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(54) **COMPOSITIONS AND METHODS FOR DETERMINING LIKELIHOOD OF AN INCREASED SUSCEPTIBILITY TO CONTRACTING JOHNE'S DISEASE**

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C12P 19/34	(2006.01)
C12Q 1/6883	(2018.01)

(52) **U.S. Cl.**

CPC ***C12Q 1/6883*** (2013.01); *C12Q 2600/118* (2013.01); *C12Q 2600/124* (2013.01); *C12Q 2600/156* (2013.01)

(58) **Field of Classification Search**

CPC C12Q 1/6827; C12Q 1/68; C12Q 1/6816; C12P 19/34

See application file for complete search history.

(56) **References Cited**

PUBLICATIONS

Settles M. et al. "A whole genome association analysis identifies loci associated with *Mycobacterium avium* subsp. paratuberculosis infection status in US holstein cattle" Anim Genet. Oct. 2009;40(5):655-62. Electronic publication Apr. 24, 2009. (Year: 2009).*

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(57) **ABSTRACT**

Collections of polynucleotides useful for estimating breeding value or detecting likelihood of an increased susceptibility to contracting paratuberculosis are disclosed. The polynucleotides are used to detect genomic sequences quantitatively associated with an increased susceptibility to contracting paratuberculosis. Methods for using the collections to estimate breeding value or predict likelihood of an increased susceptibility to contracting paratuberculosis are also provided. Kits comprising the collection of polynucleotides are also provided.

9 Claims, 3 Drawing Sheets

Specification includes a Sequence Listing.

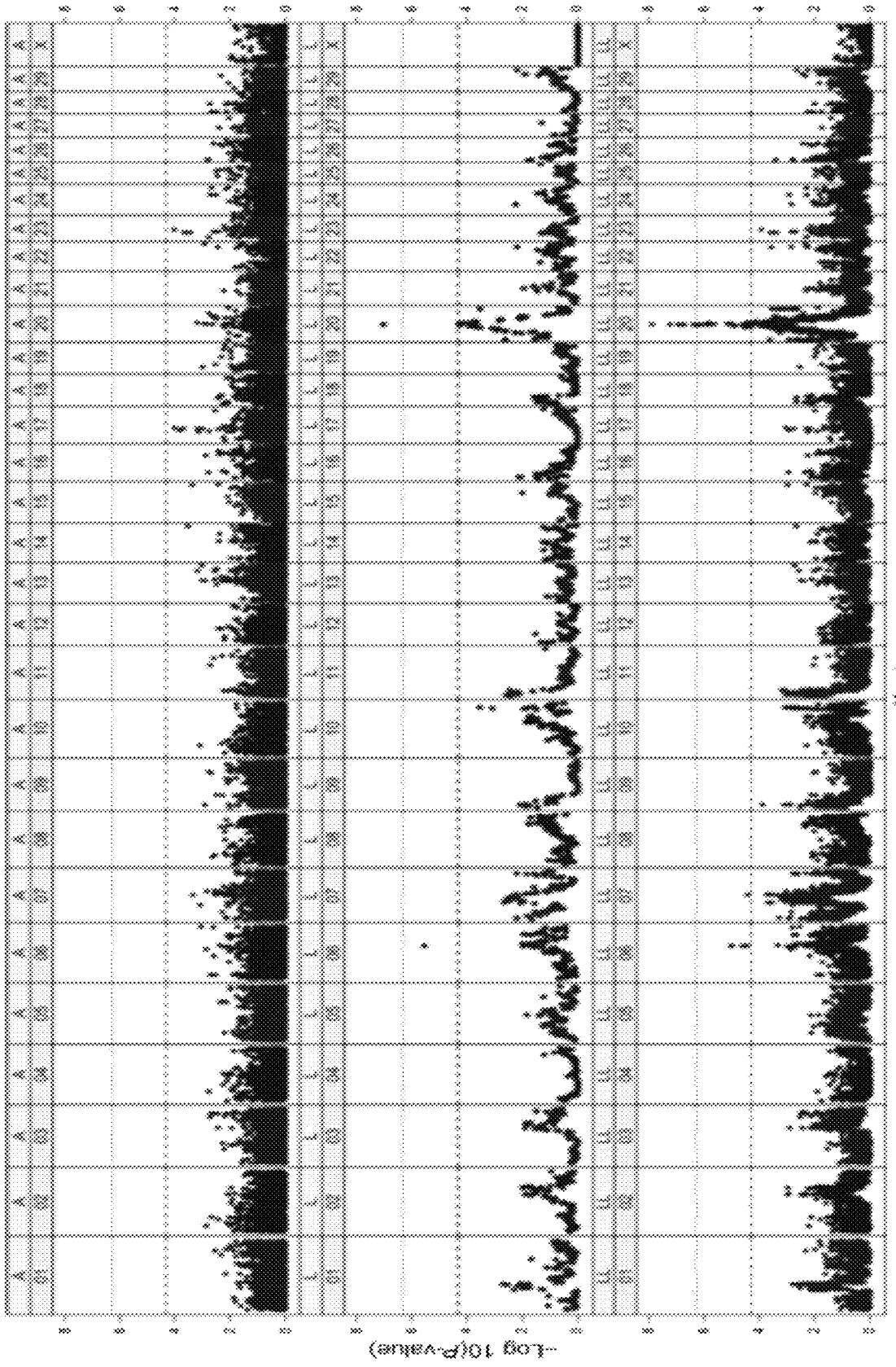

Figure 1

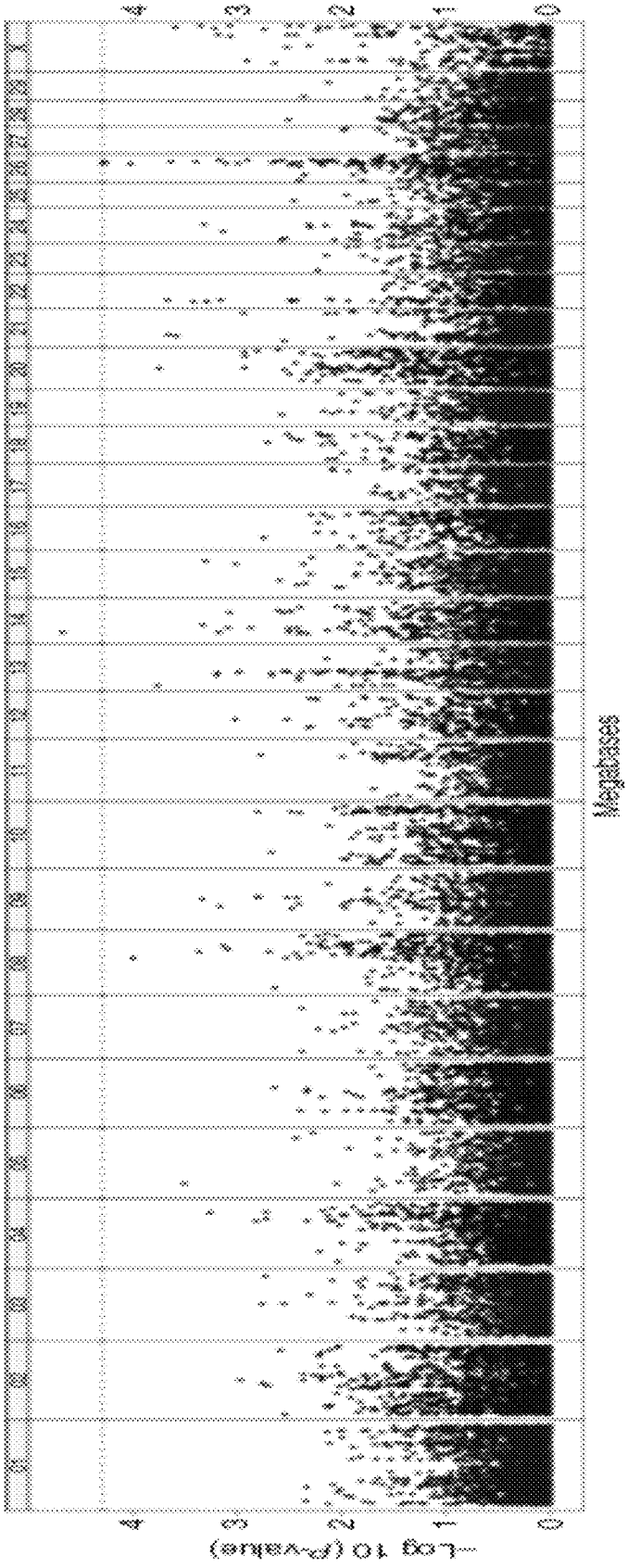
4
3
2
1
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
X
Y
Megabases
−Log 10 (P-value)

Figure 2

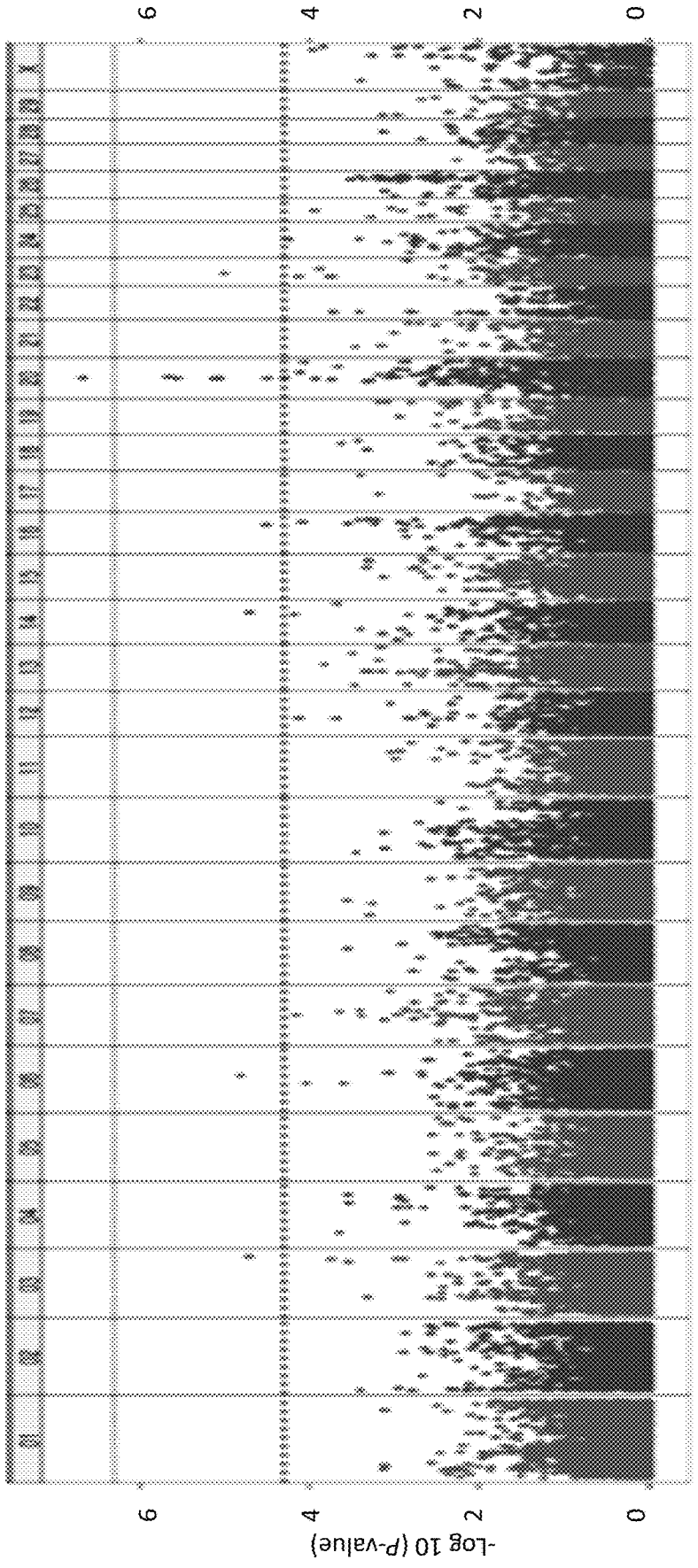

Figure 3

COMPOSITIONS AND METHODS FOR DETERMINING LIKELIHOOD OF AN INCREASED SUSCEPTIBILITY TO CONTRACTING JOHNE'S DISEASE

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation of U.S. patent application Ser. No. 12/861,482, filed Aug. 23, 2010, which is incorporated by reference herein.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

This invention was made with government support under 2007-35205-17884, 00-52100-9621 and 01-CRHF-0-6055 awarded by the USDA/CSREES. The government has certain rights in the invention.

FIELD OF THE INVENTION

This related generally to animal genetics and improvements in cattle breeding. More particularly, it relates to compositions and methods for predicting an increased susceptibility to contracting paratuberculosis in cattle.

BACKGROUND

Paratuberculosis, commonly called Johne's disease, is a chronic infection of the small intestine caused by *Mycobacterium avium*, ssp. *paratuberculosis* ("MAP"). Paratuberculosis occurs in a wide variety of animals, but most often in ruminants, especially cattle. The disease presents with symptoms including diarrhea, severe weight loss and decres=ased milk production. Cattle normally become infected with MAP as calves, but because of the slowly progressive nature of the infection, clinical signs of paratuberculosis are usually not seen until animals are adults. There is no cure for the disease and infected animals ultimately become emaciated and must be removed from the herd much sooner than their non-infected counterparts.

Since the signs of paratuberculosis can be confused with the signs of several other diseases, a diagnosis can be confirmed only by use of laboratory tests. The best way to avoid paratuberculosis is to be as certain as possible that animals brought into the herd are not infected with MAP. There are currently three common ways to test animals for paratuberculosis: culture of fecal samples, DNA probe on fecal samples, and blood tests for antibodies to MAP. The fecal culture tests take 8 to 16 weeks because of the extremely slow growth rate of MAP. MAP bacteria can also be detected in fecal samples by use of sophisticated DNA probe tests. DNA probes are much faster than culturing the organism and can be done within three days. Unfortunately, the commercial kit for doing the DNA probe tests are not yet as sensitive as culture and are only able to detect infected animals when their infection has progressed to the stage where large numbers of MAP are being excreted in the feces. Therefore, animals in early stages of the infection are not detected. There are several blood tests for paratuberculosis, but ELISA tests are considered the most accurate and best standardized. Three ELISA-based tests are licensed by the U.S. Department of Agriculture for detection of MAP-infected cattle. The ELISA tests are fast, simple, inexpensive and able to detect animals that are infected before they show signs of paratuberculosis.

However, all of these test results come too late. The animal is already infected. In addition, tests performed on individual animals are not 100% sensitive, meaning they cannot detect 100% of all infected animals. Instead, the tests are performed on a group of animals to extrapolate that if an entire group tests negative, then the probability the group is free of MAP infection is very high.

Methods for paratuberculosis control depend on the type of animal and the patterns of husbandry. In principle, two strategies must be employed at the same time:

1. newborn animals must be protected from infection by being born and raised in a clean environment and fed milk free of MAP; and
2. adult animals carrying the MAP infection must be identified by laboratory tests and removed from the herd, flock or enclosure.

A national study of US dairies, Dairy NAHMS 96, found that approximately 22% of US dairy farms have at least 10% of the herd infected with paratuberculosis. The study determined that infected herds experience an average loss of $40 per cow in herds with a low paratuberculosis clinical cull rate, while herds with a high paratuberculosis clinical cull rate lost on average of $227 per cow. This loss was due to reduced milk production, early culling, and poor conditioning at culling. The cost of paratuberculosis in beef herds still needs to be determined.

Therefore, there remains a need for methods of predicting animals that have an increased susceptibility of contracting paratuberculosis and selectively breed away from that increased susceptibility. Paratuberculosis is a good candidate for genetic selection because a) an effective vaccine is not available, b) the disease is not curable, c) it causes significant economic losses, and d) it is potentially zoonotic. Selective breeding to reduce disease susceptibility would be a low cost, sustainable practice.

Previous reports of association of DNA markers with paratuberculosis susceptibility have been limited, and frequently focused on candidate genes. The nucleotide-binding oligomerization domain containing 2 gene (NOD2), previously referred to as the caspase recruitment domain 15 protein gene (CARD15), is a well characterized gene that contributes to predisposition to Crohn's disease in humans (see recent reviews by Hugot (2006) and Radford-Smith and Pandeya (2006)) and has been the subject of study in cattle as a candidate gene. Taylor et al. (2006) identified 36 NOD2 polymorphisms in a screening of 42 animals from ten different breeds. Association of these polymorphisms with infection could not be adequately tested owing to a paucity of infected animals (n=11). Subsequently, Pinedo et al. (2009a) tested association of three of the NOD2 polymorphisms identified by Taylor et al. (2006) in a case-control study using cattle of dairy (Holstein, Jersey) and beef (Brahman×Angus) types. An association significant at a nominal $P<0.01$, after controlling for breed, was found for a non-synonymous SNP in the leucine-rich repeat domain of the gene. Evidence for this association came principally from the Brahman×Angus subset of the data. The same data was subsequently re-analyzed considering effects of predicted SNP haplotypes. A haplotype based on two non-synonymous NOD2 SNPs was found significantly associated with infection status (nominal $P<0.0001$) in an analysis that did not account for breed. The effect attributable to this risk haplotype was due to greater incidence of infection in animals heterozygous for the haplotype (i.e. overdominance). This is in contrast to the effects associated with NOD2 alleles associated with susceptibility to Crohn's disease in humans where the affects manifest in a partial

recessive fashion with genotype relative risk increasing exponentially between risk allele heterozygotes to homozygotes or compound heterozygotes (Economou et al. 2004). Analysis of the NOD2 locus in US Holstein cattle in the author's laboratory (unpublished) revealed additional polymorphisms, but none of nine previously or newly identified SNPs genotyped were significantly associated with infection status in a case-control study using 169 case (positive to either ELISA or fecal culture tests or both) and 188 control cows. In addition, only weak evidence of SNP association with infection status was observed for bovine chromosome 18 (location of NOD2) in whole-genome association analyses reported herein. Pinedo et al. (2009a) point out that the NOD2 allele showing association is more frequent in the Brahman×Angus cattle than in the Holstein cattle they utilized which could account for the lack of association observed in the current work with Holsteins.

Only two whole genome scans for paratuberculosis susceptibility have been previously reported. Our earlier study of three large sire families (264 to 585 daughters per sire) from Population 1 examined 159 informative microsatellite markers across all 29 autosomal chromosomes. One significant (chromosome-wide P-value=0.032) region on chromosome 20 was found, but the wide spacing of the markers made it impossible to more narrowly localize the region (Gonda et al., 2007). Power of this study was lessened by low marker density and the consideration only of linkage effects. The other previously reported whole genome scan utilized the recently available bovine 50 k SNP set to greatly improve marker density. Settles et al. (2009) used 218 Holstein cows in a case-control design to assess marker association with MAP infection under various definitions of infected phenotype. Phenotypes were assigned based on culture of MAP from fecal and tissue samples (ileum, ileo-cecal valve and ileo-cecal lymph nodes). 112 animals were negative to both tests, with the remainder positive to one or both fecal or tissue culture. Composition of case and control groups varied depending on definition of phenotype (fecal-positive vs. fecal-negative, tissue-positive vs. tissue-negative, etc.) leading in some instances to a small number of case samples (range 25-90). Suggestive associations ($p<5\times10^{-5}$) were found under various phenotypic definitions on chromosomes 1, 3, 5, 7, 8, 9, 16, 21 and 23. Correspondence between the results reported here and results reported by Settles et al. (2009) are slight, and none are the specific SNPs that Settles et al. found most significant.

Crohn's disease in humans bears some similarity to Johne's disease in cattle in its manifestation, and as a consequence, genes implicated in the development of Crohn's disease have been considered as candidate genes in the study of Johne's disease. Whole genome association (WGA) studies of Crohn's disease in humans (Barrett et al. 2008; Raelson et al. 2007; Welcome Trust Case Control Consortium 2007; Parkes et al. 2007; Rioux et al. 2007; Libioulle et al. 2007) have been more numerous and of larger scale than the study reported herein. Validated results from human Crohn's disease WGA studies, compilation viewable at www.genome.gov/26525384 (Hindorff et al. 2009), have now implicated more than 30 unique chromosomal regions in humans. The correspondence between results reported here or by Settles et al. (2009) for cattle and the results from humans is limited. Applying an arbitrary and liberal constraint of significant human and bovine markers being within a distance of 4 Mb, only the associations reported by Settles et al. (2009) on proximal BTA9 show correspondence with human WGA results and only associations on BTA7 and 20 reported herein show correspondence. Prostaglandin E receptor 4 (PTGER4) and the immunity-related GTPase family, M gene (IRGM), have been identified as candidate genes for the regions corresponding to BTA7 and 20, respectively in human studies. Regarding PTGER4, Libioulle et al. (2007) identified and validated SNP associations in a 1.25 Mb gene desert on HSA5 adjacent to PTGER4 and found SNP associations with variation in PTGER4 expression. Prior work has found that PTGER4 knock-out mice develop severe colitis upon treatment with dextran sodium sulphate, unlike knock-outs for other prostaglandin receptors (Kabashima et al. 2002) supporting its consideration as a candidate gene. Regarding IRGM, The most significant SNP on BTA7 is located within 2 Mb of the location of IRGM, a candidate gene for Crohn's disease in humans based on results from three whole genome association studies (Barrett et al. 2008, Welcome Trust Case Control Consortium 2007, Parkes et al. 2007) and subsequent studies. The SNPs significantly associated with Crohn's disease in this case flanked the IRGM gene, and subsequent analyses failed to reveal non-synonymous SNPs with the IRGM coding regions leading to speculation that functional polymorphism might alter regulation of IRGM. Subsequent work by McCarroll et al. (2008) identified a 20 kb insertion—deletion polymorphism upstream of IRGM that correlated with differences in IRGM expression, and the authors have speculated that this difference in IRGM expression may related to differences in autophagy.

SUMMARY OF THE INVENTION

This disclosure relates generally to identification and the use of a collection of polynucleotide sequences, or polynucleotides, for detecting (by any means known in the art) an at least partially complementary sequence in a cow genome relating to paratuberculosis.

The presence or absence of the at least partially complementary sequences, i.e. the sequences in the cow genome, is quantitatively associated with the trait of an increased susceptibility to contracting paratuberculosis in a cattle population. In various embodiments, the collection comprises at least one sequence that is quantitatively associated with an increased susceptibility to contracting paratuberculosis with statistical significance of at least $p\leq0.01$. Preferred are those collections comprising at least one sequence that is quantitatively associated with an increased susceptibility to contracting paratuberculosis with statistical significance of at least $p\leq0.001$, or even less.

Also provided herein are methods of using the collections for predicting or estimating the likelihood of an increased susceptibility to contracting paratuberculosis. The methods generally comprise the steps of:

a) providing a collection of one or more polynucleotides, each of which is at least partially complementary to a sequence in a cow genome, comprising at least one sequence that is quantitatively associated with an increased susceptibility to contracting paratuberculosis with statistical significance of at least $p\leq0.01$;

b) using the collection to determine the presence or absence of sequences complementary to one or more polynucleotides from the collection in one or more members of the cattle population genome, wherein the presence or absence of the complementary sequences is quantitatively associated with the trait of an increased susceptibility to contracting paratuberculosis in a cattle population; and

c) estimating the likelihood of an increased susceptibility to contracting paratuberculosis based on the results of step b).

Kits providing the collections and instructions for using them in predicting the likelihood of an increased susceptibility to contracting paratuberculosis are also provided.

Other and further objects, features, and advantages of the present invention will be readily apparent to those skilled in the art.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1**: Results of whole genome scan of Population 1 for genetic marker association with susceptibility to infection of cattle by MAP. Vertical panels denote individual chromosomes as indicated at the top of each panel. Each point represents the −log 10 of the P-value (y-axis) from linkage disequilibrium (top; "A"), linkage (center; "L") and combined linkage-linkage disequilibrium (bottom; "LL") analyses, relative to genomic location of the SNP marker (x-axis). A total of 35,772 polymorphic SNP markers were included in the analysis. The dashed and dotted lines represent p-values of 5×10^{-5} and 1×10^{-7}, respectively, corresponding to suggestive and significant results.

FIG. **2**: Results of whole genome scan of Population 2 for genetic marker association with susceptibility to infection of cattle by MAP. Vertical panels denote individual chromosomes as indicated at the top of each panel. Each point represents the −log 10 of the P-value (y-axis) from tests of difference in allelic (top; "A") and genotypic (bottom; "G":) frequencies for case (cows ELISA-positive for MAP infection) and control (Holstein artificial insemination sires, as described in the text). Minus Log_{10} (P-value) is plotted relative to genomic location of the SNP marker (x-axis). A total of 35, 772 polymorphic SNP markers were included in the analysis. The dashed and dotted lines represent p-values of 5×10^{-5} and 1×10^{-7}, respectively, corresponding to suggestive and significant results.

FIG. **3**: Results of whole genome scan for genetic marker association with susceptibility to infection of cattle by MAP combining information across populations. Vertical panels denote individual chromosomes as indicated at the top of each panel. Each point represents the −log 10 of the P-value (y-axis) from a linkage disequilibrium analysis (allelic association: top panel, "AS") or a combined linkage-linkage disequilibrium analysis (bottom panel, "LL"), relative to genomic location of the SNP marker (x-axis). A total of 35,772 polymorphic SNP markers were included in the analysis.

DETAILED DESCRIPTION

The present application incorporates by reference SEQ ID NO: 1-197 provided herewith on a the files titled All_SNP_081810.txt and Preferred_SNP_081810.txt, created on Aug. 18, 2010.

Definitions

the following abbreviations may be used herein:

cM, centiMorgan;

CWER, comparison-wise error rates;

FDS, false discovery rate;

HWE, Hardy-Weinberg equilibrium;

IBD, identity by descent;

Kb, kilobase;

LD, linkage disequilibrium;

LLD, linkage-linkage disequilibrium;

LRT, log-likelihood ratio;

MAF, minor allele frequency;

MB, megabase;

NCBI, National Center for Biotechnology Information;

PEV, prediction error variance;

PTA, predicted transmitting ability;

QTL, quantitative trail loci;

SNP; single nucleotide polymorphism;

The term "individual" when referring to an animal means an individual animal of any species or kind.

The term "animal" is used in a general sense and means a human or other animal, including avian, bovine, canine, equine, feline, hicrine, lupine, murine, ovine, and porcine animals. Preferably the animal is a mammal, particularly a bovine. Unless otherwise specified, or clear from the context, the term "mammal" herein includes human.

As used herein, "linkage disequilibrium" (or "LD") refers to allelic association between specific alleles at two or more neighboring loci in the genome, e.g., within a population. LD can be determined for a single marker or locus, or multiple markers. LD is sometimes expressed herein as r^2 values where $r^2=1/(4N_ec+1)$ where c=recombination rate (M), and Ne=effective population size. (Sved, 1971)

As used herein, "allele" refers to one or more alternative forms of a particular sequence that contains an SNP. The sequence may or may not be within a gene, and may be within a coding or noncoding portion and such a gene, and may be within an exon or an intron of a particular gene.

"Quantitative trait locus," (or "QTL"), as used herein is a genomic sequence that is associated with a particular phenotypic trait. Multiple QTL may be identified for a particular trait, and they are frequently found on different chromosomes. The number of QTLs that associate significantly with a particular phenotypic trait may provide an indication of the genetic architecture of a trait, the number of genes that affect the trait, or the extent of the affect of one or more of those genes. One or more QTL that significantly associates with a trait may be candidate genes underlying that trait, which can be sequenced and identified. The significance of the degree of association of a given QTL with a particular trait can be assessed statistically, e.g. through QTL mapping of the alleles that occur in a locus and the phenotypes that they produce. Statistical analysis is preferred to demonstrate whether an observed association with a trait is significant. The presence of a QTL, and its location identify a particular region of the genome as potentially containing a gene that is associated, directly (e.g., structurally) or indirectly (e.g., regulatory) with the trait being analyzed. The probability of association can be plotted for various markers associated with the trait spaced across a chromosome, or throughout the genome.

A "polynucleotide" includes single-stranded or a multi-stranded nucleic acid molecules comprising two or more sequential bases, including any single strand or parallel and anti-parallel strands of a multi-stranded nucleic acid. Polynucleotide may be of any length, and thus, include very large nucleic acids, as well as short ones, such as oligonucleotides.

The term "oligonucleotide" typically refers to short polynucleotides, generally no greater than about 50 nucleotides. It will be understood that if a nucleotide sequence is denoted represented by a DNA sequence (i.e., A, T, G, C), the corresponding RNA sequence (i.e., A, U, G, C, wherein "U" replaces "T") is also included.

As used throughout, ranges herein are stated in shorthand, so as to avoid having to set out at length and describe each and every value within the range. Any appropriate value within the range can be selected, where appropriate, as the upper value, lower value, or the terminus of the range. For

example, a range of 0.1-1.0 represents the terminal values or 0.1 and 1.0, as well as the intermediate values of 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, and all intermediate ranges encompassed within 0.1-1.0, such as 0.2-0.5, 0.2-0.8, 0.7-1.0, and so on.

As used herein and in the appended claims, the singular form of a word includes the plural, and vice versa, unless the context clearly dictates otherwise. Thus, the references "a", "an", and "the" are generally inclusive of the plurals of the respective terms. For example, reference to "a SNP", "a method", or "a trait" includes a plurality of such "SNPs", "methods", or "traits." Reference herein, for example to "an association" includes a plurality of such associations, whereas reference to "chromosomes" includes a single chromosome where such' interpretation is not precluded from the context. Similarly, the words "comprise", "comprises", and "comprising" are to be interpreted inclusively rather than exclusively. Likewise the terms "include", "including" and "or" should all be construed to be inclusive, unless such a construction is clearly prohibited from the context. Where used herein the term "examples," particularly when followed by a listing of terms is merely exemplary and illustrative, and should not be deemed to be exclusive or comprehensive.

The methods and compositions and other advances disclosed here are not limited to particular methodology, protocols, and reagents described herein because, as the skilled artisan will appreciate, they may vary. Further, the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to, and does not, limit the scope of that which is disclosed or claimed.

Unless defined otherwise, all technical and scientific terms, terms of art, and acronyms used herein have the meanings commonly understood by one of ordinary skill in the art in the field(s) of the invention, or in the field(s) where the term is used. Although any compositions, methods, articles of manufacture, or other means or materials similar or equivalent to those described herein can be used in the practice of the present invention, the preferred compositions, methods, articles of manufacture, or other means or materials are described herein.

All patents, patent applications, publications, technical and/or scholarly articles, and other references cited or referred to herein are in their entirety incorporated herein by reference to the extent allowed by law. The discussion of those references is intended merely to summarize the assertions made therein. No admission is made that any such patents, patent applications, publications or references, or any portion thereof, are relevant, material, or prior art. The right to challenge the accuracy and pertinence of any assertion of such patents, patent applications, publications, and other references as relevant, material, or prior art is specifically reserved. Full citations for publications not cited fully within the specification are set forth at the end of the specification.

Details

In a first of its several aspects, this disclosure relates to a collection of polynucleotide sequences, or polynucleotides, each of which is at least partially complementary to a sequence in a cow genome. The presence or absence of the at least partially complementary sequences, i.e. the sequences in the cow genome, is quantitatively associated with the trait of an increased susceptibility to contracting paratuberculosis in a cattle population. In various embodiments, the collection comprises at least one sequence that is quantitatively associated with an increased susceptibility to contracting paratuberculosis with statistical significance of at least $p \leq 0.01$. Preferred are those collections comprising at least one sequence that is quantitatively associated with an increased susceptibility to contracting paratuberculosis with statistical significance of at least $p \leq 0.001$, or even less. In various embodiments, the statistical significance of the quantitative association with an increased susceptibility to contracting paratuberculosis is $p \leq 0.001$, $p \leq 0.0009$, $p \leq 0.0008$, $p \leq 0.0007$, $p \leq 0.0006$, $p \leq 0.0005$, or even less. Most preferred are embodiments that have statistical significance of $p \leq 10\text{-}4$, 10-5, or even 10-6, or lower. Thus, the more highly significant (i.e., the lower the p value) the association is, the more useful the polynucleotide collection can be for predicting an increased susceptibility to contracting paratuberculosis. In certain embodiments, polynucleotides useful for indicating the presence or absence of genomic sequences whose association with an increased susceptibility to contracting paratuberculosis is, from a statistical view, only suggestive, may be useful herein. More preferred are those polynucleotides useful for indicating the presence or absence of genomic sequences whose association with an increased susceptibility to contracting paratuberculosis is highly suggestive, significant, or even highly significant. The skilled artisan will understand that the statistical significance levels deemed suggestive, highly suggestive, significant, or highly significant will vary based on the particular statistical measures used, and the underlying data used to generate the measures of association. Examples of such statistical measures are shown in the working examples.

The collection of polynucleotides is useful for predicting an increased susceptibility to contracting paratuberculosis rate or likelihood of an increased susceptibility to contracting paratuberculosis within an individual member of a population, or within a herd, and is also useful for other purposes, such as estimating breeding value in cattle, whether for genetic purposes (e.g. breed improvement, herd management, and the like), or for economic considerations (e.g., determining or estimating sale or replacement value of an animal or reproductive material from an animal, predicting the value of offspring, estimating gain or loss for milk or meat production (e.g., practical cost or impact of an increased susceptibility to contracting paratuberculosis for farmer) or the like), or a combination thereof.

The polynucleotides in the collection can be any sequences, for example, they could encompass a portion of structural genes, regulatory genes, or other sequences, e.g., SNPs, microsatellite sequences, or other sequences of any length found in a genome. The polynucleotides of the collections may correspond to either strand of a nucleic acid heteroduplex. In some embodiments, the polynucleotides are completely complementary to a portion of a genome, while in others they may be less than completely complementary, provided that they are useful for detecting at least a partially complementary sequence in the genome. For example, in various applications the polynucleotides may be used as primers for amplifying specific sequences to be detected, which may not require 100% complementarity. In other embodiments, the polynucleotide may be used as probes for binding to various sequences to be detected. In one presently preferred embodiment, each polynucleotide is useful for detecting the presence or absence of one allele of an SNP in the cow genome. In other embodiments, each polynucleotide comprises one allele of an SNP in the cow genome, or its complement.

The collection can comprise sequences distributed throughout the genome. In one embodiment of the collection, at least one of the polynucleotides is complementary to

a sequence located on any bovine chromosome. In one embodiment, the preferred chromosomes include one or more of chromosomes 2, 3, 4, 5, 6, 7, 9, 10, 13, 14, 15, 16, 17, 18, 20, 21, 22, 23, 25, 26 and 29.

In another, bovine chromosome 13 (BTA13) is preferred. Especially preferred are particular regions of chromosome 13, including those that are near or encode certain genes. In another embodiment, at least one of the polynucleotides is complementary to a sequence that maps between 4-71 Mb of BTA7. In various embodiments, the collection comprises one or more polynucleotides complementary to a sequence that maps at either of 4-6 Mb, 31-34 Mb or 70-72 Mb of BTA7.

In another, bovine chromosome 16 (BTA16) is preferred. Especially preferred are particular regions of chromosome 16, including those that are near or encode certain genes. In another embodiment, at least one of the polynucleotides is complementary to a sequence that maps between 21-70 Mb of BTA16. In various embodiments, the collection comprises one or more polynucleotides complementary to a sequence that maps at either of 21-23 Mb or 60-70 Mb of BTA7.

In another, bovine chromosome 20 (BTA20) is preferred. In one embodiment, at least one of the polynucleotides is complementary to a sequence that maps between 31-67 Mb of BTA20. Especially preferred are particular regions of chromosome 20, including those that are near or encode certain genes. In various embodiments, the collection comprises one or more polynucleotides complementary to a sequence that maps on BTA20 at either of 31-35 Mb or 65-68 Mb of BTA20. In a currently preferred embodiment, at least one of the polynucleotides is complementary to a sequence that maps between 31-35 Mb of BTA20.

In another, bovine chromosome 21 (BTA21) is preferred. Especially preferred are particular regions of chromosome 21, including those that are near or encode certain genes. In another embodiment, at least one of the polynucleotides is complementary to a sequence that maps between 19-68 Mb of BTA7. In various embodiments, the collection comprises one or more polynucleotides complementary to a sequence that maps at either of 19-25 Mb or 61-69 Mb of BTA7.

In another, bovine chromosome 26 (BTA26) is preferred. In one embodiment, at least one of the polynucleotides is complementary to a sequence that maps between 34-40 Mb of BTA26. Also useful are polynucleotides that can identify the presence or absence of sequences which map to various overlapping or more specific locations, as set forth in the Examples below.

In one presently preferred embodiment, the collection comprise at least one polynucleotide complementary to a sequence located with high LD to a genomic sequence for Prostaglandin E receptor 4 ("PTGER4"). In another presently preferred embodiment, the collection comprises at least one polynucleotide complementary to a sequence located with high LD to a genomic sequence for immunity-related GTPase family, M gene ("IRGM"). Certain preferred collections of polynucleotides feature one or more sequences that can be used to identify the presence or absence of, for example, SNPs within PTGER4 or IRGM. PTGER4 and IRGM each has been identified herein as a positional candidate that is significantly associated with an increased susceptibility to contracting Crohn's disease. However, of the more than 30 unique human chromosomal regions implicated by previous studies, correspondence between results between cattle and human is limited.

The collection can also comprise at least one polynucleotide useful for detecting one or more specific SNPs. For example, the SNPs given in Table A have been quantitatively associated with an increased susceptibility to contracting paratuberculosis, and are thus sequences for detecting their presence are useful herein.

In various embodiments of the collections or the methods below, the SNPs comprise one or more of the SNPs listed in Table A.

TABLE A

SNPs Useful for Predicting An Increased Susceptibility To Contracting Paratuberculosis

	SNP_ID	BTA/Mb	Chi-squared	P-value
SEQ ID NO 1	Hapmap57166-rs29020401	13/34.10	38.57	4.21E-09
SEQ ID NO 2	ARS-BFGL-NGS-63936	20/36.42	30.03	3.01E-07
SEQ ID NO 3	ARS-BFGL-NGS-84088	20/35.59	29.61	3.71E-07
SEQ ID NO 4	ARS-BFGL-BAC-13827	13/33.53	29.51	3.9E-07
SEQ ID NO 5	Hapmap52062-rs29027270	26/43.49	28.74	5.75E-07
SEQ ID NO 6	ARS-BFGL-NGS-95663	20/33.46	28.5	6.48E-07
SEQ ID NO 7	Hapmap48854-BTA-69129	3/103.69	28.34	7.02E-07
SEQ ID NO 8	Hapmap51130-BTA-105627	23/32.11	27.96	8.47E-07
SEQ ID NO 9	ARS-BFGL-NGS-38328	13/33.67	27.65	9.93E-07
SEQ ID NO 10	ARS-BFGL-NGS-38574	20/38.27	27.55	1.04E-06
SEQ ID NO 11	ARS-BFGL-NGS-23255	26/34.93	27.24	1.22E-06
SEQ ID NO 12	BTA-13956-no-rs	14/64.31	26.75	1.55E-06
SEQ ID NO 13	Hapmap54042-ss46526396	22/12.41	26.22	2.02E-06
SEQ ID NO 14	BTB-00261837	6/66.68	25.88	2.4E-06
SEQ ID NO 15	ARS-BFGL-NGS-16165	16/64.91	25.53	2.86E-06
SEQ ID NO 16	ARS-BFGL-NGS-114768	26/38.92	25.11	3.52E-06
SEQ ID NO 17	ARS-BFGL-NGS-84831	21/21.94	24.82	4.07E-06
SEQ ID NO 18	ARS-BFGL-NGS-55787	12/36.31	24.8	4.11E-06
SEQ ID NO 19	ARS-BFGL-NGS-18067	22/12.45	24.72	4.28E-06
SEQ ID NO 20	ARS-BFGL-NGS-114979	23/16.63	24.71	4.31E-06
SEQ ID NO 21	Hapmap41410-BTA-104176	7/63.04	24.67	4.4E-06
SEQ ID NO 22	ARS-BFGL-NGS-84327	13/5.54	24.39	5.05E-06
SEQ ID NO 23	ARS-BFGL-NGS-116261	19/61.05	24.27	5.36E-06
SEQ ID NO 24	BTB-00779241	20/35.78	24.19	5.6E-06
SEQ ID NO 25	Hapmap51169-BTA-122103	7/56.17	24.11	5.82E-06
SEQ ID NO 26	ARS-BFGL-BAC-31757	20/67.43	23.8	6.79E-06
SEQ ID NO 27	Hapmap51780-BTA-93959	18/38.44	23.62	7.41E-06
SEQ ID NO 28	BTB-00553468	14/18.76	23.47	0.000008

TABLE A-continued

SNPs Useful for Predicting An Increased Susceptibility To Contracting Paratuberculosis

	SNP_ID	BTA/Mb	Chi-squared	P-value
SEQ ID NO 29	Hapmap42075-BTA-114094	16/69.88	23.28	8.79E−06
SEQ ID NO 30	BTB-01278461	4/85.43	23.14	9.43E−06
SEQ ID NO 31	ARS-BFGL-NGS-12828	26/37.06	23.1	9.63E−06
SEQ ID NO 32	BTA-116871-no-rs	17/28.19	23.07	9.77E−06
SEQ ID NO 33	Hapmap46604-BTA-35152	14/60.13	23.06	9.82E−06
SEQ ID NO 34	BTA-15204-no-rs	20/34.74	23.05	9.86E−06
SEQ ID NO 35	BTA-61435-no-rs	26/36.89	22.96	1.04E−05
SEQ ID NO 36	Hapmap51346-BTA-89239	9/6.17	22.92	1.05E−05
SEQ ID NO 37	Hapmap49609-BTA-43790	18/51.49	22.88	1.07E−05
SEQ ID NO 38	Hapmap38462-BTA-110556	20/58.48	22.81	1.11E−05
SEQ ID NO 39	Hapmap30871-BTA-158348	8/64.55	22.72	1.16E−05
SEQ ID NO 40	ARS-BFGL-NGS-106176	23/23.10	22.58	1.25E−05
SEQ ID NO 41	ARS-BFGL-NGS-31976	13/71.05	22.19	1.52E−05
SEQ ID NO 42	BTA-21660-no-rs	12/35.67	22.16	1.54E−05
SEQ ID NO 43	BTB-00170785	4/25.67	22.08	0.000016
SEQ ID NO 44	ARS-BFGL-NGS-10383	10/47.26	22.01	1.66E−05
SEQ ID NO 45	Hapmap56950-ss46526304	3/114.08	21.99	1.68E−05
SEQ ID NO 46	ARS-BFGL-NGS-14399	12/36.16	21.62	2.02E−05
SEQ ID NO 47	ARS-BFGL-NGS-114316	26/38.21	21.6	2.04E−05
SEQ ID NO 48	BTB-01219956	26/12.53	21.57	2.07E−05
SEQ ID NO 49	Hapmap24928-BTC-010710	14/28.42	21.52	2.12E−05
SEQ ID NO 50	ARS-BFGL-NGS-34049	20/35.27	21.38	2.28E−05
SEQ ID NO 51	ARS-BFGL-NGS-116806	20/36.51	21.2	2.49E−05
SEQ ID NO 52	ARS-BFGL-NGS-13451	16/70.81	21.18	2.52E−05
SEQ ID NO 53	UA-IFASA-8974	20/31.97	21.14	2.57E−05
SEQ ID NO 54	Hapmap27079-BTC-039967	6/51.32	21.11	2.61E−05
SEQ ID NO 55	ARS-BFGL-NGS-84112	4/102.05	20.77	3.08E−05
SEQ ID NO 56	ARS-BFGL-BAC-32359	20/47.27	20.73	3.15E−05
SEQ ID NO 57	ARS-BFGL-NGS-101744	15/69.30	20.63	3.31E−05
SEQ ID NO 58	Hapmap41219-BTA-29565	24/32.30	20.53	3.48E−05
SEQ ID NO 59	Hapmap50053-BTA-61516	26/38.98	20.49	3.55E−05
SEQ ID NO 60	ARS-BFGL-NGS-115504	25/21.17	20.45	3.62E−05
SEQ ID NO 61	BTB-00780124	20/35.88	20.22	4.07E−05
SEQ ID NO 62	ARS-BFGL-NGS-101940	21/19.58	20.16	4.19E−05
SEQ ID NO 63	ARS-BFGL-BAC-34694	16/58.70	20.14	4.23E−05
SEQ ID NO 64	Hapmap59495-rs29020511	24/32.95	20.03	4.47E−05
SEQ ID NO 65	ARS-BFGL-NGS-3711	13/48.43	19.82	4.96E−05
SEQ ID NO 66	BTB-01342789	1/18.87	19.76	5.12E−05
SEQ ID NO 67	ARS-BFGL-NGS-91446	3/109.35	19.73	5.19E−05
SEQ ID NO 68	Hapmap50774-BTA-76325	6/51.29	19.7	5.26E−05
SEQ ID NO 69	ARS-BFGL-NGS-32123	15/43.28	19.7	5.26E−05
SEQ ID NO 70	BTB-01843749	9/35.20	19.57	5.63E−05
SEQ ID NO 71	ARS-BFGL-NGS-29032	16/61.38	19.45	5.98E−05
SEQ ID NO 72	Hapmap49679-BTA-61690	26/42.56	19.38	6.18E−05
SEQ ID NO 73	BTA-90616-no-rs	20/29.25	19.32	6.37E−05
SEQ ID NO 74	BTA-100341-no-rs	26/34.88	19.31	6.42E−05
SEQ ID NO 75	ARS-BFGL-NGS-30004	23/16.66	19.29	6.48E−05
SEQ ID NO 76	ARS-BFGL-NGS-41833	20/66.58	19.21	6.73E−05
SEQ ID NO 77	Hapmap55208-ss46526613	2/0.56	19.14	6.99E−05
SEQ ID NO 78	UA-IFASA-7062	14/28.50	19.12	7.05E−05
SEQ ID NO 79	Hapmap43556-BTA-33007	13/56.98	19.04	7.35E−05
SEQ ID NO 80	ARS-BFGL-NGS-26323	9/29.68	19.01	7.43E−05
SEQ ID NO 81	ARS-BFGL-NGS-52539	10/18.96	18.96	7.62E−05
SEQ ID NO 82	Hapmap43854-BTA-43847	18/56.40	18.93	7.76E−05
SEQ ID NO 83	ARS-BFGL-NGS-111520	15/76.24	18.83	8.14E−05
SEQ ID NO 84	Hapmap43873-BTA-50695	20/45.91	18.64	8.96E−05
SEQ ID NO 85	BTB-00617870	15/78.61	18.55	9.38E−05
SEQ ID NO 86	BTA-28297-no-rs	10/19.03	18.47	9.75E−05
SEQ ID NO 87	BTA-61688-no-rs	26/42.60	18.42	0.0001
SEQ ID NO 88	ARS-BFGL-NGS-112293	15/63.04	18.36	0.000103
SEQ ID NO 89	BTA-60642-no-rs	25/8.65	18.09	0.000118
SEQ ID NO 90	ARS-BFGL-NGS-36892	17/67.75	17.91	0.000129
SEQ ID NO 91	BTB-00310653	7/46.58	17.68	0.000145
SEQ ID NO 92	Hapmap49429-BTA-107409	16/69.99	17.65	0.000147
SEQ ID NO 93	ARS-BFGL-NGS-17676	20/39.04	17.62	0.00015
SEQ ID NO 94	BTA-114108-no-rs	1/26.10	17.58	0.000152
SEQ ID NO 95	Hapmap32845-BTA-152047	26/35.72	17.57	0.000153
SEQ ID NO 96	ARS-BFGL-NGS-36809	13/31.48	17.5	0.000159
SEQ ID NO 97	Hapmap38112-BTA-50631	20/42.72	17.35	0.00017
SEQ ID NO 98	ARS-BFGL-NGS-86252	23/16.59	17.15	0.000189
SEQ ID NO 99	ARS-BFGL-NGS-42452	7/65.74	17.09	0.000194
SEQ ID NO 100	Hapmap41054-BTA-67528	3/34.52	17.02	0.000201
SEQ ID NO 101	Hapmap48202-BTA-118947	20/30.16	17.02	0.000201
SEQ ID NO 102	BTB-01731152	17/28.15	16.95	0.000208
SEQ ID NO 103	BTB-01337853	12/66.70	16.73	0.000233

TABLE A-continued

SNPs Useful for Predicting An Increased Susceptibility To Contracting Paratuberculosis

	SNP_ID	BTA/Mb	Chi-squared	P-value
SEQ ID NO 104	Hapmap56001-rs29023690	16/62.05	16.66	0.000241
SEQ ID NO 105	Hapmap55502-rs29014080	6/72.21	16.14	0.000313
SEQ ID NO 106	Hapmap38405-BTA-35996	14/18.90	16.11	0.000318
SEQ ID NO 107	Hapmap43792-BTA-122725	13/83.21	16.08	0.000323
SEQ ID NO 108	ARS-BFGL-NGS-55607	29/5.03	16.05	0.000327
SEQ ID NO 109	Hapmap48185-BTA-112403	24/27.36	16.01	0.000333
SEQ ID NO 110	BTA-119803-no-rs	11/83.28	15.66	0.000397
SEQ ID NO 111	Hapmap49750-BTA-76652	6/72.25	15.43	0.000447
SEQ ID NO 112	Hapmap52400-rs29025316	7/54.59	15.39	0.000456
SEQ ID NO 113	BTA-121819-no-rs	7/105.09	15.37	0.000459
SEQ ID NO 114	ARS-BFGL-NGS-100092	26/36.33	15.37	0.000459
SEQ ID NO 115	ARS-BFGL-NGS-23638	26/41.14	15.29	0.000478
SEQ ID NO 116	Hapmap43736-BTA-98788	13/26.26	15.21	0.000497
SEQ ID NO 117	ARS-BFGL-NGS-43032	16/14.39	15.18	0.000504
SEQ ID NO 118	ARS-BFGL-NGS-101723	10/11.22	15.14	0.000515
SEQ ID NO 119	BTB-01887959	22/9.23	15.13	0.000519
SEQ ID NO 120	Hapmap47541-BTA-22031	20/39.61	14.99	0.000556
SEQ ID NO 121	Hapmap39665-BTA-59836	25/26.31	14.83	0.000602
SEQ ID NO 122	ARS-BFGL-NGS-1808	14/83.04	14.8	0.00061
SEQ ID NO 123	ARS-BFGL-NGS-21527	25/25.75	14.76	0.000624
SEQ ID NO 124	UA-IFASA-4794	28/22.77	14.71	0.000638
SEQ ID NO 125	ARS-BFGL-NGS-76451	1/138.44	14.61	0.000674
SEQ ID NO 126	BTB-00360436	8/76.85	14.31	0.00078
SEQ ID NO 127	BTB-01790614	6/3.21	14.25	0.000806
SEQ ID NO 128	ARS-BFGL-NGS-86477	21/67.62	14.2	0.000826
SEQ ID NO 129	Hapmap25321-BTA-156840	22/9.37	14.17	0.000838
SEQ ID NO 130	BTB-00783271	20/41.21	13.76	0.00103
SEQ ID NO 131	Hapmap47083-BTA-71984	4/100.70	13.72	0.00105
SEQ ID NO 132	BTB-01092452	8/81.40	13.46	0.0012
SEQ ID NO 133	Hapmap48829-BTA-61554	26/39.68	13.41	0.00123
SEQ ID NO 134	BTA-19348-no-rs	8/64.88	13.35	0.00126
SEQ ID NO 135	ARS-BFGL-NGS-33495	8/88.53	13.18	0.00137
SEQ ID NO 136	BTB-01475042	20/51.95	13.17	0.00138
SEQ ID NO 137	ARS-BFGL-NGS-113490	3/109.84	13.05	0.00147
SEQ ID NO 138	ARS-BFGL-NGS-32966	9/38.39	12.74	0.00171
SEQ ID NO 139	ARS-BFGL-NGS-2600	24/19.69	12.69	0.00175
SEQ ID NO 140	Hapmap51600-BTA-50467	20/36.77	12.66	0.00178
SEQ ID NO 141	BTB-01112664	2/19.39	12.64	0.0018
SEQ ID NO 142	UA-IFASA-1789	14/34.76	12.44	0.00199
SEQ ID NO 143	Hapmap45971-BTA-102151	11/69.73	11.88	0.00263
SEQ ID NO 144	ARS-BFGL-NGS-7597	4/102.25	11.48	0.00322
SEQ ID NO 145	ARS-BFGL-NGS-23298	19/60.94	11.2	0.00369
SEQ ID NO 146	ARS-BFGL-NGS-103845	7/56.99	11.19	0.00371
SEQ ID NO 147	Hapmap59876-rs29018046	2/14.00	11.08	0.00392
SEQ ID NO 148	ARS-BFGL-NGS-102130	24/41.61	10.89	0.00431
SEQ ID NO 149	BTA-72108-no-rs	4/108.78	10.85	0.0044
SEQ ID NO 150	BTB-01839787	17/30.34	10.69	0.00478
SEQ ID NO 151	Hapmap56784-rs29012419	20/52.23	9.89	0.00714
SEQ ID NO 152	ARS-BFGL-NGS-84716	15/82.47	9.74	0.00767
SEQ ID NO 153	Hapmap43830-BTA-29180	13/82.90	9.73	0.00772
SEQ ID NO 154	ARS-BFGL-NGS-34254	5/27.55	9.48	0.00873
SEQ ID NO 155	ARS-BFGL-NGS-49057	3/72.95	9.42	0.00901
SEQ ID NO 156	Hapmap50205-BTA-107882	9/78.41	9.04	0.0109
SEQ ID NO 157	ARS-BFGL-NGS-18128	17/21.16	8.98	0.0112
SEQ ID NO 158	ARS-BFGL-NGS-21860	17/24.67	8.74	0.0127
SEQ ID NO 159	Hapmap40908-BTA-121388	23/6.69	8.67	0.0131
SEQ ID NO 160	BTA-111934-no-rs	9/52.95	8.62	0.0134
SEQ ID NO 161	UA-IFASA-8351	23/36.28	8.6	0.0136
SEQ ID NO 162	ARS-BFGL-NGS-16677	29/37.34	8.28	0.0159
SEQ ID NO 163	BTA-27242-no-rs	5/20.21	7.74	0.0209
SEQ ID NO 164	ARS-BFGL-NGS-109845	29/19.50	7.66	0.0217
SEQ ID NO 165	ARS-BFGL-NGS-118058	2/23.36	7.65	0.0218
SEQ ID NO 166	Hapmap58939-rs29011360	3/43.09	7.59	0.0224
SEQ ID NO 167	ARS-BFGL-NGS-106807	15/41.61	7.31	0.0259
SEQ ID NO 168	ARS-BFGL-NGS-74054	24/42.08	7.16	0.0279
SEQ ID NO 169	ARS-BFGL-NGS-53471	6/116.93	7.1	0.0287
SEQ ID NO 170	ARS-BFGL-NGS-112793	12/86.28	6.92	0.0314
SEQ ID NO 171	Hapmap55067-ss46526268	23/18.58	6.88	0.032
SEQ ID NO 172	Hapmap45550-BTA-32092	13/36.23	6.43	0.0402
SEQ ID NO 173	ARS-BFGL-NGS-75935	21/24.69	6.3	0.043
SEQ ID NO 174	BTA-100864-no-rs	13/9.08	6.2	0.045
SEQ ID NO 175	ARS-BFGL-NGS-117518	17/28.09	6.2	0.0451
SEQ ID NO 176	Hapmap26742-BTA-156593	17/42.53	6.1	0.0472
SEQ ID NO 177	ARS-BFGL-NGS-39305	13/4.74	5.71	0.0575
SEQ ID NO 178	Hapmap60394-rs29020827	13/71.23	5.54	0.0627

TABLE A-continued

SNPs Useful for Predicting An Increased Susceptibility To Contracting Paratuberculosis

	SNP_ID	BTA/Mb	Chi-squared	P-value
SEQ ID NO 179	UA-IFASA-2293	20/59.45	5.47	0.0648
SEQ ID NO 180	ARS-BFGL-NGS-114525	7/53.19	5.28	0.0714
SEQ ID NO 181	BTB-01250562	7/82.51	5.01	0.0816
SEQ ID NO 182	Hapmap43880-BTA-54826	22/52.10	4.8	0.0909
SEQ ID NO 183	ARS-BFGL-NGS-115608	21/24.71	4.79	0.0912
SEQ ID NO 184	BTA-54617-no-rs	22/45.42	4.55	0.103
SEQ ID NO 185	BTB-01011603	29/21.15	4.45	0.108
SEQ ID NO 186	ARS-BFGL-NGS-102205	2/94.47	4.05	0.132
SEQ ID NO 187	ARS-BFGL-NGS-24141	9/91.47	3.94	0.139
SEQ ID NO 188	ARS-BFGL-NGS-39985	13/71.17	3.83	0.147
SEQ ID NO 189	ARS-BFGL-NGS-101621	13/76.41	3.61	0.164
SEQ ID NO 190	ARS-BFGL-NGS-23356	13/5.26	3.6	0.165
SEQ ID NO 191	ARS-BFGL-NGS-55380	16/22.06	3.34	0.188
SEQ ID NO 192	Hapmap51102-BTA-97964	6/54.36	2.87	0.238
SEQ ID NO 193	BTA-34427-no-rs	2/112.67	2.8	0.247
SEQ ID NO 194	ARS-BFGL-NGS-79435	29/16.50	1.23	0.54
SEQ ID NO 195	BTB-01195060	7/54.86	0.74	0.69
SEQ ID NO 196	ARS-BFGL-NGS-64241	9/76.67	0.74	0.691
SEQ ID NO 197	ARS-BFGL-NGS-3747	27/37.86	0.39	0.822

In various embodiments of the collections or the methods below, the SNPs preferably comprise one or more of the SNPs listed in Table B.

TABLE B

Preferred SNPs Useful for Predicting an Increased Susceptibility To Contracting Paratuberculosis

	SNP_ID	BTA/Mb
SEQ ID NO 4	ARS-BFGL-BAC-13827	13/33.53
SEQ ID NO 8	Hapmap51130-BTA-105627	23/32.11
SEQ ID NO 12	BTA-13956-no-rs	14/64.31
SEQ ID NO 14	BTB-00261837	6/66.68
SEQ ID NO 15	ARS-BFGL-NGS-16165	16/64.91
SEQ ID NO 16	ARS-BFGL-NGS-114768	26/38.92
SEQ ID NO 25	Hapmap51169-BTA-122103	7/56.17
SEQ ID NO 29	Hapmap42075-BTA-114094	16/69.88
SEQ ID NO 34	BTA-15204-no-rs	20/34.74
SEQ ID NO 35	BTA-61435-no-rs	26/36.89
SEQ ID NO 36	Hapmap51346-BTA-89239	9/6.17
SEQ ID NO 37	Hapmap49609-BTA-43790	18/51.49
SEQ ID NO 41	ARS-BFGL-NGS-31976	13/71.05
SEQ ID NO 45	Hapmap56950-ss46526304	3/114.08
SEQ ID NO 53	UA-IFASA-8974	20/31.97
SEQ ID NO 57	ARS-BFGL-NGS-101744	15/69.30
SEQ ID NO 60	ARS-BFGL-NGS-115504	25/21.17
SEQ ID NO 61	BTB-00780124	20/35.88
SEQ ID NO 62	ARS-BFGL-NGS-101940	21/19.58
SEQ ID NO 71	ARS-BFGL-NGS-29032	16/61.38
SEQ ID NO 74	BTA-100341-no-rs	26/34.88
SEQ ID NO 76	ARS-BFGL-NGS-41833	20/66.58
SEQ ID NO 78	UA-IFASA-7062	14/28.50
SEQ ID NO 85	BTB-00617870	15/78.61
SEQ ID NO 86	BTA-28297-no-rs	10/19.03
SEQ ID NO 89	BTA-60642-no-rs	25/8.65
SEQ ID NO 95	Hapmap32845-BTA-152047	26/35.72
SEQ ID NO 96	ARS-BFGL-NGS-36809	13/31.48
SEQ ID NO 102	BTB-01731152	17/28.15
SEQ ID NO 112	Hapmap52400-rs29025316	7/54.59
SEQ ID NO 128	ARS-BFGL-NGS-86477	21/67.62
SEQ ID NO 129	Hapmap25321-BTA-156840	22/9.37
SEQ ID NO 133	Hapmap48829-BTA-61554	26/39.68
SEQ ID NO 141	BTB-01112664	2/19.39
SEQ ID NO 144	ARS-BFGL-NGS-7597	4/102.25
SEQ ID NO 149	BTA-72108-no-rs	4/108.78
SEQ ID NO 150	BTB-01839787	17/30.34
SEQ ID NO 154	ARS-BFGL-NGS-34254	5/27.55

TABLE B-continued

Preferred SNPs Useful for Predicting an Increased Susceptibility To Contracting Paratuberculosis

	SNP_ID	BTA/Mb
SEQ ID NO 162	ARS-BFGL-NGS-16677	29/37.34
SEQ ID NO 164	ARS-BFGL-NGS-109845	29/19.50
SEQ ID NO 171	Hapmap55067-ss46526268	23/18.58
SEQ ID NO 173	ARS-BFGL-NGS-75935	21/24.69
SEQ ID NO 176	Hapmap26742-BTA-156593	17/42.53
SEQ ID NO 177	ARS-BFGL-NGS-39305	13/4.74
SEQ ID NO 183	ARS-BFGL-NGS-115608	21/24.71
SEQ ID NO 185	BTB-01011603	29/21.15
SEQ ID NO 187	ARS-BFGL-NGS-24141	9/91.47
SEQ ID NO 190	ARS-BFGL-NGS-23356	13/5.26
SEQ ID NO 191	ARS-BFGL-NGS-55380	16/22.06
SEQ ID NO 192	Hapmap51102-BTA-97964	6/54.36
SEQ ID NO 193	BTA-34427-no-rs	2/112.67

Still other SNPs that are useful in connection herewith include various SNPs on BTA20, particularly SNPs within the PTGER4 region, and BTA7, particularly SNPs within the IRGM region.

In one embodiment, the collection comprises a group of SNPs comprising one or more of those give in Table A. In another embodiment, the collection of polynucleotides comprises each of the foregoing SNPs. In one presently preferred embodiment, the following table (Table C) using exemplar SNPs can be used to construct a polynomial equation for predicting the association of a particular SNP or collection of SNPs with the trait of an increased susceptibility to contracting paratuberculosis.

TABLE C

Factors for predicting an increased susceptibility to contracting paratuberculosis using specific SNP
Table C. Coefficients for SNPs in final model: P < 0.01 threshold.

Parameter	Estimate	SE[1]	P-value
Intercept	5.395	1.074	5.05×10^{-7}

Parameter	Estimate 0 vs 2	SE[1]	P-value	Estimate 1 vs 2	SE[1]	P-value	0/1/2
BTB-01342789	−0.140	0.256	5.85×10^{-1}	0.671	0.260	9.85×10^{-3}	TT/TC/CC
BTA-114108-no-rs	−0.200	0.282	4.77×10^{-1}	−0.543	0.184	3.23×10^{-3}	AA/AC/CC
BTB-01112664	1.138	0.327	5.04×10^{-4}	−0.397	0.195	4.19×10^{-2}	TT/TG/GG
ARS-BFGL-NGS-118058	0.444	0.187	1.73×10^{-2}	0.152	0.148	3.06×10^{-1}	AA/AG/AG
Hapmap58939-rs29011360	0.875	0.289	2.45×10^{-3}	−0.196	0.191	3.05×10^{-1}	AA/AG/AG
BTB-01278461	−1.393	0.460	2.48×10^{-3}	−0.086	0.481	8.59×10^{-1}	TT/TC/CC
BTA-72108-no-rs	−0.525	0.355	1.39×10^{-1}	−1.536	0.406	1.57×10^{-4}	TT/TC/CC
ARS-BFGL-NGS-34254	−0.016	0.164	9.24×10^{-1}	−0.541	0.165	1.06×10^{-3}	TT/TC/CC
BTB-00261837	0.755	0.211	3.35×10^{-4}	0.158	0.155	3.08×10^{-1}	TT/TC/CC
ARS-BFGL-NGS-103845	−0.183	0.180	3.09×10^{-1}	0.514	0.148	5.17×10^{-4}	TT/TC/CC
Hapmap41410-BTA-104176	−1.821	0.943	5.35×10^{-2}	−0.121	0.961	9.00×10^{-1}	TT/TC/CC
ARS-BFGL-NGS-32966	0.984	0.573	8.61×10^{-2}	−0.111	0.314	7.24×10^{-1}	AA/AG/AG
ARS-BFGL-NGS-64241	0.828	0.368	2.42×10^{-2}	0.021	0.218	9.23×10^{-1}	TT/TC/CC
BTA-28297-no-rs	−0.965	0.231	3.06×10^{-5}	−0.238	0.231	3.03×10^{-1}	GG/GC/CC
Hapmap57166-rs29020401	−0.773	0.207	1.87×10^{-4}	0.149	0.219	4.98×10^{-1}	AA/AG/AG
Hapmap43556-BTA-33007	−0.452	0.252	7.30×10^{-2}	0.613	0.284	3.05×10^{-2}	AA/AG/AG
ARS-BFGL-NGS-32123	−0.092	0.179	6.08×10^{-1}	0.666	0.152	1.10×10^{-5}	TT/TG/GG
ARS-BFGL-NGS-55380	−0.817	0.169	1.32×10^{-6}	−0.140	0.159	3.78×10^{-1}	AA/AG/AG
BTA-116871-no-rs	0.699	0.183	1.33×10^{-4}	−0.941	0.157	2.26×10^{-9}	TT/TC/CC
Hapmap26742-BTA-156593	1.085	0.299	2.82×10^{-4}	0.099	0.311	7.51×10^{-1}	AA/AG/AG
Hapmap49609-BTA-43790	−0.363	0.170	3.25×10^{-2}	−0.532	0.162	1.06×10^{-3}	AA/AG/AG
UA-IFASA-8974	0.709	0.192	2.13×10^{-4}	−0.683	0.155	1.10×10^{-5}	AA/AC/CC
ARS-BFGL-NGS-41833	0.333	0.245	1.74×10^{-1}	−0.582	0.172	7.08×10^{-4}	TT/TG/GG
ARS-BFGL-NGS-75935	0.399	0.198	4.37×10^{-2}	0.714	0.208	5.79×10^{-4}	TT/TC/CC
Hapmap54042-ss46526396	1.278	0.216	3.30×10^{-9}	−0.250	0.155	1.07×10^{-1}	TT/TC/CC
Hapmap51130-BTA-105627	−0.569	0.207	6.04×10^{-3}	−0.165	0.152	2.79×10^{-1}	AA/AG/AG
BTA-60642-no-rs	−0.768	0.194	7.19×10^{-5}	−0.196	0.194	3.13×10^{-1}	AA/AG/AG
ARS-BFGL-NGS-115504	0.884	0.275	1.28×10^{-3}	−0.003	0.178	9.86×10^{-1}	AA/AG/AG
BTA-100341-no-rs	0.267	0.188	1.56×10^{-1}	0.682	0.153	8.37×10^{-6}	TT/TG/GG
ARS-BFGL-NGS-109845	0.597	0.180	9.27×10^{-4}	−0.134	0.152	3.79×10^{-1}	TT/TC/CC

[1]Standard error of coefficient estimate.

In one embodiment, the collection comprises a group of SNPs comprising one or more of those give in Table B. In another embodiment, the collection of polynucleotides comprises each of the foregoing SNPs. In one presently preferred embodiment, the following table (Table D) using exemplar SNPs can be used to construct a polynomial equation for predicting the association of a particular SNP or collection of SNPs with the trait of an increased susceptibility to contracting paratuberculosis.

TABLE D

Factors for predicting an increased susceptibility to contracting paratuberculosis using specific SNP
Table D. Coefficients for SNPs in final model: P < 0.001 threshold.

Parameter	Estimate	SE[1]	P-value
Intercept	5.395	1.074	5.05×10^{-7}

Parameter	Estimate 0 vs 2	SE[1]	P-value	Estimate 1 vs 2	SE[1]	P-value	0/1/2
BTA-114108-no-rs	−0.274	0.248	2.70×10^{-1}	−0.366	0.158	2.10×10^{-2}	AA/AC/CC
BTB-01112664	1.045	0.264	7.51×10^{-5}	−0.357	0.161	2.61×10^{-2}	TT/TG/GG
ARS-BFGL-NGS-118058	0.392	0.152	9.93×10^{-3}	0.271	0.126	3.09×10^{-2}	AA/AG/AG
BTB-01278461	−1.326	0.496	7.51×10^{-3}	0.174	0.513	7.34×10^{-1}	TT/TC/CC
BTA-72108-no-rs	−0.396	0.280	1.57×10^{-1}	−1.333	0.325	4.19×10^{-5}	TT/TC/CC
BTB-00261837	0.860	0.181	2.09×10^{-6}	0.027	0.129	8.37×10^{-1}	TT/TC/CC
Hapmap41410-BTA-104176	−1.751	0.900	5.16×10^{-2}	−0.069	0.913	9.40×10^{-1}	TT/TC/CC
ARS-BFGL-NGS-32966	1.114	0.467	1.70×10^{-2}	−0.167	0.257	5.15×10^{-1}	AA/AG/AG
Hapmap57166-rs29020401	−0.498	0.164	2.38×10^{-3}	0.459	0.177	9.53×10^{-3}	AA/AG/AG
ARS-BFGL-NGS-32123	−0.175	0.149	2.38×10^{-1}	0.521	0.125	3.13×10^{-5}	TT/TG/GG
ARS-BFGL-NGS-55380	−0.769	0.142	6.31×10^{-8}	−0.043	0.130	7.40×10^{-1}	AA/AG/AG
BTA-116871-no-rs	0.649	0.154	2.42×10^{-5}	−0.817	0.131	4.44×10^{-10}	TT/TC/CC
UA-IFASA-8974	0.644	0.153	2.59×10^{-5}	−0.671	0.129	1.90×10^{-7}	AA/AC/CC
Hapmap54042-ss46526396	1.021	0.185	3.68×10^{-8}	−0.290	0.133	2.93×10^{-2}	AA/AG/AG
Hapmap51130-BTA-105627	−0.346	0.175	4.74×10^{-2}	−0.194	0.130	1.35×10^{-1}	AA/AG/AG
ARS-BFGL-NGS-115504	1.237	0.234	1.20×10^{-7}	−0.158	0.151	2.93×10^{-1}	AA/AG/AG

TABLE D-continued

Factors for predicting an increased susceptibility to contracting paratuberculosis using specific SNP
Table D. Coefficients for SNPs in final model: P < 0.001 threshold.

BTA-100341-no-rs	0.474	0.160	2.98×10^{-3}	0.384	0.125	2.19×10^{-3}	TT/TG/GG
ARS-BFGL-NGS-109845	0.748	0.152	8.37×10^{-7}	−0.169	0.129	1.89×10^{-1}	TT/TC/CC

[1]Standard error of coefficient estimate

In another of its several aspects, this disclosure provides for methods of detecting sequences in a genome that provide an estimate of an increased susceptibility to contracting paratuberculosis probability or which have predictive value regarding an increased susceptibility to contracting paratuberculosis likelihood. In one embodiment, methods for estimating the likelihood of an increased susceptibility to contracting paratuberculosis in one or more members of a cattle population are provided. The methods generally comprise the steps of

1) providing a collection of one or more polynucleotides, each of which is at least partially complementary to a sequence in a cow genome, comprising at least one sequence that is quantitatively associated with an increased susceptibility to contracting paratuberculosis with statistical significance of at least p≤0.01;
2) using the collection to determine the presence or absence of sequences complementary to one or more polynucleotides from the collection in one or more members of the cattle population genome, wherein the presence or absence of the complementary sequences is quantitatively associated with the trait of an increased susceptibility to contracting paratuberculosis in a cattle population; and
3) estimating the likelihood of an increased susceptibility to contracting paratuberculosis based on the results of step 2).

The method, as the skilled artisan will appreciate, encompass use of collections of polynucleotides, for example, as described above, which are useful for detecting the presence or absence of sequences in a genome that are predictive of an increased susceptibility to contracting paratuberculosis. In one embodiment, the estimating step comprises a laboratory analysis. In such embodiments, the method comprises a statistical calculation. In other embodiments, the method comprises a field test. In many such embodiments, preferred tests are conveniently used to provide a threshold estimate or a visual indicator of acceptability. Preferably no actual statistical calculation is required for such field tests. Such tests may require the use of a chart, reader or other device to provide a measurement of an increased susceptibility to contracting paratuberculosis rate, or other useful measurement or result that reflects the likelihood of an increased susceptibility to contracting paratuberculosis.

Preferably, the methods provided herein feature a collection of polynucleotides that comprises at least one sequence that is quantitatively associated with an increased susceptibility to contracting paratuberculosis with statistical significance of at least p≤0.01. In other embodiments, the collection comprises at least one sequence that is quantitatively associated with an increased susceptibility to contracting paratuberculosis with statistical significance of at least p≤0.005. Most preferred are methods wherein the collection comprises at least one sequence that is quantitatively associated with an increased susceptibility to contracting paratuberculosis with statistical significance of at least p≤0.001.

The methods preferably are useful for estimating breeding value in cattle, thus preferably feature a collection of polynucleotides that is useful for estimating breeding value in cattle.

In various embodiments, the collection is useful for detecting the presence or absence of one allele of a SNP in the cow genome. Preferably, at least one of the polynucleotides in the collection is complementary to a sequence located on bovine chromosome 20 (BTA20). In another embodiment, at least one of the polynucleotides in the collection is complementary to a sequence located on bovine chromosome 26 (BTA26). In another embodiment, at least one of the polynucleotides in the collection is complementary to a sequence located on bovine chromosome 13 (BTA13). In another embodiment, at least one of the polynucleotides in the collection is complementary to a sequence located on bovine chromosome 16 (BTA16). In another embodiment, at least one of the polynucleotides in the collection is complementary to a sequence located on bovine chromosome 21 (BTA21).

In certain embodiments of the methods, at least one of the polynucleotides in the collection is complementary to a sequence that maps between 4-71 Mb of BTA13. In various embodiments, the collection comprises one or more polynucleotides complementary to a sequence that maps at either of 4-6 Mb, 31-34 Mb or 70-72 Mb of BTA13.

In certain embodiments of the methods, at least one of the polynucleotides in the collection is complementary to a sequence that maps between 21-70 Mb of BTA16. In various embodiments, the collection comprises one or more polynucleotides complementary to a sequence that maps at either of 21-23 Mb or 60-70 Mb of BTA16.

In certain embodiments of the methods, at least one of the polynucleotides in the collection is complementary to a sequence that maps between 31-67 Mb of BTA20. Especially preferred are particular regions of chromosome 20, including those that are near or encode certain genes. In various embodiments, the collection comprises one or more polynucleotides complementary to a sequence that maps on BTA20 at either of 31-35 Mb or 65-68 Mb of BTA20. In a currently preferred embodiment, at least one of the polynucleotides is complementary to a sequence that maps between 31-35 Mb of BTA20.

In certain embodiments of the methods, at least one of the polynucleotides in the collection is complementary to a sequence that maps between 19-68 Mb of BTA7. In various embodiments, the collection comprises one or more polynucleotides complementary to a sequence that maps at either of 19-25 Mb or 61-69 Mb of BTA7.

In certain embodiments of the methods, at least one of the polynucleotides in the collection is complementary to a sequence that maps between 34-40 Mb of BTA26. Also useful are polynucleotides that can identify the presence or absence of sequences which map to various overlapping or more specific locations, as set forth in the Examples below.

In a presently preferred method, at least one of the polynucleotides in the collection is complementary to a sequence located in a genomic sequence for Prostaglandin E

receptor 4 ("PTGER4"). In another presently preferred method, at least one of the polynucleotides in the collection is complementary to a sequence located in a genomic sequence IRGM.

In other embodiments useful with the methods, the collection comprises at least one polynucleotide useful for detecting one or more of the SNPs: SEQ ID NO: 3; SEQ ID NO: 4; SEQ ID NO: 5; SEQ ID NO: 6; SEQ ID NO: 9; SEQ ID NO: 10; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 17; SEQ ID NO: 20; SEQ ID NO: 21; SEQ ID NO: 24; SEQ ID NO: 25; SEQ ID NO: 26; SEQ ID NO: 34; SEQ ID NO: 37; SEQ ID NO: 41; SEQ ID NO: 42; SEQ ID NO: 46; SEQ ID NO: 47; SEQ ID NO: 48; SEQ ID NO: 51; SEQ ID NO: 55; SEQ ID NO: 57; SEQ ID NO: 59; SEQ ID NO: 60; SEQ ID NO: 61; SEQ ID NO: 66.

In currently preferred embodiment embodiments useful with the methods, the collection comprises at least one polynucleotide useful for detecting one or more of the SNPs: SEQ ID NO: 4; SEQ ID NO: 5; SEQ ID NO: 6; SEQ ID NO: 10; SEQ ID NO: 11; SEQ ID NO: 14; SEQ ID NO: 17; SEQ ID NO: 20; SEQ ID NO: 25; SEQ ID NO: 34; SEQ ID NO: 37; SEQ ID NO: 41; SEQ ID NO: 47; SEQ ID NO: 55; SEQ ID NO: 57; SEQ ID NO: 60; SEQ ID NO: 61; SEQ ID NO: 66.

The collection can also feature at least one polynucleotide that is in high LD to any of the above SNPs useful for detecting one or more of the SNPs. These polynucleotides would be able to be determined by an average practitioner skilled in the art once the practitioner knows the above-given SNPs.

In yet another of its several aspects, this disclosure provides kits that comprise one or more of the collections of polynucleotides useful for detecting sequences in a genome that are quantitatively associated with an increased susceptibility to contracting paratuberculosis, and instructions for use of the collection(s) for estimating breeding value or predicting the likelihood of an increased susceptibility to contracting paratuberculosis.

These and other aspects of the invention will be further illustrated by the following working examples which are included to augment, not limit the understanding and communication of the invention, as expressed in the appended claims.

Examples

The invention can be further illustrated by the following examples, although it will be understood that these examples included merely for purposes of illustrating and better describing certain aspects of what is disclosed herein. The examples do not limit the scope of the invention unless otherwise specifically indicated.

Two resource populations of approximately 5,000 cows each were used to identify genomic regions associated with susceptibility to infection by MAP. The first population (Population 1) consisted primarily of twelve Holstein paternal half-sib families of daughters of sires heavily used within the breed. Cows were specifically chosen to be in second or later lactation to increase the likelihood of identifying cows manifesting evidence of infection. The second resource population consisted of cows from six Holstein herds in Wisconsin. Blood samples were obtained from all cows in these herds over a period of 15 months in 2006-07.

Phenotype for MAP infection in Population 1 was based on both fecal culture of MAP and evidence of antibody titer to MAP as based on an ELISA test. Samples had been previously tested using the IDEXX ELISA (Gonda et al., 2006), but were re-tested for this study using a more recently developed ELISA with higher sensitivity (Shin et al., 2008). Phenotypes for Population 2 were ELISA results, also with the recently developed, higher sensitivity test.

Samples from both populations were genotyped with bead chips. Animals with fewer than 95% successfully scored genotypes and markers that were successfully scored for fewer than 90% of the samples in either of the two resource populations were removed prior to statistical analyses. In addition, SNPs with unknown genomic location or with minor allele frequencies below 5% were not included in analyses. After exclusion for these various reasons, a total of 35,772 SNPs remained.

Given the known paternal half-sib family structure in Population 1, female samples were checked for paternity relative to potential sires using a subset of 200 SNPs with high minor allele frequency. Of 233 females, 205 were verified as daughters of project sires.

Analysis of data from Population 1 accounted for the paternal half-sib family structure in the population. Inheritance of paternal and maternal haplotypes in Population 1 was determined using a Fortran program (de Roos et al., 2008) that compared sire and offspring genotypes. Paternally inherited haplotypes at each marker bracket were evaluated for deviation from a frequency of 0.5 expected under the null hypothesis of no linkage using a z test calculated as:

$$z = \frac{\hat{p} - 0.5}{\sqrt{\hat{p}\hat{q} * (1/n)}},$$

where p is the frequency of sire haplotype 1, q is 1-p and n is the number of offspring in the family. To combine linkage results across families, p-value for the 12 families were multiplied, and then compared with an empirical distribution of corresponding values obtained by simulation. For the simulation, 12 families of the same size as those in Population 1 were created with sire haplotypes one and two generated under the assumption of equal frequency (null hypothesis). The simulation was repeated one million times to generate an empirical distribution of results for determination of an empirical p-value.

Frequency of maternally inherited alleles from daughters in paternal half-sib families were used for a case-control analysis, in combination with allele frequency estimates from 28 positive cows which were not daughters of the 12 project sires. Maternally inherited allele frequencies were estimated using a single locus, maximum likelihood estimator. The control samples for the case-control analysis were not matching negatives, but rather an extensive sample of Holstein bulls used as artificial insemination (AI) sires. Bull genotype data was obtained from the USDA and Cooperative Dairy DNA Repository (CDDR) cooperators. Bulls were chosen based on birth year to represent population allele frequencies corresponding to the alleles from the MAP infection-positive cows. For Population 1, the sires selected were born between 1979 and 1990 and totaled 748. For Population 2, the selected sires were born between 1987 and 1998 and totaled 2,937. For combined analyses of Populations 1 and 2, the combined set of sires spanned birth years from 1979 to 1998 and totaled 3,271. These sire birth years were chosen considering the average difference in birth year of sires and daughters (9 yrs.) and average difference in age

of dams and daughters (3.5 yrs.). Additionally, for Population 1, the alleles considered from cases are those inherited from the cows' mothers. These sire samples provided an accurate estimate of Holstein population allele frequency for comparison with the allele frequency observed in positive cows. The two separate pieces of information (linkage, case-control i.e. linkage disequilibrium) were subsequently combined to yield a combined linkage-linkage disequilibrium result.

Allele frequencies were estimated directly in the second population without consideration of family structure, owing to the use of a large number of sires within the six commercial herds. Genotype data from Population 2 was examined for evidence of stratification or clustering using multidimensional scaling plots and IBS clustering as implemented in PLINK v1.05 (Purcell et al., 2007). There was no evidence of stratification or clustering related to herd or otherwise. As in the analysis of data from Population 1, allele frequency estimates from affected cows were compared with allele frequencies estimated from 6,283 US Holstein AI sires. In contrast to Population 1, where allele frequencies were estimated using maternally inherited haplotypes, and comparison of genotype frequencies with the control group was not feasible, it was also possible in Population 2 to test differences in genotype frequency with the exception of the X chromosome.

A combined analysis across populations was conducted by calculating a weighted average for allele frequency using the estimates obtained as described above for the two populations. The combined allele frequency estimates were compared as described above with population allele frequency estimates based on genotypes from 3,271 Holstein AI sires. This result was combined with results from the linkage analysis from population 1 for an overall linkage-linkage disequilibrium analysis.

The most significant markers from separate and combined case-control and linkage-linkage disequilibrium analyses (n=1,356) were used in logistic regression analysis to identify a subset of markers which could be used in genomic selection. The data set was comprised of the 521 cows from resource populations 1 and 2 positive for MAP infection, as described above, and the 3,271 Holstein AI sires. These 3,792 samples were randomly assigned to ten groups. For model development and cross-validation, nine of the ten groups were combined to comprise a training data set, and the model developed from the training data set was applied in prediction using the remaining group or testing data set. Model efficacy was evaluated by determining percent concordance. A pair of observations with different observed responses (case vs. control) was concordant if the observation with the lower ordered response value had a lower predicted score than the observation with the higher ordered response value. This analysis was repeated for all ten possible combinations. Models were constructed using a forward-stepwise approach with a minimum probability for SNP entry of $P<0.005$ and a minimum probability for continued inclusion in the model of $P<0.001$. SNPs chosen for each of the 10 training sets were tabulated, and SNPs appearing in models for at least half of the training sets were used in a final model, with model coefficients estimated from the full data set.

Given the limited family and population size, power of the across-family linkage analysis of Population 1 was relatively low. Additionally, the modest family sizes likely created some errors in haplotype estimation leading to some spurious results (e.g. the strong but isolated linkage result near the telomeric end of BTA5). However, a strong and consistent linkage signal ($p<1\times10^{-3}$) was observed on chromosome 20 (FIG. **1**), strengthening and refining a previous observation based on a subset of the population and within-family linkage analysis of microsatellite marker data (Gonda et al., 2007). Suggestive individual SNP associations ($p<5\times10^{-5}$) were observed in multiple genomic locations including BTA6, 7, 8, 11, 13, 17, 18, 22, 27, 28 and X. However, no individual marker associations surpassed a more stringent level of 1×10^{-7} adopted for significant linkage.

The pattern of results from allelic and genotypic tests of Population 2 were generally consistent, though the specific markers with strongest association varied between tests (FIG. **2**). Markers on all chromosomes surpassed a threshold of $P<5\times10^{-5}$ for either test while at a higher threshold (1×10^{-7}) significance was observed on BTA1, 2, 3, 4, 6, 7, 9, 10, 11, 12, 13, 16, 17, 21, 22, 25, 29 and X. In general, results from analysis of Population 2 were more significant than Population 1, owing in part to the larger number of bulls used as a control group. Correspondence between the most significant associations from Populations 1 and 2 was not striking.

The combined analysis of Populations 1 and 2 for individual marker association identified significant results ($P<1\times10^{-7}$) on BTA1, 2, 6, 7, 9, 15, 21 and 24 (FIG. **3**). Combining this information with linkage analysis results from Population 1 added BTA5, 20, 22 and 29 to the list.

A total of 1,356 of the most significant markers from the separate and combined analyses were considered in a stepwise logistic regression analysis to identify a subset of markers that could together be used in predicting genomic merit for susceptibility to MAP infection. The cross-validation analysis identified 30 SNPs that appeared in more than half of the models developed with the various subsets of the data (Table 1, FIG. **4**). SNPs from seventeen different chromosomes were included, with two or more SNPs included from BTA2, 3, 4, 7, 9, 13, 15, 20, 21, 22 and 29. In one case (BTA21) pairs of SNPs on a common chromosome were in relatively close proximity (<1 Mb), while the remainder were most often in distinct locations (i.e. separated by >20 Mb). A model incorporating the 30 SNPs identified through the cross-validation model development procedure was used on the full data set for purposes of estimating model coefficients (Tables A and B). Based on the concordance of observed and predicted values in the cross-validation testing sets (Table C), a concordance of approximately 72% could be expected.

SEQUENCE LISTING

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c 121

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c 121

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a 121

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t 121

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a 121

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a 121

<210> SEQ ID NO 11
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 11

aggaatacac acagttacat gtggtccaga gagtcgtaca aagtagccac tgcagggcca 60

cgctgctgat tgctgaccac ttgcccctct gctggcactc ctacatattg tttgccgaac 120

a 121

<210> SEQ ID NO 12
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 12

tgaccttgag taatgaggct cttcagctgc ggcaattttg aggtgggctg atagccgagc 60

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gctgcctgcc tgcagcccgc tcaacagctg agaatagaaa tccttcagac ttgaaaggga 120

a 121

<210> SEQ ID NO 13
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 13

cataaaagct gcctccggcc tggccttcta gcctcagccc agtcaaaagt cccaccttta 60

ccatttgatt tggtgtgtgc ccttagaggg aattcagagc tccgttaggc tcatagaggg 120

g 121

<210> SEQ ID NO 14
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 14

aaaacttctt gtttcctggt tatgcatcct catcttattc tttttatagt catagtagta 60

ctttttcccc atttactacc attttaaaga ttatatgaaa tgacaatgta actgttgttt 120

a 121

<210> SEQ ID NO 15
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 15

aaagtgtggc tggggacaca tcagaatgca tatggcgggc agatcagaca gtgtggcctc 60

gagcacatga taaaaagaca ttgtctgtaa tggatattga agtccctagc ctgacctcca 120

g 121

<210> SEQ ID NO 16
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 16

gacagaaaaa agaatataag gggtgccagg aggcaaaaag gcggggcccc aggaccacag 60

cgttccctgc cagcagcccc cttcaccctc cttccactca tctgccccag tcctaaaggt 120

c 121

<210> SEQ ID NO 17
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 17

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gtgtgtattg tctccctaag agtcctcaca ggtgctagtt gttgcttgca ggctgagttg 120

c 121

<210> SEQ ID NO 18
<211> LENGTH: 121
<212> TYPE: DNA

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<213> ORGANISM: Bos taurus

<400> SEQUENCE: 18

gagctgtgca gaacagaagc tttttataag ctgtagggcg gggcaaggaa gtcatagcaa 60

gaggaaagaa agggttattt ggggccagga catcgttttt tgggcaaaag gactggttta 120

a 121

<210> SEQ ID NO 19
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 19

cttgacatca ttcatcatgg atgggatgtc tttgactgca aaatggaaac tcaaagtagt 60

gtttcctggc ccctggggag ggggctgttg ggggaggatg ggggctgggt tcggagcccc 120

a 121

<210> SEQ ID NO 20
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 20

aaaaattaaa ttaaaatatt ttgtgggccc ctgaaagtat tgcaggcctt tggcactgtg 60

cctcctgtgg atacgactca agccacttag cagcagcagc agctcctgtg gataagctgg 120

c 121

<210> SEQ ID NO 21
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 21

agcacataaa actagaacat ggtctctgca cactggttct aagtcagtgt gacagatgac 60

gcatgtgtgt gctcactcag tcatgtccgg ccctttggga ccccatggac tggagcccac 120

c 121

<210> SEQ ID NO 22
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 22

aggcttcaat cctgcagaga ctgtgagtct gtgagtctga ctggggcccg gggttctacg 60

ctgctcacaa gcccccaggt gatcccccac tgccggacca cccttctcca agtatgtacc 120

a 121

<210> SEQ ID NO 23
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 23

tcctctgtgt tgtacagcag aaactgacag agcattttaa aacagttaca ttccaataaa 60

gaagaagaaa aatgtctggc cccatttttt ttgtggcatg aaactttggc tttagttttc 120

a 121

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<210> SEQ ID NO 24
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 24

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gacttcagga tgttcgtgat gaattttaag tttccccgag gacagtcagt tctggagaaa 120

t 121

<210> SEQ ID NO 25
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 25

atattataaa tattcatcca agccttcctt gaagggatct gtagacattt acaaatttaa 60

cgagagttat taggtactga ctcggtactg aagcaagccc cctgagaccc aaacactact 120

g 121

<210> SEQ ID NO 26
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 26

caccaatgtg cttgttcttg agtctgctga gactgggtct ggagctggaa tatgggtggg 60

gatggaggga aagtgtccgg tggggcaacg ttcatagact tacacgattc ctcagcagga 120

c 121

<210> SEQ ID NO 27
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 27

aaggttttct tgagtctttt ctgagccttt tcctgagcat gtgaaattac tttctaattt 60

cctccatata ttagttgttt taaatgttct aatgtctagc tcccagagtc tttattggta 120

t 121

<210> SEQ ID NO 28
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 28

tagtggtata gatctgtggg tagcgtcgac gcagagcaca taaagcagct tcagagcata 60

ctgacttgat atctgcacca cagtatccta tccaaggcaa ccaaaaaaga aaaaaaatta 120

a 121

<210> SEQ ID NO 29
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 29

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aggtgctatt atgcaggtac tacttttgaa aacttttttcc ttctgattgt cttttcctaa 60

cctgttccct tttgtctcct ctctcgtaga atattattga ttcctaatga ttttaccatc 120

c 121

<210> SEQ ID NO 30
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 30

catatcttaa ggaatttttt tgtgacctgt agtaatcctg aaatatttga gattggacct 60

catccaattt ctggatcaat aaggtacaga gtacctgtat tatgctgaag atatatgaga 120

a 121

<210> SEQ ID NO 31
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 31

ggggtggagg gacatcccag ggacccctgc tgacctctct gaaacttggt cagaacatcg 60

gagttaggaa tccattaaag gccgcctcga ggaacctgcg acttccctcc aaggaggagc 120

a 121

<210> SEQ ID NO 32
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 32

aattactctt ccattctgtc ctgatggcgc aggccatgga tttccttagg tctgctccty 60

cggagctgta acattcactt tcatttcttt caaaagtttt tcttactctc acttttcaat 120

a 121

<210> SEQ ID NO 33
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 33

caccgccacc aaaaaaaaga tacatggggt gaggagatga atttaataga aggttttaaa 60

tttacatctt aaatatagaa gggcatgtgc acatgtgctc agtcgtttca gtcgtgtccg 120

a 121

<210> SEQ ID NO 34
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 34

tcaacagtaa tgtattgtac acttaacatt tgttaaatga aggtatattt tatgctgttt 60

cttatcataa taaaattaaa ttaaaaagta cacacatgtg cacacacata catacaaaaa 120

a 121

<210> SEQ ID NO 35
<211> LENGTH: 121

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<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 35

gggcccctcc taagtctcag tgccccacag ggcccatgtg gctgcccact ccttctcgtc 60

ctcagctagc agaccccgaa agcagggtga ggcccattag ccttggctat cacccggtca 120

a 121

<210> SEQ ID NO 36
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 36

tagaatcaga atctaaaaat catcactaga atcactgaaa ccaaaggagt gtatagtagt 60

gggtataatt ctaccaatga tattgtaagt tagtgttatc tcattaggta taccaggaaa 120

a 121

<210> SEQ ID NO 37
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 37

aaggctggaa aaaaaatttt ttttaatcta tctccctcaa aaaagcaagc aaacaagaca 60

cagcaacatt gttttctaga aaaatggcag tattacactg aaaatcaaga acaacccaag 120

a 121

<210> SEQ ID NO 38
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 38

acagtcaaca agttgtgtgc tgtttgttcc tggcccattg acaccacgtc aaggcttgag 60

caaaaaagaa ttaaactctt caacccaaat ctcctcttca ttctgtcagg gccacccaaa 120

g 121

<210> SEQ ID NO 39
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 39

catgttctca tctggaagac agaagttcta tcatgagtcc tgcacatacc cctggatgat 60

cggactaggg atatgagagt gccttgaaaa caatgaaatg ctatttaagt gagagctacc 120

a 121

<210> SEQ ID NO 40
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 40

attttgttta aactgtttct tttggctgtc aacctttgat ggccttcttt gctatgcaaa 60

gaaatgttca ataagacctg attgtaacca atagcacaga atcattaatt tccgccttag 120

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c 121

<210> SEQ ID NO 41
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 41

gacctcagct tatggtacag agggtgcaag acggatctct cgtcacggaa ctaagatccc 60

gtgtgacttg tggccaagga agccaaaaca taaagcagga acaatatcgt gacaaattca 120

a 121

<210> SEQ ID NO 42
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 42

actagacttg tcatcagttt gtagtgtata caaataataa ataatgctgt atacctgaaa 60

cttggaagga aagttatgac caacctagat agcatattca aaagcagaga cattactttg 120

c 121

<210> SEQ ID NO 43
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 43

ccgaaatgaa acttcttaag gatgaaataa aattattatt agcagatggt tattttaatc 60

gtcttcaaag cttttgggga gtctagcatt gtcaggcaga tgcagtggca tcacacacat 120

a 121

<210> SEQ ID NO 44
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 44

ccataggctg tgctttgttc ccagagctca cctaacagcc cacacaaatg agtaattatc 60

cgtggccagc atggtcttta caaagaagag acaggggtgc cttaggccag gtgaggtaag 120

g 121

<210> SEQ ID NO 45
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 45

gcctgaggaa ttgaggggct gtcgctgcgc cccagctgct cttccagacg ctgacgggac 60

ggaggagtga aatgccgcct ttccttcctc tgccctcccc cccagacggc gtcagaaccg 120

c 121

<210> SEQ ID NO 46
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 46

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atgtgggttc gcggtgggcg aggaggggca gcgctgcgct tggccgagtg cctgcttgtt 60

gctcccccaa acctcacagg cagactcaca ggcaaacgtc tccttgagtt tcctgtgtga 120

c 121

<210> SEQ ID NO 47
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 47

tgcttaattt cacaccaaaa ggagagcgct ttgggtgtga gggagggccc aaggggggcaa 60

cgcccccaaa aagaaagatg aaggatgtcc ttacatgaaa acgagtgaag ccaacatccc 120

a 121

<210> SEQ ID NO 48
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 48

ctctagatca tcatgaggtt ccaattctag ttcagagtgt aagtaaagtt atggttataa 60

cctctgtcac agaaaaaata aatatatctt ggcaacacat tagtagtttt gctgatgaga 120

a 121

<210> SEQ ID NO 49
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 49

ggtctgtgga gttgtgggtg tcagagtgga aacaaatcca gggcacattc tcaggattgg 60

ctgacagagg tgggatggag ctgagggaca tggagtgagg ggtcaagaga gaggccaggg 120

a 121

<210> SEQ ID NO 50
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 50

gccagaagcc acccatgaat acagaggatc cccaggaaga tgagagcccc accaagactg 60

cggctccaca gagagggccc ctggtccccc tggcagccaa ggccaagtct ggccctttga 120

a 121

<210> SEQ ID NO 51
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 51

acatgaaggt gaaggcattt ggttcttcta agaatggcaa cagcaatgac aattttagat 60

gtatcaagtt ctgatgaggg ccgaggtaac caggttctgg gactcactgt ggcagcctct 120

c 121

<210> SEQ ID NO 52

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<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 52

ccccctttct ggagctgctt gtccccttga tggatagttc aggcctgtgg tgtggatagc 60

gccttctgca tggctcctgc tgctgctttg aagacatttc actgtctgtg gttccctaac 120

c 121

<210> SEQ ID NO 53
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 53

aactgggggt agaatcagca tcttaatcct tgaaaacaaa attttgtttt gatgtaagtt 60

cctcattctc atttcaaaag acagaaataa aatattgaca atattattac taatataaag 120

t 121

<210> SEQ ID NO 54
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 54

gagtggttga taagctctgt tcctgtgtgt aatgaaggta gaagaaatag ctattcacca 60

ctattaattt aagcattgag cacttgatat cagagtttga ctataagtaa tacatcatgg 120

a 121

<210> SEQ ID NO 55
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 55

gatggtttcc atttgtaatt attactgaaa agcatgtggt cttgtgggcc ctctcatagc 60

cgttcacaag ggggtggacc tgtgaagagg tctggacagt gtacctggtt ttaaaccagg 120

c 121

<210> SEQ ID NO 56
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 56

aaatattaca ttatgtatag tacttgaact atgcatatga tattctaaga tttttaaatc 60

caagtgtagt catttaacat ttgtggaagt ggtttcattc tttgatacgt agtaatgcat 120

g 121

<210> SEQ ID NO 57
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 57

gatgtgaagg tgaatgccat cagggtcagg tgtgaatgag gttgcggcct gccctccatc 60

cgccgttgct gacgatcctt cagctctaca cctcccacct cctgttggaa acccttgcag 120

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a 121

<210> SEQ ID NO 58
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 58

agagtaaaat acttaggagt taagtgtgtg cctggcttgg atcttaacca tccttggact 60

gtctgggctt tgtgctagtc acgcttctgc ttgtctgtgt tctgctgcct gatcagctgt 120

g 121

<210> SEQ ID NO 59
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 59

agttaactgc ccacttttt taaaaaaaaa tcagtttctt cagaggaaca caacaaaatc 60

cgggggctct acaatatata tcattcatga atggatacta cgcaaaatac taagtacatg 120

a 121

<210> SEQ ID NO 60
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 60

ctaactttca gcggcccact ggaatctctg cttggagccc acggccatct cacactgagc 60

gtttctttct tgctcctctt gggtttttttc tgtggagtat cactgtcctc cttctcaccc 120

a 121

<210> SEQ ID NO 61
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 61

agaagaactg ctatcagttc cccaccatca aacaccattc cgtttctatg gattacgggc 60

caaggtccat cttctgtaac ttcgtcttga cacagtgtgc tgtattctca gagtggaaga 120

t 121

<210> SEQ ID NO 62
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 62

aatgaagaag ccttcgaagt gctagtggga agctgctgta taacacaggg agctcagctc 60

ggtgtcttgt aatggcctag aggggtgaag aatcagcctg caatgtggga gacccagatt 120

c 121

<210> SEQ ID NO 63
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

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<400> SEQUENCE: 63

ctatgatttc atggtgaaat acttgggatc tcccaccaca tctgtctcca tactggttgc 60

cctagataag aacttggtaa tttgagttga tttaacaagg taatttgatt gttatttaaa 120

a 121

<210> SEQ ID NO 64
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 64

actgagggac tatgagaaaa gtagtagact aggggctgaa ggaaagataa agaaatcaga 60

ggagagtcta aggaacttca ctgacagcag agcatcagta aagcaaggag agaatagaag 120

a 121

<210> SEQ ID NO 65
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 65

agggcactga aaaccaagag aggaccacag atgatgctgg ccatctctga cacctccact 60

cacacagtcg ttttccactt catttcaaac aaacaggagc tggagggagg ggtatggtag 120

g 121

<210> SEQ ID NO 66
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 66

ccacttgtat gagcctatga cataggccac ctcactgatt ttagggatca gtcaaaagga 60

cttkatgtcc cacccagttc tctataaaat aagcaaagtg agcctcctac tcattttctg 120

a 121

<210> SEQ ID NO 67
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 67

cctagccggc aacaggacta ttgagctccc tatgaccttt cttcctgcaa acggcccccg 60

cgggagaagt cgaggctgga ccccagaaag gacttccttt gattaaaatg tggcaatgac 120

g 121

<210> SEQ ID NO 68
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 68

agatcagtta actatactta caagggttta ttttagtatt ttctgttctg ttgttttgtt 60

gttgtttatt tgctaagtcg tgttggcctc ttttgcaacc ccatggagtg tggagccacc 120

a 121

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<210> SEQ ID NO 69
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 69

ggtctctgag cccagaaccc cgctctctgt tcctgtagcc cattggagat ggttccagtt 60

ggggcccttc agagttctca gatgttgaat ggattcaagt cctggtgttg attggtttgc 120

a 121

<210> SEQ ID NO 70
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 70

actctttttg ttttttcagc aaacattgtt cactacttac ttggcccctg acaaccttaa 60

cgcatctgaa atggaacact ccctatgtgc atggccatgt ccaatcactg agcaagagag 120

g 121

<210> SEQ ID NO 71
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 71

acacaatagg tgctcagtat atatatttat ggaacacacg tggataggaa caaaggggcc 60

cactcactct ggagctaggt ttctccgggc ttcaacttgg caattcccag tgcccacaga 120

g 121

<210> SEQ ID NO 72
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 72

cgcccacggc atctctctgt ctttgtcact gccttgcctt ctttattctc taacttggct 60

cccctagtca cacattaagg aaggctttcc ctggtggcgc tgtggataag aatccggcga 120

c 121

<210> SEQ ID NO 73
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 73

ctcctgcatt gcaggcagat gttttaccct ctaagccaga gtaaactctt caataatagc 60

cttatattgg tccatatact ctcatttgtg gcatttaaa attctgttca ctccttcccc 120

a 121

<210> SEQ ID NO 74
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 74

atcgaccctg agataagaat ccctgcctta gatgcttgcc atatttgaaa agaaagctaa 60

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ggttttatca tttcacagca gtcttagtac cctggagagc ctctgtattt taagttgctc 120

a 121

<210> SEQ ID NO 75
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 75

agctgatcct actgaggcag cctgggttca gtcctcccag ccctggcccc cagtttccgg 60

cgcagctgtt cccgagatac ctgagcaaag ccctgagcga tcctgggcgc gtggcaggca 120

a 121

<210> SEQ ID NO 76
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 76

gagaggagcc ttttcttctg cagtgctgcc cgccccacat cctcttgggt ggagctccac 60

gtccctgttg cagatggcct tctcctcttg tgccttcaaa tggcagaggg tgatagagag 120

a 121

<210> SEQ ID NO 77
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 77

aataatacaa tgttaataga aatgggccat gtattgagtc gtcatttaaa cataagtaat 60

ctcttggtcc aaattagtga aaccttaaaa aaaaaaaagg attgtctcta gagaacatca 120

t 121

<210> SEQ ID NO 78
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 78

tgacggcaga aggctggggg cctgctttgt gattttcccc cttgggcttg acacatgtta 60

cacacagctt ctgctccccc tgccagtacc tccaatacct gctgcaggga ccctgatgac 120

a 121

<210> SEQ ID NO 79
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 79

agttagtcta gcatccaact tttatgattc accctaagaa aataattgga aaagtgtgca 60

gagatgattg tgtgagatca ttaaagtatt atttataata gtgaacaaac acaaacaagc 120

a 121

<210> SEQ ID NO 80
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

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<400> SEQUENCE: 80

ataataactc tacctcactt tagcacaggt tcctgcacag aagtctggta ccaggaaaac 60

ggcgaaacca gaaaggagca aggccctgaa tagcacccgg gaattgtccc cagtggcctt 120

g 121

<210> SEQ ID NO 81
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 81

attatctatt tggtttgcaa ttctatttac ttatttatct ttttggccat attgtgtggc 60

ttgcaggatc ttaatccctg accagggatt gaacccgtat gctctgcatt gagagcacag 120

a 121

<210> SEQ ID NO 82
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 82

ccaggaaact ctgattaaaa aaaaaaacaa acaacctaaa aaactaagaa agcaattaag 60

cttcacttat gtttaacatg ccaagtaaca ggtatatgct atgcattgga aatgcaggct 120

c 121

<210> SEQ ID NO 83
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 83

tcctaggtag gtgggccctt gctgacccaa caggcagtga taatcgagga aaggccaagg 60

gtttggctag tatctcccat ccctctgcta gccttcccca gtgtctgtcc tagtttctga 120

a 121

<210> SEQ ID NO 84
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 84

catttctatg tctgcctctc cccacaaaga gttttcttaa tctactggtc ttcatttaca 60

gtcttatttc cagaacacaa aatcaggcat ggaagatgct cagtaaatgt taggagaact 120

a 121

<210> SEQ ID NO 85
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 85

cttgaattca aaaatagact gttttgatac ggggaggaca attagctatt aataccagct 60

gaattttctc actcgttcta ataaaggctt tcttcctgtt ataggtttcc accatgaatg 120

a 121

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<210> SEQ ID NO 86
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 86

aattaaagtt ccaatgataa tagatttgaa aatataataa ataagaggat agtaatgaaa 60

gtaatattaa gggagtagga gagtatggct acaaatttct tctaaaagga aaagatggat 120

g 121

<210> SEQ ID NO 87
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 87

gacaaatttt aagtatacct caagtgttcc tataaattta agacatttag taatacttca 60

gggtggcttg caacttaaat tctataactt ttgttaggaa gtgtaggatt ccattgtgga 120

a 121

<210> SEQ ID NO 88
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 88

gagttccagt gtttggggac aaacactgct gtggaaggaa cgtgtgaaaa ggccacagtc 60

ctgtcagtga atgaggaagg ctgtgctttc tgtgtgcttc aagcagggaa gctgtcactc 120

a 121

<210> SEQ ID NO 89
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 89

aaatgctttc aggttttcac cattgagaat gaaatttgct gtgggttcgt catatggctt 60

ctattatgtt aaggtagttt ccctctatgc ccactttctg gagagttttt ttatcataca 120

t 121

<210> SEQ ID NO 90
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 90

gactgaactc cttccaaaac agacctgttc tgtcactctc tttcatctca ggcaatagca 60

cttctatcct tggggccctt cctgactact gtctctctcc ccaacccacg accaatccat 120

c 121

<210> SEQ ID NO 91
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 91

caacagtatt gtagccagat atccaaacta gtagaacatt ttaacctctt tgacctcttg 60

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gatacctgct ttttttttta aattgaagta tagttgattt acaatatagt gttagtttca 120

a 121

<210> SEQ ID NO 92
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 92

agaatatcca agagactagt gaaaggccac tgaattatgg gtataccaaa taaatacgat 60

ggcacctaac aaccaaagct gcaatgacat cacccccagg aaaatgctgg ctgtcaaatt 120

c 121

<210> SEQ ID NO 93
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 93

ctggaggact agaatcaatt agacatggac ttgggggcca tcacaccaca gagcccctca 60

cccacaggag tccgtgggtg agacctcctt cccttcctca caggacatgg ttatacttgg 120

c 121

<210> SEQ ID NO 94
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 94

ggcataataa atataatgca cttgaatcat cctaaaacca tcctccctgc ctccccactc 60

ccaccagtcc atggaaatat tgtcttccat gaaaccggtc cctgcagcca aaaagtttgg 120

a 121

<210> SEQ ID NO 95
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 95

attatttggt caatttggat ttcgcagaca attaaactgg ttaattcaga tcaaaatttc 60

ctcttcagat tctgacttat caggattggc acctacatta atttaattag tggaccaatg 120

g 121

<210> SEQ ID NO 96
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 96

gtatttattt agacctcttt agaattgttc atgttttcaa ctcatacttt cgtaagtgga 60

cggcctgcta aggaaagcgc ctgacagtgc tgttgatgct tctgtaaagt ttggagcagt 120

a 121

<210> SEQ ID NO 97
<211> LENGTH: 121
<212> TYPE: DNA

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<213> ORGANISM: Bos taurus

<400> SEQUENCE: 97

attgcagaga gtaagaactg aaacaaggat gcccaagtgt gaaatctgca aaacaggtgc 60

gctgggtgtc ctgagctgtt ttctaatcct caccccccttg ctctgtgagc tgtcttctgt 120

g 121

<210> SEQ ID NO 98
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 98

ccacaacata tctgaattta gaacacctca tcatgggcca aaatatcctg tttgtaatca 60

cgcttgccca cgacagaaac atatacaatc atccctgtca tctgcagggc attggttcca 120

g 121

<210> SEQ ID NO 99
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 99

actgtccccg gaagggaagg gtgtcaagtg aatacaggca tggaggtgcc gatgaaaaga 60

gcctgggcct tgttcactca gctgtcgttc tcagtcagag tccgctccca ggaagactgc 120

t 121

<210> SEQ ID NO 100
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 100

ataaggaaac aagtgtctta ccccacaaag caccagccct ccacagggtc cctcttatgg 60

gagaaagaca gctcagaact catgatcctt gaagtagggc aggagctagt taacacacac 120

a 121

<210> SEQ ID NO 101
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 101

tgccatcatc tccattacat acaagaggaa cctaggtctt gagcagatta agtcaacttt 60

cccaggccat caatcatgag caaaagtctg tgatgtttcc ctggagacca cttcattccc 120

a 121

<210> SEQ ID NO 102
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 102

cactgactga gttccaatga cttcagaaag aagagagaaa ggcatagctt gcatttacag 60

gagtatcatg tccatgtgaa ttttagcgtg caaagaattt tatgctatgg ttgaaatcag 120

a 121

<210> SEQ ID NO 103
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 103

gaagaactat ggtgtaatct ttccaatagc cttgtaaaca gagaacaaat cctcacaaaa 60

ggtatctttt acttgtggga caaagtaaac ttctggcaga tgtcaaatgt ttatactcgt 120

c 121

<210> SEQ ID NO 104
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 104

ggaagccctt gcctaagtct aggcaggatc ttaagaatcc atggtggagg aatcttcata 60

tgctaaacaa aagtagtatt tcacatataa tagtttgcat gtgcaggtac tggtgatgac 120

c 121

<210> SEQ ID NO 105
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 105

aaatcatatt tatctttgta tcaatcaatt cagtttaagt ttatatacat ttaatctgga 60

ccacctttgt aattacctgt ttactgtttg ttttcagaca gactgtaaat tcaaagaggc 120

a 121

<210> SEQ ID NO 106
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 106

gaaccatcct tgtactgaag ccctctatac cagttagcct aacctgaatc accatgacag 60

gcaagtttct gccactgatt aattatttttt aataagttct gtctcagaca aggtggtact 120

a 121

<210> SEQ ID NO 107
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 107

agcaattcat caaatactca ctgactacct gcattcttcc ttttagtaat gtaacagata 60

cttattgatt ccctactaca tgcaaaaaac ttggtacagc attgagaaaa gtaattatga 120

a 121

<210> SEQ ID NO 108
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 108

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ggcagatcaa gggttcctct gtgataccat ctttcatgga cgcctttagg ggattgaact 60

ccttgtgtat gaatggccat tctgggggcc ttcctgtgag tctctggatc agcagagagc 120

c 121

<210> SEQ ID NO 109
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 109

caccaacgac acagcctcag caggaacttc tctcttaatt agccttgagt aagaatttct 60

caacagagtg ctggaaccac tttgtcccaa atagcattat gattttcttc taatcagttc 120

a 121

<210> SEQ ID NO 110
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 110

acctggatca agtccggtct gcggcctctc tgagtctggg cttcttgatt atgtggactg 60

gtatattccy ttttagacgt aagccagttt gagtcgcatt tgttaccact tgcaacctga 120

t 121

<210> SEQ ID NO 111
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 111

gccaagtaag tccctacaac tcctctttca tcccaagttg aaaacttagg tttcaaccct 60

caacccacct ctattcactt cctttctcac attctcaggg ggaagcttag agaacccatg 120

a 121

<210> SEQ ID NO 112
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 112

ctttaggata acaaaagggt ctgatattca aatgagagtg attttcaaat gaatttcaaa 60

gggaagtgag gtggagtggt agggattccc accctcacac cacctgcccc cacagccctt 120

a 121

<210> SEQ ID NO 113
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 113

atgtcactta tggttcccca gatactgctg tttaatcgct ttcaattacc tcaccccatg 60

cctacccaag ccaaatgaag tggtgagtca agcgattgtc tcgtgaatgg gatcaataca 120

g 121

<210> SEQ ID NO 114
<211> LENGTH: 121

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<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 114

ccagccattt ctgagctcag aaaactatga aactcaccat tctttggcca ttctttgccg 60

cgccttattc ctttgaggaa acagtggaaa tttaaatgta tttgaagttc tttttctgca 120

g 121

<210> SEQ ID NO 115
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 115

accctgagtg tgcactgcca gtgctgggct gtctgccaag cgcttagtat gaatgatcac 60

gcggccctga agccacactg tgcatagcag aaattctgtt cttgtctctg cctcaaagat 120

g 121

<210> SEQ ID NO 116
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 116

cgtccatggg gtcccaaaaa gtcagacatg actgagtgac tgaattgact gactgactga 60

caaggataat ctttagtttg tcataactat tgcaactatt ttgttcttat ttgacattaa 120

c 121

<210> SEQ ID NO 117
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 117

gggagtcctg aaacaggagc tcccctgtac agggaaattc cttcgcagcc gggcctaagg 60

gggagctgca gagtcttgaa aaaccaggca aagcagggac ttagagggca ggaaacagag 120

a 121

<210> SEQ ID NO 118
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 118

gagggaagga tctgttccag gcctctctcc tcagcctact gatggccagc ttccctctcc 60

gcatacctgt atccaaattt ccccttttta taaggacacc agttatattg gattagggcc 120

c 121

<210> SEQ ID NO 119
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 119

gtatttttc ctcctttgct tatatttaga gagtaattta aaaatagatt acagaaagat 60

ggaacactct agagtggctg gctttcctag ctgagctctt aaaagcactc cagattgtta 120

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a 121

<210> SEQ ID NO 120
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 120

actcctcctg aaaatagaga aaccctctgt ctgacttcca gggcaaaccg catggaagca 60

cacaccagaa aagattctgt ggcagaaaat agaaatggct gctggataat actggagctg 120

a 121

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

<400> SEQUENCE: 121

actggtgact ttcaatcaca gtgaagactg agtcccagcc attttatgac agtggtcacg 60

cgattcttac cccatcatct gcctctaggc tgggccatgg caacagggcc ggtgaggggt 120

g 121

<210> SEQ ID NO 122
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 122

cctatacata acctggctct gtggtcagca gggcttgtag gcatggggcc tacaagatca 60

cgaccagtag ataaagagtt tttaaacagc tccctagccc ttatgtacca gaggcgatag 120

a 121

<210> SEQ ID NO 123
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 123

gagaattcca aagtgacacc cacaggcact gggatcagca aagtggcctg aaattgcaaa 60

gatggctccc tccggtttct cagttcccag ggagcatcca aaatgggtcc agcagatgct 120

c 121

<210> SEQ ID NO 124
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 124

acagtcacca agagaagaca gaagtcagat tgcatagcag ccagaaggaa tcaaaaacag 60

gctcagctga cccaaaggct acaaggccac aaatgtcaag ttcttccctc agtgcctgct 120

g 121

<210> SEQ ID NO 125
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 125

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ccattcctcc ctgctggcaa ccacaagtct atttttttgtt tctgggccca catgtacttc 60

gaattgttaa atgcaattca attccatttg gtttatgaac gtgtcactcc ttcccatgaa 120

c 121

<210> SEQ ID NO 126
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 126

gaggctggaa tcaaaggagg catttccagg catatcttta tttttacatt accagaaatc 60

ccatatgggg ttgactagtt agtttagatg ctcagggctt tggtttcagg gctaatgaca 120

a 121

<210> SEQ ID NO 127
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 127

acctttccat caagcaatca tttcctctct ttcctgtaag tcttagaatg gttaatagcc 60

gagtcttccc tttcttttga ccaattctca cctctggttt gttcctcatt gttgtgacat 120

a 121

<210> SEQ ID NO 128
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 128

gtgctgcgaa cagaccccta aaggaaaagg cttctccagg gaactgggaa gaaagggaag 60

cagaacagaa ggccctgcca gaccttctaa ccttcctctg aggcttcttt tttaatcatc 120

a 121

<210> SEQ ID NO 129
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 129

aattccatga atggaggagc ctcgtgggct acagtccatg ggatcgcaaa gaaacacaac 60

ctcgaggcta aacaacaaca acaagggtac cgttctaagt acatacatat caagttcctg 120

a 121

<210> SEQ ID NO 130
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 130

agaaaagaga atctctcctt taagaaaagg atttacgtaa attactgtca aatgttctac 60

ccctgagcta tatacccttt gtttcaattg aaaccacttt tttttttttc cagtgaaata 120

a 121

<210> SEQ ID NO 131

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<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 131

cagtatgaag gaaagttacc aaaactgact tgtaggaact tcctagcagt tcagtgggta 60

cggctcagtg ctcccaacgc agggggcctg ggttcaatcc ttggccaggg aactgagtct 120

c 121

<210> SEQ ID NO 132
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 132

agaattggcg tggagctgtc atgtcaatag acagtcttcc cacagaggga caacccaacc 60

gtccctaaaa gttctcacag gacatttggc agcatctcca gtaactcagc caatattact 120

c 121

<210> SEQ ID NO 133
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 133

atactttgtc tctgtttgtc gccccagcct aaaaagatcc aatccagggt ggcaagatat 60

ctccatattt gctactgact taagaactga ctcatttgaa aagaccccga tgctgggaaa 120

g 121

<210> SEQ ID NO 134
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 134

ctgagggtcc agtctcagcg atggggcttg ccgggctgcg ctcttccgca gtaggctctg 60

gggggacggg ggcaggcacc aggagaaagg ataaaggtca cagtgagact atgctgggtc 120

a 121

<210> SEQ ID NO 135
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 135

atgtttctgt atgatggaag tgaggcaagg tggaagactg gctcccagtt tgacctgctg 60

gaaccacagg ggccgtggcc tattgcaatg acagcctaca atcaagtatc tcttgactgt 120

a 121

<210> SEQ ID NO 136
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 136

acaaaataat catagttact aatatttgaa tctattcaca aaaatagagc aagccctcaa 60

caatagcacg atctaaatga caaacttttc aacaaaacta ggtaggatgg tatcctcaca 120

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a 121

<210> SEQ ID NO 137
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 137

ggagggacca aaaacaagac agacaaacag attccttttt aaggctgagt aaacgaagat 60

cgtggcatct ggccctgtca cttcatggga aatagatggg gaaacagtgg aaacagtgtc 120

a 121

<210> SEQ ID NO 138
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 138

agcagtcgct catggagtca gaattcagat gggaactggg gctgtggcag aaatctgccc 60

ggtggaaact gtggccacag aacggacttc tagaaagaga tggaattacg gagactccga 120

t 121

<210> SEQ ID NO 139
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 139

atgaacaact atagccagga gcaatggaga aatcaccttg ctagcaggcc caagggaatt 60

gccaccgagt gcctgcactg ctgtgggctg gcaggaccca gagatgcact gtcaggcggg 120

g 121

<210> SEQ ID NO 140
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 140

atcttgactg aagtggtgat tacaggtgta tacgtttgtc aaaatttgaa aagggtgcat 60

cctgtatttt attgtgaata aactatacct caataaaact gaattaaaaa gaaaatccaa 120

a 121

<210> SEQ ID NO 141
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 141

acacatatag cataagaaga tgggaccaaa atgtcttcac ttttacactc aaggacttgt 60

gttttttttt gcggatgggt ggcaggggag aagggtgtcc acaactgctt aaggaccaag 120

a 121

<210> SEQ ID NO 142
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

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<400> SEQUENCE: 142

ggttatgaag ctctactata cttacgcaag accacgactt ttcagggaaa ctgggaaaag 60

ggcatactag ctctttctga attatttctt acaactgcat gagaatctac aacaatatcc 120

a 121

<210> SEQ ID NO 143
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 143

agccctggtc agcaccatgt gaagcagaag aaatgcctgg gcaatgcaca gaaccacgag 60

tgagagtaca tgttgttact gtaagtctct agggcttagg agatttgtta cccagcaata 120

g 121

<210> SEQ ID NO 144
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 144

acatggaaat agctttgttt cataacactc tctttgtatt ttttggttgt tgttataatg 60

gaattttgtt gtatatggcc ctgaattcta ctaagtgctt cagacttgaa gagtttggtt 120

g 121

<210> SEQ ID NO 145
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 145

caggtccttt gaatttcctt tgggctcagc cagtgggagg ccacagtggg agtgaagaga 60

gaagggctgg gtcacctttc tgtcctgtgt ccccctctct gtggggtctg cttaggctgc 120

c 121

<210> SEQ ID NO 146
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 146

agtcagacac aactgtgcaa ccaacacaac acacactgac taacccctcc ttgccacttc 60

cactgcctgc tctctggcca tccctacttt ttatctggat ctcctaactt gccttccatc 120

c 121

<210> SEQ ID NO 147
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 147

ctgaaacaaa tactgggata tcagacaggt ctctagagaa cccacccaca aaaaaagatt 60

ctaatataag acaaactacc tgtagttttc tgtttttctt tttctttttt tgatattgac 120

a 121

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<210> SEQ ID NO 148
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 148

caagaagcac ccgggctcca ggggaaggca tgtgggcagg cttccacctg tcccttgggg 60

cgctaaggcc agaagggaag agggggtagg atggagagca accccagctg tgaacacaac 120

c 121

<210> SEQ ID NO 149
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 149

actggatgag tgtataatta tgtgcatcca caattatatt ttcataaaga gtaatttcac 60

cgtcctgaga gtcccctctt cctctctcac tactagtccc tggtaaccac tgatatcttg 120

a 121

<210> SEQ ID NO 150
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 150

aactaaagac ttgagaagag taaattgata gagcataata gtgtttggca caaggaaagg 60

catgtgtaga tgagagcgtg ctgggaaaag gtgcttacat ataacacaag caaaattaca 120

c 121

<210> SEQ ID NO 151
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 151

tgcaccaaaa ttccttttct aaaacttagt aagacttggc accaattgcc aacattgcta 60

gttgtctttc tgatttttt ttttttttt gcatctctta gtcttacaaa ctactgcaca 120

a 121

<210> SEQ ID NO 152
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 152

agaaaaaaaa aaaagaccag caaggtaagg gaaagagagt ggccactgac cacctccccc 60

ggatcaatcc ccttctagct ctctccccga gagggcttat ctcttgtagg gagaggtctc 120

t 121

<210> SEQ ID NO 153
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 153

accatccttc ttcccctcta gaatatgcta tctgtaattt tatttccagt gcttggtacc 60

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gtaattggaa tataaactgt ttatcaaata catgttgaat caaggctaag cacagagcaa 120

a 121

<210> SEQ ID NO 154
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 154

acaggaattt tgacccatag cttgtggtcc accagagcag ccacagggcc tccgccagca 60

cgctaaatgt tctatccctg cttctgccaa ggaatgttga tcagatcatg tagccctgtc 120

c 121

<210> SEQ ID NO 155
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 155

cctagcctca tgcttcgttc aaaaaccaat agccatttta ttggtttctc aagaaagaaa 60

gaaagtaaaa gcaatcatag gccatcacca taggccatct gatggcctgt atgctagcac 120

a 121

<210> SEQ ID NO 156
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 156

cagctttctt caccgtccaa ctctcacatc catacatgac tactggacaa ttggactatc 60

cgtatttaag cttgtctcct ttttgaggta gtcatttctt aagttggcaa gtgtctttat 120

g 121

<210> SEQ ID NO 157
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 157

aacagggctc tatgtccaag gaaaccagcc agtcacccgg tggcaggatg atcataggtg 60

gttcttttca atatggagag gccagagact agtcctcaga aaaataaacc tcttggatat 120

g 121

<210> SEQ ID NO 158
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 158

aaaggagagt acaccctcaa ggcatgaggg tgagtggacc ccaaaggaga ggccttaatc 60

catcttgacc ttctcctttt atatgtttgt cttctcccca ccttgagcct gccttctgca 120

a 121

<210> SEQ ID NO 159
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

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<400> SEQUENCE: 159

taaacatgac taggtcattt gaatgtctct ttgagaaaat ttaccatggc acttactcta 60

gtcattgggc ttcccccatg gcactagtgg taagaaccca ccgaccaatg caggagatgc 120

a 121

<210> SEQ ID NO 160
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 160

tgagcatgag tgttgcagag cagcagaaag aagtagaata cttcttagct tccgtggtgg 60

ctacttatgt caatagttgt gtggagcgct tgccccacgg tggccctctg atgccaaaac 120

a 121

<210> SEQ ID NO 161
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 161

agtttgctgt tatttgtgaa ggatactttt gctaaatata gaaatcttgg ttgacagttt 60

cgttctctga gtaccgaatg catcactcca ctgtctttga cctctgttgc ttctgatgag 120

a 121

<210> SEQ ID NO 162
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 162

agtactgcgg aaatggattg cagtcacaac tggctttgaa gaggccaatt acaaggtaaa 60

ttttccatat atcctttaag gtaaagaaaa aaagaataaa aatccccaaa tggccagaga 120

a 121

<210> SEQ ID NO 163
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 163

agagggttat aaacacatca taaaatctga cctttccaag aggggattat ctataaataa 60

ctgtggtgct aggcataagc ctggtggagg ggctgagagg agggtaattt cctctactcc 120

c 121

<210> SEQ ID NO 164
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 164

catccatctt gtagccctga aaacaacagc aagaagataa acagagcact gagagggaca 60

cggccgtcca ctcagaccca gaacacagac aactcccagg aaactgcagt ggacagaagc 120

c 121

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<210> SEQ ID NO 165
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 165

aatcaggccc cagacagggg gaaaaaaaaa tgctaagcaa gactgctata gggggtcctg 60

gaactaggga agcttcttca gggccttttc tctgtgggtg ataatctttt cacttcccca 120

c 121

<210> SEQ ID NO 166
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 166

atatgttctg tctttttcat tatatttgtc aatgtcttgg ttctcccttt attatctctt 60

gcctggactc ttcaagtagt cttacaaatg tcttcagctt ctctccaacc ccttcaatta 120

g 121

<210> SEQ ID NO 167
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 167

ctttttcacc agctgccttg gctgtgtgaa cttctctctc gataatcatc ccttatccca 60

catcccagtg tggccctgct tcccctatca agccctaact gatacactag gtaaatgaga 120

c 121

<210> SEQ ID NO 168
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 168

ccttccctcc ctggagggga gggttctcca cagcttccac ggtggccaga gggctccccc 60

cacaaccaca cctgtgaaca gtctcctctg ctccaccttа gggcagggag gagccccatc 120

c 121

<210> SEQ ID NO 169
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 169

cgccaggctc ggaatgggac ctcacccaca ccttcttctc gcccaggtgt ctgttcttac 60

gttcagggca gccccctgg tggcccccag ggttgggact taaagccact gtccgcaagt 120

c 121

<210> SEQ ID NO 170
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 170

gcaatgcagc ttggttagtt cccttaggct ccaccagcgc tgtgttatgg agcacgtgac 60

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cggtcgtggg ccatcaccat ctgacatacg acagtcatga gctactagaa acattcagtc 120

c 121

<210> SEQ ID NO 171
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 171

aatttagcaa agaagcctag cttttataaa agatcaaaca tttcacttta taaaaacact 60

cccagtgatg gtcacttgac tttcctcaag acttttagct gtggtgataa aacaacagga 120

c 121

<210> SEQ ID NO 172
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 172

aaagtattat aaacctatta catttttct tgctttttac caagcaaatt gacaacattt 60

gaaaaaggat cattgaaaga atatgaggaa tcacatattg gtgggaatgc aaagtgtaag 120

t 121

<210> SEQ ID NO 173
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 173

agacacgtat ttgcatcatg catttgtgtg tccccttcct aaagagacgt ctcttgtaga 60

cgtcactgtg tggcctgtat tcctagcctc agccgaggcc tcctcattga acaccagtca 120

c 121

<210> SEQ ID NO 174
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 174

cccagacaca caatcacacg taattgaatt ggagtcctgg taaacatgtg tggcttcttt 60

ctttaatagc tgggtgaatt gccattccaa ataaaattgg gattattata aatgaagaag 120

g 121

<210> SEQ ID NO 175
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 175

tagtatggcc agaacttgat cattacaggg aaagcgtgaa ggtggaattt ggagaagaag 60

gtatagaaca gcttctgcat ggcccattaa agaagtatgg gttttatgta aagagtattg 120

a 121

<210> SEQ ID NO 176
<211> LENGTH: 121
<212> TYPE: DNA

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<213> ORGANISM: Bos taurus

<400> SEQUENCE: 176

acaggacagc tgaaaaagag caatacaagt cccgtgtttt aaaagtagaa gataagacat 60

gctggagcag gtagagagaa aggacttctc ctacactgtt ggtgggaata taagttgggg 120

c 121

<210> SEQ ID NO 177
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 177

cccggcatca gtaatgacac ttgttattaa caattaggtt gcattatgtt gcttcagaac 60

gcggctcctt gtcagcagca ctggcctgcc agttgctcgc ttacagcctg gccctcagaa 120

g 121

<210> SEQ ID NO 178
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 178

ggggcatgtt ccagacaatg ctaaatgcag atatgaacct cttcagggtg ctgaatcccc 60

cctgtgctga gatccccagc tccgactaag cctctgccct ccaagatggt cagatttctg 120

a 121

<210> SEQ ID NO 179
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 179

caccagagct aatgagccct tttcctatca tgaagcctgg aaaggagttg gagaggcaaa 60

ctcgaatcag aaacatctct ctggggactt ttttcttttt gcaaagggac cagaaagaaa 120

g 121

<210> SEQ ID NO 180
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 180

acactcctat ggtgcactcc ccactccctg cgcatgatga aaggactttg caaacactca 60

gtgggcacag caggcccaag aggtgaggga agttgtcgac cccatcttac ggataaggaa 120

a 121

<210> SEQ ID NO 181
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 181

gcatataatc catcaaatga gggtaactgt tctattttgt atttttaata cctgagtgtt 60

ggtcatacaa tctcttccta agggaagcta taacttagta gagctctaat tacaatgcaa 120

a 121

<210> SEQ ID NO 182
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 182

ggattcttta ccactgagcc accttgggaa acccccattc acttttgtac ttaaggccaa 60

gatgtatctt ttctcataaa tatgtcctct gttagtaaat cttatgagaa tgttttaagc 120

c 121

<210> SEQ ID NO 183
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 183

aagacacact tgtaggagcc tgctggaaca ctccagggac aaggcccggt gggtgacacc 60

gtcatactct ccctttgccg tgctccggag gtccagaatc tcccaggaga aagcttatac 120

t 121

<210> SEQ ID NO 184
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 184

tccctcccac catcaacctg gcttgctctc ctgcttccct aatgcaagtt gaaagaagaa 60

cctatgtgcc tgctgccatc cactattcaa ccaaaactgg atcccagcat caccaaataa 120

a 121

<210> SEQ ID NO 185
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 185

caagttctag atgggtgaaa acctacgtct gtctttcctt ttgtagccag tcttccttat 60

gcatagcaga agctcacaaa cggtaattta ataggaataa aaggagtgta tctttgaacc 120

g 121

<210> SEQ ID NO 186
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 186

caactttatt ttttttattc tacaaacaat ttattgctct gtgaaaagta ttcaatgaaa 60

gtttcaggcc caattgagtt gcgtcccttt ggccacgtgc ccttcatttt ggcaaagggc 120

c 121

<210> SEQ ID NO 187
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 187

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aactcctcat cttcatctaa cccagacaat ctacaatatt cattaccact cttggccagg 60

gattagggag taagtgctta gaaaatagtg gttctgaaaa attaccatct attggatatg 120

c 121

<210> SEQ ID NO 188
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 188

ccacgaggaa gtgaaacctg tcaacaccaa ccacaggggt gagcttggaa gtggatctgt 60

cggccctagt tgagccttga gatgacagca gaccaggctg acacctccac tctaacttca 120

a 121

<210> SEQ ID NO 189
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 189

agcaacgaga cggaaggggc ctgggcccct ggtgctggcc ccgccctttg ggcagctaac 60

gggagaaaga gtcggctttc cactcttgaa gctgccagcc ggcatctctg gcgtcgcaaa 120

c 121

<210> SEQ ID NO 190
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 190

tctctttctc tctggctaga agcaaatgac cccatgatgg cagagccaca ccatgaagag 60

cctgggcctc tgagtcagtg cttacaggat gaggggggcca ggaggtcctc ttgccggggc 120

a 121

<210> SEQ ID NO 191
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 191

caagaacagg gtatagtttt gtgatagctt gaaggcaaga gagcacatgg cctattctgg 60

gaactatagg aatagaatgg ctctgtcata ggattgaagt ggtaaaagaa gacatgggag 120

a 121

<210> SEQ ID NO 192
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 192

aacctcagga gtctatagat taaaatattt gcttgacctt taatacaagc aggaacccaa 60

caattccagc aataattaca aaaatattac tacctcccgt ttattaagca tttattttcc 120

t 121

<210> SEQ ID NO 193
<211> LENGTH: 121

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<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 193

tgtcgcctct gtaaatggag gtaatcttag actccacctc aaagggctca tgtgacgatc 60

gcaggagaca atgcccataa aattctgggg acagtgcctg actcagagaa agcgctgcac 120

a 121

<210> SEQ ID NO 194
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 194

ctcccaacca ggtttcttga gctataatca aaacaaatgg taggccaggt gggggatgag 60

gcatttactc ttagttaagc acagactgca ttttttttaat ataggaaaat cttaaaatgg 120

c 121

<210> SEQ ID NO 195
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 195

cctggctatg gatttgtata caggcaggag ttttgttcag gttgtctttt aatttctaga 60

gcttagcaca gataccctat tgatacaata aacatttgag aaagggaaga gaaataaagg 120

a 121

<210> SEQ ID NO 196
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 196

actctcagca gaaaacacat tgagcaggga gggtcttaga gacaggacaa gaactatccc 60

cggacaattt tactctccct gaaggcccct cctctttcac tctctacccc attcttcaca 120

t 121

<210> SEQ ID NO 197
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 197

ccacagaagt ggaatcgtgt cgtatttgtc ctttcatacc tggcctcttt cagtttgtgt 60

gacggcttcc aggtttatcc acgctgtacc aggtgtcaga atttccttct ttttttgagg 120

c 121

We claim:

1. A method of prophylactically treating paratuberculosis in a population of cattle, comprising the steps of:

1) genotyping a biological sample obtained from one or more members of the cattle population, and detecting a genotype selected from the group consisting of:

(a) SNP BTA-72108-no-rs T/C, wherein one copy of BTA4 comprises SEQ ID NO: 149, and the other copy of BTA4 comprises SEQ ID NO: 149 wherein the 61st nucleotide base is T;

(b) SNP BTA-116871-no-rs T/C, wherein one copy of BTA17 comprises SEQ ID NO:32, and the other copy of BTA17 comprises SEQ ID NO:32 wherein the 61st nucleotide base is T;

(c) SNP ARS-BFGL-NGS-41833 T/G, wherein one copy of BTA20 comprises SEQ ID NO:76, and the other copy of BTA20 comprises SEQ ID NO:76 wherein the 61st nucleotide base is T;

(d) SNP ARS-BFGL-NGS-75935 T/C, wherein one copy of BTA21 comprises SEQ ID NO: 173, and the other

copy of BTA21 comprises SEQ ID NO: 173 wherein the 61st nucleotide base is T;

(e) SNP BTA-28297-no-rs G/G, wherein both copies of BTA10 comprise SEQ ID NO:86;

(f) SNP BTA-60642-no-rs A/A, wherein both copies of BTA25 comprise SEQ ID NO:89 wherein the 61st nucleotide base is A;

(g) SNP UA-IFASA-8974 A/A, wherein both copies of BTA20 comprise SEQ ID NO:53 wherein the 61st nucleotide base is A;

(h) SNP BTB-01112664 T/T, wherein both copies of BTA2 comprise SEQ ID NO: 141 wherein the 61st nucleotide base is T;

(i) SNP BTB-00261837 T/T, wherein both copies of BTA6 comprise SEQ ID NO: 14 wherein the 61st nucleotide base is T;

(j) SNP BTA-116871-no-rs T/T, wherein both copies of BTA17 comprise SEQ ID NO:32 wherein the 61st nucleotide base is T;

(k) SNP Hapmap54042-ss46526396 A/A, wherein both copies of BTA22 comprise SEQ ID NO: 13 wherein the 61st nucleotide base is A;

(l) SNP ARS-BFGL-NGS-115504 A/A, wherein both copies of BTA25 comprise SEQ ID NO:60 wherein the 61st nucleotide base is A;

(m) SNP ARS-BFGL-NGS-109845 T/T, wherein both copies of BTA29 comprise SEQ ID NO: 164 wherein the 61st nucleotide base is T;

(n) SNP Hapmap26742-BTA-156593 A/A, wherein both copies of BTA17 comprise SEQ ID NO: 176 wherein the 61st nucleotide base is A; or

(o) SNP ARS-BFGL-NGS-103845 T/C, wherein one copy of BTA7 comprises SEQ ID NO: 146, and the other copy of BTA7 comprises SEQ ID NO:146 wherein the 61st nucleotide base is T; and

2) either:

(a) selectively breeding together two or more members of the cattle population that were genotyped in step 1) as SNP BTA-72108-no-rs T/C, SNP BTA-116871-no-rs T/C, SNP ARS-BFGL-NGS-41833 T/G, SNP ARS-BFGL-NGS-75935 T/C, SNP BTA-28297-no-rs G/G, or SNP BTA-60642-no-rs A/A; or

(b) screening for the presence of *Mycobacterium avium*, ssp. *paratuberculosis* (MAP) or physically separating from the cattle population any of the one or more members of the cattle population that were genotyped in step 1) as SNP UA-IFASA-8974 A/A, SNP BTB-01112664 T/T, SNP BTB-00261837 T/T, SNP BTA-116871-no-rs T/T, SNP Hapmap54042-ss46526396 A/A, SNP ARS-BFGL-NGS-115504 A/A, SNP ARS-BFGL-NGS-109845 T/T, SNP Hapmap26742-BTA-156593 A/A, or SNP ARS-BFGL-NGS-103845 T/C;

whereby paratuberculosis in the cattle population is prophylactically treated.

2. The method of claim **1**, wherein in step 2)(b), any of the one or more members of the cattle population that were genotyped in step 1) as SNP UA-IFASA-8974 A/A, SNP BTB-01112664 T/T, SNP BTB-00261837 T/T, SNP BTA-116871-no-rs T/T, SNP Hapmap54042-ss46526396 A/A, SNP ARS-BFGL-NGS-115504 A/A, SNP ARS-BFGL-NGS-109845 T/T, SNP Hapmap26742-BTA-156593 A/A, or SNP ARS-BFGL-NGS-103845 T/C are screened for the presence of MAP.

3. The method of claim **2**, further comprising the step of physically separating from the cattle population any of the one or more members of the cattle population that were genotyped in step 1) as SNP UA-IFASA-8974 A/A, SNP BTB-01112664 T/T, SNP BTB-00261837 T/T, SNP BTA-116871-no-rs T/T, SNP Hapmap54042-ss46526396 A/A, SNP ARS-BFGL-NGS-115504 A/A, SNP ARS-BFGL-NGS-109845 T/T, SNP Hapmap26742-BTA-156593 A/A, or SNP ARS-BFGL-NGS-103845 T/C and found through the screening of step 2)(b) to be positive for the presence of MAP.

4. The method of claim **1**, wherein in step 2)(b), any of the one or more members of the cattle population that were genotyped in step 1) as SNP UA-IFASA-8974 A/A, SNP BTB-01112664 T/T, SNP BTB-00261837 T/T, SNP BTA-116871-no-rs T/T, SNP Hapmap54042-ss46526396 A/A, SNP ARS-BFGL-NGS-115504 A/A, SNP ARS-BFGL-NGS-109845 T/T, SNP Hapmap26742-BTA-156593 A/A, or SNP ARS-BFGL-NGS-103845 T/C are physically separated from the cattle population.

5. The method of claim **4**, wherein before the one or more members of the cattle population that were genotyped in step 1) as SNP UA-IFASA-8974 A/A, SNP BTB-01112664 T/T, SNP BTB-00261837 T/T, SNP BTA-116871-no-rs T/T, SNP Hapmap54042-ss46526396 A/A, SNP ARS-BFGL-NGS-115504 A/A, SNP ARS-BFGL-NGS-109845 T/T, SNP Hapmap26742-BTA-156593 A/A, or SNP ARS-BFGL-NGS-103845 T/C are physically separated from the cattle population, these one or more members of the cattle population are screened for the presence of *Mycobacterium avium*, ssp. *paratuberculosis* (MAP).

6. The method of claim **1** wherein step 1 is performed using a bead chip.

7. The method of claim **1** wherein step 1 comprises a field test.

8. The method of claim **1** wherein step 1 comprises using a visual indicator.

9. The method of claim **6** wherein the bead chip is useful for estimating breeding value in cattle.

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