATAAGGCCCTCCATGTGC
GAAAGCCCAGAGGGAGCGCGGGCAGGGTCCCCAGCGCGGGACGGCATCTCCCGAACGGCCCTCTCG
CCTCCGCAGGGACAGCGCTGGCCCCGTGGCGCCCGGCCCTCCGCACCCGCCAGCCGGAGCCCTGC
CGCCGCCACGCCAACACCAATGCCCTGGCCCCGACGCCCGCGGGCTGCTGGCAGTGGATGGC

CGTGG

SEQ. ID. NO:202 BF044377
AGAAGGAGAAGATGATTTCTCCTCTTAGGATAAAATGAAACCTGTTTATGTAAGAACATCAGATG

ACCAAATTGACCTCGGTCTGAATGGCCCCACAGGTTGTCTATGATGTAGAGCCCTCAAGTAAAGC
AGGAAGAGAGTGAGAAGAGAACCACTCTTGTCTTGCTTTGCAAGTTCATCTTAACCTCTGGGAAGA
AAAAGGACTCCTCTTTAGAGATGAGGGAAAAGAAGGTTACATTAAAGAACAGGGAAAAAGTGG
AAATCCTAAAAGTGTACTGGGAGAAGTCAGTCATTCTGTCTTTGACCCCTGTGATAATTAAACCCGC
GCAATACCATGTTAAGATGCATTAGAATAACAAAATTAAAACCTGACATAAGATCTCATTTCA
GAGATTACAGACCAACAGAGGGAAATCATGGGGCGTATTGACAGGCAACTCTGAGAAAGTTGTG
CTGAA

-continued

AATGTAATTCTAACCAGTTCTCCTTGTAAAGAAGAACATCCACTTGTTAGAATTCTGA
GTTTTGTTAACATCCACTAAAGCTCTTCAACCCAACCTATACAGTTGAAAT

SEQ. ID. NO:203 BM362629
GCACGAGGTGCGTCAGCTCGCGTACCGCTGCTCGCTGTTGGAGAAACCCAAATACCGCTG
CCCCGCCTGCCCGTGCCTACTGCTCCITGCCCTGCTTCCGAAGCACAAAGAGCAGTCAGGCCCTGCAGCT
GGTCCTGTCGAGAAAAAAAATAAAGATCAGCTCTGACTGCAAAACTAAAGCCTGTGGAAAAGGAAGGTTC
CTTAGATGATGACTCTGCTGAGTATTCATAAGTGAGGAAAGAGGACAGAGTGTCTTGAGAAT
TTAAAGAATTAGGGAGTCTGCAGCACTGAGGAGCTACTGCTCAATCCACACCTCAGACAGCTGATGGTC
GACCTCGATCAGCGGACGACAAGCCAAGCTGCGAGCCTGCATGCAGGAGCCCTGTTGTGGAGTT
GCTGACTGCTGCTTGAGTATGCTGGAGCCGCTCAGAACGAGGAGCTT

SEQ. ID. NO:204 BM366480
GCACGAGGTGATGCAAACAGAAATCCACCGCCTCCAGATACTATCATGTCATGTTCACAG
GCTCCACAAGCTTGAGCTCAGACTGCTCGGTCACTTGCAAGGTGAGCAGGCTCAAGACTCTGCTCCCCAGCC
AGGAGAAGATGACTGACACTGAGTTGGTACGTTACGGGCTGGCTGAGGACTATCTGAAATATGTGTTGC
AGATAACAGCAACCTGGATCCAAGCCAAGCAGAAAATTGCCAAGAGGTCAAAGATCAAGTCTTGTGAAAGT
TTATAATTATAATCACCTCATGCCACAAGGTACTCTGTTGATATCCCCTGGACAAAATGTTGTCAACAAAG
GATGTCCTCAGAGACCCCTGCTCTCAACGCAAGGCCGACGAGAGGCAAGGTCAAGTTGAGGAGAGATA
AAGACGGGCAAGAACAAATGGTCTTCCAGAACGCTGCGGTTTAGGTCTGCTCA

SEQ. ID. NO:205 AW465210
TACAGTGTGCCTTGGAGTGCTATGGTCGGTAGGTTGCTGTCAGCAGAGGCCGTACACAG
CCAGCGCAGGGAAACTACACCAACTACACTAAAATTACCATATTTATATGGTCAGAAATCTGTTCAAAGCA
AAAGATAATTGAGAGGGACTTGGATCAAGAAATGGATTCTCTTAACATACACAGCATGTGATTGAGCTGT
GGAAACTGAGAATCAAAGTGACAAGTCTTCCTCTGGTAGCAGCTTATTTAAACTCAGTGTGTTCTGTCCCA
CCTAAACGGAGGCAAAGAAACTATTAGAAATTGTTACATACCCAAAATCTCAAGCAACAGAGTCA
TCTAGTGACTCATCTATAGAGCCAAGACCAACTGACTTTAAAGCTATTTGAAAGATTCAAAAATAAGAAA
CGTAAACGTAAAAAGAAGAAATACAAGCCAACGGGAAGATCAGTGGGAAGACC

SEQ. ID. NO:206 BF043768
GATTGGATAACCGGCTGCCACGGGCTGGTGGGGCCTCTCCTGGTGATCATGGGTATTCCAGC
GTTACCAAGCTCTAAAGGATGGGAACGTGAGCAACCCCTGGCCCTGTGTTGTCACAGACCCGTGGCTCGT
GTGTACAGTGTAGAGATCCTCTTCTACACAAAAGGACTGTGGGGTGGAGGAGTAAGGTCTAGCTCAAAGG
GCTTGCAAAATTAAATATTTAAACAGAGGCATCTGCTAGAAAACCTCTATTGTATAAAACCGAGCT
TTAAAAAAAAAAAAAAAAAAAAAAAAAAAAACCAA

SEQ. ID. NO:207 BF045850
CCAGACTCACTCCGCTGCCGGGATGTGGCGGGCTTCCGCCGAAACCGCACTGCTTAGCCCC
CTGGCGGTCCGGGCTGAGGAGGCCGCCGCTGGGCTCGAAAGTGAAGAACGTTGGGCCACGTGTGAC
ACCGCCAAGNNNCNNNTCCATACTCCGGTTGCCAGAGGGTCCCTCCGGGGCCCCCGGATGGAGAGGC
CAGTCTCCCCGAGAGAGGGCGCCGGGGCGGCTCTGAGCAGGACGAGCTCCCTCCGAGCTCGAACCTANNTG
GTCAGAAGTGTGGCGCTGGCTGGGGCGGAGGCCCTCAAGCCTGGCCCCGGAGGGAGAGACC

SEQ. ID. NO:208 BM365541
GCACGAGAAGGAAAGACTGTGAAATAAGAGCTGTGGTGAACAGGACTGCCTAGACCTATGGCCA
GTAGTGGACTTTGACCCCTGCCAGCACGGTATGATGTGAAGCTCTCAGTCATAAGAACATCCACAGCCTCTTCA
GAGTCCTGGTAACCAGGTCTGCTTCAAGTTGGTGTCTTGAGGTTGGATTCTGAAATCAGCTTCTCAAGA
CTTGGAGGCTCAGACCTCTGTGCTCACAGAGCTGGCACATAGCTGCCCTTATGCAGAGGTGACACAGG

-continued

GCAAGAACAGTAGTAGAGGTGGTAGAGCCCCAGAAGTTCTGGAAC TGCCCTCCCAAGAAGCACTAT
 TACAAAATCCTACAGAGAACAGTGTGCCAAATGTTCTTCACATATAAACAGAGGTCTGTGGA
 CATGTGAGGATAAGAATAAAGACAAAATCTGCTTTACATGTGTATCTCGGCTTCACTGTGGAGAGAT
 AAC CAGAAAACAAGGAAGAGATGTGAGAATAAAACT

SEQ. ID. NO:209 BP230001A20G6
 AGGACTTGGGAGTCNTTATCTGCTCCATCTCAGCCACTGCCACANTCAGAGGATATGCCANGGAG
 GTCAGGGGACTGCTCCAGATCCTCTAGAACGANTACTTGGAAAGTCCAAGAGGCCAAGATTNGATGG
 TCCTCGAAGATTGAGGATTAGGGTCAAGGTGTGAAGGACCGAACCCAAAGGGCTTGTGTTGAAGGAAA
 TCGCCCCGATGGGCCAAGNACCCANATTGAAGGTACCCACNAGCAGGGCACTAAAAGCAANATGGGNA
 ATGTATTCCCCGGGGCCAAGCATTAAAGTTNCTATATTACCCCCCANTACATCCCTTCANCCCTCNGACA
 GANTTGGACCACAGGTGAAAGGCCAACCCAACTTTGGACAAGCAACATCANNCAANCAACCTAAA
 GTTCACAAGCCAGTAACCAAGGAAANAAAA

SEQ. ID. NO:210 AW462359
 GTCATCGACGATCAATTCAAAGCAGTGACGTACGTACAGGAATGTCAGTCCCAGATCAGAAGAGTG
 TTATTTGAAAAGCTGAGGGAAAGGTTGGAGTGTAAAGTGGATGGAGGATGTATAACAGGGGGCTTC
 AACTAAAAATATTTCTTTCTTTAAAGAAAAGAGAAAATTCAAAACGTGAAAGACTGTTAAGAGTAGATA
 AGCTATGAGGTGATGGGATATTCATATTGTTTCTACTTTCTGTAGGCTTCAGATATTTTAAAAAA
 ACCATTGAGTGACTTGTGATGCAACACAGTGCTACGTACAGACATTGGAAACAGTTAACGACC
 TGGGAAACTACACGTGTACATAGGCTGTAAAGAGGAAGAGAGCGCCTCTAGATCTGATGCCACGTTTC
 TAGTGCTGCAGTTCTTCGACCAAGTTGAAACA

SEQ. ID. NO:211 BF440272
 TTTTTTTTTTTTTTATAGATACATATTAAATAATAAAATGTGATTGTTACAGATACTATTG
 GTGCTTATCAAGTACTATGAATTCCAGAGTACACAAACACGTGGGATACAAATTGAAGATAAACACAATT
 GTTCCTAAATGAAAACATGGGATACATGCTGATGAATGGATTCAAACCTTCATTCCACTTTCTCCA
 GGCTGGTCTCTGAAGATGAGTGCAAGTGTAGCAGTCTTAAACACTCAGTCCCCAAATTCTAATA
 ACATGTAATATGAAAAGAACTTTGGC

SEQ. ID. NO:212 AW461819
 ATTTTCGAAGATTGTCAGGGCACTGCCAGCGAACTCAAAGATCGAGGAGAATTGAAACCGAACAA
 GGAGAGCAGAAAGTCTGCAGGTCAAGCTGAATGGCTGGGAAATTGCTGGAATAATGATGAAACTTAC
 GGCTACAAAGATGGCAAACCATGTGTCATTATAAGCTCAACCGAGTTCTGGCTCAAACCTAACGCTCCC
 AAGAATGAGTCCTGGAGAGTTACCCAGTGATGAAGTATAATCGTATGTCCTGCTGTTCACTGGCA
 AGCGAGACGAAGATAAGGAGAAAGTGGAAAGCATAGAGTACTTTGGACTGGCGGCTACCTGGTTCCCTC
 TGCAAGTATTACCTACTACGGCAAGCTTCTGCAGCCAAAGTACCTGCAGCCTC

SEQ. ID. NO:213 AW463150
 GCAACAAATGCTTCTGATCCAGTGAAAGCTTAAAAAATCCAAAGAACAGAACATT
 TCATCATCTGGTTTCAGAGGATTTAAAAAAAGTGTGTTCTGGACGCCGTTAAACCTTTCTT
 GTCGAAGGCTGCCATGAGCTGCACTTTGGGTGGGAAGGGTGAATGCCGCTGGGATAGGGGGACAG
 GGGCAGGGGCTGCTGGATGAGGGCTGCTGGCTGCGGGGGAGGAGTCCTGCTCGAACCTCACCCCA
 CCAGCCAGGGGACTTATTCTAAGACCCGTGCATGAGGAATGGTGGCCAGTGTGTTCTAGATCGACAAGGT

-continued

GTTGGTTCTCTGTAGGCTGTAACCTTTAAAAATAAAGAGTTATTAAGGGTATGCTGCACTAGTATTCTTA
AGNGGAAACTGTCCCTACAGCTAGGAAAGGGAGTGGGCA

SEQ. ID. NO:214 BF039065
ATCACACACGATATTGAGGAGAAGGGCGTCGGCATGAAGCTGACAGTCATCGACACGCCGGCTC
GGGATCACATCAACAATGAGAACTGCTGGCAGCCATCATGCAGTTCATCAACGACCAGTACGAGAAGTAC
CTGCAAGAGGAGGGTCAACATCAACCGGAAGAACGCGATCCGGACACCCGCGTCACTGCTGCCCTGACTTC
ATCCCCGCCACCGGCCACTCCCTCAGGCCCCTGGACATCGAGTTCATGAAGCGCTGAGCAAAGTGGTCAAC
ATCGTCCCAGTCATCGCCAAGGCTGACACGCTGACCCCTGGAGAGGGTCACTTCAAACAGCGGATCACT
GCGGACCTGCTGTCCAATGGCATTGACGTGTACCCCCAGAAGGAGTTGACGAGGACTCTGAGGACCGGCTG
GTGAATGAG

SEQ. ID. NO:215 BM365510
GCACGAGGTTGTCTGCACTGTTGAAATCTGCCCGCTCCCTGCCCTACTTCCTGAATGAA
ATGCTTCTGAGGTGTTATGAAAGGAGTGATCCTTGGCAGGCAGGAGGGCAGTGGCTTATGGCTCCTTGG
AGTTACTGTTGATCTTGACCTCTCTTGGCTACCTTGAGACAAAGAATATGCCAATACTTGGGCTCTGAGTT
TTATAGTCATATTATTTGTATCATCTTTGTCTAGGAATGAAAAGTGACTIONTAAACTAAGATGTGTAATA
AAAAATCAGATTTATTGTACCTCCAAAAAAAAAAAAAA

SEQ. ID. NO:216 BM365938
GCACGAGGACCTTCGACCCCCATCCAGTTCTGTCCTCTCGGTTGCTTTAGGTGGATCCCTG
GAGGCAGAAGCAGCCAGGACTGATCCCAGGTACTCTGTGTAGCAAACAAACTGTGAATTCTGACTCCCTT
GCCCTTCTTCAGCTGTAGGTGCTCCCTCTGATCGCCTGGGAGGGGACTGAAGAAAGGCAAGGGCAAGA
TGCTGCTACTTCTGACCCCTCTCTGGGGCAGGGCAGGAGGGAGCCTGGTTCATGTGCCACATTCATAC
CCGTGCAGGCATGGCGAGCGACTGGCACCCCTTCCGGCCTAAAGCCCTCCCTGCAGTGAAGCAGGGCAG
GAGGAAGAGGCCAGATTGGGTTGGATTCTAGAGGGACATGATGACCGTCAGGGCAAGTGCAGA
AATCTTGCCCTTGCTACCATTCTGTATGAGAAATAAAGTCACCAAGGTTTGTGTAAAAAAA
AAAAAAAAAAAAAA

SEQ. ID. NO:217 BF039954
AGCTCAGCTCGCTCGTGTGAATTTCATGTCACGCCCTTGCCTCTGAGTCTGCTTCCATCCATAAT
CAAGGGAACTTTGACATCTCATAAAGCGTGGATGAGCCTTCACGTTCTGAAAGAATAGTGTGCTGGCGCA
TAGAAAGTGTGGTAGATGTATCTGTTAAAGATCTTCTCATGTGGTGTAGGCTGCGAGGGACAGGAAA
ATATCTGAAGCCATAAAATAGTTCATCAGCTATTCTAAAGCGAATGGTTTCTTCTGTTTCTGAA
TGGCAAAGGTACGGATGGGAGAGATGACAGGAGGAGATGAAGAGATAGGACAAGACTGGTTCTACGCT
TCATTGTTGATCATGTTATCGTCCGGTGCATTAGCCACCGTCCATTAAAGCAGAAGGTCAAGTCA
AACAGGGAACTCTGTTCAATGTTATGGCAGCCTGGAAGGGAGTTGGGGAGAATGGATACTG
ATGTATA

SEQ. ID. NO:218 BF040540
GTGGGAGCCAGGACAGAGACCTAGCACATACGGGGACAGCCTGCTGGCTGGCTTCTGT
GGAAGGGCTGAATCCCTGGCAGACAAGATCAAGGTTCCAGATATGGCAGAGATCCAGTCTGCCCTGGCCT
ACGTGTCCCTCGCTGCGACAGCTGGAGGTTGTGAAGTCCAGCTCCTACTGTGAGTACCTGCCCAACCGATCGA
CTGCTTCAAGACCATGGACTCGGGAGTTGACCCAGATCTATGATGTGGCTACCGATGAGTCACCGTC
TTGGGGCTGGAGCCGGGGCACATCATTGAAAAGATTCTCACAGACCGGTGGCTGCCACCTGAACGAG
AGCCGCCGTGCACTGCTGCCCTCCCCAGCTGGCTCACCGACTTGGCGGAGATAGTGTCCCAGTC

-continued

AGCCGCCACCACGAGCTACGTTCGGTTCCGACGGTGTGCTGATGGGAGGAGTCGGACTGTCTGACGG
AGTATGAGGAGGACGCGGGCTGAGTGCTCACGGGACG

SEQ. ID. NO:219 BM366584
GCACGAGGGACGAAGCCAGAGATGGTATATCCAGCATGAAGGTGTAGACCATGAGGTCTCGCAG
GTTCCTAGATGGCCGGGTGAGGGCTATGACCTGAGGATGGGGCAGCTTCTCAGACTACGTGGGAGCC
CCATCACCTGCATCTGCTTCAGCCGGATGGCAGTGCACCCCTGGTGTCCAGGCTAGACTCTACCTGCGCCT
TCTGGACAAGGACACAGGGAGCTGGCGAGTACAGGGGCCATAAGAACAAAGGAGTATAAGCTGGACT
GCTGCCTGAGCGAGCGCATAACATGTGGTCAGCTGTGAGGACGGAAAGGTTCTTCTGGGACCTGG
TGGAAAGGTGCCCTGGCGCTGGCCCTGCCTGTAGGTCTGGTGTGGTCAATCGCTGACCTACCCCCACAGA
GCCCTGCCTGCTGACTGCCATGGGGGAGCATCCAGTGCTGGCGGGAGGAGACCTACGAGGCTGAAG

SEQ. ID. NO:220 BF043047
GGTTCACTGCCCTGGTCAATTCTCCATCTGCGCTCTGGTGGCTGTCTGGGAGGACTCAG
ACAGTCCCAGGAGACCTGGAAATGGACTCATGGCCTTGAGGATGTGGCTGTAAACTTCACCCCTGGATGAG
TGGGTTTACTGGATTCCCTCACAGAGGAAACTCTACAGAGATGTGATGCGGGAAAACCTCAGGAATGTAGTC
TCAGTAGAACAGGAAAGATCAGGACATTGACGATCAGGAGAAAACAGGAGAGAAATTACGAA
ATCCAAGGCAGAGAGACACTCGAAAAGAAGATATTAACTCTGAAGAAAGCTCAACCTTATTCAA
CTCCCAATGTGAAGAGAACTCGTGAATAAACCATGGGAATGCGAGAGCATGTGGAAAGTCTCATGTATC
ATTCATCCCTTACTAGACACATGAAATGTCACATTGAAAACAGATCAGATGCCGAAAGTACC

SEQ. ID. NO:221 AW461654
AGCCAGCTACCTCGTAACCTCAATTCACTGGTAACTTCAGGTTAACCTCCCTAGGGAACAGTGCAGGTGTCCACGGAC
ACCGCCTCCTCGGTGGGTGGGGCTGCCACTTCGGAGGGGTTGGCACGGACCTGCCTGGCTCTGCATTGG
GGTGGTTCCCTCCCCATCTTGTCTTGGTTCCGACGGTACAAGGCTGCCCCGGCTCCCCCCCC
GGGAGCCTCACTCTGGTCTTCAACAGGACTGGCGTCAGCTCCCCGCCGGCTCCACCCGCCGGAGTGGC
TCCC

SEQ. ID. NO:222 AW462133
AGAAGCTTAAATATTAGTGTTCATCAAATTGGCTTAATTAAAGAGAACACCCAGTCAGCTTCAGACGAGCTGTTCA
GAGCTCTAAAGCGACGAGGTTCACTGGTGGCTTCCATGATGTAACCTGGCTTCTGGTTAAAT
ATTTACAGGGTATTGCACATAGGAGACAGATGACAGAACCCGAAAGGCTTATGACACACAGATAATCA
CACGTGAAAATAAAATCCACAGGACCAATAGCGCATCTTAAACTCTTCATACTTAGAAAAATATTTTA
AATAGCAGTCTGCATAATTCCAGTCCTCAGGAAACTAGAGAGAACGCTAAATAGGAAGTCCCTGAATGGCAA
GTACTGATCTTGGCAGCATTAAAGGGAACAGGAGTAAAGACCT

SEQ. ID. NO:223 AW462711
GATACTACATTCTGGGTTTGCTGACCAAGCTGTGACTTCAGTGCAGGTCTGACGGAC
GCTGCAGTGTGACGCTTTAAATACGATGGATTGTTAGTGTGCTGTCAGTGATAATGCTAGCCTACTTCTAT
TTGACTTTAGTACAGAGTTATAATTGTGTAACCTCTAGAACATTACATGGAGCCTGGTCCCTTTCCCTAC
TTGATGATTGACTTATTCTTCTCGATCGCTACTTCCTGATTCTCAAGGACCAATTCTCCAGTGAG
CACTGGAGCGTGTCTCCAGGGTAAGCCAAGGCTGCGCTCCTCAGCCTCTAATTGTTCTGCAGCTGCCTCTGG
CAGGCACAAGTAGCCCCACTGTGTGAGGAACACATGCCAAGGAA

SEQ. ID. NO:224 AW466082
ACCTGCCCTTGTGCTGGCTGGGCCAGCCGTGGTCCCTGGAACCCCTCAAGTTGGGGCTGCGCCCTT
GGGATGGGGGTGCGAGGGGGCTGCTGCTTCCAGGCAGTGGCCACCGGTGCGCTGGTCCAGCTGCGGGTCA
GAGCCCCGAGCAGGGTGCAGCGCACACCGCCCTGAGGATGCCGCCCCGCGGGTCCCGTGTGGTCCCTGCT

-continued

GAGGCCCGCTTCGCCCCGACCTGGTCGGCATCACAGAAGTCTCCAGAACATCCTGCTCGCAGCGTTCTCCT
 GCAGACTTAACAACCTGGACGCATTGGCAGTTGGACCCAGGGCGGGCTGGTGTCTGTCGGGGGA
 CGTTTCCAGAGGCANCTGGTCCCCTCACTCTGCCTGCCCTGCCCGGGCATCACTGGTCACTGCCTCTG
 CCAGGGAC

SEQ. ID. NO:225 BF045301
 GCGCTCTCTCGGGCAACATGGCGGTGTGGAGGAGGCAGCGCTCGCGGAGGCCACCTGAATGGCG
 ACCTGGATCCAGACGAAAGAGAGGGAGCTGCCTCTACGGCTGAGGAAGCGGCAAGAAAAAAAACG
 GAAGAAGAAGAAGAGTAAAGGGCTGCCACAGGGCAACAGGAACCTGATAAGAAGCAGGAGCCTCAGTT
 GATGAGGTGACAAGACAATTGAAAGACAAGCATTGAAAGAGAAAGAAAAGATGATGATGATGAAAGGTA
 GGATTATCGATTGTGCTTTACTGTCACTTTAATCCAAATATGATACTATTATAAGCTGTCAAAGATGCC
 ACTAACACTGGAATAAGTGTGCCGAATTGATGTTCGTCTGTGATGTTGGTAGGCTATCCAAGAAGTTA
 TGAATCCTATGAAGTTGAAATAGATGGAAGACATATCAAGGCTCCAAGAACAAAACATTGTTAAATGT
 CATCAATGAAAACCTTGGCACTTGCCTCTGCCAGATGGCTGGATGTTGGAGAAAGTAAATACTTG
 ATGGCTCTGAAGAATCTGTGACTGGGCATTGTAGNGCCATATCCACCATTATGTGACATTAAAGGATCAT
 ATACAGCACAGTTGAACACACCACTT

SEQ. ID. NO:226 AW461425
 TTTGTTTTTTTTTTTTGCTTTGGTGTGAGCCTTAGTCCTGCCATGGCAGGCTGGTCTATT
 AAAATACATCAAAACATATCCTAATGATTCCATGTCATCTCGCGACTTGTCAATACCAAGATGTGATTG
 ATGCTAGCATACCGAGCAGTGCANTGAGATTATCTTCTGTATGGATGTGTTGCCTGTGCTGTGTC
 TCTGTACTTTGGCAAACCAAAATCAATAAGGATAACTTATTACAGTGACGCCAATACCCATTAGGAAG
 TTATCTGGTTAATGTCTGTATGACATATTGATTACTGATCATCTGGTGAGC
 TAACATAAGTACAGTTCAATTGAAACCTTCTGAACAGAAATTGAAGGNNNCTCAAGGCTGGTCCAAG
 AAGATCCATAACTAGCACGTTAGTCTGTTCTGACCATACCC

SEQ. ID. NO:227 AW465281
 AGAGAGAGAAAAATCCATGATGCTTACCTGTAACCCCTAGAACCCAAGTGCCAGAATTAATTCC
 TAGATGCTGCTCTGTTGAATAAAAGTCACTGCTTTACACTGAAAAACACTAAAAATGTTCAACTCC
 ATGAAAACCTGTTGGCTTAAGAAAATGTTGATGTTAACCTGTTGATTGCCATTCCACCAAGTAA
 TTGTTGGTTGATTGCACTGCACACTGGGTTGGGGA

SEQ. ID. NO:228 BF045176
 GAGGACAACATGGCTCTCTGGCATGTTAATTGTGATGTTAACGGACATCCTGCAGTTAAG
 ATGACACTTTAAAATTCCTCTAATGATGACTTGAGCCCTGCCACTCGATGGAGAACAGCAGAA
 CCTGTAGGATCTTTGCAATTGACATTCTCTATTGTAATTGTTCTTATTGTTAAATTGTTCTTGT
 TTCACTGGAAAGGAAAGATGATGCTCAGTTAACGTTAAAGTGTACAAGTTGTTACAATAAAACT
 AAATGTGTACACAAAGGATTGATGCTTTCTCTCAGATAACCTTAATATGACTTCCAAGTTGACTGTGTA
 ATGTTATTGTCAAACCTTGTCAACCTATCTGTATTGATACGCACTTGCAGGATGACCTCAGGGCT
 ATATTGATGAGTAAAGGGATTGAATCAATGTTAATGTCTCCATAGCTGGAACCCATCATGGGTATAAT
 TTGCCATTAGTTCTGAAATCTTCACATCATTGAGGATACCAGATTGCTGAAAACCTGGTTCTGAATGTGTTG
 TACTTTGATTTGTATCTCAAATCATT

SEQ. ID. NO:229 BF045836
 AACTGCTGGGTCTGCTCTGCCGCCGCCAGTCAGTCAGCCTCGCTGCCGCTGCGCCGCTC
 AGCGGTTCCGGTAGTCTTAAGCCGCCACACCTTCCCCGCCCTCCGGAGCCTCGGGTGTGTTCTGT
 CGGCCNCACAGGCCGCCGACCGCTGCGCTTCTCGGCCGCCCTGCCGCTCCGGCGACATGAGTGG

-continued

GGACCATCTCCACAACGATTCCCAGATCGAGGCAGATTCCGACTGAATGATTCTCATAAACACAAAGATAA
 GCATAAAGATCGAGAACACCGGCACAAAGAGCACAAGAAGGACAAGGAGAAAAGACCGNNAAAGTCCAAG
 CACAGCAACAGTGAACATAAAGATTCTGAAAAGAACACAAAGAGAAGGAGANGACCACAAAGATG
 GAAGTTAGAGAACATAAAGAACACAAAGACAGAGAACAGNAAGAAGGAAAGAGAAGATTAA
 AGCTTCGGGGATGCAAAAATAAAAAAG

SEQ. ID. NO:230 BM364051
 GCACGAGAAAAGATCAGTGAGGATGAGATCCCGCCTCCAGTGGCCTGGCAGGAGGCCCTGGTC
 CCCCAGGAAACAACAACTAACAGGGCCCTGAAGCAGAACCCCCAGCTGCCCCCTCCGTGGAGCCAGATAACCCC
 TCCCAGCCTGAGACAAGCCTTGGCAGCCCTGGTATTTCTGCCCAACCGACTCAGACCCGGACCCACGGG
 CCCTGCTGTTGGCCCGGAGAGAGTACAAAGTGGCTGCTGAATGCCAACGGCTGGAGACCTAGACC
 GTGCCGAGAGTCATGAGGGTGGGAAGGAGATTGCTGCTGGAGGCCCTGGAGAAGGGCAGCCTG
 TGGACCTGAGTGCCATGCCCATCACAGAGGACCTGAAGCCCTTCCACAGGCTCCAAAGCCCGACAG
 CGCCCTCCGATGCCACCCCGGAGTGGAGCGAATGCACCCAGTGTGGCCTGACATCCAGCA

SEQ. ID. NO:231 AW464893
 AGAATTCTAGTGTCTGCAGTTAGATAATATAACTGCTAGCTGTTAAAGACAGATTGTTATGTTA
 AAATTCTCTTCTTTGTTCACTGAGGTTGGATATATTGACACTGTAGATTCTATATGAAAAATATCT
 CCCAGTAAAAAAATGCCCTTCTTTCTCCTCCTTCTTCTCTTAACTAAGAACATTTATCATCACT
 CAGGTTGAATTAAATTAACATCTCAAGCTAAAGCTCTGTAATTGAGGTTGCCCTGGAGAAGATAGGAAAC
 ATTGACAATGCAAACCTCTAACATGCTGTTGAGCTTTACGTATGAGTAATCCCTTGATGTAGNTAAAGC
 TTTACCTGTTACTTTAAGGACACACTNNNATCATTGAACTCAGTTAAATCCANTTATACTATGGATA
 TCACAACCCATGCATAAAATTAAAC

SEQ. ID. NO:232 AW465985
 AAAAATGCTGGAGGGATGGACCTTGAGGATTATTCAATTAAAGATGTAGCTTTGTTGTTCC
 GGCAATTATGTATAAAGCAGATTATTATGACCAAGTTAATGTAAGTGTAGCTGAAAGTGAAAT
 CTAAACCCCTGCTCCAGCGGGAAACGCTCGGCCGACAATCACAGCCCCAGCCAGGGGCCGTGGCAGT
 GCCTCCTCTGTCGGTCCCACCTCACCCATCGCCTGTCGCTCGGTGAGCAGCCATCGGATGGAGGAGC
 ACCTACAAGAGTCTCGGCCGCTGCAATAAGGCCTGGAGGCTGCC

SEQ. ID. NO:233 BF042374
 GCCAGGGCCAGACCCAGCCCGCGGGCCGAGTCCAGCCACTGCCCTGCCAACCTTCTCCTG
 TCTTGAAATCTGAGGCACAGCCCAGGGCCGCTCCCTCCCGGGGGAAAGGGCTGGAGGTGGAGGAAGC
 GTCTTGTTGTTAAATTCGTGAGTCCAGCTGTTGCAAACCTTCTCTGTAATGTTAAAGTCATT
 TTGATTCTAAACTTTATTTAGAGGGTACTGTTGTTGCTTCAGTGTCTGTTGGTGTAAACCTTG
 TTAGGTTGTAAGCGAATTGAAAATTCCTACCCGATCTGAACTGCCAAGGAAATAAGCGAACTGG
 CCCTGTCCGGCTTGAACTGCCCACTCTGAAAGGAAAGTCTTATAAATTGAAAAGGAAATGTAATT
 GCCTATTCCTTACTTTAACGCAACTATTAAAAATCTGTTCTATGCAATATAAGCATTGAGTCAT
 TCTAAGTAATGCGTATTGAGTTTCAAATAATTTCACATTGATAATTACTATGCTGTGGCTGACC
 ATTTGTTCAATTTCCTGCTACTATAG

SEQ. ID. NO:234 BF043142
 TGCAACCTGAGTGCCAGCCCCATCTGCAGTCCTGCACCATCTCCCTGAGCAGTAGGCTCCACTG
 ACGGGGAGGCTGTGGACCAAGTCCACTTGACCCCTTGGTGGTGGAACACTTGCTGGGGCCTGGAA
 CAGACAAGGGAGCCTGACAGGTCTCCCACATATTATTACTCTTCTCAACCCGTGAGACCTGGA
 ACCCAAGTGCCTGTTGGCAATGACCAGAAATGCCTCGCACCAAGTACACTGGTCAGCTAACAGACCTT
 CCCAGTGCAGAAGTGAATTCTACAAAGTCTGGAGAGAAGGTGGTACACCTATGGTTCTCAGGCCATAAGGA

-continued

AGACACCAGACCTTCGTGCCCTGTTAGGGAAACCCCTAGTTTCTCAGGAGCAGCTGCTCTCGGTCC
 ACATGGGGCTTGAGTGCCTTGAGTGCCTGAGGCCACCCACTGCCGAACCTAGTG
 TTGTGTGTGAAGTCCATGGAGCAGGTACACAC

SEQ. ID. NO:235 BF043207
 CATCCGGATGATGCCAACCCAGCTCCGCCAGCAGGACTCAAGCGCTTCAGGCCAACCTGAG
 GCCAAGTGGNNNCCGGCCCCGTGCCGCCAGGAGGCAAGGCNGCAGGAGAAACTGTGGAAGAGAGACG
 TAGNCCTCAGGAAATAAGCGAAAAGAGCCGGTGGAGGACCCAGCTGAGCGGGCTGCCTGGCTCAAACAT
 TTCCCTGCAAGAGNNCAAGTAGGTGAACCAACCACCCCCAACCGAAGTACCCATGGTTCTCCAGCTA
 CAGGACTGGGCCATGGGC

SEQ. ID. NO:236 BF043909
 TGCCTGCAGTCGGCCGGCGCGACTGCGTCTGCCAACAGGGTGGCCCTTCAGCTCAAGAAG
 ACGGACGACGACCGCTGGGCCACGTGGTGTGGCGCCCTGTGGATCCCCGAGGTGGCTTCGCCAACACCGTG
 TTCATCGAGCCCACGCGCGTGGAAACATCCCGCCGCGCTGGAGCTGACCTGCTACCTCTGCAAG
 CAGAAGGGCGTGGCGCTGCATCCAGTGCACAAGGCAACTGCTACACCGCTTCCACGTGACGTGCGCC
 CAGCGCCGCCCTACATGAAGATGGAGCCCGTGCAGCTGGCCGGCGCCACCTTCTCCGTC
 AGGAAGACCGCTTACTGTGACGCCACGCCGGCTGCACCCGCAAGGCTCTGAACATTACGGGAC
 GTGGAGATGAAAAACGGCGTGTGGAGGAGAGTCGGTCAAAGCGGT

SEQ. ID. NO:237 BM365156
 GCACGAGGTTCTGTAATCCTGTTGGCAAGATTTCTTATGATGTAACAACAAAGGTTACAG
 TTTAGTACTAAACAGCAGTTAATAGTGATTTCTCCCAGGCAGAGTAACAAAAGCACCTGTGAAAATCG
 CAAAGAAAAACTAGGGACAGGACAAGAGGCAGCGGAAGCCTGGCTGCTGAAACTGGTGTGACCCCTGCAT
 TCCAGCAAGGGCAGGGAGCCAGAATCACCAGCTGCTTCCTCAGGACTGAAATTGACAGTTTCCAAAC
 TATCTNNNTACTGNNGCATTCACTGTACCCAGTTAAATATAAGAATTAGTCTTCTTAATAAAATCACCT
 TTCAGNNGAACTATAACACATTAAAAAAACTACTGATTGTTCCCTCGTCTTTTTCTTGAACCGA
 GGTGATTGAGTCTCCTGTGTTCTTCTTACACC

SEQ. ID. NO:238 BF039394
 CAGTCAGGTGGACGGAGAACATGGTTAGCCTCCAGGGATTATCAAGATCGTCACAAGAAC
 GAGCTCAGATGTCACCAGGGACAGGGCTTGAAAGCACCCCTGAAAGTCTGGAGATAAGCAGAAATGTG
 ATTCGGGTAAGGCAAGTCTCGAACGCACTGTACATCCAGCACGCCGCCAGCTGGCACGGAGGAAGTGT
 CTCAGATGCAGCTGTGCTCGAGGCCGAGCTCATCACCAGGATCTGCGATGCCACCATCCACT
 GTCTATTGGAGCAGGAGCTGGCCACGCCGCGTGAACGCCCTGCTCCACGCCCTGAACAAAGCCAACCCACGCT
 TCCCAGAGAGTCTTACAAGAGACACTGCCACTGAAATAGCCATCAATGTGAAGGCCATATATAACGAAACAG
 AATCTTACTAGTGGCAGGGTCTTGCAATTGAATCTCACATGAAGAGCGAGTATCCAATGCCCTACA
 TTCCNNNGAAGTGGAGCTACAGAAGTTAACAGAGATTCCATGGCTTATTATATCTTACACCGAATGAGGA
 TGAGGAGCCCCCATGGATT

SEQ. ID. NO:239 BF039014
 GGCCAGGTGGTGGCTGGGACTCCACACAGTGTGCATCTGTTCCCTGTGCAGTGAATGTCA
 CGACCCAGTACATCTGCTCGTAAGAGGATGGCCAATTGACAATGTTACTCCATTGGATTCTGACTGCC
 TTTGGTAGATGAAAATACCAAGGAAAAGAAGGGAAAGGAAGTTCCAGTTAAAGTCCAAAAGATCGAG

-continued

GCTGTGAGACGCATAGAGGTATAACAGAAAAGCTGAGGCCAGAACGCTCTGGTGGTGGGCAGATGGAG

GCAGC

SEQ. ID. NO:240 AW465409
 GTTTTAATAATTCCCTGAGAGATGTCCTGGAAGAAAAGTGTGAAACTATGACTATTTTG
 GGACAAAAATGACAACCTTAAGCTAATTCTTAAACAGTAGGATAACTTCAGGACAATATTGCTCACAA
 CCCTGCTCACATTGAGAAGTCTTTTCGTTCCCTTAGCTGACTGGATTTCTACAGAAGCTATG
 GAAGATTATCTGTTCTCGTTGCTATTCTGCTACTTTAAGAAATATAACATAGAAATGGTGC
 ATCTTAAACATTGTTGACATGTATAAAATGCTGTATTGTTAATCGTTTACATGTAGCAACACGAATT
 GTTCAAGGGTAAGCCACACATCTAAAATCACTCTAGATACGAACAATAAGGAAAAAAATGGTACCG
 ATTTAGGAGGAAACAAAGCCGCTGCGTGGGTTCTGTGAGCCTGCAGTGACTTCCGACACAGNNAG
 AAGCTGTCACTGTAACCAAGTCATCCTGTTGGAGAGCGCCACAGCCTGCTGCTT

SEQ. ID. NO:241 BM366532
 GCACGAGCCAACACTACAAAAGCCTCGCACCCGACCCTCTCCACCTCTGTGCATCTCCCAGTC
 GACGTCGTCGTTACAGGGAAAGAAGCAGGGTGGAGAAAACCTCTGTTCCACCGTTGCCATTCTGCAG
 ATTGTTCCGAGGCCAGGGCCTTGTGAGGAGATGGTCATGGCCTGAGCCCCCTGTTGGTCTTC
 TACTGGTCTGGTCTGACCCAGTGGCCCGCTCAAGATGACTACAGATAACACTTCCTGACCCAGCA
 CTACGATGCCAACCAAAGGGCGGAATGCAAAATGGTTAACATGATGAGAAAATGACGCCGACAG
 ACCTTGCAAAGACCGAACACCTTATTGCAAGAACAGATGACATTAGGCATCTGTGAGGACAGAAA
 TGGACAGCCTAACAGAGGCGATCTCAGAATAAGCAAGTCTGAATTCCAGATCACCCTGCAAGCATAAAGG
 AGGTTCCCTCCGCCATGCCGGTACGGAGCCACAGAAGACTCCAGAGTCATT

SEQ. ID. NO:242 AW462090
 TTGACCGCCGTGGCCAGAGCGAAGAGGTGGAGCGTGGCCAGGGCAAGCAGGTGCATCCCAGC
 CCGCACCCCTGGCACCCCGCAGGCCGCGTCTCAGAGCTCAAGACCAAGCAGCAGATCTGAAGCAGC
 GCGCCGAGCCAGAAGATGCGCTCCTGCAGCGTGGGGCCTGAAGCAGCTCTGCCGCAACCGGC
 GAGCCCAGGAGCTGCAAGGGCGCTTGGCGGGGTGCCCCCTTCAAGAAGGGCAAGATGAGGAAGAG
 ATGTAAGAAGGTGACACAGCCCGGATTCCCTCGTTGGTCCAGGCGTGGCATCAGCAGCGTTCCCATG
 ACCGCTGTCCTGGCCCTGAGTTGGTGGCTGGGG

SEQ. ID. NO:243 AW462739
 TTTTTTTTTTTTTCTTCAAGGNNNGTTATTCAAAATTATGAAGATTATATATTATTT
 TTATTACATAACAATAAGGGGTTAGCTTAAAGTAAAGCTTCACATTAAAGTTTATTTAAAAAGATA
 TTTTAAAATGTAGACCTTAAACACCAAAAGCTGAATATATCTGCAGCGTAGGTTATCCTTAAAT
 ATTACACATCTCAATGCTGTTAGAAAAAGTTAAAATGGCTAAACATTACCTGGCAATGATT
 AAAATCTCATCTGACAGAGCATATTATGGCACATAATGAATTACTGTCACAAGCATTTAACAGTTAAT
 GGGTACGTAGTTTATCAGTACACAA

SEQ. ID. NO:244 BF039410
 AGGACCTGACCAGCTGAGCTTCCAGCGAGGGGAAGTGCTGCGTGCATGCCACTGTGGATGAGGAC
 TGGCTCCGCTGTTGGAGGGATGGAGCGGAGGGCTGGTACCCGTGGGTATACCTCCCTGTTCTAGGCCT
 AGCACCTGTCCTTCTGCACCTCTCTCCCTGTCACCTGGGAATGGAATGCCGTGAAACTCACC
 ATGTACTGACTGTCCTTCAAGTATCTTCCCTGTCACCTGAAACTTCCCTGTCACCTGGCAATTTCTGCTA
 ATACCTAAAATAACTTTCTCCCTATACCCATCTATAAGGTGAAATCTGCTTCAAAATATATA
 AAAACGAATTCCCTCCATGCCATCTTCCCTTCAATCTGATTCTGCAAATGGAAACTAGCCCC
 GTATCTCTCCATAAGTGGACTGCACCTCTATACGCCAGTTCCCAAGACTTGAAGGGCTCTATA

-continued

GTCTTCTTCCTGTGTATGGAACCTTCCCCCACCTCACCCATCCCGATTGCCGTATTTATGATGTAACCATGC
TGGACTANGTGTGAAAGTCTGGACACCCCTGGTGGGTGGGCCTGTGGGGTCAGTCTGT

SEQ. ID. NO:245 BF045989
TTAAGGTGAAACAGGTCACTTTGTTCTGCTTTAAATCTAATGCTTATAAAAGAGGTGTGTT
TATCCCTAGACCACAGTGCCTTGCAACCCACCACCACTTGGTAAATGGCATTAGATGCTGCACAAGCCT
TTAGGGCACTATTTGGTAGCTATAAAAGTTATCCAGAAACTGTACCTGGTGTCTCAGTTATTGTCAATTCAA
CTTGTTCATGAATATTAACATTTCCAGGGTTGTTAGAAGGAAGAATTGATCTGTTCTTAGTTACTATAT
TTTTTTTCTGGTGTAAAATGAGCCAGAAAATAGCCTTATTGCTAAGTAATTATATAAACCCACATAATCC
CTGCATAAGATCCCCTCACACACTCACTATATGTATGTGGATTGGATAGAAAATGATGTTGCCAGCATTA
CCAGTTTAAATACTGACTATACAGATTGATGGAATAAAATTATTAAGTGTGTTCAAGGAACCTAATCCAT
ATGTCACCAACAAAGATTCTACAGTGTATAAGGTATGTAATATTCCAATTCTGTAAACATTGGTTAGA
TAAAGAGTTTCTTTTGGATAAACACAGTTGTACTT

SEQ. ID. NO:246 BF440222
TTTTTTTCTTTATCTTTAAATGGAAGCAAGTGTGTTGACAGAAATCAGATGGCTGCTATAAGA
GCCGATCTAGGAGTAATTCACTGGGCTTCTCGGATAGCTGGATTAAAAAGAAAAAGACAAAACA
AGAAAAATAACCCACAGAGCGTCAAACACCAACTCTGAGCCTGGTGGGAATCGTTCTAAATAAGCCAT
AAGCTACACATTCAAGGTCAAATAACTGGCTCTGCCTTATGCTCCAAGCCATATTCCCTATGGTGTTC
ACCACCAACAAACAATTGCTCACTTAATTAAATTGGGTATCAGAACCTTAGAACATTCTGAATCTTAATAAT
GAAGGTCTTCAGCAGATTGTGTGATAAGAACACATACAGGCTGAAATATAACCACGTAAATTGGTT
TCTTATATCTATTCCACTTGAGTATTAAAGCACACACGTACACACAAACACAAACATTCAAAT
ACCCGTAAACT

SEQ. ID. NO:247 AW464311
AGGCTTATAAGGAACAAATAAAAGAGAGAGTGTCTGACTGCTACAAGCATTAAATAATCCAAT
AGTGAAGGCACGATAACGAAACGTTTATTAGGGTGAGAATCCCTTGAAATTCAAGATCATTCTCAAGATCA
ACAAATAGAAGGAGATGAGGAGGGAGGAAAGATTGACGAACCTGTGAAAGAGGAGGAAGAGGAG
GAAGAAGAGGAGGAAGTGGGGAGGGGA

SEQ. ID. NO:248 BF040466
ACGGCAGCTAAAGGAAGGACTTCTGCTTGAGTCTCCTGCAGAAAATGAAATTACTGTTCAACTTA
CCAAAATGCCTTACACATTCTTACAAATAACCAACCGACACAGCGTTATCGGGCCCAACTCGGTAGCTC
TGAGAAGCCATAAGACAAGAGTTCTTAGCACCAGAAAGTAGATCTCCAGACCCAGTTGTACAAGAAGAA
CCTTGTCACATTGAGAAACATATGCCCTGGCCGGCCCTGGACCACAGCCAGCAGACGCCAAGCCC
TCGTCAAGCCGTGGCACAGACCCAGGGCTTCTGGAGGGGGGGGGTCTGTATGTCAGTCAGTGAA
TTGTGTCTTCGCGGGGTTGGGGTGGTCTAGTGTGAGTCCTAAGGCTGAGAGCAGACTGGAA
GGTCACAGCCAGCGAGGCAGCAGCCCCAGTCCCAGAAGATGCTGCCAGAACCGACCGTGACTCCTGG
GTGTTAATGCCATTAAACCCGCGTGTGCCCGGCAAAAAAAAAAAAAACAAAT

SEQ. ID. NO:249 AW465742
TTGAAAAGCTGTAATTGGCCTCAGTATGTGAAGGATAGAATTCCACTTACATGTAATTAGCA
GGAAGTATTGGCTAACAGCTTGTCTGCTGGCAGTGAGCAGAACTCCTGCTCATGAACTTCATGATGA
GAGGCTTGGATAACCATTGGCAGACCTTGCAGCCATGATTGGAGCTGGAATGCTGGTACAGTCATATC
ATACGAGCAGAGTCCAGGCCAAAGCACCTGCTGGTTACTACATTCTGGTAAATGGGTGCTGGTGGCT
CCTCTGACGATCCTAGGGGGCCTTCTCCTCAGAGCTGCGTGGTACACGGCTGGCATCGTGGAGGTCT

-continued

CCACCGTGGCCATGTGCGCCCAGTGAGAAGTTCTGAACATGGGGCCCCCTGGTGTGGCCTCGGTG

TCGTCTTGTGTCCTCACTAGGATCGATGTTCTTCACCTACAC

SEQ. ID. NO:250 AW463923
 TCCTCTAAACTATTTCTGTGGTCCGAGGGCAAGTTGCTACTCATCTTGAGTAATCTTGCTCTCT
 TTCCATGGCATTGACCTTAAGTCATTGAAGCATTCTGATCTCACCTCCATAATGGGATATGGAAAGA
 CATCTACCTTCCATTAGGAGATATGATTCTCTAGTTGAGAGAAATATGCGAATGGAGCTCCTCCCCATATTAA
 ACCAGCTCTAAATGGATTATTCTGACCTCGAGTCAGTGTGCCATGATTCCCAGGTGTTGCTCATGTTCTC
 GCTTGAGAACCATTCCTTGTGTTCTTCCACCACCTCCGTATGAGGTAATGGCACCTGCCATTGGA
 TGGTTGGACTCTGCCCTTCCCGTGCAG

SEQ. ID. NO:251 AW466175
 TAAAGACTCAAAGACTGACTCTGCTAGTGTAGCATTCCCTGGGGATTGGTTAACTTAGA
 CGGTTCACTGCTACTGTGAGTGCAGGGATGGCGGACATGGTAGGGGTAACCCAGCGACACCAGCACTG
 ATTGGACGGCCCTCACCAATCAGAAGCTCAGTGCCCAGTGGCCGCTGTGACTTGAATCATGTTGTGCA
 CTATAGTCACATGTAAGTAAAAGGGATGTGAAAAACAGAAAGCGAGACCTGCTACTAGAAAAG
 TGGGAAGGGAAATGAGTAAACTCTTCTTGTGCGGACAGATGTGACATAGCCCTAGTAAACCAGCCTCA
 AACAGAATGCTCATAGCTTAATAATAAGCTGTGCA

SEQ. ID. NO:252 BF044437
 TTTATCCTCTCTTCAAGGGTAGATTCTGGATAGCTAGTAGTGTAGGCATCTGAAATAGCATTGA
 GGGGTGGGTGGTATTCAAGGGTAGTTCTGGCTGAAGAGCTTCTGCTTAACCTTCTTGCTGTT
 AATAGGTCTTATTGGTTCTTCTGCTAGGGTATGCAATTAGCTTAAGAACTTTAAATTGTGGGGCA
 GTAAGAAAACTTGAATGCCGGCCCTGCACCTCTCTAGAACAGCAGCCAGAGGGTTAGTGTATCTG
 TTAGCAGGAGAGCTCTCTAGAAGGTCCATTGGTACCTCTCACACCCACAGCTTGTGCTATGGTTGGCCCT
 CCTCCTCTGATGAATCCATGCCATGACCCAGTGTAGCTGAATCTCATGTGCTCTGAAAGCCATTGAAAG
 GCACGTGTTGC

SEQ. ID. NO:253 BF039323
 GCAGAATGGATTGTTGATTTAACAGGCACTTATATAATGTGTTCTGTTAGTTATCAA
 GACTCCTCAGAGATAAGAACCTTTAACAGTGAGCAAGGCTGGGAGTGAATGGAGTCAGAGGTGGAG
 CGTCAGGCCAGGGTGTGGCCCAAGGTCTGCCCTCCAGCCTCAGTTCTCAGATGTAGAGGGAAAG
 ACCACCACTCCCCGCCACATGTTCTAGGAGGAAACTCTGTGCCCCATTGCACTTAGTTCT
 TTTCGGCTCTGACTTTACATATATACCTTTCTTGTGCTGTGCTNTGGGGATTATTCCCC
 AACTAGGGATCGAATCTGTGCCCCCTGCATTGAAGCACGCACTAACCACTGGACCGCTAGAAAAGTCCCC
 TTATCTGTTTATTATTTGTACATTACTTGTGGGATG

SEQ. ID. NO:254 AW462705
 TTTGAAAATTAATTGTTGATTATGCATTCTGATTTGCTAGTGTGATAATTCTAAATTATCAT
 ATTCCAGTAGATTAGGGGAATTGATACCTTGTGAGTTGAAATAAAAGTGTGATAATTCTAAATTATCAT
 TTATAAAATTCTTAGAGCTAACATTGCGTCATCACAGGCTGATTAGTATTGTTGATTAAGGAAAG
 CTTTCCCTTCTGCTGCCATTCTCGTGCACAGGCTTAAAGAAGAAATAGCCAAGT
 TGACTGTTACACCTCATCCAAACAGACACATCACAAACATACAGGAGGGGAGCTGGCTGGGATGGACGTGGT
 ACTTCTCAGTCTGCCCTGTTGAGAGAAGAGCAATTAGCATGCCACGTACCTGTGCTGAAAGTGGAAAAC
 TTAAAGATCGGAAAATTAAAGTCAGATCAGGGATTACAGCTACTTTGGTAGT

SEQ. ID. NO:255 BF040988
 GGTAAGATCATAGTGGATGTGGGTCACAAATATGTAGATGGCCACATGAAGATAGGCAGAGACTG
 GAGTTATGATGCTGAAAGTCAGGAATATGTGGGCCATCAGAAGCAAGAAGAGTCAGGAAAGGTTGGAAG

-continued

GATTCTCCTTGGAGTGCAGAGGGTACATGCCCTGCTGACACCTTAATTTGGTTCTAACGACCAGAATG
 GTGAGAAAATCAATTCTGTAGTTAAGCCACACAGTTAGGGTAAATTATACAGCAATTCTAGGAAACTA
 ACACAGTCACCAAAACTGATTATCTTGCTAATTATGATAAATTATGTTTATCATGTTACATAAGCAGATG
 AAATGAGTGTGAAGAGTTGTAGTTCTGTGAAAACCAAGTTGAATACTTGGAAAAGCTAGATGAAAGTGTG
 TTGCTTCCCCATGCCAATTAAATGATTGGTTAATTATGGTAAACAGTTGAAAGACTGGCCAGCAA
 TGTACTAAAAATCCACAGGTATTCACTACAGTGTACAACATATAACGTAACACATATGATT

SEQ. ID. NO:256 BF044083
 GCAACTAGAGAGTAACCCCTGCTCCACAACAGAGAAAAGCCATGCAGCAACGAAGACCCAGC

ACAGCCAAAAATAAATTAATAAAATAAAATTTTTAAAAGAAGGTCCCTGTAGGAGAAAAGCCCTCA
 AAATACCTCGAATCCAGACTATAACCTGCCAGTGAAGAAGAGTAGCTTATTCAATTCTGTGTGCTG
 TGTGGATCGCAAGGCCAGGCATGGAGCAGGACTCCAGTGATGCTGGCTGAATGGACAAGTGGAGAATTG
 AGAGGAGTGCTCGGATCAGGTATCAGAGGAGCTGGAGCTGCCTGTAATATCATCTATTGGTATTTGC
 GCAGACTCACTAACCTCTAGCTCACGCTATTGGCTGTCAGATGGAGCTGAGAAGACTTGCTCAAGGATT
 GTTTCGAGCAGCCTGAAGAAGCTGATGAAAGCAGATCCTCAGGAGCCTATAAAACAACACGGATTGG
 TGCAACCGCATGTCAGTCACCGCGT

SEQ. ID. NO:257 BF045148
 GCATTTGTTTTTTTTTTTTTTTTAAATGACTCTGAAACTTAATTACAGATACTTATCAACATCT
 GAAAGTGTGGATTCGTTCTTTCTGCGGAAAGGCTGGCACGGTTGTTCCCTACACCATGCTTTCTGCT
 CCTGCTCTTCTTATGTAaaaaaaaaaaaaaaATGCTGGATCACAGTCCCACCAACTCTGCTCTGCATCCCTGC
 TGGGAAC

SEQ. ID. NO:258 BM363855
 GCACAGGGACATACTGGACCTGAAAGAGATGGTCAGACAAGTGACGGGAAGATCCCCATCTTCTC
 TATTACACTATGGCTTACTGCAGAAAAGTGGCCAAGGCCAACCCAGAGATGCCACAGACAGGTGCTGC
 CGTGAACATGACTGCTGCTACCGTCACCTGAAATCTGACAACGTGACATCAGCTCGACCAACTATGACTACA
 CCTTTTCCAGGGAAAGTCAGTGTCCACCAAGGGAGCTGGTGTGAGCAGCAGCTGTGCGCCTGTGACA
 AGACGTTGGCCTCTGCTGCAGCGAACCTGAACACCTAACAGAACCTCACCTGCGACGTGTCCAGATGCG
 AGGGCGAGACTCTAGCCTGTCCCCCTGCATCTGAGCTCTGGGGAGGCCAGGACACTGCCACAGC
 CCCGACCTCTGCTGGAGCCTTAAAGCACTCTGGAAGAGGAAGGGGCTGGCCTGCCCCTAGCTACCAC
 TGCCCTTGGACCTCTGAATCTCCAGGCTGTCTGTTCCGGAGGGTGGATTGAGATC

SEQ. ID. NO:259 BF044419
 AGATGTTCACTTAAACAAATGCAAAACTTAAGACAAAAGTGATATGTGAAGAAGTCTTTACAG
 TAAAATATATCTGAATCCATATAGGTCGTTCATATTGAGTCTCTCTGAGTACCTTCTAACACGTAG
 ACAAATGTAAGACAGTGACAGCGCTTTCTAGAGGTGTTAACCTGTTAACACTGTGAAACAAAG
 AATTTCTACTTTACTAATGTTGTGGTTAAACAGTTATTTCTAACATCAGTCTCACCCCTAAATT
 TACTAAAACGTAAATACATTAGAAATGATTTGTAATACAGTATATGAAGTCAAGTTAATTGGGGAC
 AGTGGAGAACCTCCAATTGGCTCTGCCCTGGCAGTTGTTGCTGGTTTTTTAAAC
 AGC

SEQ. ID. NO:260 AW465703
 TCATTTCTATTGCAGCTGGGGGACCGCCACAAACGCAGCGACGTAAACCGCAGGAGCGTGTGCT
 GACAGTCCAGGGGTGTTCTCGGCAGAGCCAGGGAGGGTCAGCGCTGTCTCCGGGGTGTAGCAGAG
 CTCAAGCCCTGCGGTAGGGCAGGGTCTGCTCTGCCGCTGTGAGCTGAAGCCATTGGCTCTGGAAGC
 CTCTGGCTGGCCGCTGGGCCCTTCCCTTCAAGCTGGCAGCTCCCTCCATGTTGGCCCTCACACGTC

-continued

CCCTGCTGCTTCCAAGGGCTGTCAATTAGGGGTCCCACGAAGATCCAGGGTCGCCGTCCGCCTGTGTCCGT
 GTCCCTGCGCTTACCGGCCGAGNGGCCGCTCGGGCCCCGGCAGGCCCTCTGCGGCAGGAGGGGC
 AGAGCTGGCTCTGCGGGCTCGCGCAGCTGTGCACGTTGCCGCCGTGAC

SEQ. ID. NO:261 BF039660
 GTGTAACACTAGTCTTGTCTTCTCTGGAGCTAGGTTGGTCCAGCTCAGACCATGGTTGCCT
 AGCCACTACTATGGGGCTGCCCTGTACTCTCTCCCTGGTCTGCCATCTGACTCTTGAGGAT
 TCTTCCCTATTGCTCATGCCCTCAGGGTCCCTGTATTCCATCATTGGTCCACTCTCTTCTCTATTACT
 CCCCCAAATAGAACATCCATCTGTAGTCAACTGCCATTGATATGCTGGTATTCCAAATATATATCTCAAG
 CCCTAACTGCCCTTATCTTAGATCTGTATTCTCACCTGCTGGATATCTCCTGGACATGTCAGATGGA
 CTCAACTCTTCTGTCCCTACTGCCAAGTATGTTCCCTGAATTCCAATCTGGTTACATTCATCACTCTCAT
 AGGCTCACCAGCTAGAACATTATGGCTTAAATTCCCTCCATATTACTAGTCAGTATATCATATCCAT
 TCCACTCCAAGTTTCTTGTGTTTGGCCCTTCTCTCCCTGCTCTACTCTAGTTCACAGGAGCTGGGATT
 TGGAGTCA

SEQ. ID. NO:262 BF039699
 GGAAAGAGAACAGCCACCAGCTTGCTCAGCCTGGGACATTGAATTGAGTATGCATCTCGATGG
 AAGGCTCTGGATGAAATGGAGAACAGCAGCGAGCAGGTTGACAGAACATCCGAGAACGCAAAGAGA
 AACTGGAGGGAGATGGAAGCAGGGCCGGCACGAGCACCGCTGATGCTCATGCCAAGATTAATGAGG
 CGTCAAGAGGAACTCAGACGTTGGAAGAACTCAGAAATCAAGAGCTACAAAAGAAAGCAAATACAGCT
 GAGGCATGAGGAAGAGCACCGTGTGAGAGGAAATGATCCGACACAGAGAACAGGAGGAGCTGAGG
 CGACAGCAGGGCTTAAGCCAAACTATATGGAAAATGAGAAAGAACATGGATGAAGCTACCTGAA
 ATTGAGCTTCTGTGAGGCCAAAGTTGAGAGCTGAGGAAACCTGCCAGAGTTCTTCAGTGGTCTTGG
 GGAGCAGGAACCTCAGCTTCTGATTATCGCTTGAGATGAGACTGATGACATCAGAGCACTGGCTT

SEQ. ID. NO:263 BF044525
 CGCAACTTTTAAAGATTCAAGTTACAGCTCTTGTAGAGCTTGTGAAAGAGGTTTCNNNTTTATTAAACTAAAT
 GGATCAAAGAACATTGTTATTTCTCTTGTTAGATATTAAATGATAACCTTGTGGAATTNTTCC
 AAAGAAAATTTTATAATTCCGTAATTAAATGTGTTCTTTCATCATCCACTCTGGCAGTGTAGGCTAT
 GTTACCTTAAATAATCTGACTCAAGATTTTATGTATGATAAAAGAAGTATTTGTGTGCTACAAAGC
 CTTTCAAATTATCAGTAATTTTTTAAAGAATGCCAGTATTGCTCAGTGTGCTGTGAAAGAACAT
 GCAGATGGAAGCTCAGNTCTTANGNAAGGGCTGGGAGATGGGTTATTTCCACCTGTGAATATGTAAA
 ACATAAAACCATTATCTGAGGGACTCTCAC

SEQ. ID. NO:264 BF041013
 CTCTTACCTTCCCTTGTGTCACCAATGGTTGCTCTTCCAGAGAACCTGGGATATGCA
 ATGATAGCCAGAACCCCTGTTCTCACCCACCTGGGCTGTAGCTGAATGTGGCTGGCAGAACAGGGACAC
 CAAGAGATGGAGAACGGGGCTCCAGCCTCCAGCAACTTCTAGCCCATAAGCAAGCACAAAGATGAGG
 CAGAGATCTGTCAGAGCTGAAAGTTCACTGGTGTGCTCACAACTCAGGTATGCACACCGTGTGGCANNNGGG
 CAGCAGGCCCTACTGACCGCAAGTCCGTGACCCAGACCTGTGGCAGATCGTGGACTCTGGCTGCCTC
 AGGCGCCGCTCTTGCATAGGTTCTCCTCATTAGTAACTACAGCCGACTCAGACATCCTCCACATTGTGC
 AACACTGGTTCTGCCCTTGTCTCGCAAGTTGATACTTGGCATTAGCATGAAACTTGTGGGTGTGGAGGGTT
 AGAGAGAATTCTAACACAAACATCCTATTAAATTGACTTGAGAGATGAAAAAACTCCTGTGTATTGAC
 AGAATTATTTATTAAATACATCCATGAGCAAAAAAAAAAAAAACAA

SEQ. ID. NO:265 AW464094
 GCAAATCGAACCTGCTTCAGCTCCGGCTGCAGCTAGCTCCAGCCCCGGCTCCGGCAGGCTCG
 GGACCACTGTACAGCTCCATCACAGACTCCGGTCAGCTCCCTGCCAGGGCCAGGGACCCCGTACCC

-continued

CACCTATCCAGGGTATCCGGGTATTGCCAAATGCCATGCCATGGCTACAATCCTATGCGTATGGCCAG
 TATAATATGCCGTATCCACCAGTGTATCACAGAGCCCTGGCAGGCTCCATACCGGGACCCAGCAGCCTT
 CATACCCCTCCCTCAGCCCCACAGCAGTCTTAATCCAGAGCAGTAATATGTCAGCTCAGAAGCTCAGCT
 GGTCAGTTCAAAGGAAAGAAATACCAACCCCTGCAATAAGTGTACTAAACTCTACGCTC

SEQ. ID. NO:266 AW464164
 GTGGCCGTGGTACCATCTCAACGAGGAGGGACCCGCTGCCTGTTGATGTGGACGAGTGCTCTCCCC
 CTCTGAGCCCTGTGGGCGGGCACCTGTGTGTAACCTCCCTGGAAGTTCCGCTGTGAGTGCAAAGCCGG
 GTACTACTTCGACGGCATCAGCAGGACATGTGTGGACATCAACGAGTGCAGGGCGTACCCAGGGCGCTGTGC

SEQ. ID. NO:267 BF045865
 CCCCACACCAACCCCCATGGAGAGTACCTGCCAGATATGGGCTGGGAATCGAGGGAGCGAAC
 CCCGCACGCCTACGNTGCTAAGAAAGGCAAGAATGGAGGAGGGCCGGCTACGAGATGCCCGGTTCA
 GCTGAGCTGACGGCGCTTCCCGCCGTGGGGCCCCGGTGAAGTTCGACAAACTGCTCTATAACGGCAGA
 CAGAACTACAACCCGNGACGGCATCTCACCTGCGAGNNNCTGGGTCTACTACTTTGTATACCACGTT
 ACTGCAAGGGGGCAACGTGTGGTTGCTCTGTTAAGAACACAGAGCCGTAATGTACACGTACGACGA

SEQ. ID. NO:268 AW462758
 AAGGGAAAGCAGTTGATTGTTTAAAAACACTTTTATCAGCTTGAGAAAACCGAAATGCAA
 CGAGAACAGCTGCTCTGAAGCCCTTCCTGTGAGGGAGAAGAAAAAAAAAAACAAAACAAA
 CAGA
 GAAAGCCGTTAGCAGCGTGAATGCCTTTCAGAAGCTAACCGGGGATTTGAAAGCCTGGCTCGTGTCT
 CAGTTTAAAAAAAGATTCCAGGCTGTAAAAGGCTTCA

SEQ. ID. NO:269 AW462782
 ACAAAAGTAGCGTTTAAATAAAAAAACACTCACAGACATAAAGATCCGTACTACCCCCAAA
 GCTGAATAAGTTAAGTTGTGTCCTGCTGCCCTGTGACGGAGGCGGGCCGTGCGCTCAGGGCTGCCCTTC
 TCCAGATGGCACAATGTTGGAGTCAGTCAGCGCAGTGAGGTAGGTAAGGCGGGTTGCCACCAGCGTGT
 TCACCATCGTCTGGTCACCGCTGGCCATTGCTGGGCTGGGCCACTTAAGGATCTGCGTGGGGCCTG
 CGGGGGGGCTGTGGTGGGGAGCGCTGCGCAGGAGGGGCTGACGTATAGATCACACGCTGCCCTGCTC
 ATCCCCCAGAGCACAAGCCCCCTGTCAAGGACAGGTGCTGAGGGAGAAGTAGGCCAGGATGGTGGCGACC
 ACTGCAGCCAAGCCAGGACTACCACAGCCACTGTGGCTGGCTGCCCGACCCCTGCCACGTC

SEQ. ID. NO:270 AW463320
 TGTTTAAGTCTTGGGTGGTGTGCTGCTGCTTAACCATGTCTGACTCTCGATCCCCCTGGACTG
 AGCCCCATCAGGCTCTCTCCATGGATTCTCCAGCAAGAATATTGGAGTGGAGTGCTATTCTCTCCAG
 ATCAGGGATTGAACCTACATCTCATATGCCCTCTGCATTGGAGAGATCCAGTGAGCTGGCTGTCTGGAAA
 ATTCTGGATCTGTGGGACACACCCCTGAGTGTGAACCTGGATACCGGACCTTGGTGGCAAATTCATCTTT
 CTCTCACTGGGTGTAATTAAAACACAGCAACATCATCTCATGATCTCCATTGCTTGGTCTCAGC
 TCAGTAAACTGAATGAAGCTTAAATGCAATCATTTCTAAACATTTCATCTGTCAGTATAAAACA
 GCCTTGAGCCTCACATATCTTCGCTACCATGAANNACCCATGTCAGCTGAAGTGTACAGCGCAGTCTTCT
 CCAAACCTTATCAAGTTACTGCACCCCTCTCCTCTGGCCTGCTACTCAT

SEQ. ID. NO:271 AW465653
 GCGGCTTGCTGCCCGGGCTGGCTGGCAGGAGCTGCGGCTCAGCTCTCGGCCGCCACCCCT
 AAGGTGCCCTGGCCCGTGTCCCATTACACGCTGGGTGAGGTGGTTGACCCGGCTGGCTGGTAGC
 ACGACCGAGGAGGGTGGCTGGACGGCTGGAGAATGAACGGAGAAGCCGACTGCCACAGACCTGGAAATGG
 CGCCCCCTAAAGGCCAAGACCGCTGGTCCCAGGAAGACATGTTGACTTGTGAAATGCATGAAGAACACA
 TTCCATCCAATGACAGCTCAAGTTCAAACACCACCGAGTCACATATGGACTGGAAAAAGTAGCATTAAAG

-continued

ACTTTCTGGAGACATGTGCAAGCTGAAATGGTGGAGATTCTAACGAGGTGAGAAAGTTCGTACATTGA
CAGAATTGATCCCGATGCT

SEQ. ID. NO:272 W465738
GTCATCACCTCCATCTGGAGAAAATGGATATATTCTGTTGCCGGTGGCCAATCTGATGGATATGT

GTACACTCATACTCACAACCATTGAGGAAGACACGGCTGTAAATCTAGAACGACCTGCATTGGTGC
TGATCCAATAGAAATTGGATTCTCATTTGGAGGAGTGGGAACCAAGTAACGACCCCTGCTCTGATACTGAT
CATGGACTCCATGCCATTCAAGTGGAGGTGAAATCGGTGGCAGATTCTTACAAATCATGGGACTTC
AAATGCCTCATGCACCTGCACAGCTACTGGCAGCTGGTGATGTATCCATATGGCTACACAACTAGCAGAGTCC
CGGATGCTGATGAACTGGATATGGTGGCACGGAATGCATCCAAAGCTATGGCTTGTGGGACTCAGT
ACCAAGTGGTTCTGCGCTTCACTGTCTATACAGCTAGTGGAACACTATTGACTGGCATATGATAATGG
CATCAAGTATGCGTTCTTTGAGTTGAG

SEQ. ID. NO:273 BF039874
AGAGCTGCTAAAGGCACCCCTACCCCGCCGAGGGACAACACAGACAGTGTGAAGGCTAATG

TGTGGCTTTACTACCCCTCCCACCCCCATTTCAGGGGTTAGGCTACATTAAATCTAACCTGCAGT
CCGTGACTTCCTATCAAGCCCCATGCATTGGTTGGTTCTGCTCTGCCCCCTTCCACTTCTCGT
ATTTGCTTATGTGCGAGTGCTGAAATGGCCCTGGAATTGAGAATTGGCTCTCCACCAAGCACCTTATCTG
CCACCTTAGCCTAAGAATGAGTATGAAGAAAAATGCACAGCCCCTCTGCCAGGGCAGTGAGAAGCCCTG
CAAGGAAGAGGTGGAGACAAGGAAAGGAACAGACAGTCACCTCCACAGTCCGAGGCTACCATGCCTCAG
GGGGCCCCAGGGATTGAGAAGGGGATATCTGGAAGTTGCTGCAGTTGTGCC

SEQ. ID. NO:274 BF042207
GCTTGGGCTATTTTGTGTATATTGATGATGAAGACATGTGCAATGTAGAATTACAGTGAACACTG

GTGACTGTGGTAGTCATTACTGAAAATGCACTGNNNTCCACACCATGAACTGGCTGGTCGCCTCTA
TTTCGGATTCTTGACACTGGTGTACTTCATTGCCAGGCATACCTCTAACTGAGTAGGAAGGAGC
CTTGTAAAGATCCTCACAGGCAGTGCTGAAAGCATGCTTGCTGTATAAAATGAGCATGAGAAAGTGT
GTATCATGTTATTTTATTATGTTCTGCTTGGTGTAGAATTCAAGCAAATTTCATCAAATCTAGCCAGAGC
CCTTCACTGCCATGATAGCTGGGCTTCACCAGTCTGTACTGTGATGATTGTAGACTCTGGTTGTATTTC
TGTATTTATTTAAATCTACCGTGTGGATATTAGTGTCTCTTAAGTTGGATTAGTGTCTAAAT
GGTGGAGTTGCTCTGAATGTTACAAATGGATCAAGGCATTTAAATGAATGAGATCTACCTTCACCAAGTACT
GATGCTATT

SEQ. ID. NO:275 BF042293
GCCTGACCCAAGGGCTTCTGGGCTCTGGGCCATCCTGAACCCAGATCCACATGGACCTC

GTGTTGAGCCAGGGTGAGGGGAGCAACCCCAACCCGACCCACTCAAGCCCTGCCAGCTCACAGGGCAG
GGGGAGGCTGGCTCTACTCACTGGAGCTGCTAGAACCTCCCTACAGTCTGGACCCAGCTAACCTGAGGG
AGCCATTGCCACCTTCCAGCACCCACCATGTGCCACCCAC

SEQ. ID. NO:276 BF044365
TGTTACCATCTGATGTTGGAGTGGCGATTGTTTTTTTTTAATGATGAAAGTAGTTAA

TATTGTCATATGTCATTGTAACCATAAGGTGAAACACAGGTCTGTTCTTCTGTAAACT
GGAGATCCTCTGCACTGCCACCTGTTAGAGGAGAGCATTAGTGCCTCCCTGAAACCTATCATCCCCCTCA
GAGCAAAACTCGATAGAAGGTGAGTGGCAGGTATGGAAGAACTGGCTTGGAGTCAATTCTTAAAGAAT

-continued

TTATTTCCAGTACTGCTTAGCTAACAGATGGCTACTTATATCTCTGAATGATTAAATTACCCCAGATCCTA
TAGCCAGTCAGAACGAGCTTATTACAGAAGTACAGCATAACCC

SEQ. ID. NO:277 BF045161
GCCTCCGGGTAGGAATTAGGTGACCCCGCTGCCGTGGAACCTGCGGTGACAGCAGCCATGGGGC
TCACCTGGCCCCGAGATACTGGGCATGCATCGTGGAGCCGATCCCCCTGCGGATGCCACTTCCGCC
GACTACGGCTTCCCCAGCGCAAGGAACGCGAGATGGTGGCCACTCAGCAGGAGATGAACGACGCCAGCT
GGTGCTCCAGCAACGCGACTACTGCGCCACTACCTCATCCGTTCTCAAGTGCAAGCGCAGCAGCTTCCCC
AACTTCTGGCCTGCAAGCACGAGCGGACGACTGGGACTACTGCGAGCACCTGACTATGTGAAGCGCATG
AAGGAGTTTGAGCGCAGCGGGCTGCTCAGCGGAAGAAGAGACGGGAGCAGAGGGAGGCCACATGG
CCAAAGGCTGGGGCCC

SEQ. ID. NO:278 BM361926
GCACGAGGTATCCCGGCATCCGGCCGGCTACTAGGCAGGCGGTACGGAGGGTACGGAGGGCTC
CCGGAGGGCCTCGTTCCCGGCAAACCTCAGGATCCGCTGTATGGTTACTTTGCTGCTGTAGCTGGACAGGA
TGGACAATAGATGCTGATGAACTGCAAAGATGCCTGACACAGTCGGCATTGCTGGAGGATAACAAACCTT
TAACCTGGAGACTTGCCTTATGGTTCAATGCTGGATAGAGACATGTCAGGCACAATGGTTCAATGA
ATTTAAAAGAACTCTGGCTGTACTGAATGGCTGGAGACAAACACTTATCAGTTGACAGTGATAGGAGTGG
AACAGTGGATCCCAAAGAATTGCAAGAGGCTGTGACAACAATGGATTANNNNNAGTCCCCAGGCTGTG
AATTCAATTGCAAAACGATACTACCAATGGAAAGATCACCTCGATGATTACATCGCCTGTTGCGTCAAG
CTGCGAGCTCTAACAGACAGCTTCGAAGACGAGATACTGCTCAGCAAGGTGTAGTAAATTCCATATGAT
GAT

SEQ. ID. NO:279 BM364516
GCACGAGGAAGGTTGTAGCTGCCGTGTGAAGTCCAGAGAGCGTAAGCCCTGTCACTGGACCCAGTC
TGACCTCTTCTGACGGCTGGCTGGTGTAACTCACTAGGAGATCTCTCACTGGAGTTACACCTTCCCCG
GTGGTACCCCTTTGTAGCTGGATGAGAACTGTGGGTCTGATCCCTCTGCATCTCGCTGGAAATTCC
CATCCCTGGAAATATCCCTAGAAAAACCTTCTGACCTCGCTGGACTCTCAGCCTCTGAGCAGTGATGGTTCAAGTTGAAAA
ATCCCATAGATTGTAATCCTGCAACCTCGCTGGACTCTCAGCCTCTGAGCAGTGATGGTTCAAGTTAATG
TGATAAAACTGTATTTGTATTGTTAAATGGCATCTCCACAAAATGTGAAAATGGTCCGGAGAAGGCAG
CTTCCTGTATGCACTGTGCTTTTAAAAAAAAAAACAGTAACAAACTCCTTGGAGAAACAATTTC
TACTTGAAATCATATCAATGAAAAGATGTATATGCACTTATAATTTCCTAATAA

SEQ. ID. NO:280 AW462100
GAGATCAGCTCCCTCAAGGACGAGTTACAGACAGCTTACGGGATAAGAAGTACGCCAGTGACAAG
TACAAAGACATCTACACAGAGCTCAGCATCGTGAGGGCGAAGGCCACTGCCAGTCAGCAGTTGAAGGA
GCAGCTGAAAGCCGCCAGGAAGCAGTGGGTGAGAAGTCCCCGGAGAACCCACCTGTGTCGGATATGACAT
CATGAAGTCCAAGAGCAACCCGATTCCTGAAGACAGACAGGTCTGTCGGCGGAGCTCAGAGGCT
CAGGTCCAAGAGTCTGAAGGAAGGCCTGACGGTGCAAGATGCCCTGAAGCTTTGAGTCCCG

SEQ. ID. NO:281 BF039681
GGCCAGAAGCTGCTGAACCTCGACCTGGGGAGCTCATCAACAAGATGAAACTGGCCAGCAGTA
CGTCATGACCAGCCTGCAGCAGGAGTACAAGAAGCAGATGCTGACAGCCGCGACCGCCTGGACG
CCAAGAACCTGCTCGACGTACCGACCGCCAGACTGAAGGCCCTGGGGAGCCAGCCAGGCGCAGNNNGCA
CGACCCGCCCTGCCCCACCCGCCACGAGGCCACCCGGCGCAGGCACACCCAGCGCAACGTTGACTGAC
GGCTGCTGGAAATCTCACATAAGTTAACTGCGTTGATTGGTTGTTGAGCTCTTAATCATG

-continued

GTGTTCAGAAAAGTCGGGATCCACAGTGCAGCATTTCTGAGAGTAAAGTTGTATGTGAGAAGCTCTTA

AAGAACGATGAAGGATAGGCTGTGCTCACGTCAAGGATACGCTTCGTGAAAT

SEQ. ID. NO:282 BM364428
GCACGAGCCTAGTCATTGCCAGAGAAGAAGGCCTTCCCTCCGTGTCAGCCCTCCCCAGAT

GGGGACAGGCAGGTATGGATTCAAGTATAGATGGCCAGTTGTGAATCTGNNGCTACAGAGGTGACAGCA

GGCGCCCTGGGACACACTTGTACAGCCGGAGTTGAAGAGACTCCTGAGGACCAGAACCCACCCAGGA

AGACGCAGAGGCCAGGTCTGCCGAGGCTCTGAAGGAGCTCAGAAATTGCTGACGGTGACCGCGAAGT

AACAGGGGAGTCCGCTGTGCTTGAGGTTGAGAAAGATAACATGAGGAGGCCCTGTTCCCAAGATATTGA

AAAAGAAGAGGAAGCAACCAAATCGACACAGAGGCCAGTCAGCATCTGCTCGGTCAAGGACAACGTG

AAGAAAGTGAAGTCGGTAGGGGGAGGCCATGGTCCAACCTCCAAGGCCAGCGGGTGGAGCTG

GGAGAATTTCAGATGCTCAGCAAACCT

SEQ. ID. NO:283 AW462966
GAATTGGAACGTTCTGCTTGGTGTGATCATGTTCTCCAGTATTACCTCAACGAGCAAGGAGAGCG

GGTCTACACGCTGAAGAAGCTTGATCCTTGGACAACAGACGTGCTGGCCACCCCTGCTCGATTCTCCCA

GACGACAAATACTCTGACACCGAACCATCAAGAAACGCTCAAGGTGCTCATGACCCAGCAGCCGCG

CCCGTCTCTGAGGATGTCTAACATTCGTGTCTCTGCTGCCAGCCCCAAGAGACTTGTGCAAG

CAGGCTCTCAGTCTGTGAGCCTGAAAGCTTGCTCCGACCCTACTCCTCGAATCCGGTCTCATTTGCCTT

GATTATGCTTGTGTGAAGCAGTCATGGTAGCATCCCCGTCCAAGGGGAGATATTGAATCTTCGTACCTT

GAATCACTGCCAGGTTATTAATGATT

SEQ. ID. NO:284 AW461868
TTTCTCTACCTTGCCCCCTAGGAGCGATCCGTTAGCTGACAGATTGAAAAAGCGGAGTATCGGAA

CTTCCAGGCTTGTCTGCACAACCTCTGGATCGAGCAGGCCGGCTGCCCTGGAGATTGAGCTGGAAGAAGA

AATGTATAGGGAGGAAAGTTGATGAGCAGGAAGAGCGTGGAGACAAAGCAGATGAAGATCTGAAAG

AAGGAGCTGCCATTACTTCGAGCCGCTTTAAAGATGACCTGAAAACCAAGTATCCCACTCAGTCAG

GCAAGCTGCCCTGTCACGTGCCCCAAGAAAGGGTGAGTCGCGCTGAGCTGCCCTTCCAAACAGAAGA

AGAAGAAGAAGAAAAGCAGCAGCCGAGGAGCAGCCGAGCCGACAAGTGCA

SEQ. ID. NO:285 AW462382
CCCTCGCCCGGCTGCCGGCGCTCTCCGCCGAGCTTCAGCACCTGCCAGAACAAATGCTAA

AGTAGCCGTGCTGGGGCCTCTGGAGGAATTGGGAGCTGCTCTTCGCTTCTCTGAAGAACAGCCGTTGGT

AGCCGCCCTGACCTCTACGATATCGTCACAGCCGGAGTGGCCGCCGACCTGAGCCACATCGAGACCAGA

GGCACCGTAAAGGCTATCTGGACCTGAGCAGCTGCCAGATTGCTGAAGGGCTGTGATGTTGGT

CCGGCAGGAGTCCAAGAAAACAGGTATGACCCGAGATGACTTCAATACCAATGCCACGATCGTGGCC

ACCCCTGACCGCTGCCGTGCCCAGCACTGCCAGCATGATCTGCATCATCTCAAATCCAGTTAACTCCA

CCATCCAAATCACAGC

SEQ. ID. NO:286 AW464067
TTTTTTTCACCGTCCAAATCTTGTCTTTATTTTTATATAAAAAATGCAATTGGAAACCCACCC

TACCTTTCCCTAACATAATGCTTTACCTCTAAAAAATAAAAAATAAAGTACTAATCCTATGTACATCACATG

TACCATAAAAAATGTATCCAAGTTCTATTGCTACCAAGTGTCTAAATCAAACGAGTTACAGAAAGCC

CCTCATTGTAACAAAAGATTACAAGTTACAAAATCAAAGCACACAGCCAGAGTCATTATACAACAAACC

-continued

AACATCCTGCTCCAAAGCAAGTTGAATTTCATGTGCCTGTATAAAAATGCATATCAATATACTCTGCAA
TTTATTTTCATTATAAGCAAATGAATACACTTCTACAATAA

SEQ. ID. NO:287 BF042174
GCTCCTTAGGTATAAAGGTAATCTTCTGATTAAGTGGTATTGAAGTGTGAGTTGTACATTT
TGCCACACGTGTTCTGCAGATGGTTGATTATAAACATACTTACCTCTCATACTAGTAAGTGTGAGTTCA
ATCATAAGTATTTTAGGTAAGAGCCCCCTGATTCAAAGAATGCTTGTGCTGCAGTTTAAACATG
GGTTTTCTGTGACACACTAAATCTCTTATTCATCTTTAGGTCTACAGCTGCTGGCTCATGAAATA
GGTTTGGAAAGCAAAGTTACAACACACCCACTGCTAAAGACAAAATGATGAACGGAAGTCATTACAGCTAC
TCCGAGAACCGTGTGAAAAGGATGCCGTACCTTACAGCCGAGGGCCAGGAACCAGCTTGAGTTGCT
CTGAAGATCGTCAGGTGCTGGTTGCAAGGAG

SEQ. ID. NO:288 BF043744
GCTTGAGAGAGATTTATCTGGTCAATCTCCCTGCAGTGTGACAACTTAACCTGGCTACTGA
AAAAGAGTGCCATGCCAACACCACTGCCAGGACCTTCCTCACCTAAAGCAGGAGTTCTCATCAATT
GGAATCTCCAGGCCAACAAATGGTATTGTTGGAAACAATAGGACTGTAGAATCTTCATCATTAACCT
GGTGGAGGCAGGGCTGGAGGGGAATAAACATCAGCAAGCCTTGAGTTAGGGGCCAGGAATACAGCTT
AGATCCATTAAATGATTCACTTCCTTTGTCATATAACTGCACAAACGGAGATGAAAGGGAAAATAGA
AAATTGACTTTAGGTGCCAATAGTACATTGCACTACACTGATCGAAGAAGTTATCCAAAGTACTGTATAAC
ATCTGTTATTATAATGTTAAAAGTGA

SEQ. ID. NO:289 BM365103
GCACGAGGCCAACGAAGGCTTGATCACCAGCTTGAGGCTTGCTGCCGGGGTACTAGTCCGACA
GGAGTCCGATCCAGGATGAATTCTGAAGAACAGATCCGGCATCACCTGCATTCACTCAGTGGAG
AGGATAACAAGCAGAAGAAGGCTACCAAGACCGCTGGCTACCTGCCTCCACAAAGATGAAAGTTAAAA
GATCCAGTCTCTGGCAAGGATGCACCAAGCTAGAAAGCGCTATAGAGAACGCCCTGCAGTATTCCGAGATCA
TATAATGACATTATCAAATCCAGGCTTTATCCGGCAACAAAGCTGTGACTACAAGACTCTCATC
AACGCCGAGGATCCGCATGATTGTTGGTGGGAAATTGTCCACCTGCTGACCAAGTGACCAGGATTT
AGGAGGAGCTGATCTTATGAAAATGCCGGAGAGGTTATTACCTTATCGTTAACAGCAGCTGGAGA
ACGACCTCAATCTCATGGATATCAAATCGGACT

SEQ. ID. NO:290 AW464273
ATCACTCCCATCTGACTGCTAATACACATGCAGGCTGGCTGGTTAGCCCAGTCAGAGTTG
CCAGCCCATGAACTACAGCATAAGAACAGTAATAATGCAATTACAGAATTGAAAGTTAAAGGAGACTTTA
GAGATAATTAAACGAATTCTTTATTCAGGGATACAAAGATATTCAACAATTGTTCAAGTTAAACCTA
ACCTTACACTGATCCACTCTCCACAGACCTGGAAATTTCACACCAGAAAACACATAGCCACAT
AAAAACTCATACGACTATTAGAGCAGCATAGTCAGGAAATGCCACCCACTCCAGTGTCTGCTG
GAGAATCCCAGGGACGGGGAGGCTGGTGGCTGCCGTCTATGGGTCCCACAGAGAAGGACACGACTGAA
TCGAGTTAGCAGTAGCAGTCACAACAGTCAGAAAGTGGAAAAGTCCACACGTCATCCACTAATGGGATAAA
CAAGTTGTGGTCATCCATATAATGGAGCGTTATTAGC

SEQ. ID. NO:291 BM366541
GCACGAGATCAAAGAGGGCTCACACTGAGCAGCAGATCCAGTCAGGAGTCCATTGAAAG
GCTCTTAGTCTAAACTGGTGGCTCAGCCACACTCCAGTGACTCCTCTCCACCCCCCGCCCCGAGAGT
TATGTATCATATTGTCAGCATGAGTGTGTTCCAGCTACCTCTATTGTTATAAAATTTAATGCTCAA
TCTGATTTGCACTTTGACTGTTCTGTTTATAGGTTGTAGGCCCTCCCTAATCTCCCTCT
GCCATCTTATCCTCCCTTTAGAAAATGAACTAACGCCAAGAACAGGTGAAACAGGCTGGATGACACCACT

-continued

TAAAGGCAGGGAAAGAGCCGAGAGAGTAGAGAATTGGTTCCAGCTTCAGGGCCTGCTTACTGTGCAGG
GCATGATGGCATAACTGTCTGCTTGACAGGCATAATGTATCATTGGGAGGAAGCATGT

SEQ. ID. NO:292 AW462227
GCGTCAACGTTTAAGTCCCACCTTACCTCCACAAGCTAGAGAAAAATCAGGACATGTTCC
CCCGTAAATTGCCACACCTTGACTAATGAGAAAATGTTTTAAAAAAATCCCCCTCACCTATGTT
ACTGTTCCCCTTCTAAAGGGCACAGATCCTCCAGGCTTTATGTCAGTTTACACGCTCG
TTCTGTCTCCGCTTGCCATGCACACTGGGGCTCAGGCTCAGGGGACTTGAGCACGTTGGCAC
GTGGACAGTATTGAAGCAGCATTGCGCTGCCAACAGTCAGGACTGTCCAGGCACCTGGAACGTGC
TGGCCAGCACAGTGTAAACAAAATTGAGCCACTTTAAATATCTGGAGATTGCAAACAAATTGGATC
CCCGAGTGAGACTAGATAGTGATGGCTTACAGTCTCGCTGTCAGTCAGATGATGGTAGAC
ACACTTAGAAAGCTGCTCTTCCCTGTGAACATTGTT

SEQ. ID. NO:293 AW466159
AAGACTCCATGCTGATAGGCCAGCAGACTGACACGCTGACCCGGAGAAGGTGGTCTCCGCTTCC
TGAAGGTGCTCCGTGTTCAAGGTGAAGCCTCGGTGCGGACAGCTGTGCAGGACGCTGAGTGC
TGAAGAAGGCCTCAGCTCGCCTCAACTCCAACGCCTCCTCACCGGCTGCTCATCACATGGGCT
GCTCAAGAGTGAAGACAAGATCAAGGCCGTGCAACCTGTACGGCCCCCTGATGGCGCTGACCCACGTGG
GCAGCAGGACTACTCCCCAAGGCCCTGCCCCCTGCTGCTAGCGTTCATGACCAAGCCAACGGGCC
GAATCCTGCTCCCTTGCCGCCAACATCTACTGCAGACGCTGACAAGGTCTAGATGCCAAGCTGGC
CCATCCCTCGCCT

SEQ. ID. NO:294 BF045523
TTTATTTAAGATTGAAAAGGGAGCGCATGTTCCCTGGAAAGGGAGAGCATTGCTGCCAGACGAAG
CTTCGTGGCATAAAAGGGGGCGGTTCGTGAGTTCTCCATGCACCCGCTCCAGCTTACCCAGTGGGCTG
CTTTGCTTGATCCACGCCCTTACAGCCCTGTCATAGATGTCCTAGATATTGGATGCTTCTTCTT
GGTAGTAAATGCTTAAGTATTAACTTTGTTGCTCTATGTTATAGAGGGTTTGGGTTGTTGTTGTT
TTGTTCTGTATTCTTAATCATGTTTCCACTCCACTGGGAAATTGGACGCTGGTCAGCTGTGGGTTTC
TAGGATGTTGGAAACCTAGATGACCTTACTGGGTGCAAACTAGCTACGTTAAAGCTAGAAACCTAC
TCACTTACTGAGATTCTGAGTATACTTCCATATTGCTTAATGTCAGTAATGTGTTATGCATTGTT
TTGACAGACATTGTCAAATATAAAACCTACTTTTATGGCACATATTGCAATAAGCCTTATTCC

SEQ. ID. NO:295 BF044848
TCTCCACAGGTAAAGTCTCGTAAATTTCGTTGTTGGAAAGAACTGAAAGAACAGAAAG
AGTGGGCGACGGTACGGTCAGCTGGGCTGGAAAGATGATGAAGACATGACACTCACAAGGGACAGGCA
TGATCATTGGGCCACCACGGACAAATTACGAAAACAGAAATATAGCCTGAAAGTGAAGATGTTG
ACCCAGAAGCTCCATCAGTTAGATTGTAACAAAATTAAATGAATGAAATAATAATTCCAGTGGAA
TGGTGGATGCACGAAGCATAACCGAGTGTAGCAAAATTGCAAAATTGATAGCATTAAAGTTGACTTC
AGCTAACAGCTTAATGATGTCACAGAAAATTGAAAGCTCCACAGCCACAGAACAGAACATAC
AATTAATTAGTGGATCTAAACTGTCTTAAATCAGCAACCTCTACTCATGTTAATGCTTGATTAA
CACAAATGCAAAATACCCACACATTAAAGTAAGATAATTCCAGCTGGTAAACATGACCTGGAC
ATATATTAAATATGTACACCCATTATGTT

SEQ. ID. NO:296 BF040663
TGAGTGGTGGCAGTGTGCAAGCTGAGACCTCAGTTAGTGGCAGCGATGTGGCTTGATTGCT
TCTTCATTAAACATGGCTGTTAGAGAGTGTACTGAGTGGTGGCAGTGTGCAAGCTGAGAC
TGGCAGCGATGTGGCTTGATTGCTTCTTCATTAAACATGGCTGTTAGAGAGTGTACTGAGTGG
GGC

-continued

AGTGTGCAAGCTTGCAGACCTCACTGGTGGCAGCGATGTGGTCTTCCCCAGACAAAGCCTTCTTACAAGAG
ATTCCCTGTTGGTGTGGTGAGCACTCACAGATAGACCTTGGTTAATTTATTTGGCTGC
ATCGGATCCTAGTTGTGGCACGTGGATCTAGTCCCTGAC

SEQ. ID. NO:297 BF042477
GCGGTACCTTCATGGTTGGAGTGTGTGGTAGCAATGCATCAAGCTCAGCTCATTCAGATTCAAGATTCA
CACATATCTGAAGGAGATGTAGCAGCACCTTGGAGGAAGAGGTATCATTAGCTGGTCGGAAAAGA
CCTCTAAGAAATATGTCTCAAAGAGCTTGCAAAGAGATTCTGTCAAAGCGAACCTTTATAAAATGGT
TGAAGGAAGCAGAGGAAGAATCTCGGGTGGTAAGATGATGATGAGATGAGAATATTGAG

SEQ. ID. NO:298 BF042245
GGAAGCAGCACGAGCTGTTCTGCTGCAAGCTGCGCTCAGGCACCTGCAGATCTCACACACGAGCG
GAAGTGGTACTCACGCAAGGACCTGGCTCGCACCGCATGCAGGGTGACCCGACACACTCACACCGCG
ACACCCCCCTCTGCAAGTCTGTGACGAGCGTACCTGGACAACGACGAGCTGCTCAAGCACCTGCGTGTGA
CCACTACTTCTGCCACTCTGCGACGCGGATGGGCCAGGACTACTACAGTACTATGCGTATGTGCGTGTGAG
CACTCCCGAGAAGCACTTCTGTGAGGAGGGCCGCTGCAGCACCGAGCAGTTCACGCACGCCCTCCGC
ACGGAAATCGACCTGAAGGCCACAGGACGCCCTGCCACAGCCGAGCCGCCAGGCCAGAACCG
CCAGATCGACCTGCAGTTCA

SEQ. ID. NO:299 AW463964
GCCTTGGCACCGCAGCGAACCTGTCCCATCACACCCACCCCTTGAGGGTGACGGGACCCAG
CCCCCTGCCCCGTGCCCCCTCCCCAGATGGCCGTGGCCAAGCCTGTGCCACCAGGCCCTACGCCGCTG
CCCATGTGCGCTCACAGTGTGCGTGTCCGTGTGTGCGTGTCTGTGTCGTTGCTGTGCGTGAAGCTGTG
CCGTCCCCCAGTCCAAAGAAGTGAATGGCCCGAGGCCACAGTTATGCAACTTCCGTGTGTTGACAG
CGTCACTGCTTTAAACTTGATAATTCTTTAGTAGAAGATGCCAACAGTCCACACAACTGTGTTGGA
CTTGCAGAGGTTTATTTTGGCCTAGAATCTGCAGGAATTAGGAGGTACCGACCCCGTGCAGCACCT
CGGCCCTGGATTGCGTTGCCT

SEQ. ID. NO:300 BF041775
CCTCGCTCCAAGTCACGGTGTCTGGCCCGATCTGGACGTCAAGGGCTCAGCTCCCTCTCG
ACAGCCAGCCCCGTGTTGCCTTGCAATTGGTGCCTATTAGGTGGCTTGGCAGGCTGAGAAGG
CCGCCGGCAAGATGTCAAAACACGTTCCAGAGCGGCTTCCATCCTCTACAGCATGGCAGCAAAC
CCCTGCAGATCTGGACAAAAGGTACGAAATGCCACATCAAAGAATCACTGATAATGACATCCAGTCCC
TGGTGCNTNGAGATTGAAGGAACAAATGTCAGCACCACTGATATCACATG

SEQ. ID. NO:301 BF440363
TTTTTTTTTTTTTTATAAGACAAATTAAATGAAATTGGTAAGTAATAATCCAAGGGCTAAA
TAGTTACATGGGACTGTATTAGAAATTAAATACAAATGTTACATGTTACATCATCTGATTCTCTTCC
TTCAAAAGATTCTTGCATATTCTCTGCCTTCCCTACATCTTAGGAACATTTCATGCTTCCATTAGTT
ATTCACCAACCAGCTGAGCTAGTCAAAAGCTTATCCTTAACCTCATCGTGTACTATGTAATTATCTT
TGCACCTCTTAAACACATCACGGCAGGTCTTCTTCATCTGAAGCTTCAATTCTGTCTTGCAGCT
GCCCTGCTTGCCTAGGCACAGCCGAATAACCATATGAAACACCGATGGTCAATCATGTAGAGCTGTG
CACCGTCATTACACTGTAAGACCCATAACATGAAACTGCAGCCAAAAGGTCTAACAGCACTGTAGAGTGTAT
ACGCGTGTACATACATGCCACTCTATCTGCAAGATGTTAGGAAATGTTATCCTAAAGTTAGATCTAA
GTTGGAAGCC

SEQ. ID. NO:302 BF040230
TGGAGATGTTGTGGGTTCTTTTTTTCCCTCCCTATTTAGTTGCATATGAATAAAC
AAATAACAACACAAGNNNGGCCTGTGTTGCCTGGTCCCTTCAGTATTCTGGGATTATTGCTTCTAAG

-continued

TAAAACCCTCTGACCAACAGCCCAGTATGTCTTAAGACCGGAGGTATGTCACCTACTTGAAAGCTCTCAC
AGCAGGGCTGCTCGCTCGGATCTG

SEQ. ID. NO:303 AW462792
GCAGCTGCAGGGAAACTCTGAGCAGGCCACCAGGTTTCCAGTCCTCCATGGGACCAGCGTTA
GCGGTCCAAGGTCAGTATACTTTCAGAACCAAATGATACCAAGTGGAAAGTACGGAGACGTCCAGCCTT
TTGGATAGTATTTGGATGGCAGCTCTAAAAACAGGCGCAGCATGAAAGTGAACCGGTGAGGAGAAGA
AACCTCATAAGCTTAAAGTAAGAACATATAGACTTTGCTGAGTGTGGTACCTGAAACAGAAC
ATGTCCTCTGTGCTATTGCTATGAGAAGGTGCGCAAGGAAACGGCAGAAATCAGAACAGATAGGGAG
CAAGAGGGGGGCCCTTCAAGGCTCTACTGTGGAGACTGTGGTGTACTCGGGGAGACACCCCTGAG
CACGATCAAGGCAAGAGGATATTGAGCGAG

SEQ. ID. NO:304 BF046632
TGCTTTGGAAAGAGGGTGCAGGGCTGGACCTTGCTTTCTCCCTCGGTTCCAGACACGCATTCA
GTCCTGTTGAAGGCCACTTGATTTCACGCATGCCACACCCAGGCCTCAAGGCCCGTGTCTGG
AGCAGAGGCCTGGCTGAGGGAGTGGCTGAGCCAGGCCTGGCATGAGGTGTCGCGCTCGTCCGG
GAAGGTGACGGCGCGAGGGGACCCAGGGCCATGGCTGCCAGGGCGTTGCTGAAAAGAACAGTTCT
GTGGGTTTCTGGTGGAGAACAAAGGCCCTTCTTGAGATGCTGCCACATCTGCTGTGAAAGTAG
TGTTCCACAGGGAGTGGCTTGGAGGGTGAG

SEQ. ID. NO:305 BF045608
AGCCGCCTGGGTAGTTCTCGCGTATTGCTGCCAGTCTGGTGGAGAGGTTGCTGTTCC
CGGTCTTCTAGCTCATCTGGTCGCCGCCGTGTTGTTCCAGTGGCCAGGTGCGTATCATGACGTCC
CTTGGAGAACTACATCAACCGAACTGTTGCTGTCATTACTCTGATGGAGAATGATTGAGAACATTGAAA
GGTTTGACCAGACCATTAATTGATACTGGATGAAAGCCATGAACGAGTGTTCAGCTTCAAGGGAGTA
GAACAAGTGGTACTAGGGTATACATCGTAAGAGGCAGAATGTTCTGGAGGTCCAGTCCAGATGGATT
TCACGAGGCTAAAAGCAAGGACTGATGCTAAAGCTAAAGCTCAACACTTGGCCAGGTGATGAAAGAGCC
AACTCACTGGAAAAGACCTTGATGCTGGGAAAGACTGAAAGCAAAGGAGAAGGCAGGAGGAGGATGA
GATGGTTAATAGCATAATCAACACGATGGACATGAATCTGAGCAAACACCAGGAGATAGTGAAGGACAGGG
GAGCCTGGTGTGCTGCAGTCCATGGGTTCAC

SEQ. ID. NO:306 BF040483
AGAAGAACCAAGCATAATACAGCACTTTTTTATAATAAGTATATCTTGTGTTCCCTAGTTG
GCCAAAATTTTAGTTAGGTGTTAATCTCCCATAGCTATTAGTTATCTCCTTATATTAGTACTTA
ACATGAACTCTGATGAGAAGTGAGCTGCTGCAGCAGCTTAAACATACAATGGCTGCCACAGTAAGGAAA
CCAATATCCTGAGATTAGGTTATTGAACTGTTAATACTTGGGCTCCCTGTTTGGAGGGTTAAACTG
AGAAATAGCTTATAATTGGCTGACTGTGACAAAATTAAACTGAGCATTAGCTGATCAGGAGAATTAGTAA
CTAGTTCTTATGTGACATAACTCATGACAACATGTCACCGTACAAAATTCCAAAATCACCTATTAG
AAGTTACTGTAACGGTATCCCTCATGCAACTTAAATCTGCTGTTCTTTGTGTTGATGTCAGATGACCT
TCAGTAATTACTAATTGTGAAAGACATACAATGAAATTCAAAGCCAAGACTGCTTAAACCAGTC
TTGGGAAATTAGTTACATATTCAAGGTTTGCTACAGTCAATTGCTT

SEQ. ID. NO:307 AW462063
TATTCACCATTAATAGTGAGGGAAACATGCTCTCTTATGCAAAGACGACAAACTCGAGTGTGAAT
GAGTAACGGTACCCACAAAAGAACATCAGGACTCTTATTCTCTTAATTCAACCTATTGGGTTGCTTAA
GAACCTCAATATAACCTCAGATTGTCGGGCCTTTCAAGCAGTGTGAGCCCCGGAGATGCTGACC

-continued

SEQ. ID. NO:308 AW461912
 GCGCTGTGAGAAAACACATTTATTTGTTAATGATAACGCATGCTTCTGTAAATAGACAATA

AATTTTGATAGTAGTCTGGGTGTTATCTTAATTCGTATTCACTGTGAAATCAGTGAATATAGCTCAA
 GTGTTAGTGGACTGGATGAAAAGAAACTGGTTACTAGGCAAGAACAGGAGGCTGAGTTACCCATGACTACT
 TTAGCTATGCAGACTAATAACATTCTGCAGGTTACAGCTCACGCACCTTCACCTTTTCACTGGTATTCATG
 TAAGGCATCAACCCTGTAACTTTGCTGATGCTGAAGCCTGCTGGAAATTGGATGCATGGCACTCATAT

TCTCCGGCATCTCCTACTA
 SEQ. ID. NO:309 AW464194
 ATTATTAGCTCATGTATTGAGGAAGAGCAGCTGTCTTTATATGTTTTGACAAATCATATTGAA

TTCTTTGTACAAAAAGAACTACTGTATTCTAGAAGAAATATGAAATGCTTAATTATAAGCggCTGGAG
 ATTTTTCAATTGTTCTTGAAAATGAAAGGGGATCATCTATTAGTTAGTTGGGCTGGAAACTTTT
 GAAAATTAATTGAGGACCAATGTTAGTGAAGCTAAGGAAGGGCAGGGTAAATAGGGCTGATTTC
 TCATTCTGTACAGACCAGCAAACCTCCCTCTGCAAGGCAGGCTCAAATCACACACCCAAGAGTGTGGCGC
 ATAAAACGCTAGTTGCTTCAGCCCCTAGTAACCTCAGGACTTGGTTGAATATAAAAGGTAGACAACGTATA
 TGTTTCACGAGTAAATATTGTCAGCCAGAACAGCTGGTGTCAAGTAAACTTTTTTTTAAGCTTT

SEQ. ID. NO:310 BF040204
 TTGAATCTGAAGCCTGGGAGGGGGCCCCAACCTGCCCTCTCCAGGGCTCAGTCAGGTCTAG
 CCAGGCCAGCCCTCCCTGCTGCCGCCCTCCCGCAATCCTGTAGCTGAATGTGCATGGTCATGGGCC
 CCAGCCCTAGAGTTCAAGACTGAGGAGGGGCGGGGAGCCGTGGCATGTGTCCTGGCTCTGGCC
 ACCAGGTCTCTCTTGAGTTGGGGTCCGCGGGCTGGACCCCTCCAGGATGCCCTCCCTGGGA
 CTACATCCAGCTCCCCGCCAACCTTGCGGGGGCTGCCACCGCCAAGGGCCCTGGCTGGAAC
 CTCCAGGGGACCTGCAAGCCTCACCTTCCAGCTCCACCTCGCTCCTCTATCTGCAGCTCCTCTGG
 TTCCCCCGCCCCCGCTTGCTGCCAGATCCGACCTG

SEQ. ID. NO:311 BF041103
 GCTCCCTAACGATGTGATGTTCAAGGACTGGTAGAGCTTTCTGGCAACTCTGCTAGAGCCAGA
 AGTACATCCCCAATGGTGGCAGGGCCTCCATTACTCCTCTAGGACCTTGGTGGGACTCTGACTTC
 ACAGGGCTTCCCAAGAGGCCAGGCCAAAGTGCAGGGAGGACTGGGTTCCCTAACCTGCAGGCTGCC
 GTGCTGGGCCATCCAGGTGCTCCCGTGAGTGAGAACCCAGGTAACGTCAAGTCAGGGATGACTAGACTCTGG
 TCAACGTTGCAACCTCTGCCTTGGCCAGGCATGACCTCATTTCCCTGCTCCCCAGACTGTCCAGTGG
 AGGCTGCAAGGCCACTCTGCTGAGCTGAGTTGGAACAGGAAGGGCAGGGTCTCCACTCCACTTGTAT
 MNNTGGCTGGGGCTGCCAGGTCCCAGGGTACAAAATGCTACACCCCTGCGTAGGCCACCCCTACGGATA
 GTAGGCAGCAGGCTGGAAGTCTCTGCCCTGCTGGATACACAACGTGCCAGACTGCCATGAGTCCA

SEQ. ID. NO:312 BF044164
 TATAGTCATTCACTCAGCATATCCAAATATTATCATTCAACATGTAATTATATAATCTTTAA
 GATAGCTTGCATTCTTGTACTAATTTTTTATTTCTGGTGTATTTACTAATTGGCTAGCCACATT
 AAGTTAATTAAACTTAATAATACACAGTCTGTATTAATCTACATATTAATTGTTGTTCTATAAGATGT
 TGTAGGAAATTCCCTAGAATCACTCTTAAGTACAAAATCTTCTGGTCTCTGAAGCCTCAGTGTGCTT
 TTAGTGTGCCCTAAGAAGTGTGAACCTTAACTAGAAATAATCAGTTAGAAATAATCAATTGTCAA
 TAAAATAAAATGATAGCCAAATATTCCTTAAAGATAACAAACTTTCATAGGACTGTTGATGGAATG
 AAAGAATATAATCTGCCCTGTCGGCAATATGATGATTATTTCTGGCTTATAGCTAGTTGTTAGAAACA
 CATGTATGTAGGAGATTTGGCATAGTACTGTTCACTACATACCTATTTTTT

-continued

SEQ. ID. NO:313 BM362196
GCACGAGGCTGAGACTTGTCCCACCGCGCGTGGGAGGAATTCAACAAGTGTCCAGTTCAAGCTGCA

GTATGGCCGTTGGCGTACATACTTGGTGAAAAGCAACCAAAAGATGACAGAAAAGAGCAAATGATAA
CTGTAGATGGCAATATATGTTGGAAAAAGCAAGCTGCGAAAAGAAATGAGAGAAAATAGGGCTGAAG
CACTTTCCGAGGGCGGAATCCACTATGTGGACAGCACCAACAGGGGACGGGAAGCCCCCTGCCGTGCAAGTTC
AGTGGCAACTGCAGTTGGAGAAGTTTACGACGACCCGAAAGCAACGATGGCAACAGTACCGCCTGCAG
TCCTGGCTGTACGCCAGCCGCCTGCTGCAGTACCGGATGCCCTGGAGCACCTGCTGAGCACAGGACAGGGTG

SEQ. ID. NO:314 BM362608
GCACGAGATATCTGAACACCTTAACAGAGAAGTGAAGGTACGCATTGTAATCTGGACAAGTGAC
CGCCATTCCATTTGGTATCATATGTACCTCGACGATGAGATTAGGTTAGATACTTCGAGTGAAGCCTCTCAC
TGGAAAGCAGGCCAGTTGTTAGATAATCCCATCCAAGTGGAAATGGGAGACGAACTTGACTCAGCATC
CAGCACCACAAAAGCAACGTCAGCATCACCATAAGCAATGAAGAGCAGATTCTAATGAAAAGTGTGGA
AGTAGAGCAGTGGGTTCCAGTTCTAGTCTGAATTAGTAGTGTGGATTGAAACATAAAATGCAGGTGTATTA
AGTCCTGAAATGGTAAATGTTTAAACATTGACATTAATAAGTGTATTAAACACCCATAACTAAAGAG
TAGCATTATTACAAAATCTACTGCAGACTTCCCTCTGGCAAAGGCTGTCTTAAATTTCAAATTAAGAA
CTTTTATT

SEQ. ID. NO:315 AW465430
GGAGAGGGCTGGACCACTCAGGGAGGGGAAAGGATCAGGGGAATGGACAGGCGCTTGCCGCTCC
AGAATCTGAGGCCCTCACCTTGAGCGATTCTCCCTCCAACCTCACGAAAGCCGCTCAAACCTCCAGCTGGAC
TCGACCAAAGGAATAAGGTTACCAAGAAACTACAGAAGAAGCCAACCCCTCTTACCATCGGTTCTGAGGGGAA
ATCGGGAAGGCCGCGCTCGAGAGCCGACGTGCGCCACCGCTGTACCTCCAGGCGCGCGTCCAGCAGGG
GTTCGCGAGCAGTGGTTCAAGAGCCCGAGGGCAGCAAGCCAGAGGCAAGAGCCTAGAGGTGCC
CTGGAGGCCGAGGATCGCGGCTGCGCTCGGAACGGCCCCCGCGCGCGGCCGGTCCCTGCCGGCCCTG
GGCGACAGGTGAGCCGAGCCTCCGCCGCCGCTGGGCCGG

SEQ. ID. NO:316 BF045069
AAACTTGGACTCCAGATAATGCATTAACTGGTTACAGGACCTCAAGATGTATGTCAGCCTCAT
TTTTACAGATTGATGGTCCTGAACCATGATAGTTGTTGATCCATGAACACAGCTTACCCAGTCATAGGAG
TTTCACACTGAACCTTAAAGAAACAAAGTTCCATTCAAGGAGGTTGATTTCTTTAACACCAGTTCTCAA
ATACCAACAAATTCTCTGGATACTACACTCTGTTAAGAATATTGTACATCTGTACAGAAACTCATGATAGA
TTTTGAATGGTAGTTCAAGTATTGTCAGTCTTAGACTGATAGGGATTTGGACAGTTTAGCCCTC
CTAGCCTACCTCAAAGGTGCTCAGAAGGTATTAAGGAAATTTCCTGGACTAATTGGTAAATGTGT
TTGCTTTATTAAGATCCGCTCAGGTCGAGATCAAGATCCAGGTCTTCAAGGCTAGAAGCAGCCGAT
CAAAGTCCAGATCTCCATCTCAAAAAGAAGGTAAAGCTAAATAATTGTTGCCATCTTAACGTCAAGTGT
GCCCTCTGCAAGATTGCTTACTNNCTACTTCCCTGAGCTTTGGAGAATTGGTGTATATGTTAAAATACT
AAATAGAGTTTC

SEQ. ID. NO:317 AW461462
AAGTGATGTGCGCAAGACACCGCGGCAGCACCGGAGCGCGCGAGCGCTGCCGTGCCGTTCGGC
CTGGCTGCACACCGCAGGAGAAGCTGTACGTGTTGAGGTCAGGAGGCGTCAAGATGGGAAGCGGGGGCCGTGCTACCGCTCTGCT
CGCTGAGAGAGTGTGCGAGTGAAGCGAGGCGTCAGATGGGAAGCGGGGGCCGTGCTACCGCTCTGCT
TGCTTGCAGCCGATCTGGACACCGCCTCGGGCAGTGCCTGAAGACGCTACGATGACGACAACCCCC
CCGTGTCTGGTGAAGTCTCTCCGAACGCCAAGTACATCTGGCCGCCACCTGGACAACACGCTGAAGCT
CTGGGACTACAGCAA

-continued

SEQ. ID. NO:318 AW461475
 TTTTTTTTTTTTTTTCAGCACTTACACTTATTTGACATAAAGAACCGTATTACACAATACATT

CATATTTAAATATGTTACACAGCTCTCCAGAAAACCACCTCCATCACAGAACAGCAGCATGTAGCTTGGGT
 TCCGTCTTAAATATTAAATCAAGTAGAAATACTCTTAATTTCATAGCCCACAGAGGGAGACTCTGAG
 GGAG

SEQ. ID. NO:319 AW461535
 CCTGGACCTGGGCAGCAACCGGCTGGGCACGCCGGCTTGCGGAGCTGTGCCCCGGCTGCTGAGC
 CCCAGCTCCAGCTCNNGACCCGTGGCTCTGGAGTGTGACCTCACCGTCAGCGGCTGCAGAGAGCTCTGC
 CGCGCTCCAGGCCAGGAGGGCTGAAGGAGCTGAGTCAGCTGGGGCAACAGCCTGGGGACGAGGGCGC
 CCAGCTGCTGTGCGAGAGCCTGCTGCAGCCGGCTGCCAGCTGGAGTCCCTGTGGGTGAAGTCCGTGCGGGTT
 ACAGNNNGCCTGCGCAGCACTCAGCTCATGCTGACCCAGAACAGCATCTCTGGAGCTGCAGCTGAGC
 AGCAACCCGCTGGCGACGCCGGCTCCACGTGCTGTGCCAGGCCCTGGCCAGCCGGACTGTGCTGCC
 GTGCTCTGGTGGCGACTGTGAGCTGA

SEQ. ID. NO:320 AW461605
 GCGTGGCCTGCGTTGGAAAGTGTGGTGTCAAGGGGGGTTGGAGACCCCCACATACGCCGG
 CGCGAGAACAGGCCAGGGCAGGCCGGGGTTGCTTAGAAAGAGCGGCTTAAACCTGCGCGCCGGCTC
 CTCTGGCAGATACCATTGTAGTTGAATCAGGAATGAAATTCTGAAAGCTAAGAGTAAAGTCTTGGC
 AGCATGGAGGACAAAGACGCCAGGCCAGTGCAAGGGAGCCTGGCTGGCTGCTAAAGAGCCAGGCCAC
 TGCTCAGCCAGCTCCACTGCTGAGAACATCTCAAACAGAGACCTGGTAAAGCCTGGATGAAACAGGAGCA
 GCATCTGCTGACAGACAGTTGTGTTCAAAGAACCCC

SEQ. ID. NO:321 AW461982
 GGTGAACCTGGCATCTTCACTTCCAGTAGTCAGTGAAACGCAGTTGATTTCTCGTTGCTTCC
 ATAAAAAATACTTGTAAAGCTCAAGCACGGTGAGCCGAAGCTCATGCTGCCCTGGACCCCTCCCACCCATT
 ACCGCAGCCAACCCCTCCACTTCATGCCCTAGCAACCGTGCGCTCATGTTAGACCGCTTCGTCTGCACATT
 AAGACGAGACAAGGCCATCAAGAAGAGAACGCCCTGTCCTTAATGCCCTGCACATCCGACACACCCAC
 CGGGGCTACGGGGCCAGGGTCCCTGGACCAAGGAGATTTGTATCTCAAGGGCCTGCAGCTGCTTGG
 AAACAAGTGGAGAGAATCAAGTGGATCTTGGAAAAAAAGAAAAAAATGA

SEQ. ID. NO:322 AW462169
 GCCATACATGGCCTTGTGCAAGCTGCTCAACCCCTCATAGGCTGCAGCTCTCACCTGGAC
 TCCGCTTGAGGCAAAATGCGTGAATTGAGAACATGCTGTGGTTGAATCTTGCTGTTATGGTTGTGA
 GAGCGAGAGCAAGAAAAGGACGATGCGATGTCGACTGTTGCCCTACATTGTTGAAAGGTGATTCTCCT
 AAACTAACAGTGAATTGCTGAAATATGAGGACCTTCAGTGGTGAATGCAAGAAAATACAGGATACCTAAAA
 ACTCTAAATTAAATAATGGATATCCTCAGTGGTGAATGAGTGTATTGATGCCCTGTATCCAAAATGTCTTGG
 GCACTTCTATTGAGAACGAGGAACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG
 AAAATAAAATTCTGGCCTACTTGTGTTCAACGACAGTTGGTCTCAGTTAGCT

SEQ. ID. NO:323 AW462456
 TTTTTTTTTTTTCCATCTCGAACATTATTCAACACAGGTTGATTCTCTCTTTGCTCTTT
 CCTCACTGGGTTTCAGGACACAGTTACGTAATCCTTGATACCTCATCAGCTAACAGTGTGGCTGCTT
 TTGATCAGTTCATGCTGTGACGTCTGAGAACCTTATCCACTCAAGTGAATGAGCACTCCAGTCTCAG
 CCAACATCAATCTTACCATGTCGCTTCCCATGGAACCACTCATTGTTGCCGGTGGAAACGCCAGGAT
 TAGCTTCATAACCTATGCCAGCACCCACCTNNNGNTGGAAATTCTGGCTCTGAGCCATAGGGATCTCC
 CATGTTCATGCTCCACCAACCCATTCTCATGTCCTTCTCTGGATCCATAGCCATCCGACTATAAC
 TTCCCTCTTTGGCGTCTCATCTGTTCTCCATCTCACGTTGACGAATCATCATCTCTTCTT

-continued

SEQ. ID. NO:324 AW462702
 ACTGTCCATCCTGAGCAATATGCTAACGATTCCCTGGATTTATTACCAACATCTTGCTAAGAGAC

TGCCCTGAGTTCATGAGGAGGAGCTGGGGAAGGGGTTGTTGCCATCTTCAAGACCTGACTGGACAGATCG
 CTTCAGTGGGGTGTGGTCAGTCTGGAGGCTGGACGGATGAGCCAAGGGAGTAAGGTTACTCCCTGTGTT
 GAATTTCTTCTTCATGTCTAGCCATCCCGAGGGTTAGTCCCAGCAGAAGGGAAACCTCTACTTGGGTT
 AACCCCTGGTCATCTCAAGAGAAATGGAAGTCTCACATGGGGAGCGTCCTCCACTCCCTGAAAGTATGCCCTT
 CCTCCCCCTGCCCTCTCAAACCCCTTCCAGTTGATTGTTCTGTTCTGTCCATCTTAAC TGCT
 ACTGTGTCTCCANNGACAGATGGCCCTTTGTATCTTCACTCTCCACCCCCAG

SEQ. ID. NO:325 AW462838
 GGATCTTCTGCAGACACTGGAGCGGGAAAGAAGCATGAAGTGGCTTGCTCCTGGCTGGTGG
 CCTCTCAGAGTCATAGTCATATGGCCTATGTTGCAACATCACATTGGAACACCCCCCTAAGGAGTTCCGG
 GTTGTCTTGACACAGGCTCATCTGACTTGTGGTGCCTCCATCAAGTCATCAGTCCTGCTGTACACAC
 ATATTACCTTCGACCACATCAAATCTCCACCTCCGGCTTACGCGCAGGCCCTCCACATCGTACGGATCT
 GGGATGATGAACGGAGTTCTTGCCTATGACACTGTTGGTAACATGGAAACAGAAGCTGAATCAGATCTGC
 ACTAACCAACCCCTCGTGGTCCCCATAGATGGCTATGTTAGATCGGGAAACTGTCAGCACTGACCAGCCG
 TTTGGCTAAGCCTGCAGCAATTGGTTGATAACGCACCCCTTGAT

SEQ. ID. NO:326 AW463978
 AGATTTCCATTCACTAGTCCTGTTGGCCATCTCCCATCAGCAGCAGTCCTCATCCTGGATTCTCT
 CCAATCCTCATGGCTCCAGCATCTAGCCATCGTGGCACCAAGTGGATTGACCTTGTGACCTTGTGAGGGTCTGCC
 TGCTCCTGCTGTTGGTGTCAAATGTAATCTTGCCAGGGTGGGAGGATTATGCACCATACTGTAAAAA
 CCAACCTGGCAACTGCCGATTCCCTCAAAGCCTGTTGAGAGAGCAACATTGGTGGCTAGCAACA
 TAGGCTGCCAGGGAAATGTTCAATGAATTGACGAAGCCCTGTTGAGGTTGGTATCAGTTGCTCCACTCG
 TGGGATGAACCTCTGCATCAGGCACTCACAGAGTTGTCACAGGAATGGAGCCTCACCTGATATCTGGCA
 AGGGCTAAAGAGATTGAGGACAAG

SEQ. ID. NO:327 AW464129
 AGAGCCAGGCTGTGAAGTTGCAATTGGACATGGCAAGGGCATGGCTTCTACACACACTAGAGCC
 CCTCATCCCACGACATGCACTCAACAGCGTAGTGTAAATGATTGATGAGGACATGACTGCTCGAATCAGTAT
 GGCGCACGTCAGTTCTCCAGTGCCCCGGCGCATGTATGCACCTGCCCTGGCTCTGAAGCTCTG
 CAAAAGAGCTGAAGACACAAACAGACGCTCAGCAGATATGTGGAGTTTGCAGTGCTTCTATGGGA
 CGGAGACGGGAGGTACCCCTTGCTGACCTCTCAACATGGAAATTGGAAATGAA

SEQ. ID. NO:328 AW464130
 TTGCGCGCTGCAAGGGGAATGGGGCGGGCGGGGGCGTGCCTGGGGCGGAAGCCAGCAGCTCGC
 GGAGGAAGAAGGGCCAGGGCTCTGCCACGGCATACCTGGTACATCTACAAATGTGGTGTGACCGCGGGGT
 GCGCTTATAGCAGTTGGTCTGGTCAGAGCATACCTGGCTAAGGGTAGCTATCATGCTTATTATTCCATTG
 AAAAGCCTTGAATTCTCAAACGGAGCTTATTGGAGATTTACACTGTGCAATAGGAATTGTTCCGTC
 TTCTGTTGCTGACTTCTTCAGGTGATGTCAGAGTTTGTAAATATGGG

SEQ. ID. NO:329 AW464611
 GTCACAGTGAAGAAAGAGGAAGAAAAGACCCCCACGTGAAGAAGCCTTTAATGCTTCACTGTT
 TATATGAAGGGAGATGAGGGCAAGGTGGTGGCTGAGTGCACCTGAAGGGAGAGTGCAGCCATCAACCAGAT
 CCTGGGGAGGAAGTGGCACACCTGCTCCAGAAGAACAGGCCAAGTACTACGAATTGGCCGGAGGAGC
 GGCAGCTTCACTCACAGCTCACCCGACCTGGTCAGCCGGACAACACTACGTACGTGCCACTCAGGCA
 GGGGCCCTCCAAGGTAAGAAAAAGAGGAAGCGAGAAAAGCAGCTGTCCCAGACGCAGTCCCAGCAG

-continued

CAGCAAGTCCAAGAGACAGACGGTGCTCTGCCCTCCAAAAGCAAGAAGCCATGTGTCAGTACCTGCCCCC

GAGAAGCCCTGTGACAGCCCTGCTTCCTCGCATGGCAGCATGCTGGACTCCCAGTACCCCTCCG

SEQ. ID. NO:330 AW464647
ATTGAAGATAGTGCAGCGGGTGGCAGTGGCAGCGTTGCTGGCTGGGTGTGAATCGCCGG

GGAGGGAGGCGGTGGAGGAAGAGGTGGCGGGTGGCGGTGGCTAGCGTGGCGAGGAGGGGGTANN

NATCAGNTGCAGGGCGAGACATGGCAACATTGCGGTGCGAGCAATCAAGCGGGAGCTCAAGGAGGTGCTG

AAGAGCGAGGAGACGAGCAAAATCAAATTAAAGTAGATCTGNAGATGAGAATTT

SEQ. ID. NO:331 AW464892
GTGAATTCACTTTACTTTAAGAAGTAGAATTATCCTGAAAAATATGAATTAAAGTGTAACTTG
ATTTGTTATGTTGAATATATTACAGTAACTTGTAAAATGTTACTCTACATGAAGGTTCACTTGGC
ATCACTGGGATATGTTACTACTAACGGGTTATTTATGAAACTAAGAGCCTCTCGTTGAATGACTAATGA
CTATTCACTGGGATATGTTAGAGCAGATTCTTGAATTGTTACGTAATCTTGCGCTGAAGGATGTAGATTCTGCTTCT
AATAGTGAACAACTAATTATGTTGGCCAGAGTGTAAATATGCTAACTTTGGCATGGGAGATTTATCA
TGAGTTTTACTATTAAAAATGTTACATTGCTACTAGTTATAATGATGTTGCCTT

SEQ. ID. NO:332 BF039385
ATTATCTCTCCCTTATCAGGGTGGACAGCGCGTCTTATCTGATTGCTGAGGCAATGCCATCCAG
GGGGCTCTCCACCCCGCAGGCCACGGGACACGGGGTCTCTCCACCGGGACTCCAGCAGTGCAGG
GGATCCATCCTCTCCATCTGACATGGATCCTCTGGAGCCTTCCCTCGGCCAGTGGTTCTGAA
CCGATGATGTGGACGCCAGTCTCCTCATCAGTAGCATGACCGTCCCTGTTAAAATGTCGNNTCTGG
GATCACTGCTCCTCATCCTGAGNACACCCATCCAAAGCAAGAGACTGGCTCATATTCTCACCTAACAG
CCACTCCTGAAACTCAAGGATTGGTCTGGCTT

SEQ. ID. NO:333 BF039551
GGATCAGCCAGGGGCCAGNATGAGCCGGAGGGAGGGCAGTCTGGTTGAATGGACAGAGCCTGCC
TGGCTAAAAATGGAGAATTAGTGGAGCCTCTGGGTCAGGAAGAGCGAGCCTGGAAGAAGTGGTCA
AGAAGCAAGGGTTGGGTGCTCTCATCCTCCCTGTTTCCCACAGAGGACCCCAGGCTGACTCCTCA
GCCTCACCCCTCCCACTTGGAGGCCAGATCCAACAGACACACAGCCTGCCCTCCTCACAAATATG
CTGAGCAGCTCTCCAGGAATATGTGCAGCACCCAGGGAGACCCCTCGGGCTGCCGGCTTCGCCCG
GCTGCCGGTGGCGATCTGAGCGACCCGGCCCGGGCACGCTGCCAGTGCCAGGCCCTGCC
GGACGCCGCGGCCGCTGCCCGCCT

SEQ. ID. NO:334 BF039606
GGGAACCTGCTCCGGAAAGCCCTGGCGTCGCTGTCTGCTGGGTGAAACGTGTACCGTCATCCGTGG
CCTGGCCATGGCGCTGCAGCTCCGGAGAGGCATCACCTGCGCGGAGCGCCGAGATCGTGGCGA
GTTCTCTCATGGCATCACAGTATTTATCAGCGTGGCTTATATCCATCGAAACCTTACTCGGGTGC
AGAAATATGGACTCACCTGCTGTAACACTGATCCTGAGCTCATAAAATACCTAAATAATGTGGATCAACT
AAAAGAATAGTTACAAGTGTTCAGTCAGAAACTGGTGGTAGTCATCTCAAACATTGAAAGTGGAGAGGT
CCTTGAAAGATGGCAGTTGATATTGAGTTCATAGATGTAAAAGATGATAGTGCACCCAGAGAGAAAAGTT
AGAAAGTATCCAAGATGAAATCTGTCAGTGGTCAGACAGATCACAGCTACAGTAACATTCTGCCACTGTT
GGAAGTTCTGTTCATTTGATCTCCTTATTTGTACAGACAAAGATCTGGTTGACTGTAAAAATGGGAGAG
TCGGGACCACAGTTACCAATTCTG

SEQ. ID. NO:335 BF039758
GTCTCTGCTCCACTTCTTATCTGAGCTTCTATGCCATCAAGGGAAAGTATCTAAAGTTAGATG
AAATTATTTCTTGCTGGTGGTAGAAAGTAAACATCAGACTGTCCTTCACAGGAGAAGAAGTCAGCAG
TGATGTCTTATCGTTACTATTAAATGGACTTAAAGCTGTAGGCTATCTACATTCTGAGAAATCATGA

-continued

ATTGGCATAAAATGGTTGAAGGTACAAACTCTCCTGGGACGAGTGTAACTGGTGTATCAAAATCAACA
 ACCCTACACCAGAAGGGCTAACCTCAGAAAAACCCACCAATTCCCCAAATTCACTGGTCATCATCCTCAG
 CTCCGTTGTCTAGTGGTGGGGAGAAGAGTACATTGAATGATGTCTGGCTCATTGTTCAATTGCTTC
 AATACTTAATTATACTGGTTCGTCGGG

SEQ. ID. NO:336 BF041379
 GCTCAACAAACCTGCTCTCGCGAAGGACGTCTGCTCCCTGGAGCACAGGCATGCAGCTCAGGTACAAC

ATTAGTCAGCTGGAGGAATGGCTCGGGGAGAAACCTGCACCAAGAGCGGAGCTGAGACCATGGAACC
 CCTGATTCAAGGCTGCCAGCCTCGAGTTAAAGAAGAAAAGCCCGAGGATGCTGAGGCCATCTGCTCCCT
 GTGCACCGCCCTCAGCACCCAGCAGATTGTCAAATTTGAACCTTATACCCCTGAAATGAATTGAAAGAA
 CGGGTGACAGTGGCTTTATACGAACAATCAGGACAACTGCAAGATCGGAATGACCCTCAGCAGCTGCTA
 TTAGACTTCAAGCACATGTTCTGTTTGTCCCCTTAATCCATCTGACCATGGACTCAATCCACAT
 CCCAGCATGTCTCAATCTGGAGTTCCTCAACGAAGTCTGAAAATGCACATGCCAGAGCTTGTGCCAGTGA
 GAGCACGAAGGAAGTACATAGGACAGTGAAGTGAATTAAAGAATCTGTTAAAATCTGTAAGGAGATCAG
 ATCAAAGTTGAGAGCCTGTCAGAGTGAACATACAGAATAAGACACATCTGTCATTAT

SEQ. ID. NO:337 BF041571
 GTGGCCACATGGGCCGGGGACGGCACTGCAGGGCTCATGGACCTGCTCTGAGGCCGTGCC

CCCGCCCAGGAGGGAGAGGCCGGGCGCTGCCCGCAGCCTGCTCCGCCACCTCGGCCAGGAACAAGCCC
 TACGTCTCGTGGCCCTCGTCAGGGGATCTGAACCCGGAGTGTCTGTGCCNNNAAGGAGTATGTCTGACCC
 GACCAGGACTTTGACAAAGAGGTGAGGTTGCCCTGGCGAAGGCGGAGGCCTGGGTCTGAGGCTCTGCTGC
 CCTGGAGTGGCACCTCGGCCCTCGTGGTCCCAGCCCCCAGAACCGCCTCTGGAUTGCTC

SEQ. ID. NO:338 BF041789
 GTGATTGCCCTGAAGAAGAACATCAAGCGTACTTGTATCTAGATGAAGCTCACAGCATGGGCTCT

GGGCCCTACAGGACGAGGCCTGGTGGACTACTTGGCTGAGGATGTGGACATCATGATGGAAC
 ATTACAAAAAGCTTGGTCTCTGGAGGATACATCGGAGGCAAGAAGGCCGTATCGACTACCTGCC
 GCATTCCNNNGCGCGGTGTACGCTNNNTCGCTGCTCCCGCTGTGGCAGAGCAGATCATCACGCCATGAAG
 TGCATCATGGGCAGGATGGCACCACTGGCAAAGAGTGTATTAGCAGTTAGCCAAAAGTCAGGTAT
 TTCAGGAGACGCTGAAAAGCATGGCTTCATCATCTATGGAAATGAAGATTCTCCAGTGGTGCCTCTGATGC
 TCTACATGCCAGCAAATTGGCCCTTGGACGGAGATGCTGAAGC

SEQ. ID. NO:339 BF041797
 GAGGAAACTGAGGTCCGGAGACAGGAATGACGCACTCCGGGATGCCCTGAGTCATCTGGTTCT

ACGCCATCCTAAAGTCTCCACAGGTTCACTGGTCTGGGCTGTTCATCTCCCTTCAACTTCTGAAAGATGC
 TGGAGATTCCGGTCAACTGCAAATGAATGCCCTCTAGTCATACACCTTATGCCAGTCTGGAGAGTGA
 GGAGTGTCCACCTCTCTGGCACAAAGAGGGACTTGGCAAAGTGGTTGGCAGTTAGCCAGAGGGTAG
 CCAGCCGCCACGGGTTGGGTTGAGAGGAGA

SEQ. ID. NO:340 BF041818
 GAAACGCTTAACAGCCAGTTGTGAAAATTGCAAGGGGGTATTAGCAGGGCTGACGCTTGAGGAGC

ACAAGATGGTTGAAACGGACAACCCACCTCTGGAACGACTGTTCCAAGATCATTCAACCAGAGGACGAACA
 CGGTGCCCTTGACCTGGTGGCCACGAGGACGGCGGGCGTGGCGTGCCTGGTAAGGCCCTGGACG
 CGGTGGACCTGGGCCCTGGAGACTGTGTACGAGAGGTTCCACCCCTCCACGCCCTTCAACGCCAGTCGTC
 CCACTACCTCAGCGGGAGCGGCCAAGGGCGTCCAGGAGACGGAGGAGATGCTGAAGGTGGGGCGCAC
 TCACGGGGTGGCGAGCTGGTCTGGACCACAGCTGCGTGCCTGCAGCCCCCAAGGGGCCGGCATGC

-continued

AGTACTACCTGAGCAGCCAGGACTTCGACAGCCTGCTGCAGCGCAGGAGTCAGCGTCCGGCTCTGGAAGG
TCCTGGCGCTGGCTTCGGC

SEQ. ID. NO:341 BF041917
TGTTTACCAAGTATTTGAGTTGGTCCACACATTCCAGAGTGCAGCAGTACAGTCTGTTC
ATTGCACGCTGGCAAACCTCTAGCTATGTGGGATGGTATGCAATGAAAATTAGATAAATTCTTTCT
TATAATTAATATAAACACTCTGGACTTGAACCTGAGCAGGAGATGCCAAAGGCAGTGGTACCGTGTATTG
TTTATATGAATTACTTTAACAGGAATGATTCAATTAAATGAATTCAATATTTCCGTAAAAACA
ATAGAATTCAGTACATGAACTATAGAAAAATATATATAAT

SEQ. ID. NO:342 BF041933
CCCACCGGGCCCCACTGCGCCGTCGCTGCAACTCTACCTCTGTGACGCCGAAACAGTGCACCTG
GTGGCCCTCGCCCTGCTTCGTTGGCGTGGCTGAGGCTGACCCGGGCTGTATGACCTGGGCCGACTG
TCCTCTGCCTTGACTTCATGATCTCACGCTGAGGCTGCTGCACATCTCACAGTCAACAAACAGCTGGGCC
CAAGATCGTCATCGTAGCAAGATGGTGAAGGATGTGTTCTTCTCTCTCGGCGTGTGGTT
GCCTACGGGTGGCCACTGAGGGCTCTTNGCCCCAGGACCGTAGCCTCCGAATATCTGCGCCGTGTCT
TCTACCGGCCCTACCTGCAAGATCTTGGCAGATCCCTCAGGGGAGATGGACGTGGCCCTCATGGAGCACG

SEQ. ID. NO:343 BF042179
GCCATTCAAGCCAGCAGTGGTTGACCATCGAGAAAGTATATGACGGGGAGTCCGGAAGTACAACA
ACAACAAACGGTGATGAAATTGCCCGCAGCAACACCTGGAGGAGCTGATGTTGGCTTCCTCACTGGACCTA
TGAGTAACTCGGGGAGAGCTGGTTAGATTGCAAGGTTGGAGAAAATTGACGGATCCATCTGTA
ATAAAACCTGAATACAAACAATCAAGAGGAATGGTGTGACCAGCCAATTAGGGGAAGATGCAATTAG
AAACTTCATTGCAAAACATCGTTGCAACTCCTGCTGCCGAAGCTCAAACCTCCGACTAAAAAGAAATGA
CTACTCCTGGAAAGGATAAAATTCTGCTTGGACTTGAATCAGGAGCTGAGGAGATTCCAGC
GGGGGAAGAGGGTAGTAATTCTCCAGAAGATCTCACAGATTGTAaaaaaaaaaaaaaaACAAAT

SEQ. ID. NO:344 BF042480
GCTAAACATAGCTGGGATTGGGTCAGAGTTGAAAGAAATGGCTATATTAAAAACGGTTGTATCA
AGCTGAGCTAACATTGCAAGCTTAGCTAACATATCGTGTAAAGTGTATGGGTGAGAACTCTATTAGC
TTCTTATTAAACATGTTCCACTCTAACAGAGTAGTAGAGAGAGTGATTGGAGTTAAATATTGGTATA
TGACGTTCATGAAGTTCAAGTTTACAGGTTGTTGCAAAACACTCATAGAACGTGGTGTGAAG
ACCTGAAGTCCTGGCTAGTGTCAATCGAGGAGCCATTATTCTCT

SEQ. ID. NO:345 BF043417
TGTGTTGCCATAGCAAAGCCTTGCCTGGAAAACAAAAACAAAAATTAAACACACCCCTCA
GTTGTTATTGGTATAGTAATTATTAAAGTGAACAAATGGTCATTCAAATCCAAAGAGAAATCTTAA
ACAGTCCTATTGGTAAAGTATTACGTGTGCTCAAATTTCATTCAAGTTGAGAATGCTTGAGACCAATT
GATTGTTTTAAACTGCTGGCCTTACATGAAAGTGTATGGTTGTGTCATTGGAGGTGTCAAGTA
TTGATGTTGAAGGTTATTCACTGAGTCAAGTAAATTGTTGGCTGGCAAGGCCATCGC
GTGCTGACCAGTGGCGGTGATGCGCAAGGCATGAATGCCGCTGTCAGAGCCGTGACTGTATGGCATTAC
GTGGGGCCAAGGTCTCCTCATCTACGAGGGCTATGA

SEQ. ID. NO:346 BF043962
TGCTTCCTCACCCCAAGGGTTCAAGAAGTACAGTTCACAACTCTGGATCAAGAAGTTTATTAA
AAGTTAAACTGAAATTGAAGAAGAGCTCAAATCCCTGGACAAAGAAATTCTGAAGCCTCGCCAGCACAG
GCTTCGACCGCCACACCTGCCAGGACTCGGGACCCAGGAGAAAAGAAGGAGGGTTTAGTTGCTCGACTGAA
TCCGAATGGGAGCAGCTGGTGGACATCCGAGACGCTGGGTGAGGAGCTGGGTAGCAGGGCAG
GGCGGCCACCTGCCGGGTTGAGGTAGAGGCTGTGCACGCCGTCTGCTGGCGGTCCCTGGCCTGGGTT

-continued

CTCTGAGATTCAAGGGTCTAGGGTGTCAAGTGCTTCCTCAGTCTGTCTGTGGCATCTGGCAACCCGGCTGT
GAGCACCTGTGCCCGAGGGTNNNTAGCCTCCCCATCAGCCCCGTAGCACCTCCCTTGGTGACAGCA
CCCCCGATGTGCCAACGTCCCCGGGTAAATGGGTCCCCTGAGAGCCTCAG

SEQ. ID. NO:347 BF043971
GATGTTCCCATTCGAAGACGCCGCTGCTCGCTGTTAGCAAGCCTCTGCTGATGGAAGCCCTGG
GATGAATCTAGGCTTTAATGGATGTCTCGATAATGTAATAACTAAACTGTTCTCAGCTTATTAATAGG
AGGAAGACTAGCATGAAATACTGTGCCAGGCCCTGGGTCTGTGCATGCTCTTAGGAATTGGATTGTTG
GGTTGTTGTTGAGGNNNNNNNAAACGGGAATCTTTCTCAGGAGTTAATGGGAGAA
TAGTTATCTAGCTAAGGAACAGACATTACTTATTTAAAAATTTTACTTATAAAATATGGAACGGAA
GGGAATTGGTTGAAAGAAGATTTAAATGAATCAGAAATACTCACACAGGATAGAGAGGAACATATGTGA
CTGAATGGTTCTGTGAAAAGACGTATAAGTTAGAAATGAACAGAATTGTAATTAGGCTAATCCA

SEQ. ID. NO:348 BF044310
GCAGGGGGCGCTTGAAGACGCCGCTGTTGGTACCTCAGTGACGGAGTTCTCCGCTTCAAC
CGCTGGCGGAAGCGTTGTTAGGGCCGCCAAGAAAGAGGCCCTCGAGGTTCTGATGGTGTCCATGA
CTTCAGCGAGCCGAGCGACCGTTCTACAGCACCCGGTCTGCCGCTGTTGCATGTCGACCGGG
CGATCATCCTGGGACCTGGTACATGGTGGTCAACCTGTTGATGGAATTCTGCTGACTGTGAGGTAACACA
CCCAAACCTCAATGCCAGCTGTCACATTCACTGATGAGTCATTGCAATTACTATCGCTGAGAGAATGGCT
GATAATGCCTGTGTTCTTTGCCGCTCTGTTATGTTATAATCAGTTCAATGCTGGTACGGAGCAAT
TTCTTATCAAGTGGTTGGCTGATTCCGTTCTCTGTTACCGCTTTGACTTGTCTAGCTGCCTGGTNGC
TATCAGTTCTGACTTACTGCCAAGAATCAAAGAATATCTGGATCAGTTACCTGATTTCCC

SEQ. ID. NO:349 BF045055
TGAGGTGCACTGGTGGATAAAATGGAAGCAGGAAAAAAAGGAAGTAGAAGGTTCAATCATG
AGGTGGGTGGACCTAGCCCCATTCTCTCCTCCAGGTCCAATGAAGGCCAAGTGGCAGTAAATCCAC
CCGGGGTTTGCTTGAAATCAACCCATGGCATTGCCATTAAATCAACCAACATGGCATCTGTGAAAAGGG
GGAGAGTCACCCATTGTAAGAACACACGCCAGTTCTATGATGGGAGGAGTCTGCTACATCATCGATGC
CAAGCTGAAGGCAACCTGGCCGCTACCTCAATGTGAGACCCCTTCGCTCACCTGTATGTGCTGGTATCC
CCTAGTCCTCACATTCTAGTTTTAAATACAACCTCCATAAAC

SEQ. ID. NO:350 BF045103
GATAAAAGTGCAGTAGTCCAGAGAAAGCTGAAGAAGCAAAATTAAAGCAAGGTATCCTCATCTGGGA
CAAAAGCCTGGAGGTTCCGATTAAAGGAAACGATTGCAAGGAAAGGGCAAAATTTGATTCTGGGAT
TACAACATGGCTAAAGCAAAATGAAGAACAGCAACTTCCTACTGCAACCCGGATAAGACAGAGGTAC
TGGTGACCACATTCCACTCCACAGGACCTCCTCAACGGAAACCATCTTGTGCTAGCAAACGGCTGG
TGATTAAGAGCTGAACTGCATGAATCTCTAATGCCATTATTCCTCTTAATATGTTACTCCTCTGCTT
TTATTCCTTTACTCCCTGTCATTGAGAGTGTGGCTTGAGGTAGCGGTAGTGTGCTGCTATT
AGGAATATACATGTGAGAGTTGATTAAACAGTGCAGTGATGAAAGAACATGTTAGAGCAACA
TAAAGTAATCTACTGAAAATTGTATATATTACCTAACCTAGTGTAGGGCTGGATCCAACAGTAAC
AACAAAGTTTGCAGTTAAATGTTG

SEQ. ID. NO:351 BF045200
TTTTTTTTTTTTTTAAACTGCAAGCCTCTTATTCATCCATCAGAGGGCAGACAGAAT
GAAAACCACAATTACAGAAAACCAACAAATGATCACAGGATCACAGCCTGTGAACTCAGTGAAC
TGAGCCATGCCGTGTAAGGCCAGGCCAGACAGACAGGTGATGGTGGCGGGTCTGACAAACCGTGGTCCATT
GGAGAAGGAAATGGCAAACCACTTCAGCATTGCGTGAGAACCCATGAATGTATGAAAGTGTGAGAA

-continued

GCAGAGAGCAAAGCTAGTGACTGGNNGCCNNNTGCCCCACAGATAAACTCAATTACATGTCATTAT
TTACAACCTTAGGGCGGTTAACAAAACAGTTGGGAGAAAAAATGGCATTTCTGACTTGCCTTAAAAAA
TCGTCAA

SEQ. ID. NO:352 BF045261
AGACAGGACTCTAAAGTTAGACTCTCTGATTTTACAAGATGCTGGACTGGAGATTAGCAAGTGC
ACATTTATCCTGGCTATGACACTGATGCTCTGGAGCTCAGGAAAGTGTTCAGTGGGTGTCACACAGAG
GCCTTGATTCTGGAGTCTTAGGTGTTAGTCATCACCCACAGTCAGAGAACGAAAGTGGCCACTGACCTGG
CAGCAAAACTCTTACTTCTTGATGAACTTGTCTCTGGAGAATGACGTGATTGAAACAAAGAAAGAAAAAGAA
GCTTCTGGGTTGGTTCTCCCTGGACAGACTCTCAGCTGGCTCTGTAAGTCATAAAGTAAACAGAGGAA
AGTAGTAGATCATCCAAAAGGCATTGGTATCCATGGATGGATTGGAAAGAACCGGTTCAAATT
CAGAGGCTAATGGATTCCAATCACACAACCTCCTGGGTAAATGTCACAGAACATGGAAGATATTGGT
GAAGTTCTTCACACTTCTTAATGA

SEQ. ID. NO:353 BM364511
GCACGAGCCATCTCTAGGGTGGTAACACTCCCTGAAATCTCTGGACTGGAATTGGTCCCAAAG
TCTTGAGTGGCTCTGGCTTATTGTGTCCTCCACCCTGGTTCTGTGAACCACCCACTCCAGATGCCAGAGCCAC
TGGGGTTGGGCCTGGACAGGGATAGGCCTGTCAGAAGGAGCTGGAGCCAGTATGCGAAGCAGCTGTAAT
GGTCTGAGTGGATTATTGACAGTGAATAAGGGCACAAAGCCCAGCCAGACTCACCTCACACACCC
CCTGCTCCCCGTGGTGGGACACCTGAGAGAGAGGAGGGTGGACAATGAGAGAACAGGAGATGGTCATA
CCAGTGGCCTCGCAGAGCAGGGCAATAAGAGCTCAGCCATTGCACTGCTGGCATGCTTCATACCTGGT
GATCTGAGGTGTCCTGTTGCTGGCTGCCGTTGCTTCTGGCT

SEQ. ID. NO:354 BM364839
GCACGAGGCTGGCGGGGAAACATGTCGGAGTCAGAGCTCGGCCGGAAGTGGGACCGGTGCTGGCG
GACGCCGTCGTGAAGATAGGTACTGGCTTGATTAGGACTTGTCTCACTTACCCCTTTAAAAGAAGAA
TGTGGCATTAGCCTTGGCTCTGGATGGATTGGAATGGCTACTCCAATTGTCAGCATGATTCCAGGC
TCCGTACCTCTACACGGAAAATACGTCAAAGAGCAGGAGCAGTGAACCTGAGAGCAGGACCCCCAGGGGG
AGGGCAGGAGAAACACGTTCTCAGGAACGCTGAAGGCCAGTGAGCCGACTCTCCGTGAGCGT
CGCCAGTAATGCTCAACTCCAGCACACTGTGCACGTGTTGAAACCAAGTCCGTTCTGTTGTATTTCTC
TCTGGAAATTGCAGGGCGGTGGCTTAAATAAAACTAAACTCGCAGCCAGAAAAAAAAAAAAAA
AAA

SEQ. ID. NO:355 BM365207
GCACGAGCTGGCCTCAGTCAGTGATGAAAACAAGGGAAAGGGACAGGGAGGGCAGTCCTCTAGGTC
AACCCCTGGGGAGGGCCCTGGGCAGGATTCACCTTCTAGTGCTCTGAGTCAGGATCCGGGGACCCCC
AGCCTTGACCCACCTGTATTCTGAGTCCTCTCTGCCCACTCAGGACTTAGAGGCACTCATCCATTGCAC
ATGTTATAAGCACCTGTTACAGCCAATCTGAAAAGGACAGACTCATGGATTAGAGTCAGTGGGAA
TTCAAGACCCCTGGTGATGATGTTGGAAAGAGGAAGCTATGAGGTGACTGCTTGCAATCTGGGGCCTAA
CTGGGCCAAGACTGGCAAGAGTCTGCAGAAGACTTGTAAAAACCTCAAGTGGAGGTCTGGGGCTGT
TGGAGGCTGGAGGCCAGTATGAGCTCCCATGGCTCTGACCCGTAATCAAGGACCCAAGGAGCTGACTTG
ACGACAGTTTGAGGAAGTGGAGCAGGT

SEQ. ID. NO:356 BM366035
GCACGAGGTACGGACAGTATGGTCCGCCGGTGCAGGTCTCTCGCTCATCAAGCTGGCCGTTAC
TCCGCCCTGTTCTCGGCATGGCCTACGGGCCAAGCGCTACAATTACCTGAAACCTGGCAGAAGAGGAG
AGGAGGCTTGAGGCCAGGAGAAGAAGAAGCAGGGATGAGCAGAACGCGCATGAGCGGGAGCTGGCGGAAG
GTGGTCATGCGTTGGCTCTCTAGATTTCCCCGCCCGGGGTTTCAGAAACAGCTGCTGCTTACAG

-continued

GAGCAGCAAGTGGAGAGGAAAGGCTGCCTCTCCATTCCACTGGCCCTGGGCCATCCTCTGCTGAGTGG
GTAGGG

SEQ. ID. NO:357 BM366605
CCACAGTCCTGCTCACCATCCACAAAAGCTCACAGGATCGCCTAGGTGACATCCGAAGCTCTGTCAC
ATACGATCTGGCTTGATCCAGGTCGGCTGATTCCTCGTGCCTGTTTGGTGGACAGGAACTGGACTTTG
ACTCGAAGAAAAACCCCTGGAGCTGGAGAGCAGCTGTGACTCCATGAAGCTGCTTATACCAAGACTGTGTGGAG
GACATGGTGAACCCATTATCCTGCGACTCAACTCTCCCTGGTGGGAGCCCATTGCCTCATCTCAGAAC
TCGGCCCCGTGCTGGCTGTCAGGACCTCTCACGGCCTCTCCCCCTTGAGAAGAACTGTGGCA
AGATCACCTTGTGAAGGGGACCTCAGTGTCAACCTGAGCTCTTAGGGCTGGAGACCCCTGGTGGTGGGAG
CTCCCTGGAGCTCAATGTTGAGCTGATGGTCCAATGAGGGCGAGGATTCTATGGAACGGTGATCAGCTTC
TACTATCCAGCAGGGCTGCCTATGACGACGTTAGCAATCCAGCAACCTGGTCAAGCAGTCCCCCTGCGC

SEQ. ID. NO:358 AW464111
ATAATCCTGGCGTAGGGCGGCTCGGGCTGCGCCCCAGCTACTCAGAAGAGGCCCCAGACTGTGGCAG
CACTTCCCAGGGTCTGCTGGAACTTGACATCTGGGCCCCACCCGGACCTGCTGATTCAAGGGCCCACCT
TTCACATGATCCCCGGAACTCTGAACATTTCAAGGCAGCCTTCTTGACAGCCCTGGCTCGGCCACA
CCCCAGGATTCTGGGAGGCAGAGAAAACCTGATGCTGGCCCCACTCCAGAGGCTCTGACTTAATGGGG
TAGGCCGGGTGTGGGTC

SEQ. ID. NO:359 AW464166
TTTTAAAAAAAAAAATAACCTTATTACAAAACCTGTAACCTAGGGATTTATGTCCGGTT
AAGCTTTCACCTGAAATTAGTGGTGGCTCTGAAAAGAGCCTTGAGGTTTCAAAGCAGGAGGTGCCGCT
GAAGATTTACTTCTTGGAGACCAGCCTTGGCCTTGTAGCCTGGTTGGCAGCTTAGGTTGGCT
CCTTGGCTTGGGCTTGGGCTTGGCCTTGGCCTTGGGCTTGGCAGCTTGGCTTGGCT
GGACTCTGGCTACTTCTTGGCAGCAGCCGAGCCGGCTTAACTTCTTAGGGCTTGGCAGC
CTTCTCGGAGTGGCCGCACCCGTGGATTCTGGTTCTAGCCGCCCCAGCAGCCTTGGCTTGGCCG
CGCCCGCCTTCTCCCC

SEQ. ID. NO:360 BF045977
TGGAAAGCTGAAGATTTCCAGAACAGAACCAAGATAAGCTGGAGTTAATGGAAGCTTTCTTGG
CTTTTCGGTTGACCTACCTCAAACCGAGTGCAGTATATAACCACCTAGACCAGAACGTTCTCTGG
AGCCAGCATAGGGCCCTTCTTGAGCAAATACCACCAAGACTCACAAACAGCTGTTACTAAGGTTTATTAA
TTTCAGAGTGCAAATATTTCAAATGCTACTAGGTTTATATACTAAGAAGCTATATTTGCCCTTAAACA
CTCCTTGTGGATTATGATTATATTACATATACTGGCCTCAAATGAGATAAAAACCAAAGTGTCTGTTATGTT
TACTTTGATATATAATTCTTAGAGCAGCGTTAGCTACTAAAGTTAACATGTTATTCTTCTCTCACA
TGCTTGATTAAGGTGAGCTAATTCTTCAAGAGTTGATTAACAGAAAACCTAAATTCAAACACTGC
TAAAGAACAGTTGATTTATGGCTCTCCTTAAGTATGAGACACATCTTATTGAAATTCTTCAATAC
CCT

SEQ. ID. NO:361 BF040267
GACTAACCTCTCGCTTCAGCTGTTCAAATTTCGCTTAACCGCCCTGCCCTCCACTTCTT
GTGCACGGCCAACGAAAATGACCTCCAGTGATTCTTTCCATTGATCTCTTCCACAGCCAACTGGCTAA
ATAGCTTTAGCTCATCACACCTCTCCCAAAGTTTGATGTAACATTGGTGAATTCCCTGGCT
TTGGCTCCAAGTCGGCTCCCGCTTTGAGACTTGAATCTGCCACAAACAGCCCTGGAGTGGAGAGG
TAGGAGCAGGCCACACTGGCCGAGAGAACCAAGTAGCCGCTTGTGTGCGCAGTTATACCGAGGTGGGG
CCACGGCTGG

-continued

SEQ. ID. NO:362 BP230002B10G5
 AACCCNTTAAACCCCCANACTTACTATAGGAAANTGGCCCTCGAGGCCAAGAATTCGGCAC

GAGGCGAAAGATGTCAGTTTNGGGGGGGNTACAATACCTGCAGTGAGGCCAGGGCGGGCCCTGC
 AGCGAAGGGCACCTCTCACAGGTGCTTAGCTACTGCCCTTGGAAAGCCAATCCTCAGCCGGGACCC
 TTGGGTATGTGTTCTGGAACATCCTGACCTCTGATAACCCCTGCCCTGACCTGACTTGCTGNNGCAAGGCATCC
 TTCCCCCTANAGCTTNTGCAAATTACTGGCTCCTTGAGCCCTGCCCTGGAGCCACCCAATCCAGCTGTAAA
 ATGAACACNCAGGAAACCACACATCTGACTCAACTTATCCAGGTATTCTGGAGTGGGCTGGGCTATA
 ATAGGCATCATGAGTTGATCACAANAGGGCTTGAGAAAGCTGAAAGGAGAGTAGGGGAGGAAGCCANT
 GTTAGACCCANAACATAGGCACACACACCTTCAGGCCAGCTNTGAGCTGTTGGAACCGTGTCTCTANTTA
 AGGCACNTGATGGTGTGTTGGAAAGAGGGGACGGGTTCTCCTTGCTGCNTGATGGACNACTCATCCATAC
 TTGATGGCGGTCTTGTGCAAGCGGGTNCCCTCCACCCCCCAGGGCAANAAACATGTCCCCCTTCACTCCC
 ATGGAATTTTCTTTATTATCCCCCCCACCCCTTGCAAGGAAACCCCTTGCAAAGAAAAAGGNCTTGA
 NACNAGNGA

SEQ. ID. NO:363 BF044279
 TTAAGATGGCTGCCGGCGGCACCTCGGACTGAAAAGATGTGGAGTGGCTGTTACCTCCTGGCC

TAATGAAAGTGTGAATTGAATTCTGACGATGATACCACATTAGAGAGCTGTGAATTAACTTACAAG
 AGGGTAAAGAAGATGGGACCTTGAAAAGACAGAGATGGTAGATATTCTACAGATGGACCAAGCACTGAA
 GCAGAGGCAAATATAATGCATATGAAGAGTGTCCCTCTGAAATTCCCTAAATATGTGGAATAAATTCAA
 GAATTGCATAAAAAGCATTGAAACAGAAAATTCAGCTCTAGATCCGAAAAGAAAAAGAAAACGCTC
 CAGAAAAGGTAAATTGAGAATGAAGAAGAATCTCATAGTGAACAATCTCAAGTGAACCCAGTGGAGG
 AGCTTACCCAGTATTTGGAGTCATGAGAGGTTGACCCCCCTGTTAAAGGAAAAAGTTGAAAGTCGG
 GACTTGAAAAGGGATAGACCAAGTGTGGAAAGAGTGGAACTTGAGAAGC

SEQ. ID. NO:364 AW466058
 TTTTAATAAGGATGGGGTAGAAGGCTGGTTGGATGTCTGGCGAGGGTCTCCGGAGGCCAG
 GCAAATCTGAGCCAATTCAATTCTCTTCCCTCTTCCCTGGCCTTACGCGAACGCTCGGCTCCTTGAAAGCAG
 CGCCAGGGCTCTGACACCCCCATGGTCAAGGCAGAACGCGCACAGGCTGGACCACGCCGGAGATCATCG
 GGTCACTTTG

SEQ. ID. NO:365 BF042062
 GAATTCTCTTCAAGTTGAAAATTCAAGTGGATAACAGTATTATCCTCGTTGGCTGTGTT
 AAGGCATTGACATATATGTGGAGGAATGAAATACTTAACCTAGAATTCTTAATAGGTTATGGTTAACTTT
 AGAGAGCACCTTGTATTTCTTACAGCTAGGACAAAATTTGATTAAGCATATGTAGCACTCATAAAA
 TGGCTATTGTGTAAGCTACAGTAAAGCAAAGCTATAGGTAGATTATAATACAGTGAAGGCACGAGGAC
 TTCAAAACGTGCCGGCAGTTGGCCATAGAAACTGGAAGTTAAAGTCACATGAAGGTCAAGATCCAGACTTA
 ACTCATGCCACTGTCTTCAGGATCTGTCTGGAGCATGAGGGAGTTGGCAAGTTAAATGTAGAAAGCAG
 GCCCAAACCTGGAAAGGTTTGTAAATCATTTGACTTAACTATGCTCAGTAGAACAGTTTAC
 TTTACTGTTTGTACCCAGGAGTTATTTACCTAGCCGTAGAGCAGGAAACTGTTCATAAATGTATCCCTTCA
 AATGTCTTGAGAAAAATGGAGGGAAAAAC

SEQ. ID. NO:366 AW464065
 GAATGAAAGATATACTAGAACACCCATCCAGGGGGAGAAGTGAATGTGATTCCCTCCAGAACCAA
 AAGCTTGCCTCAGACTCCTAGGCCAGGAGTCGTTCTCCATCTCCCGGAGCTAACAAATAAGTGTCTTAC
 CCCTCAGAGAGAGAGAAGTGGGTAGAGTCATCAGTTGAACAGAACAGACTGTGGCTAGGACACCTCTGGCA
 GAGACGTCGGCTGGATCTCTCAGGAACCTCGATGGAAACCCAGTGCATCCCTCAGGAGAGAAGTGAAGTC
 AGACTCTCTCCAGATTCTAAAGCTAAAGATACGAATGCCACTCAGGCAGAGGAGTCACTCTGGATCCTCTCCG

-continued

GAGGTGGACAGCAAATCCGGCTTCTCCTCGCGTAGCAGGTCTGGCTATCCCCTGAGGTAAAGAGAAG

CCAAGAGCAGCACCCAGGGCACAGA

SEQ. ID. NO:367 AW464444
GCGGTGCCGCCGCCCTCGCGCTCTCGAGCCGGAGGCCGCCAGGGGATGCGGGAGCCCCG

GTGGGGAACAGAGAGGCAGGGGGAGCCGAGGACGGCATGTCCCAGGCCAGGGAGCTCAGCCAAGC
CCGCCCTCGTACCGAACGGCAACGCCCTGGAGCTCTGTGCCGTGCACGCCCTAACAAACGTCTGCAGC
AGCAGCTTCAGCCAGGAGGCTGCCGATGAGATCTGCAAGAGGTTGGCCCAGACTCCGGCTGAACCCCC
ATCGCAGCCTCTGGCACCGCAACTACGACGTCAACGTGATCATGGCTGCCCTGCAGGGCAGGGCTGG
CTGCCGTGTGGTGGGACCGAAGGAGGCCCTGTCCCAGCTGGCGCTGCCCGGGACTGGGCTGATCCTGA
ACCTGCCGTGCGCGTCTCGC

SEQ. ID. NO:368 AW461405
TGCAGGGTTACGTTGCAGTCAGTCAGTCAGTTGCAAAATTGTGCGGGCTCGCAGCGCTCTCG

GGCTCCGCCAGGACCCGAACCGGGGCGCTAACGCTGCGCAACTTGAGTTGCATGAACCTCCCGCGCT
GCAGGCACGNNGCCGCGCTCCGACTGCAGACCGCAAGCCTCCGTGTTTACAGCAGCGGGACNNNT
TTCCAACCGACATGGATGTGCTCCAATGTCAGCATCTTCAGGAACCTCCAGATTGTCAGGAGACTGNN
NACTCTCGGCCCTGCCCTCCCTGGAGGAATACTGCAACAGACCTGCCCTGGAGTTGAACTTACCTGCAG
AGCAGGCGCTGCTACGTGTCAGCCTCCGAGATCAAATTGACAGCCAGGAAGATCTGGACCAAAATCATC
TTGGCTCGGGAGAAA

SEQ. ID. NO:369 AW461482
GAGTACAGCATCTCGCTCCCTCTCCCGATGGAGGCCAGACTCCAGTTGAGACTCCACAGAGAACCTAATGATA

CCTACGGGCAGCTCATTGCCAGGGGCCATCCCTCTGTAGAGGACTCCCTACAGAGAACCTAATGATA
ACTCTGTTCTGGCAATCTGCTTCTGCTACAGATCCTGCCAGGACATGACTCCAGGGAGCACCTCTGG
TGCCCGCCGCCAGCGGGCGCTGTATGCCGCCCTGGTGCCTGCTTCGCCGTGGGCTGCTTCCC
CGAACCAACCCCCAGCCGGACCCCTGAAACAGATCCAGGCCACACCATCCACTGCTCCCTGAGACC
TTAGATGGCAGCACAGGTCCAGCCCCAT

SEQ. ID. NO:370 AW461511
GGAGGCTGATGAAGGAGCTTGAAAGAAATCGCAAGTGTGGGATGAAAAACTTCCGTAACATCCAGG

TCGATGAAGCTAATTGCTGACTTGGCAAGGGCTATTGTCCTGACAACCCCTCCCTATGATAAGGGGCCTT
CAGAATCGAAATCAACTTCCAGCAGAGTACCCCTCAAACCAACCGAAGATCACGTTCAAAACGAAGATCTA
CCACCCGAACATCGACGAGAAGGGCAGGTGTCTGCCGTGATTAGTGTGAAACTGGAAGCCAGCAAC
CAAAACCGACCAAGTCAGTCAGCTGACTGGTGAACGACCCCCAGCCGGAGCACCGCTCCGGC
TGACCTAGCCAGAGAATACTCTAAGGACCGTAAAAATTCTGTAAGAATGCTGAAGAATTACAAAGAAATA
TGGGGAAAAGCGACCTGTGGACTAAAATCTGCCGAATGGATTCCAGCGAGTGTGAGC

SEQ. ID. NO:371 AW461572
TTTTTTTTAAAACAAACAAAAGTTATTAAAGTGTCTTAATGCTCGAAACGGAAAAGATTCCCA

AATATACAGATGCCCTTTCTCATAGAAATAGATTATTTTATGATACAAAAAAAAGGCCAAAAAAA
AAAAAAACCAACAAAAACAAAAACACATCAACAGCAACACCCGTAGGAACATCTTAAGCGATTACT
CAGGGCCCGGCTGACAGTTACACGTGGTTGCCGTAGTCCCGTGTACACACCGTTAGCCATGTTAACCG
ATTGCATCAACTCGAAACCGGGCCGCCGGCGCCGGAGAGGGGGTGGCAGGAGGAGGCAAGA
GTTTATCATTCTGTACACATAGACATCTCTTAAATAACACCGCGGGCGCCCGTCTGCACGT
GCG

-continued

SEQ. ID. NO:372 AW461591
 AGCAAGGACAGCGAGCAGGGCTGAGCTGGGGTGCCTGGCTGCTACGGCCGCCACCTCCATCAC

ATGCACCTCTGCACCCCTGCTGCCTGACTCAGGAGTGGGGGGGGGTCTGTGCTTCCTCACTCCAGACC
 CACGGTGCTGACCCAGTGCACCCACCTGGTCCCTAGTGCGGACCTGGCCACAGGGCTCTGTGGGCCACG
 CTGATCCGCCCTGGTCCCTCATAAAGAACCTTGTAGCAGCAGGCCAGGGAGCCAGGAGGCTCCAGT
 GTGCTGTGTCATCTGCCTCCAGCCCCTCCAGACACTGCGCATCATGCCCTCCACCCCCACCCA
 CACTGGCAGGAGGAACAGACAGGGAGACCACACAGAGCTCGTTATAAATCTTGCTGGCTCATCG
 GTCTGTTGTCATGTATATCTGTATATCTCTATG

SEQ. ID. NO:373 AW461600
 CTTTGATTGAGCATGCCCTCAAGTAGACAGCATGCTCTGGTCCCTGGGGCAACACCTGATCC

AGATGGTAGGGCTGCTGCCTAGACCCAGNNNGTGGTGAGAACGGGAGCAGAACGCCGTGAGTCAGAG
 GNNGCCTCTGGCAGCCTCAGCTGAGCAAAGGCCAAAGAAAGTAGCCAGCGGAAGCAGCCAAAGAGGCC
 GGAGGCCCCACGTGGGAGAAGCAAGGGGTCAGACCTGACCAGGGCGCTCACGTGCCCTCCCCCTGC
 ATCCACTCCAAGGTTGACTGCTGGCTCCGGCAGCACTGTCCGTGGCCCAAGCATGCTGAGGGCTTCTGGT
 GACCCATGTTGAAA

SEQ. ID. NO:374 AW461650
 TCCTGAGAGCCCCGAGGAACCCCTCCCGCCAACATGGCCAACAAGGGCTCTCTATGGCATGA

GCGGGAAAGTCAGTCAGAAATCGAGAAGAAGTATGACGAGGAGCTGGAGGAGCGGCTGGGGAGTC
 GTAATGCAGTGGGGCCCGATGTTGGCGCCCGACCGCGGGCGCTGGCTCCAGGTCTGGCTGAAGAAT
 GCGGTGATTCTGAGCAAGCTGGTCAATAGCCTGTATCCTGATGGCTCCAAGCCAGTGAAGGTGCCGAGAAC
 CGCCCTCCATGGTCTCAAGCAGATGGAGCAGGTGGCTCAGTCCTGAAGGCAGCTGAGGATTATGGCGTC
 ACCAAGACTGACATGTTC

SEQ. ID. NO:375 AW461778
 CGGGCCCCCGCGCAGCGCTGGCCCTCAGCCCCCGCCCTGCCGACCCGCCCTAAAGC

TGTCACGATGCCAGCCCGCCCGCCCTCCGCCCTGGGCTCTCTCTGCTGCTGCTGAGTCGGGGCAGTC
 GCGGACTGTGGTGACATCCGGAGACGGCCTCGTGTGCTATAACGGCGCAGGCCAGCCATGCGGT
 CACGCAGGCCTGCTCCATGGCGAGCTGCTGCAGTGCAGGCCAGGCGCCCGAGGCCGGCCCCACCCG
 ACCCCCCGGCCTGCCAGGCACCCCTGGGCCCCCGGCCGGATCCCCGACGGCAGCGCTGCCCTGGGA
 GTGGGGAGGCTGGCGCAGCAGTGGACTTCGGGAGCAGAAAGTCAGGCTCT

SEQ. ID. NO:376 AW462000
 TACAACCTACCGGAAGTCTACCTTGATCGAGCTTCAATTGGAGGAATTGTCCTGTCTGGGT

GTGCAGGCTGTAATTTCTTCTATAAACTCTGCAAATCTAAAGAACAAACTACCAACTCTGTAAAGAG
 ACCCACTAAATTAAACAGGACTGGCGTAACTCACTGAAACCAAATATTATCTTCAAGATGTCCCACATG
 GAAGACGCTATTCTAGGATCTTAATTTCAGGATGCACTAGGAGCATCACCCCTGAAGAAGAACATCAGT
 TCAGTCACTTGCTCAACGGCCTATTAAAGTACGCTGCATGAGTCCTGGCTGTCTTCATTTACATGG
 CTGCTGCTGTGGATTGTGTTCTCTGCTTGACATGCCAAATGTAACTTAAGTGTGATGGAAAACATTGCT
 GCG

SEQ. ID. NO:377 AW462221
 ATTACTCTGTTATGGCAGCAGTCATTGACTGAACAAGTACACACTGCTCAATATGTTGATGC

TATGTCCAAAATGTTCTTAGCATTGGCAACAGAGGAAGCTATATTCAAGGAAGCTGGAGATGAGGATAGA
 TGCCCTAGAGGAAGCAATTGCAATTGAAATGAATTGAGGCTTAAAGTGAAGATTGGACTGTCTG
 TCATGCCGACTATCGGTGGATTGTGTAACACCCCTGAAAGTAAATGAGACAGATTGACTG

-continued

SEQ. ID. NO:378 AW462277
 GGAAAACCCACTGCACCTCCTCCACCCATCCCATCAGCATGTGGATCTGCATTCTGCACTCCCGGAAA

GCCAGAGCTTGTCTGCCAGGCCAAGGAGCTGCTGCCACCCACCTCCACAGAATTACATTGATTGATCTGTCC
 ATTATTTAGATTTCCAGAGTTAGTAACCTTCGGTAGAAGTGCAGGATAAGATTCTTAAGATTGTTGATA
 ATGTAATGGATTCATGGTTTTTTCTCTTCTGTTACTCTGAATTAACTTAACTTAAAAAGAGAGAGAAA
 AGGGTGTAGTGTCCACATTCTGTCTCTTCTACCTCCATGGTCTAGTGTTCACAGTGGTGTGATA
 CTCTGGGGAGGGGGCGCGTGCCTCCTGCGCGTATAAAGGCATGTTGGCACCGTGGAACCTGTGGCGA
 CGGTGCTCCTCTTCCCACAAAGCTTGAAGTTAAGAATAGAAGCTAAGCTCCCGGATTGCC

SEQ. ID. NO:379 AW463060
 TCCTTAGATTTATTATGCCTGTAATAAGAAAACCTAGCAAATGGTCACTGGATTTCTTCTTG

AATTTTCAGGATCTGCATATAAAATCTCAGCGGGTAGATGGTACTCTGAAGAAGAAAAGGCTTTGAT
 AACAGAAACAATTCTGGGTGGCTGGAGACAGTGGTATTGCTGAGTCTTGACCTCCTAACATTGTCTG
 TTATTCTTCTGAAAAGAACATGAAATTGCTCTGGTTCACCTGTGTTATTCTACTGAGTATTGATAAACTTA
 AATTTTAAAAATTGCCTCAGTTGGAGAGAAAGGAACCTTATATTCTAAGAGATACTTGATAGTTCT
 TAAAGCAGCACACAAAAAGAAAAACCTTGCACACTTGCACATTCTCCCAACAGTGCCTGTAATCTC
 ATTAGTATTTCGATTGCATTATTTGTTGTTAGCATTGGAAAACGA

SEQ. ID. NO:380 AW463121
 AGCTGCTGCAAGACTGTGGTGCCTGCTGGGGCGGACCACGCCCTCAACATCTACAAAGTGG

AGGGCGGCTGCATCACCAAGCTGGAGACCTCATCCAGGAGCACCTGAGGATCATGGGGCCGTGGGCTGG
 GCATTGCCTGTGTACAGGTGTTGGGATGCTCTCACCTGCTGCCTGACAAGAGCCTGAAAGCTGGAGCACTA
 CTG

SEQ. ID. NO:381 AW463263
 TGCTGAAGCGGCTCAAGGAGCGCTCGTGGACACGCTGCTGGAGGCGGTGGAGTCCCGCGGCG

TGCCCGGCGGCTGCCTGGTGCCTGGCGCGCCGACCTCCGCTGGCGNNCAGCCCGCGCCGCTAGCTGC
 TGCTCGGACGCCCTCTCCGCTGGCCCGACCTGCAAGCACGCCGTGGAGCTAAGCCCTGTGCGNNNTGCCACA
 GCTTCGCGCCGCCGCCGACGGCCCCACAGTGTGCTGCAACCCCTACCACTTCAGCCGCTCGGGCCAG
 AATCACCGCCACCGCCCTACTCTGGCTGTCTCTCGCGACGAGTACAAGCCACTGGATCTATCTGATTCCAC
 ATTGTCTTACACTGAAACAGAGGCCAACCTCCCTCATCACAGCTCCGGTGAATTCTCAGACGCCAGCATG
 TCTCCGGACGCCACCA

SEQ. ID. NO:382 AW463937
 TGAGAGACTTCACCTTCATTTTCACTTCACTTCACTTCACTGTATTGGAGAAGGAAATGGCAAC

CCACTCCAGTATTCTGCCTGGAGAATCCCAGGGACCTGGAGCCTGGTGGAGCTGCCGTATGGGGTACAC
 AGAGTCGGACACAACATGAAGCAACTTAGCAGCAGCGGATTAAGATAAGGCCTCAGCTGAAACAAACCTGA
 GCTGGCTGGAGGTCTGTACTCTGTCGTGATGTTGAAGAGGATTTCTTACTGAACCTCACTGCACA
 TCCACGGTCTGTCGCCAGGCTCATGACTCTGAATTAAAGTCCCTGCTGTTGGAGCTCCTC

SEQ. ID. NO:383 AW464391
 AAAGAAACAAGGAAAGAAAAAGAGAGATTACTTCAGAAGCATGAAATCGAGTCCAAGTTATT

TGGGGATCCAGACGAGTCCCGCTGCCCATCTCTGCAGCCCTCCGGCAGTATTACCTCCAAGCTGAGCAC
 TCCCTGCCAGCACTCATCCAGATAAGGCATGATTGGGATCAGTACCTGGTGCCTGATCATCCCAAAGGCA
 GCTCCATTCTCAAGGATGGTCTTCCCCGCTCCCAAGCAACGACATCTGGCAACCGCTGTTAAGCTGCA
 TTAGTAAAAGACGTTGCAGGAGTGTATCCAGCCAAGGCTCCTCAGCTGAGTATCAGCGATGCTGCCGT
 CTTGTACAGTAGACCAAAACTCTGTGTGGCATTGCCCTGCCAGNGGTACACTTCCCTCGCTCTGTCTCA
 GCC

-continued

SEQ. ID. NO:384 AW465097
 GAGCGAGTGGAAAGATGAATGCCAGAGGACTTGGATCTCAGCTAAAGGACAGTATTCCAGTTACTGA
 GCTGTCAGCAAGTGGACCTTTGAAAGTCATGATCTTCGAAAAGGTTCTCTGTGTAAAAATGAACCTT
 CTGCCAGTCATCCTCTGAAATTATCAGAAAAAAATTCCAGCTCAACCAAGACAAGATGAACCTCTCCACAC
 TGAGAACATCCAGGTCTTTGCACCACTAAAACGATGGAATTCAAGGCAGTGCAGCAGGTTCAGC
 GTCTCCATTCTCCAAGCTCAAACCTTCACTGGATATTTGAGGGTAACGATGAGACTATTGGATTGAA
 AGATATTCTTAATGACCCATCACAAAGTAACATAATGGGAGAACCGCATTGATGGTTGAATATAAACTTGG
 CTTACTGTAATGCCATGTGCTGTTCATGGAAGTAGNGGGCTGCGCTNNNTAGTTGCTTTCTATAA
 TTTGATGTGCACAACATTAAGTACTAACACATGAG

SEQ. ID. NO:385 AW465151
 GGGAAAGTTTATTCTCTCAGCTATTCTACCATCTGAGCTCCTCTTCTACCCACCCAAGAAAG
 GTGCCTGGTGCTCTGGGCCTGTCTGGACACTCTGGGAGAAAGTCTGGCTGGCTGGCTGGCTCT
 AGTTACTCTGTTCTCTGAGGCCACTAGCGTCTCTCTGGGCTTATAGTGTGCTTGATTACAAATGAG
 GACAAGAGGCTTGCTGCTCAGAATATATTCCCCATGTGGCTCGGGCAAGTCAGCCCTTTCTGAACCTT
 ACTTTCTGTCAAGTGGCATTGGAGGAATTAGAGCTCACATTAGGGCTGTATGTGAGGGCAAGTGG
 GCTCTGGCAGTGAGAATGCACTTACGAAATGATTGAGTCCCAGAAGTTGAGAAGAAGGAGTGGTTAATAG
 TTAGAGTTCTAGTTGCCCTAGTGTGAATCTTGAAG

SEQ. ID. NO:386 AW465276
 CGGGCAAGGGCGCTTTTCGCGATGCCAGGGCAGCCGCCAAGGGCTGGAGCTGTCGAGAGGAT
 CGAGAGTTCTGGAGGCCTGAAGCGGGCGGGAGGCCAGCTCCGAGGACATGGCCGGAGACTC
 TGGGACTGCTTCGCCCATCATACGGACCACCGCTGGAGCAATGGAGGGAGCTGATGAACTGATCCGA
 GAGAAGGCGGGAGGATGACGCCGCAACCTCAGAGACCACAGTGGCAACATGGTGCAGAGGTGCTC
 AGGATCATCCGGGAGGAGTATGGCAGACTCATGGACGCAGCAGAGCGATCAGCAGGAGTCTTGCA
 CAAACTCTGACATCCGGGGCCTGAGCGAGGATTCCGTTCCATTATGCTCAACTCCAGTCCAACATCATT

SEQ. ID. NO:387 AW465299
 GCTTCGGCCAGTGGCAGTGGAGCTGAATGCTTCCGGCTGCCACCCCTGAAATGGATTCTGCG
 ACGATGACAGTGTGCAGGTGCCAGCCTGGCTGGCAGGGTCCCTGTGACCGAGTGCCTGACCTTCCG
 GCTGTGTGAACGCCCTGCGTGGAGCATGGCAGTGCATCTGCAAGGACGGCTGGACGGCACCTCTGTG
 ACCTAGACATCCGGGTTGCACCTCGACCCCTGCGCCAACAACGGCACCTGCTGAACCTCGATGACGCC
 AGTACGAGTGTCTGCGCCCCGGGTTCTCAGGAAAGGATTGTCAAGGAAATGGATGGCCCTGCGTGGTGA
 ATGGCTGCCCTGCCAGCACGGAGGCAGCTGCGTGGACATGAGGGCCGGCCCCCACGCTGTGCGCTGT
 GCCCCCTGGCTCTGGCAACCTCTGCGAGATGTCAGGAAACAGCTGCATCCCCAACCGTGCAG

SEQ. ID. NO:388 AW465351
 AGAAGACTCAAAAGACGTGAAGATCGCACCTGGAGCAGTTGTTGTAGAGAGCGAAATCAGAG
 GTGATGTCACTATAGGACCCAGGACAGTGTACCTAAAGCACGAATCATCGAGAACCGGTCCAATAG
 TGATCGCGAAGGCAACCTAATAGAGGAGCAGGCCATCATATAATGTCACCCCTGATAATATCACTCCTG
 ATGCAGAAGATCCAGAACCCAAACCTATGATCATTGGCACCAATAATGTTGAGTTGCTGTACTGCCA
 AGCCATGAAAATAGGAGATAATAATNNNATCGAGTCAAAGCGTATGTGGCAGAAATGTGATACTGA

SEQ. ID. NO:389 AW465482
 GCCACAGACCAACCTGCACCATAAGCCCTGACTCCTGCCATACCAACCCACCCATGGCCTCGAA
 CCAGGCCAGCGTCTGCTGACATGGTAACACAGTGGAGGACAGCAGATGAATGGAAACCTGAGCAGA
 GGAGCGCAGGACCAAGGCCAGAGCAGGAGCTGACCTGGAGCTGGGGCTACCGGCTAGAAGGCCCTGG
 ACAGGGTCAAGGCCATGGCCCCCCCACCGCCACTGGCCCCAGCACCCACTCCTGCATGGCAGTTGGCT

-continued

CCTACCCAGACCGCGGCCACGCTTCGCCCTCACTCTCACACCACAAGCCCTGCACATACAGCGGTTGCGCCC

AAAGCCCGAGGCCCGGCCCGGGTGGCCTGGCTGGTACCGAGGTCTCAGGCTGCTGCACCCCTGCGAG

CCGAAGCCCCCTGGACTCAGCAGCCTACTTCTGCGTCTACACCTACCCCC

SEQ. ID. NO:390 AW465514

GAGCGGGTGAGAGGGCAGCGATATGGCTCCCTCGGCTCTGGTCCGGCTCTGGCGCTCCGGAG

GTTGACGAGCTGTTGACGTGAAGAACGCCCTCATATTGAGCTACCAGCAGTCAGTCATCACAGGGCGAG

CGGGTGAAGCCATCCAGCCGGAGAGAGATGGAGCGGGATGTTCTCTGTACAGAGCATACCTGGCCAG

AGGAAGTACGGCGTGGTGTGGACGAGATCAAGCCCTCCTCCGCCCCGAGCTGCAGGCCGTGCGATGTTT

GCTGAGTAGCTGGCCAGCGACAGCCGGCGGGATGCGATCGTGGCCGAGCTGGACCGAGAGATGAGCCGGAG

CGTGGATGTGACCAACACCACCTCCTGCTCATGGCTGCCTCCATCTATTCTACGACCAGAACCCAGATGCA

GCCCTGCGCACCCCTACCAAGGGGACAGCCTGGAGTGCATGCCATGACAGTGCAG

SEQ. ID. NO:391 AW465560

AGGGGGCGCCCTTCCATCCTGGGGCAGCCCTTGGCGTCCGGCTCTGACAGATCCGTTCCAC

CCCCAGATGGATGGTCTGTTGAGGTCACTGTCGAGCTGTCTCAGAATTCAAGGTTCCCTCGGTCTGTCAGTA

CTGGCCCGTGGAGCCGATGGCCGGCCCTCCCGTGGAGGATGGCCGGCAGCCCTGTCTCCGACAGCC

CCCTCCCTCCAAAGAAAAATGTCACTGCTTCTGCTCCGTGTGTTACTATGCAGCTGCTCTGCAAGAAATCAGC

GATTTCCTGTGAAATAAGGTGGTCCCAAAGTAGGCAGAAAGGAATATATATATATTTAGTAATTATAT

AGATGTCAGCAATTAGGCAGGTCAAGCTGTAGTTTCACTGTTAAAATAAGCTTACATAGTTCTT

AAAAGCCTGTGTGTCCTTAAAGAGGTTTTAACACTAGGGTGTCAATGTGAAACACAGTTTCATT

GTTCACCTCGAAACAAAAGTTGTGTTGCCAAAGCCAACCCAGGTTACCGGA

SEQ. ID. NO:392 AW465567

AGGCGTGCCTGGTACTCTGGAGAACCTCGAACAGGCTCACATCTCTGGTGGAAAGCTGCTAGGAA

CACGATGAGTCAGTGGACTGCAGTCGCCACCTCCTCATGCGGAGGTCTCGCTGTGCTGCTCTGC

ATTCCCTCATTCTCCAAAAGATGGCAGAACAGATTTCAAGTCCCGCTTGAGTTGGTAGTGCACATATG

GCAACACCTTCTTGTTGTTCTCATGGTCATCCTGTGCTACTGGCATTGATGCTGTTGAGATTGCAAG

TATGATGATGTGACAGAGAACGGTGAACCTCCAGAACAAACCTGGGCTGTGGAGCAGTCCACATGAAGCTT

TTCCGTGCCAGAGGAACCTCTACATTGCTGGCTTTCCCTGCTGTGCTTCTGCTANNCGCTGGTAC

TCTCATCTCCCAGCAGGCCACGCTGTTGCCCTCAACGAAGCCTTAAAGCAGGCAGAGAGCGCCAGTGA

TGCA

SEQ. ID. NO:393 AW465831

GTCGGCTGTCTCCAGTGCCTGGCCACGGCGGCCCTGGAGCAGNGGTGGAGCATCCCCATTG

CGTCAAAGATGAAAGGCTGGGGTGGCTGGCCCTGCTCTGGAGCCCTTGGGAACTACCTGGCCCGGA

GGAGGCCAGGATCACACTGTGGAGCTGCAGGGCTCTGGTGGATGAACTTGTAGGGAAATTGCCAGGTGG

ATCCCAAGAAGACCATTCACTGGCTCTTCCGAATCAATCCAGATGGCAGCCAGTCAGTGGTGGAGGTGC

CTTATGCTCGCTCAGAGGCCACCTCACAGAGCTGCTAGAGGAAGTATGCGACCGATGAAGGAGTATGGGG

AACAGATCGACCCCTCCACGCACCGCAAGAACATATGTACGTGTCGTGGCCGATGGAGAATCCAGTGAAC

TGGACCTACAGGGCATTGAATTGATTCAAGACATCAGTGGCACCCCTCAAGTTCGCGTGTGAG

-continued

SEQ. ID. NO:394 AW466194
 GGATCGGAGGCAGCTGTGTGGCAAGTGGCGCGCCGGTACGAGCTGAGGGCAGGGTGCCCCGG

GCAGGGGGAGGTGACCCGGACAGTCAGGCCGGAGAATAGACCCGCGACCTCGAGGGAAATCTGAGC
 GTTCAGACCGTGAGCGGATGTAAAATTGACCAAGTCTGGGGCCAGAAACTGATCAGCGCTGCCGGCTTAA
 CTACGCGCCGGCGGGAGCGTTCTCGGTGGCGGGGAGCAGGTGAACAGGTCTCACTCCCAGCTCCAC
 GCCCTACCGCCTCTGCCAGGAGCCAGGTTCCGCCGGCAGCCATGGGCCCGCTCAGCCGTGCCGCC
 GCGTCCTACGCCGTGCTCGCATGCTCGCTTGTGGTGGCCGAAGCAACCGCGCCCTCCGCCCTCAA
 CCTGGACACCCGATTCT

SEQ. ID. NO:395 BF041753
 CGCCCTGCACTCTGTCCTCACTCGCCGCCACGGCCTGTCGTCACCCGACGTGCGCCGCTGC
 CCCGNAAATGCTCGATTACCCGAGTCCTCGTCAAATGAGGCCAGTGTCCAGGGCACTGGCTCCTCATC
 TCACTCGGGTTATGCCAAAGATGTAAAATTGGTGCAGATGCTCGAGCCTTAATGCTCAAGGTGTNGACCT
 TTAGCCGATGCTGTAGCGTTACTATGGGCAAAGGGAAAGGACAGTGATTATTGAACAGAGTTGGGAAG
 TCCCAAAGTGACAAAAGATGGTGTACTGTTGCAAAGTCTATTGATTAAAAGATAAAATAAAAATATTGG
 CGCTAAACTTGTCAAGATGTTGCAATAACACAAATGAAGAGGGGGGATGGCACCAACTGCTACTGT
 ACTGGCACGCTATTGCCAAGGAAGGCTCGAGAAG

SEQ. ID. NO:396 BF042071
 AGTTGGATGCCATGGCTCAGACAGATCCGAAACCAATGACTGAAGCCTGCCACCCCTCTGG
 AGACTCTTGTCAAGTCACACATGTGTAATAACTTAGGATAACAGATGGAGAAAGCTGACTGATACTGA
 AAGGACCTATCATATAAGGCTCTGGACTGACTGCCACCAGTTGTGCATCTAGTGTGTTCTTTACTTTG
 ATACTATGTTGATGAAACCTTTTTCCCTCTGACTGGGTTGGTTGTTGTTATTGGGGGGAGGG

SEQ. ID. NO:397 BF043039
 CGCGAGCGGCTCCAGGGTGCAGAACGCCGGAGCGGTTCCAGAAGATGGCCTCGAAGCGCAGGCC
 ATCGGCAGGACCTTCAGGGCTCGGCTCCGAGGCCACGTGGCTGGCGAGGCTATCCGTGCGTGGCTGAC
 ATACTGGCGAGACTTACAAAGACGACATCGGGCCACCTGGAGACGCTCATCAGAAGCTACCCGACATC
 AGGCATTGCGGATCGGCATCGGGCCCTGCTGCCCTCGTCACTAGGTTCCGAACCTCTGCC
 GGCCTCAGAGGCCGTTCCATCAGGTTGCTTCTCCGTCCTCGCCGGTCTTGACCCCTCAAGACCCAGG
 CACCCCCCAGAACGCTGGGTGCCCTATGCTTCCAGTCCAGGCCCCGGGTCCCCCTGCCCTAGGGTCCA
 GGGTGTACTGGAGCTGCGCTCTACAGCAGGGGCCGTGTCTCTGCAGGCCAGACGTGCC
 TCCTGGCGCTCTCCACTGGCCGCCGTCGAACCAGCACTCNTGCGCACGCCAGGCCGCTGCTGAGGG

CTG

SEQ. ID. NO:398 BF043954
 GTTGGAGCGCCGCTTGTGTTTTTTTTTACAAAAACATGCATACATACACA
 GGGTATAGTCTGGGAAGACACACGCACCGACTTGCAACGACACACACTCCCTCTTTCACTCGCACACGCGTGC
 ATGCACGCGCGCACACACACATACACACAATACACACACTTCCCTTGCCCCAGGCCCTAACCCAGAACGCTCG
 AAGACTGTGCCAGGGTAGCCTCCCTCCCCATGTCTTCCATCCACTCTCCACCCACTCTCCCTCAGCCA
 AGCTAGTCCTATGTAGGGCAAGAGTCAGCTGGGTCCAGGAGACCCGAAAAGAGAGAAGGCTCATGGAGG
 GGGGCATGGTACTGAGGGAGCCCTGGGGGGTCATGCTGTGCTCTGAGGAGAGATGAAGGGTTGGCACC
 ATTGGATCAGGAAGCAGGAACCTCAAGAGCACCTGCTGCTCCACCAGGGCACTG

-continued

SEQ. ID. NO:399 BF044362

TGCGGAGACTGCTGGGCACATCGTCCCCCTGCCTCGGTTCCCTGCGGCCGAAGAGCCTGCTAG

GATTGGGGATCTGGCCTAGGCTTCGGCGCCCGCGGGGCGGAATGGCCGCGGAAGAAGAGGACGAG

GTGGAATGGGTGGTGGAGAGCATCGGGGTTCTGCGGGGCCGGACTGGTCCATCCCCATCTGGACTT

SEQ. ID. NO:400 BF044484

GCTGGCCTGATGCAGTCATCAGCCTCACTTCCGCTGTGTTGCTGAAGCCTGGTAGGAGTATGAC

CACACCACCTGGTCAAGTTCTGTGGCTAAGGAAATGTAAGATAATGTCCTGCTCCAAGGTAGGCTGG

AGCCCCCTTAACAGCCTGACTCTCCTATAAGAGATGAGTTGAAGATTNNNGCTTCAAAGTGATCCTGTG

ATTTAAAATCATACAAATGGTAGCAGTGAGGGTAGTCAGGCTGAATATTGATTCCTCCAAAGACTGGCT

CCAGGCCAGGTCTAATGACCAGCTCTCCTCTGTGAAGTGAAGGGACTCAACCACCAATGTCACCCATCATC

SEQ. ID. NO:401 BF044941

GACACCTACTATCCAGTGGGAATGGGAATGGACACCTTGAGTTGAAACAGAACCGGCCAGAT

CAAGTACTGTGATGTACATATGTCATCCTGAATCTAACATGAAATTCTTCAGTAGCTGAAGTTACAATTG

TGAATATGAAGTTGTCATTTGACACCCTTGTGAATCATCCTAAATATAGATTCAAGACATCTCCGTG

AATGACATATTTGCCAGTCACTACCAGGATGCCGTTAACCCCTCACCTGAGACAGTTGAACAAACAG

GAAGAAAATACTAAGGGTGCCTTTAGGAGAAACAAAGAGGAAGATTGCAATCAACTAAGGAAGAGAGATT

TCCAGCAATCCAAACCCATTGCTGTTGCTCAGCCAATGCTACTGTTGAAACAACCCACATATCCAA

TTGACAGATGACC

SEQ. ID. NO:402 BF440189

GCAATATGGCAATTTACTGGGGTTAACCTACCTAGGATGATTGCTGGCTNGCAACA

GGGTCCAGTTCACACTTAGCACTAAATTAATCTTATTGAATAATATAATACAAACAAAATGCATTCAA

TGCTAAAAAAAAATCAATTAAAGGCCTTCTATTCAAGCTAATGACAACACAATAAAGGCAGATATGC

TAGTTAACATAATTGGCTGATTTATACAGCACTTATATCTTGTCCACAAGTATATTAAATGATAGA

GAACATCTAACACCATTCTACAGAACTAGGAATAATTCTAAGAAAGAAAGATTACAGACCCCA

TCTTTATACCAACCCACAGTCTAACNNNAAAGAGGATAAAGCCAATGCCCTCACAAGAGCTACG

ACTAATGTCGCTTGCTATCAAATCTGTATTCTGATCC

SEQ. ID. NO:403 BF440274

TTTTTTTTTTTTTTACTGTTAAACATTATTTATATATAAAAAAATTAATATATAATAATAATAATA

TATAGTGTGTTGAGACTAAAATATAGTACATAATTAAAAAGGAAATGAAAAAGGAGAATA

GGAAAAGTGTGAGGGACACAGATACACATTGCTAAAATCTACGATGGCTGTTCTAACAAAATAATT

TTTCCTCTTAAATTATCATCATGGACCCATTATTATTGGGCTTGAGTGGAGAAAATTAACTGGAGCCAGA

AATGGTGGTTGTAATCCAAGAAGAGTGGGTTAGAAAACGTGACCACAGGGAGCCCTGGACCTCATTCTGG

TGTGACTGGAGGGCAGCAAATCCTGGGTCACTATTGCTAGCAAGATTGTGTC

SEQ. ID. NO:404 BF440607

ACGACGCCAACACGCCAAGGCCGTGGTAAGACCTCCACGAGACGCTTAACGCTGTGGTCCAA

CACGCTGATGAGACTGACCACCTCTGTGCTCAAGAACAGCCTGTGTCCTCCAGCGGCCAACGTCTACTAAT

TTGTTCAAGGAGGACTGCCATGGAAAGATCGACGAGCTTCTCGGGAAACTGTNCCTCATGGCATCGCG

-continued

GCCATCGTGGTCGCTGTGATCATGATCTCGAGATGATCCTGANCATGGTCTCTGCTGTGGCATTGGAAACA
 NCTCGGTCTGAAGCTGCCCGCTGAAGGCTCCAGGAANGGCCTCAGGGAACCCCGCAGCCCCCGA
 TTATCCAAAANTTCCAAAANGGCCCCACNTTTTNACCCNTTNCNNACNTNNNNCTT
 TTTTAAAGTTTNTTCNAAACCCNTTANTCCTTGTTGGGGATTCTGGGGTCC

SEQ. ID. NO:405 BM362313
 GCACGAGGGTTGATAGCTCTGGAGTTCGTATCAGGAGATGATGTTATTAGGCAAAACAGTC
 ACCTTGCTGAAATGAAGATGAATTGGAGGGCAATAAGACGCTATAACAAAGAGAGACTGTAGCACTTT
 CTCAGGACTAGTGAGACGGCATTGTGGATCAGGTTATGTAACCTCAACCAAGAAGGATATAATTG
 AAAATAAGGTACGCTCTGTTAGAATTCCACAGATTGGAGACAAATTGCTAGTCGACATGGTCAAAGGGT
 ACTTGTTATTCACTAGACAGGAGGATATGCCCTTCACCTGTGAAGGTATCACCCCTGATATCATCAA
 ATCCCCATGGCATCCCTCTGATGACCATTGGTCACTTGATTGAATGTCTCAAGGAAGGTATCAGCTAA
 CAAGGGTAAATTGGTATGCCACTCCATTCAATGATGCTGTTAATGTCAGAGAAGNTTCTAATCTTTATCT
 GATTATGGCTACCATCTC

SEQ. ID. NO:406 BM364049
 GCACGAGCGCGACCGGGAGCTACCGGATCGGTTGAGATGGCAGAGGTGGAGGAGACCTGAAGC
 GACTCCAGAGCCAGAAGGGCGTCAGGGAAATCATCGTGTAAACACAGAAGGNNTCCCCTCAAGAGCACC
 ATGGACAATCCCACCAACACAGTACGCCAACCTCATGGACAACCTCATCTGAAGGCCGGAGCACCGTG
 CGCGAAATTGACCCCGAGAATGACCTCACTTCCCTCGAATTGCTCCAAGAAAAATGAAATTATGGTGAC
 CAGATAAAAGACTATTCTGATTGTGATTCAGAACTCAAGATAAGCTGCTTCTGGCTCCCTGCGTCATT
 CCTTAATTAAATGCCCTCAAGATAATAGCTTAAATCATGTCATTGACGGCACGTGAAAGGCACGTTGGA
 GCCCTCCCAGGCTGGTCCGTGACCCG

SEQ. ID. NO:407 BM366788
 GCACGAGGAGAACAGATGAATATGAGTCCACCTCCGGCAATGCTGGCCAGTGATCATGTCCATT
 GAGGAGAAGATGGAGGCTGATGCCGTTCCATCTATGTTGGCAATGTGGACTATGGTCAACAGCAGAAGAG
 CTAGAACACACTTCATGGCTGTGGTCAGTCACCGCGTAACCTACTCTGTGACAATTAGTGGCCATC
 CGAAAGGGTTGCGTATATAGAGTCTCAGACAAAGAGTCAGTGAGGACTTCCCTGGCCTAGATGAATCCTT
 ATTAGAGGAAGACAGATCAAGGTGATCCCTAACGAACCAACAGACCCAGGCATCAGCACAAAGAGCGAG
 GCTTCCCACGAGCCGATAACCGTCCCCAACCAACTACAACAGTCCCGCTCGATTAGAGTGGTT
 TAACAGCAGGCCGGGTGCGTACAGGGCCGGCTAGAGCAGATCATGGTATTCCCTTACTAAAA
 AAAAGTGTGATTAGAGGAGAGAGGAAAAAGAGGAAAGAA

SEQ. ID. NO:408 BP22000602103
 TTTTAAATTGTAATTGAAACAAATACAACTTGGATGGATTGAGGCAAATTGTC
 CATAAGCAGATTCTTAAGTGGTAAACAAAGTTAAAAGCAAGTTAACATAAAAGAAAATGTTCTG
 GTATAGGACGAGCAGTACAAAAAAATAGTGTACGAGTACCTGGATAAAACACCCGTTGCAATAGTGCAC
 TTTAAGTACATATTGTTGACTGCGTAGTCACCGAGAGTTACAACTCCACACTCAACAAACATGCTGA
 CAGTTCCCTAAAGAAAATCTCAAAAAAAAAAAGGCATAACCCAGATGTTCCCTCATTTGACCAACTC
 CATCTAAAGTTAAATGTGCAAGAGGCTTAAATATCCAGAGTAAGGCCATGCAACATGTTACTTGATCAA
 TTTCTAAAATAAGGNTTCAGGACAATGAC

TABLE I

List of differentially expressed genes in blood that predict PTA for milk production

SEQ ID NO: GenBank ID (cattle)	Fold Change (hi/lo)	Raw P	FDR-adj. P	Gene Name	Gene Symbol	GenBank ID Best Hit	UniGene
1 BM362588	0.5597	7.33E-08	0.000538	upregulated during skeletal muscle growth 5	USMG5	BQ276559	Hs. 171625
2 BF440243	9.7889	9.57E-06	0.01434	Sjögren syndrome antigen B (autoantigen La)	SSB	CA77787	Hs. 309316
3 BM361928	0.7393	7.73E-06	0.01434	<i>Homo sapiens</i> mRNA, ribosomal protein L22	BM684505	BM046402	Hs. 336425
4 BM364471	0.6569	1.27E-05	0.01434	pre-mRNA branch site protein p14	RPL22	CD177296	Hs. 326249
5 BM365159	0.5563	4.33E-06	0.01434	SON DNA binding protein	P14	BU845655	Hs. 177861
6 BM365446	0.6692	1.15E-05	0.01434	polymerase (RNA directed) polypeptide B, 140 kDa	SON	AA256916	Hs. 430541
7 BM365732	0.6456	7.14E-06	0.01434	CDC37 cell division cycle 37 homolog (<i>S. cerevisiae</i>)	POLR2B	BM695397	Hs. 149353
8 BF046007	0.6706	1.962E-05	0.01941	CDC37 cell division cycle 37 homolog (S. cerevisiae)	CDC37	AI845310	Mn. 300203
9 BF044446	0.6752	2.36E-05	0.02079	similar to RIKEN cDNA 1700029H17	na	AF280545	Hs. 368746
10 BF040826	0.7777	3.61E-05	0.02854	neuropilin 2	NRP2	AJ000334	Hs. 427212
11 BF039212	0.6584	4.98E-05	0.03585	asparaginyl-tRNA synthetase	NARS	AW194846	Hs. 5753
12 AW461477	0.7712	0.0001175	0.04477	inositol(myo)-1(or 4)-monophosphatase 2	IMPA2	TC186760	
13 AW464361	2.3429	0.0001041	0.04477				
14 AW466044	0.7038	9.21E-05	0.04477	<i>Homo sapiens</i> cDNA FLJ11392 fis, clone HEMBA1000575.		AK021454	Hs. 435773
15 BF039490	0.6409	0.0001139	0.04477	FK506 binding protein 12-rapamycin associated protein 1	FRAP1	BF0440695	Hs. 338207
16 BF042320	0.6329	0.0001166	0.04477	hypothetical protein FLJ22635	FLJ22635	AW024744	Hs. 353181
17 BF043074	0.6854	0.0001157	0.04477	GLI-Knuppel family member GLI4	GLI4	BW931804	Hs. 404905
18 BF044776	0.7804	9.888E-05	0.04477	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	UBE2A	BU158774	Hs. 379466
19 BF046287	1.9876	9.685E-05	0.04477	<i>B. taurus</i> mRNA for segotin protein	SMARCD3	BI046287	Br. 3352
20 BM362351	0.6658	0.0001188	0.04477	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3		AA844170	Hs. 444445
21 BM366715	0.6512	8.58E-05	0.04477	TOMM7	CD385108	Hs. 112318	
22 BM366099	2.5611	0.0001297	0.04466	HIST1H4I	BI873793	Hs. 248172	
23 AW464526	0.7209	0.0001295	0.04491	FK506 binding protein 12-ribonucleic acid-binding protein lark	PLK2	AL0910871	Hs. 4994
24 BF046202	0.3598	0.0001513	0.04491	hypothetical protein similar to RNA-binding protein lark	EIF4G3	AW996674	Hs. 398157
25 AW466043	0.7904	0.0001663	0.05189	polo-like kinase 2 (<i>Drosophila</i>)		CD513621	Hs. 402697
26 BF040403	1.6932	0.0001705	0.05189	eukaryotic translation initiation factor 4 gamma, 3		NT_05014.3	
27 BF039168	0.6560	0.0002049	0.06005	low molecular mass ubiquinone-binding protein (9.5 kDa)	QP-C	BM548444	Hs. 146602
28 BM362530	0.6724	0.0002202	0.06223	RPL30	CD173453	Hs. 400295	
29 AW461980	0.7649	0.0002409	0.06356	ribosomal protein L30	HIG1	BG700494	Hs. 7917
30 BM364411	0.7130	0.0002389	0.06336	likely ortholog of mouse hypoxia induced gene 1	DMAP1	BI907542	Hs. 8008
31 BF039456	2.1686	0.0002711	0.06684	DNA methyltransferase 1 associated protein 1	RPS24	AA262289	Hs. 356794
32 BF042632	1.9846	0.0002732	0.06684	ribosomal S24	WBSR14	BC012925	Hs. 284681
33 BF044457	0.7183	0.0002787	0.06684	Williams Beuren syndrome chromosome region 14		CD176013	Hs. 292457
34 BF040573	2.3798	0.0003118	0.07238	<i>Homo sapiens</i> cDNA clone IMAGE: 392795, partial cds	ASB9	BE271724	Hs. 19404
35 BF042198	0.6730	0.0003201	0.07238	ankyrin repeat and SOCS box-containing 9	RASA1	BC033015	Hs. 758
36 BF045424	3.4732	0.0003324	0.07309	RAS p21 protein activator (GTPase activating protein) 1	MGC52057	AL831852	Hs. 21929
37 BF043765	0.7528	0.0003908	0.08359	hypothetical protein MGC52057	MRPL35	AL524400	Hs. 433439
38 BF039771	0.7461	0.0004176	0.08370	mitochondrial ribosomal protein L35	NDUFAB1	BQ435266	Hs. 5556
39 BF041569	0.6950	0.000423	0.08370	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8 kDa		BX370120	Hs. 509314
40 BM366529	0.5912	0.0004218	0.08370	hypothetical protein LOC285148	ABCC3	B1177942	Hs. 90786
41 AW465571	0.4533	0.0004821	0.08476	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	PRO1073	BF885638	Hs. 187199
42 BF043043	0.6526	0.0004937	0.08476	PRO1073 protein	RAB9A	U44103	Hs. 444327
43 BF043765	1.5783	0.0004822	0.08476	RAB9A, member RAS oncogene family	GTF2H2	AF078847	Hs. 422901
44 BF044823	0.7903	0.000496	0.08476	general transcription factor IIIH, polypeptide 2, 44 kDa	NCOA1	NM_147233	Hs. 386092

TABLE I-continued

List of differentially expressed genes in blood that predict PTA for milk production							GenBank ID	Best Hit	UniGene
SEQ ID NO: GenBank ID (cattle)	Fold Change (hu/o)	Raw_P	FDR-adj_P	Gene Name	Gene Symbol	GenBank ID			
45 BF044893	0.6222	0.0005033	0.08476	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	SERPINE1	CA489491	Hs. 414795		
46 BF046610	1.5839	0.0004799	0.08476	v-ski sarcoma viral oncogene homolog (avian)	SK1	XI_5218	Hs. 2969		
47 BF440261	1.6370	0.0004687	0.08476	isocitrate dehydrogenase 3 (NAD ⁺) beta	IDH3B	BL1680835	Hs. 416405		
48 BM362515	0.6810	0.0005569	0.09183	COX17 homolog, cytochrome c oxidase assembly protein (yeast)	COX17	BG539943	Hs. 16297		
49 AW465165	0.7421	0.0005733	0.09260	<i>Homosapiens</i> cDNA FL131058 fis, clone HSYRA2000828.		BQ575646	Hs. 102495		
50 AW464987	3.0054	0.000628	0.09941	Transcribed sequences		TC213365			
51 AW462906	0.7563	0.0006593	0.10246	polyamine-modulated factor 1		AW462906	Bt. 9710		
52 AW463449	1.3041	0.0006914	0.10246	mitogen-activated protein kinase-activated protein kinase 2	PMF1	BMS26376	Hs. 408848		
53 BF040406	1.8294	0.0007112	0.10246	mitochondrial ribosomal protein S18A	MAPKAPK2	AA865261	Hs. 75074		
54 BF042130	0.6805	0.0006681	0.10246	oxyster binding protein 2	Mps18a	NT_029419.10	Min. 287443		
55 BF043536	0.6957	0.0006753	0.10246		OSBP2	BC004340	Hs. 7740		
56 AW464569	1.6029	0.000759	0.10728			TC214576			
57 BF040351	2.3854	0.0007892	0.10958	DKFZP434D146 protein	DKFZP434D	AK022655	Hs. 240845		
58 BF440195	1.6557	0.0008235	0.11255	no hits					
59 BM362654	0.7062	0.000839	0.11255	cerebellar degeneration-related protein 1, 34 kDa	CDR1	BQ222662	Hs. 370504		
60 AW462632	0.5710	0.0008762	0.11413	<i>Homosapiens</i> cDNA clone IMAGE: 6272440, partial cds		CA43730	Hs. 448680		
61 BF040216	0.7157	0.0008796	0.11413			NT_016297.15			
62 BF045874	0.6316	0.0009077	0.11588	protein BA28	FLJ10359	BM105793	Hs. 257300		
63 AW461973	0.6999	0.0010677	0.11638	Transcribed sequences		AW517093	Bt. 3126		
64 AW461973	0.5475	0.0006191	0.11638	Transcribed sequences		BM105795	Bt. 3126		
65 AW461973	0.8947	0.3710353	0.11638	Transcribed sequences		BM105795	Bt. 3126		
66 AW462202	0.6132	0.0010445	0.11638	UDP-N-acetyl-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12)	GALNT12	AJ132365	Hs. 47099		
67 AW465524	0.7456	0.0009858	0.11638	Transcribed sequences		AW465524	Bt. 15671		
68 AW465958	0.6437	0.0010688	0.11638	<i>Homosapiens</i> cDNA clone IMAGE: 30374935, partial cds		BM906968	Hs. 381096		
69 BF041193	0.7937	0.0011008	0.11638	translocase of outer mitochondrial membrane 22 homolog (yeast)	TOMM22	BM554645	Hs. 285005		
70 BF042630	1.5578	0.0010138	0.11638		KLHL3	BQ446837	Hs. 434434		
71 BF043059	2.0344	0.0010778	0.11638			TC216947			
72 BF043236	3.0393	0.0010698	0.11638	poliovirus receptor		BF043236			
73 BF043635	0.3645	0.0010793	0.11638	Transcribed sequences		BQ678871	Hs. 171844		
74 BF043736	0.8297	0.0010712	0.11638	hypothetical protein MGC15677	PVR	BF046146	Bt. 9988		
75 BF044851	0.7832	0.0009527	0.11638	colony stimulating factor 1 (macrophage)	MGC15677	NM_032878	Hs. 71941		
76 BF045170	0.3654	0.001114	0.11638	<i>Mus musculus</i> 2 days neonate thymus thymic cells cDNA, RIKEN	CSF1	BF045203	Bt. 366		
77 BF045305	2.0218	0.0009861	0.11638	full length enriched library, clone: C920020J23 product: unclassifiable, full insert sequence		B1367957	Min. 280066		
78 BM362735	0.6969	0.0011274	0.11638	ribosomal protein S12	RPS12	CD390104	Hs. 380956		
79 BM366522	0.6615	0.0011341	0.11638	malate dehydrogenase 2, NAD (mitochondrial)	MDH2	BX460531	Hs. 405860		
80 AW461513	0.7629	0.0011951	0.11715	Transcribed sequences		AW461513	Bt. 12230		
81 AW462120	1.9638	0.0012245	0.11715	<i>Homosapiens</i> , Similar to DNA segment on chromosome X and Y (unique) 1.5 expressed sequence, clone IMAGE: 4430810, mRNA		BG684898	Hs. 21595		
82 AW463593	2.5733	0.0011645	0.11715	prolactin	PRL	BG202290	Hs. 1905		
83 AW465056	0.6840	0.0012285	0.11715	keratinocyte associated protein 2	KRTCAP2	BQ774375	Hs. 374854		
84 BF046404	1.5250	0.0011851	0.11715	phosphodiesterase 4D, cAMP-specific phosphodiesterase E3 dimer homolog, <i>Drosophila</i>	PDE4D	A4481397	Hs. 28482		

TABLE I-continued

List of differentially expressed genes in blood that predict PTA for milk production

SEQ ID NO: GenBank ID (cattle)	Fold Change (hu/o)	Raw_P	FDR-adj_P	Gene Name	Gene Symbol	GenBank ID	Best Hit	UniGene
85 BM366368	2.4188	0.0012245	0.11715	integrin, alpha D	ITGAD	U37028	Hs. 381264	
86 AW462010	0.8053	0.0012627	0.11758	ankyrin repeat, family A (RFXANK-like), 2	ANKRA2	AA442702	Hs. 239154	
87 AW465551	1.3113	0.0012588	0.11758	mutL homolog 1, colon cancer, nonpolyposis type 2 (<i>E. coli</i>)	MLLH1	U07343	Hs. 433618	
88 AW462774	0.6958	0.0012818	0.11797	AP2 associated kinase 1	AAK1	NM_014911	Hs. 135941	
89 AW462049	0.8134	0.0013687	0.12310	C-terminal binding protein 1	CTBP1	BC011655	Hs. 196083	
90 AW463986	0.7326	0.0013684	0.12310	<i>Homo sapiens</i> transducer of erbB-2 related gene, mRNA (cDNA clone IMAGE: 5785687), partial cds		AW297010	Hs. 161441	
91 AW462385	0.6816	0.0015179	0.12587	syntaxis 1A (brain)	STX1A	B0848697	Hs. 75671	
92 AW462546	1.3394	0.0014366	0.12587	coatomer protein complex, subunit zeta 2	COPZ2	CA415465	Hs. 37482	
93 AW463148	2.0428	0.0015425	0.12587	pepsinogen 5, group I (pepsinogen A)	PGA5	NM_014224	Hs. 432854	
94 AW464583	0.7143	0.0015369	0.12587	GTP binding protein 1	GTPBP1	BQ050866	Hs. 233677	
95 AW465767	0.7315	0.0014903	0.12587	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	UBE2G2	BG323625	Hs. 250387	
96 AW466125	0.7502	0.0015419	0.12587	sorting nexin 2	SNX2	BQ937470	Hs. 11183	
97 AW466146	0.7903	0.0015274	0.12587	ribosomal protein L17	RPL17	BQ429282	Hs. 374588	
98 BF042961	0.5447	0.0015301	0.12587	<i>Homo sapiens</i> gene product KIAA0063	KIAA0063	B0197344	Hs. 3094	
99 BF043647	1.3414	0.0014482	0.12587	<i>Homo sapiens</i> similar to hypothetical protein MGC32132 (LOC375270), mRNA		BC016181	Hs. 444182	
100 AW462175	0.6779	0.0016538	0.13196	peroxisomal D3,D2-enoyl-CoA isomerase	PEC1	BG400978	Hs. 15250	
101 AW464554	0.7914	0.0016507	0.13198	KIAA1181 protein	KIAA1181	BX410080	Hs. 180428	
102 AW464010	1.2116	0.0017134	0.13352	GATA binding protein 2	GATA2	BI518454	Hs. 367725	
103 BF045005	2.1250	0.0016951	0.13352	neutrophil cytosolic factor 4, 40 kDa	NCF4	BG398359	Hs. 196352	
104 BF045561	0.6227	0.0017206	0.13352	EAP30 subunit of ELL complex	EAP30	BG685756	Hs. 127249	
105 BF046270	1.8447	0.0017527	0.13469	<i>Homo sapiens</i> transcribed sequences		CA307924	Hs. 8882	
106 BF043456	1.4696	0.0017865	0.13596	carboxypeptidase D	CPD	U65090	Hs. 5057	
107 BF040324	0.6462	0.0018316	0.13807	<i>Homo sapiens</i> , clone IMAGE: 6254355, mRNA		BU741494	Hs. 133864	
108 AW462307	2.7603	0.0019144	0.13924	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	SLC11A2	AB004857	Hs. 57435	
109 BF043382	0.7925	0.0018925	0.13924	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)		NUPP98	BQ218203	Hs. 112255
110 BF043624	0.6949	0.0019175	0.13924	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	UBE2H	A0939244	Hs. 372758	
111 BF440494	1.6291	0.0018752	0.13924			NT_004836.15		
112 AW461523	1.4122	0.0019196	0.13976	hypothetical protein MGCL5716	MGCL5716	AK074191	Hs. 282111	
113 AW461688	0.7684	0.0019507	0.13976	chromosome 7 open reading frame 11	COrfl1	CA418873	Hs. 129159	
114 BM362465	0.7065	0.0019862	0.14047	ubiquitin-cytochrome c reductase (6.4 kD) subunit	UQCR	BF667634	Hs. 8372	
115 BF440206	1.2735	0.0020052	0.14045	deltex 4 homolog (<i>Drosophila</i>)	DTX4	T98251	Hs. 62264	
116 AW464711	0.5956	0.0020555	0.14264	ADP-ribosylation factor-like 1	ARL1	AA622011	Hs. 372616	
117 AW465606	0.7520	0.0021085	0.14264	APG7 autophagy 7-like (<i>S. cerevisiae</i>)	APG7L	B0880961	Hs. 278607	
118 BF042255	1.3021	0.0021045	0.14264	DnaJ (Hsp40) homolog, subfamily B, member 1	DNAJ1	BX364826	Hs. 82646	
119 BF042909	0.8137	0.0020837	0.14264	<i>Homo sapiens</i> hypothetical protein 1SE1,2, mRNA (cDNA clone IMAGE: 6200931), partial cds		AA373890	Hs. 441127	
120 BF042997	0.7728	0.00217	0.14556	hypothetical protein FLJ32954	FLJ32954	B0204243	Hs. 9905	
121 AW461908	0.7908	0.0022189	0.14667	glioma tumor suppressor candidate region gene 2	GLTSCR2	BM562778	Hs. 421907	
122 AW462811	0.7074	0.0022237	0.14667	CAA-X box 1		BG424569	Hs. 250708	
123 AW461534	0.6298	0.0023319	0.14898	Transcribed sequence with strong similarity to protein homolog		NT_011512.9		
124 AW461574	1.3357	0.002363	0.14898	ref: NP_056441 (<i>H. sapiens</i>) pre-mRNA processing factor 31		AW461574	Bt. 1660	

TABLE I-continued

SEQ ID NO: GenBank ID (cattle)	Fold Change (hu/o)	Raw_P	FDR-adj_P	Gene Name	Gene Symbol	GenBank ID	Best Hit	UniGene
125 AW465706	0.8093	0.0023563	0.14898	topoisomerase I binding, arginine/serine-rich tumor necrosis factor, alpha-induced protein 8	TOPORS	U82939	Hs. 446279	
126 BF041813	1.6655	0.0023578	0.14898		TNFAIP8	AA574013	Hs. 17839	
127 BF041863	0.4895	0.0023642	0.14898	Transcribed sequence		NT_008705.15		
128 BF044557	1.5444	0.0024093	0.14898		CB460423	Bt. 19405		
129 BF046723	2.2140	0.0022784	0.14898	guanine nucleotide binding protein (G protein), gamma 2	GNG2	NT_029419.10		
130 BF440382	0.6036	0.0024066	0.14898	AD023 protein	AD023	BC020774	Hs. 112928	
131 AW463169	0.7644	0.0024841	0.15068	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10 kDa	NDUFV3	CA488406	Hs. 325631	
132 AW463234	0.7892	0.0024826	0.15068	hypothetical protein MGC10120	MGC10120	AA179564	Hs. 199471	
133 BF039617	0.8087	0.0024944	0.15068	similar to RIKEN cDNA 24100041.22 gene (<i>M. musculus</i>)	MGC20533	AA884267	Hs. 34906	
134 BF039493	0.7468	0.0025265	0.15149	adenylate cyclase 3	ADCY3	BM090919	Hs. 69280	
135 AW461726	0.7637	0.0027019	0.15385	myosin, light polypeptide 9, regulatory	MYL9	BX094242	Hs. 188402	
136 AW463524	1.6407	0.0026607	0.15385	cytochrome P450, family 4, subfamily A, polypeptide 11	CYP4A11	BQ717137	Hs. 433814	
137 AW463396	2.5572	0.0027016	0.15385	protein tyrosine phosphatase-like (proline instead of catalytic	S67581	Hs. 1645		
138 AW465666	0.6545	0.0026717	0.15385	arginine), member b	PTPLB	AK074605	Hs. 5957	
139 BF040830	2.6732	0.0026583	0.15385	MAX dimerization protein 4	MXD4	NT_022517.16		
140 BF040980	0.7352	0.0026874	0.15385	Transcribed sequences		CA308842	Hs. 511752	
141 BM364711	2.1553	0.0026345	0.15385	hypothetical protein KIAA1833	KIAA1833	BM364711	Bt. 11098	
142 BF039094	1.6600	0.0027501	0.15548	chromobox homolog 6	CBX6	XM_114611	Hs. 443139	
143 BM366975	0.7709	0.0028343	0.15910	testis-specific kinase 2	TESK2	CA424188	Hs. 511952	
144 BF044410	2.0975	0.0028648	0.15968	fibrosin 1	FBS1	AB057597	Hs. 8980	
145 AW465824	1.3873	0.0029221	0.16174	RelA-associated inhibitor	RAI	BU196391	Hs. 247186	
146 BF045830	0.7629	0.0030885	0.16976	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	DYRK3	BU860066	Hs. 324051	
147 BF046712	1.3724	0.0031245	0.17055	plasminogen-related protein A		BC015501	Hs. 164267	
148 BF039623	1.9607	0.0031532	0.17094	LOC285189		XM_351480	Hs. 449164	
149 AW465584	2.0554	0.0031759	0.17100	cyclin-dependent kinase inhibitor 1C (p57, Kip2)		TC214223		
150 AW462929	0.7037	0.0032092	0.17163	splicing factor 3b, subunit 5, 10 kDa	CDKN1C	BU742010	Hs. 106070	
151 BM366972	0.7576	0.0032364	0.17192	Transcribed sequences	SF3B5	CA411860	Hs. 111695	
152 BF041965	0.7803	0.0033066	0.17342	ribosomal protein S27 (metallopanstimulin 1)		BU774419	Bt. 22285	
153 BM365835	0.7417	0.0033085	0.17342	inositol polyphosphate-4-phosphatase, type II, 105 kDa	RPS27	CD248629	Hs. 337307	
154 BF045124	2.1781	0.0033633	0.17514	transcribed with strong similarity to protein sp. P13995	INPP4B	BC017924	Hs. 153687	
155 BF040256	2.8742	0.0034738	0.17971	(<i>H. sapiens</i>) MTDC_HUMAN Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial precursor Includes:		CB421959	Bt. 20862	
				NAD-dependent methylenetetrahydrofolate dehydrogenase;				
				Methylenetetrahydrofolate cyclohydrolase]				
156 BM364415	0.7048	0.0035667	0.18278	cytochrome c oxidase subunit Vb	COX5B	TC209958		
157 BM365799	0.7019	0.0035794	0.18278	transforming growth factor beta 1 induced transcript 1	TGFBI1	AA527583	Hs. 1342	
158 AW462329	1.4275	0.0036045	0.18288	leucine proline-enriched proteoglycan (leprecan) 1	LEPRE1	BC032545	Hs. 25511	
159 AW462136	0.7972	0.0036677	0.18344	chromosome 20 open reading frame 7	C20orf7	NM_19952	Hs. 437656	
160 BF041338	2.0406	0.0037081	0.18344	cerebroside (3'-phosphoadenyl)sulfate: galactosylceramide 3')	CST	D88667	Hs. 17958	
161 BF041765	0.7198	0.0036978	0.18344	sulfotransfase				
162 BF045167	1.4258	0.0036793	0.18344	protein-O-mannosyltransferase 1	POMT1	AK074874	Hs. 209205	
163 BM362349	0.7401	0.0037621	0.18495	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8 kDa	NDUF1A2	CA455540	Hs. 163867	
164 AW462081	0.7895	0.003842	0.18562	epithelial membrane protein 1	EMP1	AW369615	Hs. 306692	
165 BF042546	2.4927	0.003893	0.18562	KIAA0703 gene product	KIAA0703	AK091051	Hs. 6168	

List of differentially expressed genes in blood that predict PTA for milk production

TABLE I-continued

List of differentially expressed genes in blood that predict PTA for milk production

SEQ ID NO: GenBank ID (cattle)	Fold Change (hu/o)	Raw_P	FDR-adj_P	Gene Name	Gene Symbol	GenBank ID	Best Hit	UniGene
166 BF043129	2.6616	0.0038096	0.18562	Transcribed sequences		TCI92095		
167 BF043441	0.3753	0.0038749	0.18562	Transcribed sequences		CB432831	Bt. 16982	
168 BF043441	0.1367	0.0003031	0.18562	Transcribed sequences		CR432831	Bt. 16982	
169 BF043441	1.0301	0.9404666	0.18562	Transcribed sequences		CB432831	Bt. 16982	
170 BM361957	0.7212	0.0038832	0.18562	ribosomal protein L34	RPL34	BG436845	Hs. 250895	
171 BM362618	0.7724	0.0039316	0.18634	ubiquitin associated domain containing 1	UBADC1	BX395764	Hs. 9194	
172 AW461418	0.7664	0.0039726	0.18716	ROD1 regulator of differentiation 1 (<i>S. pombe</i>)	ROD1	NM_005156	Hs. 374634	
173 AW461640	0.7853	0.0041372	0.18865	eukaryotic translation termination factor 1	ETF1	AA812738	Hs. 77324	
174 AW461984	1.2745	0.0041471	0.18865	p21(CDKN1A)-activated kinase 6	PAK6	BC035596	Hs. 21420	
175 BF041453	1.5013	0.0041268	0.18865	solute carrier family 4, sodium bicarbonate cotransporter, member 5	SLC4A5	NM_133478	Hs. 321127	
176 BF042148	0.6408	0.0041056	0.18865	pellino homolog 1 (<i>Drosophila</i>)	PELI1	AA255632	Hs. 7886	
177 BF042689	1.5422	0.0040901	0.18865	hypothetical protein FLJ14494	FLJ14494	NM_032795	Hs. 150458	
178 BF045165	1.2746	0.0040777	0.18865	hypothetical protein DK7Zp434N2030	DK7Zp434N2030	BC035136	Hs. 494204	
179 AW461802	0.7532	0.0042274	0.18995	p8 protein (candidate of metastasis 1)	P8	BG708311	Hs. 418692	
180 AW464520	1.5809	0.0042958	0.18995	low density lipoprotein-related protein 2	LRP2	BG3399349	Hs. 253938	
181 AW465157	1.5354	0.0042351	0.18995	short stature homeobox 2	SHOX2	AK095538	Hs. 55967	
182 BF039056	3.1018	0.0042953	0.18995	Trophoblast Kunitz domain protein 3 (TKDP3) mRNA, partial cds		BF043269	Bt. 262	
183 BF040869	2.4647	0.0042797	0.18995	Ileucine-rich repeat-containing G protein-coupled receptor 8	LGR8	NM_130806	Hs. 348481	
184 BF043917	0.8532	0.0043968	0.19227	evolutionarily conserved G-patch domain containing	EGCP	AF434677	Hs. 55014	
185 BF045154	2.0875	0.0043767	0.19227			NT_004668.16		
186 AW461470	0.8559	0.0044878	0.19389	Transcribed sequences		AW461470	Bt. 10716	
187 AW464274	1.6622	0.0045074	0.19389	noncarboxylate transporter 13	SLC16A13	XM_1154384	Hs. 448010	
188 BF044013	0.7111	0.0045045	0.19389	HSPC039 protein	HSPC039	BH23160	Hs. 406542	
189 AW461516	1.5622	0.0048622	0.19683	G protein-coupled bile acid receptor 1	GPBAR1	BG698138	Hs. 160954	
190 AW462075	0.7630	0.0046049	0.19683	serine protease inhibitor, Kunitz type, 2	SPINT2	B1889025	Hs. 31439	
191 AW462448	1.3243	0.0046701	0.19683	Transcribed sequences		AW462448	Bt. 13259	
192 AW462519	0.7746	0.004574	0.19683	choline kinase-like	CHKL	B1568477	Hs. 439777	
193 AW464128	0.7198	0.0048382	0.19683	vesicle docking protein p115	VDP	D86326	Hs. 325948	
194 AW465040	0.5985	0.0047972	0.19683	RIKEN cDNA 11I0003P22 gene		11I0003P22R	Mm. 41420	
195 AW465639	0.7636	0.0049111	0.19683			NT_010194.16		
196 AW465776	0.7988	0.0046489	0.19683	Transcribed sequences		AW465776	Bt. 12588	
197 AW466079	3.4285	0.004949	0.19683	glutanyl aminopeptidase (aminopeptidase A)	ENPEP	L14721	Hs. 435765	
198 BF039189	0.8475	0.0048752	0.19683	SH2 domain binding protein 1 (tetraarginine repeat containing)	SH2BP1	B1839172	Hs. 173288	
199 BF042267	2.0691	0.0047925	0.19683	Rab geranylgeranyltransferase, beta subunit	RABGGTB	BC020790	Hs. 78948	
200 BF043458	0.6814	0.00471	0.19683	KIAA1623	KIAA1623	AL567190	Hs. 421680	
201 BF043688	1.5270	0.0049295	0.19683	follistatin-like 1	FSTL1	BQ010153	Hs. 433622	
202 BF044377	0.2382	0.0046789	0.19683	thyroid hormone receptor interactor 3	TRIP3	CD701615	Hs. 2210	
203 BM362629	0.8571	0.0049635	0.19683	ribosomal protein L27	RPL27	BU852832	Hs. 405528	
204 BM366480	0.7655	0.0049735	0.19683	hypothetical protein MGC3306	MGC3306	BX416823	Hs. 335750	
205 AW465210	0.7042	0.0051562	0.20304	BRF2, subunit of RNA polymerase III transcription initiation factor,	BRF2	BQ018062	Hs. 274136	
206 BF043768	2.0210	0.0052193	0.20447	BRF1-like				
207 BF045850	1.3545	0.0052441	0.20447	Transcribed sequence with moderate similarity to protein NP_073596.1 (<i>H. sapiens</i>) hypothetical protein FLJ211865 [Homo sapiens]		BE664132	Bt. 6206	

TABLE I-continued

List of differentially expressed genes in blood that predict PTA for milk production

SEQ ID NO: GenBank ID (cattle)	Fold Change (hi/lo)	Raw_P	FDR-adj_P	Gene Name	Gene Symbol	GenBank ID Best Hit	UniGene
208 BM365341	1.8091	0.0052774	0.20476	choline/ethanolaminophosphotransferase	CEPT1	AW797250 XM_085151	Hs. 363372 Hs. 303775
209 BP230001A20 G6	0.6732	0.00535565	0.20681	chromosome 14 open reading frame 170	C14orf170	AW315111	Bt. 9321
210 AW462359	0.7978	0.0054161	0.20810	Transcribed sequence with weak similarity to protein sp: Q9UKK3 (<i>H. sapiens</i>) PPOV_HUMAN Vault poly			
211 BF402272	1.5176	0.0054499	0.20839	regulator of G-protein signalling 5	RGSS	B1494221	Hs. 24930
212 AW461819	0.4857	0.0056347	0.21105	ATPase, Na+K+-transporting, beta 1 polypeptide	ATP1B1	AA418647	Hs. 78629
213 AW463150	0.7574	0.0056553	0.21105	<i>Homosapiens</i> mRNAs cDNA DKFZp434H068 (from clone DKFZp434H068)		AA148248	Hs. 506074
214 BE039065	1.5715	0.0056271	0.21105	MLL septin-like fusion	MSF	BU931075	Hs. 288094
215 BM365510	0.7674	0.0055744	0.21105	kinesin family member 3B	KIF3B	BUN90106	Hs. 301206
216 BM365398	0.3500	0.0055484	0.21105	sestrin 2	SIESN2	AI700180	Hs. 8026
217 BF039954	1.8391	0.0058891	0.21884	neuropathy target esterase	NTE	AJ004832	BF039954
218 BF040540	1.3105	0.0059515	0.21990	hypothetical protein MGC4238	MGC4238	NM_032332	Hs. 511760
219 BM366584	1.1928	0.0059732	0.21990	similar to Zinc finger protein 136	LOC199692	AA141213	Hs. 334626
220 BF043047	1.6391	0.0061858	0.22667	protein inhibitor of activated STAT protein PIASY	PLASY	T8436	Hs. 14831
221 AW461654	1.3075	0.0063001	0.22980	echinoderm microtubule associated protein like 5	EML5	BF590352	Hs. 105779
222 AW462133	1.5404	0.0063331	0.22994	Transcribed sequences		AW462711	Hs. 410913
223 AW462711	0.8294	0.0063974	0.23104	echinoderm microtubule associated protein like 5		Bt. 7917	
224 AW460882	1.3508	0.0066451	0.23104	Transcribed sequences		CB449171	Bt. 6244
225 BF045301	0.7722	0.0066472	0.23104	methylaminopeptidase 2	METAP2	CA443908	Hs. 164906
226 AW461425	0.7595	0.0066545	0.23125	casein kinase 1, alpha 1	CSNK1A1	BQ231001	Hs. 318381
227 AW465281	0.7778	0.00665567	0.23125	<i>Homosapiens</i> transcribed sequences		BX4833510	Hs. 105636
228 BF045176	0.8483	0.0066875	0.23125	SET translocation (myeloid leukemia-associated)	SET	M93651	Hs. 436687
229 BF045836	0.6667	0.0066603	0.23125	topoisomerase (DNA) I	TOP1	BC004475	Hs. 253536
230 BM364051	1.4620	0.0066546	0.23125	KIAA1836 protein	KIAA1836	BE88083	Hs. 318773
231 AW464893	0.6690	0.0066645	0.23170	STAR1 domain containing 4, sterol-regulated	STARD4	AL8232599	Hs. 93842
232 AW465985	0.7679	0.00668628	0.23472	phosphatidylinositol transfer protein, membrane-associated 2	PITPNM2	BC040063	Hs. 272759
233 BF042374	0.7915	0.0068134	0.23472	neolin-like 2	NDNL2	BC041166	Hs. 512642
234 BF043142	1.5254	0.0068748	0.23472	cyclin M4	CNNM4	A2291802	Hs. 175043
235 BF043207	0.7376	0.0069098	0.23472	hypothetical protein FLJ20244	FLJ20244	BC040126	Hs. 411456
236 BM365490	0.7258	0.0068881	0.23472	bromodomain containing 1	BRD1	NM_014577	Hs. 307080
237 BM365156	0.8537	0.0067749	0.23472	MK167 (FHA domain) interacting nucleolar phosphoprotein	MK167IP	AA564743	Hs. 367842
238 BF039394	1.4396	0.0069435	0.23486	diacylglycerol kinase, etc.	DGKH	NM_152910	Hs. 378969
239 BF039014	0.7831	0.0070139	0.235624	<i>Homosapiens</i> clone IMAGE: 4815142, mRNA		BQ326465	Hs. 349568
240 AW465409	0.7396	0.0070867	0.23767	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit 45 kDa	PAFAH1B1	BUN72064	Hs. 77318
241 BM366332	3.4966	0.0071489	0.23875	angiogenin, ribonuclease, RNase A family, 5	ANG	BQ773604	Hs. 283749
242 AW462090	0.7769	0.0074169	0.24666	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	DDX54	BM794682	Hs. 203581
243 AW462739	0.8437	0.0075239	0.24735	chromosome 6 open reading frame 83	C0f83	CA142928	Hs. 284765
244 BF039410	0.5371	0.0075627	0.24735	RUSC1	CA1418193	Hs. 226499	
245 BF045989	0.4548	0.0075315	0.24735	chromosome 10, open reading frame 74	C10orf74	AA730643	Hs. 352398
246 BF40222	1.4891	0.0075193	0.24735	coronin, actin binding protein, 1C	CORO1C	CA444755	Hs. 17377
247 AW464311	0.8173	0.0076248	0.24835	hypothetical protein FLJ20403	FLJ20403	BUS21884	Hs. 306221
248 BF046466	0.7542	0.0077081	0.25004	ribosone binding protein 1 homolog 180 kDa (dog)	RBP1	AA77671	Hs. 986114
249 AW465742	0.8104	0.0078784	0.25452	growth hormone inducible transmembrane protein	GHITM	CD701404	Hs. 352456
250 AW463923	1.1798	0.0081087	0.26063	HLA-B associated transcript 1	BAT1	BG675992	Hs. 254042

TABLE I-continued

List of differentially expressed genes in blood that predict PTA for milk production

SEQ ID NO: GenBank ID (cattle)	Fold Change (hu/o)	Raw_P	FDR-adj_P	Gene Name	Gene Symbol	GenBank ID	Best Hit	UniGene
251 AW466175	0.7750	0.0081335	0.26063	ubiquitin specific protease 47	USP47	CA944859	Hs. 441028	
252 BF044437	1.8758	0.0081949	0.26154			NT_022184.13		
253 BF039223	0.6587	0.0082671	0.26279	copine III	CPNE3	NT_079592.1		
254 AW462705	0.7869	0.0084481	0.26325	B-cell linker	Blnk	BE877797	Hs. 14158	
255 BF040988	2.1454	0.0084317	0.26325	Transcribed sequence with strong similarity to protein prf_2202255A, AT motif-binding factor 1 [<i>Homo sapiens</i>]	DVL3	NT_011757.13	Mm. 9749	
256 BF044083	0.8398	0.0083968	0.26325	paraspeckle component 1	PSPC1	BB612232	Br. 6456	
257 BF045148	0.7724	0.0083655	0.26325	KIAA0007 protein	KIAA0007	CF767756		
258 BM363825	2.5268	0.0083926	0.26325	phospholipase A2, group IID	PLA2G2D	BM153087	Hs. 189507	
259 BF044419	1.7185	0.0085132	0.26424	<i>Homo sapiens</i> cDNA FLJ31099 fis, clone IMR32100023.0.	DVL3	BC020929	Hs. 177633	
260 AW465703	0.8349	0.0086112	0.26627	Transcribed sequences	RANBP10	AW465703	Br. 9668	
261 BF039660	0.8068	0.0086939	0.26650	dishvelled, dsh homolog 3 (<i>Drosophila</i>)	PDCD61P	D86963	Hs. 381928	
262 BF036969	0.6363	0.0087206	0.26650	paraspeckle component 1	FBLN1	AF448795	Hs. 16364	
263 BF044425	0.6176	0.0086956	0.26650	KIAA0007 protein	COL8A1	CB133931	Hs. 90315	
264 BF041013	0.7677	0.0088577	0.26965	Ran-binding protein 10	AL137299	Hs. 6343		
265 AW464094	0.8530	0.00889577	0.27089	programmed cell death 6 interacting protein	CA748765	Hs. 9663		
266 AW464164	0.5096	0.0089669	0.27089	fibulin 1	BU553419	Hs. 445240		
267 BF045865	1.4010	0.0090141	0.27128	collagen, type VIII, alpha 1	CA448060	Hs. 114599		
268 AW462758	1.5861	0.0094557	0.27545	hypothetical protein DKFZp434K1815	DKFZp434K	AW462758		
269 AW462782	0.8041	0.0092383	0.27545	hypothetical protein DKFZp434K1815	BQ773994	Hs. 274135		
270 AW463320	1.4604	0.0095422	0.27545	mitochondrial ribosomal protein S18A	18.15			
271 AW465653	0.7926	0.0094217	0.27545	upstream binding transcription factor, RNA polymerase I	Mpr18a	NT_009952.14	Mm. 287443	
272 AW465738	2.4055	0.0092567	0.27545	carboxypeptidase A4	UBTF	BQ440761	Hs. 89781	
273 BF039874	1.4597	0.0095609	0.27545	prostaglandin F2 receptor negative regulator	CPA4	NM_016352	Hs. 93764	
274 BF042207	0.7473	0.0094044	0.27545	mitogen-activated protein kinase kinase 1	PTGFRN	XM_040709	Hs. 418093	
275 BF042293	0.6981	0.0095702	0.27545	cytochrome c oxidase subunit VIII	MAP2K1	BMP81116	Hs. 132311	
276 BF044365	2.0515	0.0093995	0.27545	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18 kDa	COX8	BL756980	Br. 11020	
277 BF045161	1.2077	0.0095371	0.27545	sorcini	NDUFB7	AA442119	Hs. 433901	
278 BM361926	0.7576	0.0094725	0.27545	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	SRI	BG574803	Hs. 433482	
279 BM364516	1.8243	0.0093859	0.27545	myosin phosphatase-Rho interacting protein	CXCL12	NM_003130	Hs. 422340	
280 AW462100	0.7429	0.0097767	0.27835	PTK2 protein tyrosine kinase 2	M-RIP	BX647204	Hs. 436042	
281 BF039681	0.7139	0.0097685	0.27835	chromosome 1 open reading frame 24	PTK2	D23673	Hs. 430725	
282 BM364428	0.7728	0.0097117	0.27835	nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs)	C1orf24	BG497514	Hs. 434281	
283 AW462966	1.1930	0.0098488	0.27940	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	NOLA3	CA430470	Hs. 48778	
284 AW461868	0.7513	0.0100302	0.27950	malate dehydrogenase 2, NAD (mitochondrial)	A1934691	AA449355	Hs. 14317	
285 AW462382	0.7440	0.0099089	0.27950	brromodomain containing 1	MDH2	AU149417	Hs. 372267	
286 AW464067	0.7689	0.010064	0.27950	Parkinson disease (autosomal recessive, early onset) 7	BRD1	BM550823	Hs. 405860	
287 BF042174	0.7999	0.0099663	0.27950	hypothetical protein LOC255743	PARK7	BU1431018	Hs. 370880	
288 BF043744	2.8509	0.0099637	0.27950	IQ motif containing GTPase activating protein 1	LOC255743	BM554785	Hs. 419640	
289 BM365103	0.7674	0.0101655	0.28133	apoptosis(APO-1)antigen 1 (FAS), member 6	IQGAP1	AA449355	D29640	Hs. 288332
290 AW464273	1.6537	0.0101655	0.28175	NHP2 non-histone chromosome protein 2-like 1 (<i>S. cerevisiae</i>)	TNFRSF16	NM_174662	Br. 4345	
291 BM366541	0.8137	0.0102164	0.28175	NHP2 non-histone chromosome protein 2-like 1 (<i>S. cerevisiae</i>)	NHP2L1	BU955332	Hs. 182255	

TABLE I-continued

List of differentially expressed genes in blood that predict PTA for milk production

SEQ ID NO: GenBank ID (cattle)	Fold Change (hu/o)	Raw_P	FDR-adj_P	Gene Name	Gene Symbol	GenBank ID	Best Hit	UniGene
292 AW462227	0.8291	0.0102891	0.28180	transforming growth factor, beta receptor II (70/80 kDa)	TGFBR2	CD110077	Hs_82028	
293 AW466159	1.4010	0.0102895	0.28180	Ran GTPase activating protein 1	RANGAP1	BUI190935	Hs_183800	
294 BF045523	0.7624	0.0103369	0.28213	myosin regulatory light chain interacting protein	MYLIP	BQ027638	Hs_443793	
295 BF049488	0.8094	0.0103891	0.28258	ubiquitin-conjugating enzyme E2 variant 2	UBE2V2	X98091	Hs_371278	
296 BF040663	2.3303	0.0105655	0.28541	eukaryotic translation initiation factor 5	EIF5	BC007728	Hs_433702	
297 BF042477	0.7538	0.0105356	0.28541	hypothetical protein LOC90850	LOC90850	BC050477	Hs_343828	
298 BF042245	1.5952	0.0106039	0.28547	hypothetical protein containing 2	EFHD2	AA565855	Hs_301342	
299 AW463964	0.7511	0.0106864	0.28575	EF hand domain containing 2	GTL3	BC05152	Hs_279818	
300 BF041775	0.7656	0.0106543	0.28575	likely ortholog of mouse gene trap locus 3	PSMA3	CA431411	Hs_246240	
301 BF440363	0.7361	0.0107527	0.28656	proteasome (prosome, macropain) subunit, alpha type, 3	MIG-6	BQ014845	Hs_111169	
302 BF040230	0.3818	0.0108203	0.28739	mitogen-inducible gene 6	MRPL32	BUR27763	Hs_50252	
303 AW462792	0.8156	0.0109467	0.28881	mitochondrial ribosomal protein L32		BF046632		
304 BF046632	0.7915	0.0109122	0.28881					
305 BF045608	0.7502	0.0110471	0.29049	LSM8 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>)	LSM8	AA328592	Hs_446179	
306 BF040483	0.7404	0.0112759	0.29553	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	SLC37A3	TC-02969		
307 AW462063	1.3490	0.0113454	0.29637		IGFBP7	B6E93370	Hs_435590	
308 AW461912	0.8007	0.0116025	0.29637	insulin-like growth factor binding protein 7	PAN3	BC017201	Hs_455795	
309 AW464194	0.7571	0.0115795	0.29758	PABP1-dependent poly A-specific ribonuclease subunit PAN3		BC024318	Hs_190153	
310 BF040204	0.8016	0.0114776	0.29758	Transcribed sequence with weak similarity to protein pir; T14756 (<i>H. sapiens</i>) T14756 hypothetical protein DKFZp564F0923.1 - human		BF040204	Bt_125110	
311 BF041103	0.6991	0.0116226	0.29758	Transcribed sequences	STARD4	BF041103	Bt_18264	
312 BF044164	0.8039	0.0115809	0.29758	START domain containing 4, sterol regulated	NDUFA10	AA807553	Hs_93842	
313 BM362196	0.8620	0.0114649	0.29758	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42 kDa	LOC90826	CA395087	Hs_198271	
314 AW465608	0.8057	0.0116549	0.29758	hypothetical protein BC004337		AA574240	Hs_29645	
315 AW465430	0.6830	0.0117439	0.29809	splicing factor, arginine/serine-rich 7, 35 kDa	BA241061	TC202901		
316 BF045609	0.6339	0.0117505	0.29809	WD repeat domain 5	SFRS7	H12245		
317 AW461462	0.8282	0.0126424	0.29938	AFG3 ATPase family gene 3-like 2 (yeast)	WDR5	BQ939873	Hs_397638	
318 AW461475	0.7230	0.0126915	0.29938	ribonuclease/angiopeptin inhibitor	AFG3L2	BL173748	Hs_436683	
319 AW461535	0.8321	0.0131623	0.29938	prostate cancer antigen-1	RNH	BX387666	Hs_130958	
320 AW461605	1.3591	0.0127436	0.29938	insulin-like growth factor binding protein 3	DEPC-1	BI037645	Hs_71917	
321 AW461982	1.2421	0.0120911	0.29938	chromosome 21 open reading frame 66	IGFBP3	AW605051	Hs_450230	
322 AW462169	0.7422	0.0131314	0.29938	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	C2orf66	NM_145328	Hs_297559	
323 AW462456	0.8042	0.0120082	0.29938	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma	SFPQ	CA441964	Hs_180610	
324 AW462702	0.8155	0.0129927	0.29938	pepsinogen F	PIP5K2C	AK075553	Hs_144502	
325 AW462838	2.2170	0.01296	0.29938	prolactin	Peptf	AK004109	Mm_34037	
326 AW463978	2.0020	0.0126404	0.29938	integrin-linked kinase	PRL	CD106017	Hs_1905	
327 AW464129	1.2890	0.0122983	0.29938	protein tyrosine phosphatase-like (proline instead of catalytic	ILK	BC001544	Hs_6196	
328 AW464130	0.8240	0.0129722	0.29938	arginine), member b	PTPLB	NM_198402	HM_5957	
329 AW464611	1.3071	0.0130407	0.29938	transcription factor 7-like 1 (T-cell specific, HMG-box)	TCF7L1	BU543840	Hs_318517	
330 AW464647	0.8230	0.013048	0.29938	huntingtin interacting protein 2	HIP2	BX427147	Hs_246603	
331 AW464892	0.7164	0.0124284	0.29938	nucleoporin like 1	NUP111	AB007870	Hs_406243	
332 BF039385	0.7836	0.0124596	0.29938	transforming, acidic coiled-coil containing protein 1	TACC1	BC041391	Hs_279245	
333 BF039551	0.8018	0.0127349	0.29938	cardinophrin 1	CTF1	BC036787	Hs_433319	

TABLE I-continued

List of differentially expressed genes in blood that predict PTA for milk production							GenBank ID	Best Hit	UniGene
SEQ ID NO:	GenBank ID (cattle)	Fold Change (hu/o)	Raw_P	FDR-adj_P	Gene Name	Gene Symbol			
334	BF039606	0.5315	0.0129139	0.29938	MAD2 mitotic arrest deficient-like 1 (yeast)	MAD2L1	U31278	Hs_79078	
335	BF039758	1.4410	0.0120723	0.29938	afiphilin protein	AFTIPHILIN	AL833962	Hs_7942	
336	BF041379	1.6597	0.0127076	0.29938	nyosin VB	MYO5B	AL133643	Hs_512590	
337	BF041571	0.5919	0.0133519	0.29938	CDC42 binding protein kinase beta (DMPK-like)	CDC42BPB	B0845217	Hs_436985	
338	BF041789	0.8041	0.0122045	0.29938	serine palmitoyltransferase, long chain base subunit 2	SPTLC2	AB011098	Hs_59403	
339	BF041797	0.8129	0.0119381	0.29938			TC219445		
340	BF041818	2.8155	0.0122444	0.29938	hypothetical protein FLJ12875	FLJ12875	BX334448	Hs_10101	
341	BF041917	0.7942	0.0127768	0.29938	SEC24 related gene family, member B (<i>S. cerevisiae</i>)	SEC24B	BC040137	Hs_7239	
342	BF041933	1.7183	0.0133203	0.29938	transient receptor potential cation channel, subfamily M, member 4	TRPM4	B0858032	Hs_31608	
343	BF042179	1.6954	0.0120724	0.29938	transient receptor potential cation channel, subfamily M, member 6	TRPM6	AF448232	Hs_272225	
344	BF042480	0.6911	0.0132416	0.29938	KIAA0020	KIAA0020	AI936509	Hs_443866	
345	BF043417	0.2095	0.0118913	0.29938	phosphofructokinase, liver	PFKL	BL544646	Hs_368741	
346	BF043962	0.6835	0.0120777	0.29938	BCL2-like 13 (apoptosis facilitator)	BCL2L13	CA405971	Hs_310922	
347	BF043971	0.8269	0.0131719	0.29938	F-box only protein 3	FBXO3	BC039291	Hs_406787	
348	BF044310	0.6726	0.0122477	0.29938	lysosomal-associated protein transmembrane 4 alpha	LAPTM4A	BL463546	Hs_111894	
349	BF045055	1.8523	0.0124084	0.29938	SET domain, bifurcated 1	SETDB1	AK095075	Hs_345058	
350	BF045103	0.7576	0.01322737	0.29938	cyclic AMP phosphoprotein, 19 kD	ARPP-19	BF794225	Hs_7351	
351	BF045200	0.5394	0.0132464	0.29938	Transcribed sequences		BF045200	Bt_6459	
352	BF045261	0.7375	0.0124415	0.29938	osteocrin	OSTN	NM_198184	Hs_526794	
353	BM364511	1.4212	0.0133152	0.29938	hypothetical protein FLJ00007	FLJ00007	AA766256	Hs_120094	
354	BM364839	0.7436	0.0130076	0.29938	<i>Homo sapiens</i> similar to protein of fungal metazoan origin like (11.1 kD) (2C514) (LOC374960), mRNA		BG111067	Hs_343588	
355	BM365207	0.2151	0.0129951	0.29938	chromosome 9 open reading frame 58	C9orf58	AA349673	Hs_4944	
356	BM366035	0.8475	0.0126785	0.29938	ATP synthase, H ₊ transporting, mitochondrial F0 complex, subunit e	ATP51	AA301789	Hs_85539	
357	BM366605	2.7408	0.0127858	0.29938	ATP synthase, H ₊ transporting, mitochondrial F0 complex, subunit e	ATP51	AA301789	Hs_85539	

TABLE II

<u>List of differentially expressed genes in liver that predict PTA for milk production</u>									
SEQ ID NO:	GenBank ID (cattle)	Fold Change	Raw_P	FDR-adj. P	Gene Name	Gene Symbol	GenBank ID Best Hit	Unigene	
358	AW464111	0.5685	0	1.32E-07			AAM50023.1		
359	AW464166	0.3883	3.00E-10	7.67E-07	histone 1, H1d	HIST1H1D	NM_005320	Hs. 136857	
360	BF045977	0.5291	4.05E-06	0.007977	epithelial V-like antigen 1	EVA1	AF275945		
361	BF040267	0.5683	0.0001496	0.220858	poly(A) binding protein, cytoplasmic 4	PABPC4	BQ422891	Hs. 169900	
					(inducible form)				
362	BP230002B10	0.7223	0.0001969	0.232606	ribosomal protein L31	RPL31	BQ028654	Hs. 375921	
363	BF044279	0.7894	0.0002679	0.263701	G5 hypothetical protein FLJ13188	FLJ13188	BC023577	Hs. 11859	
364	AW466058	4.1302	0.0004149	0.350087	CD14 antigen	CD14	BG002906	Hs. 75627	
365	BF042062	4.1572	0.0005552	0.375487	solute carrier family 40 (iron-regulated transporter), member 1	SLC40A1	AI138761	Hs. 409875	
366	AW464065	0.6322	0.0005722	0.375487	serine/arginine repetitive matrix 2	SRRM2	AB002322	Hs. 433343	
367	AW464444	0.6123	0.0006706	0.39608	hypothetical transmembrane protein SBB154	SBB154	BM010343	Hs. 116708	

TABLE III

List of differentially expressed genes in blood and liver that predict PTA for milk production

SEQ ID NO:	GenBank ID	Contrast Blood	Raw_P Blood	Contrast Liver	Raw_P Liver	Gene Name	Gene Symbol	GenBank ID	Best hit	UniGene	
368	AW461405	-0.1525	0.0542	-0.3213	0.0727	core promoter element binding protein low density lipoprotein receptor-related protein 10	COPEB	BU151389	Hs. 285313		
369	AW461482	-0.1409	0.0884	-0.2659	0.0171		LRP10	CA488630	Hs. 28368		
370	AW461511	-0.2193	0.0495	-0.2481	0.0272	ubiquitin-conjugating enzyme E2L_3	UBE2L3	BU625673	Hs. 108104		
80	AW461513	-0.3904	0.0012	-0.1598	0.0968	Transcribed sequences		AW461513	Bt. 12230		
319	AW461535	-0.2651	0.0132	-0.2119	0.0112	ribonuclease/angiogenin inhibitor	RNH	BX387666	Hs. 130958		
371	AW461572	-0.1757	0.0300	-0.1998	0.0632	CCAAT/enhancer binding protein (C/EBP), beta	CEBPB	BX417468	Hs. 99029		
372	AW461591	0.285	0.0597	0.2631	0.0204	Transcribed sequence with strong similarity to protein		AW461591	Bt. 6019		
373	AW461600	0.3389	0.0942	0.3447	0.0371	pif: 2102256A (<i>H. sapiens</i>)		AW461600			
173	AW461640	-0.3487	0.0041	-0.3797	0.0086	eukaryotic translation termination factor 1	ETF1	AA812738	Hs. 77324		
374	AW461650	-1.4783	0.0346	-0.8129	0.0172	transgelin	TAGLN	D17409	Hs. 410977		
375	AW461778	0.259	0.0943	0.5802	0.0703	wingless-type MMTV integration site family, member 6	WNT6	NM_006522	Hs. 29764		
308	AW461912	-0.3206	0.0116	-0.3695	0.0441	insulin-like growth factor binding protein 7	IGFBP7	BC017201	Hs. 435795		
29	AW461980	-0.3867	0.0002	-0.2313	0.0689	likely ortholog of mouse hypoxia induced gene 1	HIG1	BG700494	Hs. 7917		
321	AW461982	0.3127	0.0121	0.4021	0.0574	insulin-like growth factor binding protein 3	IGFBP3	AW605051	Hs. 450230		
376	AW462000	-0.4442	0.0867	-0.3556	0.0237	CD164 antigen, sialomucin	CD164	BC040317	Hs. 43910		
100	AW462175	-0.561	0.0016	0.8753	0.0084	peroxisomal D3,D2-enoyl-CoA isomerase	PECI	BG400978	Hs. 15250		
377	AW462221	0.668	0.0163	0.5385	0.0508	<i>Mus musculus</i> adult male medula oblongata cDNA, RIKEN full-length enriched library, clone: 6330410L21		AKR031828	Mm. 252481		
378	AW462277	-0.2909	0.0643	-0.1792	0.0336	Transcribed sequence with moderate similarity to protein ref. NP_116212.1 (<i>H. sapiens</i>)		CF764638	Bt. 5043		
192	AW462519	-0.3685	0.0050	-0.2515	0.0686	choline kinase-like	CHKL	BUT568477	Hs. 439777		
324	AW462702	-0.2942	0.0130	-0.213	0.0817	phosphatidylinositol-4-phosphate 5-kinase, type II,	PIP5K2C	AK075553	Hs. 144502		
379	AW463060	-0.185	0.0654	0.2311	0.0498	calpastatin	CAST	BG28205	Hs. 440961		
380	AW463121	-0.2674	0.0332	-0.2756	0.0761	CD151 antigen	CD151	BUT528765	Hs. 512857		
381	AW463263	0.4021	0.0329	0.1067	0.0814	MAD, mothers against decapentaplegic homolog 6 (<i>Drosophila</i>)	MADH6	AF043640	Hs. 153863		
382	AW463937	0.525	0.0696	0.3736	0.0217	Transcribed sequences		CB452876	Bt. 18990		
286	AW464067	-0.3792	0.0101	-0.3797	0.0694	bromodomain containing 1	BRD1	BU431018	Hs. 370880		
265	AW464094	-0.2674	0.0090	-0.2342	0.0342	programmed cell death 6 interacting protein	PDCD6IP	CA748765	Hs. 9663		
383	AW464391	0.377	0.077	0.3149	0.0394	PDCD7		NM_005707	Hs. 143253		
384	AW465097	0.1522	0.0646	0.2588	0.0372	C13orf12		BI463840	Hs. 268742		
385	AW465151	-0.2231	0.0242	0.2027	0.0790	chromosome 13 open reading frame 12		NT_011630.14			
386	AW465276	0.4732	0.0463	0.2469	0.0792	eukaryotic translation initiation factor 2B, subunit 2	EIF2B2	AF055280	Hs. 497429		
387	AW465299	-0.229	0.0668	0.3145	0.0065	delta-like 1 homolog (<i>Drosophila</i>)	DLK1	BX438936	Hs. 169228		

TABLE III-continued

List of differentially expressed genes in blood and liver that predict PTA for milk production									
SEQ ID NO:	GenBank ID	Raw_P Contrast Blood	Raw_P Blood	Raw_P Contrast Liver	Gene Name	Gene Symbol	GenBank ID	Best hit	UniGene
388	AW465351	-0.3094	0.0484	-0.3639	0.0849	dynactin 6	DCTN6	D84145	Hs.158427
389	AW465482	-0.2549	0.0206	-0.2398	0.0320	sphingosine kinase 2	SPHK2	BU542495	Hs.444484
390	AW465514	-0.2266	0.0584	-0.3396	0.0050	coatomer protein complex, subunit epsilon	COPE	CA489097	Hs.10326
391	AW465560	-1.3432	0.0395	-0.3041	0.0682	collagen, type IV, alpha 1	COL4A1	X03963	Hs.437173
392	AW465567	0.212	0.0910	-0.2997	0.0866	B-cell receptor-associated protein 31	BCAP31	BM843607	Hs.381232
271	AW465653	-0.3354	0.0094	-0.2781	0.0610	transcription factor, RNA polymerase 1	UBTF	BQ640761	Hs.89781
138	AW465666	-0.6116	0.0027	-0.1812	0.0502	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	PTPLB	AK074605	Hs.5957
260	AW465703	-0.2604	0.0086	0.366	0.0860	Transcribed sequences		AW465703	Bt.9668
393	AW465831	-0.1632	0.0760	-0.2589	0.0435	transmembrane protein 4	TMEM4	BX406238	Hs.8752
394	AW466194	0.4396	0.0889	0.367	0.0645	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	ITGA3	BC015344	Hs.265829
11	BF039212	-0.6029	0.0000	-0.3867	0.0241	asparaginyl-tRNA synthetase	NARS	AJ000334	Hs.427212
69	BF041193	-0.3333	0.0011	-0.2739	0.0718	translocase of outer mitochondrial membrane 22 homolog (yeast)	TOMM22	BM554645	Hs.285005
395	BF041753	-0.4868	0.0478	-0.2771	0.0633	heat shock 60 kDa protein 1 (chaperonin)	HSPD1	AU133536	Hs.79037
338	BF041789	-0.3145	0.0122	-0.4083	0.0569	serine palmitoyltransferase, long chain base subunit 2	SPTLC2	AB011098	Hs.59403
396	BF042071	-0.2126	0.0977	0.2389	0.0678	DKFZP547E1010 protein	DKFZP547E1010	AA314101	Hs.323817
297	BF042477	-0.4078	0.0105	-0.214	0.0895	eukaryotic translation initiation factor 5	EIF5	BC007728	Hs.433702
397	BF043039	0.1179	0.0774	-0.5652	0.0377	chromosome 14 open reading frame 73	C14orf73	BU607548	Hs.37712
398	BF043954	-0.2387	0.0420	0.5434	0.0113	histone deacetylase 7A	HDAC7A	BQ646129	Hs.200063
399	BF044362	-0.7126	0.0144	0.3266	0.0665	similar to RIKEN cDNA 4931428D14 gene	MGC15407	BI603780	Hs.23128
400	BF044484	0.2955	0.0732	-0.3049	0.0166	XTP3-transactivated protein B	XTP3TPB	BU929539	Hs.438336
401	BF044941	-0.3714	0.0347	0.2297	0.0145	replication factor C (activator 1) 4, 37 kDa	RFC4	BM979151	Hs.35120
402	BF440189	0.328	0.0491	-0.1995	0.0208	kin of IRE like (<i>Drosophila</i>)	KIRREL	CA446859	Hs.375003
58	BF440195	0.7274	0.0008	0.2697	0.0765	proteasome (prosome, macropain) subunit, alpha type, 3	PSMA3	CA431411	Hs.246240
403	BF440274	0.1769	0.0878	0.2317	0.0270	CD81 antigen target of antiproliferative polypeptide 1	CD81	BM920185	Hs.544577
301	BF440363	-0.442	0.0108	-0.1713	0.0943	polymerase (RNA) II (DNA directed) polypeptide B,	POLR2B	AF055028	Hs.149353
404	BF440607	0.2531	0.0349	0.2189	0.0341	dynein, cytoplasmic, light polypeptide 2A	DNCI2A	BU932718	Hs.100002
405	BM362313	-0.4653	0.0620	-0.4666	0.0475	malate dehydrogenase 2, NAD (mitochondrial)	MDH2	BX460531	Hs.405860
406	BM364049	-0.382	0.0275	-0.3626	0.0366	poly(A) binding protein, nuclear 1	PABPN1	BU68740	Hs.117176
79	BM366522	-0.5962	0.0011	-0.4707	0.0191	calmodulin 2 (phosphorylase kinase, delta)	CALM2	CA441246	Hs.425808
407	BM366788	-0.2606	0.0614	0.4313	0.0448				
408	BP22000602103	0.3438	0.0164	-0.2543	0.0106				

TABLE IV

Genetic estimates and pedigree information of selected animals used for microarray experiments

No.	Classification	Barn/Ctrl ²	Identification	Registration	PTA Milk ¹	PTA Protein	PTA Fat
1	Low	#7298	Illini Mason Susan	#60046145	-68	9	5
2		#7321	Illini Leader Lassie	#60046168	-151	4	-2
3		#7350	Illini Leader EDI-TW	#60274143	-203	2	-15
4		#7351	Illini Leader Edeth TW-	#60274144	-203	2	-15
			TW				
5		#7355	Illini Premier Karen	#60274148	-17	-2	11
6	High	#7305	Illini Marty Glee	#60046152	1178	34	18
7		#7344	Illini Conviner Suzanne	#60274137	1416	33	42
8		#7361	Illini Storm Glee	#60274154	1108	34	48
9		#7367	Illini Emerson Della	#60274160	953	27	31
10		#7368	Illini Emerson Klara	#60274161	1111	33	35
11	Low	#7497	Illini Progress Edith	#60274290	-219	-9	15M
12		#7556	Illini Roman Tillie	#60712800	304	6	16
13		#7584	Illini Outside Milly	#60712828	507	12	24M
14		#7589	Illini Estimate Leota	#60712833	194	17	41M
15		#7590	Illini Luck Tillie	#60712834	115	12	26M
16	High	#7499	Illini Marshall Suzanne	#60274292	1987	49	34M
17		#7518	Illini Inquirer Romance	#60274311	1536	35	40M
18		#7536	Illini Kino Joyce	#60712780	1569	30	27M
19		#7553	Illini Emerson Kara	#60712797	1257	44	38
20		#7554	Illini Jasper Suzanne	#60712798	1240	33	54

¹Herds were selected based on PTA Milk values. Values of PTA protein and fat are cited for reference.

²Age - 7298, 7305-13 month; 7321, 7344-11 month; 7350, 7361, 7351, 7367, 7355, 7368-11 month; 7367, 7368-10 month.

PUBLICATIONS CITED

The following documents are incorporated by reference to the extent they relate to the materials and methods of the present disclosure.

Ashburner et al. (2000) Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. *Nature Genetics* 25(1):25-9.

Band et al. (2000) An ordered comparative map of the cattle and human genomes. *Genome Research* 10(9):1359-68.

Band, et al. (2002) A 3,800 gene microarray for cattle functional genomics: comparison of gene expression in spleen, placenta, and brain. *Animal Biotechnology* 13(i): 163-72.

Benjamini, Y. and Hochberg, Y. (1995), "Controlling the False Discovery Rate: a practical and powerful approach to multiple testing," *Journal of the Royal Statistical Society. B*, 57, 289-300.

Brown and Botstein (1999) Exploring the new world of the genome with DNA microarrays. *Nature Genetics* 21, 33-37.

Cook, R. D. (1977) Detection of influential observations in linear regression. *Technometrics*, 19, 15-18.

30 Diehl et al., (2000) Manufacturing DNA microarrays of high spot homogeneity and reduced background signal. *Nucleic Acids Research* 29(7).

Eisen et al. (1998) Cluster analysis and display of genome-wide expression patterns. *PNAS (USA)* 95: 14863-14868.

35 Hegde et al. (2000) A concise guide to cDNA microarray analysis. *Biotechniques* 29(3):548-50.

Huang and Madan (1999) CAP3: A DNA sequence assembly program. *Genome Research* 9(9):868-77.

40 Klecka, W. R. (1980), Discriminant Analysis, Sage University Paper Series on Quantitative Applications in the Social Sciences, Series No. 07-019, Beverly Hills: Sage Publications.

Smith and Green (1999) (Unpublished) Repeatmasker, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>.

U.S. Pat. No. 6,548,740.

<http://gowhite.ans.msu.edu>.

Yao, J. et al. (2001) Generation of EST and cDNA microarray resources for the study of bovine immunobiology. *Acta Vet. Scand.* 42(3): 391-405.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 408

<210> SEQ ID NO 1
<211> LENGTH: 385
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 1

gcacgaggcg ggatcgaggg gcagcagcgt acggtaagg acacaggccg tggagtttga

60

-continued

accccttcaa agattgaaat catggcaggt ccagaagctg atgcccagg ttccat	120
ggtatcaaaa aatatttcaa ctcttacact ctcacaggga gaatgaatg ttttgtggcc	180
acatacggaa gtattgcttt gatagtctta tacttcaagt taaggctaa aaaaactcca	240
gttgtgaaag caacataaac agattcttag ctgtacatta tctgttaagt tcccatgcct	300
gaagaagcta atgtcaactc atcatgtgat actcaatttg tacaataaat tatgaacctg	360
aaaaaaaaaaaa aaaaaaaaaa aaaaa	385

```

<210> SEQ ID NO 2
<211> LENGTH: 565
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (114)..(117)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (311)..(312)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (392)..(393)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (484)..(485)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

```

<400> SEQUENCE: 2

tttttttttt ttttttgac tatctacaaa aattttattgt ctatTTTACAG aagaaaAGCA	60
tgcgtatcat taaaacaaat aaaatgtgtt ttctcacagc gcagtgatTTTNNNNAAA	120
aaaatTTTTT taagctgtat cacagaaaca agacacaagg atTTTTAAAG agagctaaAC	180
actcatcatt cgaggtgcaa tactcatgga catgagttcc tggaaacaaca gtttgcacGC	240
ataaggcatt cgaaccaaAG agatctgggt tttatTCGG cagccccCTGC attcgatGT	300
atgggttcTG nngttcgaa ttgcCATTAT tccacaaAGA ttgcaaacGT gAACCTGATA	360
cggatctgac gcctcaaACA acctctCCCT tnnaaACTGG gctgctccat gCGCGATCTG	420
acagtctcgt tccatctctc caaaACGCA GCCACCATCA CGAGATCTAC CCTCCATCGG	480
ctgnntattt agaatctgaa taggtccccG agcacgagaa tgaatTTTAT catccaccat	540
atgcttcaa CGCTGGTAGT aagta	565

```

<210> SEQ ID NO 3
<211> LENGTH: 478
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

```

<400> SEQUENCE: 3

gcacgagAGC CGGCGTCTCA gaggagtGCA gacgctGCTG GTGACCCGTG GGCGeGTCTC	60
tgtggggcCA ggaactgaaa gagagccaa atggctgaaa atgggtataa tgaaaaATG	120
gtgtgtctgg aggccaaat ctgtcatcaa attgagtatt atTTTGGAGA CTTCAATTG	180
ccacgggaca aattttaaa ggaacagatc aaactggatg aaggctgggt acctttggag	240
ataatgataa agtttaatAG gttaaACCgt ttaacgacAG acTTTAATGT aatAGTAGAG	300
gccctgagca aatcaaAGGC agaactcatG gaaataAGTG aagataAAAC taaaATTAGA	360
agatctccaa gcaaaACCTCT CCCTGAAGTG ACTGATGAGT ataaaaATGA tggaaaaaac	420
agatctgttt atattaaAGG CTTCCGACA gatgcagCTC ttgatgacat AAAAGAAT	478

-continued

<210> SEQ ID NO 4
<211> LENGTH: 566
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 4

gcacgagcgg	cgaggagcgg	caccacacc	gtgtgtcgcc	ggtgagtccc	ggccagcccc	60
agctgcacgt	cccagccccc	gggagacgcc	ggaaaaaaacg	gaaggacctg	ggattccaga	120
gcagtcgccc	ctgactgctg	ctctccctgcc	gttgcccgcc	cgaggagcttc	cgcaactcgcc	180
gtctgaagacg	cgcccttgac	aggccttagag	gcctaggcgc	ggccctccga	gccccacgtg	240
ttggcccgcc	tgcagctgtg	agtaatccga	gegctctctc	cacggccgtt	tacagattaa	300
aatggaggaa	atttccttgg	ctaaccttga	tactaacaag	ctggaggcca	tcgctcagga	360
gatatacgtt	gacctgatag	aggattcttg	tttgggcttc	tgctttgagg	tgcacccggc	420
agtcaagtgt	ggctacttct	accttggaaatt	cgcagagact	ggtaacgtga	aggattttgg	480
cattcagcca	gttgaagata	aaggagcgtg	tcgcctcccg	ctttgtccc	ttccctggaga	540
atctggaaat	gggcctgatc	agcagc				566

<210> SEQ ID NO 5
<211> LENGTH: 465
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 5

gcacgagatg	gcgcctgtga	aaaagcttgt	ggcgaagggg	ggcaaaaaaaaa	aagaagcaag	60
tccctaaatt	cactctggac	tgtacccacc	ctgtagaaga	tggaatcatg	gatgtgccca	120
attttgagca	gttttttcag	gagaggatca	aggtgaatgg	aaaagctggc	aacctggcg	180
gcgggtgtgt	aacaattgaa	agaagcaaga	gcaagattac	tgttaacttcc	gaggtgcct	240
tttccaaag	gtatattgaaa	tatcttacca	aaaaatattt	gaagaagaat	aatctacag	300
atgggttacg	cgttagtcgt	aacagcaaag	aaagttacga	attgcgttac	ttccagatta	360
atcaagatga	agaagaggag	gaagatgagg	attaaaactc	aatctggaat	atttgataa	420
gttcttaaat	aaaatttac	aactgaaaaa	aaaaaaaaaa	aaaaaa		465

<210> SEQ ID NO 6
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 6

gcacgagggt	gatgtcctgt	atctgatgcc	ttgttgcgg	cgaaagtaag	cgagctccag	60
aggagtgcgg	agaaattcaa	gttccctctg	ctgttaacttc	atcagccgc	caagatggcg	120
atgcaagcgg	ccaagagggc	gaacattcga	cttccaccag	aagtaaatcg	gattttgtat	180
ataagaaatt	tgccttacaa	aatcacagct	gaagaaatgt	atgatattat	tggaaatata	240
ggacctattc	gtcaaattcag	agtggggAAC	acacctgaaa	ctagaggaac	agcttatgtg	300
gtctatgagg	acatcttga	tgccaagaat	gcatgtgatc	acctgtcagg	attcaatgtt	360
tgtaacagat	acctt					375

<210> SEQ ID NO 7
<211> LENGTH: 374
<212> TYPE: DNA

-continued

<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (329)..(331)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 7

gcacgaggga	cgcgcattggcg	accacacatcg	agcagatttt	taggtcttc	gtggtcagta	60
aattccggga	aattcaacag	gaactatcaa	gtgaaaggag	tgaaggacag	ctcaatggtg	120
aaacaaaacac	acctattgaa	gaaaccagg	caggtgtatgc	agctgcctct	gccaggaacc	180
tacccaaatga	agacatagtt	cagaagatag	aggaagtact	ttctggggtc	ttagatacag	240
aattacgata	taagccagac	ttgaaggagg	catccagaaa	aagttagatgt	gtgtctgtcc	300
aaacagatcc	tactgtatgaa	attcttacnn	naaagtcgaa	gaagcataaa	aagcacaaaa	360
aaaaaaaaaa	aaaa					374

<210> SEQ ID NO 8
<211> LENGTH: 546
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 8

tctctgtctg	cagtggtcca	caccatct	ccgcataacc	cggcctcagc	ctggctgcca	60
cgggcgcgc	acctgcccgg	gctgcctcta	gaggcggcaa	gatgttgagc	gcggcacgga	120
ggatccaggc	ctactggcct	agtctggggcg	agagccggaa	ggccacgtgg	ttctcaggcg	180
cagtggaaaga	agccggaccc	tgtgtggcc	acgcctgtct	ccacgcgcag	gccctcgccg	240
ccctgtgtcg	cggtgtgacg	gttccagaa	tgtcccagta	gtatgtctt	gacacacagg	300
atttatgttgc	gccagaagat	tccaggatga	ctgaagctaa	cctttcttgt	gagtgaagag	360
gacatgacag	ggatgaaacg	aaagcctcg	gaccgggtt	ccccccgtt	tttaactggc	420
agtgcctgac	actgaagtaa	ctgaaaatac	cacccgttca	ctggagocgt	ccttttagaat	480
aagacctgtt	gccagtaaag	ctgtcttcat	ctgtgcggat	ctacagagtt	gggagagaac	540
caaaaa						546

<210> SEQ ID NO 9
<211> LENGTH: 272
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (126)..(126)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 9

tttttttttt	ttttttttct	tgtcccccgtc	cttctttctct	tcttccttctt	catctgagcc	60
aacatcttct	atctcgggct	tgtcatcaa	ctccctttct	tctttctct	tctcttcctc	120
tttgtnttcc	ttctcttctg	cttcatcatc	actaactct	ttatcacgtt	cctttccac	180
cttcaaaagga	ggacaaaatct	tgtcacctct	ccatcacaaa	accgggggaa	aaaagctaaa	240
ggagactgca	gcacttacac	caacgcccacc	tg			272

<210> SEQ ID NO 10
<211> LENGTH: 605
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base

-continued

<222> LOCATION: (507) .. (507)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<400> SEQUENCE: 10

tttttttttt	tttaaggca	acaaaaagct	tcaatctctt	ctccaagtaa	acagaactag	60	
tacagtata	tat	ttctgg	aacatgtacc	cccgagaag	taacacaaga	gttaaagggg	120
gc	cctctctg	aacacactca	cacactcccc	cctaccccaa	tgaaccagtc	tctctctcac	180
acc	ccacgcac	acacagagct	attcacaggc	gcaaatgtat	actatgtaca	aacacacaga	240
tccgggtt	tc	cctcaagtc	tctggcaga	ctgcccacca	gagaggaggg	atgggctaag	300
gcaagg	gggaa	gaaacaagga	accagtct	ggaaggaaac	cagctgagcc	gtgagtttg	360
agg	tgcttag	ggcgtgtct	cttctcgat	tccaagatgc	agcattgtag	agttggggtt	420
ggcgg	tttgc	aatcaacaa	aaggaaaaca	aaagaacccg	aggagaatgg	tcgggatgga	480
ta	cagagtgc	cagggttgg	gcccagngac	agagatgtct	gagcgttcac	acagagacta	540
ggc	cgaggagg	aaaaagtgc	aatcgaggca	acgtgttgc	agtcttctt	gtttgatttgc	600
gg	tg	tc					605

<210> SEQ ID NO 11
<211> LENGTH: 452
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (397) .. (398)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<400> SEQUENCE: 11

gcattttttt	tttttaagag	gcagtctgtt	cttccatga	accgttgtct	60	
ctccctaaag	ctctgggggt	tggggggacc	gatcatggct	tgcagcgctg	gacaaaccga	120
gggtacaaac	acacatctcg	gatgtggat	ctgtccagaa	tccaggttaa	gaatcgatcc	180
aaggcccaggc	catagccgccc	atgtggacac	gtgccatatt	ttctctgatc	cgtgtaccag	240
taatagggag	tggatcaat	cccttctt	ttgtaacctg	ccaggatctc	ttcattatcc	300
cagatacgc	tggagccacc	cacgatctca	ccaacattgg	gcatcaacac	gtcgacagat	360
tcggtgagcc	gggggtgatg	acggagcgcg	ccttcannat	tttggacatg	ttctccccgc	420
ggatcatcat	gtgtctgttgc	ttgagctgga	cg			452

<210> SEQ ID NO 12
<211> LENGTH: 251
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<400> SEQUENCE: 12

ttttttttt	ttttttttt	tgagggaaac	ataagcagag	tggcgtaact	tggtttattg	60
tattctgaag	tgtcatgggg	ggccggggag	gggtgctgaa	aacaagcctg	ctttatcagc	120
agttctaaag	ccttatcacc	tgagatttgc	attctggaaa	caaaatcatg	attgcagttat	180
cagcacatat	gtcctgtgag	atctgggttc	cagccctgg	ggatggctgg	actaacctga	240
cgtgagg	tca	c				251

<210> SEQ ID NO 13
<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:

-continued

```

<221> NAME/KEY: modified_base
<222> LOCATION: (120)..(121)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (132)..(133)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (149)..(151)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (184)..(185)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (266)..(266)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 13

atccgaccac gtgacgactg gcatcctcggtcaagcccc agagtctgg gcgggacacc      60
ggactggccc agcccaagctt gggggccccc tcgttagctgc caaaggagaa ggaaacacgn     120
nccgtggagc tnncaccaag cgggtgcgnnc nccgccccac cgaaaccggc agagtctgct     180
tctnncccaag tgaggagcag cgtctgttag gtgcagccaa acggggacaa agtgaacaac     240
gecccgctgcc cgcagtcaca ctcagnccgt agtacacaccc ccagaacaag cagctccca     300
gggacagacg agcagcccttg tgccggaaagc tcgtggcga                         339

<210> SEQ ID NO 14
<211> LENGTH: 400
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (319)..(319)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (321)..(323)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 14

tttacagaat aatatgcaga aatgccacta tcttagttact tggctctaca taagcaaaga      60
ctatcctgtc ttttgtgtga ctgaacttag aatgtctcc tctggaaatg gaaaagtacc     120
tgtttaggaa gctaagtgac agaaggagtt atcaaacttg actccatata gataatgaac     180
agtttaggg aagcattttt cttggaaacta agaaggactt acctgacatt ggcttcattc     240
tggccttcac ttgttcataa gaatcatgga accagagttt gagttaagaa acttggaaaa     300
agcagctgaa aacatctcng nnncactta acaatttaaa aattccactt aagatgctaa     360
ataatccatt gcttatgttag caactcaacg atgttctcaa                           400

<210> SEQ ID NO 15
<211> LENGTH: 523
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 15

tttatgagca gctagaatgt gctgcaacag aagaagctgc gacacgcccag tggggccaac      60
atcactaactcg cagccactgc tgctaccaca gcggccacgg ccactgcccac caccaccagc    120
accgagggca gcaacagcga gagcgaggct gagagcaccc agaacagccc taccggctt     180
cctctgcaga agaaggctac tgaggatttg tccaaaaccc tcttgatgtca cactgtccct    240

```

-continued

gtgttcagg gtttccgg ttccatctcc ttgtcacgag gcaacaacct ccaggacacg 300
 ctcagagtcc tcacattatg gttgattat ggtcaactggc cagatgtaaa tgaaggctta 360
 gtggaaagggg tgaaagcaat ccagattgac acttggttac aggttatacc acagetcatt 420
 gcaagaattt atacgccaag gccccgttg ggacgttta tccaccagct tctcacagac 480
 attggtcggt accacccca ggcctcatc tacccactga cag 523

<210> SEQ ID NO 16

<211> LENGTH: 383

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 16

ggggttcagg atcaccaggg ccggtctgac tttcaacccc atgtgtccgg tggggatctc 60
 tgcagtgtgt gtctctggca tctcttacca ggggagcagg ctgtacttct ccctctctgt 120
 gggcttcgtg acagtcgagg tcacggccca ggcagggcct tggggccctt ctctggaaac 180
 cgagctgtgg ccgtacgta ctcgcctccc cctgcctcca ggacggagag tctgtttcc 240
 ctgctcagcg ggtcgatatac aaaggtcagg cctgtaggcc gcacgegctg ccccacgaac 300
 ttccctggag gctttctaaa gacgttgaac agctgccccg agcccgagg ccccgctctg 360
 ggacaccctt gggccctgaa gct 383

<210> SEQ ID NO 17

<211> LENGTH: 512

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 17

cgctcgaaag gtccccggtg tgcactcctt cagcaggccct tgggggaaga tggcgccct 60
 gggggacggt caggagcccc ctcatgtctt gtcccccggtc agtttcgagt cacccggac 120
 acctggagcc caccaccatg aagcccaact tcacctccac ctccatggtc atcaacatgc 180
 agcagccctg aggtgccctc ccagccccca caggagccgt cagacctgga cttcaagag 240
 gtggcagagg tccatgtcg cagagacacc tgctggtcag gttctgagtc ggagccggag 300
 caggccccgt cgtctccag cccgcacggt cctaagacga ggtgcaccag gccggaggcg 360
 tgctgaggac cctgtcgagg agccttcccc gcagacccgg gggtggggac cgctttggc 420
 aggagccag cctggagccgg tcagcaggcc agacaccgag ggctggccccc cgcttccaga 480
 agagagacac ctggctcggt tcgcaggggg cc 512

<210> SEQ ID NO 18

<211> LENGTH: 635

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 18

gccccggtgt actctgggggt ggtgttaagg cggcgccaga tcgaccctcg actgaggaga 60
 ggcagtgcgg ttcccttagg cgcttctccg ttgggttctc cggcttccctc agcctctca 120
 ccacccggcg ggacccgaga gtcgggtgtc tgccccaccc ctgaccggc tagagacatg 180
 tccaccccggtc tccggggcg tctcatgagg gacttcaaga ggttgcagga ggatcctcca 240
 gecggagtc gccccggctcc gtctgagaac aacatcatgg tttgaaacgc ggtcatttt 300
 gggcctgaag ggacccggtt tgaggatgga accttaagc ttacaataga attcactgag 360

-continued

gaatatccaa ataaggcacc aacggtaga tttgtctcta agatgtcca tccaaatgtc	420
tatgcagatg gtagcatatg tctggacata cttcagaacc gttggagtcc aacctatgat	480
gtgtcttcca tttaaacatc catacagtct ctactggatg aacccaatcc caatagtcca	540
gcaaatagcc aggctgctca gctgtaccag gagaacaagc gggagtatga aaaacgtgtt	600
tctgcgatag tagaacagag ctggcggtac tgttg	635

<210> SEQ ID NO 19

<211> LENGTH: 617

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 19

ggaggagtag gacggggaaa acactttctc ccccacaaaat tcataaaaaaag agcatttaaa	60
cgtcgagtaa attccacaaa acaacttctg aatgccggca gaggacatca ggcacccaga	120
aaagcaaccc aactcttcga aaggagtttt taccaacgct tcagacccga gtttctggtg	180
agaaatggct tcactgatgc gtcatctctt gccgtgtgca aaagtgtgg gcacagcacc	240
caattccgca gacagtggag ccaagtgggc tgcgtcgact ggccgtataa acagcagctc	300
tacaggtggc ttcttttaag caatctgtg gaagcatgtt cggcctgtcc accagtctgt	360
caactgaagt tatgttcaag aatttccaaac tctaggggaga ataaatcaca caagttctac	420
ctaccttaaa gacgactgtg agatttgaga ggtactgaag atgaaaggcac ttccaatgtg	480
tgaggaggtt aaaaaaatgt tactcatcat tatgataaaa ataaccataa tgatgaagat	540
gttggtaact gctctaattt gttttttttt tgttttatct cacacagacc atatgcaatt	600
aaagcttta ttaaattc	617

<210> SEQ ID NO 20

<211> LENGTH: 572

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (481)..(481)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 20

gcacgagccc aatccctcctc ccaccctagt tgccaaatgac cacacggctg ttatcaggta	60
aatgacccctt aatccagcccc ctgcctcgcc cacaaggctt cgggggtgac agccaggccc	120
caggggacag gccggggcag ggccggggac cctcageggc acgattcccc agcgegccta	180
ggtgttgcgt acgaccagcg actgctccag ctctgcctg cgctgtggta tctgttaagga	240
aaggagagca ggcgcagggt accagttgtt ggcgcgcgcgc agggcccccctt caccttggagg	300
tcccgactct gggagcggag gaggtcctgg atgtageccct tggggctctt ggagaagctc	360
agcatgaagt ccctctggat cttgagctgg ttgtatggact caatcgctc gtggatctgc	420
agtgcgcaggc tccagccccca ctttactgtc cagagcgctg atctccctgtt ggttggccgt	480
ngacagcagg aagctgctca tctgtccctt caggggtcc tccacttcca cgtcaatgtc	540
gttagcagcc gtctttttt ggtccgacgg gt	572

<210> SEQ ID NO 21

<211> LENGTH: 420

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 21

-continued

gcacgaggc gcaatggtga agctgagcaa agaggccaag cagaggctgc agcagcttt	60
caagggagga caattgccca tccgctgggg ttttattcct ctgcgtgattt acctgggatt	120
taagagggggt gcagatcctg gaatgcctga accaactgtt ttgagettac tttggggata	180
aaggactgtt tggcatctg gtttggaa cagtcaatgc agaggaacaa catggaaagg	240
gtgctctctg gctggataa gagatggac atcggtcaga cggtcaccag ttggatggca	300
cagggctctt acttctcaga tgcatctgtt gcagagtgg aacctactg acttatttat	360
gatagactgt attaaaataa atgttttaa caatgttaaa aaaaaaaaaaaaaaaact	420

<210> SEQ ID NO 22

<211> LENGTH: 274

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 22

gcacgaggc gcctggccc ccgtgggtgt gttaaacggg tttctgggtt catctacgag	60
gagacccgcg ggggtgtgaa ggtgttcctg gagaacgtga tccgggacgc ggtcacctac	120
accgagcacg ccaagcgcaa aactgtcacc gccatggacg tggtctacgc gctgaagcgc	180
cagggacgc ctctctacgg ctteggcggt taagttccag gcagccattt ggcatagtct	240
aataaaacca aaggccctt tcagggccac acaa	274

<210> SEQ ID NO 23

<211> LENGTH: 439

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 23

tgtactttt acccagtctg acttggtttt gttttgttct gtttttttcc cccctggaat	60
acaggacggg accaggggccc ttgtactcgg agccaagctg ctctccaggc attgtgttaag	120
cctcttgtgt tggctctct ttcaggttagg ataattgcgg actgaaccct cgggctgcgg	180
tcatatatga gaacttgctc cgccgcggtcc ccttgcggg gatgtttcca ttgcttcatg	240
tttcagtaaa caaaggagtt tggatccaaat tatgttttct ttcttaattt aattcttcta	300
cattcacttt tctctcttcc tggtactagt ctctgttagcc ttctgttcc tctcggtccc	360
agectctgag cagccctagg taaggattat gttggcgtcc ctttctcct gtacaggggg	420
atcccttta tcttgcttt	439

<210> SEQ ID NO 24

<211> LENGTH: 239

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 24

atgatgtct tcaatgtatgg caccttcag gtgaatttct accatgatca taaaaata	60
atcatctgta gccaaaatga agaatacctt ctcacccata tcaatgagga caggatatct	120
acaacttttta gactgacaac tcttctgtatg tctggctgtt cgtagaaatt aaaaaatcga	180
atggaatacg ctctgaacat gctcttacag aggtgtactt aggagattc ttgaacgga	239

<210> SEQ ID NO 25

<211> LENGTH: 524

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

-continued

<400> SEQUENCE: 25

ttgatecaacc	tgccaaatgg	ctacggatgt	tttttggattg	cctgtatgac	gaggaggtga	60
tctctgagga	tgccttctac	aagtggaga	gcagcaagga	ccggcagag	cagaatggga	120
agggtgtggc	cctgaagtct	gtcacggcgt	tcttcacatg	gctgcgggaa	gcagaagagg	180
agtctgagga	taactaaaac	ttcaaataca	caaaacgaaa	aaaaagaaaac	aatttaagta	240
ttttttaaa	aagtttacg	tcttcgcca	tcacagtgc	gcaaggccaa	ttctcgacaga	300
aaccccccacg	tgtgcacgag	tgggaaaggg	gaaagagaaa	aaaaaagggtg	atcatggagg	360
aaaaaggtac	tggaaaaaaaaa	gtaaaacttca	aacctgaggg	cgggagact	aaaacccaaa	420
tacatgtatt	atttatagaa	aatatttct	gtttaatct	tttctttta	aatgaggact	480
catactttaa	aaaaaaacac	atctgtttag	caaaaaaaaaa	aaaa		524

<210> SEQ ID NO 26

<211> LENGTH: 519

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 26

agggtccctt	ccaccaccta	ggccttggg	tgggggtctt	ggtcttgca	ccccatgcac	60
gtctgtttcc	tatgaggctg	agcagggacc	agggcctgag	agggaggcgt	ggcccgagg	120
agaggtgagg	ccttgctcag	ggccctgggc	ctcagttcc	ctctgtgaaa	tgggtgtatg	180
caggctcg	ggggccggca	gggttggagc	ttctgttgtt	tggagctgcc	cacccttcca	240
cacgcccagg	gatgacgagg	gtgggcagtc	tcacctcccg	gtccccagc	caaacctggg	300
ggggccatct	gtacccctcc	tcgtttctg	gtgtcggtt	cctgaccctg	aggtaagct	360
acctgatctg	actggatgtt	cagggccctt	tatgtcaatt	ctgaccctg	aaccctcagt	420
cccttccatg	gtctggggga	ggggccacc	tgcttccaca	cccgcttgc	acagecccg	480
caggttagatg	ogtatacagcc	aataaaggcc	cccgccctga			519

<210> SEQ ID NO 27

<211> LENGTH: 534

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 27

tgtgggtgtgg	cgggcagggtg	acctcgaggc	tgcggtgacc	atggggccgc	agtttgggca	60
tctgacacgg	gtgcggcatg	tatgacaccta	cagctgtcg	cccttgcgc	agcgcgcctt	120
cccgcaactac	ttcagcaagg	gcattccaa	cgttctgcgc	cgaactcggg	cgtgcattct	180
tccgcgtcg	ccgcgtgagt	gccctggccg	ggcggagagg	ctagactccc	atccacagag	240
ggtattgcgg	gtcccccctag	tgagcaactt	gcagctgc	ataaacacgc	tttctcttc	300
agtagtcctg	aatgcgttg	aactggtcat	gtcttcgc	tcttacagat	aaaggagtt	360
ggtcacacag	aaatgactgg	ctcaaggta	cttgtgtat	tccagggtct	ccctctgagc	420
tcacctttac	ccacttctt	cctagcagt	aactgtttt	tgttaaaggt	gcagcagatt	480
gtgatgatag	ttgcacattt	cgactttgt	aaaacccaca	gaagtgtaca	tttc	534

<210> SEQ ID NO 28

<211> LENGTH: 453

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 28

-continued

gcacgagctt ggttggggc gtccgcata taaggcagga agatggtggc cgcaaagaag	60
acgaaaaagt cactggagtc gatcaactct aggctccagc tggtatgaa aagtggaaag	120
tacgtgtcg ggtacaaaca gactctgaaa atgatcagac aaggcaaagc gaaactggc	180
attctcgcca acaactgccc agccttgagg aaatctgaaa tagagtatta cgccatgtt	240
gccaactg gtgtccatca ctacagtgcc aataatattt aattggcac agcatgtgga	300
aaatactaca gagtatgcac actggctatc attgatccag gtgattctga tattattaga	360
agcatgccag aacagactgg tgaaaagtaa atcatgtaca attttcttt aataaaactg	420
gccagagctt gttttaaaaa aaaaaaaaaaaa aaa	453

<210> SEQ ID NO 29

<211> LENGTH: 374

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 29

ttgaaggtgt ctgaagagtc ttcaatcact atgtcaagcg acacagatat ttctttct	60
tcatatgtat aagatcaggg atctaaactt atccgaaaag ctagagaggc accatttgc	120
cccatatggaa tggcagggtt tgcagcaatt gttgcataatg gattatataatg attgaagagc	180
agggggacata ctaaaatgtc tggtcacctg atccacatgc gtgtggcagc ccaaggctt	240
gttggggag caatgactct tggtatggc tattccctgt atcaagaatt ctggggaaa	300
cctaaacctt agaagaggag atgctgttgg ggtcgcttgg gtggcgctt cttagttag	360
acatctcata ttga	374

<210> SEQ ID NO 30

<211> LENGTH: 496

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 30

gcacgagagt ggagccgctg ggccgcagcc gggaaagctta gatgtggagg cgctgagact	60
taggagacac ctggggccgt tagggagact caggtggcg gacactggg ggtatcccac	120
ctgaccctgg gccagtctcg ttctcgccgc ccgcctctcc acccccccc cacttgggc	180
tgaagtggct ccgcctctg atctgagcct ggtccctt caggcactga cccttgcacct	240
cggggcgctc cccatcctt tggcgcgat ggctacaggc gcggatgtcc gggacattct	300
agaactcggg ggtccagagg gagacgcgc ctctggacc atcagcaaga aggacattat	360
caatccggac aaaaaaaagt ccaagaagtc ctcggagaca ctgacccatca agaggcccga	420
gggcacatgcac cgggaggct atgcactgtct ctactctgac aagaaggacg cgccccact	480
gttacccact gacact	496

<210> SEQ ID NO 31

<211> LENGTH: 552

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 31

tgattcagaa atagaatcgc tctgtatgtct gaaggccc tctgtcccaa aactaaaaag	60
ttcttattga accgtcttct ctccaggaag caaatggctt tggaaagtctt ccacccagc	120
caagccaatg tttccaagga aaagcttggt gaactcatttgc ttaagaagtt caaggctgac	180

-continued

gccaagaacg ttgtcacctt cgggttccac actcacttcg gtgggtggcag aagtactgga	240
ttctgcttgg tatacgacaa ccgtgactac ttgttgaagt acgaacccaa atacagactc	300
agaagactga aaatcttgg accaaagctt aacaacagaaa aggccagaaaa ggaattgaga	360
accaagagaa agaaggctcg aggaaaggaa aagtccaaga tccaagccgg aaagaagaag	420
ttaaggatca tatgctccct ttatatggct ggtcgactcg gaatatttgc tgctgtattt	480
gttctttct atgtgcgcgt atagttcatg catgaatctg aaaactgaaa ccataattta	540
gcaaacaaaa ag	552

<210> SEQ ID NO 32

<211> LENGTH: 453

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 32

gccgtccaga cagcaagaca gaaaaccggc gcatcacaca catctctgcg gagcagaaga	60
ggcggttcaa catcaagctg ggcttgaca cgctgcacgg gctggtgagc acactcagca	120
cccagccaa cctcaagatg agcaaggcca ccacgctgca gaagacggcc gagtacattt	180
ccatgtgcgca gcaggaggcgc gcccggcaaggc aggaggaggc ccagcagctc cgggaccaga	240
tcgaggagct caatgtgcgc attaacctgt gccagcagca gctgcctgct accgggggtgc	300
ccatcacaca ccageggttc gaccaaattgc gagacatgtt cgatgactat gtccggaccc	360
geacgctgca caactggaaat ttctgggtat tcagcatttc catccggccc ctgtttgagt	420
ccttcaacgg gatggtgtct acagcaagcc tgc	453

<210> SEQ ID NO 33

<211> LENGTH: 454

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 33

ttgggagcag atcatagctg ctaggttaag aaattgattt tcccccagaa acaatggatt	60
tcgggtgtgc ggaactgtta cgtggagatg ctaagatgca aaggtacatt tcaaaacacg	120
ccggacaata ttggctggaa aatgacttgg ttaaaacctg atgatcttac cagcattctg	180
caggttgcgtg aatactaattg aagctgtgca tgtcaactgag cagcttcatt ttaaatgagg	240
ggttgtgtc tgcctgtgt ctgcctgggt tgctgtgaca ttttgaaggt ggaaacattt	300
ctggctagtg ctgcgagatt tacttgtctg tcttatgaaa atctgggtat tggaaaacc	360
tccaatggat gtggaaagaa agttcaagat gaattacatt tttacattgg tttgtaaata	420
gattctgaac cagcatcgag tctagataat gcat	454

<210> SEQ ID NO 34

<211> LENGTH: 582

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (504)..(504)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 34

gagaccatgg ccttaaaaata ccttttatta aacccagaac atggctttaa gcagtaccat	60
attacttctt gataatagt ttaaatctt tatgcttca gtgaaggaaa ggaaaagtct	120
tggatcaatg aaacctatgt gtgacttgct ttatcatctt tctccaggcc cctttcttt	180

-continued

gatgcaggtta tgccgcctta gaattcggaa gtgtttggg atcaagcagc atcataagat	240
cactgagctc aacccctcg aggagctgaa acggtttctc ctccacattt aaatgtgtca	300
agcgaatggc gacacagaca acagacaaat gttattgagt gttgagacca ctgggatTTT	360
caagttaaGT caggTTATA gagttcagCT aagtTTTGT tGTTTGAGT gagaCgttA	420
tTGTAGCTC gtACTAGGTT CTTTGCGCT GTTGGTTGG AGGGTATGAA AAATTATCTC	480
CCCTGCCTGG AAGAGGGTGG CTANGATATC CATGGTGTG AATATCTTAC CCAGCACTGA	540
GCTGGGAACC CTTATGCTT TGTCTAATTt AGTCCCACtC TT	582

<210> SEQ ID NO 35

<211> LENGTH: 515

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (405)..(405)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 35

ggcctcgggt gcctaccggg cggtgtgtcg ggtgaagatc cccggggccc tgcccggtgc	60
ccgcgcgcgc cccttcctg ggctggcgga ggccggcggt ggcgcgactc taggtggcg	120
agccgcgtctg gggtcaggct tcctgggagc tgggtctgtg gccccggaccc cggggggagt	180
cggaCTgtca gccggaggcg ctggccggg cgtggctggt gtgcggcgcg ccggccgcgg	240
agccggcggg gagatggctt tcgccaagggg gaccacttcg ttgcctactg agaccttcgg	300
ggccggcgcc ggattccctc ctctggccgc gcctccctc cagttgccca ctttggcg	360
tggcctggaa acagtggacg aaggtagtgc tctggatggc ccagnatacg aggaggaaga	420
ggtaggcacat cccgtgaccg ctccctccgac taaccagtaa gtcaagaccc gcgTTTGGG	480
ggaagctgac tcgtcgaaaa aaaaaaaaaaaa aaaaa	515

<210> SEQ ID NO 36

<211> LENGTH: 489

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 36

gttggcctca gggTTTTC tcATGGTTc ctcagtggtg ctgtccgaga agtattcagg	60
tggtgaccat caCTGgtatg agtttctcg cagggtttagg gcatatctt gcatggactt	120
cggTGAATC attactgatt aggaggacag ttgttggggg ccatctgccc tgcacaggaa	180
gagatcttgg actcatgaaa tgagatacc ctcacccccc aaggaccaa atggaaactg	240
acatcagaaa ctctgataca aaatcattt aattgcatca aatggccta attctgagtt	300
tggtaggctt atcaaatatgt tgcttacagt tggggtaggg gaagtagagg gagagaaac	360
aagacatTTA ttTactaAGC acctcttagg tgccagacgc taggctaAGC actttacgt	420
agctgggtca tataaggccct gtgagaaccc tGtaaggaat gttactagta ttTACACTG	480
acagatgaa	489

<210> SEQ ID NO 37

<211> LENGTH: 526

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 37

-continued

atgtggcag actgccacag tcctcaatag aatggccctc ttgcctccga acgtcctgaa	60
gccaccaggc agaactgtaa cgtaactgcag ttcgagaaaa ggcaagagga agactgtgaa	120
agctgtcatc tataggtttc ttgcacttca tagcggcctg tggctaagga ggaaggctgg	180
ttataagaaa aaattatgga aaaagacggt tgcaagaaaa agacgcttga gggaaatttgt	240
cttctgcaat aagaccaga gtaagcttta agataaaatg acaacgttct tctggaagag	300
gcgaaaactgg tatgctgatg atccttatca gatgtatcat gatcgaacaa acttgaaagt	360
atagatcaga agatccatga ttctctagtt attaactgtatctgtgtg tgtatgggt	420
cttgcaaag atgaagtggt ataagacatg atgtaaatgg taccaactga tacttggAAC	480
atgggttacc aacattaaac ttaacaatgt tttaaaactt aatgga	526

```

<210> SEQ ID NO 38
<211> LENGTH: 602
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (418)..(418)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (523)..(525)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

```

```

<400> SEQUENCE: 38

tgggtcgcca tagccatggc ggctcggtgc ctttgcgcct gtgtccgcgg acttccccacg 60
gccttcgcccgc cgctgccccag gctccccacg ctggccgggg cccggccgcgt cagcactacc 120
ctcttcgcccgg cggagaccccg gacggggccct ggggctccgc tgccggccctt ggtgtcgcg 180
caggttccag gcagagttac acagctgtgc cgccagtata gcatgcacc acctttgaca 240
ttggaggggaa tcaaggacccg ttttttttac gtctgaaac totatgacaa gattgaccca 300
aaaaagcttt cagtaaattt ccatTTTATG aaagacctgg gtttagacag tttggaccaa 360
gtggagatta tcatggccat ggaggaccaa tttggggggaa aatTCCTGA tatacatncg 420
gagaagttaa tttttccaca agaaatttta gattacattt cagataagaa ggatgtatat 480
gaataaaata tcaagacccct ttttttttac gagagaaggc ttnnnnagatg ctggcgatgt 540
tctggcggtt agaacgcatt tctgcattcat tgctgacttt gcatgttattt ctgttttagac 600
tt 602

```

```

<210> SEQ ID NO 39
<211> LENGTH: 333
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (141)..(141)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (143)..(143)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (157)..(160)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (306)..(306)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

```

```
<400> SEQUENCE: 39
```

-continued

atactggtgt ggtcaggccc tttcccttg aagaggtaag gtgaatctgg cttattttga	60
ggcttcagg tttcagttt tttgatctt aaagtatccc tcaacctgtg gtgc当地aagc	120
agaaactatg gctggattag ntnatgaata ttacgnnnm ttgtaaatata acttttaca	180
ttgagaacag cactgattag ggagatgtc agattcttt ttaaatacac tgtaatgacc	240
tagtgaacat aggcatgttag tggtttgtg tgagggttaac cagacacaga tttactttt	300
gccttnaaga caaagggaga taaaagcaac aag	333

<210> SEQ ID NO 40
<211> LENGTH: 565
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (505)..(506)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 40

gcacgaggtg aagctgagcg tgtacttggta ttacgccaag gctgtggac tctggacccgc	60
tctggtcatac tgcgtgtgt atgggggtca aagcgacgt gctattgggg ccaacgtgtg	120
gtcagtgcg tggactgtatg aggctgcgggt ggacagccag cagaacacgca cctccatcag	180
actagggtgtc tacggccctt tggaaattct gcaagtgtact ccctgaccgg ccctagcagt	240
ctacactgcct ctggacactgt ctggctcatac ctgcgtatgc cctgccttgc agtgcacatgc	300
ccaagggtcat tgctaataatg aggcagagcc cagactagtc cccgggtctt ctgattccca	360
atgtggcgat atttccacac tgtactgttttataatcattt caagggatga cctccctacc	420
ccccatgattt ttgttatattt ctgtctgaa gtgttttcg ttttgtttt aaataaagct	480
ttctcccttctt tgaacagaag actgnnaggt caggccatcc ctggaaactg agtccaatac	540
tcattaaaaa tggagcactg atgaa	565

<210> SEQ ID NO 41
<211> LENGTH: 539
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (472)..(472)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 41

ggcgctaagc ttttttttt aagattttc aggtacccct cactaaaggc accaaaggct	60
taaaggtagga caaccatggta gtcttcctgt ggcaagagag acaacaaagc gctattaact	120
aagggtcaatc aaaatggtgtt cgccctcaca gccccatctt ctgttagaaa tgaggacttg	180
actcaaccccc ctgacaatg tgcattgggg ctctctgggg gagcggcat ttaaaaggaaat	240
gtttgagttac ttgttatata tattccctgtt cttgtcttaa tatttaattt ggctgtttc	300
atagcagctg ttaatgaagc ctgaaacttca agtgtatgtt gaaggggggg gaaagggggaa	360
aaggcggcaa ccactttcc ctggctttc cagaaggctg ttaaaaagca aggtctcccc	420
acaagggtact tctctgccac atcgccaccc tggcccttttgcctagcgca gncccttcac	480
ccctcacctc gatgtgtgtt gtagcttggta tccttgggg catgtccat aatcgctt	539

<210> SEQ ID NO 42
<211> LENGTH: 573
<212> TYPE: DNA

-continued

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 42

ggcgactata cctactttga aacgagtgca aaagatgccaa cgaatgtcgc tgccaggcttt	60
gaggaagcag ttcaagagt gctcgctacc gaggataggt cggtatccctt gattcagaca	120
gacacggctcc gtctgcaccc gaagcccaag cccagctcg ttttgtgtgg aagtttagaga	180
ggtagccagt gcaacctgac cagtcaccc acatgcgcag atgggctctg ggccggagaag	240
agggtacgcg tggcagcaa cgcacatcat actcaaccat taaccgtgct gtcgcctgtc	300
agtgggtggg ggaagcgaca catccccca tgggagaatc cattttactca gtaatggcgc	360
ctgacacacgttcc cccattgtaa cggctgtcta ataatgttta attttaaatat gtatgttaca	420
gagctaataa gtgaaatgac caagacttta taattaaaac acttaagtat cctagaagtt	480
actgtctttt ccctggaaat atggagaact actttttctta ttttgtatatt tttatgtaat	540
taqcatctq ttctctqqtcc aqgqaaqca tqt	573

<210> SEQ ID NO 43

<211> LENGTH: 536

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (500) .. (500)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 43

ggaaaaccct	ctttcagcat	ggcgcatctg	gatagcaaca	ctgaggccagg	acttacattg	60
ggagggtatt	tctgccccca	gtgtcgggca	aagtactgtg	agcttcttgt	cgaatgtaaa	120
atctgtggtc	ttacttttgt	gtctgctccc	cacttagcac	gatcttacca	tcatttattt	180
cctttggatg	cttttcaaga	aattcccccta	gaagaacata	atggagaaag	gttttgttat	240
gcctgtcagg	gggaattgaa	agaccaacat	gtctatgttt	gcagtgtgt	ccagaatgtg	300
ttctgtgtgg	actgtgatgt	ttttgttcat	gactcttcc	attgttgtcc	tggctgtatt	360
cataagattc	cagttcccttc	aggattttga	ttccagcatg	taatacacat	tgaatgtatt	420
aaaaagaaaat	ttgcaactgt	aaataaaatg	attctttagt	agaaaactcca	gttaaaaacac	480
gaagaacagt	ttgaaaggan	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	536

<210> SEQ ID NO 44

<211> LENGTH: 546

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 44

tgttaccatt ctcttcattt gttgtatctg atcgactgtc ttcttcaata tcttcattt	60
gtctggttt acacttaagc tgtcaatgtc actgatgttgcagacaata actcagctag	120
ctcttccaaa tattttttt cttgctccct gcgcctttt tcagtgtttt atgcagggtt	180
gtcacatggt gaccctttc tcttatgtga gtctgggtta gcagggtcag atgaactgtc	240
cccaaggcca ctcatgttga aaaacttac acctgggaga cttctttgtt cataatgagt	300
cctcaaaaca gatatggtca aatatggtgc tccgttaggtt agttccagt ggaatggggg	360
aacactctt tccagagatg gctcttagta gtcttccac tcttacactca tttaaggcca	420
gttatgcaaa caacttgaat accttagagt aagtagaagt tataaatgtc ggtgtttca	480
tttggaaagca aaaattctta ctgcctgtatc ttgtctgggtt gtccgttattttatcatca	540

-continued

gagtcg

546

```

<210> SEQ ID NO 45
<211> LENGTH: 592
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (539)..(540)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 45

aggcgctgca gaaagtgaag attgaggta atgagagcgg cacgctggcg tcctcctcca      60
cagcccttgt agtctcagcc cgaatggccc ccgaggagat catcatggac agacccttcc      120
tcttcgtggt gcggcacaat cccacaggaa ctgtcctgtt catgggcaa gtgatggAAC      180
cctgaccatg gggaaaggcag ccctcatctg ggacagaatg gagatgtcca agaggaagaa      240
agtccggagc aaagaatttt tattaattca tttttctgaa aaaagagaag atgtttattt      300
atttatTTT ccatggtaaa ttctttgaa tctgcctctt agacctaact ctgggctctc      360
tcaggagggg caaagaggac ctttgagta aaccctccaa tggagaccct gggaaagact      420
gggaggcata acacccagcc ggcctccaa ctggactgta ggactccag gaccgctggc      480
ccagctgctt ctgccccatcg ttctgcctgg ttgggttttg ggtcctggat cccaccgann      540
ccctggtagg atggcaccac aaggcctaca tgaaggagct ttgtgtgtt ca      592

<210> SEQ ID NO 46
<211> LENGTH: 314
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 46

cgtggccccc aacgtggccc tggcccccggc agcccagcac aaggcagtga gcagccacc      60
ctgtgccacg gtcgtctccc gggccctgtg gcccctcccc gcctgcattcc agccccggaa      120
gcggaaagctg cctgcggaca cccctggagc cccggagaca ccagcaccgg ggcctgcccc      180
cgaggaggac aaggactcggtt aggccgaggtt ggaggtggag agccgagagg agttcacctc      240
ctccctgtcc tcgctgtcctt ctccatcctt tacctcatcc agctccgcctt aggacctgag      300
ctccccaggc ctgc      314

<210> SEQ ID NO 47
<211> LENGTH: 502
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (120)..(122)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 47

tttttttttttttta agagtcatac catgttttat tggacatctt aacatgggtg      60
tgggtgggac ctatgggttg gacaggcac caatgacagc ctcagtgaag tcttggcagn      120
nngcataacc acccatgtca gaagttcgaa cctgttagggg agaattgtt tcatctctgt      180
ggcctggccc ccatccctaa ccccccacca cctaactgtt ccctaaggaa gccagctccc      240
aacaaacccatg gctctgcccga aaggttaattt atggcttaaa agtataggc tcttctctgg      300
tccacagtagc tgaaggaggagg tggatggcc ttgtgaggtt ggagggaaata aagggtctta      360

```

-continued

gccccccatag ggggtgcagggt ggccgatgac agacttgatg aagtccggtg tggtgctgta 420

gcccggccatg tctcgagtcg gtaccttgc aaccttaatc accttttca ctgcctctgc 480

aatcatgttg gagtgatgct cg 502

<210> SEQ ID NO 48

<211> LENGTH: 303

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 48

aggccctgcc ccatctgagt cgcaggagaa gaagcccgctg aagccctgct gcgcctgccc 60

ggagaccaag aaggcgcgcg atgcgtgcat aattgagaaa ggagaagagc aatgtggaca 120

cctaattgaa gcccacaagg agtgcgttag agccctggga tttaagatata gaaatgggtga 180

gcatgggtgt ctgctctggg agtgaatagt tcctgaaaaaa tgaagaagat tcagtaactt 240

tgggagttcc ttgctgaaaa ttgataaata aaaaattattata tataatttat taaaaaaaaa 300

aaa 303

<210> SEQ ID NO 49

<211> LENGTH: 319

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 49

ttttttttttttttttttt ttgaattttt atacaagtct ttattttacaa cttgtttaac 60

aactgtacac ttttgcagc cttgaaaaca tttttgtact tgaatggaa aatatagttt 120

gaccacaaatct taacttttatt cttcatatac atatacatat attatatgca tacatataaa 180

catatacata taattaatac cataacaagt tggcagtcat aaaattaaaa tgaataagt 240

acatcaaag gaaataacaat ataagatttc aaaaaattaa aaatctgtct tctggggatt 300

tcttggactt catgttttt 319

<210> SEQ ID NO 50

<211> LENGTH: 328

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 50

ctttagtgcc ccaagctctg tattaacatt ttgcctgaat tattctatta accattctaa 60

gtgtccctca agageggaaa tggaggcatg gagatgacat taagtgcata atttgctct 120

taacatggca ggtcccaact ctctcaggta aagccacttt gatgatattt tcctgctct 180

gtctcaggga agatgttagga tggaggtact tatgaaaaca atatctttt catgacagat 240

ggggaaagtg aggcatgggg acactgtaaag cacagtatta taaaaaacaa gaacacagag 300

gatgctgggtt ctgttactta ttcccttc 328

<210> SEQ ID NO 51

<211> LENGTH: 323

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 51

tcttcccta agacgtaccc gggacatgtc tttggtgtgtt ggtggaggca gtgagacgtg 60

ccttgcctt ggggtgcacgc cgcctccctt ccacctgttag ttgatcggtt tttcatagtg 120

gaactcttagc tagctggggaa gaaagagaat ctctgcagca ggaatcccgt gtcttcagat 180

-continued

gcagggtaaaa ccgttaagga atccccggaa ttcccatctt aataactgaga caggaaggaa	240
gccagatggc taacgcacag tcactttgtt agttagggca gcattagaaa tcgagctcc	300
taaagtgttt tcttcttcgt agc	323

<210> SEQ ID NO 52	
<211> LENGTH: 448	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 52	
gagcagcgta acgttaggca gcccgtgtgc agaaaaaggccc gaggaat tgtctcagga	60
acctgegcgc cccggacta acattcggat ggtgaagctt ttgcacacca tggtggacac	120
tttcctccag aagttggcg ctgcgggag cttccagagg ttcaactgact gttacaagcg	180
cttctaccag ttgcagcctg agatgaccca ggcacatctat gacaagtttga taactcagtt	240
gcagacttct atccaggagg aaatctctga aatcaaagct gaggaaacc tggaaagctgt	300
cctgattgca ttggacgcga ttgttggaaa aagcaaaagac cgcaaggaggc aagcctggcg	360
ccccagtgaa atccccggaga aggacctcgccgcg cagcgcctatg ggcgcctact tgctgcagca	420
gcgggatgccc ctgcagcgta gtgtcgag	448

<210> SEQ ID NO 53	
<211> LENGTH: 235	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (76)..(78)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<400> SEQUENCE: 53	
agggtgttcgg tccgcagccc cttggggcg agcgccgcac ccctgtggcc tctgcaagt	60
tccgtggcgc ggcctnnngg gtgggtgggg gaggctttgc accaaagatg tccagactct	120
gcccccttc caccagccgc tccccggccc cgcggccaaa caactcagcg acatatccag	180
gcccagtgtgg ggtggggagg cctcgtgtta acctgagcac tgtggggagg gcccc	235

<210> SEQ ID NO 54	
<211> LENGTH: 370	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (250)..(252)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<400> SEQUENCE: 54	
aacaaaatttt attgttagggt tgcttttat gggttattga aattacaaaa ataaatgaag	60
catgctttgt atcaccaagg ttattgactt tagtaagggt gatatacacy taaaaaaaggaa	120
attacagttc agtaatcttgc ctataataga ggtatgtaca cagcactgtt ggaatattga	180
aaaaggtgtg actttaatttgc cagggtccctt gaggaaagggt tcgcaaagta aacataccct	240
ggccggccaaa nntcctttctt ccttttttttcaaatggaaaac ctttttaagt tggaaaaatg	300
gcacctaagg caattcttggaa gtcttaggaa gaccgattgc agtcagccac tgtttggct	360
aagccactcc	370

<210> SEQ ID NO 55

-continued

```

<211> LENGTH: 493
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (373)..(373)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 55

gaagtgtga cccgggttct ctcaagcccc caggtgcccc gggctccca cccgccttca      60
ccatggactc gggcccccctg gggcccccag ctccagttcc cacaactcag gcaggctgg      120
ccaggccctg ggctgcctca gtcaccagcc ccccaggag gaacccggccc ctcccgaggaa    180
gccacttccg agtttttag aaaaagttat ctcccatattc tttttagccca agatgtttag     240
taaatatttt tagtacagca ctttagtgac cacttcataa ctgtgttttc ttgccacaca     300
agtgtcctgg caagagcccc ttctctttaa gacatcagga agccagccag acccttttgg     360
gtcaggagcgt ctntgcagcc ccaatagcaa ggctgtctgt gtctgagctg ccggccccccc 420
ggaagcccaag gaccccaaga ggaaggagcc aggagagcac aagtctctgg agctgcagcc     480
ccacccatgg ttg                                         493

<210> SEQ ID NO 56
<211> LENGTH: 558
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (528)..(528)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 56

gttctagaat tttaaattt tggAACatta gtcaagtttt aatttggaca tatgttgaaa      60
ttcttcacat acacatTTTg tcctcatata tatgaagttg gggcttaaat atcagtattc     120
tcagaataatc attaattaat gaaattaatt aattgattaa ttggatttgt gtacctattt     180
gtcatgaaa aaattccttc aggtcttcag aattctcaac tacctatgtat tttttttttt   240
actgtcaact ctttgacag caactggta aagaaattga tccaaagact taaggaggcaa     300
cttcttcctt ggtttatgag tgcactttca ttataccag aataagcatg tacatataagg   360
caactattaa ggtatTTAGC aggttagtaat atctagtttgc gaccttagtt ctctgacaga   420
gttaggtctgt catgtcaggt gttgtctgt tagttttgtt ggagcatgaa atatataaac   480
tctgacacct cggctagttt acatattgga agttaactca ctttcagnng ttgagagttt   540
aataacaatg ttgttaag                                         558

<210> SEQ ID NO 57
<211> LENGTH: 603
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 57

agatttcaaa aggaactgct cgagttctga aggtgagcccc agcctttcta aacctcttct  60
cagaaaaaggg aaactgacac ttgaatTTTt gtcacccctt tcctcattgg aagggaaagga 120
gccttagaaag attttcttt ctaactctgg tcttaggtaa atatattcta ataaaacata 180
ggctactcta acaacataga attagatgc ctcacgtacg tgagaaaatc ttgaatataag 240
gacaagggttc ctgttttttta aaaacagact caactgagct gatttagatga cgtgaggccg 300
ctttgccttc aataacatga agtttggac agttcctact cctatttgca gaaggaaatt 360

```

-continued

ggctgaaaaca tactttaacc atttcaaaga aggtaaaatt ggacctaaa aggtatcaag	420
aaggccagcat ggtacttaat tacaacataa catttgacc ttaatggaa ctcattttat	480
ttgcactaaa ggccttgctt gctgaagtct cttaacttct atctgttagaa ctttatct	540
tccactagta caaggagaga gaagagttct tataattgaa tgttatcata aagagggaat	600
gga	603

<210> SEQ ID NO 58

<211> LENGTH: 504

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 58

ttttttttt tttttttaa atcaaagact aagaacaagt caggagctaa gtgacttctg	60
agttcaatga ctgaccatc agagattgc caaggcctct cagatggctc gccaagcctt	120
gcgttgtaac actgatctt taatgtggca cacttgcctt tttctcacag aaatatacg	180
atgggaagtgc gatcatatat gggcagtc cagcccagaa gtaactcaac aaagacattg	240
taaacttctt acttatatgt ttaatgagaa ccatacgatctt ctgcgttgc acctaccaa	300
taagagcacc ttgttttct tctttctaga gaggttattc gggggatctg acgggtggAAC	360
tgcacacatgc accaatgttag aagatctaga caagtaccctt aggggtcacg tggccccaa	420
agtccgtctt gcagcgttc aggttgcctt tcttactttt aatgtgtaaa ttctactcct	480
cagtcctagg ggggtggagca atca	504

<210> SEQ ID NO 59

<211> LENGTH: 427

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 59

gcacgaggc cgatgtctc aagagtatca acaatgccgaa aagagaggc aaacgccagg	60
tccttattag gccgtgtccaaatgc tcaggttctt aacagtgtatgc atgaaggatcg	120
gttacattgg cgaatttgc atcattgtatgc atcacaggc tggaaaattt gttgtgaacc	180
tcacaggcgc gctaaataag tggggatgttc tcagccctatgc atttgtatgtt caactcaaa	240
atcttagaaaa atggcagaat aacctgtcc catccgtca gtttggtttc attgtactga	300
caacctcagc tggcatcatgc gaccatgaag aagcaagacg aaaacataca ggaggaaaa	360
tccttggatt tttttctatgc ggtatgtata catacaataaa aatgcctca gaggactctg	420
atgcgttc	427

<210> SEQ ID NO 60

<211> LENGTH: 212

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 60

tgttcgggtt cggggcctc acagacatataat ctagttaaaa agatcgtaa ataaacggcg	60
tcagccatcg caatgcaaaa ataaatataca atcctccggc cacagcgccaa gctgcgtgc	120
gecccaagtc ccatcgcccg cgcctaaatca ttataaaaatgttccagcgag agtgggtcg	180
cgtgagtgtg aacgggtgtg cgcgcgggggtt	212

<210> SEQ ID NO 61

-continued

```

<211> LENGTH: 530
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (328)..(328)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (383)..(385)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (422)..(422)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 61

agtgttcttg octtagaaat cccatggaca gaggagtctg ctgggttaca gtccatgggg      60
tcacaaaaga atcagacaca actaagtgc taaacaataa cattaagatg acagagaagt      120
tcatcagact cctcataatg ttgggcctgg agtactgagc tctggcggtt agcactgagc      180
tgtggtgtaa cagccagaga ctaagtggaa ccttaagacc tgaaaagtga aagtgcctc      240
ctctaactag ctaatttagt gcacaggcac atcttagagt gtggagagaa tgcaagccca      300
ttataagtga agagcttctg ctgcctngt ggaaataag taaaagagat tccatcaaat      360
gaatttgctc aactgcagca agnnntccat ttataataa tcaaataatg gctaataatg      420
tnngctgaatt gctctctgaa ataaccgtgc caaccaacag caataacttta tcagtgtatg      480
ggaatagcta ctgcacataa agtagaataa atgcacataa agtagaataa      530

<210> SEQ ID NO 62
<211> LENGTH: 341
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (104)..(106)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (159)..(161)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 62

aattacttct tagaagtttg ggaattacct tccatcaatt cagctaagaa cggaatggat      60
tctggtaaca agacgata attctcttc agtttttcag ccannnctaa cacagttatc      120
agagcagcaa atcgaacctg aaaagatgaa gaatcatnn ntaaaaacca aagaactatt      180
atagctctgt ttgttaattt atgatctaac ttgagacatg ctctgaatct taaactggta      240
tttcactctc catcaagct tcatcttagc ataccagttc attaacagt ttgagatctg      300
tttaataaca cggcaacct tgtaagtac agccttcaa t      341

<210> SEQ ID NO 63
<211> LENGTH: 341
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (199)..(201)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (237)..(237)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 63

```

-continued

atgcacccatc taataccatc actttgtgtg tgtgtgtgtg tggtaagca cgcacacg	60
cacgcattgt tatgttcgtt catgtccaa tctctgcagt ctatggact gtagecccacc	120
aggctttctt gttaatggaa tttccaggc aatactgagt gggttgccat ttccatcgcc	180
agggtatctt cctgaccnn naatcgagcc tgcatactccgtgtctcg cattagnnc	240
agattctta ccactgagcc acctggaaag cccatttt ggaatttaga atttccacat	300
aggaatttta aaggcacaca aatattcaa tcatggaccc t	341

<210> SEQ ID NO 64

<400> SEQUENCE: 64

000

<210> SEQ ID NO 65

<400> SEQUENCE: 65

000

<210> SEQ ID NO 66

<211> LENGTH: 441

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 66

cagtgtccgc gcagctgaag tgtggatgga tgaatttaaa gagctctact accatcgaa	60
tccccaggcc cgccctggagc cttttggggc cgtgacagag aggagacaac tccgtcaag	120
gtttgggtgt aaggacttca agtgggttctt gaataccgtt tatccagagc tgcacgtgcc	180
tgaggacagg cctgggttctt ttggatgtctt ccagaacaaa ggactgagag attactgttt	240
tgactacaat cctcccaatg agcacgagat cacaggacac caggtcatc tgcgtccgt	300
tcacggatg ggtcagaacc agtttttgcataccatcc cagaatgaaa tacgctacaa	360
cacccaccag ccagaaggct gcgtggcagt ggtggaaagga acagacgtcc tcatcatgca	420
tctgtgttag aacaccaccc c	441

<210> SEQ ID NO 67

<211> LENGTH: 476

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (96)..(96)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (442)..(442)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 67

agcagagacc cacatcagac agtccttaca cgtgcccgtt gaacagggtt ttctcttgg	60
ctgggagggtt tgactgttca cctgtccctt ctcagnggtt gccccaccc ccatcttcc	120
agtggaaagtc tggtaacaca agttccgttc ccactcaggat atgcaaaatg cccacggaga	180
tcaagctgtt gggggaaatgt ttacgttcc tctaaacata cccctaaaca tactcttgt	240
tagtgttaac gttaggcaaa tggaaagaaag accaggtcga attctgaaat aatttttcag	300
cctccccatcc ttgtccactt catacaccac catgctgcag aatgttccctt atttcttaag	360

-continued

gatgagtggtg cctgttgaat acaaattgtac tgctgctgtc taacttgcga gatgcattgc	420
gtatgttacc gtgctggcc antgtcgtt cttaaatgcc catcgtaaat accatg	476

<210> SEQ ID NO 68

<211> LENGTH: 481

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 68

acaaacctag acagcgtatt aaaaaggaga gacattactt tgccaacaaa gagtcacca	60
cccccacctc tggcctggac gaccctctc ctgccagcct tgggaacctt tcgggtcagc	120
cagagtgtgg gccagggtcc tgcaatgtca gagagctgcc tgaatccgag gggcagccgc	180
ctcgccccc octgccccctc ttcttcctga cgctggggc cgactggca gaggccaagg	240
ctcgctgggg tctggctgg gaggcccacg tgtacggggt aggccgcgtc ttggcctgg	300
tggccttgcg ggccgtgtcg ggcctagccc tccctggccctg ggcgtgcggc cccggcgctc	360
cctgcctggc gctgtggac atgctctgc tctcggtgg gaccacgcgg gccttccgc	420
tcttctacga cgcctacggg caccgcgacc ggctgcggc gctggtggc ctgtgtgc	480
a	481

<210> SEQ ID NO 69

<211> LENGTH: 436

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 69

tggttttcc ggtcgctttt gaaaactgaga agttacagat ggagcaacag cagcagctgc	60
agcaacggca gatacttcta gggcttaata caggcgtgtc aggaggaatg ccggggggtc	120
tacccctacttccctggaaaa atcttagattt ctactgttat atttgacccctg tcttgggtaa	180
gaagtttggaa aattcaatag tgtttgaact gctgattttt ggatttttt tttttttttaa	240
actttggcac atggcttat aaacctgggt gcaggaattt tcccccacatt ggctcatggaa	300
gagacttctc acttgcagct gtgccttcca ctgtcctgac ttatcccttc tctccatcaat	360
gctgatacca gagagcagca acgcagacgg ttactccagg tctggccacc caccggccct	420
cactaaatta ctcctg	436

<210> SEQ ID NO 70

<211> LENGTH: 475

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 70

gttaattcatg ggactggagc atttggagca acaaattgtac ccgggtgtac gttctcacct	60
ttggttatga gattcaagt tattttatcc cttttcagt ggcaataaga accttttttg	120
gacttctgt ttaattcgta cataatgtgt aaaacacttt ctttggaaacg aaattcaagg	180
cactgaatct gtatgtctgt gtgggtgtc tgcgtccatt ggcaggcaga	240
cttgatccct gacccctgt acaccacact gcatgagtca ggccttgcgtt cgggtgtct	300
ctgcttggat ggttaggaacc acagagctta tggaaagaaca cttgtcacct gtcacatcg	360
ttacagtgtc agctgaggaa aacagttctt cacatgtattt ctttaacag gactcggtt	420
ctagttccct gtaattttat ttcccttaat ttaataaaaa gctgaactgt gaaaa	475

-continued

```

<210> SEQ ID NO 71
<211> LENGTH: 504
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (4)..(5)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (354)..(354)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 71

agcnnaatga aagttaagtc tgtgatccct ggtgccccca gcccgctgag tgtgcctcca      60
ggctcagacg ctgggttccg aagctggct ctgacaaggcc ccagtgctc ccaccagggt      120
ggagagcagg tcctgcttgc ggcaaggcc gcagggtttg aaaagttaa tgtgaaagac      180
cctccccaga gccctggctt gtctggagg gccgtcagtc catggtatg ttgagacccc      240
cgaaaccctc ccctgttccct ctaagtgagg agctggctt gtgcaggatt tgtgtgtgt      300
tgtaaagagg atctgatgtg tttgtcttac tgtccgagcc ctgtgcagaa gagnctggaa      360
gggcagggggt gggcttgaa agggcaccc ctcccttaggg agagcccagg gccctatgag      420
gtgtcagacg tggagacttgc ggctggccct ggccgggtct gagtgccggc tccgtctcac      480
cggttcgggg ctgactgggt ctta                                         504

<210> SEQ ID NO 72
<211> LENGTH: 392
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 72

gggaatgag cagcggtctac agagggaggc agccggact gctggccctt ccttcctgca      60
tctccagggaa cccaggacca gccactgcaa ctaacggctt aactcatgat acacccccc      120
ttcattccaa agggaaagtc gatgtctgct tatctatcac cacttgcctc atctgcttt      180
gctttgttttgc ctttcctcagtt acttctgcct gctgtttccc tggctcgctt ttattgcac      240
gtgtccttctt tgactaaacg tggttactga caactgacgt taactctgca ctttggc      300
acctggagtt cagccactgg ctcacagacc gcagctctgg ctgaggaccc tcatccccag      360
ggatgttttgc tggatccctgtt cattcctccaa tg                                         392

<210> SEQ ID NO 73
<211> LENGTH: 529
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 73

gagggttacctt cacaggaaacc aggggcaaaag ggccacatct ttttttgaac aaggtaatc      60
cttcctgca aagttagggcc acacagaatg ttgcaactac cggagggttt tttgataaga      120
atttgacttc cagccttaag cttctaaatt tctgatcttgc ttgaaatcttgc gtagaaacca      180
gaggccggaa ctcagctgcc ccaggactgtt ccaaggagca ggagcaagtgc gtggccctga      240
actgtatgcgg tgcccgaaa gcatctgtgg ccagcgtctt ggggttaaca agacccgggt      300
catccaccga ggaaagcagg aagttgtttc caaaacaagg agaaaaaaat agatgctgaa      360
gaatcagaag ctacagctgtt gcagcacagg ctgcctcaag acctggatgg acatagccca      420
agcccaaga ogaaaagctt ctgtgataca ctgacatgtt tataactgtc cgtgatcttgc      480

```

-continued

ggggcaggca ccagaattcc tctgtctgtt ggagaaaata ggcata	529
--	-----

<210> SEQ ID NO 74	
<211> LENGTH: 341	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (185)..(185)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
 <400> SEQUENCE: 74	
tgtgtgatc ctatccaaca acaaaaaaaag aagccttag gaagagacag gtagaggggt	60
cccttcactt tgaacttggt ggaaagcagt gaggggactc cgggtggca gctctgggt	120
cggctttggg gctggctgtgt cgcccgaggag aggaagaccc cagccccctt tctgctcaa	180
gaagnctgg acgtttcttt ctccccatgt cattggacca gaacagcgga caaggggtg	240
ccctcgaacc caagaagcgt tcccaagatcc agcatcgctg aaggggggcc gtcggaa	300
tcccgatcca cgacaccaat gccgccttgt ttgagactcg t	341
 <210> SEQ ID NO 75	
<211> LENGTH: 514	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
 <400> SEQUENCE: 75	
ggatctcca aagagttagg ggtcccttag gaggtcagag tgctaccaac cactaggata	60
ttccataatgg gggctccttg gtgccagagc tccttggtt ggtgcctca gcatccatc	120
atccccc accgtgggctc cccatcccc gggggatgtt tctgagcga ctgccaccat	180
ggctccagcg ctacgtggac aaagtgtctg acctcagcc ttttgggggt ctccagcca	240
accacgtctc tggtaaccat tatctgcctg gggagggcat catgccccac gaggatggc	300
cactgtacta cccgaccgtc agcactatca gcttgggttc tccacccatg ctggacctct	360
acgagccctcg gcagccagag gatgataacc cgacagacgca gccccggccc cggccccggc	420
cggccacctc tctgtgtgtt gaaccgcgca gctgtgtgtt gtcgggtggc accgectaca	480
cgcgcctcctt ccatggcatc gccgcagcca gctgtgtgtt	514
 <210> SEQ ID NO 76	
<211> LENGTH: 561	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
 <400> SEQUENCE: 76	
ggcgagctc gacggcaaat aggctttga aattgaggcc ctgccttgc ggtgtggca	60
ggggtcagca ccccgatcc ccccgctgg cctcttccc tgtccaggcc cctgtccca	120
ccacagtcca aaggtgtctg tcagcagaca cctgggtga ggggtgtccc ttcaggagcc	180
cgggaggcccg ggacccctc ctgtctgtt cccacccctc actagcatca tctctgtta	240
caggtgagcc aggggtggag agggacttgg agagtccagg catctgcctc cagtctgcct	300
tgagggcctc agctccctcg agccggccagg ggctgcgagt tctgggtt ggggtgacagg	360
ccagtagact gccttcagcc tttgtgtac tgtgtccctc ctcttgc gtcggggcc	420
ctccaccaag agatcctgtt ggacttggcc gctggaccgg ggcctatgag cttccctcc	480
tgcccttgc aatgaggatc ctctggccc tgcctgcctt gttgttatcc attgaggaaa	540
ggcgagcttgc gaaacttccc a	561

-continued

<210> SEQ ID NO 77
<211> LENGTH: 505
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 77

cctcaaaaccg cagggcccgat	tgtccccagg cgggggctcc	actctgggtt tggggtcacc	60
ccgtccccctc	tggggagggg ctggagctt	gtttcattt aatgacctt gagcgttga	120
gggaaactga	ggcagggaag aagtcttgc	tgcctaaacg gtcaactcct cctctaaact	180
tgaagggtggc	accctcttctt ctgttaagt	tgtgtgtgtg tgtgtgtgtg tgtctgtgcg	240
tgcgaacagt	cggtcaacttt	tgtccactg ttggaccctg ctgcccctgg gctgtgggtt	300
tcccggtcc	agggegcgcc	ctttctccca ggagctggca ttgaagactt gtcacttctg	360
gcagggctt	gtgacccccc	tctgcccgcg agtattttggg ttatgtccag agggaaactag	420
gtatcatggt	tcccttggac	ttgttaagtt caggattgct cagtaatgaa tgaaaacatc	480
acgggagaca	tggggaaagag	cagtg	505

<210> SEQ ID NO 78
<211> LENGTH: 516
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (404)..(405)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 78

gcacgagccg	agccgcgcgg	aggcggaggc	tcgggtgcat	tcaagattcg	gctccacccg	60
taacccaccc	ccatggccga	ggaaggcatt	gctgctggag	gtgtaatgga	cgttaataact	120
gctctgcaag	aggtactgaa	gaccgcctc	atccacgatg	gcttagcacg	tggattcgc	180
gaagctgcga	aagctttaga	caagcgccaa	gccccatctgt	gtgtgctcgc	atccaactgt	240
gatgagcccta	tgtatgtcaa	gttgggtggag	gcccccttgc	ctgagcatca	aatcaacctg	300
attaaggttg	atgacaacaa	gaaacttaggg	gaatgggtag	gcctctgtaa	aattgacaga	360
gaggggaaac	ctcgtaaagt	ggttggttgc	agttgtgtgg	tggnnaaagga	cstatggcaaa	420
gaatctcagg	ccaaggatgt	catcgaggag	tacttcaaata	gcaagaaatg	atgaaataaa	480
ctgatttctt	gttttccaaa	aaaaaaaaaa	aaaaaaa			516

<210> SEQ ID NO 79
<211> LENGTH: 557
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 79

gcacgagccg	tggcgcaatg	aagggtgaagg	ccgcctcgc	cgccggccga	ggtgttcaag	60
gegaaggccg	gagcgccgctc	tgcccccctg	tccatggcat	acgctggagc	ccgccttgc	120
ttctccctcg	tggacgcgtat	gaatggaaag	gaaggagtcg	tcgaatgttc	ttcgatggtaag	180
tcccaagaaa	cggaactgtcc	gtatcttcc	acaccgttgc	tgctggggaa	aaaggccatc	240
gagaagaatc	taggcacatcg	caaggtctcc	ccttcgaag	agaagatgtat	tgctgaggcc	300
atccctgaggc	tgaaaggctc	catcaagaaa	ggagaggagt	ttgtcaagaa	catgaaatga	360
gaaggcgctt	agcgagcagt	cggtctcctt	aacttattaa	ggcatcatgt	cactgtaaag	420

-continued

ccgtttcaga tactttgtc gttcaattt gttcgttg ggaggattgt attaacgaac	480
cacccttgc caatcttggc cagtctgtcg gtgcataat aaaagcagcc tttgatttc	540
aaaaaaaaaaa aaaaaaaaa	557
<210> SEQ ID NO 80	
<211> LENGTH: 265	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (99)..(101)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (128)..(128)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<400> SEQUENCE: 80	
tttttttttttttttaat ggtatgcgtgg taccacctgc tagggctgtc catcctcaca	60
aagctggat tcttggccac agtggccctc gcgcggagnn nacagaccct ccagccacac	120
acgcagcnng agaaacagga agggacaggg cgtcccccttc gcagggcagc aaaggacaaa	180
actccatttt aagataaaagt cattgcagaa gaaaaaaaaaa aagtcttttta agagacaatc	240
cttcacaaag gggaaacgca gcacc	265
<210> SEQ ID NO 81	
<211> LENGTH: 425	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 81	
ttcattggaa aaaaagattt tattttacca taaaaatgca aactggaata aacaccatct	60
ctcctaagggt ggacgttaca gctattttta agtatttcca agttccctt ggagaagctg	120
acaattataa aatttaacaa gtttgcagcc ttaaatctga aacgttccaa gtaaaaataaa	180
tttagcaaaa cggcttctta aaaaaaccac acaggctaaac ctgtactaga aaccaaagct	240
aattttaaac cagcctgctt ttttgtttta tgctgaatga ctgtgatgg taaaaagtga	300
atgtctggaa cccctgtgtt ccacctgacg ctcttctgtt gtatgtgaa tgactgtaat	360
tcgtacaaag tgaatgtttt ggactcttct gtatcccgtc tgaccaggcc cacgeccgta	420
aagag	425
<210> SEQ ID NO 82	
<211> LENGTH: 504	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 82	
aggagtccct accctggat cattccacaa tccccatggc tccagctccc agttccgtg	60
gacaccagggt gacttacaac cctgtccgag ggtcctgcct gctgctgctg ctgctcatgt	120
ctaattctgtt cctgtgccaa ggcaaatcat gcccgtctg cgggtctgac gtgtttttt	180
ccttacggaa atcccttaca gacagggtta tgaatgccgc cagcctctcc catgacttct	240
ataaccccttc cacaataatg ttcaatgagt ttgatgaaaa atatgcccag ggcaaaactat	300
atatatatcaa tgtcaccaag agctgccaca ccaattccctt ccatgctccc gaagaaagag	360
atataatgtcca gcagacgaac attgaagacc ttagtaagt gacactcggtt ttgctgtact	420
cctggaataaa tcctctgtcat catctagtca cggagctgca gcatatgaaa gaactgtcaa	480

-continued

acgccttcct atcaagcgcc acaa	504
<hr/>	
<210> SEQ ID NO 83	
<211> LENGTH: 483	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 83	
gggaccaacg ggatccccctc taccccacca acccgggagg acgagttggg gtccggagttg	60
ggtgtggactag ctteccctggt cctctccca cagagctgac gtgtccctggg ttccaggcgaa	120
tgggcatttc cacggggcgg gagggttcgg gtgggtggta caggcacgtc gctggcgctt	180
tcctccctcc tgcctctgct gcttcgtcgt gggatgcaga tgtatagtcg ccagctggcc	240
tccaccegagt ggctcaccat ccagggcggc ctgcttggtt ccggcctttt cgtcttcct	300
ctcaactgcct tcaataatct ggagaatctt gtctttggca aaggattcca agcaaagatc	360
ttccctgaga ttctccctctg cctccctgtt gctctctttt catcaggcct catccacaga	420
gtctgtgtca ccacttgctt catcttctcc atgggtggtc tgtactacat caacaagatc	480
tct	483
<210> SEQ ID NO 84	
<211> LENGTH: 508	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (383) ..(384)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<400> SEQUENCE: 84	
attttttctt tttttaaatt ttcaaacact actggggaaa ttatttttgtt ccaataatta	60
ttaaaaagtct ttgcacttg agcacatgga caaatgaact tgatttgaaa ctagagccat	120
aggccatgca tgtagtact ttattttttt gcttcctgcc atgttaggaa aacaaaatat	180
aaaaaaaggtc atttttttta aaccatggaa tttttcttca actaagatga atcaaatttc	240
cttatgtatg taaattcata cattaacaca aagttttata tcatgccagt tcacatagca	300
tagtggagtc accattctct agaatgtgtg tttctgcgaa acttaacttg cttagaatt	360
ttaaattttta accttgcgca gannccagct cccgaaagct atgaaaaatt cccagtggct	420
gatgtggaaa cctctttcca ctgctgccc gcccctcaggta tgtgcaacctt agtgaagga	480
gagaatcttt ttcttaggaaa aatgagcc	508
<210> SEQ ID NO 85	
<211> LENGTH: 545	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 85	
gcacgagcag cagccggact tccagaccca gatgccaagc agtcttgtc tggactgctc	60
catcgctgac tgcctgaggt tccgctgtga catccccctcc ttccggcgatcc aggaggaact	120
tgacttcatc ttgaaggggca acctcagttt cggctggcc agccagttgc tgcagaagaa	180
gacattggtc gtgagttatgg ctgaagtcac attcaacaga tctgtgtaca cccagatttc	240
aggacaggag gcatttttga gagcccgagg agagatggtg ctagaagagt atgaggtcta	300
cagccccatg cccctccctt tgagcagctc catggggagga ctgctgtcc tggccctcat	360

-continued

caagccctta ctgtacaagt	gtggcttctt	caaacgtcaa	tacaaggaaa	tgtatggataa	420	
caaggcctgaa	aacactgcac	tcaatgggga	agatatccac	catgagaccc	cagatctacc	480
tttgtccgaa	taatccactt	tctcatttat	gtctattccc	attggctgac	cttggttca	540
cctac						
<210> SEQ ID NO 86						
<211> LENGTH: 239						
<212> TYPE: DNA						
<213> ORGANISM: Bos Taurus						
<400> SEQUENCE: 86						
acaagaaaaat	gttatcaacc	acacggacga	agaaggattt	acccctctga	tgtgggctgc	60
agcacacacggg	caaatacgctg	tggtagagtt	tctacttcag	aatggcgctg	atcctcagct	120
tttagaaaaa	ggtcgagaaaa	gtgctctgtc	attggcctgt	agcaagggt	acacagatata	180
tgtcaaaatg	ctgctggatt	gtggagttga	tgtaaatgaa	tatgatttga	atggagggaa	239
<210> SEQ ID NO 87						
<211> LENGTH: 426						
<212> TYPE: DNA						
<213> ORGANISM: Bos Taurus						
<400> SEQUENCE: 87						
ttcttagcagt	gggaccaggc	agcaggacga	ggagatgctt	gaactccctag	ctcctgtgc	60
agtggctcg	aagagtcaagg	ccttagagga	cgatgcacaa	atgagggtcg	cagacctggc	120
cgagaagaga	gggccttctt	ccagccccga	gaaccccaga	aagagacctc	gggaagactc	180
tgtatgtggaa	atgggtggagg	atgcattcccg	aaaggagatg	acagccgtt	gtaccccccgg	240
gagaaggatc	atcaacctta	ccagtgttct	gagtctccag	gaggagatca	acgagcgggg	300
ccatgagagt	acctctcccg	gagatgctgc	ataaccactc	ctttgtgggc	tgcgtgaatc	360
ctcagtgggc	cttggcacag	catcagacca	agttataccct	tctcaacacc	accagactta	420
gtgaag						426
<210> SEQ ID NO 88						
<211> LENGTH: 517						
<212> TYPE: DNA						
<213> ORGANISM: Bos Taurus						
<400> SEQUENCE: 88						
tgcccaattc	caaatgtaca	gaactctccc	attctacaa	agtcctctga	accagtgaaa	60
gccagtgagg	cagctgcaaa	gaagaccagg	ccaaaggcca	gactgacaga	tcccttccca	120
actacagaga	cgtcaattgc	accccgccag	aggcctaaag	ctgggcagac	tcagcccaac	180
ccaggaatcc	tcccccattcca	accagccctg	acccctcgga	agagggccac	agttcagccc	240
ccgcctcagg	ccgcaggatc	cagcaatcag	cctggctttt	tagccagtgt	tcctcaacca	300
aaaaaccctg	cccccaccca	gtcaaccctt	accacagtct	cagcccaagc	agcctcaggc	360
tccgccccacc	tcacagcagc	cgcctccgc	gccggccagg	gtctctgccta	cccaggccca	420
ggccacgccc	cagcaccaggc	agcaactctt	cctcaagcag	cagcagcagc	agcagacagc	480
gecgccccca	cagcagccag	cgggacacgtt	ctaccag			517
<210> SEQ ID NO 89						
<211> LENGTH: 274						
<212> TYPE: DNA						
<213> ORGANISM: Bos Taurus						

-continued

<400> SEQUENCE: 89

```
ggtatecgcc cccagatcat gaacggcccc ctgcacccccc gccccctgggt ggccgtgtc 60
gacggcagag actgcaccgt agagatgccccc atcctgaagg acctggccac cgtggcccttc 120
tgcgacgcac agtccaccca ggagatccac gagaagggtt taaacgaggc agtcggtgcc 180
atgatgtatac acaccatcac gctcaccagg gaggacctgg agaagttcaa ggccctgaga 240
gtgategtgc ggataggcag cggttatgac aacg 274
```

<210> SEQ ID NO 90
<211> LENGTH: 247
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 90

```
gtctggctga gcctgacacc cccagggaa agcagtgcag aaaccactgg tttcccagcc 60
gcccggggat ctgcactttt gtttgtttt gaccaaaaaaaa aaaaggtagt cagtgggg 120
ctaaggagac atccagcctc tgatacctaa gaggagaagt ccctggactt ggaccctcct 180
atttgtgtac ctcagccca ggtgggaact gctaccgtga gtacctgggg aggagggat 240
gggagtt 247
```

<210> SEQ ID NO 91
<211> LENGTH: 478
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 91

```
tggagagtgg gaaccccgcc atcttgctt ccgggatcat catggactcc agcatctcga 60
agcaggccct gagttagatt gagacacgccc acagcgagat catcaagctg gagaacagca 120
tccggggact gcacgacatg ttcatggaca tggccatgtc cgtggagagc caggcgctgt 180
cttcccaaaa tccctcctcg ggcccccctcg ccgcctggag gggggccctc tggagctgg 240
gtgccccctgg ccctgcaggg ggagatgatt gagaggattt agtacaacgt ggaacattcg 300
gtggactacg tggaggggc cgtgtctgac accaagaagg ccgtcaagta ccagagcaag 360
gctcgccgga agaagatcat gatcgatc tgcgtgtgg ttctggcat cgtgtcgcc 420
tccacccctcg gggcatctt cggatagaaa ccaccccgcc tgccactctg ctctggac 478
```

<210> SEQ ID NO 92
<211> LENGTH: 430
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (146)..(148)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (345)..(347)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 92

```
ttttttttttttttt tggcaggaga caaaaggcagg tttatgggg ctctggggcc 60
agggatgcct aagggtgtgag ttaaggcaac tcagctgggt gtcaatgccca aaagggcagg 120
ccagggggagg gagaagggtt gactcnnnat tgaagccaaat tctctgcatt tcaagtccct 180
ggccggagac ctggggagtc agttctggga gggcatgggt ttcttagtgg tccctgggtc 240
```

-continued

tctgtgttt tgcttaggatt gggggaaatgg tctggggca ggagcettga atgcacagcc 300

ttcacatttcag taacgaccat ttaatttgtt ccttggcaga ctgannnacc tggccacac 360

tgtgttccgt caagccgctg tcatccgccc taaaattcac tttctggatc acttgctggg 420

ggtcactttc 430

<210> SEQ ID NO 93

<211> LENGTH: 213

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 93

actgcgcctt caagcctaca tcatcaagat tcaaaacagc tgccgcagcg tctttcaagg 60

aggcacagaa aatacgcttc taaacacacgt gatccttggat gatatacttcc tgaggcagta 120

cttctcggtt tttgatcgta aaaatagaag gattggcctg gtcggccag tgtaaatgct 180

tggactatca gcaaggatctt gactaaatca gtc 213

<210> SEQ ID NO 94

<211> LENGTH: 225

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 94

tgcgcgcgcg gtcgcgcaggc gcctcgccctc cccacgcctt ccgggcctcg gggctttctc 60

cggccccgtc ccccacccccc caccgcctcc gggccgtct gtccgggtct cccgcctgt 120

tctcgccctc cccgtacccctc tgacgcgtgt cccctgccccg ctggcgcccg agctccccgt 180

cggagccccct tccctccggcc ctcgggtgggt gttgtgtgggg ggggg 225

<210> SEQ ID NO 95

<211> LENGTH: 418

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 95

ccggccctcg gcgggaggga agagagcata ggaggcgagg ctgaaggcgc agctgttgcc 60

tggacgatgg cggggacggc actcaagagg ctgatggccg agtacaaca actaacgtcg 120

aatcctccag aaggaattgt ggcaggcccc atgaatgaag agaattttt tgaatggag 180

gcattgtatca tggggccaga agacacctgt tttgagtttgggtgtttcc tgccatctcg 240

agtttccac ttgattaccc gttaaatccc ccaaagatga gatttacctg cgagatgtt 300

caccccaaca tctaccaga tggcagagtc tgcatactcca tcctgcacgc tcctggcgac 360

gaccccatgg gctacgagag cagcgccgag cgctggagcc cctgtcagag cgtggaga 418

<210> SEQ ID NO 96

<211> LENGTH: 460

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 96

ctcgcgcaagt cgtctggcg agcgaagatg gggggcgaga gggagcctcc tccgttaggg 60

gacgggaagc ccaccgactt tgaagagctg gaggacggag aggacctgtt caccagcact 120

gtctccaccc tggagtcaag tccatcatct ccggatcccg ctatgtttct tgcaagaat 180

attagtacaa actccaatgg tccaaaacct gcagaagttt cgcttagatga tgacagagaa 240

gatcttttg cagaagctac agaggaagtt tctctggaca gtccagaaag ggaacctata 300

-continued

ctctcctccg aactttctcc tgcagtcaca cctgtgaccc ccacaacact cattgctccc	360
agaattgaat caaagagtat gtctgctct gtgatcttg atagatccag ggatgagatt	420
gaagaagaag caaatggaga tgaaaaatggat atagaaatttgg	460

<210> SEQ ID NO 97
<211> LENGTH: 466
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 97

gctgtccctgc gaccctcttt ccggaaagggt ggatagtgcc cgtgggattt gtggccgttag	60
ttaggaact cacatccggg acaatgggt gcattccctg catcgcttatt ccagttctgc	120
tctgggtcta caaaaagttc ctggagccat atatataccct tctgatctcc cccttttta	180
gccccatgtgc gcctcgaaa gctatacgag aaaccaatga taaaaacaaa ggcaaagtag	240
actataagggtt tcacacata aatggattac caacaaggaa accaacagaa atgtgtgata	300
aaaagaaaaga ctaaactgtat tgcccgaaag gatctcattt ttataaaaat ggacctgata	360
ctatgaagca cttttttgtt aattgtctctt gatcttttc caagaccaga atttgggtta	420
gatattaaca gtttagacat ttacctatgc taatcaggaa atacct	466

<210> SEQ ID NO 98
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 98

gtgggtctcaa ggcagggggg caggcagggg tggcctgttc agccctcac agatcagtgg	60
tcttggcagg tctgagagct gccccactgg ccagactcctt ctccagcagc agagccagcc	120
tggggcttgc atgtccagcc tgagcaagct taacaggatg aagctgagggc tttctccca	180
ctgtgactgg agtgcattt tacaccagca cttttctgc acatgtatct tcaatccac	240
cacaggggagc tcgtcaccctt tgccacaatga cattccaacc accaccagcc agaagttaca	300
gccaaccttg ctgactgtca caagcaggac cttgggtccca ttggcacggc cagtgtatgt	360
agc	363

<210> SEQ ID NO 99
<211> LENGTH: 566
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (481)..(482)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 99

gaacttgagg gccccaaaggct tatctcagcc tttcctcaat acggggttcc gttggactgg	60
ggctcctcca tgccttagtga gaattccatg tggcctcaga agacttgggc atgcagggtgc	120
cgctgtgtat gtgtcgctgt tggtcgac acacagtggaa agctggaaattt gatggccat	180
gaagggtttac cccacacaca cctgcaggct cccagatca agtaggtgtt ttccctggc	240
agtctggca acggagacca acaagaaaca ttttttaggtt gttttaaattt cttttttta	300
aacttgcagt ttattgcgtt ctgagatgtt atcacaaccc ccatgttca taagcggacg	360
ccatgtttagg gtcaaacgtt ggcaccatga gtcctccgtt gtcctggac agagacccac	420

-continued

ctcaagatca gaagcccttt ggatggcggtt gcagatctca ttgctcaatt agcctcgaa	480
nnntctaattc tcataccact ctcagttgga ttttctggca ctcttctgc atcgagtctt	540
ctgggactga accaagctct gtggtt	566

<210> SEQ ID NO 100
<211> LENGTH: 391
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 100

gtactcgggc ggcgcggcg gggttggcag gcagggttgc caggcgctgg ttctctggc	60
ttctcggcag cccccctgcag gtcccagcc ttggggttaca cgtgcgcggc cccgcctgc	120
tagccagcca gaaggacttt aacaacgcgg tgagccaggt gaagctcttg aaggaggatc	180
cgggcaatga ggtgaagctg aaactctacg cgctctacaa gcaggccact gaaggacctt	240
gtaacgtgcc caaaccaggt atgctggact ttatcaataa gaccaaattgg gatgcattgg	300
acgctttgg cagtctgtcc aaggaagctg cccgacagaa ctacgtggac ttggtgtcca	360
ggctgagtgc ttccctctgag tccccccagcc c	391

<210> SEQ ID NO 101
<211> LENGTH: 368
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (162)..(162)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 101

acgcctttcc tttccttaccc agaagtagaa gcccagtggc agggcagcag cctgcata	60
ctcaagtctg cccactggtc actggggcgt tgggtggctcc tgggttcatgt gctacccctt	120
tcccccagaat ttaatttttag ataaatttaca ctgcctgaag tngggggacc ccttttttc	180
cctgaggaggc cccaaagacca gagacaaggc caggacagct tggggacaca ctccctggag	240
aggtgcagtc cttccctgt tggggggaaag cccagaccca tgccaatcag ctgcagccca	300
ggctttgaca atctcgccgc cctcacgatt tggtcccact ggccacttgg gttctctcc	360
gggcaggc	368

<210> SEQ ID NO 102
<211> LENGTH: 311
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 102

caccacgctg tggcgccggaa acgccaacgg ggaccccggt tgcaacgcct gcccgcctta	60
ctacaagctt cacaacgtga acaggccgtt gaccatgaag aaggaaggca tccagacccg	120
gaaccggaaat atgtccagca agtccaagaa gagcaagaag gggtccgagt gcttcgagga	180
gctgtccagg tgggtgcagg acaaggccctc cccattcage gcccgcggcc tggcggggca	240
catggcgccct gtggggcacc tgccgcctt cagccactcc ggtcacatcc tgcccacccc	300
gacgccccatc c	311

<210> SEQ ID NO 103
<211> LENGTH: 609
<212> TYPE: DNA

-continued

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 103

gatgcgaata cctgcctca acgcctacat	gaagcaccc tcagcctgc ccatctgggt	60
gctgatggac gaggacgttc gcacatcttctt	ctaccagtgc tcctacgacg ccgagcagg	120
gcctcaagcg ctccggcgcc	tccggccgcg caccggcgca gtaaaaagcg agtccccaca	180
agctgctggc attgaccgca tggcagctcc	acgagcagag gcccgtttt atttactgg	240
gaacagcaaa catgagctga atttcaaagt	tggagatgtg atttccttc tcagtcggat	300
caataaaagac tggctggagg gcactgtcc	ggaaaccaca ggcatcttcc cagtgtcctt	360
tgtgaagatc ctcaaggact tcccagagga	ggaagacccc accaactggc tacgctgcta	420
ttactatgag gacaccatca gcaccatcaa	ggacattca gtggaggagg acctcagcag	480
caccccaactc ttcaaggact tgctggagct	catgaggctt aaaggctgt ggaccttcc	540
cgaactctga tctctccac ccaggcgccg	ggtccagaga gaggacatcg ccctcaacta	600
ccgacgctg		609

<210> SEQ ID NO 104

<211> LENGTH: 296

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 104

ggatccgggg aagtggagac cgggggtccc	ggcagcgggg cggcccgccg gccacgcgg	60
ggatgcacctc tcgtgggtg ggagctggcg	ccatcgccaa gaagaagctt gcccggcca	120
agtacaagga gcgaggagact gtctggctg	aggaccagct ggcccgatg tcaaaggcagt	180
tggacatgtt caagaccaac ctggaagaat	ttgccagcaa acacaaggcag gagatccgga	240
agaatctga gttccgggtg cagttcaag	acatgtgtgc caccattggc gtggat	296

<210> SEQ ID NO 105

<211> LENGTH: 525

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 105

agcccttag atttccttga gtggaccggc	accacttctg acttcctca gagaccttga	60
atctgagctc ttacagccaa ggtatcttgg	ggctcaagc ctggggaggg accaggatg	120
ggaagataga aactggatc agtgggacat	ttctggaatc tgccgaagag ggaccacaga	180
gaacatcttc agtctcttct	ttgtctctc ttacccttc ccagagatag ttccaccccg	240
agtttctta ccctcttctc	aggccatcc agaagctgt agccttaggtt ggatgtgcc	300
taaggaatgtt ggattccaag tctatacttg	attctgactg tggtaatcc ctgccttc	360
cataacctgt ggagggttctc	ttcccttca tagaggagga agtgtatcagg tctgaaggtt	420
aaaaaaatgtt ccatacagcc aagcaaaacc	caggatctta cagaggcaat ggcactgggtt	480
gaggccttcca taccttctca tttcaattt ctttcttattt ggatc		525

<210> SEQ ID NO 106

<211> LENGTH: 585

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (495) ..(496)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

-continued

<400> SEQUENCE: 106

gaattccacct tatgccatcc atgaatcctg atgggtatga aaaggcccag gaaggagatc	60
tagtaagtgt aatcgccaga aacaacagca acaacttgc cctgaaccgg aatttcccg	120
accagttcgt tcagatcaca gagccccccc aaccagaaac tattgtgtg atgagctgga	180
tgaagaccta tccatttgt ctgtcagcaa acctgcattgg aggtactttg gtggtaact	240
accctttga tcatgtgaa caaggcattt ccacatata gaaatcacca gatgtgtg	300
tgttcacaaca aatagcactt tcttattcca agaaaaactt acagatgtt caaggtagac	360
cttgtaagaa catgtaccctt aatgagtatt ttccctcatgg aataacaaat ggagccagtt	420
ggtacaatgt cccaggtggt atgcaggact ggaacttattt gcaaacaat tgcttgaag	480
tgactattga actannttgcgt gtaaatacc catttgagaa agacctgccaa aaattttggg	540
cacagaatcg aagatcccta atccagttt taaaacaggat gacta	585

<210> SEQ ID NO 107

<211> LENGTH: 578

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (496) .. (496)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 107

ggagttagtc cggccggct ccctcgcccg cegagtcaac ccaggectca gtgacacttg	60
cgcagtcct gcagctggtc cagcaggggcc aggagctccc cggcctggag aggccggcagg	120
tgcgtgcac ctttgacgaa cccacggcgt cccgactccc gggataccca aagccctggg	180
aggccggcgcttccggag cacccagcgc cacagttcca gactggggac cggggctcg	240
cgcacccctcc gagtgggcag aggaaccgc tggaggagcc tggctcgccc gtttctgagg	300
ctccagggtcc ttgcagctg tgaataaaa attttgtgc cctgtggca aaggacactg	360
cagccccaaag ggacacccccc agaatggagg aaggcctgac tactactgaa ccctcagcca	420
ctgcggacac tcccaaccgt gcacccttag gtgcctccgg atggataga ataagatact	480
ggccttggac agctanggtt catagcaaag gaatgtatattt agtgagcccg gactttatg	540
acttcctatg catgaaaaa gctaaattct ttgtatgt	578

<210> SEQ ID NO 108

<211> LENGTH: 382

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 108

ggtccttatac atctgttcca tcaacatgtt ctttgcgtg gtttatgtcc aggtatgttgg	60
gcataatggta ttgtatgtgg tggctgcgtt ggtcagegtt gtttatctgtt gctttgtgtt	120
ttacttgggtt tggcgtgtt tcattgcactt gggcatgtcc ttccctggact ctggacacac	180
acgcttatgtt acctatctt ctgtatggatg gaggtgttgcag tgccattgaa ggatacggaa	240
agagattgtt ccacgtgtt ctcttccgtt actccaaat gactacaattt tgattattt	300
taaagatgtt gtttcaggat tcctcaaaat ctacgactct tggttcaaa gccattgtc	360
aatgtttatgtt ttgtatgttca ct	382

<210> SEQ ID NO 109

<211> LENGTH: 570

-continued

<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (456)..(458)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 109

gggttcttgg aagacatggc acctctggag cgcgatggcc taatccagga ctggaaaca 60
tctgggcttg tttacctgga ctacattagg gtcattgaaa tgctccgtca tatacagcag 120
gtggattgtc cagggttatga actcgagcac ttgcacacca aagtgcaccc actgtgcac 180
aggatagacaa aaatccagtgttacaatgcc aaggacccgc tggctcagtc agacatggcc 240
aaacctgttag ccaacctgtctgggttgccttgc acatgcctc tgatacaacc 300
tccgactcaa cgccagaccc tcagcgagtc cctttgcgc tggcttgcctcc 360
cgccccccca tgcctgagga ctatgccttg gaggaactgc gcagcctcac acagtctac 420
ctgcggaaac tgactgtcgg gagccagtga gccctnnnct cctccacca cactcacatg 480
cttggcaca ctcaccacac agagggtc tgcataaagt tgattgcctt gtttgcctt 540
ctctggcttg gccatggaat cccccctccc 570

<210> SEQ ID NO 110
<211> LENGTH: 405
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 110

tttctttccc cctcacaagg cttccagaag ccctagttgg ctttgaccc acacttcctt 60
tttattaggc gtcctgttgg ggtggctgag aatcatgaaa aacagatcct ctgctagcc 120
ccatgatgaa gttgttagac accagcttc tggaaactcg tggatgtttaatggca 180
tgtgaccctt ctgtgttctg gggactcaat cagaaaggta aaagccatta aaaaaagtt 240
gtaaagattt tattcatctc atatcttctt gcctgggttc acggccttac tgactgaaat 300
aaaatcattt ctgattggac gcagacctgc gtttcttgg acttctgaat ccatgttcat 360
attttctctg gccactgaac accttggaga ttccgtttag ggact 405

<210> SEQ ID NO 111
<211> LENGTH: 515
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 111

agtttcttgg aaatcttgc acgttcaat atttagaccc atttagttct aatacaagtt 60
catctttattt gtcaaaagtaa aagcaatattt cttgtataatc ttaactatgt aatgcaat 120
gagaaccccttc ttctcagagt acttctcagc ctcttaggatt tactaattct tcctccccc 180
ctcttaataa gggtaatgttcaaggcca acaaagagca gttctttgg attttgataa 240
agagaaaattt tggttataca tttagcaagtg tgctgtatgt aagcagctaa acacaatagc 300
cagcatgatc attaacactg cctgacatat tcaagaaaaga actggcatag ctaaatgtga 360
tttgatgtgtt tttattgtca gaatcaaaaac ttcttagagt ccacgggtgt gtgtgaacac 420
actggatgtt ttcatcatca gctcaattaa atgggttcac tggatggaaagg gaaaaaagcc 480
aatgaaaaggat atctacaggc agacccattt ttaact 515

<210> SEQ ID NO 112

-continued

<211> LENGTH: 432
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 112

aaaaaaaaatgg cgccgacgtg agcgcgagcc cgggccacc gaaggagtgc ccgcacgcctt
agtggagcc gctgaagccg cggaaacaag aggctgaacc aagctgagga tggatgagga 60
accctcgaaa cccagctgg acatgcggc tactgcagag cccagtcga gtgagaccga 120
caagggggtg tccccagttc tggctgtat agacaaatcc tttcttatgg aggaggagcc 180
ggggcctgac cgggcaacca caccggcact gtggaaacgt ggagggccca ccggaggac 240
ccagcagggt gcctcccccag cccagacag tggccattcc ggacctggac acacccttgg 300
cccaaccaggc actgtctccg ggaccagtga ggacctgegg cctcccaagac gacgccacc 360
accaggaaag ca 420
432

<210> SEQ ID NO 113
<211> LENGTH: 536
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 113

tttttttag aaagacaac tgctttat taaaacactg gaaaaaacat taaaaggcaa 60
atgtccatta tataaccaag aatgttaagc atttggaaaa tgttaatctt ctaaattgtg
gtaggcactt ccagagact aaatattgca aattatccta ccagatgtct tctgtataac 120
caaaaataact tgatatgtg aaacacacaa ctaattaccc aaagtccacca tggtaggttt
caatttaatt acaagtaaaa gtttgcacca agatgttctt gacacatgaa gcttcaggatt 180
gaatttcaga aatgttaaca aaagtatctt cttttttgc ctgtaatgt ttgggtattt 240
ctgtattgtt ggcttataatc cactacagat actggttcta ggccagccca agggttctca 300
agcattgaag gcttgcataa actctccaa tcattagaca ttctctttc tctaccacgc 360
cctgatccaa atgggtttaga tggcccttggaa gacccctggg ggtgggtctg ctgctg 420
536

<210> SEQ ID NO 114
<211> LENGTH: 406
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 114

gcacgaggcc agggtcaccc tgagcaggaa aagcaccccg atgctgacca ggttccctggg
cccgcgcatcgat cgccagctgg ccagaaactg ggtccccacg gcgaggctgt ggggcgtgt 60
gggtgcgtg gggctggat gggccactga ctggcggctg attctggact gggtgcccta 120
catcaacggc aagttcaaga aggatgacta gactcacaa ctcaggcccc tctgtatgtct
gtgtgtgtgc ctctgcctat ctgcattctgg aactgcccag gctctctggaa tggactctag 180
gaagtccctg gcacgaggatc atttctctttt ttgggtggaaa taacttttgt gtgtggacac
acagcattaa acctcactt gaaacctgaa aaaaaaaaaa aaaaaaa 240
300
360
406

<210> SEQ ID NO 115
<211> LENGTH: 237
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 115

acattttat acatatttac gtgcaacgtt gtttggaaa taagttgggtt aaaaactttt 60

-continued

catttcagtg ggctgttagt acattaaaag tctcagagt taaaggtata ctggtttat 120
 ccgattcagt aatcttcaag aactcatagg gaagtcagta tcagcaggaa agtggttagc 180
 ttggctgaaa catacccaaca aaacccccag aggtgaggga aggcattta atgctta 237

<210> SEQ ID NO 116
<211> LENGTH: 482
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 116

attttttca ggccttcttc caggagcatg tggtcccagt gtaccgcaaa gtactaacag 60
 tatataactg acatcggttc atatgttgc aggcactccg gatgggcaaa ctgtcttatt 120
 catataccctt atgtccagta tggtgcctgg cacattatgg cacctcaaaa tatgttcatg 180
 gttaaaaatg gtaggctgta tggttgcag cttagaaaaac agtacatcag cacttttac 240
 ttgggtccct ttctggtcag tggcacatat ctcgtgttag acttgtactt aaatggataa 300
 gcactcccca gtgggtcacg aacactgega aaacagaagt atggggaggt gcaaccctgg 360
 caggcaaatg ctgcctgaca aataccctt gtagcaaagg cctgcactt gatgtctg 420
 atccctctgg tttgtcacga agaataggat gggataaata gagcatacat tgacattaac 480
 ct 482

<210> SEQ ID NO 117
<211> LENGTH: 401
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 117

accattttgtt ttttttattt tagacaaaaac cgctttggaa agggaaagtc 60
 tcatgcaggt tataaggcttt tctctgtcta ggtttcaggt gtttgcactt ggactgcaga 120
 ctcttaccaa tcacgggcat tttacctttt ctgaacactg cagtttgcata ggcttagagct 180
 gaagttggag gagcctgttag tgcttcacac agtgcgtat gttttaatgg ataaaaatag 240
 ctggtttcta ttaactgtat agacagtaaa caaaaaatcc ttaataactt actagctct 300
 tttcagaatg cgtttatttt ttgtcagttt cagtcctaga tataacttact gctggtacag 360
 ttgtactcta agatttgcata ttgatatcca cgttactccc t 401

<210> SEQ ID NO 118
<211> LENGTH: 446
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 118

aatatattac aatcttcaa aatcgatcac tcctcagttt ctattgtgtg atcagttgt 60
 gttttatattt gtatattgtct ccccatattt gcccttcttc taagaaaccc tatttctct 120
 ttgcctatct caaatggaga atctcaactc tggttgcgtga actgcctggc cagctccac 180
 aagcaataacc tcccttgcac cagcaggacc aaggagccg gccttactg agtgcgttac 240
 ttgtgcactt gcctctccct caagggtcgg ggaccttggc tggagtcctg accctggct 300
 cccagacaga gatcttcgac ttcccttgcgt gtcggcaat ctttggcac acctggatt 360
 tccccatgac ccaggtcatt tttttttgt tcaacggact ctggactctc aaaaggatct 420
 gatccttttgcata aatttgcac agccct 446

-continued

<210> SEQ ID NO 119
<211> LENGTH: 552
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 119

gcacgcctta acagtgcgt tgctcagact attctctagg acttgaattt ggagcagaaa	60
caaaacagca cctggtcctc agttacagag tggggccttg gtaggataa atcaaattat	120
ttagttact gaggggaaca agcatctggc ttcttcatc ttagcatctt taaatctgag	180
aatgctagct gagggtgaaa agcctggga taggcctgcc tgaacactcc tctgctgctt	240
attacaatct tagctgagca ccttc当地 cttttcctt tatatgc当地 tagttccaa	300
taatagcatt atcttataag acttgacagg aagctaaattt atgaagcatc tcgcccaggt	360
cctgacacct gggaggtgct gaataactggt cagtttcttc cgttaggtacc cgccagaaaa	420
gttggcaggg gactgaacca tatatctgac ctctgc当地 ctttccaggtt ctttagattat	480
gggggtcagt ggtataattt aggttgtta acagcagtag ccagtattgg agttatttac	540
cacataatcg ag	552

<210> SEQ ID NO 120
<211> LENGTH: 546
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 120

tttttgtgaa ttgatttaaa tatttttattt aaggaaatatt tctgaagact atagttcatt	60
atttatagga aaaatataaa gcatacatgt ttaaagatca tttttagtgc acattatagg	120
aaatagattt ctccaaataa cataattatgt tttttagtgc taccagtggat atgcattctg	180
cagaaacatgt gttttacctt cagatctgag cacactgccc ttacatcaa aaaagaaaaa	240
aggataataa aaaaaaaaaa cacaactttt attagttaa attttttagta gaccacatct	300
gattttgtga agagcaagtt ctttttattt cctcttcaag gaagtgc当地 ttttttccac	360
ctctttctga gcatctttat cctcttggt aatacaaggaa agcaacaccc ccaaattaca	420
gaacttcata gcactgtcga tttgattaag atcggc当地 cacttggcca tgaacatgt	480
attggactta gaaaacccag gctgttagttc ttcaacctta aggaaatttt gcaaagctc	540
ttgtac	546

<210> SEQ ID NO 121
<211> LENGTH: 394
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 121

ggcttcttgg ggctgc当地 cacgtcagtg gatccagcgc tgaggaggcg ggc当地aggc	60
ccaagaata agaagcgagg ctggaggcg ctcgctcaag agcctctggg actggaaatc	120
gatcagttct tggaggacgt gccc当地gc当地 gagcgc当地 gatggccccc cctatg	180
gtgtgacattc tgc当地tcca tctccaggatg gcttgc当地tgc当地 agaggcccccc gatgagaaac	240
ttttcttcgt ggacactggc ttcaaggata aagaactgaa caagaagagg accaaaggcc	300
agaagaggtc actgettctc aagaagcccc tccggagcgc cctc当地ctt gagaacaccc	360
ccaaaggccc tggccaaa gacgtcctcg ccc	394

-continued

-continued

```

<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (490)..(491)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 126

tacagatgag gaaattaagg cgagagaaac taggaaattt gcctgaggc acgtaggct      60
cgtgtcaaaa ccagttata ttaataaaac cttatccc ttaatgtat atataggggg      120
aaaaaaaaaa cagtccatgt aacatcatta gctcagagag gagtggcag tgccctctg      180
aatggattt tcacataatg gcattttaga agttatcaa atcatacaga tctgaccgt      240
tctgggtatg gtttatgca aagaatctt aatgaagttt tcaacatggc tcctaattt      300
gggcatttc atggtaaaa ttttggtcc cttctggAAC ttcaagggtgc ttccaattaa      360
caataactt gaacactgac tcctgcagta tggatgcct cccctgccag gtggcattc      420
tgtggatact catggcactc tacgtgcccc caaccaagac aagcagaggt tcaccactgt      480
attccccagn ngaggtatgg cattgattn aaacttcaac attatccc aggttgagaa      540
actggaaaca tcggagcaag taagctaaa aatagcctt gtttttctg gttactat      600
cttcatata gaactcaaaa ttagtgaaaa g                                         631

```

```

<210> SEQ ID NO 127
<211> LENGTH: 498
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (225)..(228)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (440)..(441)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 127

ttttttttt ttttttgag cagcgcttga tttattagca taaaaaaaaac ccagttcata      60
tataaaaaac aagctgattt ttgttgtcaa gtgttaaaag cactcctta aaattaaata      120
caatttaaaag catggattaa tgagttgatt tcctggaaag cacttcagtg aatgaatatt      180
tgccaatgga aacatcagat gcacaccacg cgggcaccag ggggnnnnng gatccacagg      240
gtgtctatc acagcgtctg accccagaca ctgttaggtgc cacacacgtc cccgggtgggt      300
attcccccta agacccaggc cgggggcacg acctgtgaaa attcacttgc acgttagaat      360
aacgaccacac ttcaagtgca acttaaacct cgcggcaggc ccacccgacg tgcaccgtg      420
agccgtgaca ctggggcgn ncagtgaaag ttctgtggac aatgttgtgt gaacgtccat      480
gtcggtgtt gggccccg                                         498

```

```

<210> SEQ ID NO 128
<211> LENGTH: 534
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 128

attcatatga agctacagag gtttctggac ttttagtggg ttttaggaacc agcccatcaa      60
cgtcagtcag ccctctgagg atgggcgtat ggccggaagt gtccattt cactgtggct      120
ggctctgtggt gaagtggctg gtctacggtg aacgtgtct aaggcatctg ctcaggagga      180

```

-continued

aagggtctg atcagtatca catataattaa gataattaga aaaatggagt aactggcaga	240
gaaaagaggaa agcgtaatt tactactata tatggatct aaaaacagac ccaacagaag	300
ttcattattt gccaggagcc agtgtgagga gctccgccc tggcaaaggt catgaggaag	360
gaggctcggc acacgcaaaag gcgggatcaa gcctcaggag tccccctgga aatttcgag	420
cttctacccc caaaccagag tctgcctact ttctgccttg tgctctcacc tacacctctg	480
actttacggg gggctgtccc ctaccacctc tctctgaaaa gagttaaatt acag	534

<210> SEQ ID NO 129
<211> LENGTH: 562
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (454)..(454)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 129

tatTTTgcca ggTTcccggt ctcaaATgca caggCTTgga ttGCTTtaca tcAtggTatc	60
ttccccatcct gggTggacaa accggcaatg agttaagatt acagccccctt aatccTaccC	120
agcaCTAGTC acactggaga cttTggggTC acccaacttc aatctggggA tcccagaagg	180
ttgacACTGCC tcaacCTGCC tagggatctg gTcccCTggA ggTTgtcaCg cctcagCCTg	240
ctcggagatc tgccAGTCCA ggggtcccAG gaggttgacg tgccTcgacc tgccTgagGA	300
tctgcACCCt gaccCaggGA agcccAGTC tcaggTTgca acagtactgg gtAggataAG	360
cttcagAAAG actcACCCt aagtaAGTCC acccatggAA atagaaggAA gcctttagt	420
tgtgggactg tgccAGTttt caacaataAC tcangAGtCC aacaAGAAcc ccATTGCCt	480
tctggAAAGt otAAAAGAGG ccCTCCCCAA gtttgccaat ctggacttag actcttaCGA	540
gggacAGGTG atttAAAGG AC	562

<210> SEQ ID NO 130
<211> LENGTH: 556
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 130

tttttttttt ttttttaat atgaAGCAGA aacataAGGT ttggggAGGG atAGCAGGAA	60
agaaATgaca tcaatTTAT ctTtacatAT tcccCTCCTC taggcAGTTC tccAGACATC	120
agatCTCTTA actTggggTG tggatCAGtC ttCACTACTCA taaAGGGGAC cAGTCTTtA	180
aaACATGCAta AGCCTGGAGA CTCCAGGATG gttCTCTCC CTCTCTTAA ATGCTGTGGA	240
ctAGAAAGGC GCCCACTTG CTAaaaACTC tacATCAGTG tccCTGGAGC CCCGAGGTC	300
ctcAGGTTCC tcCTGAAGAC ttaaAGGATA GCACAGAAAA ACTTCTCTC CCTAAATGGG	360
ttttCTGAAG CGGAAACAGG TGTcAGGAGG ggatCTTCTC tggcatgcgc ttCACAGTAG	420
gCCATCAAAT CTGCAgCTGC CTTGGACACC ttTATCCTAT CGATGTGGC ttCCATCTC	480
AGCTGTTCTA CCAGTTCTC GGCTTGTGT atGCTGGCgg tGTTGTTGCT GGCATTTGA	540
ATGCTGGGTA GGTTTC	556

<210> SEQ ID NO 131
<211> LENGTH: 248
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 131

-continued

aagagtacca gactcgggag cagcttcag cccgctcccgtcagggctgg gtctgtacg	60
tcaccttat ctgcaacatc tttgactacc tgagggtgaa caacatgcct atgatggccc	120
tggtaaccc tgtctacgac tgcccttcc ggctggccca gcccgacagc ctgagcaagg	180
aggaggaggt ggactgcctg gggctgcagc tgcatacggtt cggggagcag ctggagaaga	240
tgaatggg	248

<210> SEQ ID NO 132	
<211> LENGTH: 426	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (59)..(61)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (356)..(357)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<400> SEQUENCE: 132	
ggcacccaaac ccaaaaaccgc agtgcccaag tcacaaggcca cggaggagtc tatgaagcn	60
natgtaaagg agaaaacaatc gcagaagata tctagatcaa aaaaaataga caaagaaagc	120
caaaagccac ttgaagttaa aaaagtcttg tctgaccgta caccgtgggg attgtccaca	180
cattcctgctg gcggtctggc gccccacccca tcaacaggaa ccagagccgg ggggcagcct	240
ccagccccctc ctcctgaggc cagagggagc cttttggaga aacaagtacc agaaggagat	300
ggggagctgg ctctccctt gttcaaaaca gaaaaattgg aaaagcaggc agcagnngga	360
atcttaaagg ctgaggaga gatttggaa gatcagctgc ccatgcaaaa tttgaagcca	420
gccccct	426

<210> SEQ ID NO 133	
<211> LENGTH: 453	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 133	
tgaattgcta cacccctcctt caggtgatct tccgaaccca gggatcaaac ccacggctcc	60
tgcagctcct gcactgcagg cagattcttt actgctgagc caccaggaa gccctagagt	120
acataggctg agtataaatg tcatacatca gaagggccct gttttttga cattcccttag	180
atcctgcctt gaactgccat ttggtcatta attccacatt ctatgtatct acacaaatct	240
taaaggatatac acatcttctg tttttttt aaagcgtacca gtgtttttttt taatgtctgt	300
gaaaatatga ataaactaac cagccgtaaag tatcttggaa tgaaagatata tgcataaac	360
attatgtatggaa actttaaaggc cttaaaccag aagtgtatgg aataattttta caatggaaaca	420
tatttttttgc tatttaatgt tcatttgtgc ttg	453

<210> SEQ ID NO 134	
<211> LENGTH: 552	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 134	
ggaaaatggc ggattcctcg gggggggggc ctgggaagcc tcctgcgttgggggggtt	60
ctgcttagggg tgcttagggc aaaggaagaa cacaagggtgg aagaatagtg gagtcgcgtt	120

-continued

acttgcagta tgaaaagaaa gcccccaagaa aggctcctgc agcagatgca ttaaaaggccg	180
gtggggacgat gcctgcaggt ggaacaaaat ccagccagct ccaaaaagagc aaagatggca	240
gtggggctgaa caaaggcaac ctgcagtcta ccttgctgga ggggcatgac actgccttgt	300
ctgacctgga tcttcagcc attcatgata aaagtgtggt ccgaaaagact ccacaactaa	360
aaaaaaaaagtc aaagaaagcc gagttgtcat cctcttctgc tgtgagtgaa aagagccag	420
atctgttaca agcaatggaa atgatggagt cccagactct ccttctgacc ctgctgaccg	480
tgaagatgga gaatggcctg tctgcattcg aagaacaggc agaaaagaac cttagaaatat	540
tgtgtaaaga ga	552

<210> SEQ ID NO 135

<211> LENGTH: 437

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 135

tttattgagt cagctcatga tcagaagtct actcataacct tgatcattgc aaaggaagta	60
gaccctgtc ctttatctct tccctttctt gtaagctcca ggccctggcc atgcaattgt	120
cttcatacctc tccttagtcca gtttagtgaac cacttctcca cataaccata gcctccgctc	180
tgctggcttt ttttggctct tgccatggga gtatgtgcaa ggccagtgca tggatgtgaa	240
aacctgtcac ttgccaggc aaaaaaagga gtcataacta cccttactgt ccgaaggccct	300
gagctgtatt ctggectcac tctaaaatgg tcttgtctta gagctgtatgg ccaaggagta	360
agctgcagggt gtgggtgcc aaggttaattc tggaaaggagc acagggggat ggtcgagcca	420
gtttggacca ccatctca	437

<210> SEQ ID NO 136

<211> LENGTH: 524

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (291)..(293)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 136

atgttctca ccatgtttgg ggagaagctg aacggcacag accctgagga cgtgatccgt	60
aacgccttcg cctgcttgcg cgaggaggcc tcaggtttca tccatgagga ccacccctgg	120
gagctgtca ccaccatggg tgaccgcttc acagacgagg aggtggacga gatgtaccga	180
gaggcgccca ttgataagaa aggcaacttc aactatgtgg agttcacccg catctcaaa	240
cacggcgccca aggacaagga tgacttaggcc atcccaagcgc cccctgccc nnnctgtcc	300
cagccacctg ctccccacata tacccgtatgc accagctcca tgcccatgag cccagagccc	360
cctctcagag gactctcccc ctgaggggcc gggggcccaag ctccgagtga aggaaacggg	420
ctgagaaagc acagcaccag gccaggggca gagccagcgg gaggccgggtg accctccaag	480
gaaacccat cttctcgaaa gctggggccag ggggctggac cggg	524

<210> SEQ ID NO 137

<211> LENGTH: 561

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 137

aagcccatca ctttcctga tggacgctcc ttacctgcag gaatcttagt ctccctctcc	60
--	----

-continued

tttatggac ttcatcacaa cccaaacgtg tggccgaatc cagagggttt tgacccaacc	120
cggttctcac cagggtctac tcaacacagc tatgccttcc tgcccttctc aggaggatcc	180
aggaactgca tcggaaagca gttgccatg aatgagttga aggtggccgt ggccctgacc	240
ttgcttcgtt ttgagctgtc accagatccc tccagggtcc ctgtgccccac tccaatcatg	300
gtgctgagat caaaaaatgg gatccacttg cagctcaggaa aactgtctga tccaggactt	360
ttgtgatttag atgaacaact catataagac agacttgttc tctgtctgg tgattaggat	420
gaggacacct gggcagccat tgctggacat gttaagtctt gtgtgaccac catcagctg	480
tctccggctc tctccagtgc ctacccatgt gtcagtcatg tggcttcccc tctcttgctc	540
tcccttaata aagtttgcat g	561

<210> SEQ ID NO 138	
<211> LENGTH: 515	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (232) .. (234)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (428) .. (429)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<400> SEQUENCE: 138	
gtcacaata tatgcccatt tgccctttgt caggcaggct ggcctgtact ccatcagttt	60
acctaacaaa tacaatttctt cctttgatta ttatgcattt ctaattctga taatgatctc	120
ttacattcca ctttttcccc agttatactt ccacatgata caccagagaa gaaagatcct	180
ttctctactt gaagaacacaca agaaatttga atagttctt cttcctgcac annncagaa	240
acaaaacttcc caatgacaaa aaatgctca gacttttca gttcccaata cgtttcatag	300
aaaaataagta agaactatTT ttaataacta aaaaaataaa taaataaacc aaaatccagt	360
gtcatgtggg cctgggggttt tctaaaaaac aaaacaaaaaa aacgaaagct gttacataaa	420
acatcctnncc cggccatTT cagcatgctc tttcaaccag aagttcccaa tattttagat	480
ggcgctggaa agggatttgg cattttatat cctcc	515

<210> SEQ ID NO 139	
<211> LENGTH: 658	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 139	
gttatctgta cctggacttg ctgctatggg aaccagctgt tgtttgcata aacaccttga	60
aaactttgaa acctgaccctt ttgaaacctt accctttatc accttttacc gcgtgccagg	120
ccctttctga ttctactgg ttgactctgc cccttcctt cccagagctg gctggaccat	180
cgctctctgg tgaccctgtgg aagttaggcg cacagcactt tccagctgcc atgcagagac	240
ctccagctca gaacaggctc gtctccgcca cgcccgacc ccctcctgtt cctcaaccag	300
tttctctctgg cgactcggaa gcatgcacac caggaaagaa accttttacc aacatgggcc	360
cttgcata tttctgtttt taagacttca aaggggccctt gaaagccaca ttttgcata	420
tttgggtttaa aatgagttgg gcacacaggat atttaatttt cttttttttt tgcacagcct	480
tagaaattttt cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	540

-continued

aagttttta ttgaaaatgg gcaagattgt taattcaagt gctcttgcc tttgggtcctt	600
gagcaaaagg atggactctc tccaagtctc cattaactcg tgggaagatg gggcttgc	658

<210> SEQ ID NO 140	
<211> LENGTH: 374	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (193) .. (193)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (219) .. (221)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (328) .. (328)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	

<400> SEQUENCE: 140	
---------------------	--

tttttttttt tttttgcagc aatgacattt aatacttctg gaatgattgg gatatctgaga	60
acacgctgtg ggccggctatg ctgggctccc ggatgtggga gctggggcccc gcctccgaa	120
gggggtccctg cccgggtggg aggagcgggc ggccgcgggg gcctgacccg gcaggcgggc	180
agcccccggcgc gcncggggagc ttccagaatg gcacagccnn nggcccatgg agaggcttca	240
aggaccggag ggtcgacacg ctcggccggg gcacaaactcc atgccttcga cgtccacttc	300
ttgctccgag tcgtcggtgg agacggcnga gcccgtgtg tcggtgacca cgcgtccag	360
gtcttgccgca gaca	374

<210> SEQ ID NO 141	
<211> LENGTH: 531	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	

<400> SEQUENCE: 141	
---------------------	--

gcacgagccc agttgagcgt ggggaagggg atgaacagcg gttacaggag gttactcagg	60
aacaaggaac cctctgagat cttcagaacc tgcactgtga gaagacagac agacaaacaa	120
acctaaggat taaaggcaca ctgcttatca tcaggctta caactcacac aggcaatgcc	180
aagactttgg tatggatcag ctgcatgtt tgcccatgca ggaagagagg ggtttggta	240
caccaatgtt cgcattctc aacaggccaa accatctgtc tgggatgtgt ttctactgt	300
atgcaaatgtt cctcagaaga aacaggagct acaaacacac actgtactct agttaaggac	360
tggccagctg gagggcttac tggtgacgtg aacttggact ttctctgca tgcacatccc	420
aaaataagat gggctgggtgg acggacagag gcagagacag ctgtgtatg tcggtgacaa	480
aagccacggg taggtttca ggcgttcatg gctcttcga cttctctgca t	531

<210> SEQ ID NO 142	
<211> LENGTH: 544	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	

<400> SEQUENCE: 142	
---------------------	--

gctgatggac ctggggagc gccagctcg gctggccctc acggagccctc gagccttgc	60
gctctgcccgtt ggacgcgtt caggccgttc ttgtccgggg tggcaatggat gatgtggcc	120
agtgcatggaa gctggacgggg ggctggcagt tgctcaggac ctggctgggg cacgagaaag	180
gtgtcaccccg gctggccagt gccatggcaa agttcgcaggccccccggctg cccctggta	240

-continued

tgaagctgct	cttcaccaca	cagagtagca	tgtatggagtt	ccagagggtc	acctccacag	300
ccttcctggc	tgagctgctc	agcagcaatg	tggtaaacga	cctgatgctc	ctggagtccac	360
tgctgtacaa	cctgatggca	cggcagaagg	acacgagcgc	ccgcgtgcgg	aggctggtgc	420
tccacggccct	ggccaaacatc	accttgggct	ccccagataa	ggtacagacc	cacagcccc	480
aactcctgac	agccatgatc	ggtgggctgg	acgacgggga	cgaccacac	agcctggtgg	540
cgct						544

<210> SEQ ID NO 143

<211> LENGTH: 464

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 143

gcacgagccg acccctgcct ttcttcgttg ggggtggtcgg accttagcatg atggggactg 60
aggccgaggg gagacaggcc cccgtcccaa gctgctgttt cctcttgct gtggcgcccc 120
agtttggaaacg ctggacacccg ttcttagggc ctccggcttc tccccctccct gccccctetc 180
tcttgcttgt gatcgcccaag gctctgtcac agcccagctt tctccaagca gcaggaggcc 240
tccactgtctc taggcagcctt cggttgcgtgc tgccagcctgg aaacgagtttgcaccc 300
tggcagagac caaaaaccccg gtttttaggcc ggggtgtggg aggacagact ggccaaagcg 360
ggggatagac gagggggggccccc ggtgtcccttc aggtatgcgg gcatgtgcag gaccgggggt 420
ctqqqqqacac qqqaaatqccaa ccccccgttggc ccccccttggg qqac 464

<210> SEO ID NO 144

<211> LENGTH: 599

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 144

acctgagggtt ctcccgatgt	agcccataaa tgaaaaggcg	gacgtgttct cttatggtat	60
catcctctgt gagatcatcg	cccgcatcca ggctgatcca	gactatcttc cccgaacaga	120
gaatttcggg ctagactatg	atgcgttcca gcacatggtg	ggagactgtc ccccgagactt	180
tctgcagotc accttcaact	gctgtaatat ggaccccaa	ctacgccccat cctttgtgga	240
gattggaaag accttggagg	aaattcttag ccgcctacag	gaggaagagc tggagagaga	300
caggaagctg cagccccacag	ccaaggggact ctggagaaaa	ggacctgggg tgaagcgaact	360
gagcttaactg gatgacaaga	taccgccccaa gtccccacgc	ccaagacgta ccatctggct	420
gtctcgaagc cagtccagaca	ttttctccaa taagccccca	cgtacagtga acgtttttct	480
gattaactcc ctgagtaaac	tgttataata atgaaaaaatg	tgctactcat ggcagtagta	540
qqtcacaaqatqccctttc	tqtqatqttt ctqqctctqa	tttcttcatc aqtatttt	599

<210> SEQ ID NO 145

<210> SEQ ID NO: 1

<212> TYPE: DNA

<212> TITLE: B.M.

<400> SEQUENCE: 145

```

ggaggggggc tcaggggtgga agagaacaaag cgggaccaca cctgccttcc cactcaactgc 60
ccctctccct gtccccatgca gggcgactcc cacaagcttg actttcgaa cgacctccctg 120
ccctgccttc cggggggccata tggggccctg cccccctggc aggagcttc ccacccggcc 180

```

-continued

gcctccctct tcactgcgac tggtgccgtc catgctgcag ccaaccctt cacggcagct	240
ccccggggccc atggaccctt tctgagtcgg agcacccaca ttgateccctt tgggcgtccc	300
acaagcttcg cctccttggc tgccctctcc aacggggcct ttggaggcct gggcagcccc	360
acattcaact cccggcgccgt ctggcccaag aaagaaagtc caggggccccc accagccctc	420
gcctcccccc cagaccatg gggccgcctg caccgcagtc ctctggcctt tcctgcctgg	480
gtccggggcc ct	492

<210> SEQ ID NO 146

<211> LENGTH: 397

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 146

cgggggtggtg tacggccctct gggactacag tgcggagttt ggggacgagc tgtccttcgg	60
agagggcgat tcggtcaccc tgctgcggag ggacggacta gaggagacgg actgggtggtg	120
ggccacgctg catggccagg agggttacgt gccccgtAAC tacttcggc tcttccccag	180
ggtaaaggct cagaggagta aggtgttagct ggagagaagg acgtttccaa gggagacagg	240
atgaaggcgc agctgccttc gtcggcggacc tccctcttcctt ctccgcgtgc atatcttgt	300
acccccaaggc ctttcggcgg gtggggctct tgccaaacaggc tctccggaaa ccctggggag	360
aacgagaacc ccagecttaa acttagaaggc ctgcctt	397

<210> SEQ ID NO 147

<211> LENGTH: 486

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (458) .. (458)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 147

gttcctgaa tggaggcggc agtgaaggtag aacagctatt tcaagacttc agcaacagaa	60
gagctgacaa ctttcagtcg gatgggtgtca acgactctga aaaatgtctt cccaccgctt	120
ctcaggagct ccggagatca tccctggaaag ccgtacacgc acacccatcg acatatggag	180
ttttggctgc atcccttcggc aactttttaac aggacagccg ctcttcctg gagaggatga	240
aggagaccag ctggccgtgt tggatggact tctggggatg ccaccagcaa aacttctgga	300
acaatccaaa cgtgccaagt actttttaaa ctccaaaggcc ctgcctcgct actgttctgt	360
gaccacgcg gccgatggga gggctgtgt tggatggggatg cgatgcggaa ggggtaaagaa	420
gcggggtccc ccaggcggca aagatgggt gacggcgtt aagggtgtg aggactactt	480
atttat	486

<210> SEQ ID NO 148

<211> LENGTH: 380

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (288) .. (290)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 148

atttctgttt tatctttaag gtcttttgg ttcatcacgg gtacagtatg ttgttagatca	60
tgcaatgaaa attgttttc tccacacccga tccctccatt gtcatgaccc acgacactgt	120

-continued

tcaaggctcg cactctgtgt gggctcccg gagagtc当地	180
aagtcaattc ttaacagaag aagatagttt atactgaaaa ctgc当地	240
ttgtactca ttaaaaatta tttttaaaat ttgttttattt ttaattgnnn gataattgt	300
ttacagtatt ctcttggtt ctgccatata tcaatatgaa tcagccatag gtatacatat	360
gtccccctccc ccttqaact	380

```
<210> SEQ ID NO 149
<211> LENGTH: 328
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (34)..(35)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
```

```
<400> SEQUENCE: 149  
acagccagg t gccgctgaga gaggtgaaga accnnagaca gcaggagaga cacagtgggg 60  
atctcgaggc aggagtgtgg gtggccagga gcctggggcc gcccggaggg cgtgttaca 120  
tgggataactg tctgtgaggc gcttggaaacc gtacctgatg gtggaaagca atcagtaaag 180  
accgttactg ccacacctgctg aagtcttgcc tttccagtc cccactgctc agggtctccc 240  
gccccggcac cgttcaggct ggacgatcgc tctccctgctc ccgtctcacc cctacatctc 300  
ctctccacq t qctqcccqat qqagcctt 328
```

```
<210> SEQ ID NO 150
<211> LENGTH: 255
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (52)..(53)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (180)..(182)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
```

```
<400> SEQUENCE: 150  
  
agattaaaca ttttatataa atgactctta aagctttaca ccttggggcc anngtactcc 60  
ttgggcagaa tacattnaga tataaaagac gttattataa cattgcacag ttgtcaaaact 120  
ttaaacacga aaccgaacgc tgctcgccgc agctgccgcg gggtgtgtct acatggacgn 180  
nnccageccga ggcccagcgc tcctctccctg tccactgccc aacgggatcc gtcagggtctc 240  
tttgagcacg aggct 255
```

```
<210> SEQ_ID NO 151
<211> LENGTH: 552
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 151

gcacgaggta aaaagcaaca atcaactagc cgaaaacgag cctctaaatt ccgtctcact 60
ccagtgccgt cttctctaaa gtttgctcca cggtccagtc acagttctca ggggtctggg 120
cggtctccca acgctgtgtt ccacaggaaa acagggtcca caggaaggca ggtcatgcgg 180
gacgcccctgg gtaagcacct gtacagccgc gataccgggg ggtctcagtt ctcctccggc 240
tttgtccggctg gtggggccgca aggctgcgcg atcttctcca tcaaggtaa gcggactcgc 300
```

-continued

gctttgtct catttcggc aatggcgaag tagtgagaa gatcgaagt gccccatgtag	360
gaggcagtagg agtgcgggtg ctggttcacc agccattccc acttcgttgt gtcccggtgg	420
ccgggtggca tgtacttggc ctgcagatgc tctagctggc tgtgaatggt gtgcggtcc	480
gtcatctcac cgctttccc tttgctccca ggtgaaaggc agccgactac aggcaactcgc	540
tctggaaacctt ca	552

<210> SEQ ID NO 152

<211> LENGTH: 511

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 152

ttgatgaggg ccagaaccag gcctggcgtc acccctgggc cccacctgtct tcctgcccac	60
cccagggtctg gagcgaccca tagaggtgcc acctccctt ctgatggcag ccccagccac	120
gtccccccag ccaagtgtc tccctcagac agccagagac acctggaaagc ctccctgtct	180
ccaccattcc tgctggaaac cctgaaggtc tctcagaggg ttgcacccctg tggccttgct	240
ccttcgggtc ctgggacccc cagtgtgtc cctgacgtct gtctggggct cacctgcgag	300
gagccgttcc ctgagctgcc ccattacccc tcccccaac taccggatgt ggtggtcctc	360
ctgcttcaag ctttgcaggc cctgggcaca ggttaggcagg cagatcctgc tgctctgcca	420
accgcggccgc tggcacctag tgggttttag ctgtgctggt tgaatgtcag caccctctgc	480
aggcactttt aaaggagtgt ttatgttgc g	511

<210> SEQ ID NO 153

<211> LENGTH: 355

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (116)..(118)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 153

gcacgaggaa gaagatcctt tgcgagaggg atgttctcg gaggatcttc ttcatccctc	60
tccagaagag gagaagagga aacacaagaa gaagcgctc gtgcagagcc ccaatnnnta	120
tttcatggat gtaaatgcc caggatgcta taaaatcacc accgtttta gccatgcaca	180
aacagtagtc ttgtgtgtt gctgctctac tgcctctgc cagcctacag gaggaaaagc	240
gaggcttaca gaaggatgct ctttcagacg gaagcagcac taaaagtacc ctgtatcaag	300
atgaacggaa aaccatccca ataaacacgt tttggataaa aaaaaaaaaaaaa	355

<210> SEQ ID NO 154

<211> LENGTH: 337

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 154

tgtaaaatgc ccaaagacag gacgtcgatg tccgtgacgc ttgaacagt ctcaatcctg	60
agagatgacg atcagttaca caaggacttc ttatccgag cactggattt tatgagaaga	120
gaaggatgcc gcatagaaaa tgtactgaag aatatcaat gcaggaagta tgcttcaac	180
atgctacacgc tcatggctt ccccaagttac tacagaccc tacagaccc cagagggac ttatggaaaa	240
gctgacaccc aagttacca acatgtaaat aaacaggaaac acaaatacgc ttccgttgaa	300
aaatctccac cgtttttgtt tttcattgtc atgaatt	337

-continued

```

<210> SEQ ID NO 155
<211> LENGTH: 546
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 155
gatgaatcat ctgaccgaag atggcttgc acctgacatt ctttgtgaa ccaggaagca      60
cacagaattt actcaagtta tagcaacacc agcaagcaca gtgcagacat cctgggttg      120
gaggagcctg accacaattt aaccccgatc cttactcatc acgcctgtt ccttggcag      180
gcacagaagc ccgcacttct atgtttagac tcattggaaa agtccctgtat gctggaaag      240
attgacggca ggaggagaag agggcgttag aggacaatggatggatcatcatttgg      300
gcaatggata tgaacttggg caaaacttcgg gagatggtaga gggacagaga ggcctggcgt      360
gctgaagtcc atggggtcat cacagagcat caagccgagt cccctgtt atatagcagc      420
ttccccatgg ctatctattt tacacaagaa gccgaagcct gctctctcc accctgcagt      480
agaggtctt ggaagacggg taagcagatt gttccagctg tttaaactac gctctgtatc      540
ccgtga                                         546

<210> SEQ ID NO 156
<211> LENGTH: 521
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 156
gcacgagcgg ggtatgggggg ggctggcag cctttcaca aggctgggg tcgcaggaga      60
gcctggcacc agcgggcttc tccccacago ctccagcagt ggaagcagct cagggccagc      120
atctcagctc caggcagacc catgggtacc ctccatggcc catcgagcag ctggcccagg      180
tttcaaccc cttccatcagc agtgccttgc tggcaggagg tggctctctc ctgagggAAC      240
acgggtgccc ctcttggcct accagttaat gcccggcac cccaggaacc cgaaatagag      300
gccagggtctc tgggccaagt agatcagaag gaaaagacag gggggagcgt gggggctctg      360
ggtccaggc actttccatc tgaccaccct gctccatgaa agggccctcg gatgtcactg      420
cagcaggagg agccaagggg ccgtgttggt gggtctggct tcctccatc gaaggagact      480
agggataac aaccagacag gcctgataag aggcaactcaa c                         521

<210> SEQ ID NO 157
<211> LENGTH: 410
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (317)..(317)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (320)..(320)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 157
gcacgagggt tactccgtgg agttggagct ttggcctccc aggccctgag ggccgggggt      60
ccaaatggag tctccgtggt gcgctctatg gcgctggag gtactcgccg gcaacgtgcg      120
ccgttgcctt cccgggggtgg tggccatgtt gatgttggatc agggcactgg gcttagagagg      180
gaggtcatgc tggctgtcg caagggacag gaccataaca atataacttgc cccaaaggca      240

```

-continued

acctcaggta ccaaggagga ccctaattta gtccctcca tcaccaacaa gcggatagtg	300
ggctgcatact gtgaagnagn caaacgtact gtcatacggt tctggctgca caaaggcgag	360
gcccagcgat gccccagctg tggaacccat tacaagctgg tgccacacca	410
<210> SEQ ID NO 158	
<211> LENGTH: 443	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 158	
gtgaccggcc gatgcgtgtc ggccctggc cgccgcttcc acccggacca cttcacctgc	60
accttctgcc tgcgcccgtc caccaaggcc tccttccagg agcgcgcggg caagccctac	120
tgcagccct gcttctcaa gcttctcggt tgaccgcgtc cccgggtcgcc cccctccggga	180
aagcggagcc acaaagacct cgccttccc cccacccct caaaagatcg ggctctctag	240
accccaaggcc ctgtgtgtt gagcttcggg ctccaccage cccggcttcc gaggcctcac	300
cccaactgcag ggactggccc tgaagatact gtacgttctc cgtggcgag ttcagaaaaag	360
gctccgtgaa cccttaaggc cacacgcctc ccgaagtggg tccgtacact gaccgatccc	420
acgtgagccc ttcaacttgt tcc	443
<210> SEQ ID NO 159	
<211> LENGTH: 376	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 159	
aggctgagag gaaggacggt agccaccccg tccacgtgga caactgcac tcgaatgccg	60
aggccctcggt gtgcataag gagccccctg cctacacttt cccggacttc agcgcacattc	120
tttatctgaa cgaagacttt gatggaggaa acttttattt cactgaacta gatgecaaga	180
cctgtatggc agaggtgcag ccccaagtgcg gaagggtctgt gggattctt tccggcacgg	240
aaaacccgc tggagtaaag gccgtccacca gagggcagcg ctgtgcacatc gccctctgg	300
tcactttgga tgctcgacac agcgagaggg agcgagtgcg ggcggacgac ctggtaaga	360
tgctcttttag cccaga	376
<210> SEQ ID NO 160	
<211> LENGTH: 564	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 160	
tgaataagga aactgttggaa aagttttcc aaacagacat tgcagaaaat gctttgaaaa	60
atgccttaga aacagaatt cctactgtca gtgttttagc tgacgaagaa tttctccct	120
tcaagaaaa tacgttgac ctggtggtta gcagtttaag tttgcactgg gtgaatgacc	180
tcccttagac acgttgcacag attcattatg ttttaaaacc agatggcggt ttcattgg	240
caatgtttgg aggtgacacg ctcttgcac tccgggttttc cttacagtta gcggaaacag	300
agagggaaagg gggctttct ccgcacgtct ccccttcac tgcgtcaat gacttaggac	360
atctgtttgg gagagctggc ttaataactc tgactgtggaa cactgtatgaa attcaagtt	420
actatcctgg gatgtttgaa ttgtatggaa atttacaaga agaaagtcca gaacattgac	480
ctaatttgc aaaacgcgtt tcaagctgagg aacacatgag aagtttgaa ggcttcaca	540
gtagttttaa gggatgggtg agag	564

-continued

```

<210> SEQ ID NO 161
<211> LENGTH: 537
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (285)..(285)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (372)..(372)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 161
ggcccgaggg agccagaggc tcccacctcg gccaacggct cggcgggagg ctgccagcg 60
cgccgggaca tcgtgttcat gaagacgcac aagacggcca gcagcacgct gctcaacatc 120
ctgttcgct tcggccagaa gcacgggctc aagttcgctt tccccaacgg ccgcaacgac 180
ttcgactatc cgcgccttctt cgcgcgcgcgc ctgggtcagg actaccggcc cggggcctgc 240
ttcaacatca tctgcaccca catgcgccttc cactacgacg aggttgcggg ccctgggtgc 300
gcaccaacgccc accttcatca ccgtgctcgc cgaccccgcc cgcctttcg agtctctt 360
ccactacttc gnctccgtgg tgcccttcac gtggaaagctc tcgggcccgc acaagctggc 420
cgagttcctg caggaccccg accgctacta cgaccccgcc ggctacaacg cccactacct 480
cgcaacacctg ctcttctcg acctggctca cgacagcgc ctggacccca gcagccc 537

<210> SEQ ID NO 162
<211> LENGTH: 529
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 162
ggtgagaagt gacgattcgg aacacaagta cagctccacg ccgctggact gggtcatgt 60
ggacaccaac atcgcttact ggctgcaccc caggaccagt gcgcagatcc acctgcttgc 120
gaacgtcgtg atctgggcct cgcgcgcct tgccacccctg gtgtacgcgg tgctgttcat 180
ctggtagctg ctcagacgcga gaaggagagt ctgcgcaccc cctgaagacc gctggctgc 240
ctgggtgctg gcccgggcgc tggtgcgggg gggctgggtc gtgaactacc tgcccttctt 300
cctgtatggag aagacgcctc tcctctacca ctacctgcgg gcgcgcaccc tccagatcct 360
gtgtgcgtcc gtggccctgg agcacatcg cgaccacctg tgcaggccc agctccaaag 420
gagcctcttc acggccctgg tcgtcgcatg gttcacctct gcctgtcactg tgtcgaacat 480
gctgcgcgcgc ctgacatcg ggtacaggcc gctgtcaccc agtgcgcgc 529

<210> SEQ ID NO 163
<211> LENGTH: 530
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 163
gcacgaggta ctagecgaga tggccggccgc tgcagcgatt cgtgggtcc gagggaaatt 60
gggtcttcgt gaaattcgta tccatttgta ccagcgctcg cccggcagcc agggcgctcag 120
ggacttcatt gagaaacgcgt atgtggagct gaagaaagcg aatcccgcacc tgcccatcct 180
aatccgcgcag tgctcggatg tgcagccaa gctctggccgc cgctacgcatt ttggccaaaga 240
gaagaatgtc tctctgaaca atttcagtgc tgatcaggta actagagccc tggagaacgt 300

```

-continued

gctaagttagc aaagcctgaa gtctccactg aggattaaaa acaacagccc cagagtctgg	360
gctctgctgg actgagaaca atgtggagaa atgtatTTt ttctgtataa agattgtgct	420
gaaaatgctg tctaaaaatg atctgattcg catccccacca actaccatt attgtcaac	480
catctgaggg aaagcagttg aataaaaaaa taaaacttat ttattctgt	530
<210> SEQ ID NO 164	
<211> LENGTH: 459	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 164	
ctctttgtta agcagagatt taactctgtg gtatttgta caaaatggga agaagagaca	60
tagtgattaa ggccaagttt gttggcttgc taaaactgaga aagaaatttt cacagtggaa	120
ggccctggggc gtggtcacaa ctcagaccag gcctcacaca gctgtccctt gtggagacct	180
cttgcctgtt actttgttt gttcttcgtc taaaagccaa gtcagactct ggaatttctg	240
ttaaggccaca aacaagcaat tcagtgggtt gggcaccaca caaattatgg gaaaaggggg	300
cagtcctaca gcaggattat atcagggtta tggttattttt aacctcttc tgcataatca	360
tgttgtataa gatgtgagag agatggacat agatccttc aactcaatct gttactttc	420
ccctaaatata taccctttt aggaagttt atctaattta	459
<210> SEQ ID NO 165	
<211> LENGTH: 551	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 165	
caaccccoctc aacgcctatgc agatcctgtg gatcaacatc atcatggacg ggccgcggc	60
gcagagctg ggtgtggc cggtggacaa ggacacactc cggcagccgc cgccggaaacgt	120
caaggaccag atcctgagcc gagcccttgtt cctgcggatc ctctctcgcc ccaccacat	180
catcagccgg accctttca tcttctggaa ggagatgccg gggacaggg caagcacccc	240
tgcaccacca accatggcct tcacctgttt cgtgttttc gacctttca acgccttgac	300
ctggccgtcc cagaccaagc tgatcttgc gatggcttc ctccggaaacc gcacgttct	360
ctactctgtt ctcggctcca tcctggaca gctggctgtc atttacacgc cgccctgca	420
gagggttttc cagacacaga gctggggggc gctggattta ttgttttaa ccggattggc	480
ctcgctgtt ttcattttt cagactttt caagctgtt gaaaagttt gctgcagagc	540
ccagaaagcc c	551
<210> SEQ ID NO 166	
<211> LENGTH: 253	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 166	
gctctctcaa cctaaagaag actggggcgc cagacatcc ctgggtccct tccggccct	60
atagggtcgc tgcagatctg tgaacgggtgc gggcgcaaaa gtcagactct ttccaggag	120
tttccccccc agttgaggat gcaccggggc gggctgtccc ggcctggaaac cagagatgg	180
aaagcagcag gaaaaccggc acgacatgc acgacatgc cgcagaagga atgcagagta gggcagttaa	240
atagagtgtt ttt	253

-continued

<210> SEQ ID NO 167
<211> LENGTH: 650
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (547)..(547)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (622)..(622)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 167

atttgttctg	tttcacctg	ccttcattaa	aaggcctgac	tcaattttgg	tgttgagaag	60
gaacaaaacc	caggcccatc	ccagtgcctc	tgcgcctcag	caccaggccc	cagcatggac	120
ctggtaagga	gggcacagtg	gatatccacc	caagacaggg	aatgaggat	tatgaggaac	180
tatgaatgt	gtggataaac	tagaccctc	tgtgcctca	gtcccagca	tgtcctcaaa	240
agcagttcaa	tgtctgggaa	ggaacaggc	tgtcatagct	caaaaccacc	aacctctacc	300
ctattttatc	ctggttcctc	cagaagcagt	gttggggaga	aacatgaata	ttcattggtt	360
ttagattacc	aaaaaaatgc	aaggcaagt	ttttgtgggg	gaagctgg	ttgtgatga	420
ggcggttgt	taattctgag	tttagtccac	agggtcgaa	ctggataaca	ctgagcgact	480
aaccgtttca	ctgagctcct	gtggtagctc	agatggtaaa	aatctgcct	gcagtgcag	540
agaccanggt	tcaatccctg	agttggagg	atcccctgg	gaagataatg	gcaacctatc	600
cagtattctt	gcctgggaaa	tnccatggag	ctgttagtctg	atgggttaca		650

<210> SEQ ID NO 168
<400> SEQUENCE: 168

000						
-----	--	--	--	--	--	--

<210> SEQ ID NO 169
<400> SEQUENCE: 169

000						
-----	--	--	--	--	--	--

<210> SEQ ID NO 170
<211> LENGTH: 432
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<400> SEQUENCE: 170

gcacgaggag	gccttcagga	tggtgca	ctgcgtac	cgtcgtaggc	tgtcctacaa	60
tacagcctct	aaaaaacca	ggctgtcccg	gaccctgg	aacagaattt	tttaccttta	120
taccaagaag	gttggaaag	cacaaaatc	tgcgtgtgg	gtgtgccag	gccgactgag	180
aggcgttcg	gtgtgagac	caaaaagtct	catgaggtt	tctaaaacga	agaaacacgt	240
cagccgagcc	tatgggggtt	ccatgtgtgc	taaatgtgtc	cgcgacagga	tcaagcg	300
ttcccttatt	gaagagcaga	agatcggtt	gaaagtattt	aaagcacaag	cacagagtca	360
gaaagctaaa	aaaaaaatga	accgttttg	agtaataat	aaaaaaaaaa	aaaaaaaaac	420
tcgaggggggg	gc					432

<210> SEQ ID NO 171
<211> LENGTH: 391
<212> TYPE: DNA

-continued

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 171

gcacgaggct	gggctggggg	cggggagcag	gtgggctgga	ggggaccctg	ccctgggtgt	60
tgggcgccag	ggccgcactc	ccgctggat	cttcctgtga	aaaacctcg	gtggcagcgt	120
gctcggttgg	cctccagcct	ctgacagtgt	ttacagacaa	ggccgtcacc	ctggaaagg	180
gtcgccccc	tccagcgtcc	cctgggctct	tgaaccgcta	cttgaattaa	ccgtaggcgc	240
tgcttgtaga	gtccacttgt	tatttgaaaac	aaggcatgtt	tcaatccaaa	gtgttatcgt	300
caaaggtaact	aacttgagta	gaagaattca	cagatgactt	ctctttaata	aataaattct	360
ccttttccaa	aaaaaaaaaa	aaaaaaaaaa	a			391

<210> SEQ ID NO 172

<211> LENGTH: 414

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (350)..(351)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 172

agtatatgg	gtatgtacatc	gagtgaagat	aatgtttaat	aagaaagaaa	atgcattgtt	60
tcaagatggca	gatgcaaatac	aagctcaact	agcaatgaat	catctgagcg	gtcaaagact	120
ttatggaaaa	gtgcttcgtg	cttactgtc	caagcatcaa	ggggttcagc	ttctctcgaga	180
gggacaagaa	gaccaagggtc	tgactaagga	tttagcaat	agtcccttgc	atcgctttaa	240
aaaacctggc	tctaaaaact	tccagaatat	tttcccccc	tcaagctactc	tgcacatttc	300
caacatcccc	ccctctgtta	cagtagatga	cctgaagaat	ctttcacan	nagctggatg	360
ttcagtgaag	gttttaat	tctccagaa	agatcgaaa	atggcactca	ttca	414

<210> SEQ ID NO 173

<211> LENGTH: 416

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 173

ggagatgatg	aatttttga	ccttcatgtac	tacttaggtag	tgcacatgg	tccggcaaaa	60
cgtgcctcac	cctccagcat	ccaaacccaag	gagcatacc	gtgggtggaa	tccaaacagat	120
ccctgcctta	caatttggaa	atttccggaa	cttaatccat	gagcatttgg	tattgaaaag	180
aaaaccgaaa	caaaaccaga	ccaaacccta	cactttgg	tgtcatgg	tcaagcgac	240
agcctacaac	tagttctaa	atgcactt	ggactaattt	aaaaaaagat	cccagtttt	300
acttttactc	gatgggtaaa	ttgggtgtc	ttgtatTTT	tggggaaaaa	acaaaaagat	360
tttttaacc	tccatacata	gaagcaaaaa	tactttaact	gctgtaaacc	ttcaaa	416

<210> SEQ ID NO 174

<211> LENGTH: 291

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 174

ggaagggtgt	ggtccaggag	ctccctggcg	gtggctctct	cctgggggtc	ccgcaccagc	60
atccggtcca	ggaagtctcg	cagcacccgg	gagaccttgc	aggagttctt	cagcttgggt	120
gggggggtgt	cccgaaaggct	cttcatggct	tgcacagggg	agtcaactgaa	gtaagggtgt	180

-continued

tctccatcca ccatctcaat caccatgtatg cccagagacc agatatctac ctcagttgca 240
tacaqagacc ttqqagatcac ttcttggqaccc atccaaqtatq qgggttccccac c 291

<210> SEQ ID NO 175
<211> LENGTH: 570
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 175

<210> SEQ ID NO 176
<211> LENGTH: 266
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 176

gaatgacagc agtgctctc tttttttttt tttaacagac cagccctaac	60
tgtgggtttg aatcctaaaa ggacatttc cacagtgtga ctcaaggaag tatttggttg	120
gcagggtagc accagtgaca gccaaatgga gggacataact tgcatggtca gtttattctc	180
taattccagg aagttctttg ctttcagaat gaagaaaaaca ttttctcccc ctttccccca	240
cccacccqgt tttttttttt tttta	266

```
<210> SEQ ID NO 177
<211> LENGTH: 509
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (318)..(320)
<223> OTHER INFORMATION: a C-g-t unknown or other
```

<400> SEQUENCE: 177

atcaggacaa ggaacctgtg gtcatcaata agccctacgg tctccctgtg cacggtgccc	60
ctggggtcaa gctctgcata agtgatgtac tgccctgtct ggcaaagata ctccatggcc	120
ccaaggcaaa gccgctgcac ctgtgccatc ggctggacaa ggaaaccaca ggtgtaatgg	180
tgttggcttg ggaaaaagaa gtggcgcata aagtccaaaga gctgtttaga acccgtcagg	240
tgacaaaagaa gtactgggcc atcacctgtc gcgtcccggt gcctgaagcg ggagtcgtgg	300
acatccccat cgtcgagnnn gagggcgcagg gccagcagca tcaccacaag atgacgcgtt	360
ccccgagcta ccgcattggac gacgggaaga tggtgagggt ggggagcagc cggAACgcac	420
agctggcagt gactcgtac cgggtgtca gcacgcgcgt gtccggccct ctcttgagc	480

-continued

tccagectat cacgggata aaacatcg	509
<hr/>	
<210> SEQ ID NO 178	
<211> LENGTH: 624	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 178	
aagatttaaa aattttctac atttaaaaaca aaactcgaaa gaattttttt ggaatgttga	60
ggaggacttc aaacctgttc cagagtgtc gataccagcg aaggaaatag aacagataaa	120
tgggaatccg atacctgtatg aaaatggaca cattcctggt tgggtcccag tggagaaaaa	180
cagcaaacag cactgtggc attcgtccgt agtcgattac gagtctgaga tcgccttgt	240
cctgaggcat catcctgacg accctggct tttggaaatc agtgcagtgc cgctctcaga	300
tcttctagaa caaacactgg agcttatagg aaccaatatt aatggaaatc cttatggtt	360
aggaagcaaa aagcatccat tacatcttct tataaccat gtagcggttc aaataagaaa	420
tctacctacc ttgaagcaca gtgtatctgtt gtctggttt gatggttgca gagaggtaa	480
aattgaagga atagtatggc attgcaatga tggttgttta atcaagggcc atcgccacca	540
tcttggttta tggcccgatccatc ttatatgaat tcaaaaaccag ttattatcaa	600
catgaatctg aacaaatatg agta	624
<210> SEQ ID NO 179	
<211> LENGTH: 457	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 179	
gacagacatt atggccacct tcccaagagc agccagccccg tccaggcagc ccccaggccc	60
agaggatgaa gatgecggtcc tagacgagta cgacacctac agcctggctc attcttaccc	120
gggagtggga ggccggaaag gtcgcagcaa gagagaagcc gocatcaaca ccaaccggca	180
cagccctggt gggcatgaga ggaagctgtt gaccaagctt cagaacacgg agcggaaaaaa	240
gtagggggca cggccctgag acaggactgg agatgaggcc agaggacgga caccacacg	300
aatggaaata ggactgagga agagccagcc cctggggccg ggatccaggc ctgcttgc	360
caccccaacc ccaggactta tccccacctg actgagactc tgggggcacc acggaggaag	420
caccccccgc cccagagaaa ggacaagatg agaagca	457
<210> SEQ ID NO 180	
<211> LENGTH: 457	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 180	
atgaaagtat ctgctgaatt ggttggat cattacattc aatgatccac tgaagaagg	60
aattgacttg gggcctttag caaatcaga agaggccacca tcctaagacc ctatagcatt	120
atcaaggaag ggaatccagg cccattttt gggtctgtt tcacacatca gcacttagt	180
ttcaatttga cctgatgaat agcatatcca tagagatgca gatgatacag aagggtgaaa	240
aaactaatttcc agttccaccc ttctgcctgt tggcattgtc caaccagaac tctgtttgt	300
attatctccc tagctaccaa gtgaacatgt ttatgttaat gtctgagaaa aagctcggt	360
ccttaagtct aagtatccctg caaagagtt gtaatctact cacatgaact tgcatttgat	420
ggaccatagg gtgatcaaca cgcttcctg gcatctc	457

-continued

<210> SEQ ID NO 181
<211> LENGTH: 470
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 181

ggcageccgc ggctcacca ggtgtccccg gagctgaagg atcgcaaaga ggatgcaaag	60
gggatggagg acgaaggcca gacaaaatc aagcagaggc gaagtccggac caatttacc	120
ctggaacaac tcaacgagct gggaaaggctt ttgtatgaga ctcactaccc ggacgccttt	180
atgcgtgaag aactgagcca acggctgggg ctgtccgagg cccgagtgcg ggtttggttt	240
caaaatcgaa gagctaaatg tagaaagcaa gaaaatcaac ttcataaagg cgtcctcata	300
ggagctgcca gccaatttga agctttaga gtagcacccct atgtcaatgt aggtgctta	360
aggatgccc ttcagcaggt tcaggcgcag ctgcagctgg acagcgcctg ggcgcacgcg	420
caccaccacc tgccacccgca cctggcccgac cacgcgcctt acatgtatgtt	470

<210> SEQ ID NO 182
<211> LENGTH: 202
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 182

atggctgcag gcagtttcc aagccccaa caaatccact ccagcctgtc ctgagggtcca	60
ctcagacaga cagatttccct gtggctaaaa ccagccagga tatagaaagc ccagtccatc	120
cccgccatcc tcaggagccc tcctgaaggc cacgaagatg agccggctct gcctctctgc	180
agcccttcctc cttctccctgg gc	202

<210> SEQ ID NO 183
<211> LENGTH: 279
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 183

gtcattggca tgagatctt cattaaagct gaaaacacgca ctcacgctac gtccatcaaa	60
atcccttgct gtgcggactg cctgatgggt gtgttatctgt tcttcattgg cctttgcgat	120
ctaaagtacc gagggcagta tcagaagttac gcgcgtgtgtt ggatggagag cttgcagtgc	180
cgccctctgg gtttcctggc catgctgtcc actgaggctt ctgtccctt gctcacatac	240
ttgaccctgg agaagttcct ggccgttgtc tttcccttc	279

<210> SEQ ID NO 184
<211> LENGTH: 488
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 184

tgtgtgggt cagatcccccc agcctccagg aagccagtca aagaggatg tggccacaga	60
aaaagaaaaca ccgaaaacac aagcacaaag gcaagcaaaa gaataaaaaa tcagagaaaa	120
gttagtagttc tgagagtaca gacagcagcg acagccagag tgaagaaggcccacagacc	180
tgtcacccca ggagttgctg agacggctga agcgtttcc actaaggagg cagtaattga	240
attctgcccccc tggccgtccc aataccagac ctcctccagg atggaaagttc attgtatcact	300
cagttaatac attgtataga ttgtatattat atgtaaatttc atgctgtgaa ataattttt	360

-continued

tttaaaacct tgacatttca aagcctgcct tggaagtgg ctgaaattga tttctat	420
taacttctgt tagtgtcaga gaaagaaatt cagactgtac agtttaatata aatggcatt	480
tttgtaaa	488

<210> SEQ ID NO 185	
<211> LENGTH: 476	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (153)..(153)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
 <400> SEQUENCE: 185	
tgtaaagcta tagtttcata agaacagggg tcttatttgc ctgaatccctt ccctccctga	60
gttcataatt ggtgctggc acatagtagg tagcttggga gaaatttgc agtaagaaaa	120
gaagggcagt gctaggccaa ggttccatc agnatgcact ccgcctgcgt tgtttcaaca	180
accccaaagg gcctataagc tgtattctgt tcccttgc ccagaggtt ccaatgcgt	240
ataatcagca cttcccaag gcctgaccct cacccattgg tcgttttaga acccctgc	300
cttctctaaa ggaatagccc attgtatag gactgttcca tgctcctcca acacttgct	360
attagtagaac cataaaattcc tataacaagt catggcact aaatagccctc cttacagaga	420
aatgaaatgt ttgaaccctg aagcacttaa ccaaaggatc aatctactgt ggagtt	476

<210> SEQ ID NO 186	
<211> LENGTH: 381	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (270)..(271)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
 <400> SEQUENCE: 186	
gggcttcgca ttgttcatc ccaacacatc acttccctta agacctctgg aagcactgcc	60
tggacacatc cgcccatggt ctctaccaca cctgcccggc gcatcccgcc tggtctcggt	120
ggttctctca attgccttgc cctgtcctgt cattgcacta aagcccagac gaacgagata	180
ctacgagccc caccctagct gaaactcgcc tcatcgctt taccctcagt aagaataat	240
caactgcctg ctgtaaacac tgaggatcn ncactgaaaa aatggacaga agccccagcc	300
ttcagggagt tattctagga caggagaaca aaccgctgac agaataagta agcagaatat	360
ctagtacatg gaagcactat g	381

<210> SEQ ID NO 187	
<211> LENGTH: 453	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
 <400> SEQUENCE: 187	
gttatttctg accttgcggg gctgtgggt tctgggtggc taggcgtatgc tgcccagg	60
cctgtggcaa gactcctgtat gctctggacc accctgactg gggtgataact ggcctgtac	120
cctgtggctg aggcccac tggcttggtg gcccgtacta tggcctacgg cttcacatca	180
ggggccctga ccccaagtggc cttctccgtg ctgcctgaac tggtggggac tggaaagata	240
tactgtggcc tggactgggt acagatggta gaaagcatcg gggggctgct gggggctc	300
ctgtcagggtt acctccggga tggacagggc aactacacag cttctttgtt ggtagctgg	360

-continued

gccttcottc tggcaggaag tggagttctc atcaacttgc cccacttctt ctgcttctca	420
gctcctacctt ccaagccccca ggtatcttgta aca	453

<210> SEQ ID NO 188

<211> LENGTH: 543

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 188

gtggccatgg ctttacgtt gtactcgctg ctgcaggcgg cccttctctg cgtcaatgcc	60
atcgccgtgc ttacagagga gcgtttctc aagaacattt gctggggAAC agaccaggaa	120
attggaggat tcggagaaga gccaggaatt aaatctcagc taatgaacct tattcgatct	180
gtaagaaccc tgatgagagt gccattgata atagtaaact caattgcaat tgtattactt	240
ttactgtttt ggtgaagatc agtggggAA acggagactc caaagaagag ctgccagcag	300
aagttattac ttcagtcttt attgaagttt acatatctta gctggctctc cttggactt	360
acaaaaatgt aaacctgaca ataaaaccag agtccctatt tatctgattt ttaaaaaatg	420
ttgtacttac agtttattt taaaagatc gtatcatcag agggcataac tgtcgaggat	480
tggatacat tggattgctg actgctgata aaagttcatg ctatggaaaa gattgttaaa	540
agg	543

<210> SEQ ID NO 189

<211> LENGTH: 464

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 189

ggccctgctg tctccacaca gtggaggtac catgacatca acggtcagga caccagacgt	60
cgcagaaggc cctgcagcac tggctggac aactccctga cactcgagg ggagcccagg	120
ctggcaaggc cacatctgtc acctacagtc atttcccagg aaaggccggt tgctagctgc	180
tagcctggtg cggacgtcaa gtttatgggc tggaaagtccct acccggaggg tgctcactga	240
agtgttaacca gccacaaggc ggatggaagg catgcctgct gctgctccag gtctcccccg	300
tccccaggcc caagatgaca tccaacagca ccagggaggt gcccagcccc gttcctgcag	360
ggggccctggg gctctccctg gcccggcaa gcctcatcg cgctgccaac ctgctccctgg	420
ccgtgggtat cgccggggac cgccgctgc gcagccgcgc cgct	464

<210> SEQ ID NO 190

<211> LENGTH: 446

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (380) .. (382)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 190

tgaaacagtt cagtctcctt gcatttcttc tctccctac cttcctcagc agagectgcc	60
tatttccttt cctctatgtat gctgagagac ttccctgggt gcacagatgg taaaagcgtc	120
tgactacaat gtgggagacc cgggttcaat ccctgggtca ggaagatctc ctggagaagg	180
aaatagcaac ccactccagt gttcttgctt gggaaatccc atggacagag gagcctggta	240
ggctacagtc catggggctcg caaagagtag gacactactg agcaacttca cttcacttta	300

-continued

tgatgtggg gaagatttag	360
tgccatcac caacttaatn nncatgagtt tgagcaagct ctgaaacaca gtaaagacag	420
ggaagtctgg catgctgaag cccatt	446

<210> SEQ ID NO 191	
<211> LENGTH: 480	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 191	
tgcaggcctg caaaaatcag gcagcaagcc agaccggccc acagaccaag tttgccaacc	60
ccttgcctag atgaccgcaa agggcctaac cctcaagaga aatgctagcc aatcaccagg	120
ctcccttgcgt ttcggcgct gatcacgtga ccagccctgg gcacacagat ccaaaggatg	180
ggctctgtcc cagggcagag gctgctcggg cgtaaaccac tgacccgagt cctgtctcc	240
tagacctctg aaaagtcagt ggccgagcag gtctgtttagg tggggctgag ctgagaggc	300
agaccggtgt tggccaga gttcacgcag gtcaggatag tcaggtgtca gagtgaacag	360
cccgtgatgt aagccccgaga cggggccgcg tgccgtcaat cagtcgtctg tcccgagca	420
gccccgggtg ctggtgacac gcatcgccgt ggggctcgtg cagccgtga cttgagtcca	480

<210> SEQ ID NO 192	
<211> LENGTH: 501	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 192	
acagcttgaa ggatgagatg ggcaacctca ggtggggca gacaggacaa ggttagggca	60
gggggtccggg agggggccgg acagagcaca ggaagtgtgg ggtgtggca cctagtgggg	120
tcctcccaag gatttgcgtca gggctggaaat caaggcttag cccacgagga tccttctgac	180
cctcccttgcgt cactctggct caggaccat gcccctgttc coctacagga agctgttaga	240
cactacccca tcaccagtgg tctttgcca caatgatatac caagaaggga acatcttact	300
gctctcagag octaaaaaca ccgacagcc catgctggtg gacttcgagt acagcagtt	360
taactacagg ggcttgaca tcgggaacca tttttgttag tgggtttacg attatactca	420
cgaggagtgcc tttttctaca aagegcagcc tgcaaactac cccactgagg gacagcagct	480
ccattttctt cgccactacc t	501

<210> SEQ ID NO 193	
<211> LENGTH: 484	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 193	
gcataacaac tgaccagctg agaccgtatt gcctgttgca tcaatagtgg aaggcagaag	60
tgttgacaca atttctccctt gtcctttctg atttttatataa aagaaacact ggaaacagta	120
gagaacagca cagcgtaata caaatggctg ctttcattt accatggaca taagaagtac	180
tacgatggct ggtcttggtg ggtttgaagg tgcatttaca gaagcaaaatg agtcttggtt	240
tacttggcag cctcgaataa cttctgatac agtattaatg gtctcagtca ggatatcagc	300
aggaactcca gtagtctctc aaaagcattt tcaaaagcaa caatttctg gattgctcca	360
ttgcttcttg ttagtgcctg cagtagtaag acgccatcat tacgtataac ttccctgaa	420
tctgctaata agtccatcaa tcttggaaaca cccatggac tgactaaaat aatttgcgtga	480

-continued

acct	484
<hr/>	
<210> SEQ ID NO 194	
<211> LENGTH: 512	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (416)..(418)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<400> SEQUENCE: 194	
gagggggttt ggctgtcagg gcccccaggag ccgttcttga aggggtcctg gtgagggtcc	60
caggttcagg atcgggtgag gttatagcct cctccgtctt cggagggtct gccccctgggg	120
cctgaggcac ggacatctcg gctccagcca cagcctcggg caccaagggc tccgggcgg	180
agacacctgcgc cctggggca tcgggtgagg cctccagagt cagtcccacc tccgtgctgg	240
ctgtgaccgt cggggccgggg accgagtcgtc aggtctgggt cagacccgtt acccatgcgg	300
gccgcgcctc cccggggggcc accagggtga ceggggcccga agtggecgta gtcactggcg	360
gccccggagc caccaccagg acggggccgg cccgagagcc gccccggggc ggcgannnnng	420
ccgcggggggc gccatgacgg cgccgggggg ccaccaggggg cgccggggccc gtctccatgt	480
ccgcggggccg cccctcacat ccccccgcag cg	512
<210> SEQ ID NO 195	
<211> LENGTH: 431	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (11)..(11)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<400> SEQUENCE: 195	
aaaccctcag ngaacagcag acagagatgt cagaggtatc aattcttc cagtgaccct	60
tcaagttagt tgggtcagta gggaaaggatg actggacagt atctcatgt ctgtcctcaa	120
ggaaatccttc cctagtcgtg ccagcttgct gtcatttgc atgaacaact cttcatcagc	180
atctaattgc cattctctga taacatagcc aagaactgca gacttcatct gtgttttgg	240
atgtccatttgc tcaatggta atacactaac gtgggttttc aggataataa gtggtcttta	300
attgctaatttgc tagagaagat tgggtgggtgt gtatctctgt aaagagatga tagcctgaaa	360
ctatcatttgc gataattccc attaaacatt atgcagacat tatcagactg ataagctccc	420
aagctgggct g	431
<210> SEQ ID NO 196	
<211> LENGTH: 463	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 196	
gaaattgaca gctgagatgt cctcagtaat taaacgtttt aactcggcag ttgattagct	60
gtggggagaga ggttcgtcct gagcgtatgtc agtttagccca cctgaaatct ctgggtgggtc	120
tgttttatgt gtgagaaaaaa ccagaagggg aggaacaacc tggctcgaa ggaagatgga	180
ggtgtgtctctt gaagatggct gtttgggtttt ggaagcatgc ttttggattt ttctgtcagg	240
ctgggtcagta aatatttact gaggatatac tatgctttac aaccttaggc aaagacaagc	300

-continued

catctaagcc tcagtgtctc ctttgttga aagtttatct tggtacgaa gagcatttag	360
agagtaaat tagttgcaa agtgcttaac cattgtaacg atgctggtgg tagctgctca	420
tctccacatg ggctaaaatg agactggtca gtagtcggag gtc	463

<210> SEQ ID NO 197	
<211> LENGTH: 347	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
 <400> SEQUENCE: 197	
tcaaggactc aaaccttatt aaaacgcagg atgtgttac agtcattcag tacatctcat	60
acaacagcta tggaaagact atggcctgga attggataca actcaactgg gaatatctag	120
tcaacaggtt tacactcaat aacagaaacc ttggccggat tgcactata gcagagccat	180
tcaacactga actacaactc tggcagatca agagctttt cgaaagatata cctgaagctg	240
gagcgggaca gaaaccttagg gagcaagtac tggaaacagt gaaaaacaat atcgatggc	300
taaaacaaaa cagggacacc ataagaaact ggtttcttga tttgaat	347

<210> SEQ ID NO 198	
<211> LENGTH: 508	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
 <400> SEQUENCE: 198	
cagccggcca ggaagcgcag gccctcaggc tccgaacagt cggacaacga atcccgtcag	60
tctgggggaa gccgcgtccgc aggctctgag atggactccc ggccccggc cccaaatgtct	120
gagtcggacc acgactccga aagagcatct gacaatgagg gtcggccccc aggttccgga	180
aatgaatctg aacccgaggg atccaacaac gaggcctcgg ataggggctc agaacgttgt	240
tcagatgata ggcacttaggc ttatattcat gaatatgtttt catctctgca ggaaactttt	300
tttttacata tgaaaactgt gataaaaaaca ttccaggtgt ttggcagtg gtgaaatttt	360
tgctaaaggca attttttcc ctatccattc gtacattact atgacccgaa gagatatttc	420
ccgtgttaga gtctaatatt tgagtctttt gagcaaaaagg tgactattct tcattatgg	480
acaattccac ctattacatg tgaaaacc	508

<210> SEQ ID NO 199	
<211> LENGTH: 590	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (285)...(287)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
 <400> SEQUENCE: 199	
ggaataaaaca acagaaccgt ggctcctaaa gagcaggaag acttctcttc ctgcaaccat	60
ggtcaccata aaatttatcg tcccaacegg ggcatttctg ggcgtaaaa ggaatggat	120
tgacaaacac cccgagacaa aaggcatcac tggacgtctt cggtaacca ggacacgct	180
caccctaaac aggacccgac atctctgact gtgcttgcac taaagggttg aggcgcacgg	240
taggacgccc accgcagcgc aggagaggcc gtgggctgctg gctcnnnacc ccgccaccc	300
ttcttccaaa tccctcaactg gtgtccggcc ggcgcgtgcgt gtatggat cacagcccc	360
ggccagggtt gaagctggc cccgcaggaa cagcgcagcc tactacctgc tggctgcca	420
gggaaccctgtt cggctctcc tgagtcaacgg agatgccaag caaatgtctg aacacccac	480

-continued

agcctcagtg caagaaggac tggatattat ctcacagggc tgtgctgagg actgaacagt	540
ttcatatatg tgaaacagct aacacagtgc caggcataaa caataataaa	590
<210> SEQ ID NO 200	
<211> LENGTH: 594	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 200	
ggttcttttg ctggagatat ctggggagaa attgatacaa gattctctt ttgtcagtg	60
gcaactttgg cactattggg gaagttggat gctattaatg tggaaaaggc aatcgattt	120
gttttatcat gtatgaactt tgatggtga ttgggttgcg gaccagggtc tgaatccat	180
gctgggcaga tctattgtt cacaggattc ttggctatta ctatcgattt gcaccaagta	240
aattctgatt tactcggtt gtggctttgtt gaacgcacgc ttccatcagg tggactcaat	300
ggaaggccag agaagttacc agatgtatgc tattcatgtt gggtgttgc ttccctaaag	360
ataattggaa ggcttcattt gattgtataga gaaaaactcc gcagttcat cctagcatgt	420
caagatgaat aaacaggagg atttgcagat aggccaggag atatggtaga tcctttcat	480
actctgtttt gaattgctgg attgtcaattt ttggggagaag aacagattaa acctgttagc	540
cctgtttttt gcatgcctga agaagtactt cgagagtgaa atgttcagcc tgaa	594
<210> SEQ ID NO 201	
<211> LENGTH: 430	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 201	
tcatccatgc ccgggttcca gcgcacccatc ccaggagccca caagagggtgg cagctgtac	60
accaggact taggtcgaa gtcagcgaa cttccctcaga cttccctctc tccgtgaagg	120
ggagggcccccc agtgcggcaga ggccggggat gcacccgaag aagcccaccc cttgtactg	180
atcagaagca ataaggccct ccatgtgcct gaaagcccaag agggagcgcg ggcagggtcc	240
ccagcggccgg ggcacggcatc tccccggaaac ggccctctc gcctccgcag ggacagcgct	300
ggcccccgtg ggcgccccgg ccctccgcac cgcgcgcagc cggagccctg cgccgcgc	360
accgcgcgcca acaccaatgc ctccggccccc gacgcggccccc gcgggctgctt ggcagtggaa	420
tggggccgtgg	430
<210> SEQ ID NO 202	
<211> LENGTH: 637	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 202	
agaaggagaa gatgattttt ctcccttta ggataaatga aacctgtttt ttatgttaaga	60
atccatgtac caaatttgac ctccgtctga atggcccccac aggttgtgtt atgtatgtaa	120
gccctcaagt aaagectacc caggaagaga gtgagaaaga gaaccacttc tttgtctttt	180
ctttgtcagt tcatctttaa ctttcttggg aaaaaaaagg actctccctt tagagatgag	240
ggggaaaaaaa ggtttacatt ttaagacagg gaaaaaaaggta gaatcaaattt ctaaaatgt	300
gactggggag aagtcaatgc tttctgtgtc ttttgaccct tttgtataattt aacccgcgc	360
aataccatgt ttaagatgca tttagataaa caaaataaa aacttgacat aagatctcat	420

-continued

tttcagaaag cagattacag accaccagag ggaatcatg gggccgtat tgcacaggca	480
---	-----

actctgagaa agttgtcgtg aaaatgtaat tccttctaac caggttcctt ttttcctt	540
---	-----

tgaaagaaga acattccact ttgttagaa ttctgagtt ttgttaatc atcccactta	600
--	-----

aaagctctct tccaacccaa cttatacagt ttgaaat	637
--	-----

<210> SEQ ID NO 203

<211> LENGTH: 477

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 203

gcacgaggc gctcagctgc ggtaccgctg tctgcgttg ctgtttggag aaacccaaat	60
---	----

accgctgccccc cgcctgcgcgt gtccttact gtccttgcctt ctgtttccgg aagcacaaag	120
--	-----

agcagtgcag gcctgcagct ggctctgtcg agaaaaaaat aagatcagct ctgactgcaa	180
---	-----

aaactaaaaa gcctgtggaa aacgaagggtt ctttagatga tgatgactt gtggctgatt	240
---	-----

ttctcaatag tgatgaggaa gaggacagag tgtctttgca gaatttaaag aatttaggg	300
--	-----

agtctgcagc actgaggagc ttactgctca atccacaccc ttagacgctg atggctgacc	360
---	-----

tcgatcaggc ggaegacaag gccaagctt a tgcggccctg catgcaggag cccttgggg	420
---	-----

tggagttgc tgactgctgc ttgagttatcg tggagccgtc tcagaacgag gatcctt	477
--	-----

<210> SEQ ID NO 204

<211> LENGTH: 484

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 204

gcacgaggat gatgcaaaca gaaattccac cggcctccag atactatcat gtgtcatgtt	60
---	----

tcaccaggctt ccacaagctt gagttcaga ctgtctcggt cacttcagg tgagcaggct	120
--	-----

caagactctg ctccccagcc aggagaagat gactgacact gagtttggct acgttcacgg	180
---	-----

gctggctgag gactatctga aatatgtt gcagatacag caacctggat ccaagccaaag	240
--	-----

cagaaaattt ccaagaggtc aaagatcaag tctttgtga aagtttataa ttataatcac	300
--	-----

ctcatgcctt caaggtactc tggatatac cccttggaca aaactgttgtt caacaaggat	360
---	-----

gtcttcagag accctgctt cttttttttt cttttttttt cttttttttt cttttttttt	420
--	-----

gagagatatac agacgggcaa gaacaaatgg ttcttccaga agctgcgggtt tttagtctgt	480
---	-----

ctca	484
------	-----

<210> SEQ ID NO 205

<211> LENGTH: 481

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 205

tcacatgtgc ttccggagt gctatggctg gtaggttgcgtt gttcgcagca gaggeccgtt	60
--	----

ccacgagcca ggcgcaggaa actacaccac tacactaaaa ttatccatat ttatatgtt	120
--	-----

cagaaatctg ttcaaaagcaa aagataattt gagagggact tggatcaaga atggatttc	180
---	-----

ttaactatac aacagcatgt gattcagctg tggaaactga gaatcaaagt gacaactttt	240
---	-----

cctctggtag cagtttattt aaaactcagt gtgttccgtt cccacctaaa cggaggccaa	300
---	-----

gaaacactat tagaaaattt gttcacatac cccaaaatac tcaagcaaca gactcatca	360
--	-----

gtgactcatc tatagagccca agaccactga cttaaaggc tatttttggaa agattcaaaa	420
--	-----

-continued

ataagaaaacg taaacgtaaa aagaagaaat acaaggccaac gggaaagatca gtgggaagac 480
c 481

<210> SEQ ID NO 206
<211> LENGTH: 333
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 206

gattggatac acggctgc当地 cggggctggt ggggc当地tc ctgggtgtgg tcatgggtat 60
tcccagcggtt accagctctc aaaggatggg aactgagcaa cc当地ggccc tgggtttgtt 120
cacagaccct gtgggctcgt gtgtacagt当地 ttagagatcc tctttcatca caaaaggact 180
gtgggtggag gagtaaggc当地 atagctcaaa gggtt当地ca aattttaat atattaaaac 240
aagaggc当地 tgcttagaaaa ccttctt当地tataaaaaccc gagctttaa aaaaaaaaaaa 300
aaaaaaaaaa aaaaaaaaaaa aaaaaaaaaac caa 333

<210> SEQ ID NO 207
<211> LENGTH: 349
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (148)..(150)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (152)..(154)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (279)..(280)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 207

ccagactcac ttccgctgcc cgggatgtgg gggggcttc cgccggaaac cgcaacttgct 60
tagccccctg ggggtccggg ctgaggagag cggccgctg ggctcgaaa gtgaagaaac 120
gtgtggccac cgtgtgacac cgccaagnnn cnntccata ctccggttgc gacgagggtg 180
cctccccggg ccccccgggc atggagaggc cagtctcccc gagagagggc gccggggcgg 240
cctctgagca ggacgagctc cctccgagct cgaacctann tggtcagaag tgtggccct 300
gggctggggg gccggaggcc ctcaagcctg gccccggagg ggagagacc 349

<210> SEQ ID NO 208
<211> LENGTH: 539
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 208

gcacgagaag gaaaagactg tgaaaataaga gctgtggta acaggactgc cttagacctat 60
ggcccgtag tag tggactttga cccctgccc当地 cacggtatga tgtgaagctc tc当地ata 120
gaatccacag ctttctttag agtctggta accaggctt gttcaagtt ggtgtctt当地 180
gtttgggatt tctgaaatca gctttctcaa gactttggaa ggctcagacc tctgtgctca 240
cagagctggg cacatagctg cttt当地tgc agagggtaca caggc当地aga aacagtagta 300
gaggtgggtt agagccccag aagtttctgg aactgccc当地 tcccaagaag cactattaca 360
aaatcctcta cagagaaaca agtgtcgcc caaatgtt当地 ttcttc当地atataaaacagag 420

-continued

gtctgtggac atgtgaggat aagaataaaag acaaaaatct tgctcttac atgtgtatct	480
ctggcctcca ctgtggagag ataaccagca aaacaaggca agagatgtga gaataaact	539
<210> SEQ ID NO 209	
<211> LENGTH: 456	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (16)..(16)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (47)..(47)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (63)..(63)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (74)..(74)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (103)..(103)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (134)..(134)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (230)..(230)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (236)..(236)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (254)..(254)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (274)..(274)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (281)..(281)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (317)..(317)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (332)..(332)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (345)..(345)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (351)..(351)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (358)..(358)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (412)..(413)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	

-continued

<222> LOCATION: (417)..(417)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (452)..(452)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 209

aggacttggg	gagtctttat	ctgtccatc	ttagccactc	gccacantca	gaggatatgc	60
canggaggtc	aggnggactg	cttccagatc	ctcctagaag	canttacttg	gaaggtccaa	120
gaggcccaag	attnatggt	cctcgaagat	tttgggattt	agggtcaagg	tgtgaaggac	180
cgagacccaa	agggccttgt	tttgaaggaa	atcgccccga	tgggccaagn	accanattt	240
gaaggtcacc	cacnacgagg	gcactaaaag	caanatgggg	naatgtattc	cccgggggcc	300
aagcatctta	aagtttncta	tattaccccc	antacatccc	ttcanccctc	ngacagantt	360
ggaccacagg	tggaaaggcc	ccaaacccaa	cttttggac	aagcaacatc	anncaancaa	420
cctaaagttc	acaagccagt	aaccaaggaa	anaaaa			456

<210> SEQ ID NO 210
<211> LENGTH: 464
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 210

gtcatcgacg	atcactttca	aaagcagtgt	acgtcacagg	aatgtcagtc	cccaagatcag	60
aagagtgttt	atttgaaaa	gctgagggaa	ggttggagtg	taagtggatg	gattggagga	120
tgtatacaag	gggggcttca	acttaaaata	ttttcttct	tttaaagaaa	agagaaaaat	180
tcaaaacgtg	gaaaactgtt	aagagtagat	aagctatgag	gtgatgggga	tattcatcat	240
atgtttttt	ctactttct	gtaggcttca	gatattttt	aaaaaaccat	tgagtgactt	300
tgttgtggtg	atgcaaacag	tgctacgtat	cagacattt	ggaaacagtt	aattgacctg	360
ggaaactaca	cgtgtacata	ggcttgtgt	agaggaagag	agcgccttct	agatctgatc	420
gccacgtttc	tagtgctgca	gttccttcgc	accaagttga	aaca		464

<210> SEQ ID NO 211
<211> LENGTH: 314
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 211

ttttttttt	ttttttata	gatacatatt	taatataata	aatgtgattt	tggttacaga	60
tacatatttg	gtgctttatc	aagtagtatg	aattccagag	tacacaacac	gtgggataca	120
aaatttgaag	ataaacacaa	ttgttcctaa	atgaaaaaca	tgggatacat	gctgtatgaat	180
ggatttccaa	actttcattt	ccactcttt	ctccaggctg	gtctcctgaa	gatgagttgc	240
aagttttagc	agtcttaaaa	aaaaactcag	tcccccaat	tctaataaca	tgtatatatga	300
aaagaacttt	tggc					314

<210> SEQ ID NO 212
<211> LENGTH: 409
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 212

attttcgaag	attgtggcaa	cgtgcccagc	gaactcaaag	atcgaggaga	attgaacaac	60
------------	------------	------------	------------	------------	------------	----

-continued

gaacaaggag agcgaaaagt ctgcagggtc aagcttgaat ggctggaaa ttgctctgga	120
ataaaatgatg aaacttacgg ctacaaagat ggcaaaccat gtgtcattat aaagctcaac	180
cagttctgg gcttcaaacc taagcctccc aagaatgagt cttggagac ttacccagtg	240
atgaagtata atccgtatgt cctgcctgtt cagtgcaactg gcaagcgaga cgaagataag	300
gagaaagttg gaagcataga gtactttgga ctgggcggct accctgggtt ccctctgcag	360
tattatccct actacggcaa gcttctgcag cccaagtacc tgcagcctc	409

<210> SEQ ID NO 213

<211> LENGTH: 470

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (433)..(433)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 213

gcaacaatgc tttctgatcc agtgaaggct taaaaaaaaaaaaatcc aagaacagaa	60
ttcatttca tcatctctgg tttcagagg attaaaaaaaaaaagttgtgtt tcctggacg	120
cccgtaaaa tcctttctt tgctgaaggc tgccatgagc tgcactttt ggggtggaa	180
gggtgaatgc cgcggtggga tagggggac aggggcggg gctgtcgat gatggggcc	240
tgtggctgcg gggggaggag tcctgtctcg caaacatcac cccaccagcc agggggactt	300
attctaagac ccgtgcata ggaatggtgg ccagtgttgt tctatgcgaa caagggttt	360
gtttctctgt aggctgttaac tttaaaaat aaacagttat ttaagggtta tgctgcacta	420
gtatttcata agnggaaact gttccttaca gctaggaaag ggagtggca	470

<210> SEQ ID NO 214

<211> LENGTH: 435

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 214

atcacacacg atattgagga gaagggcgctc cgcatgaagc tgacagtcat cgacacgccc	60
ggcttegggg atcacatcaa caatgagaac tgctggcagc ccatcatgca gttcatcaac	120
gaccagtacg agaagtacct gcaagaggag gtcaacatca accggaagaa ggcacatccc	180
gacaccccgcc ttcactgctg cctgtacttc atccccgcctc cccggccactc cctcaggccc	240
ctggacatcg agttcatgaa gcgcctgagc aaagtggtca acatcgccc agtcatcgcc	300
aaggctgaca cgctgaccct ggaggagagg gtctacttca aacagcggat cactgcggac	360
ctgctgtcca atggcattga cgtgtacccc cagaaggagt ttgacgagga ctctgaggac	420
cggtctggta atgag	435

<210> SEQ ID NO 215

<211> LENGTH: 329

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 215

gcacgagggt gtcttgact gtttggaaat ctgccccgc tcctccctgc cctcacttcc	60
tgaatgaaat gcttctgagg ttgtttatga aaggagtgtat cttggggcag gcaggaggca	120
gtggggcttta tggctccttg gagttactgt tgatcttgc accttcttgc gctacatgt	180
gacaaagaat atgccaatac ttggggctct gatgtttata gtcaatatattt atttgtatca	240

-continued

tctcttgc taggaatgta aaagtgactc taaaactaaga tgtgtataaa aaatcagatt	300
tattgtacct caaaaaaaaaaaaaaa	329

<210> SEQ ID NO 216

<211> LENGTH: 516

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 216

gcacgaggac ctccgcaccc ccatcccagt ttctgtcccc tctcggttgc ttttaggtgg	60
atcccttggaa ggcagaagca gccaaggact gatcccaggact ctctgtgtaa gcaaacaac	120
tgtgaattct gactccctt gcccttc tccatc cagctgttagg tgccctccct ctgatcgcc	180
gggagggggac tgaagaaagg caagggccaa gatgctgcta cttctgaccc tcctctctgg	240
ggcaggggcag gagaggagcc tgggttcatttg tgccacattt catacccggtt caggcatggg	300
cggcgcactg gcacccctt ccggcctcaa ageccctccct gcagtgaagc agggcaggag	360
ggaagaggcc ccagcattgg gggttggatt ctagagggaa catgatgacc gtcagggtca	420
agtgcagaaa tctttgcctt tgctaccatt tctgtatgtat gagaataaaa agttcaccaa	480
ggttttgttt tgtaaaaaaaa aaaaaaaaaaaa aaaaaaa	516

<210> SEQ ID NO 217

<211> LENGTH: 510

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 217

agctcagtc gctcgtgtga atttgtcac gccccttgc ctctctgagt ctgcttc	60
atccataatc aaggaaatc tttgacatct cataaaagcgt ggatgagcct tcacgtttct	120
gaaagaatag tgctcggcgc atagaaatgt ctggtagatg tcatctgtta aagatcttt	180
cttcatgtgg tggtagctgc gaggacagg aaaatatctg aagccataaa atagttcat	240
cagctattcc taaaggcgaa tggttttttt ttctgtttt cctgaaatgg caaaggtagc	300
ggatggggag agatgacagg aggagatgaa gagataggac aagactgggt tctacgcttc	360
atttgtatca tgttatcggtt cgggtgcatt ttttttagcc accgtcccat tttaaagcag	420
aaggcagtc ataacaggaa actctgttca atgttatggg cagcctggaa gggaaaggag	480
tttggggag aatggataca tgtagtata	510

<210> SEQ ID NO 218

<211> LENGTH: 541

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 218

gtggggagcc aggacgacac agacccatgc acatacgggg acagcctgtc tggctgggtgg	60
cttctgtggaa agcggctgaa tccctggca gacaagatca aggttccaga tatggcagag	120
atccagtctc gcctggccta cggtcctgc gtgcacagc tggaggttgt gaagtccagc	180
tccactgtg agtacccatgc cccacccatc gactgcttca agaccatggaa ctccggaaag	240
ttcgaccaga tctatgtatgtt gggctaccag tatggatcga ccgtctttgg gggctggagc	300
cgccggcaca tcattgaaaa gatttcaca gaccgggtggt ctggcgcacct gaacgagagc	360
cgccgtgcag acgtgtcgcc tttcccccagc tctggcttca ccgacttggc ggagatagtg	420

-continued

tcccgatcg agccgcccac cacgagctac gtttcggttt ccgacggtg tgctgtatggg	480
gaggagtccg actgtctgac ggagtatgag gaggacgcgg gccctgagtg ctcacgggac	540
g	541

<210> SEQ ID NO 219

<211> LENGTH: 495

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 219

gcacgagggc cgaagccaga gatggtatat ccagcatgaa ggtgtcagac catgaggtcc	60
tcgcagggttc cgtagatggc cgggtgaggc gctatgacct gaggatgggg cagctttct	120
cagactacgt gggcagcccc atcacctgca tctgcttcag cccggatggc cagtgcaccc	180
tggtgtccag octagactct accttgcggc ttctggacaa ggacacaggg gagctgtgg	240
gcgagtagcac gggccataaag aacaaggagt ataagctgga ctgctgcctg agcgagcgcg	300
atacacatgt ggtcagctgt tctgaggacg ggaagggtttt cttctggac ctgggtggaa	360
gtgccctggc gctggccctg cctgttagtc ctgggtgtggt gcaatcgctg acctaccacc	420
ccacagagcc ctgcctgtg actgcctatgg gggcagcat ccagtgtgg cgggaggaga	480
cctacgaggc tgaag	495

<210> SEQ ID NO 220

<211> LENGTH: 489

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 220

ggttcaactgc octggtcatt ctccgtcattt ttctgtcgct ctgggtggctg tctctggag	60
ggactcagac agtcccagga gacctggaaa tggactcattt ggcctttgag gatgtggctg	120
taaacttcac octggatgag tgggttttac tggattctc acagaggaaa ctctacagag	180
atgtgatgcg gaaaaacttc aggaatgttag tctcagtaga agcaaaacag gaatgcagg	240
acattgacga tcaggacaaa aaccaggaga gaaaattacg aaatccaaag gcagagagac	300
actccgaaaa gaaagatatt aattcctctg aagaaagctt caaccttatt ccaactccca	360
atgtgaagag aactcggtat ataaaaccat gggaatgcag agcatgtggg aaagtctca	420
tgtatcattc atcccttact agacacatga aatgtcacat tgaaaacaga tcagatcgcc	480
gaaagtacc	489

<210> SEQ ID NO 221

<211> LENGTH: 290

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 221

agccagactc ctccgttaact ccaattcagg ttaacttccc tagggAACAG tgccagggtgc	60
cacggacacc gccttctcg tgggtgggg gctgccactt cggagggggtg gcacggacct	120
gcctggcctc tccatttggg gtgggtctc ccccatcttcc ttgtctttgg gtttccgac	180
gggtacaagg cctgccccggc tccccctcc cccgggagcc tcactctggt cttccaacag	240
gactggcgt cagccccccg cccggctcca cccggcccccc agtggctccc	290

<210> SEQ ID NO 222

<211> LENGTH: 475

-continued

<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<400> SEQUENCE: 222

agaagctta aatattagtg tttcatcaa ttgggcttaa tttaagagaa tccattgaca	60
cgaaaatgaa agagaatgtat cttagggttt caagcttctt aaacgaacac cccagtcgt	120
ccttcagacg cagctgttca gagctctaaa gcccaccagg ttcaacttgcgttgggttt	180
ccatgtatgtactcggcctt ttctgggtttt aatatttaca gggtatttgcataaggagac	240
agatgaccag aacccgaaag gctctattgc acacacatg aatcacacgt gaaaataaaa	300
atccacagga ccaatagcgc atctttaact tcttcataact tagaaaaata tattttaaa	360
tagcagtctg cataatttcc agtcttcagg aaacttagaga gaagctaaat aggaagtcc	420
tgaatggcaa gtactgatct ttggcagcat ttaaaggaa caggagtaaa gacct	475

<210> SEQ ID NO 223
<211> LENGTH: 408
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<400> SEQUENCE: 223

gatactacat tctgggtttt gcttgaccac cagtgtcatt ctgactggca gtcagggtcc	60
tgcggacgc tgcagtgtgc acgctttta aatacgtgg attgttttag tgctgtcagt	120
gataatgcta gcctacttctt attttgcatt tagtacagag ttataatgt tgtaactcct	180
agaacattac atggagccct ggtccctttt ccctacttgc tgatttgact ttattcttt	240
tctcgatcgc tcactttctt gattctccaa ggaccaaattt ctccagtgag cactggagcg	300
tgtctccagg gtaagccaaa ggctgcgcgc ctcagctctt aattgttctg cagctgcctc	360
tggcaggcac aagttagcccc actgtgtgc ggaacacatg ccaaggaa	408

<210> SEQ ID NO 224
<211> LENGTH: 439
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (373)..(373)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<400> SEQUENCE: 224

acctgccttc ttgtggcgtc gggcccgacc gtggcccttg gaaccctcaa gttggggct	60
gcggcccttgg gatgggggggt cgccagggggg ctgtgttcc ccaggggttgc cccaccgggt	120
cctgggtccag ctgcgggtca gagccccgag cagggtgcgc cacaccggcc ctgaggatgc	180
cgcggcccgcc ggtccccgtg ctggcccttg ctgaggcccc gttcgcccc gcacccgttc	240
ggtcatcaca gaagtctcca gaatcctgtc cgccagggtt ctcctgcaga cttaacaact	300
ctggacgcatttggcagggtgg gacccagggg cgggcttgggt gttctgttcc gggggacgg	360
tttccagagg canctggtcc cctctcactc tgccctgcacc tgccccgggc atcactggtc	420
acttgcctctt gccaggcac	439

<210> SEQ ID NO 225
<211> LENGTH: 670
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (606)..(606)

-continued

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 225

gcgcgtctc	ggcaacatg	gcgggtgtgg	aggagggcgc	gtcctgcggg	agccacctga	60
atggcgacct	ggatccagac	gaaaagagagg	agggagctgc	ctctacggct	gaggaagcgg	120
ccaaagaaaa	aaaacggaag	aagaagaaga	gtaaaggggc	tgcccacaggg	caacaggaac	180
ctgataaaga	agcaggagcc	tcagttgatg	aggtgacaag	acaattggaa	agacaagcat	240
tggaagagaa	agaaaaagat	gatgtatgt	aaggttaggt	tatcgattgt	gctttactg	300
tcactttaa	tcccaaataat	gatacattat	taaaagctgt	caaagatgcc	actaacactg	360
gaataaaagt	tgccggaatt	gatgttcgtc	tctgtatgt	tggtgaggct	atccaagaag	420
ttatggaatc	ctatgaagtt	gaaatagatg	ggaagacata	tcaaggcttc	caagaacaaa	480
acacttgtt	aatgtcatca	atgaaaactt	tggcactt	gccttctgcc	gcagatggct	540
ggatcgtttg	ggagaaaagta	aatacttcat	ggctctgaag	aatctgtgtg	acttggccat	600
tgtagnccca	tatccaccat	tatgtgacat	taaaggatca	tatacagcac	agtttgaaca	660
caccatactt						670

<210> SEQ ID NO 226

<211> LENGTH: 484

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (169)..(169)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (415)..(415)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (417)..(418)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 226

tttgtttttt	tttttttttt	ttgttttttt	gttgcagcct	ttagtcttg	ccatggcagg	60
ctgggttctat	taaaatacat	caaaaacatat	cctaatttatt	ccatgtcatc	tcggcgactt	120
tgttcaatac	caagatgtc	attgtatgt	gcataccgag	cagtgcant	gagattttt	180
tcttctctgt	atggatgtg	ttgccttg	ctgttgtctc	tgtactttt	ggccaaacca	240
aaatcaataa	ggaataactt	attacagt	cgcccaatac	ccattaggaa	gttatcttgt	300
ttaatgtctc	tgtgtataaa	attctttgt	tgcacatatt	cgatttact	gatcatctgg	360
tcagctaaca	taagtagt	tttcatttg	aaccttcttg	aacagaatt	gaagngnct	420
tcaaggctgg	gtccaagaag	atccataact	agcacgtt	agtcttttc	ctgaccatac	480
cacc						484

<210> SEQ ID NO 227

<211> LENGTH: 252

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 227

agagagagag	aaaaatccat	gatgcttacc	tgtaaccccc	tagaacccaa	gtgccagaat	60
taatttcttag	atgctgcttc	tgtttgaata	aaaagtca	gttttacac	ttgaaaaaca	120
ctcaaaaaat	gttcaactcc	atgaaaactg	ttttggctt	taagaaaactg	tttgatgtt	180

-continued

aactgtttcc tttgattgcc attcacccag taaaattgttg gttgattgc actgcacact	240
gggggttgggg ga	252

<210> SEQ ID NO 228
<211> LENGTH: 612
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 228

gaggacaaca tggcttc tttggcatgt ttaattgtga tgtttaacgg acatcctgc	60
agtttaagat gacacttta aaataaaatt ctctcctaattt gatgacttga gccctgcac	120
tcatgggg aatcagcaga acctgttagga tcttatttgc aattgacatt ctctatttga	180
attttgttcc tgtttatttt taaattttc ttttgttcc actggaaagg aaagatgtg	240
ctcagttta aacgttaaaa gtgtacaagt tgcttgcata caataaaact aatgtgtac	300
acaaggatt tgatgtttt ctctcagata aacttaatat gactttccaa gtttgacttg	360
tgtatgttta ttgtcaact ttttgtcacc ctatctcgat attttttgtat acgcacttg	420
caggatgacc tcaggctat attgatttag taaagggatt tgaatcaatg tattaatgtc	480
tccatagctt ggaaccatc atgggtataa tttgcattt gtttctgaaa tctttcacat	540
cattgaggat accagattgc tgaaaactcg gttctgaatg tgttgtactt ttgatttgc	600
tctcaaatca tt	612

<210> SEQ ID NO 229
<211> LENGTH: 524
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (149)..(149)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (344)..(345)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (409)..(409)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (471)..(471)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 229

aactgctggg gtctgcttc gcccggcc cgccagtcag tcagcctgc tgccgctgtc	60
gcccgcctcag cgggtccgggt agtcttaagc ccggccccacc acctttccc cgcgcctccc	120
ggagcctccg ggtgtttccct gtccgcccnc acaggccggc cgccgaccgtc tgcgtttct	180
cgccgcacctt ccggcgtccg gcccgcatttga gtggggacca tctccacaac gattcccaga	240
tgcaggccggaa tttccgactg aatgatttcataaaacacaa agataagcat aaagatcgag	300
aacacccggca caaagagcac aagaaggaca aggagaaaaga ccgnnaaaag tccaagcaca	360
gcaacagtga acataaaagat tctgaaaaga aacacaaaga gaaggagang accaaacaca	420
aagatgaaag ttcagagaag cataaagaca aacacaaaga cagagacaag naaaaacgaa	480
aggaagagaa gattaaagct tctggggatg caaaaataaa aaag	524

<210> SEQ ID NO 230

-continued

<211> LENGTH: 492
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 230

gcacgagaaa agatcagtga gnatgagatc ccgcctccag tggccttggg caggaggccc	60
ctgggtccccc agggaaacaac taacaggagc cctgaagcag aaccccccagc tgcccccctcc	120
gtggagccag ataacccttc ccagccttag acaagcctct tgggcagccc tggtaattct	180
gccccacccg actcagaccc ggacccacgg gccctgtgt tggccggca gagagagtac	240
aaaagtggctg ctctgaatgc caagcgggct ggagacctag accgtgcccag agagctcatg	300
agggttggga agagatttg tgcgtcctg gaggccctgg agaaggggca gcctgtggac	360
ctgagtgcca tgccccatc accagaggac ctgaagcccc ttccacaggc ttcccaagcc	420
ccgacagcgc cctccgatgc acccccgga gtggagcgaat gtcacccagt gatggcctct	480
gacatcccaag ca	492

<210> SEQ ID NO 231
<211> LENGTH: 460
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (355)..(355)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (391)..(393)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (421)..(421)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 231

agaattttgtt gttctgcagt tatgagtaat ataaaactgct agctgttaaa gacagatgt	60
tcatgttaaa attctttca ttttgttgtt cactgaggtt ggatataattt gacactgttag	120
atttctatat gtaaaaatat ctcccagtaa aaaaatgcct ttctttctc tcctcttttc	180
tttttcttc ctaactgaag aacattttat catcaacttag gttgaattaa attaacatct	240
caagctaaaa gctctgtaat tgaggttgc tctggagaag ataggaaaca ttgcacaatg	300
caaactccta atgtctgtt agcttttacg tatgagtaat tccctttgtat gtagnaaaa	360
gttttacctg tttactttta aggacacact nnnatcattt gaatcagttc taaaatcca	420
ntttatacta tggatatcac aaccctatgc ataaattaac	460

<210> SEQ ID NO 232
<211> LENGTH: 333
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 232

aaaaatgtct ggagggatgg gacttcagg atttattcat attaagatg tagtttttg	60
ttgtttccgg cattatgtat aaagcgcacga ttatTTTATG gaccaagttt taatgttaact	120
gttgcagtga aagtgcataa tctaacccttcc tgcgtccagc gggaaacgct cggcccgaca	180
atcacagccc cagccagggg cccctggcc agtgcctctt cctgtcggtc ccacccatcacc	240
ccatctcgcc tgcgtccctcg gtgagcagcc atccggatgg aggacacact acaagagtt	300
cggcccgccct gcaataaagg cctggaggct gcc	333

-continued

```

<210> SEQ ID NO 233
<211> LENGTH: 611
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 233

gccaggggcca gaccccgacc cgcggggccg agtccagcca ctgcctcgtc cccaaacctt 60
tccctgtct cttgaatct gaggcacagc ccagggcccg ctccctcccc ggggggaagg 120
gtcgagggtg ggaggaagcg tcttgctgt ttaaattcggt ggttagttcca ggacgtgttt 180
gcaaactttt cttcttgtaa tgtttaagt cattttgatt ctaaactttt atttagaggg 240
tgacttgtt tgttttgtt cagtgtctgt gtttttgggt gtaaccttgt taggtttgtta 300
aagcgaattt gaaaaacttcc tacccctgatc tggaaactgcc aaggaaatat aagcgaactg 360
gcccttgccc ggccttgaa ctgccttcaact ctgtaaaggg aaagtcttta taaattgaaa 420
acgaaaatgt aattgcattt attccctttt actttaacgc aactattttt aaaaatctgtt 480
ttctatgcataaagcattt tgagtcatc taagtaatgt gctgttttgc gttttccaa 540
ataattttt acattgataa ttactatgtt gtgtggctga ccattttgtt caattttttt 600
tgctactata g 611

```

```

<210> SEQ ID NO 234
<211> LENGTH: 538
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 234

tgcaccctga gtgcggccagc cccatctgca gtccctgcacc atctccctga gcagtaggct 60
tcccactgac gggggaggctg tgggacccaaa gtccactttt accctttgggt tgggtggAAC 120
acttgcgtggg gggcctggaa cagacaaggg agcctcgaca ggtcttccca catattttt 180
attcacttct ttcctcaacc cgtgagacct ggaaccccaa gtgcgtgtt ggcaatgacc 240
agaaaaatgcc tcgcaccaag tatactggtc agcttaacag accttcccag tgacagaagt 300
gattcctaca agtctggaga gaagggtgggt acacctatgg gttctcagcc ataaggaaga 360
caccagaccc tctgtggccctg ttcaaggaaa ccccttagtt ttctccagga gcagcttgct 420
cttcgcgtcc acatgggggc ttgcagtgcg gttttcctgg ggcctgagtg ctgcctgagc 480
ccacccactg cccgaaccta gtgtttgtt gtgaagtcca tggagcaggt acacacac 538

```

```

<210> SEQ ID NO 235
<211> LENGTH: 301
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (78)..(80)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (112)..(112)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (142)..(142)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (223)..(225)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

```

-continued

<400> SEQUENCE: 235

catccgggat gatgccacc	ccagctccc	ccagcgagga	ctcaaggcgt	tccaggccaa	60
ccctgaggcc aactgggnn	ccccggcccc	tgcccgccca	ggaggcaagg	cngcaggaga	120
aactgtggaa gagagacgta	gnctgctcca	aaataagcga	aaagagccgg	tggaggaccc	180
agctgagcgg gctgcctggc	tcaaaacatt	tccctgcaag	agnnncaagt	aggtgaacca	240
aaccacccccc caaccgaagt	acccatgggt	tctcccagct	acaggactgg	gccaatggc	300
C					301

<210> SEQ ID NO 236

<211> LENGTH: 477

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 236

tgcctgca	ccggggcccg	gccccgactg	cgtgctctgc	cccaacaagg	gtggcgcc	60
caagaagacg	gacgacgacc	gctggggcca	cgtgggtgtc	gcccgtgga	tccccgaggt	120
gggcgttcgc	aacaccgtgt	tcatcgagcc	catcgacggc	gtgcggaaaca	tcccgccgc	180
ggcgttggaa	gtgacctgtct	acctctgcaa	gcagaaggcc	gtggggcct	gcatccagt	240
ccacaaggcc	aactgttaca	ccgccttcca	cgtgacgtgc	gcccagcgcc	ccggcctcta	300
catgaagatg	gagccgtgc	gcgagctggc	cgccggccgc	gcccccttct	ccgtcaggaa	360
gaccgtttac	tgtgacgtcc	acacggccccc	cggtgcacc	cgccaggccctc	tgaacattna	420
cgggggacgtg	gagatgaaaa	acggcgctcg	tccgaaggag	agttcggtca	aagcggt	477

<210> SEQ ID NO 237

<211> LENGTH: 467

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (292)..(293)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (299)..(301)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (364)..(365)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 237

gcacgagggtt	ttctgtatc	ctgtttggca	agattttctt	tatgtatgg	taacaacaaa	60
ggttacagtt	tagtacttaa	accagcagtt	aatagtgttt	ttctcccgag	gcagagtaac	120
taaaaggcacc	tgtgaaaact	gcaaaagaaaa	ctagggacag	gacaagaggc	agcggaaagcc	180
tggctgttgt	aaactggtgt	gcacccctgc	attccagcaa	gggcagggg	gccagaatca	240
ccgactgctt	tcctcaggga	cttgaattga	cagtttttc	ccaaactatct	tnntactgnn	300
ngcattccac	tgttacccagt	taaatataaa	gaatttagtct	tcttaataaa	atcaccttt	360
cagnngaact	atacacattta	aaaaaaaaat	cactgattgt	gtttccttcg	tcttttttc	420
tttgaacttg	cagggtgattt	agtctcctgt	gtttcttctt	ttacacc		467

<210> SEQ ID NO 238

<211> LENGTH: 591

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

-continued

<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (504)..(505)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 238

cagtgcagg	ggacggagaa	gcatgggtc	agcctccagg	gattatcaag	atcgtgcaca	60
agaacagagc	tca	accagggaca	gggccttga	aagcacccctg	aagtcttggg	120
aagataagca	gaaatgtgat	tcgggtaagc	cagttctccg	aacgcacttg	tacatccagc	180
acgcggcgga	cctggccacg	gaggaagtgt	ctcagatgc	gctgtgctcg	caggeggccg	240
aggagctcat	caccaggatc	tgcgatgcgg	ccaccatcca	ctgtctattg	gagcaggagc	300
tggcccacgc	ggtgaacgcc	tgctcccacg	ccctgaacaa	agccaaacca	cgcttccag	360
agagtcttac	aagagacact	gccactgaaa	tagccatcaa	tgtgaaggcc	ctatataacg	420
aaacagaatc	tttacttagt	ggcagggttc	ctttgcattt	ggaatctcca	catgaagagc	480
gagtatccaa	tgccttacat	tccnnnngaa	tggagctaca	gaagtttaca	gagattccat	540
ggcttttatta	tatcttacac	ccgaatgagg	atgaggagcc	ccccatggat	t	591

<210> SEQ ID NO 239
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 239

ggccagggtgg	tggcctggga	ctcccaacac	agtgtgcac	tgttccctg	tgcagtgaat	60
gtcagtcga	ccagtagatc	tgctcgctaa	gaggatggtc	caatttgaca	atgttactcc	120
cattcggatt	ctgtactgcc	ttttggtaga	tgaaaactac	caggaaaaga	agggaaaggga	180
agttcccagt	taaagttccc	aaaagatcga	ggctgtgaga	cgcatacagg	tatacagaaa	240
gctgaggcga	gaacgctctg	gtggggggc	gtgcagatgg	aggcagc		287

<210> SEQ ID NO 240
<211> LENGTH: 562
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (501)..(502)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 240

gttttaata	attcctgaga	gatgtctctg	gaaggaaaag	tgttttggaa	actaatgact	60
attttgagg	acaaaaatga	caacttaa	taatttctta	aatacgttag	gataactttc	120
aggacaatat	tgcctcacaa	ccctgctac	attgagaagt	cttttttcg	tttccctta	180
gttgttctga	ctggattttt	ctacagaacg	tatggaat	tatctttgtt	ctcggttgct	240
gttatttcct	gtcctacttt	aagaaatata	aatacataga	aatggtgcat	ctttaacatt	300
tgtttgtaca	tgtataatg	tcttgttattt	taattcgttt	ttagcatgt	gcaacacgaa	360
ttgttcaagg	gtaagccaca	acatctaaaa	atcactccta	gatacgaaca	ataaaggaaa	420
aaaaatggta	ccgatttagg	aggaaacaaa	gccgctgtcg	ctgggtttc	tgtgcagcct	480
gcagtgactt	ccgacacacg	nngagaagct	gtcactgtaa	accaagtcat	ccttgggg	540
agagcgcac	agcctgctgc	tt				562

<210> SEQ ID NO 241

-continued

-continued

<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (591)..(591)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 244

aggacctgac	cagctgagct	tccagcgagg	ggaagtgtcg	cgtgtcatcg	ccactgtgga	60
tgaggactgg	ctccgcgtgt	ggaggggatgg	agcgggggggg	ctggtaccgg	tgggtataac	120
ctcccttgtt	ctctaggcct	agcacctgtt	ccttcctgc	acctctctct	cccttctgtc	180
acctggaaat	ggaatggcct	gtgaaatactc	accatgtat	actgactgtc	cccaaagtat	240
cttccctgtc	tgcaaaatga	cactttcctc	ccatagccat	ttctgctaatt	acctaaaataa	300
aacttttttc	cttccttcct	ataccatct	ataagggtgaa	atctgcttt	cgaaaatata	360
taaaaaacgaa	tttccctcca	tgccatctct	ttcctcttcc	caatctgtat	tctgcaaaat	420
ggaaatctag	ccccctgtat	cttcttcctc	cataagtgg	ctgcacccct	atatacgcct	480
cagttcccaa	gacttgaagg	gcctctatag	tcttcttcct	gtgtatggaa	ccttccccca	540
cctcaccat	cccgcattgc	ctgtatttat	gatgtactca	tgctggacta	ngtgetgaag	600
tctggacacc	cctgggtgggt	gggcctgtgg	ggtcagtcgt	t		641

<210> SEQ ID NO 245
<211> LENGTH: 627
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 245

tttaagggtgg	aacagggtcat	tttttgttt	ctctgctttt	aatctaatt	cttataaaaag	60
agggtgtttt	atcccttagac	cacagtgcct	tgcaccccac	caccaccatt	tggtaatgg	120
gcatttagatg	ctgcacaagc	ctttagggca	ctattttgg	agctataaaa	gtttatccag	180
aaactgtacc	tgggtctca	gtttattgtc	attcaacttg	ttcataata	ttaactattt	240
ccaggggttt	tttagaagga	agaattgtac	tgttctttag	tttactata	tttttttttc	300
tggtgtaaaa	atgagccaga	aataagcctt	attgctaatt	aattatataa	acccacataa	360
tccctgcata	agatccctc	cacacacttc	actatatgt	tgtggatttg	gatagaaaat	420
gatgttgcca	gcattaccag	ttttaataac	ttgactatac	agattgtatgg	aataaaatta	480
ttaaagtgtt	ttcagggAAC	ttaatccata	tgtcaccacc	aaagatttct	acagtgttat	540
aaaggatgtta	aatattccaa	atttctgtaa	acattggta	gataaagagt	ttttctttt	600
tttttggaaat	aacacagttt	gtactct				627

<210> SEQ ID NO 246
<211> LENGTH: 516
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 246

ttttttttct	tttatctttt	aaaatggaaag	caagtgtttc	gacagaatac	gatggctgct	60
ctataagagc	cgatcttaga	gtaattca	gggtcttctc	tccgatagct	cggtttaaa	120
aaaagaaaaaa	agacaaaaca	agaaaaataa	cccacagagc	gtcaaacacc	aactctgagc	180
ctgggtgggg	atccgttcat	taaataagcc	ataagctaca	cattcaggc	agaataactg	240
getcctgcct	ccttatgtct	ccaaaggcata	tcccttatgg	tgtttcacca	ccaaacaacaa	300
ttttgtcac	ttaattaatt	gggtatcaga	accttagaac	atttctgaat	cttaataatg	360

-continued

aaggctttca gcagattgtt ttgataaaaga aacacataca ggcttgaata taaaccactg	420
taattattgg tttctttata tctcattatc cacttgagta tttaaagcac acacgtacac	480
acaaaaccac accaaacatt caaataccct gaaact	516
<210> SEQ ID NO 247	
<211> LENGTH: 238	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 247	
aggcttataa ggaacaataa aaaagagaga gtgtcttgac tgctacaagc attttaataa	60
atccaatagt gaaggcacga tacgaacgtt ttattaaggg tgagaatccc tttgaaattc	120
aagatcattc tcaagatcaa caaatagaag gagatgagga gggagaggaa aagattgacg	180
aacctgtgga agaagaggag gaagaggagg aagaagagga ggaagtgggg gaagggga	238
<210> SEQ ID NO 248	
<211> LENGTH: 558	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 248	
acggcagctc aaaggaaggc acttctgtct gagtctcctg cagaaaatga aattactgtt	60
caacttacca aaatgcctta cacattcctt acaaataaac caaccgacac agcgatatcc	120
ggggccaaact tcggtagctc tgagaagcca taaagacaag agtttcttag caccagaagt	180
agatcttcca gaccctgttt gtacaagaag aacctttgtc acattcgaga aacactatcg	240
ccctggcccg gccctggacc accagccagc agacgc当地 gcccctcgta gccgtgc当地	300
agacccaggg otgtttctgg gaggcgggccc cggggctctgt atgtcagtca gtgcaattgt	360
gtctttcgcg ggggtggggg tcgggtgggtt ctatgtctga gtccctaagg ctgc当地agca	420
gacttggagg tcacagccag cgaggcagca gccccagtc当地 cggaaagatg ctgccccag	480
aaccgc当地gc tgactcctgg gtgttaatgc cattaaaacc cgc当地gtc当地 cc当地ggcaaaaa	540
aaaaaaaaaa aaacaaat	558
<210> SEQ ID NO 249	
<211> LENGTH: 478	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 249	
ttgaaaaagc tgtaatttggtt cctcagttatg tgaaggatag aattcattcc acttacatgt	60
acttagcagg aagtattggc ttaacagtt tgc当地tgc当地 ggc当地gtgagc agaactctg	120
ctctcatgaa cttcatgatg agaggcttt ggataaccat tggc当地caacc tttgc当地gcca	180
tgattggagc tggaaatgtt gtacagtcaa tatcatacga gcagagtc当地 gccc当地aaagc	240
accttgc当地tggt gttactacat tctgggttaa tgggtgtctgt ggtggctct ctgc当地egatcc	300
tagggggccc tcttctc当地tca agagctgc当地 ggtacacggc tggc当地atc当地gtg ggaggctct	360
ccaccctggc catgtgtgc当地 cccaggatgaga agtttctgaa catggggccc cccctgggtg	420
tgggc当地ctgg tgc当地gtcttt gtgc当地ctc当地 ac taggatc当地gt gtttcttccca cctaccac	478
<210> SEQ ID NO 250	
<211> LENGTH: 393	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	

-continued

<400> SEQUENCE: 250

tccctctaaa ctatttcattt gtggtccgag ggcaagttgc tactcatctt gagtaatctt	60
tgcctctctt tccatggcat tttgaccta agtccatttga agcattctga tcttccacct	120
tcctaatggg gatatggaa gacatctacc ttcccttatgg agatatgatt ctccctagg	180
agagaatatg cgaatggagc tctccccat attaaaccag ctctaatggga tttattctga	240
cctcgagtca ctgttgccat gatttcccag gtgtttgtt catgttctcg ctttgagaac	300
cattttccctt tggtttcttt cctccaccac ctccgtatgg ggtaatggca ctttgccatt	360
ggatggttgg actctgcctt ttccctccgtg cag	393

<210> SEQ ID NO 251

<211> LENGTH: 393

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 251

taaagatcta actcaagact gactctgcta gtgttagcatt tccctggggg attttggttt	60
taatttagacg gttcactgct actgtgttgtt gcggggatgg ccggacatgg ttaggggta	120
acccagcgc accagcactg attggacggc cttcaccaa tcagaagctc agtgcggcagt	180
ggggccgtgt gtgacttggg atcatgttgtt gcactatagt cacatgtact gtaaagtgaa	240
aaggggatgtg caaaaacaga aagcgagacc tgctactaga aaagtggaa ggggaaatgag	300
taaacttctt ttcttgccga cagatgtgca catagccgct agtaaaacca gcctcaaaca	360
gaatgctcat agcttaataa taaaagctgt gca	393

<210> SEQ ID NO 252

<211> LENGTH: 446

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 252

tttatecctct ctcttcagg gtagatttct ggatagctag tagttagatggc atctgaaata	60
gcatttgagg ggtgggttgtt attcattttag taacccgagc ttttgctga agagcttctg	120
cttaactctt ctttgtgtt tcaataggctc ttatatttgtt ttcttcctgt cttaggttgc	180
gcattttttgc ttaagaactt ttaaatttgtt gggcagtaa gaaaactttg aatgcctggg	240
gcctgtcaact tctcttcctt aacgcggccag agggttttagt gtgtatctgt tagcaggaga	300
gtcttctaga aggtccattt ggtacctctc acacccacag ctgtgtgcta tggttggcc	360
ctccctctctt cctgtatgaaat ccatgcccattt acccagtgtt gctgtatctc atgtgtctg	420
aaaggccattt gaaaggcaccg tggttgc	446

<210> SEQ ID NO 253

<211> LENGTH: 476

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (344) .. (344)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 253

gcagaatggaa ttgttgattt taatccagag gcactttata taatgtgttc tctgttttag	60
tttatcaaaatcactcctcaga gataagaacc ctttaacag tgagcaaggc tcggggagtg	120

-continued

aaatggagtc agagggtggag cgtaaggcc agggtgtgg cccaggtctg cctgtccctc	180
ccagcctcag tttcctcaga tgttagaggga agaccaccac tccccgccc ccacatgtt	240
ttcttaggagg aaaactctgt gtccccattt ttgcacatta gttttttt cggcctgac	300
ttttacatat atatatactt ttttttttc ttttgtctgt gctntgcggg attttatcc	360
ccaaactaggg atcgaatctg tgccccctgc atttgaagca cgcacttaac cactggaccg	420
ctagaaaagt cccctttatc tgtttattt tttgttaca ttactttgt gggatg	476

<210> SEQ ID NO 254

<211> LENGTH: 495

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 254

tttgaaaatt aatttgtat tatgcattct tgatttggtt catcagtagg tgcttattt	60
catcctgtga ttccagtaga tttagggaaat tgataccctt ttgcagttt gaataaaagt	120
gttgataatt tctaaattat cattataaaa attcttagag cttcaacatt ttgcgtcatc	180
acaggcgtat ttagtattgt tttgtattaa aatagtccctt ttcccttgc tgctgccatt	240
cattccgtgc cattagtccct taaaatgcgt ttaaagaaga aatagccaag ttgactgtt	300
cacctcatcc aaacagacac atcacaaaca tacgagggcg acagtgccctg ggatggacgt	360
ggtaacttctc agtctgcctg ttctgagaga agagcaatta gcatggccac gtcacctgt	420
gettgaagt gaaaacttta agatcgaaaa aattnaaagt cagatcaggg atttacagct	480
atctactttg gtatg	495

<210> SEQ ID NO 255

<211> LENGTH: 566

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 255

ggtaagatca tagtggatgt ggggtcacaa atatgtagat ggccacatga agataggcag	60
agactggagt tatgtatgcgt aaagtcaagg aatatgtggg gocatcagaa gcaagaagag	120
tcaaggaagg ttggaggat tttcccttgg agtgcagagg gtacatggcc ctgctgacac	180
cttaattttg ggttctaaag caccagaatg gtgagaaaat caatttctgt agtttaagc	240
cacacagttt gtggtaattt attacagca ttcttagaaaa ctaacacagt cacaaactg	300
attatctttg ctaattttatg ataaatttat gttttatca tgttacataa gcagatgaaa	360
tgagtgtgaa gagttgtatgt ttctgtgaaa accaagttaa atactttggaa aagcttagat	420
gaaagtgtgt tgctttcccc atgccaatt taaatgtattt ggttaatttt tggtaaaaca	480
gttgtaaaag actggccagc aatgtactaa aaatccacag gtattcatta ccagtgtaca	540
actatataaac gtaacacata tgattt	566

<210> SEQ ID NO 256

<211> LENGTH: 526

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 256

gcaactagag agtaacccct gctctccaca actagagaaaa agcccatgca gcaacgaaga	60
cccagcacag caaaaataa attaataaaat aaataaaattt tttttaaaaa gaaggccct	120
ctaggagaaa gcccttcaaa atacctcctg aatccagact ataacctgcc ccagtgaaag	180

-continued

<210> SEQ ID NO 257

<211> LENGTH: 225

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 257

```
gcattttttt ttttttttaa atgactctga aactttaatt acagatactt 60  
atcaacatct gaaagtgtgg attcgttctc ttttgcgga aaggctggca cggttgtcc 120  
cttacaccca tgtctttcc tgctccctgt ctcttctta tgtaaaaaaa aaaatgtctg 180  
gatcacagtc ccaaccaact ctgctctgca tcccttgctg ggaac 225
```

<210> SEQ ID NO 258

<211> LENGTH: 558

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 258

cgacgaggac atactggacc tgaacgagat ggtcagacaa gtgacgggaa agatccccat 60
cttcttctat tcacactatg gctgttactg cagaaaaggt ggccaaggcc aaccaggaga 120
tgccacagac aggtgctgcc gtgaacatga ctgctgtac cgtcacctga aatctgacaa 180
ctgtgacatc agcttcgacc actatgacta caccttttc caggggaaag tccagtgttc 240
caccaagggg agctgggtgtg agcagcagct gtgcgcctgt gacaagacgt tggccttctg 300
cctgcagcgg aacctgaaca cctacaagaa tcacctgcga cgtctgtcca gatgcgagg 360
cgagactcta gcctgtccccc ctgcatttg agctctgggg aaggcccccc aggaccactg 420
gccccacggcc cgacacctgc ctggagcctt taaagcactc ctggaagagg aaggggctt 480
gcctcgcccc tagctaccac ttgccttcttgc gaccttctga atctcccaagg ctgtgttcc 540
cqaaqqqtqqa ttqaqatc 558

<210> SEQ ID NO 259

<211> LENGTH: 439

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 259

atgttttca cttataacaa atgcaaaaac tttagacaaa agtgatatgt gaagaagtct	60
tttacagtaa aatatatcct gaatccatata ggttcgttc ataatttgagt ctcttcttga	120
gttacccctt ctaacacgta gacaatgtga agacagtgc acgtccctt tctagaggtg	180
ttaacctgt tcttacaaac tgtaaaaaca aagaatttc tactttacta atgtttgtgg	240
ttttaaacag ttatttcat tctaatcagt tctctaccct ctaatttcta ctaaaacttgt	300
aaatacattt agaaatgata ttgtaaata cagtatatga agtcaagttt attttgggga	360
cagtggagaa cctcccaatt ggctctggct tggcagttt gttttttgtt gttgtgggtt	420

-continued

ttttttttt ttaaacagc	439
---------------------	-----

<210> SEQ ID NO 260
<211> LENGTH: 481
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (384)..(384)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 260

tcatttccta ttgcagctgg	60
ggggaccgcc acaaacgcag	
cgacgtaaac ccgcaggagc	
gtgtgctgac agtccagggg	120
tgttcctcg gcagagccca	
gggagggtca gcgtcctgtc	
tcgggggtg tcagcagagc	180
tcagccccgt cggttagggcc	
aggtcctgtct cctcgcgt	
gtgagctgaa gcccttattt	240
gcttctggaa gcctctggc	
tggccgctcg ggcccttcc	
tcttccaagg tggcagctcc	300
tctccatgt tggccttca	
cacgtcccct gctgtttca	
agggctgtgc aattaggggt	360
cccacgaaga tccagggtcg	
cccgtccgcc tgcgtccgt	
tcctcgctc taccggcccg	420
cagngccgg ctccggccccc	
ggcggccagg cctccctgcg	
gcaggagggg cagagctggc	480
tctgcgcggc tccggcgeage	
tgtgcacgtt gccgcctga	
c	481

<210> SEQ ID NO 261
<211> LENGTH: 597
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 261

gtgttaactca gtcttgctt	60
ccttctggga gctctaggtt	
tgcctccagc tcagaccatg	
gttgccctcta gccactacta	120
tggggctgcc tcctgtactt	
ctcttcctcc tctggttctg	
ccatctctga ctctctttag	180
gatttttccc ctattgtca	
tgccttcagg gtccctgtat	
tcacatattt gtccacttct	240
ctttcctctc tatttactcc	
caaaatagaa tcacatccat	
tgcattgtcaac tgccattgtat	300
atgcgttgta ttcccaaata	
tatatctcaa gcccctaactg	
ccctttatct ttagatctgt	360
attttatca cctgctggat	
atctccttgg acatgtccag	
atggactcaa ctcttctgt	420
ccctactgca aagtatgttc	
ctcctgaatt ccaatcctgg	
ttacattcat cactttcat	480
aggttcacca gctagaaaca	
ttttatgggc ttaaattcct	
tcccatatcc tactagtcag	540
tatatcatat ccattccact	
ccaagtttcc ttgttttgg	
ccctttctt cccctctgcc	
tctactctag ttcacaggag	
cttgggattt ggagtca	597

<210> SEQ ID NO 262
<211> LENGTH: 563
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 262

ggaaagagaa cagccaccac	60
gttttgctca gcctggaca	
tttgaatttg agtatgcac	
tcgatggaaag gctctggatg	120
aatggagaa gcagcagcgc	
gagcaggatg acagaaacat	
ccgagaagcc aaagagaaac	180
tggaggccga gatggaagcg	
gcccggcacg agcaccagct	
gatgctcatg cggcaagatt	240
taatgaggcg tcaagaggaa	
ctcagacgtt tggagaact	
cagaaatcaa gagctacaaa	300
aacgaaagca aatacagctg	
aggcatgagg aagagcacgg	
tcgtcgtaa gaggaaatga	360
tccgacacag agaacaggag	
gagctgaggc gacagcagga	

-continued

gggccttaag ccaaactata tggaaaatga gaaaaggaaa catggatgaa gctacctgaa	420
atttggctc ctgtgtgagc ccaaagttga gagctgagga aaacctgcc aagttccct	480
tcaagtgtct tggggagcag gaacctcagc ctttcttgat tatcgcttgt gagatgagac	540
tgtatgacatc agagcactgg ctt	563

<210> SEQ ID NO 263
<211> LENGTH: 470
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (48)..(50)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (382)..(382)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (388)..(388)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (390)..(390)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 263

cgcacacttt taaaagattc agttacagct ctttgaaga ggtttcnnn ttttattaa	60
actactaatg gatcaaagaa caattgtta ttttttctc ttgggttta gatattaatg	120
ataaaccttgt tggaattttt ttccaaagaa aatattttta taattccgta atttaatgtg	180
ttccctttca tcatccactc ttggcagtgt taggctatgt ttaccttaaa ataaatctga	240
ctcaagattt tttatgtatg tataaagaag tattttgtgt gctacaaaag cctttcaaa	300
ttatcgtaa tttttttttt ttaagaatgt agccagtatt tgctcagtgc tctgttaaggg	360
aacatgcaga tggaaagctca gntcttangn aagggctggg gagatggggtt tattttccc	420
acctgtgaat atgtaaaaca taaaaccatt atctctgagg gacttctcac	470

<210> SEQ ID NO 264
<211> LENGTH: 630
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (278)..(280)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 264

ctcttacctt ttcctttgt tccaccaaat ggttgcttctt ttccagagca gaaactggcg	60
gatatgcaat gatagccaga accccctgttc ctcacccacc ttgggtctgtt gctgaatgt	120
ggctggcaga acagggacac caagagatgg agaagggggc ttcccagcct cccagcaact	180
tccttagcca taagcaagca caaagatggatg gcagagatct gtccagagctg aaagtccatt	240
tgggtgctca caactcaggt atgcacacccg tgtggcannn gggcagcaga gccctacttg	300
accgcaagtc ccgtgcaccc agacctgtgg ccagatcggt gactctggct gcctcaggcg	360
ccgcctttt gcatagggtt ctcctccatt agtaactaca gcccactcag acatcctcca	420
cattgtgcac actgggtctg ctttgcctt cgcaagttga tacttggcat tagcatgaaa	480
cttgggggtt tgggggggtt tagagagaat tctaacaacaa aacatccat taaattgtac	540

-continued

ttgagagatg aaaaaactcc tgggttattt tgacagaatt attttatata aaatacat	600
ccatgagcaa aaaaaaaaaaaa aaaaaaaaaaca	630
<210> SEQ ID NO 265	
<211> LENGTH: 419	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 265	
gaaaatcgaa ctccctgttc agctccggct gcagctctag ctccagcccc ggctccggca	60
ggctctggga ccactgtacc agtcccatca cagactcccg gttcagctcc cctgcctcag	120
gcccaggAACccccgtaccc cacctatcca gggtatcccg ggtattgccaa aatgcccatt	180
cccatggggct acaatcccta tgcgtatggc cagtataata tgccgtatcc accagtgtat	240
caccagagcc ctgggcaggc tccataccgg ggaccccagc agccttcata cccctccct	300
cagcccccac agcagtctta ctatccacag cagtaataatg tcagctcaga agctcagctg	360
gttcagttca aaggaaaga aataccaacc ctgcaataag tgtactaaac tctacgctc	419
<210> SEQ ID NO 266	
<211> LENGTH: 212	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 266	
gtggccgtgg ctaccatctc aacgaggagg gaacccgctg cggtgtatgtg gacgagtgtc	60
ctccccccctc tgagccctgt gggccggggc acctgtgtgt gaactccctt ggaagttcc	120
gtgtgtgatgtg caaagccggg tactacttgc acggcatcag caggacatgt gtggacatca	180
acgagtgcggc gcggtaccca gggcgctgt gc	212
<210> SEQ ID NO 267	
<211> LENGTH: 352	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (82) ..(82)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (226) ..(226)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (249) ..(251)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<400> SEQUENCE: 267	
ccccgacacc accacccat ggagagtacc tgccagatat ggggctggga atcgaggagg	60
cgaaacccccc gcacgcctac gntgctaaga aaggcaagaa tggaggaggc ccggcctacg	120
agatgeccgc gttcaccgct gagctgacgg cgcccttccc gcccgtgggg gccccgggtga	180
agttcgacaa actgtctat aacggcagac agaactacaa cccgcngacg ggcacatctca	240
cctgcgagnn ncctgggtc tactactttg tataaccacgt tcactgcaag gggggcaacg	300
tgtgggttgc tctgttaag aacaacgagc ccgtaatgta cacgtacgac ga	352
<210> SEQ ID NO 268	
<211> LENGTH: 251	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	

-continued

<400> SEQUENCE: 268

aaggaaagc agtttgattt gtttaaaaaa cacttttat cagtttggaa	60
atgcaaacga gaacagctgc tctgaagccc ctcccttgta cagggagaag	120
aaacaaaacc aaaactcaga aagccgttca gcagcgtgaa atgcctttc agaagcta	180
cgggggattt tgaaagcctg gctccgtgtc tcagttgaa aaaaagattc caggtgtaa	240
aaggctttca t	251

<210> SEQ ID NO 269

<211> LENGTH: 489

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 269

acaaagtgc gtttaataa aaaaaaaaaac actcacagac ataaagatcc cgtcactacc	60
cccaaagctg aataagttaa gttgtgtcc tgctgcctg tgacggagc gggcccggtc	120
gctcaggcgt cgcccccttc ccagatggcg acaatgtgg agtcagttagc cgcaagtgg	180
taggtaaagg cgggggttggc caccacgtg ttccacatcg tcttggtcac cgtctggccc	240
attgcctggg gctggggcca cttaaggatc tgctggggg cctgcggggc ggtctgttgt	300
ggggagcgct ggcgcaggag gggcctgacg tcatagatcc acacgctgcc ctgctcatcc	360
ccgcagagca caagccctt gtcaggacag gtgtgtggg agaagtaggc caggatgtg	420
ggcgaccact gcagccaagc caggactacc acagccactg tgggctggct gccccgaccc	480
tgcacacgtc	489

<210> SEQ ID NO 270

<211> LENGTH: 558

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (470)..(471)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 270

tgttaagtc ctttgggtgt ggtgtgtgt tgcttaacca tgtctgactc ttgcgtcccc	60
ctggactgta gccccatcagg cttctctctc catggattc ttccagcaag aatattggag	120
tggagtgtca tttcctctcc agatcaggga ttgaacctac atctcatatg cctcctgcat	180
tggagagatc cagtgagcct gggctgtct ggaaaattct tggatcctgt gggcacacac	240
cctgagtgtg aacctggata ccggacactt gttggcaaaat tcatctttct ctcactgggg	300
tgtatTTTT aaaacacagc aacatcatct cattgatctc tccatttgc tttggctca	360
gctcagtaaa ctgaatgaat gaagttaaa tgcatttcatt ttctaaacat tttacatctg	420
tcagtataaa caactgcctt gagcctcaca tatcttcgc taccatgaan nacccatgtc	480
agctgaagtg tacagggca tgctttctcc aaacttatca agtttactgc accctctctc	540
ctctggcctg ctactcat	558

<210> SEQ ID NO 271

<211> LENGTH: 447

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 271

-continued

gcggcggctgct	ccccggcggt	cggctgcggc	ggagctgcgg	ctcagcttt	cgccccccg	60
ccccccctaag	gtgcggcttgg	cccggtgc	cattcacacg	ctcggttgag	gtggcttga	120
ccccggcttg	cctggcttagc	acgaccgagg	agggtggctgg	acggctggag	aatgaacgga	180
gaagccgact	gccccacaga	cctggaaatg	gccgcccccta	aaggccaaga	ccgctggtcc	240
caggaagaca	tgttgacttt	gttggaaatgc	atgaagaaca	acattccatc	caatgacagc	300
tccaagttca	aaaccaccga	gtcacatgtg	gactggggaa	aagttagcatt	taaagacttt	360
tctggagaca	tgtgcaagct	gaaatgggtg	gagatttctta	acgagggtgag	aaagttcgt	420
acattgacag	aattgtatcct	cgatgtct				447

<210> SEQ ID NO 272

<211> LENGTH: 533

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 272

gtcatcacct	ccatcttgaa	gaaaatggat	atattcttgt	tgccgggtggc	caatcctgtat	60
ggatatatgt	tcactcatac	tcacaaccga	ttatggagga	agacacggtc	tgtaaatcct	120
agaagcacct	gcattgggtc	tgtatccaaat	agaaattggg	attctcattt	tggaggagtg	180
ggaaccagta	acgacccttg	ctctgatacg	tatcatggac	tccatgccca	ttcagaagtg	240
gaggtgaaat	cggtggcaga	tttcattaca	aatcatgggg	acttcaaatg	cctcatcgac	300
ctgcacacgt	actcgcagct	ggtgatgtat	ccatatggct	acacaactag	cagagtcccg	360
gatgctgatg	aactggatat	ggtggcacgg	aatgcatacc	aagctatggc	ttccttgcg	420
ggcactcagt	accaagtggg	ttctgtcgcc	tccactgtct	atacagctag	tggaaacact	480
attgactggg	catatgataa	tggcatcaag	tatgcgttct	cttttgagtt	gag	533

<210> SEQ ID NO 273

<211> LENGTH: 491

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 273

agagctgcta	aaaggcacc	tctacccccgg	ccgagggaca	acacagacca	gtgctgaagg	60
ctaatgtgt	gttttacta	ccctccccac	cccctatttt	ccaggggggtt	taggetacat	120
ttaaaatcta	aacctgcagt	ccgtgacttc	ctatcaagcc	caaatgcatt	ttggtttgg	180
ttttctgctt	ctctgcccct	ttccacttct	ttcgtatttg	ctttatgtgc	gagtgtctaa	240
atggccctgg	aattgagaat	ttggctctcc	accaagcacc	ttatcttgcc	accttagcct	300
taagaatgag	tatgaagaaa	aatgcacacg	cccttctgtc	cagggcagt	agaaggcctg	360
caaggaagag	gtcgagaca	aggaaaggaa	cagacagtca	ctccccacagt	tccgaggct	420
ccatgectca	ggggccccca	gggattgcag	aaggggata	tcctggaagt	tcgatttctg	480
cagtttgc	c					491

<210> SEQ ID NO 274

<211> LENGTH: 591

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (107)..(109)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 274

-continued

gcttggggct attttgtgt atattgatga tgaagacatg tgcaatgtag aattacagtg	60
aaactctgggt gactgtgggt agtcattctt actgaaaact gcactgnnnt tcccacacca	120
tgaactggct ggtcgcctct atttcggga ttctttgaca cttggtggtta cttcatctt	180
gccaggcata cttcttaact gagtaggaag gagccttgta agatcctca caggcagtgc	240
atgtgaagca tgctttgtcg ctataaaaat gagcatcaga aagtgtgtat catgttattt	300
tattatgttc ttgctttgg tgtagaattc agcaaatttt catcaaatac tagccagagc	360
ccttcactgc catgatagct ggggcttcac cagtctgtct actgtgtatga tttgttagact	420
tctgggtgta tttctgtatt tattttaaa tctaccgtgt ggatatttag tgctatgtct	480
ctttaagttt ggatttagtgc ttctaaaatg gtggagtgc tctgaatgtt acaaatggat	540
caaggcatta aaatgaatga gatctacatt tcaccaagta ctgtatgtat t	591

<210> SEQ ID NO 275

<211> LENGTH: 255

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 275

gcctgaccca aggcccttc ctggggcttc tggggccat cctgaaccca gatccacatg	60
gaccttcgtg ttgagccagg gtgaggggag caaccccccac cccgacccac tcaagccct	120
gcccagcttc acagggcagg gggaggctgg ctcttactca ctggagctgc tagaacccctc	180
cctacagtct ggacccagct aacctgaggg gagccattgc caccttcca gcaccaccca	240
tgtgccccca cccac	255

<210> SEQ ID NO 276

<211> LENGTH: 406

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (104)..(104)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 276

tgttaccatt ctgatgttgg agtggccgca tttgtttttt tttttttttt taatgtatcaa	60
agtagttaat atttggtaaa tatgtccatt gtaaccataa ggtngaaaat gaaacacagg	120
tctgtttctt ttcctgtaaa ctggagatcc tctgcactgg ccaccttggt agaggagagc	180
attagtgcct ccctgcaacc ctatcatccc cctcagagca aaactcgata gaaggtgact	240
gccaggtatg ggaagaactg gtcttggag tcaatttctt aaagaattttt tttccagttac	300
tgcttttagct aaacagatgg ctacttatat ctcttgaatg atttatattttt cccagatcct	360
atagccagtc agaaacgagc ttattcacag aagtacagca taaccc	406

<210> SEQ ID NO 277

<211> LENGTH: 443

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 277

gettccgggt aggaattagg tgaccccgcc tgccgctggc acctgcccggc acagcagcc	60
tggggggctca cctggccgg agatacctgg gcgatgcata ggtggagccc gatccctgc	120
ggatgccccac ttcccgcccc gactacggct tccccgagcg caaggaacgc gagatggtgg	180

-continued

ccactcagca ggagatgaac gacgcccaga tggtgctcca gcaacgcac tactgcgcc	240
actacctcat ccggtttctc aagtgcaga gcgacagct ccccaacttc ctggcctgca	300
agcacgagcg gcacgactgg gactactgcg agcacctcgca ctatgtgaag cgcatgaagg	360
agtttgagcg cgagcggcgg ctgctccaga ggaagaagag acgggagcag agggggcgg	420
acatggccaa aggccctgggg ccc	443

```

<210> SEQ ID NO 278
<211> LENGTH: 573
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (406)..(410)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 278

```

gcacgaggta tcccgccat cctggcgccg gcccggcta ctacgcaggc gggtaacggag	60
gggctcccg agggectgcg ttcccggc aaactcagga tccgctgtat ggtaactttg	120
ctgctgttagc tggacaggat ggacaatacg atgctgtatc actgcaaaaga tgcctgacac	180
agtcggccat tgctggagga tacaacattt ttaacctgga gacttgccgg cttatggtt	240
caatgctgga tagagacatg tcaggcaca tgggttcaa tgaatttaaa gaactctggg	300
ctgtactgaa tggctggaga caacacttta tcagttcga cagtgtatagg agtggAACAG	360
tggatccccca agaattgcag aaggccctga caacaatggg atttannnn gagtccccag	420
gttgtaatt caattgcaaa acgatacagt accaatggaa agatcacctt cgatgattac	480
atgcctgtt gctcaagct gcgagctcta acagacagct ttcaagacg agataactgct	540
cagcaaggtg tagtaaattt cccatatgtat gat	573

```

<210> SEQ ID NO 279
<211> LENGTH: 561
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 279

```

gcacgaggaa gttttagct gccgtgtga agtccagaga gcgttaagccc tgcactggaa	60
cccaagtctga cttccctttc tgacggctgc ctgggtataat cactaggaga tctctactg	120
ggagttacca cttcccccg gtggtacccc cttttgttagc tggatgagaa ctgtgggtc	180
ctgateccctc tgcatttcg ctggaaattt tcccatccct tggaaatatac ctttagaaaa	240
accttcatgt cccctaagga gaccactgac attgcaagt taaaaatcc catagatgt	300
atccctgca cctcgctgga ctctcagct ctgagcgtg atgggttcag tggtaatgt	360
gataataact gtatTTGTA ttgtttaat ggcatctccc aaaaaatgtg aaaatggtcc	420
cgggagaaggc agttccctgt atgcgtgtg ctttttaaaa aaaaaaaaaaaa aaaacaagta	480
acaactcctt ttgagaaaca atttctactt tggaaatcata tcaatggaaa gatgtatag	540
cacttataat ttccctaata a	561

```

<210> SEQ ID NO 280
<211> LENGTH: 344
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 280

```

gagatcagct ccctcaagga cgagttacag acagcttac gggataagaa gtacgcccagt	60
---	----

-continued

gacaagtaca aagacatcta cacagagctc agcatcgta gggcgaaggc cgactgcac	120
gtcageaggt tgaaggagca gctgaaagcc gccacggaag cactgggtga gaagtccccg	180
gagaaccac ctgtgtccgg atatgacatc atgaagtcca agagcaaccc cgattcctg	240
aagacagaca ggtcatgtgt cggccggcag ctcagaggcc tcaggtccaa gagtctgaag	300
gaaggcctga cggtgcaaga tcgcctgaag ctctttgagt cccg	344

<210> SEQ ID NO 281	
<211> LENGTH: 479	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (202)..(205)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<400> SEQUENCE: 281	
ggcccagaag ctgtgaact ccgacctggg ggagctcatc aacaagatga aactggccca	60
gcagtagtc atgaccagcc tgcagcagga gtacaagaag cagatgtga cagccgcgca	120
cgcgctggcc gtggacgcca agaacctgtc cgacgtcatc gaccaggccca gactgaaggc	180
cctggggcag ccgaggccgc annnngcacg acccgccctt gccccacccg ccacgaggcc	240
acccggcgcga ggcacaccca ggcacaacgt tttgactgac ggctgtttgg aaatctcaca	300
taagtttaac tgcgtttga ttgggttgt tttgtttca gcttttaat catggtttc	360
agaaaaagtcc gggatccaca gtgcagcatt tttctgagag taaaagttgt atgtgagaag	420
ctcttaaaga acgtgaagg ataggctgtg ctcacgtcag gatacgctt cgtggaaat	479

<210> SEQ ID NO 282	
<211> LENGTH: 524	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (119)..(120)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<400> SEQUENCE: 282	
gcacgagcct agtccattgg ccagagaaga aggccattcc ctccctgtgt ccagccctcc	60
cccagatggg gacaggcagg tcatcgattc aagtatacat ggcgcgttgg tgaatctgnn	120
ggctacagag gtgacagcag ggcgcctggg cacacacttg tcacagccgg agttggaga	180
gactcctgag gaccgagaac ccacccagga agacgcagag cccaggtctg ccgcaggctc	240
cttgaaggag ctcagaaatt tgctgacggt gaccgcccggaa gtaacagggg agtccgtgt	300
gcttgagggtt gagaaagata cacatgagga ggccttggg ccccaagata ttgaaaaga	360
agaggaagca acccaaatcg acacagaggc cagtcaagca tctgcttcgg gtcaggacaa	420
ctgtgaagaa agtgaagtcg gtgaggggga ggcgcgttgg ccaactccca aggccaggc	480
cagcggggtg gagctggag aattccaga tgctcagccca acct	524

<210> SEQ ID NO 283	
<211> LENGTH: 462	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 283	
gaatttggAAC gttctgtttt ggtgtgatca tgtttctcca gtattacctc aacgagcaag	60

-continued

gagagcgggt ctacacgctg aagaagcttg atcccttggg acaacagacg tgctcgcccc	120
accctgctcg attctccca gacgacaaat actctcgaca ccgaatcaccc atcaagaaac	180
gcttcagggt gctcatgacc cagcagccgc gccccgtctt ctgaggatgt cttaacattt	240
cgtgtgtctt ctgctgcctg ccagcccca agagactttg tgcagccagg ctcttcagtc	300
tgtgagcctg gaagcttgct ccgaccctta ctcctcgaat ccggctctat ctttgcctt	360
gattatgctt gttgtgaagc agtcatggta gcatccccgt ccaaggggag atatttgaat	420
ctttcgtac cttgaatcac tgccaggta taaaaatgat tt	462

<210> SEQ ID NO 284

<211> LENGTH: 410

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 284

tttcttacc ttgcccctag gagcgaatcc gttagctcg acagattgaa aaagcggagt	60
atcggaaacctt ccaggcttgt ctgcacaact cttggatcga gcagggccgcg gctgcctgg	120
agattgagct ggaagaagaa atgtataggg gaggaaaagt tgatgagcag gaagagcgtc	180
ggagacaaaaa gcagatgaag atcctgaaga aggagctgcg ccatttactt tcgcagccgc	240
tgtttaaaa tgacctgaaa accaagtatac ccactcagtc aggcaagctg cccctgtca	300
cgtctgcccc aagaaagggt gagtccgcgc tgagctgcct ttccaaacag aagaagaaga	360
agaagaaaaaa gcagcagccgc caggagcgcg cgccagccgag cacaagtgc	410

<210> SEQ ID NO 285

<211> LENGTH: 445

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 285

ccctcgcccc ggctgccccgc gcccgtctcc gcccgcgtt cagcacctcg gcccagaaca	60
atgctaaagt agccgtgtg ggggcctctg gaggaaattgg gcagccttt tcgcttcttc	120
tgaagaacag cccgttggtg agccgcctga ccctctacga tatcgtctcac acgccccggag	180
tggccgcgca cctgagccac atcgagacca gagcgcacgt gaaaggctat ctggacactg	240
agcagctgcc agattgcctg aagggtgtg atgtgggtt cattccggca ggagtccaa	300
gaaaaccagg tatgaccgaa gatgacttgt tcaataccaa tgccacgatc gtggccaccc	360
tgaccgctgc ctgtgccccag cactgccccgg aagccatgat ctgcacatc tcaaattccag	420
ttaactccac catccaaatc acagc	445

<210> SEQ ID NO 286

<211> LENGTH: 404

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 286

tttttttca ccgtccaaat cttgacttta tttttttat ataaaaaatg caatttggaa	60
aacccaccctt acctttccc ctaacataat gcttttaccc cttaaaaataaaaataaagt	120
actaatccta tgtacatcac atgtaccata aaaaatgtat ccaaagtttc tattgttacc	180
aaagtgttctt aatcaaaaac gagttacaga aagccctca ttgtaaacaa aagattacaa	240
gttacaaaat caaagcacac acagccagag tcatttatac aacaaccaac atcctgcctcc	300
caaagcaagt tgaattttta tggctctgtta taaaaatgca tatcaatata cttctgc	360

-continued

tttatttttc attataaaagc aaatgaatac actttctaca ataa	404
---	-----

<210> SEQ ID NO 287
<211> LENGTH: 468
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 287

gctccttagg tataaaggta aatctttctg attaagtggt tattgaagtg ttttgagtt	60
gtacatTTT gccacacgtg ttctgcagat ggTTgattat aaacataactt tacctctcat	120
actagtaagt gTTtagttc agaatcataa gtatattttt aggttaagagc cccctgattc	180
aaagaatgt ctTgttgcgt cagTTTTaa aacatgggtt ttTctgtgtc cacacttaaa	240
tctcttatt catTTTTta ggtcttacag ctctgctggc tcatgaaata ggTTTggaa	300
gcaaagtac aacacaccca cttgtctaaag acaaaatgtt gaacggaaatg cattacagct	360
actccgagaa ccgtgtggaa aaggatggcc tgatccttac cagccgaggg ccaggaaacca	420
gctttgagtt tgctctgaag atcgtcgagg tgctgggttgg caaggagg	468

<210> SEQ ID NO 288
<211> LENGTH: 467
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 288

gcttgagaga gatTTTtatc tggtgcaatc tccctgcagt gtgtgtgaca acttaacctg	60
gctactgaaa aagagtgcac tgcccaacac cactgccagg acctttccctt cacctaata	120
caggagtttc tctcatcaat tggaatctcc aggccccaca aaatggattt gTTTTggaa	180
caataggact gttagaatctt tcatcattta acttgggtggaa ggcaggggctg gagggggaaat	240
ataaaatcagc aagcTTTga gtttagggcc agggaaataca gcttttagatc catttttaat	300
gattcatttc ctTTTggtc atataactgc acaacgggag atgaaaggaaa aaaatagaaaa	360
atttgacttt taggtgccaa tagtacattt cactacactg atcgaagaag ttatccaaag	420
tactgtataa catcttgTTT attatTTat gTTTctaaa agtggaaa	467

<210> SEQ ID NO 289
<211> LENGTH: 535
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 289

gcacgagggc caacgaaggc ttgatcacca agttcaggc ttgctgcggg gggtaacttag	60
tccgacagga gttccgatcc aggatgaattt tcctgaagaa acagatccc gccatcacct	120
gcattcagtc tcagtggaga ggatacaagc agaagaaggc gtaccaagac cgcttggctt	180
acctgcgtc ccacaaagat gaagttataa agatccagtc tctggcaagg atgcaccaag	240
ctagaaaacgc ctatagagaa cgcctgcagt atttccgaga tcatataaat gacattatca	300
aaatccaggc ttTtatccgg gcaaacaag ctcgtatga ctacaagact ctcataacg	360
ccgaggatcc gcctatgatt gtggccggaa aatttgcgttca cctgctgcac caaagtgacc	420
aggatTTca ggaggagctc gatcttatga aaatgcggga agaggTTattt acccttatcc	480
gttctaaccacca gcaagctggag aacgacccatca atctcatggaa tatcaaatac ggact	535

<210> SEQ ID NO 290

-continued

<211> LENGTH: 538
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 290

atcactccca tctgactgct aatacacatg caggctgcag gctgggttta gcccacagtc	60
agagttgcca gccccatgaac tacagcataa gaaacagttaa taatgcattt acagaatttt	120
gaagttaaag gagacttttag agataattt accgaattcc ttatattcag ggatacaaag	180
atattcaaca atttgttcaa gttttaacc taaccttatac actgatccac tctccacaga	240
cctggaaatt tcacaccaga aaaaccaaaa acacatagcc acataaaaaac tcatacacga	300
ctattnagag cagcattagt caaggaaatg gcaacccact ccagtgttct tgcctggaga	360
atcccaggga cgggggagcc tgggtggctg ccgtctatgg ggtcccacag agaaggacac	420
gactgaatcg acttagcagt agcagtcaca acagtcagaa agtgaaaag tccacacgtc	480
catccactaa tggataaac aagttgtgtt ccatccatat aatggagcgt tattnagc	538

<210> SEQ ID NO 291
<211> LENGTH: 562
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 291

gcacgagatc aaagagggtc cacaactgaa gcagcagatc cagtcacatcc agcagtccat	60
tgaaaggctc ttatgtctaaa ctgggtggct cagccacact cccagctgac tccctctccac	120
ccccccgccc ccgcagagtt atgtatcata ttgtctgtta gcatgttagt gttccagcta	180
ccttctattt tgataaaaata tttaatgtt caatctgatt ttgcatttt tgcactgttg	240
tcttggttta taggttgtca gcccctcccc taatctcccc ttccctctcg ccatcttatac	300
ctccctttta gaaaaatgaa ctaacgccaa gaacagggtgg aacaggctgg atgacaccac	360
ttaaaggcag ggaagagccg agagagtaga gaattggttc cagcttcag gggctgtt	420
cctactgtgc agggcatgtat ggcataactg tctgctgtt cccctcatcc ccatgtacag	480
gatcggttgc cgtgtgtctg aatcatcgag gggtttctt tgctctgcag ggcataatgt	540
atcatttggg gagaaagcat gt	562

<210> SEQ ID NO 292
<211> LENGTH: 549
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 292

gggtcaacgt ttaaagtccc atctttacc tccacaagct acagaaaaat caggacatgt	60
tttccctacc cgtgaaattt ccacacctt tactaatgaa aaaaatgttct tttaaaaaaa	120
atccccccctt ccacctatgt tactgttccc catttctaa aagggcacag atctcccttc	180
caggctttt atgttcagtt ttcatcagc ctgggtttct gtcttcgcgt tgccatgcatt	240
cactgggtgg tctcaggctc cagggggact tgagcaegtt ttggccacgt ggacagtatt	300
gaagcagcat tgcgtgttcca cagtcaggac tgcgtgttcca ctggaaacgt gcatcttgct	360
tggccagcac agtgtttaac aaaattgagc cacttttaa atatctggag attttgc当地	420
caaattttgg atccccgagt gagacttagat agctgatggc ttacagttct cgctgtgttcca	480
cgtcatttcac agatgtgttgcgtttagaaagct gctctttcc cctgtgttcca	540
ttcgtgtttt	549

-continued

<210> SEQ ID NO 293
<211> LENGTH: 443
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 293

aagagttcca tgctgata	60
ccagcagact gacacgtctg accccggagaa ggtggtctcc	
gccttcctga aggtgtcctc cgtgttcaag gatgaaggct cggtgcggac agctgtcag	120
gacgctgttag atgcgttgat gaagaaggcc ttcatcgctg ccgcctcaa ctccaaacgcc	180
ttcctcaccc ggctgctcat ccacatgggg ctgctcaaga gtgaagacaa gatcaaggcc	240
gttgccaaacc tgcgttggcc cctgtatggcg ctgacccacg tggcagcggc ggactacttc	300
cccaaggccc ttgcggccct gctgttgcgg ttcatgacca agcccaacgg cgccctggaa	360
tgcgttgcct ttgcggccca caatctactg cagacgtgt acaaggctta gatgecaagc	420
tggcctctgc ccattccctcg cct	443

<210> SEQ ID NO 294
<211> LENGTH: 585
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 294

tttattttaa gattgaaaag ggagcgcattt ttccttggaa gggagagcat tgctcgccga	60
gacgaagctt cgtggcatac aaagggggcg gttcgtgagt tctccatgc accctgtcc	120
agcttcaccc agtggggctg ctttgcttg atccatccag cttttacag ctttgtcata	180
gtatgttctatg atattggatg ctttcttct ttttggtag taaatgttta agtattaact	240
ttttgttgc cctctatgtt atagaggggtt ttcgggtttt tttgttttt tgtttctgt	300
ttcttaatca tggggggccca ctccccactt ggaattttgg acgctggtca gcttgggt	360
tttcttagat gttggaaac ctagatgacc ttactgggtt caatacttagc tacgttaaag	420
ctagaaacctt acactgtcac tttactgaga tttctgatgtt tactttccat attgcctttaa	480
tgttagcagta atgtgtttat gcattttttt ctttgcacac acatttgtc aaatattaaa	540
actctactttt ttatggcac atattagcat ataaggcctt attcc	585

<210> SEQ ID NO 295
<211> LENGTH: 603
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 295

tctccacagg tggtaaagtt cctcgtaatt ttcgtttgtt ggaagaactt gaagaaggac	60
agaaaggagt gggcgacgggt acggtcagct ggggcctggaa agatgtgaa gacatgacac	120
tcacaagggtg gacaggcatg atcattgggc caccacggac aaattacgaa aacagaatat	180
atagcctgaa agtagaatgt ggacctaattt acccagaagc tcctccatca gtttagattt	240
taaccaaat taatatgaat ggaataataa attccagtgg aatgggtggat gcacgaagca	300
taccagtgtt agcaaaatgg caaaaattcat atagcattaa agttgtactt caagagctaa	360
gacgtctaat gatgtccaaa gaaaatatga agttccaca gccaccagaa ggacaaacat	420
acaacaatta attttagtgg atctcaaact tgcgtttaat cagcaaccctt ctactcatgt	480
taatgttcttgc attaaatatc acaatgcaaa atacccacac attaaagtaa gataattcca	540

-continued

```
gctggtaaac atgacctgga cgttgcataatataatataatgtac acccattatg 600  
ttt 603
```

<210> SEQ ID NO 296

<211> LENGTH: 403

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 296

tgagtgggtgg	gcagtgtgca	agcttgcaga	cctcacttag	tggcagcgat	gtggcttga	60
tttgtgttttc	ttcacatttaa	catggctgtt	agagagtgtt	ctgagtggtt	ggcagtgtgc	120
aaggcttgcag	acctcactta	gtggcagcga	tgtggctttt	atttgtgttt	cttcatttttta	180
acatggctgt	tagagagtgt	actgagtggt	gggcagtgtt	caagcttgca	gacctcactt	240
ggtgtggcagcg	atgtggtctt	ccccagacaa	ageccttctt	acaagagaat	tcccttggtt	300
ctgttgggttg	agcactctca	cagatagacc	ttttgggttt	taatatttat	ttatttggct	360
qcatacqgatc	ctaqtqtqqq	cacqtqqqat	ctaqtccct	qac		403

<210> SEQ ID NO 297

<211> LENGTH: 274

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 297

gcgggtacctt cttcatggtt tggagtgtgt ggttagcaatg catcaagctc agctcatttc	60
caagattcca catabttga aggagatgta tgacgcagac cttttgagg aagaggtcat	120
cattagctgg tcggaaaaga cctctaagaa atatgtctca aaagagatgg ccaaagagat	180
tctgtgtcaaa gcggaacctt ttataaaatg gttgaaggaa gcagaggaag aatcttccgg	240
tggtaagat gatgtatgtat atgagaatat tgag	274

<210> SEQ ID NO 298

<211> LENGTH: 447

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 298

ggaaaggcaga cgagctgttc tgctgcaagg tggccctcg agacacctgcag atcttcacac 60
acgagcggaa gtggtaactca cgcaaggacc tggctcgga ccgcattgcag ggtgaccccg 120
acgacacttc acaccggcga caccctctt gcaagttctg tgacgagcgc tacctggaca 180
acgacgagct gctcaaggcac ctgcgtcgta accactactt ctgccacttc tgcgacgcgg 240
atggggccca ggactactac agtgaactatg cgtatctgcg tgagcacttc cgcgagaagc 300
acttcctgtg tgaggagggc cgctgcagca ccgaggcagt cacgcacgcc ttccgcacgg 360
aaatcgacct gaaggcccac aggacggcct gcccacagcc cagccgcgc gaggccccgc 420
agaaccccccataatcgacctg cagttca 447

<210> SEQ ID NO 299

<210> SEQ ID NO 2
<211> LENGTH: 456

<211> LENGTH: 43

<212> TYPE: DNA

<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 299

```
gccccatggcc cagcgacggg aacctgtccc atcacaccca ccccttgagg gtgcacgggg 60  
accccaaaaa ccctggccca tccccctccc cagatggacc ttggccaaac ctgtggccacc 120
```

-continued

agccaggccc tacggggctc cccatgtcg ctcacacgtg tgcgtgtccg tgcgtgtcg	180
tgtctgtgtc cggtgtgtc tcgtgaagct gtgcggccaa acaagtgaat	240
ggccgcggag gccacagttt tgcaacttcc cgtgtgtgtt gtgcacagcgt cactgtttt	300
taaacttgat aatttttat tttagtaaga tgccccaaa gtccacacaa cttgtgtgg	360
acttgcagag gttttatttt ttggcccta gaatctgcag gaattaggag gtaccgaccc	420
ccgtgcagca gcctggccc tggattgcgt ttgcct	456

<210> SEQ ID NO 300
<211> LENGTH: 334
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (293)..(293)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 300

cctgcgtcca agtccagggtg tctgtggccg cegatctggc cgtcaggggc tcaagttccc	60
ttcttcggac cagccagccc cctgtttgc ctttgccat tggtgcctat atttaggtcg	120
gctttggcga ggctgagaag gcccggca agatgttcaa aaacacgttc cagagcggct	180
tcctctccat cctctacagc atcggcagca aaccctgca gatctggac aaaaaggtagc	240
gaaatggcca catcaaaga atcaactgata atgacatcca gtcctgggt ctngagattg	300
aaggaacaaa tgtcagcacc acgtatatca catg	334

<210> SEQ ID NO 301
<211> LENGTH: 592
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<400> SEQUENCE: 301

ttttttttt ttttttata agacaaaaat ttaatgaaaa ttggtaagta ataatccaaag	60
gggctaaata gttacatggg actgtattag aaatttaata tacaatgtt acatgtttatc	120
atcatctgtat tcatcttctt ctttcaaaga ttccctggca tatttctctg cctctccct	180
tacatcttta ggaactattt catgtcttcc attagttatt tcaccaaccc agctgagctc	240
tagttcaaaa gctttatcct taacttcattc gtgtactatg taaattatct ttgcaacttc	300
tttaacaaca tcacggcagg tcattttttt catctgaagc ttttcaattt ctgtcttgc	360
agectgcctt gctttgccaa tggcacagcc ccaataacca tatgaaaacac ccgatgggtc	420
aatcatgttag agctgtgcac cgtcattcac actgttaagac ccttaacatga aactgcagcc	480
aaaaggctta acagcactgt agagtgtata cgcgtgtaca tacatggcca ctctatctgc	540
aagatgtttt agtggaatgt tataatccaaa gtttagatcta aagttggaaag cc	592

<210> SEQ ID NO 302
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (85)..(87)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 302

tggagatgtg tttttttttt tttttttcc ctccccattt tttagttgcatt	60
---	----

-continued

atgataataac aaatacacaaca caagnnnggc cttgtgttc ctgggtctc ttcagtattt
cctggggatt atttgcttcc taagtaaaaac cttctgacc aacagcccag tatgtcttaa
gaccggaggcatgtcacct actttggaaag ctctcacagc aggctgtcc gctcgatct
g 240

<210> SEQ ID NO 303
<211> LENGTH: 458
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 303
gcagctgcag gggaaacttc tgcaagccg accaggtttt tccagtcctc catggggacc 60
agcgtagcg gtccaaaggc cagctatatt ttcaacaaca acaaatacg ccagtggaaag 120
tacggagacg tccagcctt tggatagttt atttggatg gcagctccta aaaacaggcg 180
cagcattgaa gtgaaccggtt gtaggagaag aaaccctcat aagcttattaa aagttaaagaa 240
caatatacgat ttttgcctg agtgtggta cctgaaacag aaacatgtcc tctgtggcta 300
ttgctatgaa aagggtgcga agggaaacccg agaaatcaga agacagatag ggaagcaaga 360
ggggggccctt ttcaaggctc ctactgtggaa gactgtgggt ctgtactcgg gggagacacc 420
ctctgagcac gatcaaggca agaggatcat tgagcgg 458

<210> SEQ ID NO 304
<211> LENGTH: 391
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 304
tgcttttggaa aagagggtgc ggggctggaa ctttgctttt tctccctcg gttccagaca 60
cgccattca gtcctgtgtt gaaggccac ttgtatttc acgcattcccc acaccaggcc 120
gtccaaggcc ccgtgtctt gaggcaggcc ctggctgagg ggagtggctt gagccaggcc 180
tgtggcatgaa ggggtgtcccg gctgcgtccg gggaaagggtt cggccgcgcg aggggaccca 240
gagcccatgg tctgccagg cggtgcttga aaagaatacg ttctgtgggt ttttctgtttt 300
ggaggaacaa aagacccctt ctttctgtt gatcgacaca tctgtctgtt aaagtagtgtt 360
ttccacacaggc agtggcctttt gggaggggttga g 391

<210> SEQ ID NO 305
<211> LENGTH: 603
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 305
agccgcctcg cggttagttt cgcggattttt gctgcgcaca gtctgtggaa gaggttgctg 60
tttcctggcg gtcctttctt gtcatctgg tcgcgcggc tgggtgtttt ccagttgcac 120
ggtcgcgtat catgacgtcc gccttggaga actacateaa cggaaactgtt gctgtcatta 180
tttctgtatgg gagaatgtt gttggaaacat tggaaagggtt tgaccagacc attaatttga 240
tactgtatgg aagccatgaa cgagtgttca gctttcaca gggagtagaa caagttgtac 300
taggggtata catcgtaaga ggcgacaatg tttctggagg tccgaagtcc agatggattt 360
cagcaggctt aagcaaggaa ctgtatgttca agctaaagggtt ccaacactt ggccagggttga 420
tgcaaaagagc caactcaactg gaaaagaccc tggatgtggg aaagactgaa agcaaaaggaa 480
gaaggcggca gggaggatg agatggttaa tagcataatc aacacgttgg acatgtatct 540

-continued

gagcaaacac caggagatag tgaaggacag gggagcctgg tgtgctgcag tccatgggtt 600
sac 603

<210> SEQ ID NO 306
<211> LENGTH: 635
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 306
agaagaacca agcattaata cagcacccat tttttataa taaagtatat ctgggtttt 60
cccttagttgg ccaaaaactttt ttttagttta ggtgttaatc ttccccatgc tatttttagtt 120
tatctcccta tattatagta cttaacatga actctgatga gaagttagct gctgcagcag 180
cttaaacata caatggctct gccacagtaa ggaaaaccaa ttccttgaga ttaggttaat 240
ttattgttact gttaataactt aggggtccctt gttttggagg gttaaacttg agaaaatagct 300
tataattggc tgacttgtac aaaattaata ctgagcatta gctgatcagg cagaattagt 360
aactagtttcc ttatgtgaca taacctcatc acaacatgtc aacggtacaa aatttccaaa 420
atcacctatt ttttagaagtt actgtAACGG tttccctat gcaactttaa atcttgctgt 480
ttctttttgtt gtttgatgtc agatgacccctt cagtaattac taatttgaa aatttggca 540
tacaatgaa ttccaaaggcc aagacttgc ttccaaaccgg tctttggaa atttagttac 600
atattcggtt ttttgcataa qttcaatttgc ctttt 635

<210> SEQ ID NO 307
<211> LENGTH: 206
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<210> SEQ ID NO 308
<211> LENGTH: 382
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

```
<400> SEQUENCE: 308  
gcgctgtgag aaaacacatt ttatggttt taatgatacg catgctttc ttctgtaaat 60  
agacaataaa ttttgtaga tagtcttggt gtgttatctt aatttcgtat ttcactgtgt 120  
aaaatcgtg aatatagctc aagtgttagt ggactggatg aaaagaaaact ggttactagg 180  
caagaacagg aggctgttagt tacccatgac tacttttagc tatgcagact aatacattct 240  
gcaggtttac agctcagcac ctccacccctt ttcaactggat atttcatgtta aggcaccaac 300  
cactgttaatt tttgtgtatg ctgaagcctg tccttgaaat ttggatgtat ggcactcata 360  
ttctccggca tcttccttac ta 382
```

<210> SEQ ID NO 309
<211> LENGTH: 506
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

-continued

<400> SEQUENCE: 309

atatttagct catgtatgg	aggaagagca gctgtcttt	tatatgttt ttgacaata	60
atattgtaa tctttgtac	aaaaaagaac tacttgtatt	ctagaagaaa tatgaaatgc	120
ttaatttata agcgggctgg	agatttttc caatattgtt	ttctttgaaa atgaaagggg	180
atcatctatt ttagtttcgg	ggtctggaa cttttgaaa	atthaatttg tggaccaatg	240
ttatgtgaaa gctaaggaag	ggcaggggta aaatagggc	tgatttctc attctgtaca	300
gaccagcaaa cttccctctg	caaggcaggc tcaaattcaca	cacccaagag tggtggcg	360
ataaaaacgct agtttgc	ttc agcccctagt aacctcagg	cttgggttga atataaaagg	420
tagacaactg atatgtttc	acgagtaaaa tattgtcagc	cagaaacagc tggtgtcagg	480
taaactttttt tttttttta	agcttt		506

<210> SEQ ID NO 310

<211> LENGTH: 473

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (423) .. (423)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 310

ttgaatctga agcctgggaa	ggggggcccg aacctgc	cttccaggc tcagctgc	60
gtcctagcca gccagccctt	cctgcgtcgcc cgccctcccc	gccaatcccg tagctga	120
tgcattggcg tcatggggcc	ccagccctag agttcaggac	tgaggagggg gcccgggc	180
cctgtggcgatg tgc	cccttgcgc gcaccaggc	tctcttgc gttgggggtc	240
cgccggcgatgg accccctccct	ccaggatgcc ctccctcc	tggactaca tccagctccc	300
cgcggccacc ttggggcg	ggggcctgcgc caccgcca	ggccctggc tgggaaacctc	360
caggggacact gcaggcctca	ccttcccg ctccaccc	ctccctctct atctggc	420
tntctctgg cttccccccg	cccccccgcc tctgcttgcc	agatccgacc tgt	473

<210> SEQ ID NO 311

<211> LENGTH: 572

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (432) .. (434)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 311

gtccctaaag catgtatgt	ttcaggact ggtagagct	ctttctggca actcttgct	60
gagccagaag tacatccccca	aatggtggca gggcctcc	tttactccctc taggac	120
tgggtggca cttctgactt	cacaggcctt ccccaagg	ccaggeccca aagtgc	180
aggactgggt tcccttaccc	gcaggctgc	tcagtgtgg gccatcagg	240
agtgagaacc aggttaactgc	aagtcaagg	tgactagact tctggtaac	300
tctctgcctt gggccaggca	tgacccat	tttccctgt ccccaagact	360
ggctgcaagg ccactctgt	ct gagctgagtt	gttggaaaca ggaaggcag	420
tccacttgta tnnntggctg	ggggctgccc	aggtccccag gtttacaaa tgctacaccc	480
ctgcgttaggc cacccctacgg	atagtaggca	gcaggctggaa agttctctgc	540
tacacaactg tgcccagact	gccatgagtc	ca	572

-continued

<210> SEQ ID NO 312
<211> LENGTH: 569
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 312

tatagttcat ttcactcgc atatccaaa tattatcatt tcaacatgta atttatataa	60
atctttaag atagcttgca ttctttgtt ctaattttt ttatttctgg tgtatattt	120
actaatttgg gctagccaca tttcaagtta attttaataa cttataataa cacagttctg	180
tattaatcta catattaatt tgggttcta taagatgtt taggaaattt cctagaatca	240
ctctcttaag tacaaaatct tttctggct ctgaaggctt cagtgttgc ttttagtgt	300
ccctaagaag tgtgaacttc ttaacatttt aaataaatca gtttagaaata aatatcaatt	360
gtcaataaaa taaaaatgtt agccccaaat atttccctt aaagataaca aactttcat	420
aggactgtt agggatgaa agaatataat ctgccttgc gcaatatgtat tgattattt	480
ctctggctt tagctatgtt gtatttagaa cacatgtatg taggagatat ttggcatagt	540
actgtttca gtacataacct attttttt	569

<210> SEQ ID NO 313
<211> LENGTH: 426
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 313

gcacgaggct gagacttgc ccaccgcgcg tgggaggaat tcatacaagt gtccagttca	60
agctgcgatc tggcccggtt gcgtacatac ttgggtgaaaa agcaaccaa aagatgacag	120
aaaagagcaa actgataact gtatgttca atatgttcc tggaaaaagc aagcttgcga	180
aagaaatagc agagaaacta ggcctgaagc actttcccga ggcgggaaatc cactatgtgg	240
acagcaccac aggggacggg aagccctgc ctgtgcagttt cagtggcaac tgcagttgg	300
agaagttta cgacgaccccg aaaagcaacag atggcaacag ctaccgcctt cagtcctggc	360
tgtacgccag ccgcctgtt cagtacgcgg atgccttggc gcacctgtt agcacaggac	420
agggtt	426

<210> SEQ ID NO 314
<211> LENGTH: 511
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 314

gcacgagata tctgaacacc tctaacagag aagtgaaggt acgcattttt aaatctggac	60
aagtgaccgc cattccattt tggatcata tgcacccatca cgtatgagattt aggttagata	120
cttcgagtga agcctctcac tggaaagcagg ccgcagttt tttatataat cccatccaag	180
tggaaatggg agacgaactt gtactcagca tccagccaca caaaagcaac gtcagcatca	240
ccataaaagca atgaagagca gatttctaat gaaaaatgtt ggaagttagag cagtgggtt	300
ccagttcttag tctgaattttt tagtgggattt gtaaccataa aatgcaggtt tattttatca	360
cttggaaatgg tcaaattttt taaaacattt gacattaataa aagtgttattt aaacacccta	420
actaaagagt agcattatca caaaaatctt actgcagact tcccttctgg caaaggctgt	480
cattaaatttt tcaaattaag aactttttat t	511

-continued

<210> SEQ ID NO 315
<211> LENGTH: 469
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 315

```
ggagagggct ggaccactca gggaggggga aaggatcagg ggaatggaca ggcgtctgc      60
cgctccagaa tctgaggcct tcaccccttag cgattccctcc ctcccaactca cgaaaagcccg    120
ctcaaacttc cagctggact cgaccaaagg aataaggta ccagaaaacta cagaagaagc      180
caacccttcc accatcggtt ctgaggggga aatgcggaaag ggccgcctcg agagccgacg     240
tgcccaccg gctgtacctc caggcgccgc cgtccagcag ggagttcgcg gagcagtggg     300
ttcagaaggc ccgaggaggc cagcaagccc agaggccaag agecttagagg tgccctggag     360
gccggaggat cgccgtgcg ctccgaacgg ccccgccgcg cgccgcggg gtccctgcg        420
gccctggcg acaggtgcag ccgcagcctc cgccgcggc tggggccggg                  469
```

<210> SEQ ID NO 316
<211> LENGTH: 667
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (606)..(607)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 316

```
aaacttggac tccagataaa tgcatttaac ttggttacag gacctcaaga tgtgtatgtc      60
agcctcattt tttacagatt gatggtcctg aaccatgata gtttggatcatgaaacac       120
agctttaccc agtcatacgg gttttcactg aacttaaaga aacaaagttt ccattcagga     180
ggttgatatt tttttttaa caccagttt ctccaaatacc acaaatttct cttggataact     240
acactctgtt taagaatatt gtacatctgt acagaaaactc atgatagatt tttgaaatgg     300
tagttccaaag tatttgcctt gtccttagact gatagggcat tttggacagt tttggccct     360
tccttagcta cttccaaagg tgctcagaag gtatttaagg aaattattcc cgtggactaa     420
ttgggtgtaaa tgtgtttgct tttattaaga tccccgtccca ggtcgagatc aagatccagg     480
tctcttcac ggccttagaaag cagccgatca aagtccagat ctccatctcc aaaaagaagg     540
taagcttaat aattttgtc catatctta ctgtcaagt tgccctctgc agaattttgc     600
ttactnncta cttccctgag ctctttggag aattgggtgct atatgttaaa atactaaata     660
gagtttc                                         667
```

<210> SEQ ID NO 317
<211> LENGTH: 371
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 317

```
aagtgtatgtc cgcaagacac cgccggcagea cggagcgcg cggcgagcgc tgccgtggc      60
ttccggcctgg ctgcacaccg caggagaagc tgcacgtgt gggtaaaagc cctctgcct     120
cctccgtgt ctcccggtgc gctgagagag tgcgcgtgt agcgaggcgt cagatggaa     180
ggggccgggc ccgtgtcac cgctctgtc ttgcatttgc gccgcattcg ggacaccgccc     240
tcggggccagt gcctgaagac gtcatcgat gacgacaacc ccccggtgtc cttegtgaag     300
ttctctccga acggcaagta catcctggcc gccacattgg acaacacgct gaagtcgtgg     360
```

-continued

gactacagca a	371
--------------	-----

<210> SEQ ID NO 318	
<211> LENGTH: 220	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 318	
tttttttttt ttttttcag catttacact ttatgtga cataaagaag ccgtattac	60
acaatacatt catatttta aatatgttac acagctctcc tagaaaacca ctccatcaca	120
gaacagcagc atgttagctt ggttccgtct taaaaatatt aatcaagta gaaatactct	180
ttaatttcat agcccatcac agaggagac tctgaggag	220

<210> SEQ ID NO 319	
<211> LENGTH: 455	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (83)..(84)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (287)..(289)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<400> SEQUENCE: 319	
cctggacctg ggcagcaacc ggctgggaga cgccggcctt gcggagctgt gccccggct	60
gtcgagcccc agctcccagc tcnnnacccct gtggctctgg gagtgtgacc tcaccgtcag	120
cggtctgcaga gagctctgcc cgctccctca ggccaaggag gcccctgaagg agctgagtct	180
ggcgggcaac agcctggggg acgaggggcgc ccagctgctg tgcgagagcc tgctgcagcc	240
cggctgcccag ctggagtccc tgtgggtgaa gtccctgcggg tttacgnnng cctgtgcca	300
gcacttcagc tctatgctga cccagaacaa gcatctcttg gagctgcagc tgagcagcaa	360
cccgctgggc gacgcgggca tccacgtct gtgccaggcc ctggggcagc cgggcactgt	420
gctgcgggtg ctctgggtgg gcgactgtga gctga	455

<210> SEQ ID NO 320	
<211> LENGTH: 393	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 320	
gccgtgggcc tgcgggtggg aagtgtggt gtcaggccgg ggttcgaga cccccacata	60
ccggccggcgg cagaacaggc ccgaggcage ccggggtttg cttaggaag agcggctta	120
aaacactgcgc gccccgtcc tctggcagat accattgtgt agtttgaatc aggaatgaaa	180
tttctgaaa gctaagagta gaagtcttgg tcagcatgaa ggacaaaaga cggcgagccc	240
gagtgcggg agcctgggct ggtctgtca agagccaggc cactgtcag ccagtc当地	300
ctgctgagaa caatctccaa cagagacctg gtaaagcctg gatgaaacaag gagcagcatc	360
tgtctgacag acagtttgtt ttcaaagaac ccc	393

<210> SEQ ID NO 321	
<211> LENGTH: 412	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	

-continued

<400> SEQUENCE: 321

ggtgaacctg	gcatacttcc	actttccagt	agtcagtgaa	acgcagttg	attttctcg	60
ttgcttccta	taaaaatact	tgtaagctca	agcacggcgc	agccgtaaac	tcatgctgcc	120
ctgggaccct	ccccacccat	tcacccgcgc	caaccctcca	cttcatgcct	tagcaacgcg	180
tgtggctcat	gtagacgcgc	ttcgtctgca	cttgcataagac	gagacaaggc	ctcatcaaga	240
agaggaacgc	cctgtccctt	aatgcctgca	catcccgaca	cacccacccg	gggctaccgg	300
ggccagggtc	cctggaccaa	ggagatattt	tgtatcttca	aggggcctgc	actgcttgg	360
aacaagtgg	gagaatcaag	tggaatcttgc	tttggaaaaaa	aaaaaaaaat	ga	412

<210> SEQ ID NO 322

<211> LENGTH: 493

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 322

gcctacatcg	gcctttgttt	gccaaggctg	ctcaacccccc	tcataaggct	gcagcttctc	60
acctggactc	cgcttgaggc	aaaatgtcgt	gactttgaga	acatgtgtg	gtttgaatct	120
ttgctgtttt	atggttgtga	agagcgagag	caagaaaagg	acgatgtcga	tgtcgactg	180
ttgcctacca	tttgtgaaaa	ggtgatttt	cctaaactaa	cagtgtattc	tgaaaatatg	240
tgggaccct	tttctacaac	acagacttca	agaatggttg	gaattactct	aaaattaata	300
aatggatatac	ttcagtgggt	gaatgcagaa	aataaaaata	cacaggata	cctaaaagca	360
cttctattga	gaatgaggag	aacttttagat	gatgatgtat	tcatgcctt	gtatccaaa	420
aatgtcttgg	aaaataaaaa	ttctgggcct	tacttggttt	ttcaacgaca	gttttggct	480
tcagttaa	tc					493

<210> SEQ ID NO 323

<211> LENGTH: 501

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (324)..(326)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (328)..(328)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 323

tttttttttt	ttttttccca	tctcgaaaca	tttttattca	acaacagggtt	gattctctc	60
tttgctcttt	tcctcaactgg	gtttcaggac	acagttcactg	taatcattga	tacttcatca	120
gtctaaacaag	ttgtggcttg	ctttttgtat	cagttcatgc	tgtgtgacgt	cttgagaact	180
tataatccact	tcaagtgaat	gagcacttca	gttctcagcc	aacatcaatc	attcttacca	240
tgtcgcttcc	catcatggaa	ccactcattt	ttgcccgtgg	aacgcccaggaa	ttagttcat	300
aacctatgcc	agcaccacca	cctnnnngntg	gaaatttctg	gcctcttgcag	ccataggat	360
ctcccatgtt	cattgtctt	ccaccaccca	ttctcatgtc	tctttctt	ggatccat	420
agcccatccg	actataactt	tcctctttt	ggcgctctat	ctgttcttcc	atctcacgtt	480
gacaaatcat	catcttttct	t				501

<210> SEQ ID NO 324

<211> LENGTH: 490

-continued

<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (447)..(448)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 324

actgtccatc ctgagacaata tgctaaggca ttccctggatt ttattaccaa catcttgcc	60
taagagactg cctgagttca tgaggaggag ctgggggaag ggggttgtg gccatctca	120
agacctgact ggacagatcc cttagtggg ggtgtggca gttctggagg ctggacggat	180
gagccaaggg agtaagggttc actccctgtg ttgaattcc tttcttcatg tctagccatc	240
ccggagggtt tagtcccagec agaaggaaat acctctactt gggtaaccc tggtcatctc	300
aagagaatgg aagtctcaca tgggggagcg tcctccactc cctgaaagta tgcccttcc	360
tccccctgccc cttctcaaac cctttccca gttgatttg ttattctgtt ctttctgtc	420
catcttaact gctactgtgt ctccanngg acagatggcc ctctttgtca tcttcactct	480
ccaccccccag	490

<210> SEQ ID NO 325
<211> LENGTH: 480
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 325

ggatcttctg cgagcacattg gagccggaa agaagcatga agtggcttgt gctcttggg	60
ctggggcccc tctcagagtg catagtcata tggcctatgt gggcaacatc accattggaa	120
caccccttaa ggagttccgg gttgtcttgc acacaggctc atctgacttg tgggtgcct	180
ccatcaagtg catcgtccct gcctgtcata cacatattac ctgcaccat cacaatctt	240
ccacccctccg gtttacgcgc aggcccttcc acatcctcta cggatctggg atgatgaacg	300
gagttcttgc ctatgacact gttcggtaa catggaaaca gaagctgaat cagatctgca	360
ctaaccacc cccctgtggt ccccatagat ggcctatgtt agatcggaa acttgtcagc	420
actgaccagc cggttggcct aagcctgcag caattcgggt ttgataacgc acccttgat	480

<210> SEQ ID NO 326
<211> LENGTH: 456
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 326

agatttcctc cattcagtcc tggggcca tctccccatc agcagcagtc ctcatcctgg	60
gatttctctc caatcctcat ggctccagca tctagccatc gtggcacca gtggatttgt	120
gacccctgttc gagggccttg cctgtccctg ctgctgggtg tgtcaaatct actcttgtc	180
cagggtgcgg aggattatgc accatactgt aaaaaccaac ctggcaactg ccggattccc	240
cttcaaaagcc tggggatggag agcaacattt gttggcttagca acaactatag gctcgccagg	300
gaaatgttca atgaatttga cgaaggccctg ttgagggttg ttatcagtt gctccactcg	360
tggggatggac ctctgcatca ggcagtcaca gagttgtgc acaggaatgg agcctcacct	420
gatatcttgg caaggctaa agagatttag gacaag	456

<210> SEQ ID NO 327
<211> LENGTH: 336
<212> TYPE: DNA

-continued

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 327

agagccaggc tgtgaagttt gcattggaca tggcaagggg catggccttc	ctacacacac	60
tagagccccat cccacga catgcactca acagccgtag tgtaatgatt gatgaggaca		120
tgactgctcg aatcgtatg gccgacgtca agttctcctt ccagtgcctt gggcgcatgt		180
atgcacctgc ctgggtggct cctgaagctc tgcaaaaagaa gcctgaagac acaaacagac		240
gctcagcaga tatgtggagt tttgcagtgc ttctatggga actggcgaca cgggaggatc		300
cctttgtga cctctccaac atggaaattt gaatga		336

<210> SEQ ID NO 328

<211> LENGTH: 337

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 328

ttgcggcgtc gaaggggaat gggggcggcg gggggcgtgc cggggccggc gaagccagca	60
gctcggcgag gaagaaggcg ccaggccctc tggccacggc atacctggc atctacaatg	120
tggtgatgac cgccgggtgg cgttatagca gtttgttgg tcagagcata cctggctaag	180
ggtagctatc atagccctta ttattccatt gaaaaggctt tgaaattctt ccaaactgga	240
gccttattgg agattttaca ctgtgcaata ggaattgttc cgtttctgt tgcctgact	300
tctttccagg tgatgtcaag agtttttcta atatggg	337

<210> SEQ ID NO 329

<211> LENGTH: 490

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 329

gtcacagtga agaaagagga agaaaagaag ccccacgtga agaagectct taatgccttc	60
atgttatata tgaaggagat gagggccaag gtgggtggctg agtgcaccct gaaggagagt	120
gcagccatca accagatctt ggggaggaag tggcacaacc tgcggcggaga agaacaggcc	180
aagtactacg aattggcccg gaaggagcg cagttcaact cacagctta cccgacctgg	240
tcaagccggg acaactacgt acgtgcccac tcaggcaccc ggggcegctt ccaaggttaag	300
aaaaagaaga ggaaggcgaga aaaggcgtg tcccagacgc agtcccagca gcagcaagtc	360
caagagacag acgggtctt ggcctccaaa agcaagaagc catgtgtcca gtacctgcc	420
cccgagaagc cctgtgacag ccctgtttcc tcgcacatggca gcatgtggaa ctccccagct	480
accccccctccg	490

<210> SEQ ID NO 330

<211> LENGTH: 265

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (136)..(138)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (144)..(144)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (252)..(252)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

-continued

<400> SEQUENCE: 330

atgtttttttt	atgtttttttt	60
cgccgggggg	cgccgggggg	120
cgaggaggcc	cgaggaggcc	180
aatcaagcgg	aatcaagcgg	240
agttagatctt	agttagatctt	265

<210> SEQ ID NO 331
<211> LENGTH: 425
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 331

gtgaatttcg	gtgaatttcg	60
cttaacttgc	cttaacttgc	120
acatgaaggc	acatgaaggc	180
atggaaactaa	atggaaactaa	240
ttgaatttgt	ttgaatttgt	300
taatttatat	taatttatat	360
catgagtttt	catgagtttt	420
gcctt	gcctt	425

<210> SEQ ID NO 332
<211> LENGTH: 395
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (278) .. (280)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (311) .. (311)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 332

attatctctt	attatctctt	60
cccttatcag	cccttatcag	120
tccagcaggc	tccagcaggc	180
gagccttcc	gagccttcc	240
tcatcgtatc	tcatcgtatc	300
tcatcctgag	tcatcctgag	360
caactcctga	caactcctga	395

<210> SEQ ID NO 333
<211> LENGTH: 453
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (19) .. (19)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 333

-continued

ggatcagcca	ggggccagna	tgagccggag	ggagggcagt	ctggttgaa	tggacagag	60
cctgcctgc	taaaaattt	gagaatttcg	agtggagcct	ctgggttcag	gaagagcgag	120
ccttggaa	gtggtaaga	agcaagggtt	tgggtgtctc	tcattcctcc	cctgttttc	180
ccaccagagg	accccaggc	tgactcctca	gcctcacccc	ttccccactt	ggaggccaag	240
atccaaacaga	cacacagcct	tgccgcctc	ctcaccaaata	atgctgagca	gcttctccag	300
gaatatgtgc	agcaccaggg	agaccccttc	gggctgccc	gcttctcgcc	cccgccgctg	360
ccggtgtggcc	atctgagcga	cccgcccccc	ggccacgctg	gcctgccagt	gcccgagcgc	420
ctgcggctgg	acgcccggc	gctggccg	ctt			453

<210> SEQ ID NO 334

<211> LENGTH: 604

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 334

gggaactgct	ccggaagccc	ctggcgctcg	tgtctgtcg	gtggaaacgt	gtaccgtcat	60
ccgtgggcct	ggccatggcg	ctgcagctct	cccgggagca	aggcatcacc	ttgcgcggga	120
gecccgagat	cgtggccgag	tttttctat	ttggcatcaa	cagtatttt	tatcagcgtg	180
gettataatcc	atcgaaacc	tttactcggt	tgcagaaata	tggactcacc	ttgcttgtaa	240
ctactgatcc	ttagtcata	aaatacctaa	ataatgtgga	tcaactaaaa	aatagttat	300
acaagtgttc	agttcagaaa	ctgggtgtag	tcatctcaa	cattgaaagt	ggagaggc	360
ttgaaagatg	gcagttttagt	attgagttca	taagatgtaa	aagatgtatg	tgcacccaga	420
aaaaagttt	agaaagctat	ccaagatgaa	atctgttca	tggtcagaca	gatcacagct	480
acagtaacat	ttctgcact	gttggaaagt	tcttgttcat	ttgatctcct	tatttgata	540
gacaaagatc	tgggtgtacc	tgaaaaatgg	gaagagtccg	gaccacagtt	cattaccaat	600
tctg						604

<210> SEQ ID NO 335

<211> LENGTH: 463

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 335

gtctctgctc	cacttcttta	tctcggtggac	tttctatgcc	atcaaggaa	gtatctaaag	60
ttttagatga	aattatttct	ttgtgggtgg	tagaaagtaa	aacatcagac	tgtccttca	120
caggagaaga	aagttcagca	gtgtatgttt	tatcgtaact	attttaatg	gacttaaagc	180
ttgttaaggct	atctacattt	tctcgaaaat	catgaatttg	cataaaatgg	tttgaaggta	240
caaactttc	cttgggacga	gtgtaatctg	gtgtatcaa	atcaacaaac	cctacaccag	300
aagggttaac	ttcagaaaaac	ccaccaaattt	cccaaaattt	atcgcatca	tcatctcag	360
ctccgttgc	tagtgggtgt	ggggacgaag	agtacattcg	aatgatgtct	ggctccattg	420
ttcaatttgc	ttcaataactt	aatttatacc	tggttcg	tcc	ggg	463

<210> SEQ ID NO 336

<211> LENGTH: 632

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 336

gctcaacaac	ctgcttc	ggaaggacgt	ctgcttc	tggacaggca	tgcagctcag	60
------------	---------	------------	---------	------------	------------	----

-continued

gtacaacatt agtcagctgg aggaatggct tcggggaga aacctgcacc agageggagc	120
tgtttagacc atgaaacccc tgattcaggc tgcccgctc ctgcagttaa agaagaaaag	180
ccccgaggat gctgaggcca tctgctccct gtgcacccgc ctcagcaccc agcagatgt	240
caaaatttt aaccttata cccctctgaa tgaatttcaa gaacgggtga cagtggctt	300
tatacgaaca atccaggcac aactgcaaga tcggaatgac cctcagcagc tgctattaga	360
cttcaagcac atgttcctg ttttgtccc gtttaatcca tcttctctga ccatggactc	420
aatccacatc ccagcatgtc tcaatctgaa gttcctcaac gaagtctgaa aatgcacatg	480
ccagagcttg attgccatgtc agagcacgaa ggaagtagcat aggacagtga agtgaattta	540
agaatctgtt aaaatctgtt aaaggagatc agatcaaagt ttgagagcct gtgcagatgt	600
aactatacag aataagacac atctgtcatt at	632

<210> SEQ ID NO 337
<211> LENGTH: 349
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (190)..(192)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 337

gtggcccaca tggggccggg cgacggcaact gcaggtgctc atggacctgc ctctgagcgc	60
cgtgcccccc gcccaggagg agaggccggg ccctgcccccc gccagectgt cccgcccacc	120
tccgcccagg aacaagccct acgtctcgta gcccctcgta gggggatctg aacccggagt	180
gtctgtgcen nnaaggagta tgtctgaccc tgaccaggac tttgacaag aggtgaggtt	240
cgccctggcga aggcggaggc ctggggctcg aggctctgta tgccctggag tggccacctc	300
gggcctccgt ggtcccccagc cccccagaac cgccttctct ggactgctc	349

<210> SEQ ID NO 338
<211> LENGTH: 476
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (218)..(221)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (236)..(238)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 338

gtgattgcc tgaagaagaa tacaaggcgt acttgtatct agatgaagct cacagcatcg	60
gggctctggg ccctacagga cgaggcgtgg tggactactt tggcctggat cctgaggatg	120
tggacatcat gatggaaaca ttcacaaaaa gcttggtgcc ttctggagga tacatggag	180
geaagaaggc gctgatcgac tacctgcgga cgcattcnnc ngcgcggtgt acgctnnntc	240
gctgtccccg cctgtggcag agcagatcat cactgcccatt aagtgcattca tggggcagga	300
tggcaccacc cttggcaaag agtgtattca gcagtttagcc gaaaacgtca ggtatttcag	360
gagacgtctg aaaagcatgg gcttcatcat ctatggaaat gaagattctc cagtgggcc	420
tctgatgctc tacatgcccag cccaaattgg cgcctttggaa cggggagatgc tgaagc	476

<210> SEQ ID NO 339

-continued

<211> LENGTH: 317
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 339

gaggaaactg aggtccggag acaggaaatg acgcactccc ggggatgccc tgagtcatct 60
ggtttctacg ccatcctcaa agtcctccca caggttcagt tctgggtgt tcatctccc 120
ttcaacttt ctgaaagatg ctggagattc cggtcaactg caaaatgaat gcgctcttag 180
tctcatacac cttatgccag tctggagatg gactggagtg tccaccctct ctggcacaaa 240
gagggacttg gcaaagtgtt tggtggcag ttagccaga ggtagccag cgcacacggg 300
ttggggttga gaggaga 317

<210> SEQ ID NO 340
<211> LENGTH: 520
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 340

aaacgccta acagccagg ttgtggaaat tgcaaggggg tgattcagcg gctgacgctt 60
caggagcaca agatggttt gAACCGGACA acccaccctt ggaacgactg ttccaagatc 120
attcaccaga ggacgaacac ggtgcctt gacctgggtgc cccacgagga cggcgcgggc 180
gtggccgtgc gcgtgctgaa gcccctggac gcggtggacc tgggcctgga gactgtgtac 240
gagaggttcc acccctccac gccgtccttc accgacgtcg tcggccacta cctcagcggg 300
gagcggccca agggcgtcca ggagacggag gagatgtga aggtgggggc gccactcacf 360
gggggtgggcg agctgggtct ggaccacacg tgcgtgcgccc tgcagcccc caagggccgc 420
ggcatgcagt actacctgag cagccaggac ttgcacagcc tgctgcagcg gcaggagtcc 480
agcgtccggc tctgaaaggt cctggcgctg gtcttcggct 520

<210> SEQ ID NO 341
<211> LENGTH: 333
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 341

tgtttcacca agtatatttt gagttggttt ccacacattt ccagagtgca gcagtacagt 60
tctctgttca ttgcacgcgtg gCAAACCTCT gtatgtatgtt gggatggat gtcaatgaaa 120
aattagataa attctttttt cttataatta atataacact tctggacttg aactttgaca 180
ggagatgcca aaaggcagtg gtaccgttattt atgaattact ttttaacaag 240
gaatgattca tattcattaa atgaattcaa tattttccct gtaaaaaacaa tagaatttca 300
gtacatgaac tatagaaaaa atatatatat aat 333

<210> SEQ ID NO 342
<211> LENGTH: 432
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (318)..(318)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 342

ccacccgggc cccactgcgc cgtegtctgc aactctacct ctctgacgccc tggaaccagt 60
gegacactgtt ggccctcgcc tgcttcgttcc tggcgtggg ctgcaggctg accccggggc 120

-continued

tgtatgacct gggccgcact gtcctctgcc ttgacttcat gatcttcacg ctgaggctgc	180
tgcacatctt cacagtcaac aaacagctgg ggcccaagat cgtcatctg agcaagatgg	240
tgaaggatgt gttcttcttc ctcttcttcc tccggcgtgtg gctgggtgcc tacggggtgg	300
ccactgaggg gtccttngg ccccaggacc gtagccccc gaatatcctg cgccgtgtct	360
tctaceggcc ctacctgcag atcttggc agatccctca gggggagatg gacgtggccc	420
tcatggagca cg	432

<210> SEQ ID NO 343

<211> LENGTH: 494

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 343

gcatttcagc ccagcagtgg ttgaccatcg agaagtata gacggggag ttccggaagt	60
acaacaacaa caacggtgat gaaattgcc ccagcaacac ctggaggag ctgtgttgg	120
cttctctca ctggacctat gagtatactc ggggagagct gctgggttta gatttcaag	180
gtgttgaga aaatttgcg gatccatctg taataaaacc tgaatacaaa caatcaagag	240
aatgggtt tggaccagcc aatttagggg aagatgcaat tagaaaactc attgcaaac	300
atcggtgcaa ctccctgctgc cggaagctca aactccggc cttaaaaaga aatgactact	360
ctcctggaag gataaattct gccttggac ttgaaatcaa aatagaacca gctgaggaga	420
ttccagcggg ggaagagggt agtaattctc cagaagatct cacacgatgt taaaaaaaaa	480
aaaaaaaaac aaat	494

<210> SEQ ID NO 344

<211> LENGTH: 332

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 344

gctaaacata gctggggatt tgggtcagag ttgaaagaaa tggctatatt aaaaacgcgt	60
tgtatcaagc tgagcttaac attgtcaagc tttagcttaac aatatcggt taagtgat	120
tgggtgagaa ctctattagc tttcttatta aaacatgttt cccactctaa gagtagtaga	180
gagagagtga ttggagttt aaatatttgtt atatgacgtt catgaagttt cagtttattt	240
tacaggttgtt tttgcaaaaa cactcataga acgtgttgtt gtgaagaacc tgaagtctg	300
ggctagtgta aatcgaggag ccattattct ct	332

<210> SEQ ID NO 345

<211> LENGTH: 471

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 345

tgtgttgcata tagcaaaggc ctttcctgg gaaaaccaaa aacaaaaat taaaaaacac	60
accctcagtt gtttattttt gtatagtaat ttatTTaaa gtgaacaaa tggtcattca	120
aatccaaaga gaatcttaaa acagtccat tctttgaaag tattacgtgt gctcaaattt	180
tcattcaagt ttgagaatgc tttgagatca ttttagattgt ttttaaaact gcttggcct	240
tacatgaaaa gtgttatgggt tttgtgtcat tatttggatgtt gtcaggattt gatgttgaag	300
gtttattcag tctatagtc ggtgatacta aatTTTTTT tgggctggca aggccatcg	360

-continued

cgtgctgacc agtggcggtg atgcgcagg catgaatgcc gctgtcagag ccgtgactcg	420
tatggcatt tacgtggggg ccaaggctt cctcatcac gagggctatg a	471

<210> SEQ ID NO 346
<211> LENGTH: 553
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (451)..(453)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 346

tgtttcctca ccccaagggg tttagcaaga tacagttca caatctctgg atcaagaagt	60
tttattaaaa gttaaaactg aaattgaaga agagctcaa tccctggaca aagaaattc	120
tgaaggcttc gccagcacag gcttcgaccc ccacacctgc caggactcg gaccaggag	180
aaagaaggag ggtttagtt gtctcgactg aatccgaatg ggcagcagct ggttggacat	240
ccgcaggacg ctctgggtg aggagctggg tcagcaggcc agggggggcc cacctgcgg	300
ggctttaggt agaggctgtg cacgcggct gctgggggtt ccctggctg gtttctctg	360
agattcaggg tctagggtgt caagtgttc ctcagtttg tctgtggcat ctggcaacc	420
ccggctgtga gcacctgtgc ccccgagggt nnntagcctc ccccatcagc ccccgtagca	480
ccttccccctt tggtagacgc acccccccgt gtgccaacg tccccgggtt aatgggtccc	540
gtgagagcct cag	553

<210> SEQ ID NO 347
<211> LENGTH: 500
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (237)..(244)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 347

gtatgttccca ttcaagacg ccgtgtctcg cgcctgtttt agcaagcctc tgctgtatgga	60
agccctggaa tgaatctagg cttttaatg gatgtctcgta taatgtcaat aactaaactg	120
ttctcagctt atattaatag caggaagact agcatgaaat actgtgccag gccctgggtt	180
ctgtgcgtat ctccctttagg aattggattt tttgggtttt ttttgtgggtt ttgaggnnnn	240
nnnnngaaacg ggaatctttt tttcttttctt aggatataat gggagaatag ttatctagct	300
aaggaaacaga cattacttta tttaaaaata tttataactt ataaaaatataat ggaaacggaa	360
ggaaatgggt ttgaaagaag atttaaatg aatcagaaat acctacacaa ggatagagag	420
gaactatgtg actgaatggt tctgtaaaaa gacgtataag ttattnaaat atgaacagaa	480
ttttaatggtaatcca ggctaatcca	500

<210> SEQ ID NO 348
<211> LENGTH: 570
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (504)..(504)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 348

gcaggggggc ggtcttgaag acgcgtcggtt tggtttgcacc tcagtgacgg agttctccgt	60
---	----

-continued

cttcaaccgc	tggcgccaag	gcgtttgtta	ggggcccg	caagaaagag	gccctcgagg	120
ttcctgatgg	tgtccatgac	tttcaagcgg	agccgcagcg	accggttcta	cagcacccgg	180
tgctgcggct	gttgcattgt	tcgcaccggg	acgatcatcc	tggggacctg	gtatcatggt	240
gtcaacctgt	tgatggcaat	tctgctgact	gtggaggtaa	cacacccaaa	ctcaatgcca	300
gctgtcaaca	ttcagtatga	agtcatggc	aattactatt	cgtctgagag	aatggctgat	360
aatgcctgt	ttcttttgc	cgtctctgtt	cttatgtta	taatcagttc	aatgtggta	420
tacggagcaa	tttcttatca	agtgggttgg	ctgatccgt	tcttcgttta	ccggctttt	480
gactttgttc	tcagctgct	ggtngeatac	agttctctga	cttacttgcc	aagaatcaaa	540
qaatatctqq	atcaqttacc	tqatttccc				570

```
<210> SEQ ID NO 349
<211> LENGTH: 401
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 349

tgaggtgcac tgggtggat aaaaatgaa gcaggaaaaa aaaggaagta gaaggccaa 60
tcatgaggtg ggggtggactt agccccatc ttctccttcc ccaggtccaa tgaagcgcca 120
agtggcagta aaatccaccc ggggtttgc tttgaaatca acccatggca ttgccattaa 180
atcaaccaa ac atggcatctg tggaaaaggg ggagagtgc cccattcgta agaacacacg 240
ccagttctat gatggggagg agtcttgcta catcatcgat gccaaagctt aaggcacac 300
ggggccgtac ctcaatgtga gaccctttc gtcacccgtt atgtgttgt tatccccctag 360
tcctcacatt tcttagttt taaaatacaa ctccataaaac c 401
```

<210> SEQ ID NO 350
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 350

gataaaagtga cttagtccaga gaaagctgaa gaagcaaaaat taaaagcaag gtatcctcat 60
ctggggacaaa agcctggagg ttccgatttt ttaaggaaac gattgcagaa agggcaaaaa 120
tatTTTgatt ctggggattt caacatggct aaagcaaaaa tgaagaacaa gcaacttcct 180
actgcaaccc cggataagac agaggtcact ggtgaccaca ttcccactcc acaggacctt 240
cctcaacgga aaccatctt tgTTgcttagc aaactggctg gctgattaaa aagagctgaa 300
ctgcatgaat cttctaatgc ccattatttc tccttaatat gttactcctc tgctttttat 360
ttccctttac tccctgtgtc atttgagagt gatggcttg caggtagcgg tagtgtgtgc 420
tgctatTTta agggaatata catgtgtaga gttttgatt agttAACAG tgcaCTgtatg 480
aaaagaacat gttAGAGCAA cataAAAGTAA tCTACTTGTAA aATAATTGTA tatattacct 540
aactccttagt gtacggctgg atccaacaag taactaaacaa gttttggact ttaaatgttg 600

```
<210> SEQ ID NO 351
<211> LENGTH: 437
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (312)..(313)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
```

-continued

<221> NAME/KEY: modified_base
<222> LOCATION: (318)..(320)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 351

tttttttttt tttttttttt taaaacttgca gaaggctctt tattttcatc catcagaggg	60
cagacagaat gaaaaccaca attacagaaa actaaccaa atgatcacat ggatcacagc	120
cttgtgtaac tcagtgaaac tatgagccat gccgtgtaaag gccagccgag acagacaggt	180
catggtggcg gggtctgaca aaccgtggtc cattggagaa ggaaatggca aaccacttca	240
gcattcttcg cgtgagaacc ccatgaatgt atgaaaatgt tgagaagcag agagcaaaag	300
ctagtgactg gnnggcnnn tctgccccac agataaaactt caatttacat gtcattattt	360
acaacttttag gggcggttta aacaaaacag ttggggagaa aaaatggcat ttctgacttg	420
cgttaaaaaa tcgtcaa	437

<210> SEQ ID NO 352
<211> LENGTH: 526
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 352

agacaggact ctaaaagttag actctcctga ttttcacaa gatgctggac tggagattag	60
caagtgcaca ttttatcctg gctatgacac tcatgtctcg gagctcagga aaagtgttct	120
cagtgggtgt cacaacagag gccttgatt ctggagtctt aggtgttcag tcatcaccca	180
cagtcagaga agcgaagtcg gccactgacc tggcagcaaa actcttaccc tttgtatgaac	240
tttgtgtctct ggagaatgac gtgattgaaa caaagaagaaa aagaagctt tctgggttg	300
gttctccctt ggacagactc tcagctggct ctgttaagtca taaaggtaaa cagagggaaag	360
tagtagatca tccaaaagg cgattggta tccctatgga tggattgga agaaaccggc	420
tttcaaatc cagaggctaa tggattccaa tcaacacaact tcttgggtg aaatgtcaca	480
gaaacatgga agatattttg gtgaagttct tcacacttct taatga	526

<210> SEQ ID NO 353
<211> LENGTH: 477
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 353

gcacgagccc atctctaggg tggtaacta ccctgaaatc tctggactg gaatttggc	60
cccaaagtct tgagtggctc tggcttattt gtgtctccac cctgggtctg tgaaccaccc	120
cactccagat gccagagcca ctgggggtgg ggcctggac agggatagc ctgtcagaag	180
gagctggcgc cagtatgca agcagctgtatggctctgag tggattttt gacagtgaat	240
aaagggcaca aagcccgagc caggcagact cacccacac accccctgtt cccctgtgt	300
gggacacctg agagagagga ggggtggaca atgagagaac aggagatgg tcataaccgt	360
ggcctcgcag agcagggca ataagagctc ageccattgc agtgcgtggcc atgtcttcat	420
acctgggtat ctgagggtgtc ctgtttgtt ggctgtccgt ttgtttctt tctggct	477

<210> SEQ ID NO 354
<211> LENGTH: 504
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 354

-continued

gcacgaggct ggcgggggaa catgtcgag tcagagctcg gcccgaagtg ggaccgggtgc	60
ttggcggacg ccgtcgtaa gataggtact ggcttggat taggacttgt tttctcaatt	120
accctctta aaagaagaat gtggccatta gcctttggct ctggaatggg atttggaaatg	180
gcctactcca attgtcagca tgatttcag gctccgtacc ttctacacgg aaaatacgctc	240
aaagagcagg agcagtgact cacgccttag agcaccccg ggggagggca ggagaaacca	300
cgttcattcc tcaggaacgc tgaagcgccc gagtgagccg cactctccgt gagcgtcgcc	360
agtaatgctc aactccagca cactgtgcac gtgtttgaaa ccaagtcgt ttcttgaaa	420
gtatttctc tctggaaatt gcagggcggt ggtcttaaaa taaataaaact aaactcgca	480
gccccagaaaa aaaaaaaaaaaa aaaa	504

<210> SEQ ID NO 355

<211> LENGTH: 529

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 355

gcacgagctg gcctcagtca gtgatgaaaa caagggagg gacagggagg ggcagtcctcc	60
taggtcaacc ctcggggagg gcccgggccc aggattcacc cttccttagtgc cctctgagtc	120
aggatcccgccg ggaccccccag ctttgacccc acctgtatttgc tttttccct tctctgccc	180
actcaggact tagaggactcatccattgc acatgtttat aacccatgtt taccagccaa	240
tactgaaaag gacagactca tggaaatttag agtcttagtgg ggaattcaga ccctgggtat	300
gaatgttggg aaagaggaag ctatgaggtg actgcattgc aatcctgggg gcctaactgg	360
gccccaaagact gggcaagagt cctgcagaag actttgaaaa acctcaagtg ggaaggctcg	420
ggggctgttg gaggctggag ccagttatgg ctccctgtac ccgtaatcaa	480
ggacccaagg agctgacttg acgacagttt ttgaggaagt ggagcaggt	529

<210> SEQ ID NO 356

<211> LENGTH: 361

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 356

gcacgaggct acggacagta tggttccgccc ggtgcaggctc tctccgtctca tcaagctcg	60
ccgttactcc gcccgttcc tcggcatggc ctacggcgcc aagcgctaca attacctgaa	120
acctcgggca gaagaggaga ggaggcttgc agccgaggag aagaagaagc gggatgagca	180
gaagcgcata gagcggggagc tggcggagg tggcatcgcc ttggctctc ctatgtttc	240
ccccggcccg cggggtttc agaaacagct gctgcttcat acggacgacg aagtggagag	300
gaaaggctgc cttctccatt tccactggcc cctggccat cctctgtca gtggggtagg	360
g	361

<210> SEQ ID NO 357

<211> LENGTH: 572

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 357

ccacagtctg tctcaccatc cacaaaagct cacaggatcg cctaggatgc atccgaagct	60
ctgtcacata cgatctggcg ttggatccag gtcggctgat ttctcgatgt gttttgggt	120

-continued

agaccaggaa ctggactttg actcgaagaa aaacccctgga gctggagag cactgtgact	180
ccatgaagct gcttatacca gactgtgtgg aggacatggt gaaccccatt atcctgcgac	240
tcaacttctc cctgggtggg gagcccatgg cctcatctca gaacctccgc cccgtgtgg	300
ctgtgggctc ccaggacctc ttacggcct ctctccctt tgagaagaac tgtggcaag	360
atcaccttg tgaaggggac ctcagtgtca acctgagctt cttaggcgtg gagaccctgg	420
tggtggggag ctccctggag ctcaatgtt cagtgtggt gtccaatgag ggcgaggatt	480
cctatggAAC ggtgtacgc ttctactatc cagcagggtc gtccatatcgA cgacgttag	540
caatccagca acctggctc agtccccctgc gc	572

<210> SEQ ID NO 358

<211> LENGTH: 303

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 358

ataatcctgg cgtagggcgg ctccggctgc gccccagcta ctcagaacag gccccagact	60
gtggcagcac ttccccaggg gtcttgctgg gaacttgaca tctcgggccc cacccggacc	120
tgctgattca gggcccacct ttcacatgtat cccctggaa ttctgaacat ttccaaggca	180
gccttccttg cacagccctt ggctctggcc acacccagg attcctgggg aggcagagaa	240
aaccctgtatg ctggccccac tccagaggct ctgacttaat ggggttaggc cgggtgtgg	300
ctc	303

<210> SEQ ID NO 359

<211> LENGTH: 454

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 359

ttttaaaaaa aaaaataat tacctttatt acaaaaactca tggtaaacct agggatttat	60
gtcccggttaa gctctttcac ctgaaattag tgggtggctc tgaaaaagac ctggaggtt	120
ttcaaaagcag gaggtgccgc tgaagattta ctcttttttgg gagacccgc tcttggcctt	180
tgtagecttg ggtttggcag cttaggttt ggctgccttggcttgggggg ctggcctt	240
ggccggactc ttagtcggct tcttcggctt ggctgccttc gccttcttcg gactcttggc	300
tacttttttgc tccccagcag ccgcagccgg ctctttaact ttcttaggggg tcttcttggc	360
agccttcttc ggagtggccg caccctgtgg tttcttgggt ttcttagccg ccccaagcagc	420
cttcttgggc ttggccgcgc ccgccttctt cccc	454

<210> SEQ ID NO 360

<211> LENGTH: 586

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 360

tggaaagctga agattccca gaacaagaac ccaagataag ctggagttaa tggaaagctt	60
tctttggctt ttccgggtgt gacctacattt ccaaccatgt ctgcagatata taaccaccta	120
gaccagcaac gttccctctgg agccagcata gggcccttct tgagcaaata ccaccagact	180
cacaaacagc tctgttacta aggtttatt taatttcaga gtgcaaataat tttcaatg	240
ctcactaggt ttatataact aagaagctat atttttggcc ttaaacactc ctgtggatt	300
atgattata ttcacatata ctggcctcaa atgagataaa aaccaaactg tctgttatgt	360

-continued

ttactttgat atattaattt cttagagca gcgttttagc tactaaagtt aacatgttta	420
ttcttcctt ctcacatgct tgattaaaag gtgagcta at tcttcaaga gtttgatta	480
at taacagaa aatcctaaat tc当地actgct aaagaacagt ttgattttt tggctctccct	540
taagtagatgag acacatctt ttttattgaa tttcttcaa tacccct	586

<210> SEQ ID NO 361

<211> LENGTH: 371

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 361

gactaatcct ctccctgcttc agctgttcaa atttcgctt taactcgccc tgccgctcca	60
ctttcttttg tgca cggccaa acgaaaatga cttcccagt gattttttt ccattcatct	120
cttccacagc caaactggct aaatagctct ttc当地gattct catcatcaac ctcttcccc	180
aagtttttga tgtaaacattt ggtgaattcc ttggctttgg ctccaaatgc ggcttccgc	240
tcttttcgag acttgaatct gcccacaaac cagccctggaa gtggagaggt aggaggcaggc	300
cacacttggg cc当地gagaac cagtagccgc cttgtgtgtt ccagttata cc当地gggtggg	360
gccccacggctg g	371

<210> SEQ ID NO 362

<211> LENGTH: 800

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (7)..(7)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (21)..(21)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (39)..(39)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (87)..(87)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (92)..(92)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (102)..(102)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (272)..(272)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (293)..(293)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (299)..(299)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (365)..(365)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (454)..(454)

-continued

```

<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (498)..(498)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (510)..(510)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (543)..(543)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (569)..(569)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (579)..(579)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (623)..(623)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (633)..(633)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (672)..(672)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (695)..(695)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (785)..(785)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (792)..(792)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (795)..(795)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (798)..(798)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 362

aacccctntta aaaccccccna nactttact ataggaaat tggccctcga ggccaagaat      60
tcggcacgag gcgcaaagat gtcagtnttt tnggggggtg gngtacaata cctgcagtga    120
ggccaggggcg ggccctgcag cgaaaggcca cctctcacag gtgtcttagc tactgccct    180
ttgggaagcc aaatcttcca gccccggacc ttgggtatgt gttcttggaaac atcctgacct   240
ctgataccct gcctgtgacc ctgacttgcg gngcaaggca tccttcccc tanagctnt    300
tgcaaaattac tggcttcctt gagecctgac ttggagccac ccaatccagc tgtaaatga   360
acacncagga aaccacacat cttgactcaa cttatccagg tcatctcgg agtgggcctg    420
gggctataaa taggcatacat gagttgatca caanaaggcc ttgagaaaag ctgaaaggag   480
agttaggggag gaagccantg tttagacccan aactataggc acacacacct tcaggccagc   540
ttntgagctg tggaaaccgt gttctctant taaggcacnt gatggtgtt ggaagagggg   600
acggggtttc ttccttgct gcntgatggg acnactcatac catacttgat ggccgtctt   660
tgcaagcggg tncccttcca ccccccaggg ccaanaaaca tgtccccctt cacttccat   720

```

-continued

ggaatttttt cttttattat cccccccacc ctttgcaggg aaacccctt gcaaagaaaa	780
aaggnccttg anacnagnga	800
<210> SEQ ID NO 363	
<211> LENGTH: 548	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 363	
ttaagatggc tgccggcggt cacgggtccgg actgaaaaga tgtggagtgg gctgttacct	60
cctggcctaa atgaaagtga tggtaattt aattctgacg atgataaccac attagagagc	120
tctgaactta acttacaaga gggtaaagaa gatgggaccc ttgaaaagac agagatggta	180
gatattccta cagatggacc aagcactgaa gcagaggcaaa atataaatgc atatgaagag	240
tgtccctctg gaattccctt aaatatgtgg aataaaatttc aagaatttgc taaaaagcat	300
tctgaacaga aaacttcage ttcttagatcc gaaaagaaaa aaagaaaaacg ctccagaaaa	360
ggtaaatttga agaatgaaga agaatctcat agtgaacaat cttcaagtga aacccagtgg	420
aaggagctta cccagtattt tggagtcaat gagaggttt acccccctgt taaaaaggaaa	480
aaagttgaaa agtcgggact tggaaagagg atagaccaag ctgttggaaaga gtggAACATT	540
gagaaggc	548
<210> SEQ ID NO 364	
<211> LENGTH: 222	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 364	
tttaataag gatggggtag aaggctgggtt ggtttagatg tccctggcgag ggtctcccg	60
agccagggca atctgagcca attcatctt cttccctctc ttccctgtgc cttacgcgaa	120
gcctcggtc ccttgaagca gcgccaggcc tcctgacacc cccatggtca aggcagaacg	180
cgcacaggct gggaccacgc cgagatcat cgggtcattt tg	222
<210> SEQ ID NO 365	
<211> LENGTH: 609	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 365	
gaattctctt ccaagtttga aaattcaagt tggataacca gtattatcct cgttggcct	60
gttgctgtta aggcatgtac atatatgtgg aggaatgaaa tacttaacta gaattctta	120
atagggttta tggtttaact ttagagagca cctttgtatt tttcttatca gctaggacaa	180
aatattgtat taagcatatg tagacttca taaaatggct atttgttaag ctacaggtaa	240
aagcaaagct atagggttaga tttataatac agtgaaggca cgaggacttc aaacgtgccg	300
gcaggttggc catagaaaact ggaagttaaa agtcacatga aggtcaagat ccagactaa	360
ctcatgccac tgccttcag gatctctgtc ttggagcatg agggagttgg caagttaaat	420
gttagaaagca ggcccaaact tggaaagggtt ttgtttttgtt aaatcatttt acttacttt	480
aacatgctca gttagaacgtt tttactttta ctgtttgtt cccaggagttt attttacct	540
agccgttagag caaaactgtt cataaaatgtt tccctttcaa atgttcttga gaaaaatgg	600
ggaaaaaac	609

-continued

<210> SEQ ID NO 366
<211> LENGTH: 453
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 366

```
gaatgaaaga tatacctaga acaccatcca gggggagaag tgaatgtat tccttcagg      60
aaccaaaagc tttgccttagt actccttaggc caaggagtgc ttctccatct tccccggagc    120
tcaacaataa gtgtttaacc cctcagagag agagaagtgg gtcagagtca tcagttgaac    180
agaagactgt ggcttaggaca cctcttgggc agagacgtcg gtctggatct tctcaggaaac   240
tcgatggaa acccagtgc a tccctcagg agagaagtga gtcagactct tctccaggatt    300
ctaaagactaa gatacgaatg ccactcaggc agaggagtca ctctggatcc tctccggagg   360
tggacagcaa atcccgccct tctcctcgcc gtagcaggcc tggctcatcc cctgaggta     420
aagagaagcc aagacgagca cccaggccac aga                                         453
```

<210> SEQ ID NO 367
<211> LENGTH: 447
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 367

```
cggtgtccgc ccgcctgcg ctctcgagc cggagccgc cgcccgagg gatggggag      60
cccccggtt ggggaaacag agaggcaggc ggggagccgc ggacggatg tcccaggccc    120
caggagctca gccaagcccg ccctccgtgt accacgaacg gcaacgcctg gagctctgtg   180
cgtgtccacgc octcaacaac gtcttgcgcg acgagctt cagccaggag gtcggatg     240
agatctgaa gaggttggcc ccagactccc ggctgaaccc ccatcgacgc ctctggca     300
ccggcaacta cgacgtcaac gtgatcatgg ctgcctgcg gggcaggcc ctggctggcg   360
tgtggtgaaa cggaaaggagg cccctgtccc agtggcgct gccccgggtt ctggggctga   420
tcctgaacct gccgtcgccc gtctcgc                                         447
```

<210> SEQ ID NO 368
<211> LENGTH: 445
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (151) .. (152)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (209) .. (211)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (284) .. (286)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 368

```
tgcagggtt acgttgcag tcagtccgtt gtttgc当地 attgtgcggg ctgcggagcg      60
cgtctccggg ctccggccag gacccgaacc cggggccgcct aatcgctgcg cacttggat    120
tgcgtact tccccggcgc tgcaggcagc nncggccgc tcccgactgc agaccgcaag     180
cctccctgtt tttacagcag cggggacgn ntcttcaac ccgacatgg tttgtccca     240
atgtgcagca tcttccagga actccagatt gtgcacgaga ctgnnnactt ctggcgctg   300
ccctccctgg aggaataactg gcaacagacc tgcctggagt tggaacgtta cctgcagagc   360
```

-continued

gagccctgct acgtgtcage ctccgagata aaattcgaca gccaggaaaga tctgtggacc	420
aaaatcatct tggctcgaaa gaaaa	445

<210> SEQ ID NO 369

<211> LENGTH: 384

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 369

gagtagacga tcttcgtcc cctctccgg atggaggccc agattgtgca gcagcaggcg	60
cctccctcct acgggcagct cattgcccag ggccatcc ctcctgtaga ggacttcct	120
acagagaacc ctaatgataa ctctgttctg ggcaatctgc gttctgtct acagatctg	180
cgccaggaca tgactccagg gagcacctct ggtgccegccc ggcgcaggcg gggccgcct	240
atgcgcgcgc tggcgcgcgc tcttcgcgc tggggcttc ttccccgaac caaccccca	300
gcccggaccc ctgaaaccag atcccaggcc acaccatcca ctgctctcc tgagaccta	360
gatggcagca caggcccgcc ccat	384

<210> SEQ ID NO 370

<211> LENGTH: 485

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 370

ggaggctgat gaaggagctt gaagaaatcc gcaagtgtgg gataaaaac ttccgtaa	60
tccaggctcgat tgaagctaat ttgtgactt ggcaagggtt cattgttccc gacaaccctc	120
cctatgataa gggggcccttc agaatcgaaa tcaacttcc agcagagtac cccttcaa	180
caccgaatg cacgttcaaa acgaagatct accacccgaa catcgacgag aaaaaaaaa	240
tgtgtctgcc tggtaatttgt gctgaaaact ggaagccagc aacccaaacc gaccaagtca	300
tccagtcctt catagcactg gtgaacgacc cccagccgaa gcacccgctc cgggctgacc	360
tagccgaaga atactctaag gaccgtaaaa aattctgtaa gaatgctgaa gaatttacaa	420
agaaatatgg ggaaaagcga cctgtggact aaaatctgcc gcaatggatt ccagcgagt	480
tgagc	485

<210> SEQ ID NO 371

<211> LENGTH: 431

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 371

tttttttta aaacaaaaaca aaagtttatt aaaagtgttc ttaatgctcg aaacggaaaa	60
gattccaaaa tatacagatg cctttttct catagaaata gatttttt tatgatacaa	120
aaaaaaaaaggcc aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	180
aaccccgtag gaacatctt aagcgattac tcaggccccc gctgacagtt acacgtgggt	240
tgcgtcagtc ccgtgtacac acgcgtttag ccatgttta accgattgca tcaacttca	300
aaccggcccg cccgcggcg cccggagagg ggggtggca ggaggagagg caagat	360
tcatatct gtacacatag acatcttcc tttaataac accgcggccg ggcgcggcg	420
ctgcacgtgc g	431

<210> SEQ ID NO 372

-continued

<211> LENGTH: 465
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<400> SEQUENCE: 372

agcaaggaca	gcgagcaggg	ctgagctggg	ggtgcgtggg	ctgctacggc	ccgccacctc	60
catcacatgc	acctctgcac	ccccctgctgc	ctgactcagg	agtggggggg	ggggtcctgt	120
gcttccttca	ctccagaccc	acggtgctga	cccagtgcac	ccacacctggc	ctcttagtgcg	180
gacctggcca	cagggctcct	gtggggccac	gctgatccc	ccctggtccc	ttcataaaga	240
actcttgagc	acatgcagcc	caggggagcc	aggaggctcc	agtgtgttgt	gtccatctgc	300
ctccctccag	cccctccga	gacactgcgc	atcatgcccc	cctccacccc	cacccacact	360
ggcaggagga	acagacaggg	agaccacaca	cagagctcgt	tgtttataaa	tctctgcctg	420
gtccatcggt	ctgtttgtcc	atgtatatat	ctgtatatct	ctatg		465

<210> SEQ ID NO 373
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (99)..(101)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (141)..(142)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<400> SEQUENCE: 373

cttgatttg	agcatgcccc	tcaagtagac	agcatgtct	ctggtccctt	ggggcaaca	60
cctgatccag	atggtgaggc	tgtctgccta	gaccgcagnn	ngtggtgaga	acggggagca	120
gaacgcgtgt	cagttagagg	nngcctctg	gcagcctca	ctgagcaaaag	gccaaagaaaa	180
gtagccagcg	gaagcagccc	aagagccgcc	gggaggccccc	acgtgggaga	agcaagggggg	240
tcagactgaa	ccagggccgc	tcaegtgc	ccctccctcg	catccactcc	aaggttgact	300
gtgggtccg	gccagcaactg	tccgtggccc	cagcatgtcg	agggtcttc	tggtgaccca	360
tgtttgaaa						369

<210> SEQ ID NO 374
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<400> SEQUENCE: 374

tccctgagac	cccgaggAAC	ccctctcccc	gccaacatgg	ccaacaaggg	tccttcctat	60
ggcatgagcc	gggaagtgcA	gtcgaaaatc	gagaagaagt	atgacgagga	gctggaggag	120
cggtggatgg	agtggatcgT	aatgcagtgc	ggccccgtatg	tggggggccc	cgacccgggg	180
cgccctgggc	tccaggatctg	gctgaagaat	ggcgtgattc	tgagcaagct	ggtaatagc	240
ctgtatcccg	atggctccaa	gccagtgaag	gtgcccggaa	acccggccctc	catggtctc	300
aaggcagatgg	agcaggatggc	tcaagtccctg	aaggcagatcg	aggattatgg	cgtcaccagg	360
actgacatgt	tc					372

<210> SEQ ID NO 375
<211> LENGTH: 409
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

-continued

<400> SEQUENCE: 375

cgggcccccg	cgcgcagcgg	ctggcccttc	agccccgccc	cctgccccca	cccgcggcc	60
ctaaagctgt	cacgatgcag	ccgcggcgc	cctcccgccc	ggggctgctc	ctgctgctgc	120
tccctgactcc	ggcgcacgtc	ggcggactgt	ggtgacatcc	gggagacggc	cttcgtttc	180
gctataacgg	ccgcaggcgc	cagecatcg	gtcacgcagg	cctgctccat	gggcgagctg	240
ctgcagtgcg	gctgccaggc	gccccgaggc	cggggcccac	cccgacccccc	cggcctgcca	300
ggcaccctcg	ggcccccgg	ccccgggg	tcccccga	gcagcgcgtc	ctgggagtgg	360
ggaggctgcg	gcga	gacgtt	gggg	gacgaga	gt cgaggctct	409

<210> SEQ ID NO 376

<211> LENGTH: 437

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 376

tacaacctac	cgccaa	ggtct	accc	tgtat	cagccagttt	cattggagga	attgtccttg	60
tcttgggtgt	gcagg	ctgt	a	tttctt	tctataaatt	ctgcaa	atct aaagaacgaa	120
actaccacac	tctgt	aaaga	gacc	actaa	attaacaagg	actggcgtgt	aactcactga	180
aacccaaaata	ttat	ctttca	agatgt	ccc	catg	ga	gac gctattctag	240
ttttcaaagg	atgc	atata	atg	cat	atc	agg	gacatcacc	300
tcaacggg	cc	tatt	aaagt	acg	ctgtc	atg	gtcactttc	360
gctgctgctg	tgg	att	gtgt	ttc	tctct	tc	ttgacatg	420
gaaaacattt	tc	ctg	cg	cg	cg	cg	cg	437

<210> SEQ ID NO 377

<211> LENGTH: 275

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 377

attacttctg	tttat	atggc	agc	agtttca	ttgact	gaa	aagtacacac	tgctcaat	60		
gtt	gat	gcta	tgt	ccaaaa	tgtt	c	tta	gcattggcaa	120		
aag	ctgg	aga	tg	aggat	aga	tg	cc	cagagga	180		
cagg	ctttaa	aag	tg	gat	gat	g	tt	aat	gtt	aaat	240
acac	ccctga	aag	taat	tg	at	g	tt	gacat	tg	ttt	275

<210> SEQ ID NO 378

<211> LENGTH: 499

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 378

ggaaaaccca	ctgcac	cttcc	c	c	c	c	c	c	60
cccg	gaa	agc	c	ag	ctt	gt	cc	at	120
attac	at	tg	at	ct	gt	ca	tt	tc	180
aag	tg	ca	gg	at	tt	gt	tt	tt	240
ttc	ctt	ctg	tt	at	ta	ta	ta	aa	300
tcc	ac	at	tt	tt	tt	tt	tt	tt	360

-continued

atactctggg ggaggggggc gcgtgcctcc tgcgcgtat aaaggcatgt tggcacgcgt	420
gggaacctgt ggcgacgggtc ctccctttc ccacaaacgt ttgaagttaa gaatagaagc	480
taagctcccc gggattgcc	499
<210> SEQ ID NO 379	
<211> LENGTH: 484	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 379	
tccttagatt tattatgcct gtaataagaa aataacctag caaatggttc actggatttt	60
cttcttgaa ttttcaagg tatctgcata taaaatcttc agcggtttaga tggtgacttc	120
tgaagaagaa aaggcttga taacagaaac aatttctggg tggcttggag acagtggat	180
ttgctgagtc ttttgcctc ctaaacattt tctgttattt tttcctgaa aagaaaactga	240
atttgcgtgg ttcacctgtt ttattctact gagtattgtt aaactttaaa tttttaaaaa	300
ttgccttcag ttgggagaga aaggaacttt atatttctaa gagatacatt tgatagttc	360
ttaaaggcgc acacaaaaaa ggaaaaacct ttgcaaactt ttgcacatcc tccccacagt	420
gcctgttaat tcatttgcattt ttttgcattt gcacttattt ttgttgcattt catttggaaa	480
acga	484
<210> SEQ ID NO 380	
<211> LENGTH: 215	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 380	
agctgctgca agactgtggt gcccggtgtt gggcgccgg accacgcctc caacatctac	60
aaagtggagg gcggtgtcat caccaagctg gagaccttca tccaggagca cctgaggatc	120
atcgccggccg tgggcctggg cattgcgtgt gtacaggtgt tgggtatgtt ctgcacatgc	180
tgccctgtaca agagcctgaa gctggagcac tactg	215
<210> SEQ ID NO 381	
<211> LENGTH: 444	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (115)...(116)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<220> FEATURE:	
<221> NAME/KEY: modified_base	
<222> LOCATION: (202)...(203)	
<223> OTHER INFORMATION: a, c, g, t, unknown, or other	
<400> SEQUENCE: 381	
tgctgaaggcg gctcaaggag cgctcgctgg acacgctgtt ggaggggggtt gaggcccgcg	60
ggggcggtcc gggcggtgtc gtgttgtgc cgcgccgcgc cttccgcctg ggccgnncagc	120
ccgcgcgcgc gtagctgtt ctcggacgc tttccgcgtt gcccgcacgt cagcacgcgc	180
tggagctcaa gccccgttgc gnnntgcaca gtttcgcgcgc cgccgcgcac gggccacag	240
tgtgctgcaa ccccttaccac ttcaaggccgc tctgcgggccc agaatcaccc ccacccgcct	300
actctcggt gtctcttcgc gacgactaca agccactggaa tctatctgtt tccacatgtt	360
cttacactga aacagaggcc gccaactccc tcatcacagc tccgggtgaa ttctcagacg	420
ccagcatgtc tccggacgc acca	444

-continued

<210> SEQ ID NO 382
<211> LENGTH: 347
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 382

tgagagactt cacttcatt tttcaacttc actttcact ttcatgtatt ggagaaggaa	60
atggcaaccc actccagtat tcttcctgg agaatcccag ggaccctgga gcctggtag	120
ctgccgtcta tggggtcaca cagagtggaa cacaactgaa gcaacttagc agcagcggca	180
ttaagataag gccctcagct gaaacaacct gagctggctg ggaggctgt gtactctgtc	240
gctgtatgtt gaagaggatt ttccttactg aactctcaact gcacatccac ggtctgtgc	300
caggcttcat gactctgaat taagtccctc gtctgttggaa gtccttc	347

<210> SEQ ID NO 383
<211> LENGTH: 435
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (402) .. (402)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 383

aaagaaaacaa aggaaaagaaa aagagaagtt ttacttcag aagcatgaaa tcgagtccaa	60
gttatttggg gatccagacg agttcccgctt ggcccatctc ttgcagccctt tccggcagta	120
ttacctccaa gctgagact ccctgccagc actcatccag ataaggcatg attggatca	180
gtacctgggtt ccatctgtatc atcccaaagg cagctccattt cctcaaggat gggcccttcc	240
cccgctcccc agcaacgcaca tctggcaac cgctgttaag ctgcatttagt aaaagacgtt	300
gcaggagtgtt catccagccca aggctccctc cagctctgag tatcagcgtat gctgccgtct	360
tgtacagtag accaaaactct gtgtggcatt gccctgcccac gnnggtacac tttcccttccg	420
tcctctgtct cagcc	435

<210> SEQ ID NO 384
<211> LENGTH: 540
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (465) .. (465)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (479) .. (481)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 384

gaggcgagtgg aagatgaatg ccagaggact tggatctca gtaaaggaca gtattccagt	60
tactgagctg tcagcaagtg gaccttttga aagtcatgat ttcttcgaa aaggtttctc	120
tttgtgtaaa aatgaacttc tgcccaactca tcctcttggaa ttatcagaaa aaaatttcca	180
gctcaaccaa gacaagatga acttctccac actgagaaac atccagggtc tttttgcacc	240
actaaaaactg cagatggaat tcaaggcagt gcagcaggtt cagcgttttc catttcttc	300
aagctcaaac ctttcaactgg atatttttagt gggttaacgat gagactattg gatttgaaga	360
tattcttaat gacccatcac aaagtgaact aatggggagaa ccgcatttga tggttgaata	420

-continued

taaaacttggc ttactgtaat gccatgtgct gttcatggaa gtagnngggc tgcgtctnn	480
ntatagttgt cttttccta taatttgtatg tgcacaacat taaaagtact aacacatgag	540
<210> SEQ ID NO 385	
<211> LENGTH: 471	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 385	
ggaagttta ttcttcag ctattctacc atctgcagct cttccctttt ctacccacc	60
caagaaaagggt gcctgggtct ctctgggcct gtctgtggac actctgggggt agtggagaaa	120
gtcttggtctg gcctggcttc tagttactct gttctcttg agggccacta gcgttccctc	180
tctggcctt atagtgtgct tggattacaa atgaggacaa gaggcttgc tgcttcagaa	240
tatattcccc atgtggcttc gggcaagtca gcctcttcc tgaactttac ttttctgtca	300
agtgggcatt tgggaggaat tagagctac attttttaggg ctgtatgtga gggcaagtgg	360
ggctctggca gtgagaatgc acttttagcaa atgattgagt tcccagaagt tgagaagaag	420
gagtggtaa tagtttagagt ttcttagttt ccctagtgtt gaatcttggaa g	471
<210> SEQ ID NO 386	
<211> LENGTH: 425	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 386	
cggcaaggc ggctttttc gcatgccag gggcagccgc caagggctcg gagctgtccg	60
agaggatcga gagtttctgt gaggcgctga agcgccggcgg cgccggccgc agctccgagg	120
acatggcccg ggagactctg ggactgcttc gccgcacat cacggaccac cgctggagca	180
atgcaggggaa gctgatggaa ctgatccgga gagaaggccg gaggatgacg gccgcgcac	240
cctcagagac cacagtgggc aacatggtcg ggagagtgct caggatcatc cggggaggagt	300
atggcagact ccatggacgc agcgcacgaga gcatgcacca ggagtctctg cacaaactct	360
tgacatccgg gggcctgagc gaggatttcc gttccattt tgctcaactc cagtcacaca	420
tcatt	425
<210> SEQ ID NO 387	
<211> LENGTH: 495	
<212> TYPE: DNA	
<213> ORGANISM: Bos Taurus	
<400> SEQUENCE: 387	
gttttcggcc gcagtgccca tggagctgaa tgcttcccg cctgccaccc tgaaaatggaa	60
ttcttgcgacg atgacagtgt gtgcagggtgc cagcctggctt ggcagggtcc cctgtgtac	120
cagtgegtga ctttcccg ctgtgtgaac ggcctctgcg tggagecatg gcagtgcac	180
tgcaaggacg gctgggacgg acacctctgt gacctagaca tccgggcttg cacctcgacc	240
ccctgcgcac acaacggcac ctgcctgaac ctgcgtacg ggcgtacga gtgcctgc	300
gccccgggt tctcaggaaa ggattgtcag gaaatggat ggcctctgcgt ggtgaatggc	360
tcgcctgccc agcacggagg cagctgcgtg gacgtgagg gccgggcccc ccacgcgtgc	420
tcgcctgtgcc cccctggctt ctgcggcaac ttctgcgaga tcgtgaccaa cagctgcac	480
cccaaccctgcgatc	495

-continued

<210> SEQ ID NO 388
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (309)..(311)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 388

agaagactca aaagagcgtg aagatcgac ctggagcagt tgtgtgtga gagagcgaaa	60
tcagagggtga tgtcactata ggaccaggaa cagtgtatcca ccctaaagca cgaatcatcg	120
cagaagccgg tccaatagtg atcggcgaag gcaacctaattt agaggagcag gcgctcatca	180
taaatgtca ccctgataat atcactcctg atgcagaaga tccagaaccc aaaccttatga	240
tcattggcac caataatgtg tttgaagttt gctgttactg ccaagccatg aaaataggag	300
ataataatnn natcgagtca aaagcgtatg tggcagaaaa tgtgataactg a	351

<210> SEQ ID NO 389
<211> LENGTH: 475
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 389

gccacagacc aaacctgcac cataaggccc gactccttgc ccataccacc cacccatggc	60
ctccgaacca ggcccagcgt cttgtgtaca tggtaacaca gtggaggacc agcagatgaa	120
tggaaacctt gaagcagagg agcggcagga ccagaggcca gagcaggagc tgacctggag	180
ctggggctac cggcctagaa gccccttggc cagggtcaag gccatggccc ccccaccc	240
actggcccccc acgcacccac tcctgtcatgg cgagtttgc tcctaccac accgcggccc	300
acgcttcgcc ctcactctca caccacaagc cctgcacata cagcggttgc gcccaaagcc	360
cgagggccgg ccccggggtg gcctggctt gctgaccgag gtctcaggct gctgcaccc	420
gcggagccga agccccctgg actcagcagc ctacttctgc gtctacaccc acccc	475

<210> SEQ ID NO 390
<211> LENGTH: 484
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 390

gagcgggtga gagggcagcg atatggctcc tccggctcct ggtccggctt ctggcggtc	60
cggggagggtg gacgagctgt tcgacgtaa gaacgccttc tacattggca gctaccagca	120
gtgcacatcaac gagggcgcagc gggtaagcc atccagccc gagagagatg tggagcggga	180
tgtcttcctg tacagagcat acctggccc gaggaagtac ggcgtggtc tggacgagat	240
caaggccctcc tccgcggcgg agctgcaggg cgtgcgcatg ttgcgtgagt acctggccag	300
cgacagccgg cggatgcga tcgtggccga gctggaccga gagatgagcc ggagcgtgga	360
tgtgaccaac accacccccc tgctcatggc tgcctccatc tatttctacg accagaaccc	420
agatgcagcc ctgcgcaccc ttcaccaggg ggacagcctg gactgcatgg ccatgacagt	480
gcag	484

<210> SEQ ID NO 391
<211> LENGTH: 559
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

-continued

<400> SEQUENCE: 391

aggggggccg	ccttccatcc	tgggggcagc	cccttggcgt	cccggcgcccc	tgacagatcc	60
gttccacccc	cagatggatg	gtctgttag	gtcaactgtcg	agctgtctca	gaattcagg	120
tccctcggtc	tgtccaagta	ctggcccggt	ggagccgatg	gccggggccct	cccggtggaa	180
ggatggcccg	gcagccctgt	cttccgacag	ccccctccct	ccaaagaaaa	atgtcagtct	240
ttctgctccg	tgtgtacta	tgcaagtcgt	cttgcagaaa	tcacggattt	cctgtggaat	300
aaaggtggtc	cccaaagtag	gcagaaagga	aatatatata	tatTTtagta	atttatata	360
atgtcagcaa	ttaggcaggt	caagctgtag	tttcatttcc	actgttaaaa	taaagcttac	420
atagttctt	taaaagcctg	tgttgtcctt	taacagaggt	tttttaaaca	ctagggtgtc	480
gaatgtgaaa	caccagttt	cattgttac	ctcgaaacca	aaagttgtgt	gttgccaaag	540
ccaaacccag	gttcacgga					559

<210> SEQ ID NO 392

<211> LENGTH: 509

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (421)..(422)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 392

aggcgtgcgt	ggtgactctg	gagaactcgg	aacaggctca	catcttctgg	tggaaagctg	60
ctaggaacac	gatgagtctg	cagtggactg	cagtcgcccc	cttcctctat	gcggaggct	120
tcgctgtgt	gtcgctctgc	atcccttca	tttctccca	aagatggcag	aagatttca	180
agtccccct	tgtggagttg	gtagtgcacat	atggcaacac	cttctttgtg	gttctcattg	240
tcatccttgc	gtactggtc	attgtatgt	ttcgtgagat	tgcggatgtat	gtatgtgtga	300
cagagaaggt	gaacctccag	aacaaccctg	gggctgttga	gcacttccac	atgaagcttt	360
tcgcgtgcacca	gaggAACCTC	tacattgtctg	gttttccctt	gtcgctgtcc	tttctgccta	420
nncgcctgg	gactctcate	tcccagcagg	ccacgctgtt	ggcctccaaac	gaagecttta	480
aaaagcaggc	agagagcgcc	agtgtatgc				509

<210> SEQ ID NO 393

<211> LENGTH: 489

<212> TYPE: DNA

<213> ORGANISM: Bos Taurus

<220> FEATURE:

<221> NAME/KEY: modified_base

<222> LOCATION: (49)..(49)

<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 393

gtcggtgtc	ttccagtgcc	tggggcacgg	cggggccct	gggagcagng	gtggagcatc	60
cccattgcgt	caaagatgaa	aggctgggt	tggctggccc	tgcttctggg	agccctcttgc	120
ggaactacct	ggggccggag	gagccaggat	ctacactgtg	gagcttgcag	ggctctggtg	180
gatgaacttg	agtggaaat	tgcggatgt	gtatccaaga	agaccattca	gtatggctct	240
ttccgaatca	atccagatgg	cagccagtca	gtgggtggagg	tgccttatgc	tcgctcagag	300
gcccacccca	cagagctgct	agaggaagta	tgcgaccgg	tgaaggagta	tggggacag	360
atcgaccctt	ccacgcacccg	caagaactat	gtacgtgtcg	tggggccaaa	tggagaatcc	420
agtgaactgg	acctacaggg	cattcgaatt	gattcagaca	tcagtgccac	cctcaagttc	480

-continued

gctgtgtgag	489
------------	-----

<210> SEQ ID NO 394
<211> LENGTH: 444
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<400> SEQUENCE: 394

ggatcgaggc	60
cccccgggc	120
ccgagggaaa	180
cagaaactga	240
cgccccggag	300
aggagccagg	360
acgcccgttgc	420
cttcaacctg	444

<210> SEQ ID NO 395
<211> LENGTH: 467
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (74)..(74)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (209)..(209)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<400> SEQUENCE: 395

gccccctgc	60
gccgctgccc	120
ccagggca	180
atgctcgagc	240
tggggccaaa	300
aagatggtgt	360
ctaaactgt	420
ctgctactgt	467

<210> SEQ ID NO 396
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<400> SEQUENCE: 396

agttggatgc	60
tccttggaga	120
gaaagctgac	180
tttgtgcata	240
tcccctctga	288

<210> SEQ ID NO 397

-continued

<211> LENGTH: 576
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (546)..(546)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 397

cgcgagcggc	tccagggtgc	gaaccggccgg	agcggttccc	agaagatggg	cctcgaagcg	60
caggccatcg	gcagcacctt	ccaggggctcg	ggctccgagg	ccacgtggct	gggccaggct	120
atccccgtgcg	tggctgacat	actggggcag	acttacaaaag	acgacatcgg	gcggcacctg	180
gagacgctca	tcagaagcta	ccccgacatc	aggcattgcg	gcatcggcat	cggggcccc	240
tgcgtgcctcc	ttcgggtcac	taggtttccg	gaacctctgc	ctgggcctca	gaggccgttc	300
ccatcaggct	tgcgtttcc	cgtctccgcc	ggtctttca	cccttcaaga	cccaggcacc	360
ccccccaggaa	cgtctgggtgc	cctaattgttt	ccagtccgag	ccccgggggtc	ccccctcgccc	420
tagggtccag	ggtgtcaactg	gagctgtcgc	gtctacagca	ggggcccggt	tgtctctgca	480
ggcgccgacca	cgtgcgtgc	atccctggcgc	tgctccgact	ggccgcgcgt	cggaaaccagc	540
atttntgctg	ccacgccccag	gccctgtca	gggctg			576

<210> SEQ ID NO 398
<211> LENGTH: 487
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 398

gttggagcgg	ccgcatttgt	ttttttttt	tttttttcc	tttttttacaa	aaacatgcat	60
acatacacag	ggtatagtct	tggggaaagac	acacgcactt	gcacgcacac	acactccctc	120
tctttcaactc	gcacacgcgt	gcatgcacgc	gcgcacacac	acatacacac	aaatacttcc	180
cttcttggcc	ccaggcctca	accccagaag	cctcgaagac	tgtgccaggg	tagctcccc	240
ctccccccatg	tctccatcc	actctccac	ccactctccc	ctcageccaag	ctagtccttat	300
gttagggcaag	agtcaagctgg	ggtccaggag	accccaaaaa	gagagaaggc	tcatggaggg	360
gggcacatgg	actgagggag	ccctgggggg	gtcatgctgt	gtttctgagg	agagatgaag	420
ggtttggcac	cattggatca	ggaagcacgg	aactccaaga	gcacctgtct	gctccaccag	480
ggcactg						487

<210> SEQ ID NO 399
<211> LENGTH: 209
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 399

tgcggagact	gctggggcac	atcgttcccc	tgtcctctcg	gttccctgcg	gccgaaaggc	60
ctgcttagat	tggggatct	ggccttaggt	tccggggcgc	cccgccccgg	cggaatggcc	120
gccccaaaga	aggacgaggt	ggaatgggt	gtggagagca	tgcgggggtt	cctgcggggc	180
ccggactgg	ccatccccat	cttggactt				209

<210> SEQ ID NO 400
<211> LENGTH: 361
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base

-continued

<222> LOCATION: (191)..(193)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<400> SEQUENCE: 400

gctggcctga	tgcagtcaat	cagecctcaact	ttccgcctgt	gttgctgaag	cctggtgagg	60
agtatgacca	caccacttgg	ttcaagttt	ctgtggccta	aggaaatgt	aagatatgtc	120
ctgctccaag	gtcaggctgg	gagccccttt	aacagcctga	ctctccata	aagagatgag	180
ttgaagattt	nnnggctttc	aaagtgtatcc	tgtgatttaa	aatcatacaa	atggtagcag	240
tcagggtagt	caggctcgaa	tattgatttc	cttcccuaag	actggctcca	ggccaggtct	300
aatgaccagc	tctccctct	gtgaagtgaa	ggggactcaa	ccaccaatgt	cacccatcat	360
c						361

<210> SEQ ID NO 401
<211> LENGTH: 442
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<400> SEQUENCE: 401

gacaccctac	tatccagtg	gaatggaaa	tggacaccc	ttagttgaa	acagaacccg	60
cccgatcaa	gtactgtat	gtacatatgt	catcctgaat	ctaagcatga	aattttca	120
gtagctgaag	ttacaactt	tgaatatgaa	gttgtcattt	tgacaccact	cttgcataat	180
catcctaaat	atagattcag	agcatctccc	gtgaatgaca	tatggcaca	gtcactacca	240
ggatcgccgt	ttaaacccct	caccctgaga	cagttggAAC	aacaggaaga	aatactaagg	300
gtgcctttt	ggagaaacaa	agaggaagat	ttgcaatcaa	ctaaggaaga	gagatttcca	360
gcaatccaca	acccttgc	tgttggttct	cagccaatgc	tcactgttgg	aacaaccac	420
atatccaaat	tgacagatga	cc				442

<210> SEQ ID NO 402
<211> LENGTH: 470
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (61)..(61)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (387)..(389)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<400> SEQUENCE: 402

gcaatatggc	aattttactg	ggggtttaac	cctacctagg	atgattgtt	gctggggctt	60
ngcaacaggg	tccagttcac	acttagca	aattaaatac	tttattgaat	aaatataata	120
ccaaacaaaa	tgcattcaaa	tgctaaaaaa	aaaatcaatt	ttaaaggcct	ttcttattcag	180
gtaatgaca	aacacaataa	aggcagat	gttagttaa	cataattggc	tgattttata	240
cagcacttat	atcttttagt	ccacaagat	attattaaat	gatagagaac	atctaatac	300
accatttcta	cagaactagg	aaataaattt	ctaagaaaga	aagattttac	agacccatc	360
tttatacc	accccaacag	tctaacnnna	aaggatataa	agccaatgcc	tttccctcaca	420
agagctcacg	actaatgtcg	cttgctatc	aaaatctgt	tttctgtatcc		470

<210> SEQ ID NO 403
<211> LENGTH: 412
<212> TYPE: DNA

-continued

```

<213> ORGANISM: Bos Taurus

<400> SEQUENCE: 403

ttttttttt tttttttact gtttaaaaca tttatattta tataatataaa aaaattaaat      60
atatataata tatagtgtgt ttgagactaa aaatatagtta cataatattt aaaaaaaagg      120
aaaatgaaaa aaggcagaat aggaaaagtg tgagggacac agatacacat tgctaaaaat      180
ctacgatggt ctgttcaac aaaataata ttttttcct cttattatc atcatggacc      240
catttattat tgggcttga gtggagaaaa tttaactgga gccagaaatg gtgggtgaa      300
tcccaagaag agtgggggta gaaaacgtga ccacaggag ccctggacct cattctggtg      360
tgactggagg cagccaaatc tcctggtca ctattgttag caagattgtg tc      412

<210> SEQ ID NO 404
<211> LENGTH: 492
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (132)..(132)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (196)..(196)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (256)..(256)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (286)..(286)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (327)..(327)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (367)..(367)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (369)..(369)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (378)..(378)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (391)..(391)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (400)..(400)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (407)..(407)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (412)..(413)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (416)..(417)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (420)..(420)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

```

-continued

<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (423) .. (426)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (447) .. (447)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (452) .. (452)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (460) .. (460)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (465) .. (465)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 404

acgacgccaa caacgccaag	60
gccgtggta agaccttcca	
cgagacgctt aactgcttg	
gttccaacac gctgatgaca	120
ctgaccacct ctgtgctcaa	
gaacagcctg tgtccctcca	
gcggcaacgt cntcaataat	180
ttgttcaagg aggactgcca	
tgggaagatc gacgagctct	
tctcgggaaa actgtncctc	240
attggcatcg cggccatcg	
ggtcgctgtg atcatgatct	
tcgagatgat cctgancatg	300
gtgctctgct gtggcattcg	
gaacanctcg gtgttctgaa	
gctgcccggc ctgaaggctc	360
caggaanggc ctcagggAAC	
cccgcagccc ccccgaatta	
tccaaanant tccaaaangg	420
gccccccac nttnnnnnn	
acccctnttt cnntgnnacn	
tttnnnnnnttt ttttttaaag	480
ttttttnttt cnnaaacccn	
tttatttcct ttgggggatt	
ccttgggggt cc	492

<210> SEQ ID NO 405
<211> LENGTH: 520
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (485) .. (485)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 405

gcacgagggt ttgatagctc	60
ctggagttcg tgtatcagga	
gatgatgtt ttataggcaa	
aacagtcaacc ttgcctgaaa	120
atagaagatga attggagggc	
actaatagac gctataacaa	
gagagactgt agcaactttc	180
tcaggactag tgagacgggc	
attgtggatc aggttatgg	
aactctcaac caagaaggat	240
ataaaatttg taaaataagg	
gtacgctctg tttagaatcc	
acagattgga gacaaatttg	300
ctagtcgaca tggtcaaaag	
ggtacttgtg gtattcaga	
tagacaggag gatatgcctt	360
tcacctgtga aggtatcacc	
cctgatataca tcataaatcc	
ccatgccatc ccctctcgta	420
tgaccattgg tcacttgatt	
gaatgtctc aagggaaagg	

-continued

atcagctaac aagggtgaaa ttggtgatgc cactccattc aatgatgctg ttaatgtgca	480
gaagntttct aatcttttat ctgattatgg ctaccatctc	520

```

<210> SEQ ID NO 406
<211> LENGTH: 455
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (119)..(120)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

```

<400> SEQUENCE: 406

gcacgagcgg cgacgccccag ctaccggatc gggtcgagat ggcagagggtg gaggagaccc	60
tgaagcgact ccagagccag aagggcgtgc aggaaatcat cgtggtaaac acagaaggnn	120
ttcccatcaa gagcaccatg gacaatccca ccaccacaca gtacgccaac ctcatgcaca	180
acttcatctt gaaggcccgg agcacccgtgc gcgaaattga cccccagaat gacctcaatt	240
tccttcgaat tcgctccaag aaaaatgaaa ttatggttgc accagataaa gactatttcc	300
tgattgtgat tcagaatcca actgaataag ctgctttctt ggctccctgc gtcattcctt	360
aatttaatgc ccctcaagaa taatagcgtt aatcatgtcc attgacgggc acgtggaagg	420
cacgttggag ccctccagg ctggtccgtg acccg	455

```

<210> SEQ ID NO 407
<211> LENGTH: 546
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (516)..(516)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

```

<400> SEQUENCE: 407

geacgaggag aagcagatga atatgagtcc acctccgggc aatgctggcc cagtgtatcat	60
gtccatttagag gagaagatgg aggctgatgc ccttccatc tatgttggca atgtggacta	120
tggtgcaaca gcagaagagc tagaagcaca ctttcatggc tgggttcag tcaaccgcgt	180
aactatactc tgtgacaaat ttatggcca tccgaaaggg ttgcgtata tagagttctc	240
agacaaagag tcagtgagga cttccctggc cttagatgaa tccttattta gaggaagaca	300
gatcaaggtg atccctaaac gaaccaacag accaggcatc agcacaacag accgaggctt	360
cccacgagcc cgataccgtg cccgaaccac caactacaac agttcccgct ctgcattcta	420
cagtgggttt aacagcaggc cccggggctcg cgtctacagg ggccgggcta gagcgacatc	480
atggtattcc ctttactaaa aaaaagtgtg tattangagg agagagagga aaaaaagagg	540
aaagaa	546

```

<210> SEQ ID NO 408
<211> LENGTH: 463
<212> TYPE: DNA
<213> ORGANISM: Bos Taurus
<220> FEATURE:

```

-continued

```
<221> NAME/KEY: modified_base
<222> LOCATION: (449)..(449)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 408

ttttaaattt taatttttt attggaaaaac aaatatacaa cttggaatgg atttgaggca 60
aatttgtgcc a taaggcagg ttctttaagt ggctaaaaca aagttaaaa agcaagttaa 120
caataaaaga aaatgtttt ggtataggac cagcagtaca aaaaaatagt gtacgagttac 180
ctggataaaa cacccgtttt gcaatagtgc aacttttaag tacatattgt tgactgtccg 240
tagtccacgc agagttacaa ctccacactt caacaacaac atgctgacag ttcctaaaga 300
aaactactca aaaaaaaaaa aaaaaggcat aacccagatg ttccctcatt tgaccactc 360
catctaagtt taaatgtgca gaagggttta aatatatcca gagtaagcca catgcaacat 420
gttaccttgat caatttctt aaataaggnt tcaggacaat gac 463
```

We claim:

1. A method of determining whether cattle are genetically elite for milk production, the method comprising:

 - i) determining a gene expression profile of cattle using as a plurality of genes SEQ ID NOS: 334, 279, 79, 156, 23, 353, 40, 73, 306, 120, 107, 149, 119, 179, 288, 32, 95, 221, 211, 152, 312, 244, 36, 105, 253 and 164;
 - ii) comparing the gene expression profile of the cattle with a Gene Expression Index constructed by
 - (a) selecting cattle with at least two specific levels of milk production;
 - (b) selecting a plurality of genes for which expression can be determined;
 - (c) comparing expression levels of the plurality of genes in cattle at each of the two levels of milk production; and
 - (d) determining a set of genes predictive of high milk production or with a Reference Expression Profile constructed by
 - (a) selecting an optimal subset of genes from the Gene Expression Index that accounts for a significant fraction of the variation in milk production;
 - (b) determining a gene expression profile of the cattle for the optimal subset; and
 - (c) designating the gene expression profile as a Reference Expression profile for high milk production; and
 - (iii) designating the cattle as elite for milk production if their gene expression profile is similar to the Gene Expression Index or the Reference Expression Profile.

2. A method for selecting male or female cattle as genetically elite for milk production, the method comprising:

 - i) constructing a Gene Expression Index comprising gene expression values for a plurality of gene sequences set forth in SEQ ID NOS: 334, 279, 79, 156, 23, 353, 40, 73, 306, 120, 107, 149, 119, 179, 288, 32, 95, 221, 211, 152, 312, 244, 36, 105, 253 and 164, wherein the Gene Expression Index is obtained from cattle having high milk production;
 - ii) determining a gene expression profile for the cattle to be tested, wherein the gene expression profile comprises gene expression values for the gene sequences set forth in SEQ ID NOS: 334, 279, 79, 156, 23, 353, 40, 73, 306, 120, 107, 149, 119, 179, 288, 32, 95, 221, 211, 152, 312, 244, 36, 105, 253 and 164; and

- iii) designating the male or female cattle as genetically elite for milk production if their gene expression profiles and the gene expression values in the Gene Expression Index are similar.

3. A method for selecting male or female cattle as genetically elite for milk production, the method comprising:

- i) creating a Reference Expression Profile comprising gene expression values for a plurality of genes set forth in SEQ ID NOS: 334, 279, 79, 156, 23, 353, 40, 73, 306, 120, 107, 149, 119, 179, 288, 32, 95, 221, 211, 152, 312, 244, 36, 105, 253 and 164, wherein the Reference Expression Profile is predictive of cattle having high milk production;

- ii) determining a gene expression profile for the cattle to be tested, wherein the gene expression profile comprises gene expression values for the genes set forth in SEQ ID NOS: 334, 279, 79, 156, 23, 353, 40, 73, 306, 120, 107, 149, 119, 179, 288, 32, 95, 221, 211, 152, 312, 244, 36, 105, 253 and 164; and

- iii) designating the male or female cattle as genetically elite for milk production if their gene expression profiles and the gene expression values in the Reference Expression Profile are similar.

4. The method of claim 2, wherein the gene expression profile is obtained by a microarray analysis.

- 5.** The method of claim **2**, wherein the gene expression profile is obtained by a quantitative polymerase chain reaction analysis.

6. A method for predicting milk production in a candidate cow, the method comprising:
i) obtaining a candidate gene expression profile of a cow

- 1) obtaining a candidate gene expression profile of a candidate cow for a plurality of genes set forth in SEQ ID NOS: 334, 279, 79, 156, 23, 353, 40, 73, 306, 120, 107, 149, 119, 179, 288, 32, 95, 221, 211, 152, 312, 244, 36, 105, 253 and 164;

- ii) comparing the candidate gene expression profile to a Gene Expression Index from cows with known milk production levels; and

- iii) predicting milk production in the candidate cow if the gene expression profile of the candidate cow and the Gene Expression Index are similar.

483

7. A method for predicting milk production in the daughters of a candidate bull, the method comprising:

- i) obtaining a candidate gene expression profile of the candidate bull for a plurality of genes set forth in SEQ ID NOS: 334, 279, 79, 156, 23, 353, 40, 73, 306, 120, 107, 149, 119, 179, 288, 32, 95, 221, 211, 152, 312, 244, 36, 105, 253 and 164;

5

484

- ii) comparing the candidate gene expression profile to a Gene Expression Index from bulls whose daughters have known milk production levels; and
iii) predicting milk production in the daughters of the candidate bull if the gene expression profile of the bull and the Gene Expression Index are similar.

* * * * *