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(54) **MYCOBACTERIAL RPOB SEQUENCES**

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(75) Inventors: **Thomas R. Gingeras**, Santa Clara, CA  
(US); **Jorg Drenkow**, Hollister, CA  
(US)

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**Correspondence Address:**

**COOLEY GODWARD LLP**  
**THE BOWEN BUILDING**  
**ATTN: THE PATENT GROUP**  
**875 15TH STREET, N.W., SUITE 800**  
**WASHINGTON, DC 20005-2221 (US)**

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(73) Assignee: **AFFYMETRIX, INC.**, Santa Clara, CA

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**ABSTRACT**

This invention provides polynucleotide probes, sequences and methods for speciating and phenotyping organisms, for example, using probes based on the *Mycobacterium tuberculosis* rpoB gene. The groups or species to which an organism belongs may be determined by comparing hybridization patterns of target nucleic acid from the organism to hybridization patterns in a database.

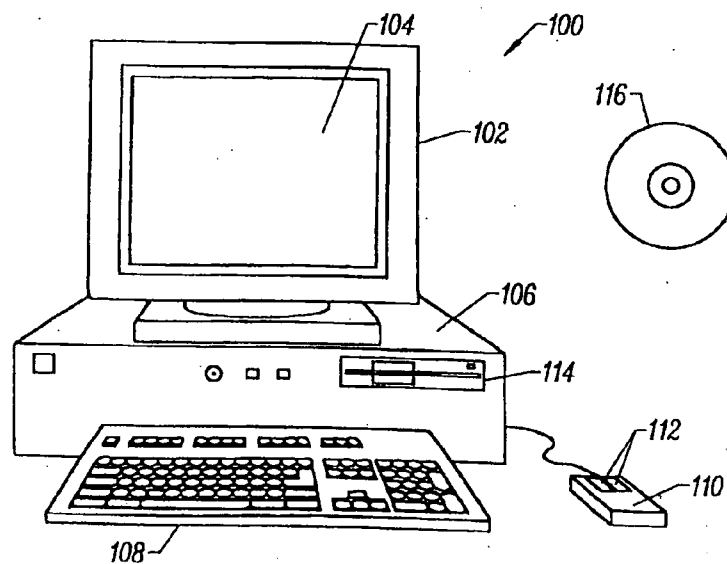


FIG. 1

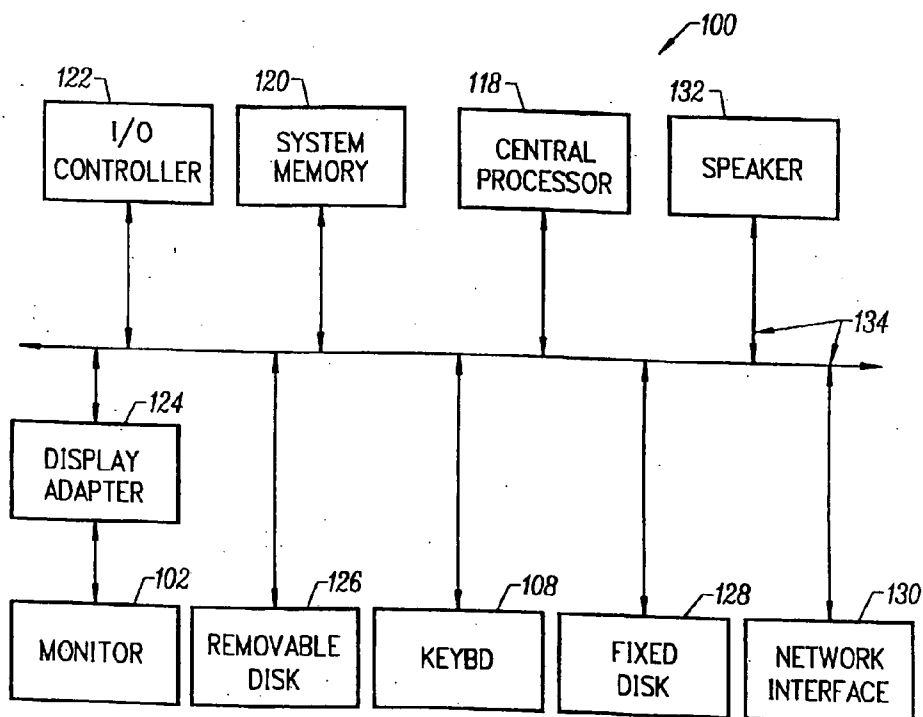


FIG. 2

## MYCOBACTERIAL RPOB SEQUENCES

### CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application derives priority from U.S. Ser. No. 60/080,616, filed Apr. 3, 1998, and incorporated by reference. Applications U.S. Ser. No. 08/797,812, filed Feb. 7, 1997, now U.S. Pat. No. 6,228,575; U.S. Ser. No. 60/011,339, filed Feb. 8, 1996; U.S. Ser. No. 60/012,631, filed Mar. 1, 1996; U.S. Ser. No. 08/629,031, filed Apr. 8, 1996, now abandoned; and 60/017,765, filed 15 May 15, 1996 are directed to related subject matter. These applications are specifically incorporated by reference in their entirety for all purposes.

### STATEMENT OF GOVERNMENT INTEREST

[0002] The work described in this application was supported in part by grant number 1R43a140400 by the NIAID. The Government may have certain rights in this invention.

### BACKGROUND OF THE INVENTION

#### [0003] 1. Field of the Invention

[0004] This invention is directed to polymorphisms in *rpoB* genes of mycobacteria and use of the same in the identification and characterization of microorganisms.

#### [0005] 2. Background of the Invention

[0006] Multidrug resistance and human immunodeficiency virus (HIV-1) infections are factors which have had a profound impact on the tuberculosis problem. An increase in the frequency of *Mycobacterium tuberculosis* strains resistant to one or more anti-mycobacterial agents has been reported, Block, et al., (1994) *JAMA* 271:665-671. Immunocompromised HIV-1 infected patients not infected with *M. tuberculosis* are frequently infected with *M. avium* complex (MAC) or *M. avium-M. intracellulare* (MAI) complex. These mycobacteria species are often resistant to the drugs used to treat *M. tuberculosis*. These factors have re-emphasized the importance for the accurate determination of drug sensitivities and mycobacteria species identification.

[0007] In HIV-1 infected patients, the correct diagnosis of the mycobacterial disease is essential since treatment of *M. tuberculosis* infections differs from that called for by other mycobacteria infections, Hoffner, S. E. (1994) *Eur. J. Clin. Microbiol. Inf. Dis.* 13:937-941. Non-tuberculosis mycobacteria commonly associated with HIV-1 infections include *M. kansasii*, *M. xenopi*, *M. fortuitum*, *M. avium* and *M. intracellulare*, Wolinsky, E., (1992) *Clin. Infect. Dis.* 15:1-12, Shafer, R. W. and Sierra, M. F. 1992 *Clin. Infect. Dis.* 15:161-162. Additionally, 13% of new cases (HIV-1 infected and non-infected) of *M. tuberculosis* are resistant to one of the primary anti-tuberculosis drugs (isoniazid [INH], rifampin [RIF], streptomycin [STR], ethambutol [EMB] and pyrazinamide [PZA] and 3.2% are resistant to both RIF and INH, Block, et al., *JAMA* 271:665-671, (1994). Consequently, mycobacterial species identification and the determination of drug resistance have become central concerns during the diagnosis of mycobacterial diseases.

[0008] Methods used to detect, and to identify *Mycobacterium* species vary considerably. For detection of *Mycobacterium tuberculosis*, microscopic examination of acid-

fast stained smears and cultures are still the methods of choice in most microbiological clinical laboratories. However, culture of clinical samples is hampered by the slow growth of mycobacteria. A mean time of four weeks is required before sufficient growth is obtained to enable detection and possible identification. Recently, two more rapid methods for culture have been developed involving a radiometric, Stager, C. E. et al., (1991) *J. Clin. Microbiol.* 29:154-157, and a biphasic (broth/agar) system Sewell, et al., (1993) *J. Clin. Microbiol.* 29:2689-2472. Once grown, cultured mycobacteria can be analyzed by lipid composition, the use of species specific antibodies, species specific DNA or RNA probes and PCR-based sequence analysis of 16S rRNA gene (Schirm, et al. (1995) *J. Clin. Microbiol.* 33:3221-3224; Kox, et al. (1995) *J. Clin. Microbiol.* 33:3225-3233) and IS6110 specific repetitive sequence analysis (For a review see, e.g., Small et al., P. M. and van Embden, J. D. A. (1994) *Am. Society for Microbiology*, pp. 569-582). The analysis of 16S rRNA sequences (RNA and DNA) has been the most informative molecular approach to identify *Mycobacteria* species (Jonas, et al., *J. Clin. Microbiol.* 31:2410-2416 (1993)). However, to obtain drug sensitivity information for the same isolate, additional protocols (culture) or alternative gene analysis is necessary.

[0009] To determine drug sensitivity information, culture methods are still the protocols of choice. *Mycobacteria* are judged to be resistant to particular drugs by use of either the standard proportional plate method or minimal inhibitory concentration (MIC) method. However, given the inherent lengthy times required by culture methods, approaches to determine drug sensitivity based on molecular genetics have been recently developed.

[0010] Because resistance to RIF in *E. coli* strains was observed to arise as a result of mutations in the *rpoB* gene, Telenti, et al., id., identified a 69 base pair (bp) region of the *M. tuberculosis* *rpoB* gene as the locus where RIF resistant mutations were focused. Kapur, et al., (1995) *Arch. Pathol. Lab. Med.* 119:131-138, identified additional novel mutations in the *M. tuberculosis* *rpoB* gene which extended this core region to 81 bp. In a detailed review on antimicrobial agent resistance in mycobacteria, Musser (*Clin. Microbiol. Rev.*, 8:496-514 (1995)), summarized all the characterized mutations and their relative frequency of occurrence in this 81 bp region of *rpoB*. Missense mutations comprise 88% of all known mutations while insertions (3 or 6 bp) and deletions (3, 6 and 9 bp) account for 4% and 8% of the remaining mutations, respectively. Approximately 90% of all RIF resistant tuberculosis isolates have been shown to have mutations in this 81 bp region. The remaining 10% are thought possibly to involve genes other than *rpoB*.

[0011] For the above reasons, it would be desirable to have simpler methods which identify and characterize microorganisms, such as *Mycobacteria*, both at the phenotypic and genotypic level. This invention fulfills that and related needs.

### SUMMARY OF THE INVENTION

[0012] In one aspect, the invention provides isolated nucleic acids comprising at least 25, 50, 75, 100, or 200 contiguous bases from an *rpoB* sequence shown in Table 1 (SEQ ID NOS: 1-181). Some nucleic acid comprise a complete sequence shown in Table 1.

[0013] The invention further provides a set of probes perfectly complementary to and spanning such nucleic acids, preferably spanning one of the complete sequences shown in Table 1 (SEQ ID NOS: 1-181).

[0014] The invention further provides methods of classifying mycobacteria. Some such methods entail providing a sample comprising a mycobacterial rpoB target nucleic acid from a mycobacteria, determining the sequence of a segment of at least 50 contiguous bases from the target nucleic acid; comparing the determined sequence to at least one sequence shown in Table 1; and classifying the mycobacteria from the extent of similarity of the compared sequences. Preferably, at least 100 or 200 contiguous bases are determined from the target nucleic acid. Preferably, the determined sequence is compared with a plurality of sequences from Table 1, for example, 10, 20, 50 or all of the sequence from Table 1 (SEQ ID NOS: 1-181).

[0015] In other methods of classification, the identity of one or more bases in the target sequence at one or more positions corresponding to one or more of the highlighted positions in a sequence shown in Table 1 is determined. The identity of the one or more bases characterizing the species of mycobacteria that is present in the sample. In some methods, the identity of at least 10 bases in the target nucleic acid at positions corresponding to highlighted positions in a sequence shown in Table 1 is determined. In some methods, the identity of at least 20 bases in the target sequence at highlighted positions shown in Table 1 are identified. In some methods, at least 20 determined bases are compared with 20 bases occupying corresponding positions in each of at least ten sequences from Table 1.

[0016] In another aspect, the invention provides sequence-specific polynucleotide probes or primers that hybridizes to a segment of a mycobacterial rpoB sequence shown in Table 1 or its complement without hybridizing to the *M. tuberculosis* sequence designated ATCC9-Mtb in Table 1 or its complement, the segment including a highlighted nucleotide position shown in Table 1. In some such probes, a central position of the probe aligns with a highlighted nucleotide position shown in Table 1. In some such primers, the 3' end of the primer aligns with a highlighted nucleotide position shown in Table 1. Some probes and primers are between 10 and 50 bases long.

[0017] In another aspect, the invention provides a computer-readable storage medium for storing data for access by an application program being executed on a data processing system. Such a system comprises a data structure stored in the computer-readable storage medium. The data structure includes information resident in a database used by the application program and includes a plurality of records, each record comprising information identifying a polymorphism or sequence shown in Table 1. Some records have a field identifying a base occupying a polymorphic site and a field identifying location of the polymorphic site. Some records record a contiguous segment of at least 50, 100, or 200 bases from an rpoB sequence shown in Table 1. Some storage medium comprise at least ten records each recording a contiguous segment of at least 50 bases from at least ten rpoB sequences shown in Table 1.

#### BRIEF DESCRIPTION OF THE DRAWINGS

[0018] **FIG. 1:** Computer that may be utilized to execute software embodiments of the present invention.

[0019] **FIG. 2:** A system block diagram of a typical computer system that may be used to execute software embodiments of the invention.

#### DEFINITIONS

[0020] A polynucleotide can be DNA or RNA, and single- or double-stranded. Polynucleotide can be naturally occurring or synthetic, and can be of any length. Preferred polynucleotide probes of the invention include contiguous segments of DNA, or their complements including any of the highlighted bases shown in Table 1. The segments are usually between 5 and 100 bases, and often between 5-10, 5-20, 10-20, 10-50, 20-50 or 20-100 bases. The highlighted site can occur within any position of the segment. Preferred polynucleotide probes are capable of binding in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991), and probes having nonnaturally occurring bases.

[0021] The term primer refers to a single-stranded polynucleotide capable of acting as a point of initiation of template-directed DNA synthesis under appropriate conditions (i.e., in the presence of four different nucleoside triphosphates and an agent for polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair means a set of primers including a 5' upstream primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3', downstream primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

[0022] A cDNA or cRNA is derived from an RNA if it produced by a process in which the RNA serves as a template for production of the cDNA or cRNA.

[0023] Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25° C. For example, conditions of 5×SSPE (750 mM NaCl, 50 mM Na Phosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30° C. are suitable for allele-specific probe hybridizations.

[0024] An isolated nucleic acid means an object species invention that is the predominant species present (i.e., on a molar basis it is more abundant than any other individual species in the composition). Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present. Most preferably, the object species is purified to essential homogeneity (contaminant species cannot be detected in the composition by conventional detection methods).

[0025] For sequence comparison and homology determination, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm

program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

[0026] Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by visual inspection (see generally, Ausubel et al., *infra*).

[0027] One example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al., *J. Mol. Biol.* 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915).

[0028] In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul (1993) *Proc. Nat'l. Acad. Sci. USA* 90:5873-5877). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic

acid is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

[0029] The term "target nucleic acid" refers to a nucleic acid (often derived from a biological sample), to which the probe nucleic acid is designed to specifically hybridize. It is the presence or expression level of the target nucleic acid that is to be detected or quantified. The target nucleic acid has a sequence that is complementary to the nucleic acid sequence of the corresponding probe directed to the target. The term target nucleic acid may refer to the specific subsequence of a larger nucleic acid to which the probe is directed or to the overall sequence (e.g. gene or mRNA) whose expression level it is desired to detect. The difference in usage will be apparent from context.

[0030] "Subsequence" refers to a sequence of nucleic acids that comprise a part of a longer sequence of nucleic acids.

## DETAILED DESCRIPTION

### I. Mycobacterial Sequences of rpoB Genes

[0031] Table 1 shows a comparison of a substantial collection of mycobacterial strains of an about 700-nucleotide conserved region of an rpoB gene. The sequences shown in Table 1 are identified as follows: SEQ ID NOS: 1-56, respectively, are shown on pages 21, 25, 29, 33, 37, 41, 45, 49, 53, 57, 61 and 65; SEQ ID NOS: 57-112, respectively, are shown on pages 22, 26, 30, 34, 38, 42, 46, 50, 54, 58, 62 and 65; SEQ ID NOS: 113-168, respectively, are shown on pages 23, 27, 31, 35, 39, 43, 47, 51, 55, 59, 63 and 66; SEQ ID NOS: 169-181, respectively, are shown on pages 24, 28, 32, 36, 40, 44, 52, 56, 60, 64 and 68. The first sequence, designated as a reference sequence, is from *M. tuberculosis*. Nucleotides are numbered consecutively starting from the first nucleotide of the reference sequences. Other sequences are from other strains of mycobacteria. For example, the sequences designated ATCC-av, M29, M30 . . . M104 are from *M. avium*. Sequences designated from ATT-chelnew, M11, M13, and M17 are from *M. chelonae*. Sequences designated ATCC-for, M53, M55, M56, and M74 are from *M. fortuitum*, and so forth. Complete correspondence between strain designations and strain types is shown in Table 2. Nucleotides in a mycobacterial sequence are accorded the same number as the corresponding position of the reference sequence when the two are maximally aligned. Differences between a sequence and the reference sequences are shown in highlighted type. Many of the highlighted positions are common to all tested members of a species. Other highlighted positions vary among different isolates in a species. Both types of variation can be useful in speciation analysis.

### II. Analysis of Species Variations

#### [0032] A. Preparation of Samples

[0033] An rpoB sequence is isolated from a sample of an unknown mycobacteria being tested. Nucleic acids can be isolated from mycobacteria by standard methods as described in WO 97/29212 (incorporated by reference in its entirety for all purposes). The rpoB sequences to be analyzed can then be isolated and amplified by means of PCR. See generally *PCR Technology. Principles and Applications for DNA Amplification* (ed. H. A. Erlich, Freeman Press, NY, N.Y., 1992); *PCR Protocols: A Guide to Methods and*

*Applications* (eds. Innis, et al., Academic Press, San Diego, Calif., 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Pat. No. 4,683,202 (each of which is incorporated by reference for all purposes). Primers for PCR preferably flank the regions of interest *rpoB* genes, although primers to internal sites can be used if it is intended to analyze only certain sites of potential species variation. Exemplary primers are described in WO 97/29212. If necessary, additional sequences flanking the sequences shown in Table 1 can be determined using probes based on the sequences in Table 1 to isolate full-length *rpoB* sequences from the appropriate mycobacterial species.

[0034] B. Detection of Species-Specific Variations in Target DNA

[0035] 1. Sequence-Specific Probes

[0036] The design and use of sequence-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Sequence-specific probes can be designed that hybridize to a segment of target DNA in one isolate of mycobacteria that do not isolate to a corresponding isolate in another due to the presence of allelic or species variations in the respective segments from the two sequences. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the sequences. Some probes are designed to hybridize to a segment of target DNA such that the site of potential sequence variation aligns with a central position (e.g., in a 15 mer at the 7 position; in a 16 mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic and species variants.

[0037] Sequence-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple potential variations within the same target sequence.

[0038] 2. Tiling Arrays

[0039] The bases occupying sites of potential variation can also be identified by hybridization to nucleic acid arrays, some example of which are described by WO 95/11995 (incorporated by reference in its entirety for all purposes). Such arrays contain a series of overlapping probes spanning a reference sequence. Any of the *rpoB* sequences shown in Table 1, or contiguous segments of, for example, at least 25, 50, 100 or 200 bases thereof, can serve as a reference sequence. WO 95/11995 also describes subarrays that are optimized for detection of a variant forms of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is a variant of the first reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (i.e., two or more mutations within 9 to 21 bases).

[0040] 3. Sequence-Specific Primers

[0041] A sequence-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of a variant form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two primers leading to a detectable product signifying the particular variant form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the site of variation and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the primer aligned with the point of variation because this position is most destabilizing to elongation from the primer. See, e.g., WO 93/22456.

[0042] 4. Direct-Sequencing

[0043] The direct analysis of mycobacterial sequences can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)).

### III. Methods of Use

[0044] The sequences and polymorphisms shown in Table 1 are useful for identifying the presence of mycobacteria in samples, and optionally, classifying the mycobacteria. The sample can be obtained from a patient or from a biological source, such as a food product.

[0045] The sequences shown in Table 1 can be used for design of sequence-specific probes or primers encompassing polymorphic sites as described above. These probes or primers can then be used to determine the base occupying a corresponding position in an *rpoB* sequence from an isolate in a sample under test. A base in one sequence corresponds with a base in another when the two bases occupy the same position when the two sequences are maximally aligned by one of the criteria described in Definitions.

[0046] Alternatively, the sequences shown in Table 1 can be used for design of tiling arrays in which one or more of the sequences serves as a reference sequence. At least one set of overlapping probes is designed spanning a segment of the reference sequence, as described in WO95/11995 or EP 717,113. Target sequences from samples under test can be hybridized to such arrays, optionally in combination with controls of known *rpoB* sequences. The hybridization pattern of a target sequence to such an array can be analyzed to determine the identity of bases at which the target sequence differs from the reference sequence, as described in WO 95/11995.

[0047] One or more of the above methods, or direct sequencing, can be used to identify the base occupying at least one and usually several (e.g., 5, 10, 15, 25, 50 or 100) sites of potential variation between the 16S RNA and/or *rpoB* gene in an unknown mycobacteria relative to bases occupying corresponding sites in one or more known strains of mycobacteria, such as those shown in Table 1. This analysis results in a profile of bases occupying particular

sites that characterizes the mycobacterial strain under test. The profile is compared with the corresponding profiles of different mycobacterial isolates shown in e.g., Table 1. In general, the unknown mycobacterium isolate is characterized as being from the same mycobacterial species as the precharacterized isolate with which it shares the greatest similarity in base profile.

[0048] In some methods, the sequence of a contiguous segment of the *rpoB* target nucleic acid is determined in a sample under test for comparison with one or more of the sequences shown in Table 1. The mycobacteria is classified by the extent of similarity. For example, if a target nucleic acid shows greater sequence identity to *rpoB* sequences from one species than any other, the sample from which the target was obtained is typically classified as arising from that species.

[0049] Alternatively, an array of tiled probes based on a reference sequence shown in Table 1 can be used for identifying and characterizing mycobacterial sequences based on comparison of hybridization patterns. Such an array is hybridized to a 16S RNA or *rpoB* target sequence from a sample, and the hybridization pattern compared with the hybridization pattern of one or more control sequences. The hybridization patterns of control sequences can be historic controls, stored, for example, in a computer database, or can be contemporaneous controls performed at or near the same time as the hybridization to the target sequence. Optionally, hybridization of target and reference sequence can be performed simultaneously using different labels.

[0050] Method of classifying unknown mycobacterial isolate by matching the hybridization pattern of a target sequence with those of control sequences from characterized species are described in more detail in WO 97/29212 (incorporated by reference in its entirety for all purposes). In an idealized case, the detection of a particular hybridization pattern in an isolate characterizes that isolate as belonging to a particular species. This can occur when the hybridization pattern detected in the isolate is uniquely associated with a specific species. More frequently however, such a unique one-to-one correspondence is not present. Instead, the hybridization pattern observed in an isolate does not bear a unique correspondence with a previously characterized species. However, the hybridization pattern detected is associated with a probability of the organism being screened belonging to a particular species (or not) or carrying a particular phenotypic trait (or not). As a result, analysis of an increasing number of polymorphic sites in an isolate, allows one to classify the isolated with an increasing level of confidence. Algorithms can be used to derive such composite probabilities from the comparison of multiple polymorphic forms between an isolate and references. Typically, the mathematical algorithm makes a call of the identity of the species and assign a confidence level to that call. One can determine the confidence level (>90%, >95% etc.) that one desires and the algorithm will analyze the hybridization pattern and either provide an identification or not. Occasionally, the call is that the sample may be one of two, three or more species, in which case a specific identification is not be possible. However, one of the strengths of this technique is that the rapid screening made possible by the chip-based hybridization allows one to continuously expand a database

of patterns ultimately to enable the identification of species previously unidentifiable due to lack of sufficient information.

#### IV. Modified Polypeptides and Gene Sequences

[0051] The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in Table 1. Some nucleic acid encode full-length variant forms of proteins. Variant proteins have the prototypical amino acid sequences of encoded by nucleic acid sequence shown in Table 1 (read so as to be in-frame with the full-length coding sequence of which it is a component).

[0052] Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example *trp*, *lac*, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

[0053] The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

[0054] The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

[0055] In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

[0056] Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

#### V. Kits

[0057] The invention further provides kits comprising at least one sequence-specific probe as described above. Often, the kits contain one or more pairs of sequence-specific probes hybridizing to different forms of a polymorphism. In some kits, the sequence-specific probes are provided immobilized to a substrate. For example, the same substrate can comprise sequence-specific probes for detecting at least 10, 100 or all of the variations shown in Table 1. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

#### VI. Computer Databases

[0058] FIG. 1 illustrates an example of a computer system that can be used to store records relating to polymorphisms of the invention and perform algorithms comparing polymorphic profiles and to classify species. FIG. 2 shows a computer system 100 which includes a monitor 102, screen 104, cabinet 106, keyboard 108, and mouse 110. Mouse 110 may have one or more buttons such as mouse buttons 112. Cabinet 106 houses a CD-ROM drive 114, a system memory and a hard drive (see FIG. 2) which can be utilized to store and retrieve software programs incorporating code that implements the present invention, data for use with the present invention, and the like. Although a CD-ROM 116 is shown as an exemplary computer readable storage medium, other computer readable storage media including floppy disks, tape, flash memory, system memory, and hard drives may be utilized. Cabinet 106 also houses familiar computer components such as a central processor, system memory, hard disk, and the like.

[0059] FIG. 2 shows a system block diagram of computer system 100 that may be used to execute software embodiments of the present invention. As in FIG. 1, computer system 100 includes monitor 102 and keyboard 108. Computer system 100 further includes subsystems such as a central processor 102, system memory 120, I/O controller 122, display adapter 124, removable disk 126 (e.g., CD-ROM drive), fixed disk 128 (e.g., hard drive), network interface 130, and speaker 132. Other computer systems suitable for use with the present invention may include additional or fewer subsystems. For example, another computer system can include more than one processor 102 (i.e., a multi-processor system) or a cache memory.

[0060] Arrows such as 134 represent the system bus architecture of computer system 100. However, these arrows are illustrative of any interconnection scheme serving to link the subsystems. For example, a local bus can be utilized to connect the central processor to the system memory and display adapter. Computer system 100 shown in FIG. 1 is but an example of a computer system suitable for use with the present invention.

[0061] The computer stores records relating to the polymorphisms of the record. Some such records record a polymorphism by reference to the position of a polymorphic site and the identity of base(s) occupying that site in one or more species. Some databases include records for at least ten polymorphic sites in at least ten of the sequences shown in Table 1. Some databases include records for all of the polymorphic sites in at least one of the sequences shown in Table 1. Some databases include records for at least 100, 1000, or 2000 polymorphic sites shown in Table 1. Some databases include records for all of the polymorphic sites shown in Table 1.

[0062] The foregoing invention has been described in some detail by way of illustration and example, for purposes of clarity and understanding. It will be obvious to one of skill in the art that changes and modifications may be practiced within the scope of the appended claims. Therefore, it is to be understood that the above description is intended to be illustrative and not restrictive. The scope of the invention should, therefore, be determined not with reference to the above description, but should instead be determined with reference to the following appended claims, along with the full scope of equivalents to which such claims are entitled.

[0063] All patents, patent applications and publications cited in this application are hereby incorporated by reference in their entirety for all purposes to the same extent as if each individual patent, patent application or publication were so individually denoted.



Table 1  
BASE NOS 1-60

ATCC9-H2b.txt	SEQ ID NO 1	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
MY621.txt	SEQ ID NO 2	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
ATCC1-av.txt	SEQ ID NO 3	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H29.txt	SEQ ID NO 4	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H30.txt	SEQ ID NO 5	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H31.txt	SEQ ID NO 6	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H32.txt	SEQ ID NO 7	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H33.txt	SEQ ID NO 8	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H34.txt	SEQ ID NO 9	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H38-new.txt	SEQ ID NO 10	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H49.txt	SEQ ID NO 11	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H64 (Hav2).txt	SEQ ID NO 12	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H65 (Hav3).txt	SEQ ID NO 13	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H67 (Hav5).txt	SEQ ID NO 14	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H69 (Hav7).txt	SEQ ID NO 15	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H71 (Hav9).txt	SEQ ID NO 16	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H91.txt	SEQ ID NO 17	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H92.txt	SEQ ID NO 18	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H95.txt	SEQ ID NO 19	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H96.txt	SEQ ID NO 20	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H100.txt	SEQ ID NO 21	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H101.txt	SEQ ID NO 22	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H102.txt	SEQ ID NO 23	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H104.txt	SEQ ID NO 24	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H105.txt	SEQ ID NO 25	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H106.txt	SEQ ID NO 26	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H111.txt	SEQ ID NO 27	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H76.txt	SEQ ID NO 28	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H451.txt	SEQ ID NO 29	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
ATCC2-chelnew.txt	SEQ ID NO 30	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H10.txt	SEQ ID NO 31	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H11-662.txt	SEQ ID NO 32	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H12.txt	SEQ ID NO 33	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H13-2-662.txt	SEQ ID NO 34	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H14.txt	SEQ ID NO 35	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H15.txt	SEQ ID NO 36	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H16.txt	SEQ ID NO 37	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H17-2-662.txt	SEQ ID NO 38	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H50.txt	SEQ ID NO 39	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H51.txt	SEQ ID NO 40	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H115.txt	SEQ ID NO 41	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H116.txt	SEQ ID NO 42	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H119.txt	SEQ ID NO 43	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H109.txt	SEQ ID NO 44	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H200.txt	SEQ ID NO 45	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H207.txt	SEQ ID NO 46	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H209.txt	SEQ ID NO 47	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H122.txt	SEQ ID NO 48	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H123.txt	SEQ ID NO 49	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H124.txt	SEQ ID NO 50	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
ATCC3-for.txt	SEQ ID NO 51	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H53.txt	SEQ ID NO 52	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H54.txt	SEQ ID NO 53	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H55.txt	SEQ ID NO 54	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H56.txt	SEQ ID NO 55	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG
H74 (Hav12).txt	SEQ ID NO 56	CCCAAGGACGTTGGAGGGCGATCACACCGCAGACGTTGATCAACATTCGGG



Table 1  
BASE NOS 1-60

M60. txc	SEQ ID NO 113	CCAGGACGTGGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
M61. txc	SEQ ID NO 114	CCAGGACGTGGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
M62. txc	SEQ ID NO 115	CCAGGACGTGGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY106. txc	SEQ ID NO 116	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY216. txc	SEQ ID NO 117	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY218. txc	SEQ ID NO 118	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY226. txc	SEQ ID NO 119	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
M109. txc	SEQ ID NO 120	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
M111. txc	SEQ ID NO 121	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
M112. txc	SEQ ID NO 122	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
M113. txc	SEQ ID NO 123	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
M114. txc	SEQ ID NO 124	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY325. txc	SEQ ID NO 125	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY718. txc	SEQ ID NO 126	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY214. txc	SEQ ID NO 127	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY224. txc	SEQ ID NO 128	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY244. txc	SEQ ID NO 129	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY339. txc	SEQ ID NO 130	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY343. txc	SEQ ID NO 131	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY358. txc	SEQ ID NO 132	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY609. txc	SEQ ID NO 133	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY817. txc	SEQ ID NO 134	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY821. txc	SEQ ID NO 135	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY824. txc	SEQ ID NO 136	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY102. txc	SEQ ID NO 137	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY105. txc	SEQ ID NO 138	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY251. txc	SEQ ID NO 139	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY256. txc	SEQ ID NO 140	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY294. txc	SEQ ID NO 141	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY354. txc	SEQ ID NO 142	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
ATCC7-acc. txc	SEQ ID NO 143	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
ATCC7-acc. txc	SEQ ID NO 144	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY121. txc	SEQ ID NO 145	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY249. txc	SEQ ID NO 146	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY372. txc	SEQ ID NO 147	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY378. txc	SEQ ID NO 148	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY484. txc	SEQ ID NO 149	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY556. txc	SEQ ID NO 150	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY563. txc	SEQ ID NO 151	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY586. txc	SEQ ID NO 152	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
ATCC8-acc. txc	SEQ ID NO 153	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
M35. txc	SEQ ID NO 154	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
M36. txc	SEQ ID NO 155	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
M37. txc	SEQ ID NO 156	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
m125. txc	SEQ ID NO 157	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY143. txc	SEQ ID NO 158	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY104. txc	SEQ ID NO 159	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY196. txc	SEQ ID NO 160	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY357. txc	SEQ ID NO 161	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY358. txc	SEQ ID NO 162	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY480. txc	SEQ ID NO 163	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY212. txc	SEQ ID NO 164	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY491. txc	SEQ ID NO 165	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY497. txc	SEQ ID NO 166	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
MY816. txc	SEQ ID NO 167	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG
ATCC10-acc. txc	SEQ ID NO 168	GGAGGCGATCACACCGCAGAC	TGATCAACATCCG	CCGGTGGTGGCCG

Table 1  
BASE NOS 1-60

M38 .txt	SEQ ID NO 169	CCCA	GGAC	CGT	GGAG	GGCG	GAT	CACA	CCGC	AGAC	TT	GAT	CAAC	AT	CCG	GT	GGT	GGCC	G
M39 .txt	SEQ ID NO 170	CCCA	GGAC	CGT	GGAG	GGCG	GAT	CACA	CCGC	AGAC	TT	GAT	CAAC	AT	CCG	GT	GGT	GGCC	G
M40 .txt	SEQ ID NO 171	CCCA	GGAC	CGT	GGAG	GGCG	GAT	CACA	CCGC	AGAC	TT	GAT	CAAC	AT	CCG	GT	GGT	GGCC	G
M41 .txt	SEQ ID NO 172	CCCA	GGAC	CGT	GGAG	GGCG	GAT	CACA	CCGC	AGAC	TT	GAT	CAAC	AT	CCG	GT	GGT	GGCC	G
M42 .txt	SEQ ID NO 173	CCCA	GGAC	CGT	GGAG	GGCG	GAT	CACA	CCGC	AGAC	TT	GAT	CAAC	AT	CCG	GT	GGT	GGCC	G
M43 .txt	SEQ ID NO 174	CCCA	GGAC	CGT	GGAG	GGCG	GAT	CACA	CCGC	AGAC	TT	GAT	CAAC	AT	CCG	GT	GGT	GGCC	G
M44 .txt	SEQ ID NO 175	CCCA	GGAC	CGT	GGAG	GGCG	GAT	CACA	CCGC	AGAC	TT	GAT	CAAC	AT	CCG	GT	GGT	GGCC	G
M45 .txt	SEQ ID NO 176	CCCA	GGAC	CGT	GGAG	GGCG	GAT	CACA	CCGC	AGAC	TT	GAT	CAAC	AT	CCG	GT	GGT	GGCC	G
M46 .txt	SEQ ID NO 177	CCCA	GGAC	CGT	GGAG	GGCG	GAT	CACA	CCGC	AGAC	TT	GAT	CAAC	AT	CCG	GT	GGT	GGCC	G
M47 .txt	SEQ ID NO 178	CCCA	GGAC	CGT	GGAG	GGCG	GAT	CACA	CCGC	AGAC	TT	GAT	CAAC	AT	CCG	GT	GGT	GGCC	G
M58 (Mav6) .txt	SEQ ID NO 179	CCCA	GGAC	CGT	GGAG	GGCG	GAT	CACA	CCGC	AGAC	TT	GAT	CAAC	AT	CCG	GT	GGT	GGCC	G
M59 .txt	SEQ ID NO 180	CCCA	GGAC	CGT	GGAG	GGCG	GAT	CACA	CCGC	AGAC	TT	GAT	CAAC	AT	CCG	GT	GGT	GGCC	G
M66 (Mav4) .txt	SEQ ID NO 181	CCCA	GGAC	CGT	GGAG	GGCG	GAT	CACA	CCGC	AGAC	TT	GAT	CAAC	AT	CCG	GT	GGT	GGCC	G

Table 1  
BASE NOS 61-120

ATCC9-H2b.txt	SEQ ID NO 1	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M621.txt	SEQ ID NO 2	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
Atcc1-av.txt	SEQ ID NO 3	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M29.txt	SEQ ID NO 4	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M30.txt	SEQ ID NO 5	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M31.txt	SEQ ID NO 6	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M32.txt	SEQ ID NO 7	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M33.txt	SEQ ID NO 8	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M34.txt	SEQ ID NO 9	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M48-new.txt	SEQ ID NO 10	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M49.txt	SEQ ID NO 11	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M64 (May2).txt	SEQ ID NO 12	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M65 (May3).txt	SEQ ID NO 13	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M67 (May5).txt	SEQ ID NO 14	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M69 (May7).txt	SEQ ID NO 15	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M71 (May9).txt	SEQ ID NO 16	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M91.txt	SEQ ID NO 17	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M94.txt	SEQ ID NO 18	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M95.txt	SEQ ID NO 19	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M96.txt	SEQ ID NO 20	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M100.txt	SEQ ID NO 21	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M101.txt	SEQ ID NO 22	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M102.txt	SEQ ID NO 23	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M104.txt	SEQ ID NO 24	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M105.txt	SEQ ID NO 25	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M106.txt	SEQ ID NO 26	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M111.txt	SEQ ID NO 27	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M76.txt	SEQ ID NO 28	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M751.txt	SEQ ID NO 29	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
ATCC2-chelnew.txt	SEQ ID NO 30	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M10.txt	SEQ ID NO 31	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M11-662.txt	SEQ ID NO 32	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M12.txt	SEQ ID NO 33	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M13 2,662.txt	SEQ ID NO 34	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M14.txt	SEQ ID NO 35	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M15.txt	SEQ ID NO 36	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M16.txt	SEQ ID NO 37	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M17 2,662.txt	SEQ ID NO 38	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M507.txt	SEQ ID NO 39	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M51.txt	SEQ ID NO 40	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M15.txt	SEQ ID NO 41	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M16.txt	SEQ ID NO 42	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M19.txt	SEQ ID NO 43	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M109.txt	SEQ ID NO 44	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M200.txt	SEQ ID NO 45	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M207.txt	SEQ ID NO 46	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M209.txt	SEQ ID NO 47	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M122.txt	SEQ ID NO 48	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M123.txt	SEQ ID NO 49	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M124.txt	SEQ ID NO 50	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
Atcc3-for.txt	SEQ ID NO 51	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M53.txt	SEQ ID NO 52	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M54.txt	SEQ ID NO 53	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M55.txt	SEQ ID NO 54	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M56.txt	SEQ ID NO 55	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG
M74 (May12).txt	SEQ ID NO 56	CGATCAAGGAGTTCCTTCGGGACGAGCCAGGCTG

Table 1  
BASE NOS 61-120

M77. .txt	SEQ ID NO 57	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M118. .txt	SEQ ID NO 58	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M721. .txt	SEQ ID NO 59	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M723. .txt	SEQ ID NO 60	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M725. .txt	SEQ ID NO 61	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M741. .txt	SEQ ID NO 62	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M715. .txt	SEQ ID NO 63	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M740. .txt	SEQ ID NO 64	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
Atcc4-go. .txt	SEQ ID NO 65	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
ATCC4-O-Gord. .txt	SEQ ID NO 66	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M78(1a). .txt	SEQ ID NO 67	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M79(1d). .txt	SEQ ID NO 68	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M80(1g). .txt	SEQ ID NO 69	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M81(11). .txt	SEQ ID NO 70	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M82(1m). .txt	SEQ ID NO 71	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M83(1n). .txt	SEQ ID NO 72	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M84(1w). .txt	SEQ ID NO 73	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M85(1b). .txt	SEQ ID NO 74	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M86(1b). .txt	SEQ ID NO 75	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M87(1n). .txt	SEQ ID NO 76	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M90(gordDB). .txt	SEQ ID NO 77	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
m126. .txt	SEQ ID NO 78	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M128. .txt	SEQ ID NO 79	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M103. .txt	SEQ ID NO 80	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M7475. .txt	SEQ ID NO 81	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M7476. .txt	SEQ ID NO 82	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M830. .txt	SEQ ID NO 83	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
Atcc5-Int. .txt	SEQ ID NO 84	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
ATCC5-0Int. .txt	SEQ ID NO 85	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M18. .txt	SEQ ID NO 86	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M19. .txt	SEQ ID NO 87	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M20. .txt	SEQ ID NO 88	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M21. .txt	SEQ ID NO 89	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M22. .txt	SEQ ID NO 90	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M23. .txt	SEQ ID NO 91	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M24. .txt	SEQ ID NO 92	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M25. .txt	SEQ ID NO 93	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M26. .txt	SEQ ID NO 94	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M27. .txt	SEQ ID NO 95	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M28. .txt	SEQ ID NO 96	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M107. .txt	SEQ ID NO 97	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M7112. .txt	SEQ ID NO 98	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M7312. .txt	SEQ ID NO 99	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
ATCC6-Kan. .txt	SEQ ID NO 100	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
ATCC6-0Kan. .txt	SEQ ID NO 101	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M1. .txt	SEQ ID NO 102	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M2. .txt	SEQ ID NO 103	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M3. .txt	SEQ ID NO 104	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M4. .txt	SEQ ID NO 105	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M6. .txt	SEQ ID NO 106	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M7. .txt	SEQ ID NO 107	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M9. .txt	SEQ ID NO 108	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M10. .txt	SEQ ID NO 109	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M57. .txt	SEQ ID NO 110	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M58. .txt	SEQ ID NO 111	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG
M59. .txt	SEQ ID NO 112	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG	CGATCAAGGAGTTCCTTCGGGACCAAGCCAGCTG

Table 1  
BASE NOS 61-120

M60.txt	SEQID NO 113	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
M61.txt	SEQID NO 114	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
M62.txt	SEQID NO 115	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY106.txt	SEQID NO 116	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY216.txt	SEQID NO 117	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY218.txt	SEQID NO 118	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY226.txt	SEQID NO 119	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
M109.txt	SEQID NO 120	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
M111.txt	SEQID NO 121	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
M112.txt	SEQID NO 122	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
M113.txt	SEQID NO 123	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
M114.txt	SEQID NO 124	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY325.txt	SEQID NO 125	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY718.txt	SEQID NO 126	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY214.txt	SEQID NO 127	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY224.txt	SEQID NO 128	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY244.txt	SEQID NO 129	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY339.txt	SEQID NO 130	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY343.txt	SEQID NO 131	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY458.txt	SEQID NO 132	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY809.txt	SEQID NO 133	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY817.txt	SEQID NO 134	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY821.txt	SEQID NO 135	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY824.txt	SEQID NO 136	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY102.txt	SEQID NO 137	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY105.txt	SEQID NO 138	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY251.txt	SEQID NO 139	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY256.txt	SEQID NO 140	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY294.txt	SEQID NO 141	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY354.txt	SEQID NO 142	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
Atcc1-ber.txt	SEQID NO 143	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
ATCC7-Orce.txt	SEQID NO 144	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY121.txt	SEQID NO 145	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY249.txt	SEQID NO 146	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY372.txt	SEQID NO 147	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY378.txt	SEQID NO 148	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY484.txt	SEQID NO 149	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY556.txt	SEQID NO 150	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY563.txt	SEQID NO 151	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY586.txt	SEQID NO 152	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
Atcc8-ane.txt	SEQID NO 153	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
M35.txt	SEQID NO 154	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
M36.txt	SEQID NO 155	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
M37.txt	SEQID NO 156	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
m125.txt	SEQID NO 157	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY143.txt	SEQID NO 158	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY104.txt	SEQID NO 159	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY196.txt	SEQID NO 160	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY357.txt	SEQID NO 161	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY358.txt	SEQID NO 162	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY480.txt	SEQID NO 163	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY212.txt	SEQID NO 164	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY491.txt	SEQID NO 165	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY497.txt	SEQID NO 166	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
MY816.txt	SEQID NO 167	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG
Atcc10-ken.txt	SEQID NO 168	CGATCAAGGAGTCTTCGGCCACGAGCCAGCTG	TTTTCATGGACCGAGAACAAACCCGCG

Table 1  
BASE NOS 61-120

M38.txt	SEQ ID NO 169	CGATCAAGGAGTTCTTCGGCAGCCAGCCAGCT	70	80	90	100	110	120
M39.txt	SEQ ID NO 170	CGATCAAGGAGTTCTTCGGCAGCCAGCCAGCT						
M40.txt	SEQ ID NO 171	CGATCAAGGAGTTCTTCGGCAGCCAGCCAGCT						
M41.txt	SEQ ID NO 172	CGATCAAGGAGTTCTTCGGCAGCCAGCCAGCT						
M42.txt	SEQ ID NO 173	CGATCAAGGAGTTCTTCGGCAGCCAGCCAGCT						
M43.txt	SEQ ID NO 174	CGATCAAGGAGTTCTTCGGCAGCCAGCCAGCT						
M44.txt	SEQ ID NO 175	CGATCAAGGAGTTCTTCGGCAGCCAGCCAGCT						
M45.txt	SEQ ID NO 176	CGATCAAGGAGTTCTTCGGCAGCCAGCCAGCT						
M46.txt	SEQ ID NO 177	CGATCAAGGAGTTCTTCGGCAGCCAGCCAGCT						
M47.txt	SEQ ID NO 178	CGATCAAGGAGTTCTTCGGCAGCCAGCCAGCT						
M48 (Mav6).txt	SEQ ID NO 179	CGATCAAGGAGTTCTTCGGCAGCCAGCCAGCT						
M49.txt	SEQ ID NO 180	CGATCAAGGAGTTCTTCGGCAGCCAGCCAGCT						
M55 (Mav4).txt	SEQ ID NO 181	CGATCAAGGAGTTCTTCGGCAGCCAGCCAGCT						





Table 1  
BASE NOS 121-180

M77. .txt	SEQ ID NO 57	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M118. .txt	SEQ ID NO 58	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M721. .txt	SEQ ID NO 59	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M723. .txt	SEQ ID NO 60	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M725. .txt	SEQ ID NO 61	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M734. .txt	SEQ ID NO 62	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M715. .txt	SEQ ID NO 63	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M740. .txt	SEQ ID NO 64	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
Atcc4-go. .txt	SEQ ID NO 65	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M78(1a). .txt	SEQ ID NO 66	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M79(1d). .txt	SEQ ID NO 67	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M80(1g). .txt	SEQ ID NO 68	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M81(1j). .txt	SEQ ID NO 69	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M82(1m). .txt	SEQ ID NO 70	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M83(1n). .txt	SEQ ID NO 71	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M84(1o). .txt	SEQ ID NO 72	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M85(1b). .txt	SEQ ID NO 73	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M86(1b). .txt	SEQ ID NO 74	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M87(1n). .txt	SEQ ID NO 75	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M90(gotdB). .txt	SEQ ID NO 76	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M126. .txt	SEQ ID NO 77	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M128. .txt	SEQ ID NO 78	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M103. .txt	SEQ ID NO 79	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M1475. .txt	SEQ ID NO 80	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M1476. .txt	SEQ ID NO 81	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M1830. .txt	SEQ ID NO 82	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
Atcc5-int. .txt	SEQ ID NO 83	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
Atcc5-0int. .txt	SEQ ID NO 84	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M18. .txt	SEQ ID NO 85	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M19. .txt	SEQ ID NO 86	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M20. .txt	SEQ ID NO 87	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M21. .txt	SEQ ID NO 88	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M22. .txt	SEQ ID NO 89	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M23. .txt	SEQ ID NO 90	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M24. .txt	SEQ ID NO 91	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M25. .txt	SEQ ID NO 92	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M26. .txt	SEQ ID NO 93	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M27. .txt	SEQ ID NO 94	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M28. .txt	SEQ ID NO 95	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M107. .txt	SEQ ID NO 96	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M1107. .txt	SEQ ID NO 97	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M1112. .txt	SEQ ID NO 98	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M1312. .txt	SEQ ID NO 99	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
Atcc6-kan. .txt	SEQ ID NO 100	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
Atcc6-0kan. .txt	SEQ ID NO 101	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M1. .txt	SEQ ID NO 102	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M2. .txt	SEQ ID NO 103	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M3. .txt	SEQ ID NO 104	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M4. .txt	SEQ ID NO 105	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M6. .txt	SEQ ID NO 106	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M7. .txt	SEQ ID NO 107	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M9. .txt	SEQ ID NO 108	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M10. .txt	SEQ ID NO 109	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M58. .txt	SEQ ID NO 110	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
M59. .txt	SEQ ID NO 111	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG
	SEQ ID NO 112	TGT CCGGG	TGACCCCAACAAGCGG	CTGTGCGGCGCTGGGG	CCCCGGCGGTCGTCTG	CGGTG

[illegible]

Table 1  
BASE NOS 121-180

M38 .txt	SEQ ID NO 169	TGT CCGGG	TACCCACAAGCG	CGCT	TCGGCGCT	GG	CC	GGCGGTCTGT	CGG
M39 .txt	SEQ ID NO 170	TGT CCGGG	TACCCACAAGCG	CGCT	TCGGCGCT	GG	CC	GGCGGTCTGT	CGG
M40 .txt	SEQ ID NO 171	TGT CCGGG	TACCCACAAGCG	CGCT	TCGGCGCT	GG	CC	GGCGGTCTGT	CGG
M41 .txt	SEQ ID NO 172	TGT CCGGG	TACCCACAAGCG	CGCT	TCGGCGCT	GG	CC	GGCGGTCTGT	CGG
M42 .txt	SEQ ID NO 173	TGT CCGGG	TACCCACAAGCG	CGCT	TCGGCGCT	GG	CC	GGCGGTCTGT	CGG
M43 .txt	SEQ ID NO 174	TGT CCGGG	TACCCACAAGCG	CGCT	TCGGCGCT	GG	CC	GGCGGTCTGT	CGG
M44 .txt	SEQ ID NO 175	TGT CCGGG	TACCCACAAGCG	CGCT	TCGGCGCT	GG	CC	GGCGGTCTGT	CGG
M45 .txt	SEQ ID NO 176	TGT CCGGG	TACCCACAAGCG	CGCT	TCGGCGCT	GG	CC	GGCGGTCTGT	CGG
M46 .txt	SEQ ID NO 177	TGT CCGGG	TACCCACAAGCG	CGCT	TCGGCGCT	GG	CC	GGCGGTCTGT	CGG
M47 .txt	SEQ ID NO 178	TGT CCGGG	TACCCACAAGCG	CGCT	TCGGCGCT	GG	CC	GGCGGTCTGT	CGG
M58 (May6) .txt	SEQ ID NO 179	TGT CCGGG	TACCCACAAGCG	CGCT	TCGGCGCT	GG	CC	GGCGGTCTGT	CGG
M59 .txt	SEQ ID NO 180	TGT CCGGG	TACCCACAAGCG	CGCT	TCGGCGCT	GG	CC	GGCGGTCTGT	CGG
M66 (May4) .txt	SEQ ID NO 181	TGT CCGGG	TACCCACAAGCG	CGCT	TCGGCGCT	GG	CC	GGCGGTCTGT	CGG



Table 1  
BASE NOS 181-240

M77 .txt	SEQ ID NO 57	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M119 .txt	SEQ ID NO 58	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M221 .txt	SEQ ID NO 59	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M223 .txt	SEQ ID NO 60	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M225 .txt	SEQ ID NO 61	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M341 .txt	SEQ ID NO 62	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M715 .txt	SEQ ID NO 63	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M740 .txt	SEQ ID NO 64	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
ATCC4-00 .txt	SEQ ID NO 65	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M78(1a) .txt	SEQ ID NO 66	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M79(jd) .txt	SEQ ID NO 67	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M80(1g) .txt	SEQ ID NO 68	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M81(11) .txt	SEQ ID NO 69	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M82(1m) .txt	SEQ ID NO 70	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M83(1ab) .txt	SEQ ID NO 71	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M84(ow) .txt	SEQ ID NO 72	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M85(1b) .txt	SEQ ID NO 73	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M86(1b) .txt	SEQ ID NO 74	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M87(1m) .txt	SEQ ID NO 75	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M87(1m) .txt	SEQ ID NO 76	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M90(gordb) .txt	SEQ ID NO 77	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M126 .txt	SEQ ID NO 78	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M128 .txt	SEQ ID NO 79	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M103 .txt	SEQ ID NO 80	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M175 .txt	SEQ ID NO 81	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M176 .txt	SEQ ID NO 82	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M1830 .txt	SEQ ID NO 83	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
ATCC5-0int .txt	SEQ ID NO 84	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M18 .txt	SEQ ID NO 85	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M19 .txt	SEQ ID NO 86	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M20 .txt	SEQ ID NO 87	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M21 .txt	SEQ ID NO 88	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M22 .txt	SEQ ID NO 89	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M23 .txt	SEQ ID NO 90	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M24 .txt	SEQ ID NO 91	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M25 .txt	SEQ ID NO 92	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M26 .txt	SEQ ID NO 93	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M27 .txt	SEQ ID NO 94	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M28 .txt	SEQ ID NO 95	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M107 .txt	SEQ ID NO 96	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M1107 .txt	SEQ ID NO 97	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M112 .txt	SEQ ID NO 98	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M312 .txt	SEQ ID NO 99	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
ATCC6-kan .txt	SEQ ID NO 100	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
ATCC6-kan .txt	SEQ ID NO 101	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M1 .txt	SEQ ID NO 102	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M2 .txt	SEQ ID NO 103	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M3 .txt	SEQ ID NO 104	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M4 .txt	SEQ ID NO 105	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M6 .txt	SEQ ID NO 106	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M7 .txt	SEQ ID NO 107	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M9 .txt	SEQ ID NO 108	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M57 .txt	SEQ ID NO 109	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M58 .txt	SEQ ID NO 110	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M59 .txt	SEQ ID NO 111	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA
M59 .txt	SEQ ID NO 112	AGCGTGGCCGGGCTTGAAGGTCCGCGACGTGCACCTCAGTACAGGCGCGATGTGTGCCCGGA



Table 1  
BASE NOS 181-240

M38 . txt	SEQ ID NO 169	A G C G	G C C G G G G C T G G A G G T C C G	G A C G T G C A C	C G	C A C T A C G G C C G G A T G T G C C C G A	210
M39 . txt	SEQ ID NO 170	A G C G	G C C G G G G C T G G A G G T C C G	G A C G T G C A C	C G	C A C T A C G G C C G G A T G T G C C C G A	220
M40 . txt	SEQ ID NO 171	A G C G	G C C G G G G C T G G A G G T C C G	G A C G T G C A C	C G	C A C T A C G G C C G G A T G T G C C C G A	230
M41 . txt	SEQ ID NO 172	A G C G	G C C G G G G C T G G A G G T C C G	G A C G T G C A C	C G	C A C T A C G G C C G G A T G T G C C C G A	240
M42 . txt	SEQ ID NO 173	A G C G	G C C G G G G C T G G A G G T C C G	G A C G T G C A C	C G	C A C T A C G G C C G G A T G T G C C C G A	
M43 . txt	SEQ ID NO 174	A G C G	G C C G G G G C T G G A G G T C C G	G A C G T G C A C	C G	C A C T A C G G C C G G A T G T G C C C G A	
M44 . txt	SEQ ID NO 175	A G C G	G C C G G G G C T G G A G G T C C G	G A C G T G C A C	C G	C A C T A C G G C C G G A T G T G C C C G A	
M45 . txt	SEQ ID NO 176	A G C G	G C C G G G G C T G G A G G T C C G	G A C G T G C A C	C G	C A C T A C G G C C G G A T G T G C C C G A	
M46 . txt	SEQ ID NO 177	A G C G	G C C G G G G C T G G A G G T C C G	G A C G T G C A C	C G	C A C T A C G G C C G G A T G T G C C C G A	
M47 . txt	SEQ ID NO 178	A G C G	G C C G G G G C T G G A G G T C C G	G A C G T G C A C	C G	C A C T A C G G C C G G A T G T G C C C G A	
M68 (Nav6) . txt	SEQ ID NO 179	A G C G	G C C G G G G C T G G A G G T C C G	G A C G T G C A C	C G	C A C T A C G G C C G G A T G T G C C C G A	
M89 . txt	SEQ ID NO 180	A G C G	G C C G G G G C T G G A G G T C C G	G A C G T G C A C	C G	C A C T A C G G C C G G A T G T G C C C G A	
M66 (Nav4) . txt	SEQ ID NO 181	A G C G	G C C G G G G C T G G A G G T C C G	G A C G T G C A C	C G	C A C T A C G G C C G G A T G T G C C C G A	







Table 1  
BASE NOS 241-300

M60. txc	SEQ ID NO 113	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
M61. txc	SEQ ID NO 114	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
M62. txc	SEQ ID NO 115	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY106. txc	SEQ ID NO 116	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY216. txc	SEQ ID NO 117	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY218. txc	SEQ ID NO 118	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY226. txc	SEQ ID NO 119	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY29. txc	SEQ ID NO 120	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY11. txc	SEQ ID NO 121	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY12. txc	SEQ ID NO 122	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY13. txc	SEQ ID NO 123	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY14. txc	SEQ ID NO 124	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY325. txc	SEQ ID NO 125	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY718. txc	SEQ ID NO 126	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY214. txc	SEQ ID NO 127	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY224. txc	SEQ ID NO 128	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY244. txc	SEQ ID NO 129	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY339. txc	SEQ ID NO 130	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY343. txc	SEQ ID NO 131	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY458. txc	SEQ ID NO 132	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY809. txc	SEQ ID NO 133	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY817. txc	SEQ ID NO 134	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY821. txc	SEQ ID NO 135	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY824. txc	SEQ ID NO 136	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY102. txc	SEQ ID NO 137	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY105. txc	SEQ ID NO 138	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY251. txc	SEQ ID NO 139	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY256. txc	SEQ ID NO 140	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY294. txc	SEQ ID NO 141	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY354. txc	SEQ ID NO 142	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
Atcc7-08e. txc	SEQ ID NO 143	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
Atcc7-08e. txc	SEQ ID NO 144	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY121. txc	SEQ ID NO 145	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY249. txc	SEQ ID NO 146	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY372. txc	SEQ ID NO 147	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY378. txc	SEQ ID NO 148	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY486. txc	SEQ ID NO 149	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY556. txc	SEQ ID NO 150	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY563. txc	SEQ ID NO 151	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY586. txc	SEQ ID NO 152	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
Atcc8-08e. txc	SEQ ID NO 153	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
M35. txc	SEQ ID NO 154	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
M36. txc	SEQ ID NO 155	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
M37. txc	SEQ ID NO 156	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
M125. txc	SEQ ID NO 157	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY143. txc	SEQ ID NO 158	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY104. txc	SEQ ID NO 159	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY196. txc	SEQ ID NO 160	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY357. txc	SEQ ID NO 161	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY359. txc	SEQ ID NO 162	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY480. txc	SEQ ID NO 163	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY212. txc	SEQ ID NO 164	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY491. txc	SEQ ID NO 165	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY497. txc	SEQ ID NO 166	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
MY816. txc	SEQ ID NO 167	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG
Atcc10-08e. txc	SEQ ID NO 168	T CGA	CCCAACATCGGG	CTGATCGGGCTCGCTGTCGGTGTACGGCA	CGGG



Table 1  
BASE NOS 301-360

ATCC9-Meb. txt	SEQID NO 1	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
MY621. txt	SEQID NO 2	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
Atcc1-mv. txt	SEQID NO 3	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M29. txt	SEQID NO 4	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M30. txt	SEQID NO 5	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M31. txt	SEQID NO 6	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M32. txt	SEQID NO 7	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M33. txt	SEQID NO 8	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M34. txt	SEQID NO 9	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M48-naw. txt	SEQID NO 10	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M49. txt	SEQID NO 11	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M64(Mav2). txt	SEQID NO 12	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M65(Mav3). txt	SEQID NO 13	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M67(Mav5). txt	SEQID NO 14	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M69(Mav7). txt	SEQID NO 15	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M71(Mav9). txt	SEQID NO 16	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M91. txt	SEQID NO 17	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M94. txt	SEQID NO 18	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M95. txt	SEQID NO 19	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M96. txt	SEQID NO 20	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M100. txt	SEQID NO 21	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M101. txt	SEQID NO 22	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M102. txt	SEQID NO 23	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M104. txt	SEQID NO 24	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M105. txt	SEQID NO 25	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M106. txt	SEQID NO 26	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M111. txt	SEQID NO 27	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M176. txt	SEQID NO 28	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
MY451. txt	SEQID NO 29	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
ATCC2-Chelnew. txt	SEQID NO 30	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M10. txt	SEQID NO 31	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M11-662. txt	SEQID NO 32	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M12. txt	SEQID NO 33	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M13-2_662. txt	SEQID NO 34	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M14. txt	SEQID NO 35	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M15. txt	SEQID NO 36	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M16. txt	SEQID NO 37	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M17-2_662. txt	SEQID NO 38	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M50. txt	SEQID NO 39	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M51. txt	SEQID NO 40	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M115. txt	SEQID NO 41	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M116. txt	SEQID NO 42	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M119. txt	SEQID NO 43	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
MY109. txt	SEQID NO 44	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
MY200. txt	SEQID NO 45	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
MY207. txt	SEQID NO 46	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
MY209. txt	SEQID NO 47	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M122. txt	SEQID NO 48	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M123. txt	SEQID NO 49	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M124. txt	SEQID NO 50	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
Atcc3-for. txt	SEQID NO 51	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M53. txt	SEQID NO 52	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M54. txt	SEQID NO 53	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M55. txt	SEQID NO 54	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M56. txt	SEQID NO 55	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT
M74(Mav12). txt	SEQID NO 56	TCAACCCGTTCCGGTTCATCGAAGCCGCTACCCGACCGTGTGTCGACGGGGTGGT

Table 1  
BASE NOS 301-360

MY77.txt	SEQ.DNO57	TCAACCCGTTCCGGTTTCATCGA
MY110.txt	SEQ.DNO58	TCAACCCGTTCCGGTTTCATCGA
MY221.txt	SEQ.DNO59	TCAACCCGTTCCGGTTTCATCGA
MY223.txt	SEQ.DNO60	TCAACCCGTTCCGGTTTCATCGA
MY225.txt	SEQ.DNO61	TCAACCCGTTCCGGTTTCATCGA
MY341.txt	SEQ.DNO62	TCAACCCGTTCCGGTTTCATCGA
MY715.txt	SEQ.DNO63	TCAACCCGTTCCGGTTTCATCGA
MY470.txt	SEQ.DNO64	TCAACCCGTTCCGGTTTCATCGA
Atcc4-go.txt	SEQ.DNO65	TCAACCCGTTCCGGTTTCATCGA
ATCC4-0-Gord.txt	SEQ.DNO66	TCAACCCGTTCCGGTTTCATCGA
MY78(1st).txt	SEQ.DNO67	TCAACCCGTTCCGGTTTCATCGA
MY79(1st).txt	SEQ.DNO68	TCAACCCGTTCCGGTTTCATCGA
MY80(1st).txt	SEQ.DNO69	TCAACCCGTTCCGGTTTCATCGA
MY81(1st).txt	SEQ.DNO70	TCAACCCGTTCCGGTTTCATCGA
MY82(1st).txt	SEQ.DNO71	TCAACCCGTTCCGGTTTCATCGA
MY83(1st).txt	SEQ.DNO72	TCAACCCGTTCCGGTTTCATCGA
MY84(1st).txt	SEQ.DNO73	TCAACCCGTTCCGGTTTCATCGA
MY85(1st).txt	SEQ.DNO74	TCAACCCGTTCCGGTTTCATCGA
MY86(1st).txt	SEQ.DNO75	TCAACCCGTTCCGGTTTCATCGA
MY87(1st).txt	SEQ.DNO76	TCAACCCGTTCCGGTTTCATCGA
MY88(1st).txt	SEQ.DNO77	TCAACCCGTTCCGGTTTCATCGA
MY89(1st).txt	SEQ.DNO78	TCAACCCGTTCCGGTTTCATCGA
MY90(1st).txt	SEQ.DNO79	TCAACCCGTTCCGGTTTCATCGA
MY91(1st).txt	SEQ.DNO80	TCAACCCGTTCCGGTTTCATCGA
MY92(1st).txt	SEQ.DNO81	TCAACCCGTTCCGGTTTCATCGA
MY93(1st).txt	SEQ.DNO82	TCAACCCGTTCCGGTTTCATCGA
MY94(1st).txt	SEQ.DNO83	TCAACCCGTTCCGGTTTCATCGA
MY95(1st).txt	SEQ.DNO84	TCAACCCGTTCCGGTTTCATCGA
MY96(1st).txt	SEQ.DNO85	TCAACCCGTTCCGGTTTCATCGA
MY97(1st).txt	SEQ.DNO86	TCAACCCGTTCCGGTTTCATCGA
MY98(1st).txt	SEQ.DNO87	TCAACCCGTTCCGGTTTCATCGA
MY99(1st).txt	SEQ.DNO88	TCAACCCGTTCCGGTTTCATCGA
MY100(1st).txt	SEQ.DNO89	TCAACCCGTTCCGGTTTCATCGA
MY101(1st).txt	SEQ.DNO90	TCAACCCGTTCCGGTTTCATCGA
MY102(1st).txt	SEQ.DNO91	TCAACCCGTTCCGGTTTCATCGA
MY103(1st).txt	SEQ.DNO92	TCAACCCGTTCCGGTTTCATCGA
MY104(1st).txt	SEQ.DNO93	TCAACCCGTTCCGGTTTCATCGA
MY105(1st).txt	SEQ.DNO94	TCAACCCGTTCCGGTTTCATCGA
MY106(1st).txt	SEQ.DNO95	TCAACCCGTTCCGGTTTCATCGA
MY107(1st).txt	SEQ.DNO96	TCAACCCGTTCCGGTTTCATCGA
MY108(1st).txt	SEQ.DNO97	TCAACCCGTTCCGGTTTCATCGA
MY109(1st).txt	SEQ.DNO98	TCAACCCGTTCCGGTTTCATCGA
MY110(1st).txt	SEQ.DNO99	TCAACCCGTTCCGGTTTCATCGA
MY111(1st).txt	SEQ.DNO100	TCAACCCGTTCCGGTTTCATCGA
MY112(1st).txt	SEQ.DNO101	TCAACCCGTTCCGGTTTCATCGA
MY113(1st).txt	SEQ.DNO102	TCAACCCGTTCCGGTTTCATCGA
MY114(1st).txt	SEQ.DNO103	TCAACCCGTTCCGGTTTCATCGA
MY115(1st).txt	SEQ.DNO104	TCAACCCGTTCCGGTTTCATCGA
MY116(1st).txt	SEQ.DNO105	TCAACCCGTTCCGGTTTCATCGA
MY117(1st).txt	SEQ.DNO106	TCAACCCGTTCCGGTTTCATCGA
MY118(1st).txt	SEQ.DNO107	TCAACCCGTTCCGGTTTCATCGA
MY119(1st).txt	SEQ.DNO108	TCAACCCGTTCCGGTTTCATCGA
MY120(1st).txt	SEQ.DNO109	TCAACCCGTTCCGGTTTCATCGA
MY121(1st).txt	SEQ.DNO110	TCAACCCGTTCCGGTTTCATCGA
MY122(1st).txt	SEQ.DNO111	TCAACCCGTTCCGGTTTCATCGA
MY123(1st).txt	SEQ.DNO112	TCAACCCGTTCCGGTTTCATCGA

Table 1  
BASE NOS 301-360[illegible]





**Table 1**  
**BASE NOS 361-420**

[illegible]

Table 1  
BASE NOS 361-420

M77.txt	SEQ ID NO 57	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M118.txt	SEQ ID NO 58	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M221.txt	SEQ ID NO 59	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M223.txt	SEQ ID NO 60	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M225.txt	SEQ ID NO 61	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M341.txt	SEQ ID NO 62	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M715.txt	SEQ ID NO 63	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M7470.txt	SEQ ID NO 64	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
Atcc4-90.txt	SEQ ID NO 65	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M78(12).txt	SEQ ID NO 66	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M79(jd).txt	SEQ ID NO 67	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M80(lg).txt	SEQ ID NO 68	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M81(11).txt	SEQ ID NO 69	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M82(rn).txt	SEQ ID NO 70	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M83(mb).txt	SEQ ID NO 71	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M84(ow).txt	SEQ ID NO 72	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M85(lb).txt	SEQ ID NO 73	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M86(lb).txt	SEQ ID NO 74	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M87(wr).txt	SEQ ID NO 75	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M90(gordb).txt	SEQ ID NO 76	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M126.txt	SEQ ID NO 77	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M128.txt	SEQ ID NO 78	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M103.txt	SEQ ID NO 79	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M475.txt	SEQ ID NO 80	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M476.txt	SEQ ID NO 81	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M4830.txt	SEQ ID NO 82	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
Atcc5-int.txt	SEQ ID NO 83	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
ATCC5-Qint.txt	SEQ ID NO 84	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M18.txt	SEQ ID NO 85	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M19.txt	SEQ ID NO 86	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M20.txt	SEQ ID NO 87	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M21.txt	SEQ ID NO 88	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M22.txt	SEQ ID NO 89	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M23.txt	SEQ ID NO 90	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M24.txt	SEQ ID NO 91	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M25.txt	SEQ ID NO 92	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M26.txt	SEQ ID NO 93	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M27.txt	SEQ ID NO 94	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M28.txt	SEQ ID NO 95	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M107.txt	SEQ ID NO 96	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M1107.txt	SEQ ID NO 97	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M1112.txt	SEQ ID NO 98	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M1312.txt	SEQ ID NO 99	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
Atcc6-kan.txt	SEQ ID NO 100	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
Atcc6-ORan.txt	SEQ ID NO 101	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M1.txt	SEQ ID NO 102	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M2.txt	SEQ ID NO 103	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M3.txt	SEQ ID NO 104	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M4.txt	SEQ ID NO 105	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M5.txt	SEQ ID NO 106	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M6.txt	SEQ ID NO 107	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M7.txt	SEQ ID NO 108	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M8.txt	SEQ ID NO 109	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M9.txt	SEQ ID NO 110	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M17.txt	SEQ ID NO 111	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M18.txt	SEQ ID NO 112	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T
M19.txt	SEQ ID NO 113	TACCTGACCGCCGACGAGGAGGACCGCCACCGT	GTGGC	CAAGGCCAA	T

[illegible]







SEQ ID NO 113  
M60. txt  
SEQ ID NO 114  
M61. txt  
SEQ ID NO 115  
M62. txt  
SEQ ID NO 116  
M106. txt  
SEQ ID NO 117  
M216. txt  
SEQ ID NO 118  
M218. txt  
SEQ ID NO 119  
M226. txt  
SEQ ID NO 120  
M109. txt  
SEQ ID NO 121  
M111. txt  
SEQ ID NO 122  
M112. txt  
SEQ ID NO 123  
M113. txt  
SEQ ID NO 124  
M114. txt  
SEQ ID NO 125  
M1325. txt  
SEQ ID NO 126  
M1718. txt  
SEQ ID NO 127  
M17214. txt  
SEQ ID NO 128  
M17244. txt  
SEQ ID NO 129  
M17244. txt  
SEQ ID NO 130  
M17339. txt  
SEQ ID NO 131  
M17343. txt  
SEQ ID NO 132  
M17458. txt  
SEQ ID NO 133  
M17809. txt  
SEQ ID NO 134  
M17817. txt  
SEQ ID NO 135  
M17821. txt  
SEQ ID NO 136  
M17824. txt  
SEQ ID NO 137  
M17102. txt  
SEQ ID NO 138  
M17105. txt  
SEQ ID NO 139  
M17251. txt  
SEQ ID NO 140  
M17256. txt  
SEQ ID NO 141  
M17294. txt  
SEQ ID NO 142  
M17354. txt  
SEQ ID NO 143  
Atcc7-aer. txt  
SEQ ID NO 144  
Atcc7-0scr. txt  
SEQ ID NO 145  
M1721. txt  
SEQ ID NO 146  
M17249. txt  
SEQ ID NO 147  
M17372. txt  
SEQ ID NO 148  
M17378. txt  
SEQ ID NO 149  
M17484. txt  
SEQ ID NO 150  
M17556. txt  
SEQ ID NO 151  
M17563. txt  
SEQ ID NO 152  
M17586. txt  
SEQ ID NO 153  
Atcc9-ame. txt  
SEQ ID NO 154  
M1735. txt  
SEQ ID NO 155  
M173136. txt  
SEQ ID NO 156  
M17337. txt  
SEQ ID NO 157  
M17125. txt  
SEQ ID NO 158  
M17143. txt  
SEQ ID NO 159  
M17108. txt  
SEQ ID NO 160  
M17196. txt  
SEQ ID NO 161  
M17357. txt  
SEQ ID NO 162  
M17358. txt  
SEQ ID NO 163  
M17480. txt  
SEQ ID NO 164  
M17212. txt  
SEQ ID NO 165  
M17491. txt  
SEQ ID NO 166  
M17497. txt  
SEQ ID NO 167  
M17816. txt  
SEQ ID NO 168  
M17816. txt

Table 1  
BASE NOS 421-480

M38. txt	SEQ ID NO 160	CGCCGATC	GA	GGGA	GG	CGCTTC	CGAGCCGCG	GTGCTGGT	GC
M39. txt	SEQ ID NO 170	CGCCGATC	GA	GGGA	GG	CGCTTC	CGAGCCGCG	GTGCTGGT	GC
M40. txt	SEQ ID NO 171	CGCCGATC	GA	GGGA	GG	CGCTTC	CGAGCCGCG	GTGCTGGT	GC
M41. txt	SEQ ID NO 172	CGCCGATC	GA	GGGA	GG	CGCTTC	CGAGCCGCG	GTGCTGGT	GC
M42. txt	SEQ ID NO 173	CGCCGATC	GA	GGGA	GG	CGCTTC	CGAGCCGCG	GTGCTGGT	GC
M43. txt	SEQ ID NO 174	CGCCGATC	GA	GGGA	GG	CGCTTC	CGAGCCGCG	GTGCTGGT	GC
M44. txt	SEQ ID NO 175	CGCCGATC	GA	GGGA	GG	CGCTTC	CGAGCCGCG	GTGCTGGT	GC
M45. txt	SEQ ID NO 176	CGCCGATC	GA	GGGA	GG	CGCTTC	CGAGCCGCG	GTGCTGGT	GC
M46. txt	SEQ ID NO 177	CGCCGATC	GA	GGGA	GG	CGCTTC	CGAGCCGCG	GTGCTGGT	GC
M47. txt	SEQ ID NO 178	CGCCGATC	GA	GGGA	GG	CGCTTC	CGAGCCGCG	GTGCTGGT	GC
M68 (Nav6). txt	SEQ ID NO 179	CGCCGATC	GA	GGGA	GG	CGCTTC	CGAGCCGCG	GTGCTGGT	GC
M89. txt	SEQ ID NO 180	CGCCGATC	GA	GGGA	GG	CGCTTC	CGAGCCGCG	GTGCTGGT	GC
M66 (Nav4). txt	SEQ ID NO 181	CGCCGATC	GA	GGGA	GG	CGCTTC	CGAGCCGCG	GTGCTGGT	GC



Table 1  
BASE NOS 481-540

ATCC9-Hcb. txt	SEQ ID NO 1	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY621. txt	SEQ ID NO 2	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
ATCC1-AV. txt	SEQ ID NO 3	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY29. txt	SEQ ID NO 4	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY30. txt	SEQ ID NO 5	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY31. txt	SEQ ID NO 6	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY32. txt	SEQ ID NO 7	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY33. txt	SEQ ID NO 8	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY34. txt	SEQ ID NO 9	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY48-new. txt	SEQ ID NO 10	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY49. txt	SEQ ID NO 11	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY64 (May2). txt	SEQ ID NO 12	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY65 (May3). txt	SEQ ID NO 13	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY67 (May5). txt	SEQ ID NO 14	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY69 (May7). txt	SEQ ID NO 15	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY71 (May9). txt	SEQ ID NO 16	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY91. txt	SEQ ID NO 17	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY98. txt	SEQ ID NO 18	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY95. txt	SEQ ID NO 19	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY100. txt	SEQ ID NO 20	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY101. txt	SEQ ID NO 21	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY102. txt	SEQ ID NO 22	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY104. txt	SEQ ID NO 23	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY105. txt	SEQ ID NO 24	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY106. txt	SEQ ID NO 25	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY111. txt	SEQ ID NO 26	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY76. txt	SEQ ID NO 27	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY431. txt	SEQ ID NO 28	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
ATCC2-Cholnew. txt	SEQ ID NO 29	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY10. txt	SEQ ID NO 30	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY11-662. txt	SEQ ID NO 31	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY12. txt	SEQ ID NO 32	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY13-2_662. txt	SEQ ID NO 33	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY14. txt	SEQ ID NO 34	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY15. txt	SEQ ID NO 35	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY16. txt	SEQ ID NO 36	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY17-2_662. txt	SEQ ID NO 37	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY50. txt	SEQ ID NO 38	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY51. txt	SEQ ID NO 39	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY115. txt	SEQ ID NO 40	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY116. txt	SEQ ID NO 41	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY119. txt	SEQ ID NO 42	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY109. txt	SEQ ID NO 43	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY200. txt	SEQ ID NO 44	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY207. txt	SEQ ID NO 45	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY209. txt	SEQ ID NO 46	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY122. txt	SEQ ID NO 47	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY123. txt	SEQ ID NO 48	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY124. txt	SEQ ID NO 49	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
ATCC3-for. txt	SEQ ID NO 50	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY53. txt	SEQ ID NO 51	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY54. txt	SEQ ID NO 52	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY55. txt	SEQ ID NO 53	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY56. txt	SEQ ID NO 54	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
MY74 (May12). txt	SEQ ID NO 55	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC
	SEQ ID NO 56	GCCGCAAGGCGGGCGAGGTGGAGTACGTGCCCCCTCGTCTGAGGTTGAGCTACATGGAACGTC







SEQ ID NO 1	ATCC9-Meb.txt
SEQ ID NO 2	ATCC17621.txt
SEQ ID NO 3	Atccel-av.txt
SEQ ID NO 4	M29.txt
SEQ ID NO 5	M30.txt
SEQ ID NO 6	M31.txt
SEQ ID NO 7	M32.txt
SEQ ID NO 8	M33.txt
SEQ ID NO 9	M34.txt
SEQ ID NO 10	M48-nov.txt
SEQ ID NO 11	M49.txt
SEQ ID NO 12	M64 (Nov2).txt
SEQ ID NO 13	M65 (Nov3).txt
SEQ ID NO 14	M67 (Nov5).txt
SEQ ID NO 15	M69 (Nov7).txt
SEQ ID NO 16	M71 (Nov9).txt
SEQ ID NO 17	H91.txt
SEQ ID NO 18	H94.txt
SEQ ID NO 19	H95.txt
SEQ ID NO 20	H96.txt
SEQ ID NO 21	H100.txt
SEQ ID NO 22	H101.txt
SEQ ID NO 23	H102.txt
SEQ ID NO 24	H104.txt
SEQ ID NO 25	H105.txt
SEQ ID NO 26	H106.txt
SEQ ID NO 27	H111.txt
SEQ ID NO 28	H76.txt
SEQ ID NO 29	H451.txt
SEQ ID NO 30	ATCC2-chelnew.txt
SEQ ID NO 31	H10.txt
SEQ ID NO 32	H11-662.txt
SEQ ID NO 33	H12.txt
SEQ ID NO 34	H13_2_662.txt
SEQ ID NO 35	H14.txt
SEQ ID NO 36	H15.txt
SEQ ID NO 37	H16.txt
SEQ ID NO 38	H17_2_662.txt
SEQ ID NO 39	H50.txt
SEQ ID NO 40	H51.txt
SEQ ID NO 41	H15.txt
SEQ ID NO 42	H16.txt
SEQ ID NO 43	H19.txt
SEQ ID NO 44	H200.txt
SEQ ID NO 45	H207.txt
SEQ ID NO 46	H209.txt
SEQ ID NO 47	H122.txt
SEQ ID NO 48	H123.txt
SEQ ID NO 49	H124.txt
SEQ ID NO 50	Atcc3-for.txt
SEQ ID NO 51	H53.txt
SEQ ID NO 52	H54.txt
SEQ ID NO 53	H55.txt
SEQ ID NO 54	H56.txt
SEQ ID NO 55	H57.txt
SEQ ID NO 56	H14 (Nov12).txt











Table 1  
BASE NOS 600-660

M77. txt	SEQ ID NO 57	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M18. txt	SEQ ID NO 58	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
MY221. txt	SEQ ID NO 59	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
MY223. txt	SEQ ID NO 60	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
MY225. txt	SEQ ID NO 61	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
MY341. txt	SEQ ID NO 62	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
MY715. txt	SEQ ID NO 63	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
MY740. txt	SEQ ID NO 64	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
Atcc4-go. txt	SEQ ID NO 65	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
Atcc4-0-Gord. txt	SEQ ID NO 66	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M78(1s). txt	SEQ ID NO 67	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M79(1s). txt	SEQ ID NO 68	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M80(1g). txt	SEQ ID NO 69	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M81(11). txt	SEQ ID NO 70	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M82(1m). txt	SEQ ID NO 71	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M83(1m). txt	SEQ ID NO 72	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M84(ow). txt	SEQ ID NO 73	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M85(1b). txt	SEQ ID NO 74	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M86(1b). txt	SEQ ID NO 75	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M87(1m). txt	SEQ ID NO 76	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M90(gordDB). txt	SEQ ID NO 77	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M126. txt	SEQ ID NO 78	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M128. txt	SEQ ID NO 79	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
MY103. txt	SEQ ID NO 80	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
MY475. txt	SEQ ID NO 81	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
MY476. txt	SEQ ID NO 82	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
MY830. txt	SEQ ID NO 83	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
Atcc5-int. txt	SEQ ID NO 84	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
Atcc5-0int. txt	SEQ ID NO 85	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M18. txt	SEQ ID NO 86	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M19. txt	SEQ ID NO 87	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M20. txt	SEQ ID NO 88	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M21. txt	SEQ ID NO 89	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M22. txt	SEQ ID NO 90	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M23. txt	SEQ ID NO 91	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M24. txt	SEQ ID NO 92	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M25. txt	SEQ ID NO 93	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M26. txt	SEQ ID NO 94	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M27. txt	SEQ ID NO 95	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M28. txt	SEQ ID NO 96	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M107. txt	SEQ ID NO 97	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
MY112. txt	SEQ ID NO 98	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
MY312. txt	SEQ ID NO 99	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
Atcc6-kan. txt	SEQ ID NO 100	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
Atcc6-0kan. txt	SEQ ID NO 101	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M1. txt	SEQ ID NO 102	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M2. txt	SEQ ID NO 103	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M3. txt	SEQ ID NO 104	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M4. txt	SEQ ID NO 105	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M5. txt	SEQ ID NO 106	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M6. txt	SEQ ID NO 107	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M7. txt	SEQ ID NO 108	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M8. txt	SEQ ID NO 109	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M9. txt	SEQ ID NO 110	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M57. txt	SEQ ID NO 111	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG
M59. txt	SEQ ID NO 112	CGA	CCGT	GCCCT	ATGGG	GC	AA	AT	GC	AG	CG	AG	CG

[illegible]

Table 1  
BASE NOS 600-660

M38 .txt	SEQ ID NO 169	CCAAACCGGGGCCTTTTATGGGGGC	5	610
M39 .txt	SEQ ID NO 170	CCAAACCGGGGCCTTTTATGGGGGC	6	620
M40 .txt	SEQ ID NO 171	CCAAACCGGGGCCTTTTATGGGGGC	7	630
M41 .txt	SEQ ID NO 172	CCAAACCGGGGCCTTTTATGGGGGC	8	640
M42 .txt	SEQ ID NO 173	CCAAACCGGGGCCTTTTATGGGGGC	9	650
M43 .txt	SEQ ID NO 174	CCAAACCGGGGCCTTTTATGGGGGC	10	660
M44 .txt	SEQ ID NO 175	CCAAACCGGGGCCTTTTATGGGGGC	11	670
M45 .txt	SEQ ID NO 176	CCAAACCGGGGCCTTTTATGGGGGC	12	680
M46 .txt	SEQ ID NO 177	CCAAACCGGGGCCTTTTATGGGGGC	13	690
M47 .txt	SEQ ID NO 178	CCAAACCGGGGCCTTTTATGGGGGC	14	700
M68 (May6) .txt	SEQ ID NO 179	CCAAACCGGGGCCTTTTATGGGGGC	15	710
M89 .txt	SEQ ID NO 180	CCAAACCGGGGCCTTTTATGGGGGC	16	720
M66 (May4) .txt	SEQ ID NO 181	CCAAACCGGGGCCTTTTATGGGGGC	17	730

SEQ ID NO 1  
 ATCC9-Mtb.txt  
 SEQ ID NO 2  
 M621.txt  
 SEQ ID NO 3  
 ATCC9-av.txt  
 SEQ ID NO 4  
 M429.txt  
 SEQ ID NO 5  
 M330.txt  
 SEQ ID NO 6  
 M331.txt  
 SEQ ID NO 7  
 M332.txt  
 SEQ ID NO 8  
 M333.txt  
 SEQ ID NO 9  
 M334.txt  
 SEQ ID NO 10  
 M348-new.txt  
 SEQ ID NO 11  
 M49.txt  
 SEQ ID NO 12  
 M64 (Mav2).txt  
 SEQ ID NO 13  
 M65 (Mav3).txt  
 SEQ ID NO 14  
 M67 (Mav5).txt  
 SEQ ID NO 15  
 M69 (Mav7).txt  
 SEQ ID NO 16  
 M71 (Mav9).txt  
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 M1451.txt

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 SEQ.DNO.55 M1225.txt  
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 SEQ.DNO.58 MY470.txt  
 SEQ.DNO.59 ATCC64-0-Gord.txt  
 SEQ.DNO.60 M718(1s).txt  
 SEQ.DNO.61 M719(1s).txt  
 SEQ.DNO.62 M801(1g).txt  
 SEQ.DNO.63 M801(1l).txt  
 SEQ.DNO.64 M823(1mb).txt  
 SEQ.DNO.65 M83(1mb).txt  
 SEQ.DNO.66 M84(1ow).txt  
 SEQ.DNO.67 M85(1b).txt  
 SEQ.DNO.68 M86(1mb).txt  
 SEQ.DNO.69 M87(1mb).txt  
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 SEQ.DNO.71 M128.txt  
 SEQ.DNO.72 MY103.txt  
 SEQ.DNO.73 MY475.txt  
 SEQ.DNO.74 MY476.txt  
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 SEQ.DNO.85 M28.txt  
 SEQ.DNO.86 M107.txt  
 SEQ.DNO.87 MY112.txt  
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 SEQ.DNO.89 ATCC6-Okn.txt  
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 SEQ.DNO.107 M67.txt  
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 SEQ.DNO.301 M261.txt  
 SEQ.DNO.302 M262.txt  
 SEQ.DNO.303 M263.txt  
 SEQ.DNO.304 M264.txt  
 SEQ.DNO.305 M265.txt  
 SEQ.DNO.306 M266.txt  
 SEQ.DNO.307 M267.txt  
 SEQ.DNO.308 M268.txt  
 SEQ.DNO.30



Table 1  
BASE NOS 660-720

M38. txt	SEQ ID NO 169	AGGC	CCGCTGGTGGGCA	CCGGATGGA	TGCGCGCGCGCGATCGACGC	CGCGACGT	670
M39. txt	SEQ ID NO 170	AGGC	CCGCTGGTGGGCA	CCGGATGGA	TGCGCGCGCGCGATCGACGC	CGCGACGT	710
M40. txt	SEQ ID NO 171	AGGC	CCGCTGGTGGGCA	CCGGATGGA	TGCGCGCGCGCGATCGACGC	CGCGACGT	720
M41. txt	SEQ ID NO 172	AGGC	CCGCTGGTGGGCA	CCGGATGGA	TGCGCGCGCGCGATCGACGC	CGCGACGT	
M42. txt	SEQ ID NO 173	AGGC	CCGCTGGTGGGCA	CCGGATGGA	TGCGCGCGCGCGATCGACGC	CGCGACGT	
M43. txt	SEQ ID NO 174	AGGC	CCGCTGGTGGGCA	CCGGATGGA	TGCGCGCGCGCGATCGACGC	CGCGACGT	
M44. txt	SEQ ID NO 175	AGGC	CCGCTGGTGGGCA	CCGGATGGA	TGCGCGCGCGCGATCGACGC	CGCGACGT	
M45. txt	SEQ ID NO 176	AGGC	CCGCTGGTGGGCA	CCGGATGGA	TGCGCGCGCGCGATCGACGC	CGCGACGT	
M46. txt	SEQ ID NO 177	AGGC	CCGCTGGTGGGCA	CCGGATGGA	TGCGCGCGCGCGATCGACGC	CGCGACGT	
M47. txt	SEQ ID NO 178	AGGC	CCGCTGGTGGGCA	CCGGATGGA	TGCGCGCGCGCGATCGACGC	CGCGACGT	
M68 (May6). txt	SEQ ID NO 179	AGGC	CCGCTGGTGGGCA	CCGGATGGA	TGCGCGCGCGCGATCGACGC	CGCGACGT	
M89. txt	SEQ ID NO 180	AGGC	CCGCTGGTGGGCA	CCGGATGGA	TGCGCGCGCGCGATCGACGC	CGCGACGT	
M66 (May4). txt	SEQ ID NO 181	AGGC	CCGCTGGTGGGCA	CCGGATGGA	TGCGCGCGCGCGATCGACGC	CGCGACGT	



TABLE 2

Affy#	SAMPLE ID#	Alt. ID	SPECIES
MY621		ATCC	<i>M. abscessus</i>
ATCC1	25291	ATCC-av	<i>M. avium</i>
M100	60300	MAC	<i>M. avium</i>
M101	60112	MAC	<i>M. avium</i>
M102	60268	MAC	<i>M. avium</i>
M103	60270	MAC	<i>M. avium</i>
M104	60272	MAC	<i>M. avium</i>
M105	60293	MAC	<i>M. avium</i>
M106	60313	MAC	<i>M. avium</i>
M107	60345	MAC	<i>M. avium</i>
M29	95-1764		<i>M. avium</i>
M30	95-1766		<i>M. avium</i>
M31	95-1768		<i>M. avium</i>
M32	95-1770		<i>M. avium</i>
M33	95-1775		<i>M. avium</i>
M34	95-1776		<i>M. avium</i>
M48	95-1765		<i>M. avium</i>
M49	95-1769		<i>M. avium</i>
M63	MAC #1	MAC	<i>M. avium</i>
M64	MAC #2	MAC	<i>M. avium</i>
M65	MAC #3	MAC	<i>M. avium</i>
M67	MAC #5	MAC	<i>M. avium</i>
M69	MAC #7	MAC	<i>M. avium</i>
M70	MAC #8	MAC	<i>M. avium</i>
M71	MAC #9	MAC	<i>M. avium</i>
M72	MAC #10	MAC	<i>M. avium</i>
M91	FM	avium-intracell. FM(MAC)	<i>M. avium</i>
M92	60040	MAC	<i>M. avium</i>
M93	60042	MAC	<i>M. avium</i>
M94	60049	MAC	<i>M. avium</i>
M95	60051	MAC	<i>M. avium</i>
M96	60110	MAC	<i>M. avium</i>
M97	60116	MAC	<i>M. avium</i>
M98	60123	MAC	<i>M. avium</i>
M99	60176	MAC	<i>M. avium</i>
M78	92-773		<i>M. bovis</i>
MY451			<i>M. bovis</i>
ATCC2	35752	ATCC-chel(new)	<i>M. chelonae</i>
M10	95A9151		<i>M. chelonae</i>
M11	95A0477		<i>M. chelonae</i>
M115	60121		<i>M. chelonae</i>
M116	52942		<i>M. chelonae</i>
M117	43192		<i>M. chelonae</i>
M118	53180		<i>M. chelonae</i>
M119	53131		<i>M. chelonae</i>
M12	95A4883		<i>M. chelonae</i>
M120	52923		<i>M. chelonae</i>
M121	52919		<i>M. chelonae</i>
M13	95A2611		<i>M. chelonae</i>
M14	95A0779		<i>M. chelonae</i>
M15	95A8654		<i>M. chelonae</i>
M16	95A8882		<i>M. chelonae</i>
M17	95A8881		<i>M. chelonae</i>
M50	95A11814		<i>M. chelonae</i>
M51	95A1102		<i>M. chelonae</i>
M75	#13	MAC#13	<i>M. chelonae</i>
MY109			<i>M. chelonae</i>
MY200			<i>M. chelonae</i>
MY207			<i>M. chelonae</i>
MY209			<i>M. chelonae</i>
M122	60025		<i>M. flavescens</i>
M123	60078		<i>M. flavescens</i>
M124	60252		<i>M. flavescens</i>
ATCC3	6841	ATTC-for	<i>M. fortuitum</i>
M53	60305		<i>M. fortuitum</i>
M54	60344		<i>M. fortuitum</i>
M55	60435		<i>M. fortuitum</i>
M56	60447		<i>M. fortuitum</i>
M74	#12	MAC#12	<i>M. fortuitum</i>
M88	CH	font. CH	<i>M. fortuitum</i>
MY221			<i>M. fortuitum</i>
MY223			<i>M. fortuitum</i>
MY225			<i>M. fortuitum</i>

TABLE 2-continued

Affy#	SAMPLE ID#	Alt. ID	SPECIES
MY341			<i>M. fortuitum</i>
MY715			<i>M. fortuitum</i>
MY470			<i>M. genevise</i>
ATCC4	14470	ATCC-go	<i>M. gordonae</i>
ATCC4-0		gord.	<i>M. gordonae</i>
M125	60068		<i>M. gordonae</i>
M126	60182		<i>M. gordonae</i>
M127	60214		<i>M. gordonae</i>
M128	60283		<i>M. gordonae</i>
M78	92-942	gord. LZ	<i>M. gordonae</i>
M79	93-692	gord. JD	<i>M. gordonae</i>
M80	94-94	gord. LG	<i>M. gordonae</i>
M81	93-1231	gord. LL	<i>M. gordonae</i>
M82	93-463	gord. RM	<i>M. gordonae</i>
M83	92-1219	gord. MB	<i>M. gordonae</i>
M84	91-1131	gord. OW	<i>M. gordonae</i>
M85	91-1478	gord. LB	<i>M. gordonae</i>
M86	92-642	gord. RB	<i>M. gordonae</i>
M87	93-1180	gord. WN	<i>M. gordonae</i>
M90	DB	gord. DB	<i>M. gordonae</i>
MY103			<i>M. gordonae</i>
MY475			<i>M. gordonae</i>
MY476			<i>M. gordonae</i>
My746			<i>M. gordonae</i>
MY830			<i>M. gordonae</i>
ATCC5		ATCC-int	<i>M. intracellulare</i>
ATCC5-0		intra	<i>M. intracellulare</i>
M18	95-1778		<i>M. intracellulare</i>
M19	95-1780		<i>M. intracellulare</i>
M20	94-1781		<i>M. intracellulare</i>
M21	95-1782		<i>M. intracellulare</i>
M22	95-1790		<i>M. intracellulare</i>
M23	95-1794		<i>M. intracellulare</i>
M24	95-1796		<i>M. intracellulare</i>
M25	95-1777		<i>M. intracellulare</i>
M26	95-1779		<i>M. intracellulare</i>
M27	95-1760		<i>M. intracellulare</i>
M28	95-1761		<i>M. intracellulare</i>
ATCC6	12478	ATTC-kan	<i>M. kansasii</i>
ATCC6-0		kans.	<i>M. kansasii</i>
M1	95A5375		<i>M. kansasii</i>
M2	95A10299		<i>M. kansasii</i>
M3	96A0020		<i>M. kansasii</i>
M4	95A3977		<i>M. kansasii</i>
M5	95A4739		<i>M. kansasii</i>
M52	95A5381		<i>M. kansasii</i>
M57	60163		<i>M. kansasii</i>
M58	60180		<i>M. kansasii</i>
M59	60207		<i>M. kansasii</i>
M59	95A2695		<i>M. kansasii</i>
M60	60294		<i>M. kansasii</i>
M61	60308		<i>M. kansasii</i>
M62	60314		<i>M. kansasii</i>
M7	95A2694		<i>M. kansasii</i>
M73	#11	MAC#11	<i>M. kansasii</i>
M8	94A9042		<i>M. kansasii</i>
M9	95A1275		<i>M. kansasii</i>
MY106			<i>M. kansasii</i>
MY141			<i>M. kansasii</i>
MY216			<i>M. kansasii</i>
MY218			<i>M. kansasii</i>
MY226			<i>M. kansasii</i>
M108	60044		<i>M. malmoense</i>
M109	60149		<i>M. malmoense</i>
M110	60211		<i>M. malmoense</i>
M111	60202		<i>M. malmoense</i>
M112	60085		<i>M. malmoense</i>
M113	60047		<i>M. malmoense</i>
M114	60185		<i>M. malmoense</i>
MY325		ATCC	<i>M. malmoense</i>
MY718		maimo	<i>M. malmoense</i>
MY214			<i>M. marinum</i>
MY224			<i>M. marinum</i>
MY244			<i>M. marinum</i>

TABLE 2-continued

Affy#	SAMPLE ID#	Alt. ID	SPECIES
MY339			<i>M. marinum</i>
MY343			<i>M. marinum</i>
MY458		ATCC	<i>M. mucogenicum</i>
MY809			<i>M. mucogenicum</i>
MY817			<i>M. mucogenicum</i>
MY821			<i>M. mucogenicum</i>
MY824			<i>M. mucogenicum</i>
MY102			<i>M. nonchromagenicum</i>
MY105			<i>M. nonchromagenicum</i>
MY251			<i>M. nonchromagenicum</i>
MY256			<i>M. nonchromagenicum</i>
MY294			<i>M. nonchromagenicum</i>
ATCC7	19981	ATCC-scr	<i>M. scrofulaceum</i>
ATCC7-0		scrof.	<i>M. scrofulaceum</i>
MY121			<i>M. scrofulaceum</i>
MY249			<i>M. scrofulaceum</i>
MY372			<i>M. scrofulaceum</i>
MY387			<i>M. scrofulaceum</i>
MY484			<i>M. simiae</i>
MY556			<i>M. simiae</i>
MY583			<i>M. simiae</i>
MY586			<i>M. simiae</i>
ATCC8	19420	ATCC-sme	<i>M. smegmatis</i>
M35	95A1072		<i>M. smegmatis</i>
M36	95A8183		<i>M. smegmatis</i>
M37	95A4990		<i>M. smegmatis</i>
M77	92-144	smeg. JL	<i>M. smegmatis</i>
MY143		ATCC	<i>M. smegmatis</i>
MY104			<i>M. szulgai</i>
MY198			<i>M. szulgai</i>
MY357			<i>M. szulgai</i>
MY358			<i>M. szulgai</i>
MY480			<i>M. szulgai</i>
TB74	C.17.96.5		<i>M. tab M160 DR</i>
MY387			<i>M. tb</i>
MY418			<i>M. tb</i>
MY437			<i>M. tb</i>
MY462			<i>M. tb</i>
TB59	C.18.96.1		<i>M. tb H37rv DR</i>
TB57	C.16.96.1		<i>M. tb H37rv DR</i>
TB73	C.17.96.1		<i>M. tb H37rv DR</i>
TB60	C.18.96.2		<i>M. tb J35 DR</i>
TB65	C.22.96.9		<i>M. tb M101 DR</i>
TB82	C.18.96.4		<i>M. tb M104 DR</i>
TB89	C.16.96.3		<i>M. tb M104 DR</i>
TB72	C.16.98.7		<i>M. tb M104 DR</i>
TB66	C.22.96.10		<i>M. tb M112 DR</i>
TB63	C.18.96.5		<i>M. tb M140 DR</i>
TB64	C.18.96.6		<i>M. tb M160 DR</i>
TB70	C.18.96.4		<i>M. tb M160 DR</i>
TB61	C.18.96.3		<i>M. tb M60 DR</i>
TB68	C.18.96.2		<i>M. tb M60 DR</i>
TB71	C.18.96.5		<i>M. tb M60 DR</i>
MY212			<i>M. terrae</i>
MY354			<i>M. terrae</i>
MY491			<i>M. terrae</i>
MY497			<i>M. terrae</i>
MY816			<i>M. triplex</i>
ATCC9	27294	Mtb	<i>M. tuberculosis</i>
ATCC9-0		TB2020	<i>M. tuberculosis</i>
N/A	93-1071		<i>M. tuberculosis</i>
N/A	93-336		<i>M. tuberculosis</i>
N/A	92-852		<i>M. tuberculosis</i>
N/A	92-1005		<i>M. tuberculosis</i>
N/A	92-243		<i>M. tuberculosis</i>
N/A	92-304		<i>M. tuberculosis</i>
N/A	92-199		<i>M. tuberculosis</i>
N/A	92-197		<i>M. tuberculosis</i>
N/A	92-484		<i>M. tuberculosis</i>
N/A	94-577		<i>M. tuberculosis</i>
TB1	936		<i>M. tuberculosis</i>
TB10	1122		<i>M. tuberculosis</i>
TB11	3407		<i>M. tuberculosis</i>
TB12	978		<i>M. tuberculosis</i>

TABLE 2-continued

Affy#	SAMPLE ID#	Alt. ID	SPECIES
TB13	3553		<i>M. tuberculosis</i>
TB14	3468		<i>M. tuberculosis</i>
TB15	2163		<i>M. tuberculosis</i>
TB16	DW	DW	<i>M. tuberculosis</i>
TB17	CB	CB	<i>M. tuberculosis</i>
TB18	PB	PB	<i>M. tuberculosis</i>
TB19	AA	AA	<i>M. tuberculosis</i>
TB2	M0404A		<i>M. tuberculosis</i>
TB20	3492		<i>M. tuberculosis</i>
TB21	1435		<i>M. tuberculosis</i>
TB22	896		<i>M. tuberculosis</i>
TB23	2268		<i>M. tuberculosis</i>
TB24	3455		<i>M. tuberculosis</i>
TB25	37		<i>M. tuberculosis</i>
TB26	173		<i>M. tuberculosis</i>
TB27	230		<i>M. tuberculosis</i>
TB28	2519		<i>M. tuberculosis</i>
TB29	T29233		<i>M. tuberculosis</i>
TB3	1231		<i>M. tuberculosis</i>
TB30	SP	SP	<i>M. tuberculosis</i>
TB31	3201		<i>M. tuberculosis</i>
TB32	3219		<i>M. tuberculosis</i>
TB33	80		<i>M. tuberculosis</i>
TB34	3442		<i>M. tuberculosis</i>
TB35	3502		<i>M. tuberculosis</i>
TB36	3759		<i>M. tuberculosis</i>
TB37	1295		<i>M. tuberculosis</i>
TB38	337		<i>M. tuberculosis</i>
TB39	394		<i>M. tuberculosis</i>
TB4	914		<i>M. tuberculosis</i>
TB40	499		<i>M. tuberculosis</i>
TB41	535		<i>M. tuberculosis</i>
TB42	607		<i>M. tuberculosis</i>
TB43	707		<i>M. tuberculosis</i>
TB44	692		<i>M. tuberculosis</i>
TB45	2408		<i>M. tuberculosis</i>
TB46	1069		<i>M. tuberculosis</i>
TB47	M3282A		<i>M. tuberculosis</i>
TB48	1338		<i>M. tuberculosis</i>
TB49	1368		<i>M. tuberculosis</i>
TB5	1145		<i>M. tuberculosis</i>
TB50	65		<i>M. tuberculosis</i>
TB51	727		<i>M. tuberculosis</i>
TB52	3455		<i>M. tuberculosis</i>
TB53	3506		<i>M. tuberculosis</i>
TB54	9500387		<i>M. tuberculosis</i>
TB55	9600173		<i>M. tuberculosis</i>
TB56	9503471		<i>M. tuberculosis</i>
TB57	9600309		<i>M. tuberculosis</i>
TB58	9600230		<i>M. tuberculosis</i>
TB6	1417		<i>M. tuberculosis</i>
TB7	SM2341		<i>M. tuberculosis</i>
TB75	2098		<i>M. tuberculosis</i>
TB76	173/1		<i>M. tuberculosis</i>
TB77	1122/1		<i>M. tuberculosis</i>
TB78	1417/1		<i>M. tuberculosis</i>
TB8	1587		<i>M. tuberculosis</i>
TB9	M7032A		<i>M. tuberculosis</i>
ATCC10	19250	ATTC-xen	<i>M. xenopi</i>
M129	60133		<i>M. xenopi</i>
M130	60200		<i>M. xenopi</i>
M131	60365		<i>M. xenopi</i>
M132	60387		<i>M. xenopi</i>
M38	95A5208		<i>M. xenopi</i>
M39	95A5399		<i>M. xenopi</i>
M40	95A3938		<i>M. xenopi</i>
M41	95A8782		<i>M. xenopi</i>
M42	95A0933		<i>M. xenopi</i>
M43	95A4320		<i>M. xenopi</i>
M44	95A478		<i>M. xenopi</i>
M45	95A2997		<i>M. xenopi</i>
M46	95A8383		<i>M. xenopi</i>
M47	95A4319		<i>M. xenopi</i>
M89	SG	xen.SG	<i>M. xenopi</i>

TABLE 2-continued

Affy#	SAMPLE ID#	Alt. ID	SPECIES
MY219			<i>M. xenopi</i>
MY250			<i>M. xenopi</i>
MY252			<i>M. xenopi</i>
MY254			<i>M. xenopi</i>
MY255			<i>M. xenopi</i>
MY107			MAC
MY111			MAC
MY112			MAC

TABLE 2-continued

Affy#	SAMPLE ID#	Alt. ID	SPECIES
MY312			MAC
M66	MAC #4	MAC #4	unique

[0064]

## SEQUENCE LISTING

&lt;160&gt; NUMBER OF SEQ ID NOS: 181

&lt;210&gt; SEQ ID NO 1

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium tuberculosis

&lt;400&gt; SEQUENCE: 1

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tgtcgggggt gaccacaag cgccgactgt cggcgctggg gcccgcggt ctgtcacgtg      180
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tcaaccggtt cgggttcacg gaaacgccgt accgcaaggt ggtcgacggc gtggttagcg      360
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&lt;210&gt; SEQ ID NO 2

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&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium abscessus

&lt;400&gt; SEQUENCE: 2

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cggacggagt tgtcaccgac gacatccact acctgacggc cgacgaagag gaccgccacg      360
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 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium avium  
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tgctggggct caccacaag cgccgcctgt cggcgctggg cccgggtggg ctgtcccggg	180
agcgggccgg gctggaggtc cgcgacgtgc acccgcccc ctacggccgg atgtgcccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcggg tacgcgcggg	300
tcaaccggtt cgggttcacg gagacgcgt accgcaaggt ggtcgacggc gtggtcaccg	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgccgatcga cggaagggc cggttcgccg agggccgggt gctggtccgc cgcaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacntkts ccgcgccara	540
tggtgtcggg ggccaccgcg atgatccgt tcctcgagca cgacgacgcc aaccgtgccc	600
tgatgggcgc caacatgcak cgccaggcgg ttccgctggg gcgcagcgan gcgccgctgg	660
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 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium avium

<400> SEQUENCE: 4

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tgctggggct caccacaag cgccgcctgt cggcgctggg cccgggtggg ctgtcccggg	180
agcgggccgg gctggaggtc cgcgacgtgc acccgcccc ctacggccgg atgtgcccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcggg tatgcgcggg	300
tcaaccggtt cgggttcacg gagacgcgt accgcaaggt ggtcgacggc gtggtcaccg	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgccgatcga cgacaagggc cggttcgccg agggccgggt gctggtccgc cgcaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tggtgtcggg ggccaccgcg atgatccgt tcctcgagca cgacgacgcc aaccgtgccc	600
tgatgggcgc caacatgcag cgccaggcgg ttccgctggg gcgcagcgag gcgccgctgg	660

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tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705
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<210> SEQ ID NO 5  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium avium

<400> SEQUENCE: 5

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg	60
cgatcaagga gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgc	120
tgctggggct caccacaag cgcgcctgt cggcgctggg cccgggtggg ctgtcccg	180
agcgggccgg gctggaggtc cgcgacgtgc acccggtcca ctacggccgg atgtgccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcggg tatgcgcgg	300
tcaaccggtt cgggttcacg gagacgcgt accgcaaggt ggtcgacggc gtggtcaccg	360
acgagatcca ctacgtgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgcgcatcga cgacaaggcg cggttcgcgg aggcccggt gctggtccgc cgcaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tggtgtcggg ggccaccgcg atgatcccg tccctcgagca cgacgacgcc aaccgtgcc	600
tgatgggcgc caacatgcag cgcacggcgg ttccgctggt gcgcagcgag gcgcgcgtgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 6  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium avium

<400> SEQUENCE: 6

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg	60
cgatcaagga gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgc	120
tgctggggct caccacaag cgcgcctgt cggcgctggg cccgggtggg ctgtcccg	180
agcgggccgg gctggaggtc cgcgacgtgc acccggtcca ctacggccgg atgtgccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcggg tatgcgcgg	300
tcaaccggtt cgggttcacg gagacgcgt accgcaaggt ggtcgacggc gtggtcaccg	360
acgagatcca ctacgtgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgcgcatcga cgacaaggcg cggttcgcgg aggcccggt gctggtccgc cgcaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tggtgtcggg ggccaccgcg atgatcccg tccctcgagca cgacgacgcc aaccgtgcc	600
tgatgggcgc caacatgcag cgcacggcgg ttccgctggt gcgcagcgag gcgcgcgtgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 7  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium avium

<400> SEQUENCE: 7

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg	60
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cgatcaagga gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgc	120
tgtcggggct caccacaag cgcgcctgt cggcgctggg cccgggtggg ctgtcccggg	180
agcgggccgg gctggaggtc cgcgacgtgc acccgcccc ctacggccgg atgtgcccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcgggt tatgcccggg	300
tcaaccggtt cgggttcacg gagacgccgt accgcaaggt ggtcgacggc gtggtcaccg	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgcgacatga cgacaagggc cggttcgcgg agggccgggt gctggtccgc cgcaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tggtgtcggg ggccaccgcg atgatcccgt tcctcgagca cgacgacgcc aaccgtgccc	600
tgatggggcg caacatgcag cgcagggcgg ttccgctggg gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 8

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium avium

&lt;400&gt; SEQUENCE: 8

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg	60
cgatcaagga gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgc	120
tgtcggggct caccacaag cgcgcctgt cggcgctggg cccgggtggg ctgtcccggg	180
agcgggccgg gctggaggtc cgcgacgtgc acccgcccc ctacggccgg atgtgcccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcgggt tatgcccggg	300
tcaaccggtt cgggttcacg gagacgccgt accgcaaggt ggtcgacggc gtggtcaccg	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgcgacatga cgacaagggc cggttcgcgg agggccgggt gctggtccgc cgcaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tggtgtcggg ggccaccgcg atgatcccgt tcctcgagca cgacgacgcc aaccgtgccc	600
tgatggggcg caacatgcag cgcagggcgg ttccgctggg gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 9

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium avium

&lt;400&gt; SEQUENCE: 9

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg	60
cgatcaagga gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgc	120
tgtcggggct caccacaag cgcgcctgt cggcgctggg cccgggtggg ctgtcccggg	180
agcgggccgg gctggaggtc cgcgacgtgc acccgcccc ctacggccgg atgtgcccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcgggt tatgcccggg	300
tcaaccggtt cgggttcacg gagacgccgt accgcaaggt ggtcgacggc gtggtcaccg	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420

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cgccgatcga cgacaagggc cggttcgcgg aggcccgggg gctggtccgc cgcaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tggtgtcggg ggccaccgcg atgatcccggt tcctcgagca cgacgacgcc aaccgtgccc	600
tgatggggcg caacatgcag cgccaggcgg ttccgctggg gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 10  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium avium

<400> SEQUENCE: 10

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtccr gtcgtggcgg	60
cgatcaagga gttcttcgcg accagccagc tgtcccagtt catggaccag aacaaccgc	120
tgtcgggtct gacccacaag cgccgcctgt cggcgctggg cccgggtggg ctgtcccggg	180
agcggggcgg cctggaggtc cgtgacgtgc acccgtsca ctacggccgg atgtgccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcggg taygcgcggg	300
tsaaccggtt cgggttcacg gagaccccg accgcaagg ggtcgacgg gtggtcacccg	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtsgtggcg caggccaact	420
cgccgatcga cgacaagggc cggttcgagg agkcccgggg gctggtccgc cgsaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tggtgtcggg ggccaccgcg atgatcccggt tcctcgagca cgacgacgcc aaccgtgccc	600
tgatggggcg caacatgcag cgccaggcgg ttccgctggg gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 11  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium avium  
 <220> FEATURE:  
 <221> NAME/KEY: modified\_base  
 <222> LOCATION: (42)...(42)  
 <223> OTHER INFORMATION: n = g,a,c or t  
 <220> FEATURE:  
 <221> NAME/KEY: modified\_base  
 <222> LOCATION: (692)...(692)  
 <223> OTHER INFORMATION: n = g,a,c or t

<400> SEQUENCE: 11

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa cntccgtccc gtcgtggcgg	60
cgatcaagga gttcttcgcg accagccagt tgtcccagtt catggaccag aacaaccgc	120
tgtcggggct caccacaag cgccgcctgt cggcgctggg cccgggtggg ctgtcccggg	180
agcggggcgg gctggaggtc cgcgacgtgc acccgtscca ctacggccgg atgtgccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcggg tacgcgcggg	300
tgaaccggtt cggcttcacg gagaccccg accgcaagg ggtcgacggc gtggtcacccg	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgccgatcga cgacaagggc cggttcgccg aggcccgggg gctggtccgc cgcaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540

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tggtgtcggg	ggccaccg	atgatccc	tcctcgag	cgacgacgc	aaccgtgccc	600
tgatggggc	caacatgc	cgccaggcg	ttccgctgg	gcgcagcg	gcgccgctg	660
tgggcaccg	catggagct	cgcgggcg	tngacgcgc	gacgt		705

<210> SEQ ID NO 12  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium avium

<400> SEQUENCE: 12

cccaggacgt	ggaggcgatc	acaccgcaga	ccctgatcaa	catccgtcca	gtcgtggcgg	60
cgatcaagga	gttcttcggc	accagccagc	tgccccagtt	catggaccag	aacaaccgc	120
tgctggggct	caccacaag	cgccgcctgt	cggcgctggg	ccgggtgggt	ctgtcccggg	180
agcgggccc	gctggaggtc	cgcgacgtgc	acccgtccca	ctacggccgg	atgtgcccga	240
tcgagacccc	ggagggtccc	aacatcggtc	tgatcggtc	gctgtcgggt	tatgcgcggg	300
tcaaccggtt	cggttcctc	gagacgcct	accgcaaggt	ggtcgacggc	gtggtcaccg	360
acgagatcca	ctacctgacc	gccgacgagg	aggaccgcca	cgtggtggcg	caggccaact	420
cgccgatcga	cgacaagggc	cggttcgcgg	aggcccgggt	gctggtccgc	cgcaaggcgg	480
gcgaggtcga	gtacgtgccc	tcgtccgagg	tggactacat	ggacgtgtcg	ccgcgccaga	540
tggtgtcggg	ggccaccg	atgatccc	tcctcgag	cgacgacgc	aaccgtgccc	600
tgatggggc	caacatgc	cgccaggcg	ttccgctgg	gcgcagcg	gcgccgctg	660
tgggcaccg	catggagct	cgcgggcg	tcgacgcgc	gacgt		705

<210> SEQ ID NO 13  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium avium

<400> SEQUENCE: 13

cccaggacgt	ggaggcgatc	acaccgcaga	ccctgatcaa	catccgtcca	gtcgtggcgg	60
cgatcaagga	gttcttcggc	accagccagc	tgccccagtt	catggaccag	aacaaccgc	120
tgctggggct	caccacaag	cgccgcctgt	cggcgctggg	ccgggtgggt	ctgtcccggg	180
agcgggccc	gctggaggtc	cgcgacgtgc	acccgtccca	ctacggccgg	atgtgcccga	240
tcgagacccc	ggagggtccc	aacatcggtc	tgatcggtc	gctgtcgggt	tatgcgcggg	300
tcaaccggtt	cggttcctc	gagacgcct	accgcaaggt	ggtcgacggc	gtggtcaccg	360
acgagatcca	ctacctgacc	gccgacgagg	aggaccgcca	cgtggtggcg	caggccaact	420
cgccgatcga	cgacaagggc	cggttcgcgg	aggcccgggt	gctggtccgc	cgcaaggcgg	480
gcgaggtcga	gtacgtgccc	tcgtccgagg	tggactacat	ggacgtgtcg	ccgcgccaga	540
tggtgtcggg	ggccaccg	atgatccc	tcctcgag	cgacgacgc	aaccgtgccc	600
tgatggggc	caacatgc	cgccaggcg	ttccgctgg	gcgcagcg	gcgccgctg	660
tgggcaccg	catggagct	cgcgggcg	tcgacgcgc	gacgt		705

<210> SEQ ID NO 14  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium avium



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&lt;400&gt; SEQUENCE: 14

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cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg      60
cgatcaagga gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgc      120
tgtcggggct caccacaaag cgccgcctgt cggcgctggg cccgggtggg ctgtcccggg      180
agcgggcccg gctggaggtc cgcgacgtgc acccgtccca ctacggccgg atgtgccga      240
tcgagacccc ggagggtccc aacatcggtc tgatcggctc gctgtcggtg tatgcccggg      300
tcaaccggtt cgggttcacg gagacgccgt accgcaagggt ggtcgacggc gtggtcaccg      360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact      420
cgccgatcga cgacaagggc cgggttcggg aggcccgggg gctggtccgc cgcaaggcgg      480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga      540
tggtgtcggg gggcaccgcg atgatcccggt tcctcgagca cgacgacgcc aaccgtgccc      600
tgatgggcgc caatcgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg      660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt                      705

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&lt;210&gt; SEQ ID NO 15

&lt;211&gt; LENGTH: 626

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium avium

&lt;400&gt; SEQUENCE: 15

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tccgtccagt cgtggcggcg atcaaggagt tcttcggcac cagccagctg tcccagttca      60
tggaaccagaa caaccgctg tcgggggtca cccacaagcg ccgcctgtcg gcgtggggc      120
cgggtggtct gtcccgggag cgggcggggc tggagggtccg cgacgtgcac ccgtcccact      180
acggccggat gtgcccgatc gagaccccgg aggggtccaa catcggtctg atcggtcgc      240
tgtcgggtga tgcgcgggtc aaccggttcg ggttcacgga gacgccgtac cgcaagggtg      300
tcgacggcgt ggtcaccgac gagatccact acctgaccgc cgacgaggag gaccgccacg      360
tggtggcgca ggccaactcg ccgatcgacg acaaggggcg gttcgcggag gcccggtg      420
tggtccgcgc caaggcgggc gaggtcgagt acgtgccctc gtccgaggtg gactacatgg      480
acgtgtcgcc gcgcagatg gtgtcgggtg ccaccgcgat gatcccggtc ctcgagcacg      540
acgacgcaa ccgtgccctg atgggcgcca acatgcagcg ccaggcgggt ccgctggtgc      600
gcagcgaggc gccgctggtg ggcacc                      626

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&lt;210&gt; SEQ ID NO 16

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium avium

&lt;400&gt; SEQUENCE: 16

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cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg      60
cgatcaagga gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgc      120
tgtcggggct caccacaaag cgccgcctgt cggcgctggg cccgggtggg ctgtcccggg      180
agcgggcccg gctggaggtc cgcgacgtgc acccgtccca ctacggccgg atgtgccga      240
tcgagacccc ggagggtccc aacatcggtc tgatcggctc gctgtcggtg tatgcccggg      300
tcaaccggtt cgggttcacg gagacgccgt accgcaagggt ggtcgacggc gtggtcaccg      360

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acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgccgatcga cgacaagggc cggttcgcgg aggcccggtt gctggtccgc cgcaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tgggtgcggt ggccaccgcg atgatcccggt tcctcgagca cgacgacgcc aaccgtgccc	600
tgatggggcg caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 17

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium avium

&lt;400&gt; SEQUENCE: 17

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg	60
cgatcaagga gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgc	120
tgtcggggct caccacaag cgcgcctgt cggcgtggg cccgggtggt ctgtccggg	180
agcggggcgg gctggaggtc cgcgacgtgc acccgtccca ctacggccgg atgtgccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcgtg tatgcccgg	300
tcaaccggtt cgggttcacg gagacccgt accgcaaggt ggtcgacggc gtggtcaccg	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgccgatcga cgacaagggc cggttcgcgg aggcccggtt gctggtccgc cgcaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tgggtgcggt ggccaccgcg atgatcccggt tcctcgagca cgacgacgcc aaccgtgccc	600
tgatggggcg caacatgcag cgccaggcgg ttccgctggt gcgcagcgaa gcgccgctgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 18

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium avium

&lt;400&gt; SEQUENCE: 18

ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg cgatcaagga	60
gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgc tgtcggggct	120
caccacaag cgcgcctgt cggcgtggg cccgggtggt ctgtccggg agcggggcgg	180
gctggaggtc cgcgacgtgc acccgtccca ctacggccgg atgtgccga tcgagacccc	240
ggagggtccc aacatcggtc tgatcggtc gctgtcgtg tatgcccgg tcaaccggtt	300
cgggttcacg gagacccgt accgcaaggt ggtcgacggc gtggtcaccg acgagatcca	360
ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact cgccgatcga	420
cgacaagggc cggttcgcgg aggcccggtt gctggtccgc cgcaaggcgg gcgaggtcga	480
gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtcgggt	540
ggccaccgcg atgatcccggt tcctcgagca cgacgacgcc aaccgtgccc tgatggggcg	600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg	660
catggagctg cgcgcggcga tcgacgc	687

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<210> SEQ ID NO 19  
<211> LENGTH: 687  
<212> TYPE: DNA  
<213> ORGANISM: Mycobacterium avium

<400> SEQUENCE: 19

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ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg cgatcaagga    60
gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgcg tgcgggggct    120
caccacaag cgccgcctgt cggcgtggg cccgggtggt ctgtcccggg agcggggccgg    180
gctggaggtc cgcgacgtgc acccggtcca ctacggccgg atgtgccga tcgagacccc    240
ggagggtccc aacatcggtc tgatcggtc gctgtcgtg tatgcgggg tcaaccggtt    300
cgggttcacg gagacccgt accgcaaggt ggtcgacggc gtggtcaccg acgagatcca    360
ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact cgccgatcga    420
cgacaagggc cggttcgcgg aggcccggt gctggtccgc cgcaaggcgg gcgaggtcga    480
gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggt    540
ggccaccgcg atgatcccg tccctgagca cgacgacgcc aaccgtgccc tgatgggcgc    600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg    660
catggagctg cgcgcggcga tcgacgc                                     687
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<210> SEQ ID NO 20  
<211> LENGTH: 687  
<212> TYPE: DNA  
<213> ORGANISM: Mycobacterium avium

<400> SEQUENCE: 20

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ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg cgatcaagga    60
gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgcg tgcgggggct    120
caccacaag cgccgcctgt cggcgtggg cccgggtggt ctgtcccggg agcggggccgg    180
gctggaggtc cgcgacgtgc acccggtcca ctacggccgg atgtgccga tcgagacccc    240
ggagggtccc aacatcggtc tgatcggtc gctgtcgtg tatgcgggg tcaaccggtt    300
cgggttcacg gagacccgt accgcaaggt ggtcgacggc gtggtcaccg acgagatcca    360
ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact cgccgatcga    420
cgacaagggc cggttcgcgg aggcccggt gctggtccgc cgcaaggcgg gcgaggtcga    480
gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggt    540
ggccaccgcg atgatcccg tccctgagca cgacgacgcc aaccgtgccc tgatgggcgc    600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg    660
catggagctg cgcgcggcga tcgacgc                                     687
```

<210> SEQ ID NO 21  
<211> LENGTH: 687  
<212> TYPE: DNA  
<213> ORGANISM: Mycobacterium avium

<400> SEQUENCE: 21

```
ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg cgatcaagga    60
gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgcg tgcgggggct    120
```

## -continued

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caccacaaag cgcgcctgt cggcgtggg cccgggtggt ctgtcccggg agcgggccgg	180
gctggaggtc cgcgacgtgc acccgtccca ctacggccgg atgtgccga tcgagacccc	240
ggagggtccc aacatcggtc tgatcggctc gctgtcggtg tatgcgcggg tcaaccggtt	300
cgggttcate gagacccgt accgcaaggt ggtcgacggc gtggtcaccg acgagatcca	360
ctacctgacc gccgacgagg aggacggcca cgtggtggcg caggccaact cgcgatcga	420
cgacaagggc cggttcgcgg aggccgggt gctggtccgc cgcaaggcgg gcgaggtcga	480
gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggg	540
ggccaccgcg atgatcccg ttctcgagca cgacgacgcc aaccgtgccc tgatgggcgc	600
caacatgcag cgcacggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg	660
catggagctg cgcgcggcga tcgacgc	687

&lt;210&gt; SEQ ID NO 22

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium avium

&lt;400&gt; SEQUENCE: 22

ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg cgatcaagga	60
gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgc tgctggggct	120
caccacaaag cgcgcctgt cggcgtggg cccgggtggt ctgtcccggg agcgggccgg	180
gctggaggtc cgcgacgtgc acccgtccca ctacggccgg atgtgccga tcgagacccc	240
ggagggtccc aacatcggtc tgatcggctc gctgtcggtg tatgcgcggg tcaaccggtt	300
cgggttcate gagacccgt accgcaaggt ggtcgacggc gtggtcaccg acgagatcca	360
ctacctgacc gccgacgagg aggacggcca cgtggtggcg caggccaact cgcgatcga	420
cgacaagggc cggttcgcgg aggccgggt gctggtccgc cgcaaggcgg gcgaggtcga	480
gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggg	540
ggccaccgcg atgatcccg ttctcgagca cgacgacgcc aaccgtgccc tgatgggcgc	600
caacatgcag cgcacggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg	660
catggagctg cgcgcggcga tcgacgc	687

&lt;210&gt; SEQ ID NO 23

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium avium

&lt;400&gt; SEQUENCE: 23

ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg cgatcaagga	60
gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgc tgctggggct	120
caccacaaag cgcgcctgt cggcgtggg cccgggtggt ctgtcccggg agcgggccgg	180
gctggaggtc cgcgacgtgc acccgtccca ctacggccgg atgtgccga tcgagacccc	240
ggagggtccc aacatcggtc tgatcggctc gctgtcggtg tatgcgcggg tcaaccggtt	300
cgggttcate gagacccgt accgcaaggt ggtcgacggc gtggtcaccg acgagatcca	360
ctacctgacc gccgacgagg aggacggcca cgtggtggcg caggccaact cgcgatcga	420
cgacaagggc cggttcgcgg aggccgggt gctggtccgc cgcaaggcgg gcgaggtcga	480

## -continued

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gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggt	540
ggccaccgcg atgatcccggt tcctcgagca cgacgacgcc aaccgtgccc tgatgggcgc	600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg	660
catggagctg cgcgcggcga tcgacgc	687

<210> SEQ ID NO 24  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium avium  
 <400> SEQUENCE: 24

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg	60
cgatcaagga gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgc	120
tgtcggggct caccacaag cgccgctgt cggcgctggg cccgggtggt ctgtcccggg	180
agcgggccgg gctggaggtc cgcgacgtgc acccgcccc ctacggccgg atgtgcccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcggtg tatgcgcggg	300
tcaaccggtt cggttcacg gagacgcgt accgcaaggt ggtcgacggc gtggtcaccg	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgccgatcga cgacaagggc cggttcgcgg aggcccggt gctggtccgc cgcaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tgggtgcggt ggccaccgcg atgatcccggt tcctcgagca cgacgacgcc aaccgtgccc	600
tgatgggcgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 25  
 <211> LENGTH: 687  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium avium  
 <400> SEQUENCE: 25

ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg cgatcaagga	60
gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgc tgtcggggct	120
caccacaag cgccgctgt cggcgctggg cccgggtggt ctgtcccggg agcgggccgg	180
gctggaggtc cgcgacgtgc acccgcccc ctacggccgg atgtgcccga tcgagacccc	240
ggagggtccc aacatcggtc tgatcggtc gctgtcggtg tatgcgcggg tcaaccggtt	300
cggttcacg gagacgcgt accgcaaggt ggtcgacggc gtggtcaccg acgagatcca	360
ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact cgccgatcga	420
cgacaagggc cggttcgcgg aggcccggt gctggtccgc cgcaaggcgg gcgaggtcga	480
gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggt	540
ggccaccgcg atgatcccggt tcctcgagca cgacgacgcc aaccgtgccc tgatgggcgc	600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg	660
catggagctg cgcgcggcga tcgacgc	687

<210> SEQ ID NO 26  
 <211> LENGTH: 687  
 <212> TYPE: DNA

## -continued

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<213> ORGANISM: Mycobacterium avium

&lt;400&gt; SEQUENCE: 26

```

ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg cgatcaagga      60
attcttcggc accagccagc tgtcgcagtt catggaccag aacaaccgcg tgcgggtct      120
gaccacaag cgctcgtctgt cggcgctggg ccccggcggg ctgtcccggt agcgcgccgg      180
ccttgaggtc cgcgacgtgc actccagcca ctacggccgc atgtgcccgga tcgagacccc      240
tgagggtccc aacatcggtc tgatcggctc gctgtcggtg tacgccggg tcaaccggt      300
cggtttcatc gagaccccg accgcaaggt cgtcgacggg gtggtcaccg accagatcga      360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgacgcg      420
cgcggacggc agcttcaccg aagaccgcgt gatggtccgc cgtaaggggc gcgaggtcga      480
gaacgtggcc ccgatcgacg tggattacat ggacgtctcg ccgcgccaga tgggtgcgg      540
cgcgacgcg atgatcccg tccctcgagca cgacgacgcc aaccgtgccc tgatgggtgc      600
caacatgcag cgcacggcgg ttccgctggt gcgtagcgag gcccgctgg tcggtaccgg      660
tatggagttg cgcgcggcga tcgacgc                                     687

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&lt;210&gt; SEQ ID NO 27

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium avium complex (MAC)

&lt;400&gt; SEQUENCE: 27

```

ggaggcgatc acaccgcaga ccctgatcaa catccgtcca gtcgtggcgg cgatcaagga      60
gttcttcggc accagccagc tgtcccagtt catggaccag aacaaccgcg tgcggggct      120
caccacaag cgcgcctgt cggcgctggg cccgggtggt ctgtccggg agcgggccgg      180
gctggaggtc cgcgacgtgc acccgtccca ctacggccgg atgtgcccgga tcgagacccc      240
ggagggtccc aacatcggtc tgatcggctc gctgtcggtg tatgcgggg tcaaccggt      300
cgggttcac c gagaccccg accgcaaggt ggtcgacggc gtggtcaccg acgagatcca      360
ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact cgcgacgcga      420
cgacaagggc cggttcgcgg aggcccggt gctggtccgc cgcaaggcgg gcgaggtcga      480
gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcgg      540
ggccaccgcg atgatcccg tccctcgagca cgacgacgcc aaccgtgccc tgatgggcgc      600
caacatgcag cgcacggcgg ttccgctggt gcgcagcgag gcgcgctgg tgggcaccgg      660
catggagctg cgcgcggcga tcgacgc                                     687

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&lt;210&gt; SEQ ID NO 28

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium bovis

&lt;400&gt; SEQUENCE: 28

```

cccaggacgt ggaggcgatc acaccgcaga cgttgatcaa catccggccg gtggtcgccg      60
cgatcaagga gttcttcggc accagccagc tgagccaatt catggaccag aacaaccgcg      120
tgtcgggggt gaccacaag cgcgactgt cggcgctggg gcccggcggg ctgtcacgtg      180
agcgtgccgg gctggaggtc cgcgacgtgc acccgtcgca ctacggccgg atgtgcccgga      240

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tcgaaacccc tgagggggccc aacatcggtc tgatcgggtc gctgtcgggtg tacgcgcggg	300
tcaacccggtt cgggttcacg gaaacgccgt accgcaaggt ggtcgacggc gtggttagcg	360
acgagatcgt gtacctgacc gccgacgagg aggaccgcca cgtggtggca caggccaatt	420
cgccgatcga tgcggacggt cgcttcgtcg agccgcgcgt gctggtccgc cgcaaggcgg	480
gcgaggtgga gtacgtgccc tcgtctgagg tggactacat ggacgtctcg ccccgccaga	540
tgggtgcggt ggccaccgcg atgattccct tcctggagca cgacgacgcc aaccgtgccc	600
tcatgggggc aaacatgcag cgccaggcgg tgccgctggt ccgtagcgag gcccgcgtgg	660
tgggcaccgg gatggagctg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 29

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium bovis

&lt;400&gt; SEQUENCE: 29

ggagggcgtc acaccgcaga cgttgatcaa catccggccg gtggtcgccg cgatcaagga	60
gttcttcggc accagccagc tgagccaatt catggaccag aacaaccgcg tgcgggggtt	120
gaccacaag cgcgcactgt cggcgctggg gcccgggcgt ctgtcacgtg agcgtgccgg	180
gctggaggtc cgcgacgtgc acccgtcgca ctacggccgg atgtgcccga tcgaaacccc	240
tgagggggcc aacatcggtc tgatcgggtc gctgtcgggt tacgcgcggg tcaacccggt	300
cgggttcacg gaaacgccgt accgcaaggt ggtcgacggc gtggttagcg acgagatcgt	360
gtacctgacc gccgacgagg aggaccgcca cgtggtggca caggccaatt cgccgatcga	420
tgcggacggt cgcttcgtcg agccgcgcgt gctggtccgc cgcaaggcgg gcgaggtgga	480
gtacgtgccc tcgtctgagg tggactacat ggacgtctcg ccccgccaga tgggtcggt	540
ggccaccgcg atgattccct tcctggagca cgacgacgcc aaccgtgccc tcatgggggc	600
aaacatgcag cgccaggcgg tgccgctggt ccgtagcgag gcccgcgtgg tgggcaccgg	660
gatggagctg cgcgcggcga tcgacgc	687

&lt;210&gt; SEQ ID NO 30

&lt;211&gt; LENGTH: 652

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium chelonae

&lt;400&gt; SEQUENCE: 30

cgcagaccct gatcaacatc cgtcccgctc tggcggcgat caaggagtgc ttcggaacca	60
gccagctgtc gcagttcatg gaccagaaca acccgctgtc gggcttgacc cacaagcgtc	120
gtctgtcggc gctggggccc ggtggtctga ctctgacgcg cgccggcctt gaggtccgcg	180
acgtgcaccc ctgcactac ggccgcatgt gcccgatcga gaccccgaa ggcccgaaca	240
tcggtctgat cggttcgctg tcggtgtacg cgcgggtcaa cccgttcggc ttcacgcaga	300
cgcggtaccg caaggtgtcc gaggtgtcgc tcaccgacga gatccactac ctgaccgccg	360
acgaagagga ccgccacgtg gtggcgacgg ccaactcgcc tgtggatgcc gacggccgct	420
tcaccgagga caagatcctg gtccgccgta aggggtggcg ggtcgagtgc gtctcggcga	480
ccgaggtgga ctacatggac gtctcgcgcg gccagatggt gtcggtcgcg accgccatga	540
tcccgctcct cgagcacgac gacgccaacc gtgccctcat gggtgccaac atgcagcgcc	600

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aggcgggttcc gctgggtgcgc agcggaggccc cgctgggtcgg taccggtatg ga 652

<210> SEQ ID NO 31  
 <211> LENGTH: 626  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium chelonae

<400> SEQUENCE: 31

tccgtcccggt cgtggcgggc atcaaggagt tcttcggaac cagccagctg tcgcagttca	60
tggaccagaa caaccgcgtt tcgggtctga cccacaagcg tcgtctgtcg gctctggggc	120
ccggtggtct gaccctgtac cgcgctggcc ttgagggtccg cgacgtgcac ccctcgcaact	180
acggccgcat gtgcccgatc gagaccccg aaggcccgaa catcggcctg atcggttcgc	240
tttcggtgta cgcgcgggtc aaccgcgttc gcttcacga gacgccgtac cgcaagggtg	300
ccgaggggtgt cgtcaccgac gagatccact acctgaccgc cgacgaagag gaccgccacg	360
tcgtggcaca ggccaactcg cctgtggatg ccgacggccg cttaccgag gacaagatcc	420
tggtccgccc taagggtggc gaggtcgagt tcgtctcggc gaccgaggtg gactacatgg	480
acgtctcgcc gcgccagatg gtgtcggtcg cgaccgcat gatcccggtc ctcgagcacg	540
acgacgcaa ccgtgccctc atgggtgcc aatgcagcg ccaggcggtt ccgctggtgc	600
gcagcgaggc cccgctggtc ggtacc	626

<210> SEQ ID NO 32  
 <211> LENGTH: 647  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium chelonae

<400> SEQUENCE: 32

tgatcaacat ccgtcccgtc gtggcgggcga tcaaggagtt cttcggaacc agccagctgt	60
cgagttcat ggaccagaac aaccgcgttt cgggtctgac ccacaagcgt cgtctgtcgg	120
ctctggggcc cgggtggtctg acccgtgacc gcgctggcct tgagggtccgc gacgtgcacc	180
cctcgcaacta cggccgatg tgcccgatcg agaccccgga agggccgaac atcggcctga	240
tcggttcgct ttcggtgtac gcgcgggtca acccgttcgg cttcatcgag acgccgtacc	300
gcaagggtgtc cgagggtgtc gtcaccgacg agatccacta cctgaccgac gacgaagagg	360
accgccacgt cgtggcacag gccaaactgc ctgtggatgc cgacggccgc ttcaccgagg	420
acaagatcct ggtccgcctg aagggtggcg aggtcgagtt cgtctcggcg accgaggtgg	480
actacatgga cgtctcgccg cgccagatgg tgcgggtcgc gaccgccatg atcccgttcc	540
tcgagcacga cgacgcaac cgtgcctca tgggtgcaa catgcagcg caggcggttc	600
cgctggtgcg cagcgaggcc ccgctggtcg gtaccggtat ggagctg	647

<210> SEQ ID NO 33  
 <211> LENGTH: 626  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium chelonae

<400> SEQUENCE: 33

tccgtcccggt cgtggcgggc atcaaggagt tcttcggaac cagccagctg tcgcagttca	60
tggaccagaa caaccgcgtg tcgggtctga cccacaagcg tcgtctttcg gcgtggggc	120
ccggtggtct gaccctgtac cgcgcggcc ttgagggtccg cgacgtgcac ccctcgcaact	180



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acggccgcat gtgcccgatc gagaccccgg aaggcccgaa catcggcctg atcgggttcgc 240
tgtcgggtgta cgcgcggggtc aaccggttcg gcttcacga gacgccgtac cgcaagggtg 300
ccgaggggtgt cgtcaccgac gagatccact acctgaccgc cgacgaagag gaccgccacg 360
tcgtggcaca ggccaactcg cctgtggatg ccgacggccg cttcaccgag gacaagatcc 420
tggtccgccc taagggtggc gaggtcgagt tcgtctcggc gaccgaggtg gactacatgg 480
acgtctcgcc gcgccaaatg gtgtcggtcg cgaccgcat gatcccggtc ctcgagcacg 540
acgacgcaa ccgtgccctc atgggtgcca acatgcagcg ccaggcggtt ccgctgggtg 600
gcagcgaggc cccgctggtc ggtacc 626

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<210> SEQ ID NO 34
<211> LENGTH: 643
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium chelonae

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<400> SEQUENCE: 34

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```

tgatcaacat ccgtcccgtc gtggcggcga tcaaggagtt cttcggaacc agccagctgt 60
cgcagttcat ggaccagaac aaccgcgttt cgggtctgac ccacaagcgt cgtctgtcgg 120
ctctggggccc cgggtggtctg acccgtgacc gcgctggcct tgagggtccgc gacgtgcacc 180
cctcgcaacta cggccgatg tgcccgatcg agaccccgga aggccgaac atcggcctga 240
tcggttcgct ttcgggtgac gcgcgggtca acccgttcgg cttcatcgag acgccgtacc 300
gcaagggtgc cgagggtgtc gtcaccgacg agatccacta cctgaccgcc gacgaagagg 360
accgccacgt cgtggcacag gccaaactgc ctgtggatgc cgacggccgc ttcaccgagg 420
acaagatcct ggtccgccgt aagggtggcg aggtcgagtt cgtctcggcg accgaggtgg 480
actacatgga cgtctcgccg cgccagatgg tgcgggtcgc gaccgccatg atcccgttcc 540
tcgagcacga cgacgccaac cgtgccctca tgggtgcaa catgcagcgc caggcggttc 600
cgctgggtgc cagcgaggcc ccgctggtcg gtaccggtat gga 643

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<210> SEQ ID NO 35
<211> LENGTH: 705
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium chelonae

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<400> SEQUENCE: 35

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```

cccaggacgt ggaggcgatc acaccgcaga cctgatcaa catccgtccc gtcgtggcgg 60
cgatcaagga gttcttcgga accagccagc tctcgagtt catggaccag aacaaccgc 120
tgtcgggtct gaccacaag cgtcgtctgt cggcgctggg cccgggtggg ctgaccgtg 180
accgcgccg ccttgaggtc cgtgacgtgc accctcgc ctagggcgc atgtgccga 240
tcgagacccc ggaaggccc aacatcgcc tgatcggtc gctgtcggg tacgcgcgcg 300
ttaaccggtt cggttcacg gagacgcgt accgcaagg ggtcgagggt gtcgtcaccg 360
acgagatccg ctacctgact gccgacgaag aggaccgcca cgtggtggcg caggccaact 420
cgccgaccga tgagaaggcg cgcttcaccg aggagcgcgt cctggtgcgc cgtaagggtg 480
gcgaggtcga gttcgtgccg tcgacggcg tcgactacat ggacgtctcg ccgcgccga 540
tggtgtcggc cgcgaccgcg atgatccgt tcctggagca cgacgacgc aaccgtgcc 600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggg gcgtagcgag gccccgctgg 660

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tcggtaccgg tatggagctg cgcgcggcga tcgacgcggc gacgt	705
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<210> SEQ ID NO 36  
 <211> LENGTH: 626  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium chelonae

<400> SEQUENCE: 36

tccgtcccg	cgtggcggc	atcaaggagt	tcttcggaac	cagccagctg	tcgcagttca	60
tggaaccagaa	caaccgcgtt	tcgggtctga	cccacaagcg	tcgtctgtcg	gctctggggc	120
ccggtggtct	gaccctgtac	cgcgctggcc	ttgagggtccg	cgacgtgcac	ccctcgcact	180
acggccgcat	gtgcccgatc	gagaccccg	aaggcccgaa	catcggcctg	atcggttcgc	240
tttcggtgta	cgcgcgggtc	aaccgcgttc	gcttcacga	gacgccgtac	cgcaagggtg	300
ccgaggggtg	cgtcaccgac	gagatccact	acctgaccgc	cgacgaagag	gaccgccacg	360
tcgtggcaca	ggccaactcg	cctgtggatg	ccgacggccg	cttcaccgag	gacaagatcc	420
tggtccgccc	taaggggtgc	gagggtcag	tcgtctcggc	gaccgagggtg	gactacatgg	480
acgtctcgcc	gcgccagatg	gtgtcggtcg	cgaccgccat	gatcccggtc	ctcgagcacg	540
acgacgcca	ccgtgccctc	atgggtgcca	acatgcagcg	ccaggcggtt	ccgctggtgc	600
gcagcgaggc	cccgcgtggtc	ggtacc				626

<210> SEQ ID NO 37  
 <211> LENGTH: 626  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium chelonae

<400> SEQUENCE: 37

tccgtcccg	cgtggcggc	atcaaggagt	tcttcggaac	cagccagctg	tcgcagttca	60
tggaaccagaa	caaccgcgtt	tcgggtctga	cccacaagcg	tcgtctgtcg	gctctggggc	120
ccggtggtct	gaccctgtac	cgcgctggcc	ttgagggtccg	cgacgtgcac	ccctcgcact	180
acggccgcat	gtgcccgatc	gagaccccg	aaggcccgaa	catcggcctg	atcggttcgc	240
tttcggtgta	cgcgcgggtc	aaccgcgttc	gcttcacga	gacgccgtac	cgcaagggtg	300
ccgaggggtg	cgtcaccgac	gagatccact	acctgaccgc	cgacgaagag	gaccgccacg	360
tcgtggcaca	ggccaactcg	cctgtggatg	ccgacggccg	cttcaccgag	gacaagatcc	420
tggtccgccc	taaggggtgc	gagggtcag	tcgtctcggc	gaccgagggtg	gactacatgg	480
acgtctcgcc	gcgccagatg	gtgtcggtcg	cgaccgccat	gatcccggtc	ctcgagcacg	540
acgacgcca	ccgtgccctc	atgggtgcca	acatgcagcg	ccaggcggtt	ccgctggtgc	600
gcagcgaggc	cccgcgtggtc	ggtacc				626

<210> SEQ ID NO 38  
 <211> LENGTH: 652  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium chelonae

<400> SEQUENCE: 38

gcagaccctg	atcaaacatcc	gtcccgtcgt	ggcggcgatc	aaggagttct	tcggaaccag	60
ccagctgtcg	cagttcatgg	accagaacaa	cccgtgtcg	ggtctgacct	acaagcgtcg	120
tctttcggcg	ctggggccccg	gtggtctgac	ccgtgaccgc	gccggccttg	aggtccgcga	180

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cgtgcacccc tcgcactacg gccgcatgtg cccgatcgag accccggaag gcccgaaacat	240
cggcctgata ggttcgctgt cgggtgtacg cggggtcaac ccgttcggct tcatacgagac	300
gccgtaccgc aagggtgtccg aggggtgtcgt caccgacgag atccactacc tgaccgccga	360
cgaagaggac cgccacgtcg tggcacaggc caactcgcct gtggatgccg acggccgctt	420
caccgaggac aagatcctgg tccgcgctaa ggggtggcgag gtcgagttcg tctcggcgac	480
cgaggtggac tacatggacg tctcgcccg ccaaatggtg tcggtcgcga ccgccatgat	540
cccgttcctc gagcacgacg acgccaaccg tgccctcatg ggtgccaaca tgcagcgcca	600
ggcgggtccg ctggtgcgca gcgagggccc gctggtcggg accggtatgg ag	652

&lt;210&gt; SEQ ID NO 39

&lt;211&gt; LENGTH: 626

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium chelonae

&lt;400&gt; SEQUENCE: 39

tccgtcccg cgtggcggcg atcaaggagt tcttcggaac cagccagctg tcgcagttca	60
tggaccagaa caaccgcgtg tcgggtctga cccacaagcg tcgtctgtcg gcgctggggc	120
ccggtggtct gaccgcgtgac cgcgcgggcc ttgaggtccg cgacgtgcac cctcgcact	180
acggccgcat gtgcccgatc gagaccccg aaggcccgaa catcgccctg atcggttcgc	240
tgtcgggtga cgcgcggggt aaccgcgttc gcttcacga gacgccgtac cgcaagggtg	300
ccgaggggtg cgtcaccgac gacatccact acctgaccgc cgacgaagag gaccgccacg	360
tcgtggcaca ggccaactcg cctgtggacg ccgacggccg ttaccacgag gacaagatcc	420
tggtcggccg taagggtggc gaggtcgagt tcgtctcggc gaccgaggtg gactacatgg	480
acgtctcgcc gcgccagatg gtgtcggtcg cgaccgccat gatcccgctt ctcgagcag	540
acgacgcaa ccgtgccctc atgggtgcca acatgcagcg ccaggcggtt ccgctgggtg	600
gcagcgaggc cccgctgggt ggtacc	626

&lt;210&gt; SEQ ID NO 40

&lt;211&gt; LENGTH: 626

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium chelonae

&lt;400&gt; SEQUENCE: 40

tccgtcccg cgtggcggcg atcaaggagt tcttcggaac cagccagctg tcgcagttca	60
tggaccagaa caaccgcgtg tcgggtctga cccacaagcg tcgtcttctg gcgctggggc	120
ccggtggtct gaccgcgtgac cgcgcgggcc ttgaggtccg cgacgtgcac cctcgcact	180
acggccgcat gtgcccgatc gagaccccg aaggcccgaa catcgactg atcggttcgc	240
tgtcgggtga cgcgcggggt aaccgcgttc gcttcacga gacgccgtac cgcaagggtg	300
ccgaggggtg cgtcaccgac gagatccact acctgaccgc cgacgaagag gaccgccacg	360
tgggtggcga ggccaactcg cctgtggatg cggacggccg cttaccgag gacaagatcc	420
tggtcggccg taagggtggc gaggtcgagt tcgtctcggc gaccgaggtg gactacatgg	480
acgtctcgcc gcgccagatg gtgtcggtcg cgaccgccat gatcccgctt ctcgagcag	540
acgacgcaa ccgtgccctc atgggtgcca acatgcagcg ccaggcggtt ccgctgggtg	600
gcagcgaggc cccgctgggt ggtacc	626

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&lt;210&gt; SEQ ID NO 41

&lt;211&gt; LENGTH: 626

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium chelonae

&lt;400&gt; SEQUENCE: 41

```
tccgtcccgt cgtggcggcg atcaaggagt tcttcggaac cagccagctg tcgcagttca    60
tggaccagaa caaccgctt tcgggtctga cccacaagcg tcgtctgtcg gctctgggcc    120
ccggtggtct gaccctgtac cgcgctggcc ttgaggtccg cgacgtgcac ccctcgcaact    180
acggccgcgt gtgcccgate gagaccccg aagggccgaa catcggcctg atcggttcgc    240
tttcggtgta cgcgcgggtc aaccggttcg gcttcacga gacgccgtac cgcaagggtg    300
ccgaggggtg cgtcaccgac gagatccact acctgaccgc cgacgaagag gaccgccacg    360
tcgtggcaca ggccaactcg cctgtggatg ccgacggccg cttcaccgag gacaagatcc    420
tggtcgcccg taagggtggc gaggtcgagt tcgtctcggc gaccgaggtg gactacatgg    480
acgtctcgcc gcgccagatg gtgtcggtcg cgaccgccat gatcccgttc ctcgagcacg    540
acgacgcaaa ccgtgccctc atgggtgcc aatgcagcg ccaggcggtt ccgctggtgc    600
gcagcgaggc cccgctggtc ggtacc                                     626
```

&lt;210&gt; SEQ ID NO 42

&lt;211&gt; LENGTH: 626

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium chelonae

&lt;400&gt; SEQUENCE: 42

```
tccgtcccgt cgtggcggcg atcaaggagt tcttcggaac cagccagctg tcgcagttca    60
tggaccagaa caaccgctt tcgggtctga cccacaagcg tcgtctgtcg gctctgggcc    120
ccggtggtct gaccctgtac cgcgctggcc ttgaggtccg cgacgtgcac ccctcgcaact    180
acggccgcgt gtgcccgate gagaccccg aagggccgaa catcggcctg atcggttcgc    240
tttcggtgta cgcgcgggtc aaccggttcg gcttcacga gacgccgtac cgcaagggtg    300
ccgaggggtg cgtcaccgac gagatccact acctgaccgc cgacgaagag gaccgccacg    360
tcgtggcaca ggccaactcg cctgtggatg ccgacggccg cttcaccgag gacaagatcc    420
tggtcgcccg taagggtggc gaggtcgagt tcgtctcggc gaccgaggtg gactacatgg    480
acgtctcgcc gcgccagatg gtgtcggtcg cgaccgccat gatcccgttc ctcgagcacg    540
acgacgcaaa ccgtgccctc atgggtgcc aatgcagcg ccaggcggtt ccgctggtgc    600
gcagcgaggc cccgctggtc ggtacc                                     626
```

&lt;210&gt; SEQ ID NO 43

&lt;211&gt; LENGTH: 626

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium chelonae

&lt;400&gt; SEQUENCE: 43

```
tccgtcccgt cgtggcggcg atcaaggagt tcttcggaac cagccagctg tcgcagttca    60
tggaccagaa caaccgctt tcgggtctga cccacaagcg tcgtctgtcg gctctgggcc    120
ccggtggtct gaccctgtac cgcgctggcc ttgaggtccg cgacgtgcac ccctcgcaact    180
acggccgcgt gtgcccgate gagaccccg aagggccgaa catcggcctg atcggttcgc    240
```

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tttcggtgta cgcgcgggtc aaccggttcg gcttcacga gacgccgtac cgcaagggtgt	300
ccgaggggtgt cgtcaccgac gagatccact acctgaccgc cgacgaagag gaccgccacg	360
tcgtggcaca ggccaactcg cctgtggatg ccgacggccg cttaccgag gacaagatcc	420
tggtccgccg taaggggtgc gaggtcgagt tcgtctcggc gaccgagggtg gactacatgg	480
acgtctcgcc gcgccagatg gtgtcggtcg cgaccgccat gatcccgttc ctcgagcacg	540
acgacgcaa ccgtgccctc atgggtgcc acatgcagcg ccaggcggtt ccgctggtgc	600
gcagcgaggc cccgctggtc ggtacc	626

<210> SEQ ID NO 44  
 <211> LENGTH: 626  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium chelonae

<400> SEQUENCE: 44

tccgtcccgt cgtggcggcg atcaaggagt tcttcggaac cagccagctg tcgcagttca	60
tggaccagaa caaccgctt tcgggtctga cccacaagcg tcgtctgtcg gctctgggcc	120
ccggtggtct gaccctgac cgcgctggcc ttgaggccg cgacgtgcac ccctcgact	180
acggccgcat gtgcccgatc gagaccccg aaggccgaa catcggcctg atcggttcgc	240
tttcggtgta cgcgcgggtc aaccggttcg gcttcacga gacgccgtac cgcaagggtgt	300
ccgaggggtgt cgtcaccgac gagatccact acctgaccgc cgacgaagag gaccgccacg	360
tcgtggcaca ggccaactcg cctgtggatg ccgacggccg cttaccgag gacaagatcc	420
tggtccgccg taaggggtgc gaggtcgagt tcgtctcggc gaccgagggtg gactacatgg	480
acgtctcgcc gcgccagatg gtgtcggtcg cgaccgccat gatcccgttc ctcgagcacg	540
acgacgcaa ccgtgccctc atgggtgcc acatgcagcg ccaggcggtt ccgctggtgc	600
gcagcgaggc cccgctggtc ggtacc	626

<210> SEQ ID NO 45  
 <211> LENGTH: 626  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium chelonae

<400> SEQUENCE: 45

tccgtcccgt cgtggcggcg atcaaggagt tcttcggaac cagccagctg tcgcagttca	60
tggaccagaa caaccgctg tcgggcctga cccacaagcg tcgtctgtcg gcgctgggcc	120
ccggtggtct gaccctgac cgcgcggcc tcgaggccg cgacgtgcac ccctcgact	180
acggccgcat gtgcccgatc gagaccccg aaggccgaa catcggcctg atcggttcgc	240
tgctggtgta cgcgcgctc aaccggttcg gtttcacga gacgccttac cggaaggctt	300
cggacggagt tgcaccgac gagatccact acctgacggc cgacgaagag gaccgccacg	360
tggtggcgca ggccaactcg cccgtggacg ccaacggccg cttaccgag gagaagatcc	420
tggttcgccg caagggcgcg gaggtggagt tcgtgtcggc gaccgaggtc gactacatgg	480
atgtttcgcc gcgccagatg gtgtcggtcg cgaccgccat gatcccgttc ctcgagcacg	540
acgacgcaa ccgtgccctc atgggtgcc acatgcagcg ccaggcggtt ccgctggtgc	600
gtagcgaggc tccgctggtc ggtacc	626

<210> SEQ ID NO 46

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&lt;211&gt; LENGTH: 626

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium chelonae

&lt;400&gt; SEQUENCE: 46

```

tccgtcccggt cgtggcgccg atcaaggagt tcttcggaac cagccagctg tcgcagttca    60
tggaccagaa caaccgcgtg tcgggcctga cccacaagcg tcgtctgtcg gcgctggggc    120
ccggtggtct gaccgcgtgac cgcgcggcc tcgaggtccg cgacgtgcac ccctcgcaact    180
acggcccgcat gtgcccgatc gagaccccg aaggcccgaa catcgccctg atcggtctgc    240
tgtcgggtga cgcgcgcgtc aaccgcgttc gtttcacga gacgccttac cggaagggtct    300
cggacggagt tgtaccgcac gagatccact acctgacggc cgacgaagag gaccgccacg    360
tggtggcgca ggccaactcg cccgtggacg ccaacggccg cttaccgag gagaagatcc    420
tggttcgccc caaggcgccg gaggtggagt tcgtgtcggc gaccgaggtc gactacatgg    480
atgtttcgcc gcgccagatg gtgtcgggtc cgaccgccat gatcccggtc ctcgagcacg    540
acgacgccaa ccgtgccctc atgggtgcc aatgcagcg ccaggcggtt ccgctgggtg    600
gtagcgaggc tccgctggtc ggtacc                                     626

```

&lt;210&gt; SEQ ID NO 47

&lt;211&gt; LENGTH: 626

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium chelonae

&lt;400&gt; SEQUENCE: 47

```

tccgtcccggt cgtggcgccg atcaaggagt tcttcggaac cagccagctg tcgcagttca    60
tggaccagaa caaccgcgtg tcgggcctga cccacaagcg tcgtctgtcg gcgctggggc    120
ccggtggtct gaccgcgtgac cgcgcggcc tcgaggtccg cgacgtgcac ccctcgcaact    180
acggcccgcat gtgcccgatc gagaccccg aaggcccgaa catcgccctg atcggtctgc    240
tgtcgggtga cgcgcgggtc aaccgcgttc gtttcacga gacgccttac cggaagggtct    300
cggacggagt tgtaccgcac gacatccact acctgacggc cgacgaagag gaccgccacg    360
tggtggcgca ggccaactcg cccgtggacg ccaacggccg cttaccgag gagaagatcc    420
tggttcgccc caaggcgccg gaggtggagt tcgtgtcggc gaccgaggtc gactacatgg    480
atgtctcgcc gcgccagatg gtgtcgggtc cgaccgccat gatcccggtc ctcgagcacg    540
acgacgccaa ccgtgccctc atgggtgcc aatgcagcg ccaggcggtt ccgctgggtg    600
gtagcgaggc tccgctggtc ggtacc                                     626

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&lt;210&gt; SEQ ID NO 48

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium flavescens

&lt;400&gt; SEQUENCE: 48

```

ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg cgatcaagga    60
gttcttcggc accagccagc tgtcgcagtt catggaccag aacaaccgcg tctcgggcct    120
gaccacaaag cgcgcctgtg cggcgctggg ccccgcggtt ctgtcccggt agcgcgcggg    180
cctcgaggtc cgcgacgtgc acgcatcgca ctacggccgc atgtgcccga tcgagacccc    240
ggagggtccg aacatcgggc tgatcggctc gctgtcggtg tacgcgcggg tcaaccggtt    300

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cggttcacgc gagacgccgt accgcaaggt caaggacggt gttgtcaccg atgacatcga	360
gtacctgacc gccgacgagg aggaccgcc cgtcgtggcg caggccaact cgcgatcga	420
tgacaacggc cgcttcctgg aggagcgcgt cctggtccgc cgcaagggcg gcgaggtcga	480
gcagatctcg tcgagcgagg tggactacat ggacgtctcg ccgcgccaga tggatcgggt	540
cgcgacggcc atgatcccgt tcctcgagca cgacgacgcc aaccgcgcc tgatgggtgc	600
caacatgcag cgccaggcgg tcccgtggt gcgcagcgag gcccgttg tcggcaccgg	660
tatggagttg cgcgcggcga tcgacgc	687

<210> SEQ ID NO 49  
 <211> LENGTH: 687  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium flavescens

<400> SEQUENCE: 49

ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg cgatcaagga	60
gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc tctcgggcct	120
gaccacaag cgcgcctgt cggcgtggg ccccggtggt ctgtccgtg agcgcgccg	180
cctcgaggtc cgcgacgtgc acgctcgca ctacggcgc atgtgccga tcgagacccc	240
ggagggtccg aacatcgcc tgatcggctc gctgtcgtg tacgcgcggg tcaaccggt	300
cggcttcacgc gagacgccgt accgcaaggt caaggacggt gttgtcaccg atgacatcga	360
gtacctgacc gccgacgagg aggaccgcc cgtcgtggcg caggccaact cgcgatcga	420
tgacaacggc cgcttcctgg aggagcgcgt cctggtccgc cgcaagggcg gcgaggtcga	480
gcagatctcg tcgagcgagg tggactacat ggacgtctcg ccgcgccaga tggatcgggt	540
cgcgacggcc atgatcccgt tcctcgagca cgacgacgcc aaccgcgcc tgatgggtgc	600
caacatgcag cgccaggcgg tcccgtggt gcgcagcgag gcccgttg tcggcaccgg	660
tatggagttg cgcgcggcga tcgacgc	687

<210> SEQ ID NO 50  
 <211> LENGTH: 687  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium flavescens

<400> SEQUENCE: 50

ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg cgatcaagga	60
gttcttcggc accagccagc tctcgagtt catggatcag aacaaccgc tctcgggcct	120
gaccacaag cgcgcctgt cggcgtggg ccccggtggt ctgtccgtg agcgtgccg	180
cctcgaggtc cgcgacgtgc actccagcca ctacggcgc atgtgccga tcgagacccc	240
ggaaggccc aacatcgcc tgatcggctc gctgtcgtg tacgcgcggg tcaaccggt	300
cggcttcacgc gagaccccgt accgcaaggt cgtcgacggc gtcgtcagcg accagatcga	360
ctacctgacc gccgacgagg aggaccgcc cgtcgtggcg caggccaatt cgcgctcga	420
cggtagcgggt cgtttcgagg aggagcgcgt cctggtccgc cgtaagggcg gcgaggtcga	480
gttcgtctcg gcgagcgagg tcgactacat ggacgtctcg ccgcgccaga tggatcgggt	540
cgcgacggcg atgatcccgt tcctcgagca cgacgacgcc aaccgcgcc tgatgggtgc	600
gaacatgcag cgccaggcgg ttccgtggt ccgcagcgag gcgccgttg tcggtaccgg	660

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catggaactg cgcgcggcga tcgacgc 687

<210> SEQ ID NO 51  
<211> LENGTH: 705  
<212> TYPE: DNA  
<213> ORGANISM: Mycobacterium fortuitum

<400> SEQUENCE: 51

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg 60  
cgatcaagga gttcttcgga acgtcgcagc tgtcgcagtt catggatcag aacaaccgc 120  
tgtcgggtct gaccacaag cgtcgtctgt cggcgctggg ccccgcggt ctgtcccg 180  
agcgcgccg ccttgaggtc cgcgacgtcc actcgtcgca ctacggccgc atgtgccga 240  
tcgagacccc tgagggtccg aacatcggtc tgatcggttc gctttcggtg tacgcgcggg 300  
tcaaccggtt cggtttcacg gagaccccgt accgcaaggt cgtcgacggt gtggtcaccg 360  
accagatcga ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact 420  
cgccgatcga cccggacggc cggttcaccg aggaccgct gatggttcgt cgtaaggcg 480  
gcgaggtcga gaacgtggcc ccgtccgacg tcgactacat ggacgtctcg ccgcgccaga 540  
tggtgtccgt cgcgaccgcg atgatcccg tccctcgagca cgacgacgcc aaccgcgcc 600  
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gccccgctgg 660  
tcggtaccgg tatggagctg cgcgcggcga tcgacgcggc gacgt 705

<210> SEQ ID NO 52  
<211> LENGTH: 705  
<212> TYPE: DNA  
<213> ORGANISM: Mycobacterium fortuitum

<400> SEQUENCE: 52

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg 60  
cgatcaagga attcttcgga accagccagc tgtcgcagtt catggaccag aacaaccgc 120  
tgtcgggtct gaccacaag cgtcgtctgt cggcgctggg ccccgcggt ctgtcccg 180  
agcgcgccg ccttgaggtc cgcgacgtgc actccagcca ctacggccgc atgtgccga 240  
tcgagacccc tgagggtccg aacatcggtc tgatcggctc gctgtcggtg tacgcccgg 300  
tcaaccggtt cggcttcacg gagaccccgt accgcaaggt cgtcgacggt gtggtcaccg 360  
accagatcga ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact 420  
cgccgatcga cgcggacggc agcttcaccg aagaccgct gatggtcgc cgtaaggcg 480  
gcgaggtcga gaacgtggcc ccgatcgacg tggattacat ggacgtctcg ccgcgccaga 540  
tggtgtccgt cgcgaccgcg atgatcccg tccctcgagca cgacgacgcc aaccgtgcc 600  
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgtagcgag gccccgctgg 660  
tcggtaccgg tatggagttg cgcgcggcga tcgacgcggc gacgt 705

<210> SEQ ID NO 53  
<211> LENGTH: 626  
<212> TYPE: DNA  
<213> ORGANISM: Mycobacterium fortuitum  
<220> FEATURE:  
<221> NAME/KEY: modified\_base  
<222> LOCATION: (340)...(340)  
<223> OTHER INFORMATION: n = g,a,c or t  
<220> FEATURE:



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<221> NAME/KEY: modified\_base  
 <222> LOCATION: (354)...(355)  
 <223> OTHER INFORMATION: n = g,a,c or t

<400> SEQUENCE: 53

```
tccgtcccggt cgtggcgggc atcaaggagt tcttcggtac cagccagctg tcgcagttca    60
tggaccagaa caaccgcgtt tcgggtctga cccacaagcg tcgcctgtcg gcgctggggc    120
ccggcggtct gtcccgtaga cgtgccggcc ttgaggtccg cgacgtgcac gccagccact    180
acggccgcat gtgcccgatc gagaccctcg aggggtccga catcggtctg atcggtctgc    240
tgtcggtgta cgcccggtc aaccggttcg gcttcacga gacgccgtac cgcaaggctc    300
tcgacggtgt ggtcaccgac cagatcgact acctgaccgn cgacgaggag gacnntcacg    360
tcgtggcgca ggccaactcg ccgatcgacg ccgacggccg cttaccgaa gaccgcgtca    420
tggtgcgtcg taaggcgggc gaggtcgaga acgtggcccc gtccgacgtc gactacatgg    480
acgtctcgcc ggcgcagatg gtgtctgtcg cgaccgcgat gatcccgctt ctcgagcacg    540
acgacgccaa ccgcgccctg atgggtgccg acatgcagcg ccaggcggtt ccaactggtgc    600
gcagcgaggc cccgctggtc ggtacc                                     626
```

<210> SEQ ID NO 54  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium fortuitum

<400> SEQUENCE: 54

```
cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg    60
cgatcaagga gttcttcgga acgtcgacgc tgtcgagtt catggatcag aacaaccgc    120
tgtcggtctt gaccacaag cgtcgtctgt cggcgctggg ccccgcggtt ctgtcccggtg    180
agcgcgccgg ccttgaggtc cgcgacgtcc actcgtcgca ctacggccgc atgtgtccga    240
tcgagacccc tgagggtccg aacatcggtc tgatcggttc gctttcggtg tacgcgcggg    300
tcaaccggtt cggtttcacg gagaccctgt accgcaaggt cgtcgacggt gtggtcaccg    360
atcagatcga ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact    420
cgccgatcga cccggacggc cggttcaccg aggaccgct gatggttcgt cgtaaggcg    480
gcgaggtcga gaatgtggc ccgtccgacg tcgactacat ggacgtctcg ccgcgccaga    540
tggtgtccgt cgcgaccgcg atgatccctg tcttcgagca cgacgacgcc aaccgcgcc    600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcccgcgtgg    660
tcggtaccgg tatggagctg cgcgcggcga tcgacgcggc gacgt                                     705
```

<210> SEQ ID NO 55  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium fortuitum

<400> SEQUENCE: 55

```
cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg    60
cgatcaagga gttcttcgga accagccagc tgtcgagtt catggaccag aacaaccgc    120
tgtcggtctt gaccacaag cgtcgctgtg cggcgctggg ccccgcggtt ctgtcccggtg    180
agcgtgccgg ccttgaggtc cgcgacgtgc actccagcca ctacggccgc atgtgcccga    240
```

## -continued

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tcgagacccc tgagggtccg aacatcggtc tgatcggttc gctgtcgggtg tacgcccggg	300
tcaaccggtt cggttcctc gagacgcctt accgcaaggt cgtcgacggt gtggtctccg	360
accagatcga ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact	420
cgccgatcga cgcggacggc agcttcaccg aggatcgctg gatggtccgg cgtaagggtg	480
gcgaggtcga gaacgtggcc ccgtccgacg tcgactacat ggacgtctcg ccgcgccaga	540
tggtgtctgt cgcgaccgcg atgatccctg tcctcgagca cgacgacgcc aaccgcgcc	600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gccccgctgg	660
tcggtaccgg catggagttg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 56  
 <211> LENGTH: 626  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium fortuitum

<400> SEQUENCE: 56

tcctgccctg cgtggcggcg atcaaggagt tcttcggaac gtcgcagctg tcgcagttca	60
tgatcagaa caaccgctg tcgggtctga cccacaagcg tcgtctgtcg gcgtggggc	120
ccggcggtct gtcccgtag cgcgcggcc ttgaggtccg cgacgtccac tcgtcgcaact	180
acggcccat gtgtccgac gagaccctg aggggtccga catcggtctg atcggttcgc	240
tttcggtgta cgcgcgggct aaccggttcg gtttcacga gacccgtac cgcaaggctc	300
tcgacggtgt ggtcaccgat cakatckact acctgaccgc cgacgaggag gaccgccacg	360
tcgtggcgca ggccaactcg ccgatcgacc cggacggccg gttcaccgag gaccgcgtga	420
tggttcgtcg taaggcgcg gaggtcgaga atgtggcccc gtccgacgtc gactacatgg	480
acgtctcgcc gcgccagatg gtgtccgtcg cgaccgcgat gatcccgctc ctcgagcacg	540
acgacgcaa ccgcgccctg atgggtgcca acatgcagcg ccaggcggtt ccgctgggtc	600
gcagcgaggc cccgctggtc ggtacc	626

<210> SEQ ID NO 57  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium smegmatis

<400> SEQUENCE: 57

cccaggacgt ggaggcgatc acaccgcaga cctgatcaa catccgcccc gtcgtggcgg	60
cgatcaagga gttcttcgac accagccagc tgcgcagtt catggaccag aacaaccgc	120
tgtcgggtct gaccacaag cgtcgtctgt cggcgctggg ccccgcggt ctgtccctg	180
agcgcgccg ccttgaggtc cgcgacgtc actccagcca ctacggccgc atgtgccga	240
tcgagacccc tgagggtccg aacatcggtc tgatcggtc gctgtcgggtg tacgcccggg	300
tcaaccggtt cggttcctc gagacgcctt accgcaaggt tgcgacggt gtggtcagcg	360
accagatcga ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact	420
cgccgatcga caccgacggt cgcttcaccg aggaccgctg gatggtccgc cgtaagggtg	480
gcgaggtcga gaacgtggcc ccgtccgacg tcgactacat ggacgtctca ccgcgccaga	540
tggtgtctgt cgcgaccgcg atgatccctg tcctcgagca cgacgacgcc aaccgtgcc	600
tgatgggtgc caacatgcag cgccaggcag ttccgctggt acgcagcgag gccccgctgg	660

## -continued

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tcggtaccgg tatggagctg cgcgcggcga tcgacgcggc gacgt 705

<210> SEQ ID NO 58  
 <211> LENGTH: 687  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium chelonae

<400> SEQUENCE: 58

ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg cgatcaagga 60  
 gttcttcggc accagccagc tgtcgcagtt catggaccag aacaaccgcg tgcgggtct 120  
 gaccacaag cgtcgctgt cggcgtggg ccccgcggt ctgtccgtg agcgtgccg 180  
 ccttgaggtc cgcgagctgc actccagcca ctacggcgcg atgtgccga tcgagacccc 240  
 tgagggtccg aacatcggtc tgatcggttc gctgtcgtg tacgcccggg tcaaccggt 300  
 cggttcctc gagacgccgt accgcaaggt cgtcgacggt gtggtctccg accagatcga 360  
 ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgacatcga 420  
 cgcggacggc agcttcaccg aggatcgcgt gatggtccgc cgtaagggtg gcgaggtcga 480  
 gaacgtggcc ccgtccgacg tcgactacat ggacgtctcg ccgcgccaga tgggtgtctgt 540  
 cgcgaccgcg atgatcccg tccctcgagca cgacgacgcc aaccgcgcc tgatgggtgc 600  
 caacatgcag gccagggcgg ttccgctggt gcgcagcgag gcccgcgtgg tcggtaccgg 660  
 catggagttg cgcgcggcga tcgacgc 687

<210> SEQ ID NO 59  
 <211> LENGTH: 687  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium fortuitum

<400> SEQUENCE: 59

ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg cgatcaagga 60  
 gttcttcgga acgtcgcagc tgtcgcagtt catggatcag aacaaccgcg tgcgggtct 120  
 gaccacaag cgtcgtctgt cggcgtggg ccccgcggt ctgtccgtg agcgcgccg 180  
 ccttgaggtc cgcgagctcc actcgtcgca ctacggcgcg atgtgccga tcgagacccc 240  
 tgagggtccg aacatcggtc tgatcggttc gcttctcgtg tacgcgcggg tcaaccggt 300  
 cggttcctc gagaccccgt accgcaaggt cgtcgacggt gtggtcaccg aycagatcga 360  
 ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgacatcga 420  
 cccggacggc cggttcaccg aggaccgct gatggttcgc cgtaaggcg gcgaggtcga 480  
 gaacgtggcc ccgtccgacg tcgactacat ggacgtctcg ccgcgccaga tgggtgtccgt 540  
 cgcgaccgcg atgatcccg tccctcgagca cgacgacgcc aaccgtgcc tgatgggtgc 600  
 caacatgcag gccagggcgg ttccgctggt gcgcagcgag gcccgcgtgg tcggtaccgg 660  
 tatggagctg cgcgcggcga tcgacgc 687

<210> SEQ ID NO 60  
 <211> LENGTH: 687  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium fortuitum

<400> SEQUENCE: 60

ggaggcgatc acaccgcaga ccctgatcaa catccgccc gtcgtggcgg cgatcaagga 60

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gtttcttcggc accagccagc tgtcgcagtt catggaccag aacaaccgcg tgcgggtct	120
gaccacaaag cgtcgtctgt cggcgtctgg ccccggcggg ctgtcccgtg agcgcgccgg	180
ccttgaggtc cgcgacgtgc actccagcca ctacggccgc atgtgcccga tcgagacccc	240
tgagggtccg aacatcggtc tgatcggctc gctgtcggtg tacgcccggg tcaaccggtt	300
cggcttcacg gagagccctt accgcaaggt tgcgcacggt gtggtcagcg accagatcga	360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgatcga	420
caccgacggt cgtttcaccg aggaccgctg gatggtccgc cgtaagggtg gcgaggtcga	480
gaacgtggcc ccgtccgacg tcgactacat ggacgtctca ccgcgccaga tgggtgtctgt	540
cgcgaccgcg atgatcccg tccctcgagca cgacgacgcc aaccgtgccc tgatgggtgc	600
caacatgcag cgcagggcag ttccgctggt acgcagcgag gcccgcgtgg tcggtaccgg	660
tatggagctg cgcgcggcga tcgacgc	687

<210> SEQ ID NO 61  
 <211> LENGTH: 687  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium fortuitum

<400> SEQUENCE: 61

ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg cgatcaagga	60
gtttcttcgga acgtcgcagc tgtcgcagtt catggatcag aacaaccgcg tgcgggtct	120
gaccacaaag cgtcgtctgt cggcgtctgg ccccggcggg ctgtcccgtg agcgcgccgg	180
ccttgaggtc cgcgacgtcc actcgtcgca ctacggccgc atgtgcccga tcgagacccc	240
tgagggtccg aacatcggtc tgatcggctc gctttcggtg tacgcgcggg tcaaccggtt	300
cggtttcacg gagaccccg accgcaaggt cgtcgcacggt gtggtcaccg atcagatcga	360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgatcga	420
cccggacggc cgtttcaccg aggaccgctg gatggttcgt cgtaaggcg gcgaggtcga	480
gaacgtggcc ccgtccgacg tcgactacat ggacgtctcg ccgcgccaga tgggtgtccgt	540
cgcgaccgcg atgatcccg tccctcgagca cgacgacgcc aaccgcgcc tgatgggtgc	600
caacatgcag cgcagggcgg ttccgctggt gcgcagcgag gcccgcgtgg tcggtaccgg	660
tatggagctg cgcgcggcga tcgacgc	687

<210> SEQ ID NO 62  
 <211> LENGTH: 687  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium fortuitum

<400> SEQUENCE: 62

ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg cgatcaagga	60
gtttcttcgga acgtcgcagc tgtcgcagtt catggatcag aacaaccgcg tgcgggtct	120
gaccacaaag cgtcgtctgt cggcgtctgg ccccggcggg ctgtcccgtg agcgcgccgg	180
ccttgaggtc cgcgacgtcc actcgtcgca ctacggccgc atgtgcccga tcgagacccc	240
tgagggtccg aacatcggtc tgatcggctc gctttcggtg tacgcgcggg tcaaccggtt	300
cggtttcacg gagaccccg accgcaaggt cgtcgcacggt gtggtcaccg atcagatcga	360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgatcga	420

## -continued

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cccggacggc cggttcaccg aggaccgcgt gatggttcgt cgtaagggcg gcgaggtcga 480
gaacgtggcc ccgtccgacg tcgactacat ggacgtctcg ccgcgccaga tgggtgccgt 540
cgcgaccgcy atgatcccg tccctcgaca cgacgacgcc aaccgcgccc tgatgggtgc 600
caacatgcag cgcacggcgg ttccgctggt gcgcagcgag gccccgctgg tcggtaccgg 660
tatggagctg cgcgcggcga tcgacgc 687

```

```

<210> SEQ ID NO 63
<211> LENGTH: 687
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium fortuitum

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<400> SEQUENCE: 63

```

```

ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg cgatcaagga 60
gttcttcgga acgtcgcagc tgctgcagtt catggatcag aacaaccgcg tgcgggtct 120
gaccacaaag cgtcgtctgt cggcgctggg ccccggcggg ctgtcccggt agcgcgccgg 180
ccttgaggtc cgcgacgtcc actcgtcgca ctacggccgc atgtgtccga tcgagacccc 240
tgagggtccg aacatcggtc tgatcgggtc gctttcgggt tacgcgcggg tcaaccggt 300
cggtttcacg gagaccccg accgcaaggt cgtcgacggg gtggtcaccg atcagatcga 360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgcgatcga 420
cccggacggc cggttcaccg aggaccgcgt gatggttcgt cgtaagggcg gcgaggtcga 480
gaacgtggcc ccgtccgacg tcgactacat ggacgtctcg ccgcgccaga tgggtgccgt 540
cgcgaccgcy atgatcccg tccctcgaca cgacgacgcc aaccgcgccc tgatgggtgc 600
caacatgcag cgcacggcgg ttccgctggt gcgcagcgag gccccgctgg tcggtaccgg 660
tatggagctg cgcgcggcga tcgacgc 687

```

```

<210> SEQ ID NO 64
<211> LENGTH: 626
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium fortuitum

```

```

<400> SEQUENCE: 64

```

```

tccgtccggt cgttgccgcg atcaaggagt tcttcggaac cagccagctg tcgcagttca 60
tggaaccaga caaccgcgtc tccggtctca cccacaagcg ccgcctctcg gcgctggggc 120
cgggcggtct gtcccgtgag cgcgcgggtc tggaagtctg tgacgtgcac ccgtcgcact 180
acggccggat gtgcccgate gagacgcggg aagggccgaa catcggtctg atcggttcac 240
tgtcgtgtga cgcgggggtc aaccggttcg ggttcacaga gacgccctac cgcaaggtgg 300
tcgacggggg cgtttccgac gagatccact acctgaccgc cgacgaggag gaccgccacg 360
tcgtggcgca ggccaactcg ccgatcgacg cgcagggccg cttcgtcgag ccgcgcgtgc 420
tggtcgcccg gaaggcgggc gaggtcgagt acgtgccctc gtcagagggt gactacatgg 480
acgtgtcgcc gcgccagatg gtgtcggtag ccaccgcgat gattccgttc ctcgagcacg 540
atgacgcaaa ccgcgccttg atgggtgcca acatgcagcg scaggcggtc ccgctggtgc 600
gcagcgaggc accgctgggtc ggtacc 626

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<210> SEQ ID NO 65
<211> LENGTH: 705
<212> TYPE: DNA

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<213> ORGANISM: Mycobacterium gordonae

&lt;400&gt; SEQUENCE: 65

```

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg      60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc      120
tgtcgggtct gaccacaag cgtcgtctgt cggcgctggg gccgggtggt ctgtcccgtg      180
agcgtgctgg tctggaagta cgtgacgtgc acccgtcgca ctacggccgc atgtgcccga      240
tcgagacgcc ggaaggccgc aacatcggcc tgatcggttc gctgtcggtg tacgcgcggg      300
tcaaccggtt cggcttcacg gagacgcctt atcggaaggt ggtggatgga gtcgtttctg      360
acgagatcca ctacctcacc gccgacgagg aggaccgcca cgtggtggcg caggccaact      420
cgccgatcga cgagagcggc cggtttgctg agccgcgcgt tctggtccgc cgcaaggcgg      480
gcgaggtgga gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga      540
tggtgtcggg ggccaccgcg atgattccgt tcctcgaaca cgacgacgcc aaccgtgccc      600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg      660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt                      705

```

&lt;210&gt; SEQ ID NO 66

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium gordonae

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: modified\_base

&lt;222&gt; LOCATION: (90)...(90)

&lt;223&gt; OTHER INFORMATION: n = g,a,c or t

&lt;400&gt; SEQUENCE: 66

```

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg      60
cgatcaagga gttcttcggc accagccagn tctcgagtt catggaccag aacaaccgc      120
tgtcgggtct gaccacaag cgtcgtctgt cggcgctggg gccgggtggt ctgtcccgtg      180
agcgtgctgg gctggaagta cgtgacgtgc acccgtcgca ctacggccgc atgtgcccga      240
tcgagacgcc ggaaggccgc aacatcggcc tgatcggttc gctgtcggtg tacgcgcggg      300
tcaaccggtt cggcttcacg gagacgcctt atcggaaggt ggtggatgga gtcgtttctg      360
acgagatcca ctacctaacg gccgacgagg aggaccgcca cgtggtggcg caggccaact      420
cgccgatcga cgagagcggc cggtttgctg agccgcgcgt tctggtccgc cgcaaggcgg      480
gcgaggtgga gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga      540
tggtgtcggg ggccaccgcg atgattccgt tcctcgaaca cgacgacgcc aaccgtgccc      600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg      660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt                      705

```

&lt;210&gt; SEQ ID NO 67

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium gordonae

&lt;400&gt; SEQUENCE: 67

```

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg      60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc      120

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tttcgggcct caccacaag cgtcgtctgt cggcgtctggg gcccggcggt ctgtcccgtg	180
agcgggcccgg cctggaggtc cgtgacgtcc acccgtcgca ctacggccgc atgtgccga	240
tcgagactcc ggaaggcccc aacatcgccc tgatcggctc actgtcggtg tacgcgcggg	300
tgaacccgtt cggcttcacg gagacgccgt atagacgagt ggtgagcgga gttgtcacgg	360
atgagatcca ctacctacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact	420
cgccgatcga cgagaacggc cggtttctcg agccgcgcgt tctggtcgcg cgcaaggcgg	480
gcgagggtga gtacgtgccc tcgtccgagg tcgactacat ggacgtctcg ccgcgccaga	540
tgggtgtcggg ggccaccgcc atgattccgt tcctcgagca cgacgacgcc aaccgtgccc	600
tgatgggtgc caacatgcag cggcaggcgg ttccgctggt ccgcagcgar gcgccgctgg	660
tgggtaccgg catggagttg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 68

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium gordonae

&lt;400&gt; SEQUENCE: 68

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtggccg	60
cgatcaagga gttcttcggc accagccagc tgtcgagtt catggaccag aacaaccgc	120
tgtcgggtct gaccacaag cgtcgccgtg cggcgtctggg gccgggtggt ctgtcccgtg	180
agcgtgccgg cctggaggtc cgtgacgtcc acccgtcgca ctacggccgc atgtgccga	240
tcgagacccc ggaaggcccc aacatcgccc tgatcggctc gctgtcggtg tacgcgcggg	300
tcaacccgtt cgggttcacg gagacgccgt accgcaagggt ggtggaagggt gtcgtctccg	360
acgaaatcca ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgccgatcga cgagagcggt cggttctcg agccacgcgt tctggtcgcg cggaaggcgg	480
gcgaggtcga gtacgtgcct tcgtccgagg tggactacat ggacgtctcg ccgcgccaga	540
tgggtgtcggg ggccaccgcg atgattccgt tcctcgagca cgacgacgcc aaccgcgccc	600
tgatgggtgc caacatgcag cggcaggcgg ttccgctggt gcgcagcgar gcaccgctgg	660
tgggcaccgg tatggaattg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 69

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium gordonae

&lt;400&gt; SEQUENCE: 69

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg	60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc	120
tttcgggcct caccacaag cgtcgtctgt cggcgtctggg gcccggcggt ctgtcccgtg	180
agcgggcccgg cctggaggtc cgtgacgtcc acccgtcgca ctacggccgc atgtgccga	240
tcgagactcc ggaaggcccc aacatcgccc tgatcggctc actgtcggtg tacgcgcggg	300
tgaacccgtt cggcttcacg gagacgccgt atagacgagt ggtgagcgga gttgtcacgg	360
atgagatcca ctacctacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact	420
cgccgatcga cgagaacggc cggttctcg agccgcgcgt tctggtcgcg cgcaaggcgg	480

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gcgaggtgga gtacgtgccc tcgtccgagg tcgactacat ggacgtctcg ccgcgccaga	540
tggtgtcggg gccaccgcg atgattccgt tcctcgagca cgacgacgcc aaccgtgccc	600
tgatgggtgc caacatgcag cgcacggcgg ttccgctggt gcgcagcgag gcgccgctgg	660
tgggtaccgg catggagttg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 70  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium gordonae  
 <400> SEQUENCE: 70

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgctg	60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc	120
tttcgggcct caccacaag cgtcgtctgt cggcgctggg gccggcggt ctgtcccg	180
agcgggccg cctggaggtc cgtgacgtcc acccgtcgca ctacggccgc atgtgccga	240
tcgagactcc ggaaggccgc aacatcgccc tgatcggttc gctgtcggtg tacgcgcggg	300
tgaaccggtt cggcttcacg gagacgcgt accgcgaggt ggtcgacggt gtggtgacg	360
acgagatcca ctacctcacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact	420
cgcgatcga cgagaacggc cgttcgtcg agccgcgcgt tctggtccgc cgcaaggcg	480
gcgaggtgga gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcggg gccaccgcg atgattccgt tcctcgagca cgacgacgcc aaccgtgccc	600
tgatgggtgc caacatgcag cgcacggcgg ttccgctggt ccgcagcgag gcgccgctgg	660
tgggtaccgg catggagttg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 71  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium gordonae  
 <400> SEQUENCE: 71

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg	60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc	120
tgctgggtct gaccacaag cgtcgtctgt cggcgctggg gccgggtggt ctgtcccg	180
agcgtgcggg tctggaagta cgtgacgtgc acccgtcgca ctacggccgc atgtgccga	240
tcgagacgcc ggaaggccgc aacatcgccc tgatcggttc gctgtcggtg tacgcgcggg	300
tcaaccggtt cggcttcacg gagacgcctt atcggaaggt ggtggatgga gtcgtttctg	360
acgagatcca ctacctcacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgcgatcga cgagacggc cggtttgctg agccgcgcgt tctggtccgc cgcaaggcg	480
gcgaggtgga gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcggg gccaccgcg atgattccgt tcctcgagca cgacgacgcc aaccgtgccc	600
tgatgggtgc caacatgcag cgcacggcgg ttccgctggt gcgcagcgag gcaccgctgg	660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 72  
 <211> LENGTH: 705  
 <212> TYPE: DNA



## -continued

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<213> ORGANISM: Mycobacterium gordonae

&lt;400&gt; SEQUENCE: 72

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cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg      60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc      120
tgtcgggtct gaccacaag cgtcgtctgt cggcgctggg gccgggtggt ctgtcccgtg      180
agcgtgctgg tctggaagta cgtgacgtgc acccgtcgca ctacggccgc atgtgcccga      240
tcgagacgcc ggaaggccgc aacatcggcc tgatcggttc gctgtcggtg tacgcgcggg      300
tcaaccggtt cggcttcacg gagacgcctt atcgggaagg ggtggatgga gtcgtttctg      360
acgagatcca ctacctcacc gccgacgagg aggaccgcca cgtggtggcg caggccaact      420
cgccgatcga cgagagcggc cggtttctg agccgcgcgt tctggtccgc cgcaaggcgg      480
gcgaggtgga gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga      540
tggtgtcggg ggccaccgcg atgattccgt tcctcgaaca cgacgacgcc aaccgtgccc      600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg      660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt                      705

```

&lt;210&gt; SEQ ID NO 73

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium gordonae

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: modified\_base

&lt;222&gt; LOCATION: (690)...(690)

&lt;223&gt; OTHER INFORMATION: n = g,a,c or t

&lt;400&gt; SEQUENCE: 73

```

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg      60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc      120
tttcgggcct caccacaag cgtcgtctgt cggcgctggg gccgggcggg ctgtcccgtg      180
agcgggccgg cctggaggtc cgtgacgtcc acccgtcgca ctacggccgc atgtgcccga      240
tcgagactcc ggaaggccgc aacatcggcc tgatcggctc gctgtcggtg tacgcgcggg      300
tgaaccggtt cggcttcacg gagacgcctt accgcgaggt ggtcgacggt gtggtgacgg      360
acgagatcca ctacctcacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact      420
cgccgatcga cgagaacggc cgcttcgtcg agccgcgcgt tctggtccgc cgcaaggcgg      480
gcgaggtgga gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga      540
tggtgtcggg ggccaccgcg atgattccgt tcctcgaaca cgacgacgcc aaccgtgccc      600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt ccgcagcgag gcgccgctgg      660
tggttaccgg catggagttg cgcgcggcgn tcgacgcggc gacgt                      705

```

&lt;210&gt; SEQ ID NO 74

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium gordonae

&lt;400&gt; SEQUENCE: 74

```

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg      60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc      120

```

## -continued

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tgctcgggtct gaccacacaag cgtcgtctgt cggcgtctggg gccgggtggg ctgtcccgtg	180
agcgtgcggg tctggaagta cgtgacgtgc acccgtcgca ctacggccgc atgtgccga	240
tcgagacgcc ggaaggcccc aacatcgccc tgatcggttc gctgtcggtg tacgcgcggg	300
tcaacccgtt cggcttcacg gagacgcctt atcggaaggt ggtggatgga gtcgtttctg	360
acgagatcca ctacctcacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgccgatcga cgagagcggc cggtttgctg agccgcgcgt tctggtccgc cgcaaggcgg	480
gcgaggtgga gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcggg gccaccgcg atgattccgt tcctcgaaca cgacgacgcc aaccgtgccc	600
tgatgggtgc caacatgcag cggcaggcgg ttccgctggt gcgcagcgag gcaccgctgg	660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 75

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium gordonae

&lt;400&gt; SEQUENCE: 75

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg	60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc	120
tgctcgggtct gaccacacaag cgtcgtctgt cggcgtctggg gccgggtggg ctgtcccgtg	180
agcgcgccg tctggaggtc cgtgacgtcc acccgtcgca ctacggccgc atgtgccga	240
tcgagacccc ggaaggctccg aacatcgccc tgatcggctc gctgtcggtg tacgcgcggg	300
tcaacccgtt cggcttcacg gagacgcctt accgggaggt tgtggacggg gtcgtcacag	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgccgatcga cgagaacggc cggtttgctg agccgcgcgt tctggtccgc cgcaaggcgg	480
gcgaggtgga gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcggg gccaccgcg atgatccctg tcctcgagca cgacgacgcc aaccgtgccc	600
tgatgggcgc caacatgcag cggcaggcgg ttccgctggt gcgtagcgar gcgccgctgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 76

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium gordonae

&lt;400&gt; SEQUENCE: 76

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg	60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc	120
tgctcgggtct gaccacacaag cgtcgtctgt cggcgtctggg gccgggtggg ctgtcccgtg	180
agcgtgcggg tctggaagta cgtgacgtgc acccgtcgca ctacggccgc atgtgccga	240
tcgagacgcc ggaaggcccc aacatcgccc tgatcggttc gctgtcggtg tacgcgcggg	300
tcaacccgtt cggcttcacg gagacgcctt atcggaaggt ggtggatgga gtcgtttctg	360
acgagatcca ctacctcacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgccgatcga cgagagcggc cggtttgctg agccgcgcgt tctggtccgc cgcaaggcgg	480

## -continued

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```

gcgaggtgga gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga    540
tgggtgtcggg ggccaccgcg atgattccgt tcctcgaaca cgacgacgcc aaccgtgccc    600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg    660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt                      705

```

```

<210> SEQ ID NO 77
<211> LENGTH: 705
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium gordonae
<400> SEQUENCE: 77

```

```

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg    60
cgatcaagga gttcttcggc accagccagc tgcgcagtt catggaccag aacaaccgc     120
tgtcgggtct gactcacaag cgtcgtctgt cggcgctggg gcctggcggt ctgtcacgtg    180
agcgcgccgg cctggaagtc cgtgacgtcc acccgtcgca ctacggccgg atgtgcccga    240
tcgagacccc ggaaggcccc aacatcggcc tgatcggttc gctgtcggtg tacgcgcggg    300
tcaaccggtt cggttcctc gagacgcctt atcggaaggt ggtcgacggt gtggtctccg    360
atgagatcca ctacctgacc gccgacgaag gagaccccca cgtggtggcg caggccaact    420
cgccgatcga cgagagcggc cggtttgccg agccgcgcgt tctggtccgc cgcaaggcgg    480
gcgaggtcga gtacgtcccg tcgtccgagg tggactacat ggacgtctcg ccgcgccaga    540
tgggtgtcggg ggccaccgcg atgattccgt tcctcgagca cgacgacgcc aaccgtgccc    600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg    660
tgggcaccgg tatggagttg cgcgcggcga tcgacgcggc gacgt                      705

```

```

<210> SEQ ID NO 78
<211> LENGTH: 705
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium gordonae
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (688)...(688)
<223> OTHER INFORMATION: n = g,a,c or t
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (701)...(701)
<223> OTHER INFORMATION: n = g,a,c or t
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (704)...(705)
<223> OTHER INFORMATION: n = g,a,c or t

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```

<400> SEQUENCE: 78
cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg    60
cgatcaagga gttcttcggc accagccagc tctcgcagtt catggaccag aacaaccgc     120
tgtcgggtct gaccacaaag cgtcgtctgt cggcgctggg gccgggtggt ctgtcccgtg    180
agcgtgcggg tctggaagta cgtgacgtgc acccgtcgca ctacggccgc atgtgcccga    240
tcgagacgcc ggaaggcccc aacatcggcc tgatcggttc gctgtcggtg tacgcgcggg    300
tcaaccggtt cggttcctc gagacgcctt atcggaaggt ggtggatgga gtcgtttctg    360
acgagatcca ctacctcacc gccgacgagg aggaccgcca cgtggtggcg caggccaact    420
cgccgatcga cgagagcggc cggtttgctg agccgcgcgt tctggtccgc cgcaaggcgg    480

```

## -continued

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gcgaggtgga gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcggg gccaccgcg atgattccgt tcctcgaaca cgacgacgcc aaccgtgccc	600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggg gcgcagcgag gcaccgctgg	660
tgggcaccgg catggagttg cgcgcgngga tcgacgcggc nacnn	705

<210> SEQ ID NO 79  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium gordonae  
 <400> SEQUENCE: 79

cccaggacgt ggaggcagtc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg	60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccccc	120
tgctgggtct caccacaag cggcgtctgt cgccgctcgg gccgggtggg ctgtcgctg	180
agcgtgcggg tctggaagtc cgtgacgtcc acccgtcgca ctacggccgc atgtgcccga	240
tcgagacccc ggaaggtccg aacatcgccc tgatcggttc gctgtcggtg tacgcgcggg	300
tcaaccggtt cggttcctc gagacgcctt atagacgcgt cgtcagcgga gttgtcacgg	360
atgagatcca ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgccgctggc cggtgcttct cactttgctg agccgcgcgt tctggtccgc cgcaaggcgg	480
gcgaggtgga gtacgttccg tcgtccgagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcggg gccaccgcg atgattccgt tcctcgagca cgacgacgcc aaccgtgccc	600
tgatgggcgc caacatgcag cgccaggcgg ttccgctggg gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagttg cgcgcgccga tcgacgcggc gacgt	705

<210> SEQ ID NO 80  
 <211> LENGTH: 687  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium gordonae  
 <400> SEQUENCE: 80

ggaggcagtc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg cgatcaagga	60
gttcttcggc accagccagc tctcgagtt catggaccag aacaacccgc tgcgggtct	120
gaccacaag cgtcgtctgt cgccgctggg gccgggtggg ctgtcccggt agcgtgcggg	180
tctggaagta cgtgacgtgc acccgtcgca ctacggccgc atgtgcccga tcgagacgcc	240
ggaaggcccg aacatcgccc tgatcggttc gctgtcggtg tacgcgcggg tcaaccggtt	300
cggttcctc gagacgcctt atcggaaggt ggtggatgga gtcgtttctg acgagatcca	360
ctacctcacc gccgacgagg aggaccgcca cgtggtggcg caggccaact cgccgatcga	420
cgagagcggc cggtttgctg agccgcgcgt tctggtccgc cgcaaggcgg gcgaggtgga	480
gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga tggtgtcggg	540
ggccaccgcg atgattccgt tcctcgaaca cgacgacgcc aaccgtgccc tgatgggtgc	600
caacatgcag cgccaggcgg ttccgctggg gcgcagcgag gcaccgctgg tgggcaccgg	660
catggagttg cgcgcgccga tcgacgc	687

<210> SEQ ID NO 81  
 <211> LENGTH: 687  
 <212> TYPE: DNA

## -continued

---

<213> ORGANISM: *Mycobacterium gordonae*

<400> SEQUENCE: 81

```
ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg cgatcaagga    60
gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgcg tctcggtct    120
gaccacaag cgtcgtctgt cggcgctggg tccgggtggt ctgtcccggtg agcgcgccgg    180
tctggaggtc cgtgacgtcc acccgtcgca ctacggccgc atgtgcccgga tcgagacccc    240
ggaaggtccg aacatcggcc tgatcggttc gctgtcggtg tacgcgcggg tcaaccggt    300
cggttctatc gagacgccgt accgggaggt tgtggacggg gtcgttacag acgagatcca    360
ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact cgccgatcga    420
cgagagcggc cggtttctgc agccgcgcgt tctggtccgc cgcaaggcgg gcgaggtgga    480
gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga tgggtgcggt    540
ggccaccgcg atgatcccggt tcctcgagca cgacgacgcc aaccgtgccc tgatgggcgc    600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggtaccgg    660
catggagctg cgcgcgccga tcgacgc    687
```

<210> SEQ ID NO 82

<211> LENGTH: 687

<212> TYPE: DNA

<213> ORGANISM: *Mycobacterium gordonae*

<400> SEQUENCE: 82

```
ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg cgatcaagga    60
gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgcg tctcggtct    120
gaccacaag cgtcgtctgt cggcgctggg gccgggtggt ctgtcccggtg agcgtgcggg    180
tctggaagta cgtgacgtgc acccgtcgca ctacggccgc atgtgcccgga tcgagacgcc    240
ggaaggcccg aacatcggcc tgatcggttc gctgtcggtg tacgcgcggg tcaaccggt    300
cggttctatc gagacgcctt atcggaaggt ggtggatgga gtcgtttctg acgagatcca    360
ctacctcacc gccgacgagg aggaccgcca cgtggtggcg caggccaact cgccgatcga    420
cgagagcggc cggtttctgc agccgcgcgt tctggtccgc cgcaaggcgg gcgaggtgga    480
gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga tgggtgcggt    540
ggccaccgcg atgattccgt tcctcgaaca cgacgacgcc aaccgtgccc tgatgggtgc    600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg tgggcaccgg    660
catggagttg cgcgcgccga tcgacgc    687
```

<210> SEQ ID NO 83

<211> LENGTH: 687

<212> TYPE: DNA

<213> ORGANISM: *Mycobacterium gordonae*

<220> FEATURE:

<221> NAME/KEY: modified\_base

<222> LOCATION: (47)...(47)

<223> OTHER INFORMATION: n = g,a,c or t

<220> FEATURE:

<221> NAME/KEY: modified\_base

<222> LOCATION: (64)...(64)

<223> OTHER INFORMATION: n = g,a,c or t

<400> SEQUENCE: 83

## -continued

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```

ggaggcgatc acaccgcaga ctctgatcaa catccggccc gtcgtcnccg cgatcaagga    60
gttnttcggc accagccagc tctcgagtt catggaccag aacaaccgc tgtccggttt    120
gacgcacaag aggcgtctgt ccgcgtggg gccgggtggt ctgtccgtg agcgggccgg    180
cctggaggtc cgtgacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacccc    240
ggaaggtccg aacatcggtc tgatcgggtc gctgtcgtg tacgcgcggg tcaaccggt    300
cgggttcacg gagacccct atcggaaggt ggtggacggg gtcgtctcgg atgagatcca    360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cggcgatcga    420
cgagaacggc cgcttcgtcg agcccggtg gctggtcgc cggaagcgg gcgaggtgga    480
gtacgtgccg tcgtccgagg tggactacat ggacgtctcg ccgcgccaga tgggtgcgg    540
ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgtgccc tgatgggcgc    600
caacatgcag cgccaggcgg ttccgctggt gcgtagcgag gcgccgttg tgggcaccgg    660
gatggagttg cgcgcggcga tcgacgc

```

&lt;210&gt; SEQ ID NO 84

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium gordonae

&lt;400&gt; SEQUENCE: 84

```

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg    60
cgatcaagga gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc    120
tgtccggtct gaccacaag cgccgctct cggcgtggg ccccgccggt ctgtccgtg    180
agcgcgccgg cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgccga    240
tcgagacccc ggagggtccc aacatcggtc tgatcggctc gctgtcgtg tacgcgcggg    300
tgaaccggtt cgggttcacg gagacccct accgcaaggt ggtcgacggt gtggtcaccg    360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact    420
cggcgatcga cgccaaggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg    480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtca ccgcgccaga    540
tgggtgcggg ggccaccgc atgatccct tcctcgagca cgatgacgcc aaccgtgccc    600
tgatgggcgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgtg    660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt

```

&lt;210&gt; SEQ ID NO 85

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium intracellulare

&lt;400&gt; SEQUENCE: 85

```

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg    60
cgatcaagga gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc    120
tgtccggtct gaccacaag cgccgctct cggcgtggg ccccgccggt ctgtccgtg    180
agcgcgccgg cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgccga    240
tcgagacccc ggagggtccc aacatcggtc tgatcggctc gctgtcgtg tacgcgcggg    300
tgaaccggtt cgggttcacg gagacccct accgcaaggt ggtcgacggt gtggtcaccg    360

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## -continued

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acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact	420
cgccgatcga cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtca ccgcgccaga	540
tgggtgcggt ggccaccgcg atgatcccggt tcctcgagca cgatgacgcc aaccgtgccc	600
tgatggggcg caacatgcag cgccaagcgg ttccgctggt gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 86

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium intracellulare

&lt;400&gt; SEQUENCE: 86

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg	60
cgatcaagga gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc	120
tgtccggtct gaccacaag cgcgcctct cggcgctggg ccccgcggt ctgtcccg	180
agcgcgcgg cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcggtg tacgcgcgg	300
tgaaccggtt cgggttcacg gagacccgt accgcaaggt ggtcgacggt gtggtcaccg	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact	420
cgccgatcga cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtca ccgcgccaga	540
tgggtgcggt ggccaccgcg atgatcccggt tcctcgagca cgatgacgcc aaccgtgccc	600
tgatggggcg caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 87

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium intracellulare

&lt;400&gt; SEQUENCE: 87

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg	60
cgatcaagga gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc	120
tgtccggtct gaccacaag cgcgcctct cggcgctggg ccccgcggt ctgtcccg	180
agcgcgcgg cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcggtg tacgcgcgg	300
tgaaccggtt cgggttcacg gagacccgt accgcaaggt ggtcgacggt gtggtcaccg	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact	420
cgccgatcga cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tgggtgcggt ggccaccgcg atgatcccggt tcctcgagca cgatgacgcc aaccgtgccc	600
tgatggggcg caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

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&lt;210&gt; SEQ ID NO 88

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium intracellulare

&lt;400&gt; SEQUENCE: 88

```
cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg    60
cgatcaagga gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc    120
tgtccggtct gaccacaaag cgccgcctct cggcgctggg ccccggcggg ctgtcccgtg    180
agcgcgccgg cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgcccga    240
tcgagacccc ggagggtccc aacatcggtc tgatcggttc gctgtcggtg tacgcgcggg    300
tgaacccgtt cgggttcacg gagaccccg accgcaaggt ggtcgacggt gtggtcaccg    360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact    420
cgccgatcga cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg    480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga    540
tggtgtcggg ggccaccgcg atgatcccg tccctcgagca cgatgacgcc aaccgtgccc    600
tgatgggcgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg    660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt                    705
```

&lt;210&gt; SEQ ID NO 89

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium intracellulare

&lt;400&gt; SEQUENCE: 89

```
cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg    60
cgatcaagga gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc    120
tgtccggtct gaccacaaag cgccgcctct cggcgctggg ccccggcggg ctgtcccgtg    180
agcgcgccgg cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgcccga    240
tcgagacccc ggagggtccc aacatcggtc tgatcggttc gctgtcggtg tacgcgcggg    300
tgaacccctt cgggttcacg gagaccccg accgcaaggt ggtcgacggt gtggtcaccg    360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact    420
cgccgatcga cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg    480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga    540
tggtgtcggg ggccaccgcg atgatcccg tccctcgagca cgatgacgcc aaccgtgccc    600
tgatgggcgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg    660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt                    705
```

&lt;210&gt; SEQ ID NO 90

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium intracellulare

&lt;400&gt; SEQUENCE: 90

```
cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg    60
cgatcaagga gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc    120
```



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tgcccggtct gaccacaag cgcgcctct cggcgctggg ccccgcggt ctgtccgtg	180
agcgcgccgg cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggctc gctgtcggtg tacgcgcggg	300
tgaacccgtt cgggttcacg gagaccccg accgcaaggt ggtcgacggt gtggtcaccg	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact	420
cgcgcatcga cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tggtgtcggg ggccaccgcg atgatcccg tcctcgagca cgatgacgcc aaccgtgccc	600
tgatgggccc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 91

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium intracellulare

&lt;400&gt; SEQUENCE: 91

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg	60
cgatcaagga gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc	120
tgcccggtct gaccacaag cgcgcctct cggcgctggg ccccgcggt ctgtccgtg	180
agcgcgccgg cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggctc gctgtcggtg tacgcgcggg	300
tgaacccctt cgggttcacg gagaccccg accgcaaggt ggtcgacggt gtggtcaccg	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact	420
cgcgcatcga cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tggtgtcggg ggccaccgcg atgatcccg tcctcgagca cgatgacgcc aaccgtgccc	600
tgatgggccc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 92

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium intracellulare

&lt;400&gt; SEQUENCE: 92

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg	60
cgatcaagga gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc	120
tgcccggtct gaccacaag cgcgcctct cggcgctggg ccccgcggt ctgtccgtg	180
agcgcgccgg cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggctc gctgtcggtg tacgcgcggg	300
tgaacccgtt cgggttcacg gagaccccg accgcaaggt ggtcgacggt gtggtcaccg	360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact	420
cgcgcatcga cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg	480

## -continued

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```

gcgagggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga 540
tggtgtcggg gccaccgcg atgatcccg tctcagagca cgatgacgcc aaccgtgccc 600
tgatggggcg caacatgcag cgcaggcggt ttccgctggt gcgcagcgag gcgccgctgg 660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt 705

```

```

<210> SEQ ID NO 93
<211> LENGTH: 705
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium intracellulare

<400> SEQUENCE: 93

```

```

cccaggacgt ggaggcgatc acaccgcaga cctgatcaa catccggccg gtcgtcgccg 60
cgatcaagga gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc 120
tgtccggtct gaccacaag cgcgcctct cggcgctggg ccccgcggt ctgtccctg 180
agcgcgccg cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgccga 240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcggtg tacgcgcggg 300
tgaaccggtt cgggttcacg gagaccccg accgcaaggt ggtcgacggt gtggtcaccg 360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact 420
cgccgatcga cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg 480
gcgagggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtca ccgcgccaga 540
tggtgtcggg gccaccgcg atgatcccg tctcagagca cgatgacgcc aaccgtgccc 600
tgatggggcg caacatgcag cgcaggcggt ttccgctggt gcgcagcgag gcgccgctgg 660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt 705

```

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<210> SEQ ID NO 94
<211> LENGTH: 705
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium intracellulare

<400> SEQUENCE: 94

```

```

cccaggacgt ggaggcgatc acaccgcaga cctgatcaa catccggccg gtcgtcgccg 60
cgatcaagga gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc 120
tgtccggtct gaccacaag cgcgcctct cggcgctggg ccccgcggt ctgtccctg 180
agcgcgccg cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgccga 240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcggtg tacgcgcggg 300
tgaaccggtt cgggttcacg gagaccccg accgcaaggt ggtcgacggt gtggtcaccg 360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact 420
cgccgatcga cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg 480
gcgagggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtca ccgcgccaga 540
tggtgtcggg gccaccgcg atgatcccg tctcagagca cgatgacgcc aaccgtgccc 600
tgatggggcg caacatgcag cgcaggcggt ttccgctggt gcgcagcgag gcgccgctgg 660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt 705

```

```

<210> SEQ ID NO 95
<211> LENGTH: 705
<212> TYPE: DNA

```

## -continued

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<213> ORGANISM: Mycobacterium intracellulare

&lt;400&gt; SEQUENCE: 95

```

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg      60
cgatcaagga gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc      120
tgtccggtct gaccacaag cgcgcctct cggcgctggg ccccgcggt ctgtcccgtg      180
agcgcgccgg cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgccga      240
tcgagacccc ggagggtccc aacatcggtc tgatcggttc gctgtcggtg tacgcgcggg      300
tgaaccggtt cgggttcacg gagacccgt accgcaaggt ggtcgacggt gtggtcaccg      360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact      420
cgccgatcga cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg      480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtca ccgcgccaga      540
tggtgtcggg ggccaccgcg atgatcccg tccctcgagca cgatgacgcc aaccgtgccc      600
tgatggggcg caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg      660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt                      705

```

&lt;210&gt; SEQ ID NO 96

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium intracellulare

&lt;400&gt; SEQUENCE: 96

```

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg      60
cgatcaagga gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc      120
tgtccggtct gaccacaag cgcgcctct cggcgctggg ccccgcggt ctgtcccgtg      180
agcgcgccgg cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgccga      240
tcgagacccc ggagggtccc aacatcggtc tgatcggttc gctgtcggtg tacgcgcggg      300
tgaaccggtt cgggttcacg gagacccgt accgcaaggt ggtcgacggt gtggtcaccg      360
acgagatcca ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact      420
cgccgatcga cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg      480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga      540
tggtgtcggg ggccaccgcg atgatcccg tccctcgagca cgatgacgcc aaccgtgccc      600
tgatggggcg caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg      660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt                      705

```

&lt;210&gt; SEQ ID NO 97

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium avium

&lt;400&gt; SEQUENCE: 97

```

ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg cgatcaagga      60
gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc tgtccggtct      120
gaccacaag cgcgcctct cggcgctggg ccccgcggt ctgtcccgtg agcgcgccgg      180
cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgccga tcgagacccc      240

```

## -continued

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```

ggaggggtccc aacatcggtc tgatcggtc gctgtcgggtg tacgcgcggg tgaacccctt 300
cgggttcacg gagaccccg accgcaaggt ggtcgacggt gtggtcaccg acgagatcca 360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgatcga 420
cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg gcgaggtcga 480
gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga tgggtgcggt 540
ggccaccgcg atgatcccg tcctcgagca cgatgacgcc aaccgtgccc tgatgggcgc 600
caacatgcag cgcacggcgg ttccactggt gcgcagcgag gcgccgctgg tgggcaccgg 660
catggagctg cgcgcggcga tcgacgc 687

```

&lt;210&gt; SEQ ID NO 98

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium avium complex (MAC)

&lt;400&gt; SEQUENCE: 98

```

ggagggcgtc acaccgcaga ccctgatcaa catccggcgg gtcgtcgccg cgatcaagga 60
gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgcg tgtccggtct 120
gaccacaaag cgcgcctct cggcgctggg ccccggcggg ctgtcccgtg agcgcgccgg 180
cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgcccga tcgagacccc 240
ggaggggtccc aacatcggtc tgatcggtc gctgtcgggtg tacgcgcggg tgaacccctt 300
cgggttcacg gagaccccg accgcaaggt ggtcgacggt gtggtcaccg acgagatcca 360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgatcga 420
cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg gcgaggtcga 480
gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga tgggtgcggt 540
ggccaccgcg atgatcccg tcctcgagca cgatgacgcc aaccgtgccc tgatgggcgc 600
caacatgcag cgcacggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg 660
catggagctg cgcgcggcga tcgacgc 687

```

&lt;210&gt; SEQ ID NO 99

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium avium complex (MAC)

&lt;400&gt; SEQUENCE: 99

```

ggagggcgtc acaccgcaga ccctgatcaa catccggcgg gtcgtcgccg cgatcaagga 60
gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgcg tgtccggtct 120
gaccacaaag cgcgcctct cggcgctggg ccccggcggg ctgtcccgtg agcgcgccgg 180
cctggaggtc cgtgacgtcc acccctcgca ctacggccgg atgtgcccga tcgagacccc 240
ggaggggtccc aacatcggtc tgatcggtc gctgtcgggtg tacgcgcggg tgaacccgtt 300
cgggttcacg gagaccccg accgcaaggt ggtcgacggt gtggtcaccg acgagatcca 360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgatcga 420
cgccaagggc cggttcgagg agtcgcgcgt cctggtccgc cggaaggcgg gcgaggtcga 480
gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga tgggtgcggt 540
ggccaccgcg atgatcccg tcctcgagca cgatgacgcc aaccgtgccc tgatgggcgc 600

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caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg	660
catggagctg cgcgcggcga tcgacgc	687

<210> SEQ ID NO 100  
 <211> LENGTH: 687  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium avium complex (MAC)

<400> SEQUENCE: 100

ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtcgccg cgatcaagga	60
gttcttcggc accagccagc tgagccagtt catggaccag aacaaccgc tgcgggtct	120
gaccacaag cgccgctct cggcgctggg ccccgccggt ctgtccgtg agcgcgccg	180
cttgagggtc cgtgacgtcc acccctcgca ctacggccg atgtgccga tcgagacccc	240
ggagggtccc aacatcggtc tgatcggtc gctgtcggtg tacgcgggg tgaaccggt	300
cgggttcacg gagacccgt accgcaaggt ggtcgacggt gtggtcaccg acgagatcca	360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgccgatcga	420
cgccaagggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggcgg gcgaggtcga	480
gtacgtgccc tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtcgggt	540
ggccaccgcg atgatccgt tcctcgagca cgatgacgcc aaccgtgccc tgatgggcgc	600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg	660
catggagctg cgcgcggcga tcgacgc	687

<210> SEQ ID NO 101  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium kansasii

<400> SEQUENCE: 101

cccaggacgt ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg	60
ccatcaagga gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgc	120
tgctgggcct caccacaag cgccggcttt cggcgctggg gccggcggt ctgtccggg	180
agcgtgccgg gctggaagtg cgtgacgtgc acccgtcgca ctacggccgc atgtgccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcggtg tacgcacggg	300
tcaaccggtt cggttcacg gagacgccgt accgcaaggt gatcgacggt ctcggtactg	360
atgagatcca ctacttgacg gccgacgagg aggaccgcca cgtcgtggca caggccaact	420
cgccgatcga cgtgagggc cggttcgtcg agccgcgcgt gctggtgcgc cgcaaggccg	480
gcgaggtcga gtacgtggcc tcgtcgagg tggactacat ggacgtctcg ccgcgccaga	540
tgggtcgggt ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgggctc	600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 102  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium kansasii

<400> SEQUENCE: 102

## -continued

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```

cccaggacgt ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg      60
ccatcaagga gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgc      120
tgtcgggcct caccacaag cgccggcttt cggcgctggg gccgggcggg ctgtcccggg      180
agcgtgccgg gctggaagtt cgtgacgtgc acccgtcgca ctacggccgc atgtgccga      240
tcgagacccc ggagggtccc aacatcgcc tgatcggtc gctgtcggtg tacgcacggg      300
tcaaccggtt cggcttcacg gagacgccgt accgcaaggt gatcgacggt ctcggtactg      360
atgagatcca ctacttgacg gccgacgagg aggaccgcca cgtcgtggca caggccaact      420
cgccgatcga cgctgagggc cggttcgtcg agccgcgcgt gctggtgcgc cgcaaggccg      480
gcgaggtcga gtacgtggcc tcgtcgaggg tggactacat ggacgtctcg ccgcgccaga      540
tggtgtcggg ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgggctc      600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg      660
tgggcaccgg catggagttg cgccggcgga tcgacgcggc gacgt                      705

```

&lt;210&gt; SEQ ID NO 103

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium kansasii

&lt;400&gt; SEQUENCE: 103

```

cccaggacgt ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg      60
ccatcaagga gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgc      120
tgtcgggcct caccacaag cgccggcttt cggcgctggg gccgggcggg ctgtcccggg      180
agcgtgccgg gctggaagtg cgtgacgtgc acccgtcgca ctacggccgc atgtgccga      240
tcgagacccc ggagggtccc aacatcgcc tgatcggtc gctgtcggtg tacgcacggg      300
tcaaccggtt cggcttcacg gagacgccgt accgcaaggt gatcgacggt ctcggtactg      360
atgagatcca ctacttgacg gccgacgagg aggaccgcca cgtcgtggca caggccaact      420
cgccgatcga cgctgagggc cggttcgtcg agccgcgcgt gctggtgcgc cgcaaggccg      480
gcgaggtcga gtacgtggcc tcgtcgaggg tggactacat ggacgtctcg ccgcgccaga      540
tggtgtcggg ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgggctc      600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg      660
tgggcaccgg catggagttg cgccggcgga tcgacgcggc gacgt                      705

```

&lt;210&gt; SEQ ID NO 104

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium kansasii

&lt;400&gt; SEQUENCE: 104

```

cccaggacgt ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg      60
ccatcaagga gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgc      120
tgtcgggcct caccacaag cgccggcttt cggcgctggg gccgggcggg ctgtcccggg      180
agcgtgccgg gctggaagtg cgtgacgtgc acccgtcgca ctacggccgc atgtgccga      240
tcgagacccc ggagggtccc aacatcgcc tgatcggtc gctgtcggtg tacgcacggg      300
tcaaccggtt cggcttcacg gagacgccgt accgcaaggt gatcgacggt ctcggtactg      360

```

## -continued

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atgagatcca ctacttgacg gccgacgagg aggaccgcca cgtcgtggca caggccaact	420
cgccgatcga cgctgagggc cggttcgtcg agccgcgcgt gctggtgcgc cgcaaggccg	480
gcgaggtcga gtacgtggcc tcgtcggagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcggg ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgggctc	600
tgatgggtgc caacatgcag gccagggcgg ttccgctggt gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 105

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium kansasii

&lt;400&gt; SEQUENCE: 105

cccaggacgt ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg	60
ccatcaagga gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgc	120
tgctgggcct caccacaag cgcgggcttt cggcgtggg gccgggcggg ctgtcccggg	180
agcgtgccgg gctggaagtg cgtgacgtgc acccgtcgca ctacggccgc atgtgccga	240
tcgagacccc ggagggtccc aacatcgcc tcgacggctc gctgtcggtg tacgcacggg	300
tcaaccggtt cggcttcacg gagacgccgt accgcaaggt gatcgacggt ctggttactg	360
atgagatcca ctacttgacg gccgacgagg aggaccgcca cgtcgtggca caggccaact	420
cgccgatcga cgctgagggc cggttcgtcg agccgcgcgt gctggtgcgc cgcaaggccg	480
gcgaggtcga gtacgtggcc tcgtcggagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcggg ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgggctc	600
tgatgggtgc caacatgcag gccagggcgg ttccgctggt gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 106

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium kansasii

&lt;400&gt; SEQUENCE: 106

cccaggacgt ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg	60
ccatcaagga gttcttcggc accagccagc tgtcgcagtt catggaccag aacaaccgt	120
tgctgggcct gaccacaag cgcgggcttt cggcgtggg gccgggcggg ctgtcccgtg	180
agcgtgccgg cctggaagtg cgtgacgtgc acccttcgca ctacggcccg atgtgccga	240
tcgagacccc ggagggtccc aacatcgcc tcgacggatc gctgtcggtg tacgcgcggg	300
tcaaccggtt cggcttcacg gagacgccgt accggaaggt gatcgacggg ctggtcaccg	360
atgagatcca ctacctgacg gccgacgaag aggaccgcca cgtcgtggca caggccaact	420
cgccgatcga cgctgacggc cgctttgtcg agccgcgcgt tctggtgcgc cgcaaggccg	480
gcgaggtcga atacgtcgcc tcctcggagg tggactacat ggacgtctcg ccacgccaaa	540
tggtgtcggg ggccaccgcg atgatcccg tcctcgagca cgacgacgcc aaccgggcac	600
tgatgggcgc caacatgcag cgtcagggcg ttccgctggt acgcagcgag gcgccgctgg	660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt	705

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&lt;210&gt; SEQ ID NO 107

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium kansasii

&lt;400&gt; SEQUENCE: 107

```
cccaggacgt ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg    60
ccatcaagga gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgcg    120
tgtcgggcct caccacaaag cgccggcttt cggcgctggg gccgggagggt ctgtcccggg    180
agcgtgccgg gctggaagtg cgtgacgtgc acccgtcgca ctacggccgc atgtgcccga    240
tcgagacccc ggagggtccc aacatcgccc tgatcggtctc gctgtcggtg tacgcacggg    300
tcaaccgcgt cggttcctc gagacgccgt accgcaaggt gatcgacggt ctcggtactg    360
atgagatcca ctacttgacg gccgacgagg aggaccgcca cgtcgtggca caggccaact    420
cgccgatcga cgctgagggc cggttcgtcg agccgcgcgt gctggtgcgc cgcaaggccg    480
gcgaggtcga gtacgtggcc tcgtcggagg tggactacat ggacgtctcg ccgcgccaga    540
tggtgtcggg ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgggctc    600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg    660
tgggcaccgg catggagttg cgcgcgccga tcgacgcggc gacgt                    705
```

&lt;210&gt; SEQ ID NO 108

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium kansasii

&lt;400&gt; SEQUENCE: 108

```
cccaggacgt ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg    60
ccatcaagga gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgcg    120
tgtcgggcct caccacaaag cgccggcttt cggcgctggg gccgggagggt ctgtcccggg    180
agcgtgccgg gctggaagtg cgtgacgtgc acccgtcgca ctacggccgc atgtgcccga    240
tcgagacccc ggagggtccc aacatcgccc tgatcggtctc gctgtcggtg tacgcacggg    300
tcaaccgcgt cggttcctc gagacgccgt accgcaaggt gatcgacggt ctcggtactg    360
atgagatcca ctacttgacg gccgacgagg aggaccgcca cgtcgtggca caggccaact    420
cgccgatcga cgctgagggc cggttcgtcg agccgcgcgt gctggtgcgc cgcaaggccg    480
gcgaggtcga gtacgtggcc tcgtcggagg tggactacat ggacgtctcg ccgcgccaga    540
tggtgtcggg ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgggctc    600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg    660
tgggcaccgg catggagttg cgcgcgccga tcgacgcggc gacgt                    705
```

&lt;210&gt; SEQ ID NO 109

&lt;211&gt; LENGTH: 626

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium kansasii

&lt;400&gt; SEQUENCE: 109

```
tccgcccggg ggtcgccgcc atcaaggagt tcttcggcac cagccagctc tcccagttca    60
tggaccagaa caaccgcgtg tcgggcctca cccacaagcg ccggctttcg gcgctggggc    120
```



## -continued

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cgggcggtct gtccccggag cgtgccgggc tggaaagtgcg tgacgtgcac ccgtcgcaact	180
acggccgcac gtgcccgate gagaccccg aggggcccaa catcgccctg atcggtcgc	240
tgctggtgta cgcacgggtc aaccggttcg gcttcacga gacgccgtac cgcaagggtga	300
tcgacgggtct cgttactgat gagatccact acttgacggc cgacgaggag gaccgccacg	360
tcgtggcaca ggccaactcg ccgatcgacg ctgagggccg gttcgtcgag ccgcgcgtgc	420
tgggtgcgcc caaggccggc gaggtcgagt acgtggcctc gtcggagggtg gactacatgg	480
acgtctcgcc gcgccagatg gtgtcgggtg ccacggccat gattccgttc ctcgagcacg	540
acgacgcaa ccgggtcttg atgggtgcc aatgcagcg ccaggcggtt ccgtggtgc	600
gcagcgaggc gccgctggtg ggcacc	626

&lt;210&gt; SEQ ID NO 110

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium kansasii

&lt;400&gt; SEQUENCE: 110

cccaggacgt ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg	60
ccatcaagga gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgc	120
tgctgggcct caccacaag cgccggcttt cggcgctggg gccgggcggt ctgtcccg	180
agcgtgccgg gctggaagtg cgtgacgtgc acccgtcgca ctacggccgc atgtgccga	240
tcgagacccc ggagggtccc aacatcggcc tgatcggtc gctgtcggtg tacgcacggg	300
tcaaccggtt cggcttcac gagacgccgt accgcaaggt gatcgacggt ctcggtactg	360
atgagatcca ctacttgacg gccgacgagg aggaccgcca cgtcgtggca caggccaact	420
cgcgatcga cgtgagggc cggttcgtcg agccgcgctg gctggtgcgc cgcaaggccg	480
gcgaggtcga gtacgtggcc tcgtcggagg tggactacat ggacgtctcg ccgcgccaga	540
tgggtgctggt ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgggctc	600
tgatgggtgc caatcgcag cgcaggcggt ttccgctggt gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 111

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium kansasii

&lt;400&gt; SEQUENCE: 111

cccaggacgt ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg	60
ccatcaagga gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgc	120
tgctgggcct caccacaag cgccggcttt cggcgctggg gccgggcggt ctgtcccg	180
agcgtgccgg gctggaagtg cgtgacgtgc acccgtcgca ctacggccgc atgtgccga	240
tcgagacccc ggagggtccc aacatcggcc tgatcggtc gctgtcggtg tacgcacggg	300
tcaaccggtt cggcttcac gagacgccgt accgcaaggt gatcgacggt ctcggtactg	360
atgagatcca ctacttgacg gccgacgagg aggaccgcca cgtcgtggca caggccaact	420
cgcgatcga cgtgagggc cggttcgtcg agccgcgctg gctggtgcgc cgcaaggccg	480
gcgaggtcga gtacgtggcc tcgtcggagg tggactacat ggacgtctcg ccgcgccaga	540

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tggtgtcggg	ggccacggcc	atgattccgt	tcctcgagca	cgacgacgcc	aaccgggctc	600
tgatgggtgc	caacatgcag	cgccaggcgg	ttccgctggt	gcgcagcgag	gcgccgctgg	660
tgggcaccgg	catggagttg	cgcgcggcga	tcgacgcggc	gacgt		705

<210> SEQ ID NO 112  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium kansasii

<400> SEQUENCE: 112

cccaggacgt	ggaggcgatc	acaccgcaga	caactgatcaa	catccgccc	gtggtcgccg	60
ccatcaagga	gttcttcggc	accagccagc	tctcccagtt	catggaccag	aacaaccgc	120
tgctgggcct	caccacaag	cgcgggcttt	cggcgctggg	gccgggcggg	ctgtcccggg	180
agcgtgccgg	gctggaagtg	cgtgacgtgc	acccgtcgca	ctacggccgc	atgtgcccga	240
tcgagacccc	ggagggtccc	aacatcgccc	tgatcggttc	gctgtcggtg	tacgcacggg	300
tcaaccggtt	cggcttcac	gagacgccgt	accgcaaggt	gatcgacggt	ctcgttactg	360
atgagatcca	ctacttgacg	gccgacgagg	aggaccgcca	cgtcgtggca	caggccaact	420
cgcgatcga	cgtgagggc	cggttcgtcg	agccgcgcgt	gctggtgcgc	cgcaaggccg	480
gcgaggtcga	gtacgtggcc	tcgtcggagg	tggactacat	ggacgtctcg	ccgcgccaga	540
tggtgtcggg	ggccacggcc	atgattccgt	tcctcgagca	cgacgacgcc	aaccgggctc	600
tgatgggtgc	caacatgcag	cgccaggcgg	ttccgctggt	gcgcagcgag	gcgccgctgg	660
tgggcaccgg	catggagttg	cgcgcggcga	tcgacgcggc	gacgt		705

<210> SEQ ID NO 113  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium kansasii

<400> SEQUENCE: 113

cccaggacgt	ggaggcgatc	acaccgcaga	caactgatcaa	catccgccc	gtggtcgccg	60
ccatcaagga	gttcttcggc	accagccagc	tctcccagtt	catggaccag	aacaaccgc	120
tgctgggcct	caccacaag	cgcgggcttt	cggcgctggg	gccgggcggg	ctgtcccggg	180
agcgtgccgg	gctggaagtg	cgtgacgtgc	acccgtcgca	ctacggccgc	atgtgcccga	240
tcgagacccc	ggagggtccc	aacatcgccc	tgatcggttc	gctgtcggtg	tacgcacggg	300
tcaaccggtt	cggcttcac	gagacgccgt	accgcaaggt	gatcgacggt	ctcgttactg	360
atgagatcca	ctacttgacg	gccgacgagg	aggaccgcca	cgtcgtggca	caggccaact	420
cgcgatcga	cgtgagggc	cggttcgtcg	agccgcgcgt	gctggtgcgc	cgcaaggccg	480
gcgaggtcga	gtacgtggcc	tcgtcggagg	tggactacat	ggacgtctcg	ccgcgccaga	540
tggtgtcggg	ggccacggcc	atgattccgt	tcctcgagca	cgacgacgcc	aaccgggctc	600
tgatgggtgc	caacatgcag	cgccaggcgg	ttccgctggt	gcgcagcgag	gcgccgctgg	660
tgggcaccgg	catggagttg	cgcgcggcga	tcgacgcggc	gacgt		705

<210> SEQ ID NO 114  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium kansasii

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&lt;400&gt; SEQUENCE: 114

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cccaggacgt ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg    60
ccatcaagga gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgcg    120
tgtcgggcct caccacaag cgccggcttt cggcgctggg gccgggcggg ctgtcccggg    180
agcgtgccgg gctggaagtg cgtgacgtgc acccgtcgca ctacggccgc atgtgccga    240
tcgagacccc ggaggttccc aacatcgccc tgatcggctc gctgtcggtg tacgcacggg    300
tcaaccggtt cggcttcacg gagacgccgt accgcaaggt gatcgacggg ctcggtactg    360
atgagatcca ctacttgacg gccgacgagg aggaccgcca cgtcgtggca caggccaact    420
cgccgatcga cgctgagggc cggttcgtcg agccgcgcgt gctggtgcgc cgcaaggccg    480
gcgaggtcga gtacgtggcc tcgtcggagg tggactacat ggacgtctcg ccgcgccaga    540
tggtgtcggg ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgggctc    600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg    660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt                    705

```

&lt;210&gt; SEQ ID NO 115

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium kansasii

&lt;400&gt; SEQUENCE: 115

```

cccaggacgt ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg    60
ccatcaagga gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgcg    120
tgtcgggcct caccacaag cgccggcttt cggcgctggg gccgggcggg ctgtcccggg    180
agcgtgccgg gctggaagtg cgtgacgtgc acccgtcgca ctacggccgc atgtgccga    240
tcgagacccc ggaggttccc aacatcgccc tgatcggctc gctgtcggtg tacgcacggg    300
tcaaccggtt cggcttcacg gagacgccgt accgcaaggt gatcgacggg ctcggtactg    360
atgagatcca ctacttgacg gccgacgagg aggaccgcca cgtcgtggca caggccaact    420
cgccgatcga cgctgagggc cggttcgtcg agccgcgcgt gctggtgcgc cgcaaggccg    480
gcgaggtcga gtacgtggcc tcgtcggagg tggactacat ggacgtctcg ccgcgccaga    540
tggtgtcggg ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgggctc    600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg    660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt                    705

```

&lt;210&gt; SEQ ID NO 116

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium kansasii

&lt;400&gt; SEQUENCE: 116

```

ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg ccatcaagga    60
gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgcg tgtcgggcct    120
caccacaag cgccggcttt cggcgctggg gccgggcggg ctgtcccggg agcgtgccgg    180
gctggaagtg cgtgacgtgc acccgtcgca ctacggccgc atgtgccga tcgagacccc    240
ggaggttccc aacatcgccc tgatcggctc gctgtcggtg tacgcacggg tcaaccggtt    300

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## -continued

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cgggttcacg gagacgccgt accgcaaggt gatcgacggt ctcgttactg atgagatcca	360
ctacttgacg gccgacgagg aggacgccca cgtcgtggca caggccaact cgccgatcga	420
cgctgagggc cggttcgtcg agccgcgcgt gctggtgcgc cgcaaggccg gcgaggtcga	480
gtacgtggcc tcgtcggagg tggactacat ggacgtctcg ccgcgccaga tgggtgcggt	540
ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgggctc tgatgggtgc	600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg	660
catggagttg cgcgcggcga tcgacgc	687

&lt;210&gt; SEQ ID NO 117

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium kansasii

&lt;400&gt; SEQUENCE: 117

ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg ccatcaagga	60
gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgcg tgcgggcct	120
caccacaaag cgccggcttt cggcgtggtg gccgggcggt ctgtcccggt agcgtgccg	180
gctggaagtg cgtgacgtgc acccgtcgca ctacggccgc atgtgccga tcgagacccc	240
ggagggctcc aacatcgcc tgatcggtc gctgtcggtg tacgcacggg tcaaccggt	300
cgggttcacg gagacgccgt accgcaaggt gatcgacggt ctcgttactg atgagatcca	360
ctacttgacg gccgacgagg aggacgccca cgtcgtggca caggccaact cgccgatcga	420
cgctgagggc cggttcgtcg agccgcgcgt gctggtgcgc cgcaaggccg gcgaggtcga	480
gtacgtggcc tcgtcggagg tggactacat ggacgtctcg ccgcgccaga tgggtgcggt	540
ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgggctc tgatgggtgc	600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg	660
catggagttg cgcgcggcga tcgacgc	687

&lt;210&gt; SEQ ID NO 118

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium kansasii

&lt;400&gt; SEQUENCE: 118

ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg ccatcaagga	60
gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgcg tgcgggcct	120
caccacaaag cgccggcttt cggcgtggtg gccgggcggt ctgtcccggt agcgtgccg	180
gctggaagtg cgtgacgtgc acccgtcgca ctacggccgc atgtgccga tcgagacccc	240
ggagggctcc aacatcgcc tgatcggtc gctgtcggtg tacgcacggg tcaaccggt	300
cgggttcacg gagacgccgt accgcaaggt gatcgacggt ctcgttactg atgagatcca	360
ctacttgacg gccgacgagg aggacgccca cgtcgtggca caggccaact cgccgatcga	420
cgctgagggc cggttcgtcg agccgcgcgt gctggtgcgc cgcaaggccg gcgaggtcga	480
gtacgtggcc tcgtcggagg tggactacat ggacgtctcg ccgcgccaga tgggtgcggt	540
ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgggctc tgatgggtgc	600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg	660

## -continued

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catggagttg cgcgcggcga tcgacgc 687

<210> SEQ ID NO 119  
<211> LENGTH: 687  
<212> TYPE: DNA  
<213> ORGANISM: Mycobacterium kansasii

<400> SEQUENCE: 119

ggaggcgatc acaccgcaga cactgatcaa catccgcccg gtggtcgccg ccatcaagga 60  
gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgcg tgcggggcct 120  
caccacaag cgcgggcttt cggcgtctgg gccgggagggt ctgtcccggg agcgtgcccg 180  
gctggaagtg cgtgacgtgc acccgtcgca ctacggccgc atgtgcccgga tcgagacccc 240  
ggagggtccc aacatcggcc tgatcggttc gctgtcggtg tacgcacggg tcaaccggtt 300  
cggtttcatc gagacgccgt accgcaaggt gatcgacggt ctggttactg atgagatcca 360  
ctacttgacg gccgacgagg aggaccgcca cgtcgtggca caggccaact cgcgcgacga 420  
cgctgagggc cggttcgtcg agccgcgcgt gctggtgccc cgcaaggccg gcgaggtcga 480  
gtacgtggcc tcgtcggagg tggactacat ggacgtctcg ccgcgcgaga tgggtgcggt 540  
ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgggctc tgatgggtgc 600  
caacatgcag cgcacggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg 660  
catggagttg cgcgcggcga tcgacgc 687

<210> SEQ ID NO 120  
<211> LENGTH: 699  
<212> TYPE: DNA  
<213> ORGANISM: Mycobacterium malmoeense

<400> SEQUENCE: 120

ggaggcgatc acaccgcaga cgctgatcaa catccggccg gtggtcgccg cgatcaagga 60  
gttcttcggc accagccagc tgcgcagtt catggaccag aacaaccgcg tgcggggcct 120  
gaccacaag cgcggctgtg cggcgtctgg cccgggtggt ctgtcgcgtg agcgtgcccg 180  
cttgagggtc cgtgacgtgc acccgtcgca ctacggccgg atgtgcccgga tcgagacccc 240  
ggagggtccg aacatcggcc tgatcggttc gctgtcggtg tacgcgcggg tcaatccggt 300  
cgggttcacg gagacgcctt atcggaaggt tgtggacggt gtcgttactg acgagatcgt 360  
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgcgaccg 420  
acccaacgag gccgggtgcc aggttttcga agaggggctg gtcctgggtc gccgcaaggc 480  
ggcgagagtg gactacgtgc ccagctccga ggtggactac atggacgtct cgcgcgggca 540  
gatggtgtcc gtggccaccg ccatgattcc gttcctcgag cagcagcagc ccaaccgtgc 600  
cctgatgggc gccaacatgc agcgcacggc ggttcgctg gtgcgcagcg aggcgcgct 660  
ggtgggcacc ggcattggagc tgcgcgcggc gatcgacgc 699

<210> SEQ ID NO 121  
<211> LENGTH: 699  
<212> TYPE: DNA  
<213> ORGANISM: Mycobacterium malmoeense

<400> SEQUENCE: 121

ggaggcgatc acaccgcaga cgctgatcaa catccggccg gtggtcgccg cgatcaagga 60

## -continued

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```

gtttcttcggc accagccagc tgtcgagtt catggaccag aacaaccgc tgtcggggct 120
gaccacaaag cgccgctgt cggcgtggg cccgggtggt ctgtcgctg agcgtgccg 180
cttgagggtc cgtgacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacccc 240
ggagggtccg aacatcgcc tgatcggttc gctgtcggtg tacgcgcggg tcaatccgtt 300
cgggttcacg gagagcctt atcggaaggt tgtggacggt gtcgttactg acgagatcgt 360
ctacctgacc gccgacgag aggaccgcca cgtcgtggcg caggccaact cgccgaccag 420
acccaacgag gccgggtccg aggttttcga agaggggctg gtcctggttc gccgcaaggc 480
gggcgagggt gagtacgtgc ccagctccga ggtggactac atggacgtct cgccgcggca 540
gatggtgtcc gtggccaccg ccatgattcc gttcctcgag cagcagcag ccaaccgtgc 600
cctgatgggc gccaacatgc agcgccaggc ggttcgctg gtgcgcagcg aggcgccgct 660
ggtgggcacc ggcattggagc tgcgcgcggc gatcgacgc 699

```

&lt;210&gt; SEQ ID NO 122

&lt;211&gt; LENGTH: 699

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium malmoeense

&lt;400&gt; SEQUENCE: 122

```

ggaggcgatc acaccgcaga cgctgatcaa catccggccg gtggtcgccg cgatcaagga 60
gtttcttcggc accagccagc tgtcgagtt catggaccag aacaaccgc tgtcggggct 120
gaccacaaag cgccgctgt cggcgtggg cccgggtggt ctgtcgctg agcgtgccg 180
cttgagggtc cgtgacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacccc 240
ggagggtccg aacatcgcc tgatcggttc gctgtcggtg tacgcgcggg tcaatccgtt 300
cgggttcacg gagagcctt atcggaaggt tgtggacggt gtcgttactg acgagatcgt 360
ctacctgacc gccgacgag aggaccgcca cgtcgtggcg caggccaact cgccgaccag 420
acccaacgag gccgggtccg aggttttcga agaggggctg gtcctggttc gccgcaaggc 480
gggcgagggt gagtacgtgc ccagctccga ggtggactac atggacgtct cgccgcggca 540
gatggtgtcc gtggccaccg ccatgattcc gttcctcgag cagcagcag ccaaccgtgc 600
cctgatgggc gccaacatgc agcgccaggc ggttcgctg gtgcgcagcg aggcgccgct 660
ggtgggcacc ggcattggagc tgcgcgcggc gatcgacgc 699

```

&lt;210&gt; SEQ ID NO 123

&lt;211&gt; LENGTH: 699

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium malmoeense

&lt;400&gt; SEQUENCE: 123

```

ggaggcgatc acaccgcaga cgctgatcaa catccggccg gtggtcgccg cgatcaagga 60
gtttcttcggc accagccagc tgtcgagtt catggaccag aacaaccgc tgtcggggct 120
gaccacaaag cgccgctgt cggcgtggg cccgggtggt ctgtcgctg agcgtgccg 180
cttgagggtc cgtgacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacccc 240
ggagggtccg aacatcgcc tgatcggttc gctgtcggtg tacgcgcggg tcaatccgtt 300
cgggttcacg gagagcctt atcggaaggt tgtggacggt gtcgttactg acgagatcgt 360
ctacctgacc gccgacgag aggaccgcca cgtcgtggcg caggccaact cgccgaccag 420

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## -continued

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```

acccaacgag gccgggtgcc aggttttcga agagggggcgt gtcctggttc gccgcaaggc 480
gggcgaggtg gagtacgtgc ccagctccga ggtggactac atggacgtct cgccgcggca 540
gatggtgtcc gtggccaccg ccattgattcc gttcctcgag cagcagcagc ccaaccgtgc 600
cctgatgggc gccaacatgc agcgccaggc ggttcgctg gtgcgcagcg aggcgcgct 660
ggtgggcacc ggcattggagc tgcgcgcggc gatcgacgc 699

```

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<210> SEQ ID NO 124
<211> LENGTH: 699
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium malmoense

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<400> SEQUENCE: 124

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```

ggaggcgatc acaccgcaga cgctgatcaa catccggccg gtggtcgccg cgatcaagga 60
gttcttcggc accagccagc tgcgcagtt catggaccag aacaaccgc tgcggggct 120
gaccacaag cgccgctgt cgccgctggg cccgggtggt ctgtcgctg agcgtgccg 180
cttgaggtc cgtgacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacccc 240
ggagggtccg aacatcgcc tgcgcggttc gctgtcggtg tacgcgcggg tcaatccgtt 300
cgggttcacg gagacgcctt atcggaaggt tgtggacggt gtcgttactg acgagatcgt 360
ctacctgacc gccgacgag aggaccgcca cgtcgtggcg caggccaact cgccgaccag 420
acccaacgag gccgggtgcc aggttttcga agagggggcgt gtcctggttc gccgcaaggc 480
gggcgaggtg gagtacgtgc ccagctccga ggtggactac atggacgtct cgccgcggca 540
gatggtgtcc gtggccaccg ccattgattcc gttcctcgag cagcagcagc ccaaccgtgc 600
cctgatgggc gccaacatgc agcgccaggc ggttcgctg gtgcgcagcg aggcgcgct 660
ggtgggcacc ggcattggagc tgcgcgcggc gatcgacgc 699

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<210> SEQ ID NO 125
<211> LENGTH: 699
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium malmoense

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<400> SEQUENCE: 125

```

```

ggaggcgatc acaccgcaga cgctgatcaa catccggccg gtggtcgccg cgatcaagga 60
gttcttcggc accagccagc tgcgcagtt catggaccag aacaaccgc tgcggggct 120
gaccacaag cgccgctgt cgccgctggg cccgggtggt ctgtcgctg agcgtgccg 180
cttgaggtc cgtgacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacccc 240
ggagggtccg aacatcgcc tgcgcggttc gctgtcggtg tacgcgcggg tcaatccgtt 300
cgggttcacg gagacgcctt atcggaaggt tgtggacggt gtcgttactg acgagatcgt 360
ctacctgacc gccgacgag aggaccgcca cgtcgtggcg caggccaact cgccgaccag 420
acccaacgag gccgggtgcc aggttttcga agagggggcgt gtcctggttc gccgcaaggc 480
gggcgaggtg gagtacgtgc ccagctccga ggtggactac atggacgtct cgccgcggca 540
gatggtgtcc gtggccaccg ccattgattcc gttcctcgag cagcagcagc ccaaccgtgc 600
cctgatgggc gccaacatgc agcgccaggc ggttcgctg gtgcgcagcg aggcgcgct 660
ggtgggcacc ggcattggagc tgcgcgcggc gatcgacgc 699

```

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<210> SEQ ID NO 126

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## -continued

&lt;211&gt; LENGTH: 699

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium malmoense

&lt;400&gt; SEQUENCE: 126

```

ggagggcgatc acaccgcaga cgctgatcaa catccggccg gtggtcgccg cgatcaagga      60
gttcttcggc accagccagc tgtcgagtt catggaccag aacaaccgcg tgcgggggct      120
gaccacacaag cgccgctgt cggcgctggg cccgggtggt ctgtcgctg agcgtgccgg      180
cttgagggtc cgtgacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacccc      240
ggaggggtccg aacatcggcc tgatcggttc gctgtcggtg tacgcgcggg tcaatccgtt      300
cgggttcacg gagacgcctt atcggaaggt tgtggacggt gtcgttactg acgagatcgt      360
ctacctgacc gccgacgagg aggaccgcca cgctgtggcg caggccaact cgccgaccag      420
acccaacgag gccgggtgcc aggttttcga agaggggctg gtcctgggtc gccgcaaggc      480
gggcgaggtg gagtacgtgc ccagctccga ggtggactac atggacgtct cgccgcggca      540
gatggtgtcc gtggccaccg ccattgattcc gttcctcgag cagcagacg ccaaccgtgc      600
cctgatgggc gccaacatgc agcgccaggc ggttcgctg gtgcgcagcg aggcgcgct      660
ggtgggcacc ggcatggagc tgcgcgcggc gatcgacgc      699

```

&lt;210&gt; SEQ ID NO 127

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium marinum

&lt;400&gt; SEQUENCE: 127

```

ggagggcgatc acaccgcaga cgctgatcaa catccgtccg gtcgttgccg cgatcaagga      60
gttcttcgga accagccagc tgtcgagtt catggaccag aacaaccgcg tctccggtct      120
caccacacaag cgccgcctct cggcgctggg gccgggagggt ctgtcccgtg agcgcgccgg      180
tctggaagtt cgtgacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacgcc      240
ggaagggccg aacatcggtc tgatcggttc actgtcggtg tacgccggg tcaaccggtt      300
cgggttcacg gagacgcctt accgcaaggt ggtcgacggg gtcgtttccg acgagatcca      360
ctacctgacc gccgacgagg aggaccgcca cgctgtggcg caggccaact cgccgatcga      420
cgcgagggc cgcttcgtcg agccgcgcgt gctggtccgc cggaaggcgg gcgaggtcga      480
gtacgtgccc tcgtcagagg tggactacat ggacgtgtcg ccgcgccaga tgggtgtcgt      540
ggccaccgcg atgattccgt tcctcgagca cgatgacgcc aaccgcgcc tgatgggtgc      600
caacatgcag cgccaggcgg tcccgtggt gcgcagcgag gcaccgctgg tcggtaccgg      660
tatggagttg cgcgcgccga tcgacgc      687

```

&lt;210&gt; SEQ ID NO 128

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium marinum

&lt;400&gt; SEQUENCE: 128

```

ggagggcgatc acaccgcaga cgctgatcaa catccgtccg gtcgttgccg cgatcaagga      60
gttcttcgga accagccagc tgtcgagtt catggaccag aacaaccgcg tctccggtct      120
caccacacaag cgccgcctct cggcgctggg gccgggagggt ctgtcccgtg agcgcgccgg      180

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tctggaagtt cgtgacgtgc acccgtcgca ctacggccgg atgtgcccga tcgagacgcc	240
ggaagggccg aacatcggtc tgatcggttc actgtcggtg tacgcccggg tcaaccggtt	300
cgggttcatac gagacgccct accgcaaggt ggtcgacggg gtcgtttccg acgagatcca	360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgcatcga	420
cgcgcagggc cgttcctcgc agccgcgcgt gctgggccgc cggaaggcgg gcgaggtcga	480
gtacgtgccc tcgtcagagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggg	540
ggccaccgcg atgattccgt tcctcgagca cgatgacgcc aaccgcgcc tgatgggtgc	600
caacatgcag cgcacggcgg tcccgtgtgt gcgcagcgag gcaccgctgg tcggtaccgg	660
tatggagttg cgcgcggcga tcgacgc	687

&lt;210&gt; SEQ ID NO 129

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium marinum

&lt;400&gt; SEQUENCE: 129

ggaggcgatc acaccgcaga cgctgatcaa catccgtccg gtcgttgccg cgatcaagga	60
gttcttcgga accagccagc tgctgcagtt catggaccag aacaaccgc tctccggtct	120
caccacaag cgcgcctct cggcgtggg gccgggcggg ctgtcccgtg agcgcgccgg	180
tctggaagtt cgtgacgtgc acccgtcgca ctacggccgg atgtgcccga tcgagacgcc	240
ggaagggccg aacatcggtc tgatcggttc actgtcggtg tacgcccggg tcaaccggtt	300
cgggttcatac gagacgccct accgcaaggt ggtcgacggg gtcgtttccg acgagatcca	360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgcatcga	420
cgcgcagggc cgttcctcgc agccgcgcgt gctgggccgc cggaaggcgg gcgaggtcga	480
gtacgtgccc tcgtcagagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggg	540
ggccaccgcg atgattccgt tcctcgagca cgatgacgcc aaccgcgcc tgatgggtgc	600
caacatgcag cgcacggcgg tcccgtgtgt gcgcagcgag gcaccgctgg tcggtaccgg	660
tatggagttg cgcgcggcga tcgacgc	687

&lt;210&gt; SEQ ID NO 130

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium marinum

&lt;400&gt; SEQUENCE: 130

ggaggcgatc acaccgcaga cgctgatcaa catccgtccg gtcgttgccg cgatcaagga	60
gttcttcgga accagccagc tgctgcagtt catggaccag aacaaccgc tctccggtct	120
caccacaag cgcgcctct cggcgtggg gccgggcggg ctgtcccgtg agcgcgccgg	180
tctggaagtt cgtgacgtgc acccgtcgca ctacggccgg atgtgcccga tcgagacgcc	240
ggaagggccg aacatcggtc tgatcggttc actgtcggtg tacgcccggg tcaaccggtt	300
cgggttcatac gagacgccct accgcaaggt ggtcgacggg gtcgtttccg acgagatcca	360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgcatcga	420
cgcgcagggc cgttcctcgc agccgcgcgt gctgggccgc cggaaggcgg gcgaggtcga	480
gtacgtgccc tcgtcagagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggg	540

## -continued

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ggccaccgcg atgattccgt tcctcgagca cgatgacgcc aaccgcgcc tgatgggtgc	600
caacatgcag cgccaggcgg tcccgtggt gcgcagcgag gcaccgctgg tcggtaccgg	660
tatggagttg cgcgcgcgca tcgacgc	687

<210> SEQ ID NO 131  
 <211> LENGTH: 687  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium marinum

<400> SEQUENCE: 131

ggaggcgatc acaccgcaga cgctgatcaa catcsgtccg gtcgttgccg cgatcaagga	60
gttcttcgga accagccagc tgtcgcagtt catggaccag aacaaccgc tctccggtct	120
caccacaag cgccgcctct cggcgtggg gccgggcggt ctgtcccgtg agcgcgccgg	180
tctggaagtt cgtgacgtgc acccgtcga ctacggccgg atgtgccga tcgagacgcc	240
ggaaggcgcc aacatcggtc tgatcggttc actgtcgtg tacgccggg tcaaccggt	300
cgggttcacg gagacccct accgcaaggt ggtcgacggg gtcgtttccg acgagatcca	360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgccgatcga	420
cgcgacgggc cgcttcgtcg agccgcgcgt gctggtccgc cggaaggcgg gcgaggtcga	480
gtacgtgccc tcgtcagagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggt	540
ggccaccgcg atgattccgt tcctcgagca cgatgacgcc aaccgcgcc tgatgggtgc	600
caacatgcag cgccaggcgg tcccgtggt gcgcagcgag gcaccgctgg tcggtaccgg	660
tatggagttg cgcgcgcgca tcgacgc	687

<210> SEQ ID NO 132  
 <211> LENGTH: 626  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium mucogenicum

<400> SEQUENCE: 132

tcctgccgt cgtggcggcg atcaaggagt tcttcggtac gtcgcagctg tcgcagttca	60
tggaccagaa caaccgctg tcgggtctga cccacaagcg tcgtctgtcg gcgtggggcc	120
ccggtggtct gtcccgtgag cgcgccggcc tcgaggtecg cgacgtccac tcgtcgcaact	180
acggccgcat gtgccgcat gagaccctg aaggcccgaa catcggtctg atcggtctgc	240
tgctggtgta cgcgcgggg aaccggttc gttcatcga gacccgtac cgcaaggctg	300
tcgacggcat cgtcaccgat cagatcgact acctgaccgc cgacgaggag gaccgccacg	360
tcgtggcgca ggccaactcg ccgctggacg cgaacggcca cttaccgag gagaagatcc	420
tcgtccgtcg taaggcgcg gaggtcgagt tcgtctcggc gaacgacgtc gactacatgg	480
acgtctcgcc gcgcagatg gtgtcggtcg cgaccgcgat gatccggtc ctggagcacg	540
acgacgcaa ccgcgccctc atgggtgcga acatgcagcg tcaggcggtt ccgctggtgc	600
gcagcgaggc ccgctggtc ggtacc	626

<210> SEQ ID NO 133  
 <211> LENGTH: 626  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium mucogenicum

<400> SEQUENCE: 133

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tccgtcccg	cgtggcg	atcaaggagt	tcttcggcac	gtcgcagctg	tcgcagttca	60
tggaccagaa	caaccgcgtg	tcgggtctga	cccacaagcg	tcgtctgtcg	gcgctggggc	120
ccggtggtct	gtcccgtag	cgcgcggcc	tcgaggtccg	cgacgtccac	tcgtcgcaact	180
acggccgc	gtgcccgc	gagaccccg	aaggcccgaa	catcggtctg	atcggtctgc	240
tgtcgtgtga	cgcacgggtc	aaccggttcg	gcttcacga	gacccgtac	cgcaaggctc	300
tcgacggcat	cgtcaccgat	cagatcgact	acctgaccgc	cgacgaggag	gaccgccacg	360
tcgtggcgca	ggccaactcg	ccgctggacg	cgaacggcca	cttcaccgag	gagaagatcc	420
tcgtccgtcg	taaggcg	gaggtcgagt	tcgtctcg	gaacgacgtc	gactacatgg	480
acgtctcgcc	gcccagatg	gtgtcggtcg	cgaccgcgat	gatcccggtc	ctcgagcagc	540
acgacgcaa	ccgcgccctg	atgggtgcga	acatgcagcg	tcaggcggtt	ccgctgggtg	600
gcagcgaggc	ccgctgggtc	ggtacc				626

&lt;210&gt; SEQ ID NO 134

&lt;211&gt; LENGTH: 626

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium mucogenicum

&lt;400&gt; SEQUENCE: 134

tccgtcccg	cgtggcg	atcaaggagt	tcttcggcac	gtcgcagctg	tcgcagttca	60
tggaccagaa	caaccgcgtg	tcgggtctga	cccacaagcg	tcgtctgtcg	gcgctggggc	120
ccggtggtct	gtcccgtag	cgcgcggcc	tcgaggtccg	cgacgtccac	tcgtcgcaact	180
acggccgc	gtgcccgc	gagaccccg	aaggcccgaa	catcggtctg	atcggtctgc	240
tgtcgtgtga	cgcacgggtc	aaccggttcg	gcttcacga	gacccgtac	cgcaaggctc	300
tcgacggcat	cgtcaccgat	cagatcgact	acctgaccgc	cgacgaggag	gaccgccacg	360
tcgtggcgca	ggccaactcg	ccgctggacg	cgaacggcca	cttcaccgag	gagaagatcc	420
tcgtccgtcg	taaggcg	gaggtcgagt	tcgtctcg	gaacgacgtc	gactacatgg	480
acgtctcgcc	gcccagatg	gtgtcggtcg	cgaccgcgat	gatcccggtc	ctcgagcagc	540
acgacgcaa	ccgcgccctg	atgggtgcga	acatgcagcg	tcaggcggtt	ccgctgggtg	600
gcagcgaggc	ccgctgggtc	ggtacc				626

&lt;210&gt; SEQ ID NO 135

&lt;211&gt; LENGTH: 626

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium mucogenicum

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: modified\_base

&lt;222&gt; LOCATION: (8)...(8)

&lt;223&gt; OTHER INFORMATION: n = g,a,c or t

&lt;400&gt; SEQUENCE: 135

tccgtccngt	cgtggcg	atcaaggagt	tcttcggcac	gtcgcagctg	tcgcagttca	60
tggaccagaa	caaccgcgtg	tcgggtctga	cccacaagcg	tcgtctgtcg	gcgctggggc	120
ccggtggtct	gtcccgtag	cgcgcggcc	tcgaggtccg	cgacgtccac	tcgtcgcaact	180
acggccgc	gtgcccgc	gagaccccg	aaggcccgaa	catcggtctg	atcggtctgc	240
tgtcgtgtga	cgcacgggtc	aaccggttcg	gcttcacga	gacccgtac	cgcaaggctc	300
tcgacggcat	cgtcaccgat	cagatcgact	acctgaccgc	cgacgaggag	gaccgccacg	360

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tcgtggcgca ggccaactcg ccgctggacg cgaacggcca cttaccgag gagaagatcc	420
tcgtccgtcg taagggcggc gaggtcgagt tcgtctcggc gaacgacgtc gactacatgg	480
acgtctcgcc gcgccagatg gtgtcggtcg cgaccgcgat gatcccgttc ctcgagcacg	540
acgacgccaa ccgcgccctg atgggtgcga acatgcagcg tcaggcggtt ccgctgggtg	600
gcagcgaggc cccgctggtc ggtacc	626

&lt;210&gt; SEQ ID NO 136

&lt;211&gt; LENGTH: 626

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium mucogenicum

&lt;400&gt; SEQUENCE: 136

tccgtcccg	tgcgtggcg	atcaaggagt	tcttcggcac	gtsgcagctg	tcgcagttca	60
tggaccagaa	caaccgcgtg	tcgggtctga	cccacaagcg	tcgtctgtcg	gcgctggggc	120
ccggtggtct	gtcccgtag	cgcgcggcc	tcgaggtycg	cgacgtccac	tcgtcgcaact	180
acggccgcat	gtgcccgatc	gagaccccg	aaggcccgaa	catcggtctg	atcggtctrc	240
tgctcgtgta	cgcacgggtc	aaccggttcg	gcttcacga	gacccgtac	cgcaaggctc	300
tcgacggcat	cgtcaccgat	cagatcgact	acctgaccgc	cgacgaggag	gaccgccacg	360
tcgtggcgca	ggccaactcg	ccgctggacg	cgaacggcca	cttaccgag	gagaagatcc	420
tcgtccgtcg	taagggcggc	gaggtcgagt	tcgtctcggc	gaacgacgtc	gactacatgg	480
acgtctcgcc	gcgccagatg	gtgtcggtcg	cgaccgcgat	gatcccgttc	ctcgagcacg	540
acgacgccaa	ccgcgccctg	atgggtgcga	acatgcagcg	tcaggcggtt	ccgctgggtg	600
gcagcgaggc	cccgctggtc	ggtacc				626

&lt;210&gt; SEQ ID NO 137

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium nonchromagenicum

&lt;400&gt; SEQUENCE: 137

ggaggcgatc	acaccgcaga	ccctgatcaa	catccgccc	gtggtcgccg	cgatcaagga	60
gttcttcggc	accagccagc	tctcccagtt	catggaccag	aacaaccggt	tgtcgggtct	120
gaccacaag	cgcgcctgt	cggcgctggg	accgggcggt	ctgtcgcgtg	agcgggccgg	180
cctggaagtt	cgtgacgtgc	acccgtccca	ctacggccgg	atgtgtccga	tcgagacccc	240
ggaaggccc	aacatcggtc	tgatcgggtc	gctgtcggtg	tacgcgcggg	tcaaccggtt	300
cggtttcac	gagacgccct	accgcaaggt	cgtggacggg	gtcgtcaccg	acgagatcca	360
ctacctgacc	gccgacgagg	aggacgccca	cgtcgtggcg	caggccaact	cgcgctgga	420
ggaggacggg	cacttcaccg	aggaccgggt	tctggttcgt	cgtaagggtg	gtgaggtcga	480
gtacgtgtcg	tccgcgagg	tcgactacat	ggacgtctca	ccgcgccaga	tgggtcggt	540
ggccacggcc	atgattccgt	tcctcgagca	cgacgacgcc	aaccgtgcc	tgatggcg	600
caacatgcag	cgccaggcg	ttccgctggt	gcgcagtgag	gcgccgctgg	tgggtaccgg	660
catggagctg	cgcgcggcga	tcgacgc				687

&lt;210&gt; SEQ ID NO 138

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

## -continued

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<213> ORGANISM: Mycobacterium nonchromagenicum

&lt;400&gt; SEQUENCE: 138

```

ggaggcgatc acaccgcaga ccctgatcaa catccgcccg gtggtcgccg cgatcaagga      60
gttcttcggc accagccagc tctcccagtt catggaccag aacaaccctg tgtcgggtct      120
gaccacaaag cgccgcctgt cggcgctggg accgggagggt ctgtcgcgtg agcgggccgg      180
cctggaagtt cgtgacgtgc acccgtccca ctacggcccg atgtgtccga tcgagacccc      240
ggaaggcccc aacatcggtc tgatcgggtc gctgtcggtg tacgcgcggg tcaaccctgt      300
cggtttcatc gagacgccct accgcaaggt cgtggacggg gtcgtcaccg acgagatcca      360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgccgctgga      420
ggaggacggc cacttcaccg aggaccgggt tctggttcgc cgtaagggtg gcgaggtcga      480
gtacgtctcg tccgccgagg tcgactacat ggacgtctca ccgcgccaga tgggtgcggg      540
ggccacggcc atgatcccg tccctcagca cgacgacgcc aaccgtgccc tgatgggcgc      600
caacatgcag cgccaggcgg ttccgctggt gcgcagttag gcgccgctgg tgggtaccgg      660
catggagctg cgcgcgccga tcgacgc                                         687

```

&lt;210&gt; SEQ ID NO 139

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium nonchromagenicum

&lt;400&gt; SEQUENCE: 139

```

ggaggcgatc acaccgcaga ccctgatcaa catccgtccg gtggtcgccg cgatcaagga      60
gttcttcggc accagccagc tctcccagtt catggaccag aacaaccctg tgtcgggtct      120
gaccacaaag cgccgcctgt cggcgctggg accgggagggt ctgtcgcgtg agcgggccgg      180
cctggaagtt cgtgacgtgc acccgtccca ctacggcccg atgtgtccga tcgagacccc      240
ggaaggcccc aacatcggtc tgatcgggtc gctgtcggtg tacgcgcggg tcaaccctgt      300
cggtttcatc gagacgccct accgcaaggt cgtggacggg gtcgtcaccg acgagatcca      360
ctacctgacc gccgacgagg aggaccgcca cgttgtggcg caggccaact cgccgctgga      420
ggaggacggc cacttcaccg aggaccgggt tctggttcgt cgtaagggtg gtgaggtcga      480
gtacgtctcg tccgccgagg tcgactacat ggacgtctca ccgcgccaga tgggtgcggg      540
ggccacggcc atgattccgt tccctcagca cgacgacgcc aaccgtgccc tgatgggcgc      600
caacatgcag cgccaggcgg ttccgctggt gcgcagttag gcgccgctgg tgggtaccgg      660
catggagctg cgcgcgccga tcgacgc                                         687

```

&lt;210&gt; SEQ ID NO 140

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium nonchromagenicum

&lt;400&gt; SEQUENCE: 140

```

ggaggcgatc acaccgcaga ccctgatcaa catccgtccg gtggtcgccg cgatcaagga      60
gttcttcggc accagccagc tctcccagtt catggaccag aacaaccctg tgtcgggtct      120
gaccacaaag cgccgcctgt cggcgctggg accgggagggt ctgtcgcgtg agcgggccgg      180
cctggaagtt cgtgacgtgc acccgtccca ctacggcccg atgtgtccga tcgagacccc      240

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ggaaggcccg aacatcggtc tgatcgggtc gctgtcgggtg tacgcgcggg tcaaccggtt	300
cggtttcctc gagacgccct accgcaaggt cgtggacggg gtcgtcaccg acgagatcca	360
ctacctgacc gccgacgagg aggaccgcca cgttggtggcg caggccaact cgcgcgtgga	420
ggaggacggc cacttcaccg aggaccgggt tctggttcgt cgtaaggggtg gtgaggtcga	480
gtacgtctcg tccgccgagg tcgactacat ggacgtctca ccgcgccaga tgggtgcggg	540
ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgtgccc tgatgggcgc	600
caacatgcag cgcacggcgg ttccgctggt gcgcagttag gcgccgctgg tgggtactgg	660
catggagctg cgcgcggcga tcgacgc	687

&lt;210&gt; SEQ ID NO 141

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium nonchromagenicum

&lt;400&gt; SEQUENCE: 141

ggaggcgatc acaccgcaga ccctgatcaa catccgcccg gtggtcgccg cgatcaagga	60
gtttcttcggc accagccagc tctcccagtt catggaccag aacaaccggt tgcgggtct	120
gaccacaaag cgcgcctgt cggcgtggg accgggagggt ctgtcgcgtg agcgggccc	180
cctggaagtt cgtgacgtgc acccgtccca ctacggcccg atgtgtccga tcgagacccc	240
ggaaggcccg aacatcggtc tgatcgggtc gctgtcgggtg tacgcgcggg tcaaccggtt	300
cggtttcctc gagacgccct accgcaaggt cgtggacggg gtcgtcaccg acgagatcca	360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgcgtgga	420
ggaggacggc cacttcaccg aggaccgggt tctggttcgt cgtaaggggtg gtgaggtcga	480
gtacgtgtcg tccgccgagg tcgactacat ggacgtctca ccgcgccaga tgggtgcggg	540
ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgtgccc tgatgggcgc	600
caacatgcag cgcacggcgg ttccgctggt gcgcagttag gcgccgctgg tgggtaccgg	660
catggagctg cgcgcggcga tcgacgc	687

&lt;210&gt; SEQ ID NO 142

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium terrae

&lt;400&gt; SEQUENCE: 142

ggaggcgatc acaccgcaga ccctgatcaa catccgcccg gtggtcgccg cgatcaagga	60
gtttcttcggc accagccagc tctcccagtt catggaccag aacaaccggt tgcgggtct	120
gaccacaaag cgcgcctgt cggcgtggg gcccggtggt ctgtcccgtg agcgcgcgg	180
cctggaagtt cgtgacgtgc acccgagcca ctacggcccg atgtgtccga tcgagacccc	240
ggaaggcccg aacatcggtc tgatcgggtc gctgtcgggtg tacgcgcggg tgaaccggtt	300
cggtttcctc gagacgccct accgcaaggt ggtcgacggt gtcgtcagcg acgagatcca	360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgcgtgga	420
ggacgacggc cggtttcggc aggaacgagt tctggtgcgc cgcaagggcg gcgaggtcga	480
gtacgtgtcg tcggccgagg ttgactacat ggacgtctcg ccgcgccaga tgggtgcggg	540
ggccacggcc atgattccgt tcctcgagca cgacgacgcc aaccgtgccc tgatgggcgc	600

## -continued

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caacatgcag cgtcaggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg	660
catggagctg cgcgcggcga tcgacgc	687

<210> SEQ ID NO 143  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium scrofulaceum

<400> SEQUENCE: 143

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtggccg	60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc	120
tgtcgggcct gacccacaag cgcgcctgt cggcgctggg cccgggtggt ctgtcccgc	180
agcgggcccg gctggaggtc cgggacgtgc acccgtcgca ctacggccgg atgtgccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcggtg tacgcgcggg	300
tcaaccggtt cggcttcacg gagacgcgt accgcaaggt ggtcgacggt gtggtcaccg	360
acgagatcca ctacctgacc gccgacgag aggaccgtca cgtcgtggcg caggccaact	420
cgcgcatcga cgcgagcggc cggttcgagg agtcgcgcgt cctggtcgcg cggaaggcgg	480
gcgaggtcga gtacgtgccg tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tggtgtcggg ggccaccgcc atgatcccgt tcctcgagca cgacgacgcc aaccgtgcc	600
tgatggggcg caacatgcag cgcagggcgg ttccgctggt gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 144  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium scrofulaceum

<400> SEQUENCE: 144

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtggccg	60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc	120
tgtcgggcct gacccacaag cgcgcctgt cggcgctggg cccgggtggt ctgtcccgc	180
agcgggcccg gctggaggtc cgggacgtgc acccgtcgca ctacggccgg atgtgccga	240
tcgagacccc ggagggtccc aacatcggtc tgatcggtc gctgtcggtg tacgcgcggg	300
tcaaacacgtt cggcttcacg gagacgcgt accgcaaggt ggtcgacggt gtggtcaccg	360
acgagatcca ctacctgacc gccgacgag aggaccgtca cgtcgtggcg caggccaact	420
cgcgcatcga cgcgagcggc cggttcgagg agtcgcgcgt cctggtcgcg cggaaggcgg	480
gcgaggtcga gtacgtgccg tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga	540
tggtgtcggg ggccaccgcc atgatcccgt tcctcgagca cgacgacgcc aaccgtgcc	600
tgatggggcg caacatgcag cgcagggcgg ttccgctggt gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagttg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 145  
 <211> LENGTH: 687  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium scrofulaceum

<400> SEQUENCE: 145

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```

ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtggtggccg cgatcaagga    60
gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgcg tgcgggtct    120
gaccacaaag cgcgcctgt cggcgctggg cccgggagggt ctgtcccgtg agcgggcccg    180
cctcgagggtg cgcgacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacccc    240
ggagggtccc aacatcgggc tgatcggtc gctgtcgtg tacgcgcggg tcaaccggt    300
cgggttcacg gagacgccgt accgcaaggt cgtcgacggt gtggtcaccg acgagatcca    360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgacgca    420
cgcgagcggc cggttcgagg agtcgcgcgt gctggtccgc cggaaggccg gcgaggtcga    480
gtacgtgccg tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtcgggt    540
ggccaccgcc atgatcccgt tcctcgagca cgacgacgcc aaccgtgccg tgatgggcgc    600
caacatgcag cgcacggcgg tcccgtggt gcgcagcgag gcgccgctgg tgggcaccgg    660
catggagttg cgcgcggcga tcgacgc    687

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&lt;210&gt; SEQ ID NO 146

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium scrofulaceum

&lt;400&gt; SEQUENCE: 146

```

ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtggccg cgatcaagga    60
gttcttcggc accagccagc tctcgcagtt catggaccag aacaaccgcg tgcgggcct    120
gaccacaaag cgcgcctgt cggcgctggg cccgggtggt ctgtcccgcg agcgggcccg    180
gctggaggtc cgggacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacccc    240
ggagggtccc aacatcggtc tgatcggtc gctgtcgtg tacgcgcggg tcaaccggt    300
cggcttcacg gagacgccgt accgcaaggt ggtcgacggt gtggtcaccg acgagatcca    360
ctacctgacc gccgacgagg aggaccgtca cgtcgtggcg caggccaact cgcgacgca    420
cgcgagcggc cggttcgagg agtcgcgcgt cctggtccgc cggaaggccg gcgaggtcga    480
gtacgtgccg tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtcgggt    540
ggccaccgcc atgatcccgt tcctcgagca cgacgacgcc aaccgtgccg tgatgggcgc    600
caacatgcag cgcacggcgg ttccgtggt gcgcagcgag gcgccgctgg tgggcaccgg    660
catggagttg cgcgcggcga tcgacgc    687

```

&lt;210&gt; SEQ ID NO 147

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium scrofulaceum

&lt;400&gt; SEQUENCE: 147

```

ggaggcgatc acaccgcaga cgctgatcaa catccggccg gtcgtcgcg cgatcaagga    60
gttcttcggc accagccagc tctcccagtt catggaccag aacaaccgcg tgcgggtct    120
gacgcacaaag cgcgcctgt cggcgctggg cccgggagggt ctgtcccgtg agcgggcccg    180
gctggaggtc cgcgacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacccc    240
ggagggggccg aacatcggtc tgatcggtc gctgtcgtg tacgcccggg tcaaccggt    300
cggcttcacg gagaccccgt accgcaaggt ggtcgacggt gtggtcaccg acgagattca    360

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## -continued

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ctacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact cgcgcatcga	420
cgcgaacggc cggttcagag agtcgcgcgt cctggtccgc cggaaggcgg gcgaggtcga	480
gtacgtgccg tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggt	540
ggccaccgcc atgatcccg tccctcagca cgcgcgcgc aaccgtgccc tgatgggcgc	600
caacatgcag cgtcaggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg	660
catggagctg cgcgcggcga tcgacgc	687

&lt;210&gt; SEQ ID NO 148

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium scrofulaceum

&lt;400&gt; SEQUENCE: 148

ggaggcgatc acaccgcaga ccctgatcaa catccggccg gtcgtggccg cgatcaagga	60
gttcttcggc accagccagc tctcgcagtt catggaccag aacaaccgc tgctgggcct	120
gaccacaag cgcgcctgt cggcgtggg cccgggtggt ctgtcccgcg agcgggccc	180
gctggaggtc cgggacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacccc	240
ggagggtccc aacatcggtc tgatcgggtc gctgtcgtg tacgcgcggg tcaaccggt	300
cggcttcacg gagacccgt accgcaaggt ggtcgacggt gtggtcaccg acgagatcca	360
ctacctgacc gccgacgagg aggaccgtca cgtcgtggcg caggccaact cgcgcatcga	420
cgcgacggc cggttcagag agtcgcgcgt cctggtccgc cggaaggcgg gcgaggtcga	480
gtacgtgccg tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggt	540
ggccaccgcc atgatcccg tccctcagca cgcgcgcgc aaccgtgccc tgatgggcgc	600
caacatgcag cgcacggcgg ttccgctggt gcgcagcgag gcgccgctgg tgggcaccgg	660
catggagttg cgcgcggcga tcgacgc	687

&lt;210&gt; SEQ ID NO 149

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium scrofulaceum

&lt;400&gt; SEQUENCE: 149

ggaggcgatc acaccgcaga ccctgatcaa catccgtccg gtcgtggcgg cgatcaagga	60
gttcttcggc accagccagc tctcgcagtt catggaccag aacaaccgc tgctgggtct	120
gaccacaag cgcgcctct cggcgtggg acccgtggt ctgtcccgcg agcgtgcggg	180
cctcgaggtc cgtgacgtac acccgtcgca ctacggccgg atgtgtccga tcgaaacccc	240
ggagggggccg aacatcggtc tgatcgggtc gctgtcgtg tacgcccggg tcaaccggt	300
cgggttcacg gagacccgt accgcaaggt tgtcgacggt gtggtcaccg acgagatcga	360
gtacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgcatcga	420
cgcgcacggg cgcttcgaag agtcgcgtgt gctggttcgc cgcaaggcgg gcgaggtcga	480
gtacgtgccg tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggt	540
cgcacggcg atgatcccg tccctcagca cgcgcgcgc aaccgcgccc tgatgggtgc	600
caacatgcag cgcacggcgg ttccgctggt gcgcagcgag gcaccgctgg tgggcaccgg	660
gatggagttg cgcgcggcga tcgacgc	687

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&lt;210&gt; SEQ ID NO 150

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium scrofulaceum

&lt;400&gt; SEQUENCE: 150

```
ggaggcgatc acaccgcaga ccctgatcaa catccgtccg gtcgtggcgg cgatcaagga    60
gttcttcggc accagccagc tctcgcagtt catggaccag aacaaccgcg tgcgggtct    120
taccacaag cgccgcctgt cggcgtggg gccgggcggg ctgtcccgtg agcgggcggg    180
cctcgaggtc cgcgatgtgc acccgtcgca ctacggccgg atgtgtccga tcgagacccc    240
cgagggtccg aacatcggtc tgatcgggtc gctatcgtg tacgcgggg tcaaccggt    300
cgggttcacg gagacccgt accgcaaggt tgcgacggt gtggtcaccg acgagatcga    360
gtacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgccgatcga    420
ccccgacggc cgcttcgaag agtcgcgcgt gctggttcgc cgtaaggcgg gcgaggtcga    480
atacgtgccg tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggttcggt    540
ggcgaccgcg atgatcccg tccctgaaca cgacgacgcc aaccgtgcc tcgatgggtgc    600
caacatgcag cgccaggcgg ttccgctggt acgcagcgag gcccgcgtgg tcggcaccgg    660
gatggagctg cgcgcggcga tcgacgc    687
```

&lt;210&gt; SEQ ID NO 151

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium scrofulaceum

&lt;400&gt; SEQUENCE: 151

```
ggaggcgatc acaccgcaga ccctgatcaa catccgtccg gtcgtggcgg cgatcaagga    60
gttcttcggc accagccagc tctcgcagtt catggaccag aacaaccgcg tgcgggtct    120
taccacaag cgccgcctgt cggcgtggg gccgggcggg ctgtcccgtg agcgggcggg    180
cctcgaggtc cgcgatgtgc acccgtcgca ctacggccgg atgtgtccga tcgagacccc    240
cgagggtccg aacatcggtc tgatcgggtc gctatcgtg tacgcgggg tcaaccggt    300
cgggttcacg gagacccgt accgcaaggt tgcgacggt gtggtcaccg acgagatcga    360
gtacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgccgatcga    420
ccccgacggc cgcttcgaag agtcgcgcgt gctggttcgc cgtaaggcgg gcgaggtcga    480
atacgtgccg tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggttcggt    540
ggcgaccgcg atgatcccg tccctgaaca cgacgacgcc aaccgtgcc tcgatgggtgc    600
caacatgcag cgccaggcgg ttccgctggt acgcagcgag gcccgcgtgg tcggcaccgg    660
gatggagctg cgcgcggcga tcgacgc    687
```

&lt;210&gt; SEQ ID NO 152

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium scrofulaceum

&lt;400&gt; SEQUENCE: 152

```
ggaggcgatc acaccgcaga ccctgatcaa catccgtccg gtcgtggcgg cgatcaagga    60
gttcttcggc accagccagc tctcgcagtt catggaccag aacaaccgcg tgcgggtct    120
```

## -continued

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```

caccacacaag cgccgcctgt cggcgctggg gccgggcggt ctgtcccgtg agcgggcggg 180
cctcgaggtc cgagacgtgc acccgtcgca ctacggccgg atgtgtccga tcgagacccc 240
cgagggtccg aacatcggtc tgatcggtgc gctgtcgtg tacgcgcggg tcaaccggtt 300
cgggttcacg gagacgcgt accgcaaggt tgtcgacgt gtggttacg acgagatcga 360
gtacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact cgcgacgca 420
cgccgacggc cgcttcgaag agtcgcgcgt actggttcgc cgtaaggcgg gcgaggtcga 480
gtacgtgccg tcgtccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggt 540
ggcgaccgcg atgatcccgt tcctcgagca cgacgacgcc aaccgtgccc tgatgggtgc 600
caacatgcag cgccaggcgg ttccgctggt acgcagcgag gccccgctgg tcggcaccgg 660
gatggagctg cgcgcggcga tcgacgc 687

```

```

<210> SEQ ID NO 153
<211> LENGTH: 705
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium smegmatis

```

```

<400> SEQUENCE: 153

```

```

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg 60
cgatcaagga gttcttcggc accagccagc tgtcgagtt catggaccag aacaaccgc 120
tgtcgggtct gaccacaaag cgtcgtcttt cggcgctggg ccccgcggt ctgtcccgtg 180
agcgcgctgg cctcgaggtc cgcgacgtgc accccagcca ctacggccgc atgtgcccga 240
tcgagacccc tgagggtccc aacatcggtc tgatcggttc gctgtcggtg tacgcccgcg 300
tgaaccggtt cggcttcacg gagacgcgt accgcaaggt cgagaacggt gtggtcaccg 360
accagatcga ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact 420
cgccgaccga cgagaacggc cgcttcaccg aggaccgct catggtccgc aagaaggcgg 480
gcgaggtcga gttcgtctcc gccgaccagg tggactacat ggacgtctcg ccgcgccaga 540
tgggtgcggt cgctacggcc atgatcccgt tcctcgagca cgacgacgcc aaccgcgccc 600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg 660
tggtgtaccg tatggaactg cgcgcggcga tcgacgcggc gacgt 705

```

```

<210> SEQ ID NO 154
<211> LENGTH: 626
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium smegmatis
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (9)...(9)
<223> OTHER INFORMATION: n = g,a,c or t

```

```

<400> SEQUENCE: 154

```

```

tccgtccgnt cgtggcggcg atcaaggagt tcttcggaac gtcgcagctg tcgcagttca 60
tggaccagaa caaccgctg tccggtctga cccacaagcg ccgcctgtcg gcgctggggc 120
cgggtggtct gtcccgtgag cgcgcgggcc tggagggtccg cgacgtgcac tccagccact 180
acggccggat gtgcccgatc gagaccccgg aaggcccga catcgccctg atcggttcgc 240
tgtcgtgtga cgcgcgggtc aaccggttcg ggttcacgca gacccgtac cgcaagggtga 300
tcgacggcca ggtcagcgat cagatcgact acctcaccgc cgacgaggag gaccgccaca 360

```

## -continued

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tcgtggcgca ggccaactcg ccgctcgacg acgagggccg gttcaccgag gacaagatcc	420
tcgtccgccc taagggcggc gaggtcgagt tcgtcgcgcc caccgaggtg gactacatgg	480
acgtctcgcc gcgccagatg gtgtcggtcg cgacggcgat gatcccgttc ctcgagcacg	540
acgacgccaa ccgtgccctg atgggtgcc aatgcagcgc ccaggcggtt ccgctgggtcc	600
gcagcgaggc cccgctggtc ggcacc	626

<210> SEQ ID NO 155  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium smegmatis

<400> SEQUENCE: 155

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgcccc gtcgtggcgg	60
cgatcaagga gttcttcggc accagccagc tgctgcagtt catggaccag aacaaccgc	120
tgctgggtct gaccacaag cgtcgtctgt cggcgctggg cccggcggt ctgtcccgtg	180
agcgcgccgg cctggaggtc cgcgacgtgc actccagcca ctacggccgg atgtgccga	240
tcgagacccc ggaaggcccc aacatcgcc tgatcggttc gctgtcggtg tacgcgcggg	300
tgaaccggtt cggtttcacg gagacccgt accgcaaggt cgtcgacggt gtcacaccg	360
accagatcga ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact	420
cgcgacatga cgacaacggc cggttcaccg aggaccgct gctggtgcgc cgcaagggtg	480
gcgaggtcga gttcgtctcc gccaccgagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcggg cgcgacggcg atgatcccgt tcctcgagca cgacgacgcc aaccgtgct	600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcccgcgtgg	660
tcggcaccgg tatggagctg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 156  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium smegmatis

<400> SEQUENCE: 156

cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg	60
cgatcaagga gttcttcggc accagccagc tgctgcagtt catggaccag aacaaccgc	120
tgctgggtct gaccacaag cgtcgtcttt cggcgctggg cccggcggt ctgtcccgtg	180
agcgcgccgg cctcgaggtc cgcgacgtgc accccagcca ctacggccgc atgtgccga	240
tcgagacccc tgagggtccc aacatcggtc tgatcggttc gctgtcggtg tacgcccgcg	300
tgaaccggtt cggtttcacg gagacgcctt accgcaaggt cgagaacggt gtggtcaccg	360
accagatcga ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact	420
cgcgaccga cgagaacggc cgcttcaccg aggaccgct catggtccgc aagaaggcg	480
gcgaggtcga gttcgtctcc gccgaccagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcggg cgctacggcc atgatcccgt tcctcgagca cgacgacgcc aaccgcgcc	600
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg	660
tggttacggg tatggaactg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 157

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-continued

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<211> LENGTH: 705  
<212> TYPE: DNA  
<213> ORGANISM: *Mycobacterium gordonae*  
<220> FEATURE:  
<221> NAME/KEY: modified\_base  
<222> LOCATION: (688)...(688)  
<223> OTHER INFORMATION: n = g,a,c or t  
<220> FEATURE:  
<221> NAME/KEY: modified\_base  
<222> LOCATION: (700)...(701)  
<223> OTHER INFORMATION: n = g,a,c or t  
<220> FEATURE:  
<221> NAME/KEY: modified\_base  
<222> LOCATION: (704)...(705)  
<223> OTHER INFORMATION: n = g,a,c or t  
  
<400> SEQUENCE: 157  
  
cccaggacgt ggaggcgatc acaccgcaga ccctgatcaa catccggccc gtcgtcgccg 60  
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc 120  
tctccggtct gacgcacaag cggcgtctgt ccgctttggg gccgggagggt ctgtcccgtg 180  
agcggggcgg gctggaggtc cgtgacgtgc acccgtcgca ctacggccgg atgtgccga 240  
tcgagacccc ggagggtccg aatatcggtc tgatcggttc gctgtcgggt tacgcacggg 300  
tcaaccggtt cgggttcacg gagacgccgt atagacgcgt cgtcagcgga gttgtcacgg 360  
atgagatcca ctacgtgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact 420  
cgccgatcga cgccgacgga cggttcgtcg agggacgcgt cctggtcgcg cgcaaggcgg 480  
gcgaggtcga gtacgtgccc tcctccgagg tggactacat ggacgtgtcg ccgcgccaga 540  
tggtgtcggg ggccaccgcg atgattccgt tcctcgagca cgacgacgcc aaccgcgcc 600  
tgatgggtgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg 660  
tgggtaccgg tatggagtgt gcgcggnga tcgacgcggg nacnn 705  
  
<210> SEQ ID NO 158  
<211> LENGTH: 687  
<212> TYPE: DNA  
<213> ORGANISM: *Mycobacterium smegmatis*  
  
<400> SEQUENCE: 158  
  
ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggcgg cgatcaagga 60  
gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc tctcggtct 120  
gaccacaaag cgtcgtcttt cggcgtggg ccccgccgggt ctgtcccgtg agcgcgccgg 180  
cctcgaggtc cgcgacgtgc accccagcca ctacggccgc atgtgccga tcgagacccc 240  
tgagggtccc aacatcggtc tgatcggttc gctgtcgggt tacgcccgcg tgaaccggt 300  
cgggttcacg gagacgccgt accgcaaggc cgagaacggt gtggtcacgg accagatcga 360  
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgccgaccga 420  
cgagaacggc cgcttcacgg aggacgcgt catggtccgc aagaaggcgg gcgaggtcga 480  
gttctgtctc gccgaccagg tggactacat ggacgtctcg ccgcgccaga ttgtgtcgg 540  
cgccacggcc atgatccgt tcctcgagca cgacgacgcc aaccgcgcc tgatgggtgc 600  
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg tgggtaccgg 660  
tatggaactg cgccggcgga tcgacgc 687  
  
<210> SEQ ID NO 159

## -continued

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<211> LENGTH: 687

<212> TYPE: DNA

<213> ORGANISM: Mycobacterium szulgai

<400> SEQUENCE: 159

```
ggaggcgatc acaccgcaga ccctgatcaa catccggccc gtcgtcgccg cgatcaagga      60
gttcttcggc accagccagc tctcgcagtt catggaccag aacaaccgcg tctccggtct      120
gacgcacaag cggcgtctgt ccgctttggg gccgggcggt ctgtcccgtg agcgggcccgg      180
gctggaggtc cgtgacgtgc acccgtcgca ctacggccgg atgtgcccgga tcgagacccc      240
ggagggtccg aatatcggtc tgatcgggtc gctgtcggtg tacgcacggg tcaaccggtt      300
cgggttcacg gagacgccgt atagacgcgt cgtcagcgga gttgtcacgg atgagatcca      360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgatcga      420
cgccgacgga cggttcgtcg agggacgtgt cctggtccgc cgcaaggcgg gcgaggtcga      480
gtacgtgccc tcctccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggt      540
ggccaccgcg atgattccgt tcctcgagca cgacgacgcc aaccgcgccg tgatgggtgc      600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg tgggtaccgg      660
tatggagttg cgcgcggcga tcgacgc      687
```

<210> SEQ ID NO 160

<211> LENGTH: 687

<212> TYPE: DNA

<213> ORGANISM: Mycobacterium szulgai

<400> SEQUENCE: 160

```
ggaggcgatc acaccgcaga ccctgatcaa catccggccc gtcgtcgccg cgatcaagga      60
gttcttcggc accagccagc tctcgcagtt catggaccag aacaaccgcg tctccggtct      120
gacgcacaag cggcgtctgt ccgctttggg gccgggcggt ctgtcccgtg agcgggcccgg      180
gctggaggtc cgtgacgtgc acccgtcgca ctacggccgg atgtgcccgga tcgagacccc      240
ggagggtccg aatatgggtc tgatcgggtc gctgtcggtg tacgcacggg tcaaccggtt      300
cgggttcacg gagacgccgt atagacgcgt cgtcagcgga gttgtcacgg atgagatcca      360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgatcga      420
cgccgacgga cggttcgtcg agggacgtgt cctggtccgc cgcaaggcgg gcgaggtcga      480
gtacgtgccc tcctccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtgcggt      540
ggccaccgcg atgattccgt tcctcgagca cgacgacgcc aaccgcgccg tgatgggtgc      600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg tgggtaccgg      660
tatggagttg cgcgcggcga tcgacgc      687
```

<210> SEQ ID NO 161

<211> LENGTH: 687

<212> TYPE: DNA

<213> ORGANISM: Mycobacterium szulgai

<400> SEQUENCE: 161

```
ggaggcgatc acaccgcaga ccctgatcaa catccggccc gtcgtcgccg cgatcaagga      60
gttcttcggc accagccagc tctcgcagtt catggaccag aacaaccgcg tctccggtct      120
gacgcacaag cggcgtctgt ccgctctggg gccgggcggt ctgtcccgtg agcgggcccgg      180
```

## -continued

---

gctggaggtc cgtgacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacccc	240
ggaggggtccg aatatcggtc tgatcgggtc gctgtcggtg tacgcacggg tcaaccggtt	300
cgggttcacg gagacgccgt atagacgcgt cgtcagcgga gttgtcacgg atgagatcca	360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgccgatcga	420
cgccgacgga cggttcgtcg agggacgcgt cctgggccgc cgcaaggcgg gcgaggtcga	480
gtacgtgccc tcctccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtcgggt	540
ggccaccgcg atgattccgt tcctcgagca cgacgacgcc aaccgcgcc tgatgggtgc	600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg tgggtaccgg	660
tatggagttg cgccggcgga tcgacgc	687

&lt;210&gt; SEQ ID NO 162

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium szulgai

&lt;400&gt; SEQUENCE: 162

ggaggcgatc acaccgcaga ccctgatcaa catccggccc gtcgtcgccg cgatcaagga	60
gttcttcggc accagccagc tctcgcagtt catggaccag aacaaccgc tctccggtct	120
gacgcacaag cggcgtctgt ccgctctggg gccgggcggg ctgtcccgtg agcgggcccgg	180
gctggaggtc cgtgacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacccc	240
ggaggggtccg aatatcggtc tgatcgggtc gctgtcggtg tacgcacggg tcaaccggtt	300
cgggttcacg gagacgccgt atagacgcgt cgtcagcgga gttgtcacgg atgagatcca	360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgccgatcga	420
cgccgacgga cggttcgtcg agggacgcgt cctgggccgc cgcaaggcgg gcgaggtcga	480
gtacgtgccc tcctccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtcgggt	540
ggccaccgcg atgattccgt tcctcgagca cgacgacgcc aaccgcgcc tgatgggtgc	600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg tgggtaccgg	660
tatggagttg cgccggcgga tcgacgc	687

&lt;210&gt; SEQ ID NO 163

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium szulgai

&lt;400&gt; SEQUENCE: 163

ggaggcgatc acaccgcaga ccctgatcaa catccggccc gtcgtcgccg cgatcaagga	60
gttcttcggc accagccagc tctcgcagtt catggaccag aacaaccgc tctccggtct	120
gacgcacaag cggcgtctgt ccgctttggg gccgggcggg ctgtcccgtg agcgggcccgg	180
gctggaggtc cgtgacgtgc acccgtcgca ctacggccgg atgtgccga tcgagacccc	240
ggaggggtccg aatatcggtc tgatcgggtc gctgtcggtg tacgcacggg tcaaccggtt	300
cgggttcacg gagacgccgt atagacgcgt cgtcagcgga gttgtcacgg atgagatcca	360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgccgatcga	420
cgccgacgga cggttcgtcg agggacgtgt cctgggccgc cgcaaggcgg gcgaggtcga	480
gtacgtgccc tcctccgagg tggactacat ggacgtgtcg ccgcgccaga tgggtcgggt	540

## -continued

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```

ggccaccgcg atgattccgt tcctcgagca cgacgacgcc aaccgcgccc tgatgggtgc 600
caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcaccgctgg tgggtaccgg 660
tatggagttg cgcgcggcga tcgacgc 687

```

```

<210> SEQ ID NO 164
<211> LENGTH: 687
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium terrae

```

```

<400> SEQUENCE: 164

```

```

ggaggcgatc acaccgcaga ccctgatcaa catccgcccg gtggtcgccg cgattaagga 60
gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgcg tgcgggtct 120
gaccacaag cgccggtgt cggcgtggg cccgggtggt ctgtcccgtg aacgggccc 180
gcttgaggtc cgtgacgtgc acccgcccc ctacggccgg atgtgtccga tcgagacccc 240
ggagggtccg aacatcggtc tgatcggtc gctggcgact tacgcgcggg tcaaccggt 300
cgggttcacg gaaaccccg accgcaaggt caacgacggt gtggtcagcg atgagatcgt 360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgccgctgga 420
ggacgacaat cgcttcaccg aggaccgggt tctggtgcgc cgcaagggcg gcgaggtcga 480
gtacgtgtcg tcggccgagg tcgactacat ggacgtctcg ccgcgccaga tgggtgcgg 540
ggccacggcc atgateccgt tcctggagca cgacgacgcc aaccgggccc tgatgggtgc 600
caacatgcag cgtcaggcgg ttcccctggt gcgcagcgag gcgccgctgg tgggcaccgg 660
catggagctg cgcgcggcga tcgacgc 687

```

```

<210> SEQ ID NO 165
<211> LENGTH: 687
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium terrae

```

```

<400> SEQUENCE: 165

```

```

ggaggcgatc acaccgcaga ccttgatcaa catccgcccg gtggtcgccg cgatcaagga 60
gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgcg tgcgggtct 120
gaccacaag cgccggtgt cggcgtggg cccgggtggt ctgtcccgtg agcgggccc 180
gcttgaggtc cgtgacgtgc acccgcccc ctacggccgg atgtgtccga tcgagacccc 240
ggagggtccg aacatcggtc tgatcggtc gctggcgact tacgcgcggg tcaaccggt 300
cgggttcacg gaaaccccg accgcaaggt caacgacggt gtggtcagcg atgagatcgt 360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgccgctgga 420
ggacgacaat cgcttcaccg aggaccgggt tctggtgcgc cgcaagggcg gcgaggtcga 480
gtacgtgtcg tcggccgagg tcgactacat ggacgtctcg ccgcgccaga tgggtgcgg 540
ggccacggcc atgateccgt tcctggagca cgacgacgcc aaccgggccc tgatgggtgc 600
caacatgcag cgtcaggcgg ttcccctggt gcgcagcgag gcgccgctgg tgggcaccgg 660
catggagctg cgcgcggcga tcgacgc 687

```

```

<210> SEQ ID NO 166
<211> LENGTH: 687
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium terrae

```



## -continued

&lt;400&gt; SEQUENCE: 166

```

ggaggcgatc acaccgcaga ccctgatcaa catccgcccg gtggtcgccg cgatcaagga      60
gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc tgcgggtct      120
gaccacaag cgcggctgt cggcgtggg cccgggtggt ctgtcccgtg agcgggcccg      180
gcttgaggtc cgtgacgtgc acccggtcca ctacggccgg atgtgtccga tcgagacccc      240
ggagggtccg aacatcggtc tgatcggctc gctggcgacc tacgcgagg tcaaccggt      300
cgggttcacg gaaaccccg accgcaaggt caacgacggt gtggtcagcg atgagatcgt      360
ctacctgacc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgctgga      420
ggacgacagt cgcttcgccc aggaccgagt tctggtgcgc cgcaaggcg gtgaggtcga      480
gtacgtgtcg tcggccgagg tcgactacat ggacgtctcg ccgcgccaga tgggtgcggt      540
ggccacggcc atgatcccg tcctggagca cgacgacgcc aaccgtgcc tgatgggcgc      600
caacatgcag cgtcaggcgg ttcccctggt gcgcagcgag gcgccgctgg tgggcaccgg      660
catggagctg cgcgcggcga tcgacgc      687

```

&lt;210&gt; SEQ ID NO 167

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium triplex

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: modified\_base

&lt;222&gt; LOCATION: (139)...(139)

&lt;223&gt; OTHER INFORMATION: n = g,a,c or t

&lt;400&gt; SEQUENCE: 167

```

ggaggcgatc acaccgcaga ccctgatcaa catccgtccc gtcgtggccg cgatcaagga      60
gttcttcggc accagccagc tgtccagtt catggaccag aacaaccgc tgtccgggt      120
caccacaag cgcgcctnt cggcgtggg gccgggcggt ctgtcgcgtg agcgcgcggg      180
cctcgagggt cgtgacgtgc acccgtcgca ctacggccgg atgtgcccga tcgagacccc      240
cgagggtccg aacatcggtc tgatcggttc gctgtcgtg tacgcgagg tcaaccggt      300
cgggttcacg gagacgcgt accgcaaggt ggtcgacggt gtggtcaccg amcaratcga      360
ctasctgrcc gccgacgagg aggaccgcca cgtcgtggcg caggccaact cgcgacgca      420
cgccgacggc cggttcgagg agtcgcgtgt cctggtccgc cggaaggcg gcgaggtcga      480
gtacgtgccg tcgtccgagg tcgactacat ggacgtgtcg ccgcgccaga tgggtgcggt      540
ggccacggcc atgatcccg tcctcgagca cgacgacgcc aaccgtgcc tgatgggcgc      600
caacatgcag cgcaggcgg ttccgctggt gcgcagcgag gcgccgctgg tcggtaccgg      660
tatggagctg cgcgcggcga tcgacgc      687

```

&lt;210&gt; SEQ ID NO 168

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium xenopi

&lt;400&gt; SEQUENCE: 168

```

cccaggacgt ggaggcgatc acaccgcaga ccttgatcaa catccgccc gtggtggccg      60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggatcag aacaaccgc      120
tgtcggggct caccacaag cggcggtctt cggcgcttgg tccgggcggt ctgtcgcgcg      180

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agcgggccgg gctggaggtc cgtgacgtgc actcgagcca ctacggccgg atgtgcccga	240
tcgaaacccc ggagggcccg aacatcggtt tgatcggtc gctgtcggtg tacgcgcggg	300
tcaacccgta cgggttcatt gagacgcctt accgcaaggt ggtcaacggc gtggtcaccg	360
acgagatcgt gtacctgacc gccgacgagg aggaccgcca tgtggtggcg caggccaact	420
cgccgatcga cgaggatggc cgcttcaccg agccgcgggt gctggtgcgc cgcaagggtg	480
gggaggtcga gtacgtgtcc tcctccgagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcggg gggcaccgcg atgatcccg ttctcgagca cgacgacgcc aaccgcgcgt	600
tgatggggcg gaacatgcag cgccaggccg ttccgttggt gcgtagcgag gcaccgctgg	660
tgggcaccgg gatggaattg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 169

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium xenopi

&lt;400&gt; SEQUENCE: 169

cccaggacgt ggaggcgatc acaccgcaga ccttgatcaa catccgcccc gtggtggccg	60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggatcag aacaacccgc	120
tgctggggct caccacaag cggcggtctt cggcgcttgg tccgggcggg ctgtcgcgcg	180
agcgggccgg gctggaggtc cgtgacgtgc actcgagcca ctacggccgg atgtgcccga	240
tcgaaacccc ggagggcccg aacatcggtt tgatcggtc gctgtcggtg tacgcgcggg	300
tcaacccgta cgggttcatt gagacgcctt accgcaaggt ggtcaacggc gtggtcaccg	360
acgagatcgt gtacctgacc gccgacgagg aggaccgcca tgtggtggcg caggccaact	420
cgccgatcga cgaggatggc cgcttcaccg agccgcgggt gctggtgcgc cgcaagggtg	480
gggaggtcga gtacgtgtcc tcctccgagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcggg gggcaccgcg atgatcccg ttctcgagca cgacgacgcc aaccgcgcgt	600
tgatggggcg gaacatgcag cgccaggccg ttccgttggt gcgtagcgag gcaccgctgg	660
tgggcaccgg gatggaattg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 170

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium xenopi

&lt;400&gt; SEQUENCE: 170

cccaggacgt ggaggcgatc acaccgcaga ccttgatcaa catccgcccc gtggtggccg	60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggatcag aacaacccgc	120
tgctggggct caccacaag cggcggtctt cggcgcttgg tccgggcggg ctgtcgcgcg	180
agcgggccgg gctggaggtc cgtgacgtgc actcgagcca ctacggccgg atgtgcccga	240
tcgaaacccc ggagggcccg aacatcggtt tgatcggtc gctgtcggtg tacgcgcggg	300
tcaacccgta cgggttcatt gagacgcctt accgcaaggt ggtcaacggc gtggtcaccg	360
acgagatcgt gtacctgacc gccgacgagg aggaccgcca tgtggtggcg caggccaact	420
cgccgatcga cgaggatggc cgcttcaccg agccgcgggt gctggtgcgc cgcaagggtg	480
gggaggtcga gtacgtgtcc tcctccgagg tggactacat ggacgtctcg ccgcgccaga	540

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tggtgtcggg	ggccaccgcg	atgatcccgt	tcctcgagca	cgacgacgcc	aaccgcgcgt	600
tgatggggcg	gaacatgcag	cgccaggccg	ttccgttggt	gcgtakcgag	gcaccgctgg	660
tgggcaccgg	gatggaattg	cgcgcggcga	tcgacgcggc	gacgt		705

<210> SEQ ID NO 171  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium xenopi

<400> SEQUENCE: 171

cccaggacgt	ggaggcgatc	acaccgcaga	ccttgatcaa	catccgcccc	gtggtggccg	60
cgatcaagga	gttcttcggc	accagccagc	tctcgagtt	catggatcag	aacaaccgc	120
tgctggggct	caccacaag	cggcggtct	cggcgcttg	tccgggcgg	ctgtcgcgcg	180
agcgggccc	gctggaggtc	cgtgacgtgc	actcgagcca	ctacggccgg	atgtgcccga	240
tcgaaacccc	ggagggcccg	aacatcgggt	tgatcggctc	gctgtcggtg	tacgcgcggg	300
tcaacccgta	cgggttcatt	gagacgcctt	accgcaaggt	ggtcaacggc	gtggtcaccg	360
acgagatcgt	gtacctgacc	gccgacgagg	aggaccgcca	tgtggtggcg	caggccaact	420
cgcgatcga	cgaggatggc	cgcttcaccg	agccgcgggt	gctggtgcgc	cgcaagggtg	480
gggaggtcga	gtacgtgtcc	tcctccgagg	tggactacat	ggacgtctcg	ccgcgccaga	540
tggtgtcggg	ggccaccgcg	atgatcccgt	tcctcgagca	cgacgacgcc	aaccgcgcgt	600
tgatggggcg	gaacatgcag	cgccaggccg	ttccgttggt	gcgtagcgag	gcaccgctgg	660
tgggcaccgg	gatggaattg	cgcgcggcga	tcgacgcggc	gacgt		705

<210> SEQ ID NO 172  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium xenopi

<400> SEQUENCE: 172

cccaggacgt	ggaggcgatc	acaccgcaga	ccttgatcaa	catccgcccc	gtggtggccg	60
cgatcaagga	gttcttcggc	accagccagc	tctcgagtt	catggatcag	aacaaccgc	120
tgctggggct	caccacaag	cggcggtct	cggcgcttg	tccgggcgg	ctgtcgcgcg	180
agcgggccc	gctggaggtc	cgtgacgtgc	actcgagcca	ctacggccgg	atgtgcccga	240
tcgaaacccc	ggagggcccg	aacatcgggt	tgatcggctc	gctgtcggtg	tacgcgcggg	300
tcaacccgta	cgggttcatt	gagacgcctt	accgcaaggt	ggtcaacggc	gtggtcaccg	360
acgagatcgt	gtacctgacc	gccgacgagg	aggaccgcca	tgtggtggcg	caggccaact	420
cgcgatcga	cgaggatggc	cgcttcaccg	agccgcgggt	gctggtgcgc	cgcaagggtg	480
gggaggtcga	gtacgtgtcc	tcctccgagg	tggactacat	ggacgtctcg	ccgcgccaga	540
tggtgtcggg	ggccaccgcg	atgatcccgt	tcctcgagca	cgacgacgcc	aaccgcgcgt	600
tgatggggcg	gaacatgcag	cgccaggccg	ttccgttggt	gcgtagcgag	gcaccgctgg	660
tgggcaccgg	gatggaattg	cgcgcggcga	tcgacgcggc	gacgt		705

<210> SEQ ID NO 173  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium xenopi

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&lt;400&gt; SEQUENCE: 173

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cccaggacgt ggaggcgatc acaccgcaga ccttgatcaa catccgcccc gtggtggccg    60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggatcag aacaaccgc    120
tgtcggggct caccacaag cggcggctct cggcgcttgg tccgggcggg ctgtcgcgcg    180
agcgggcccg gctggaggtc cgtgacgtgc actcgagcca ctacggccgg atgtgccga    240
tcgaaacccc ggagggcccg aacatcggtt tgatcggctc gctgtcggtg tacgcgcggg    300
tcaacccgta cgggttcatt gagacgcctt accgcaaggt ggtcaacggc gtggtcaccg    360
acgagatcgt gtacctgacc gccgacgagg aggaccgcca tgtggtggcg caggccaact    420
cgccgatcga cgaggatggc cgcttcaccg agccgcgggt gctggtgcgc cgcaagggtg    480
gggaggtcga gtacgtgtcc tcctccgagg tggactacat ggacgtctcg ccgcgccaga    540
tggtgtcggg ggccaccgcg atgatcccgt tcctcgagca cgacgacgcc aaccgcgcgt    600
tgatggggcg gaacatgcag cgccaggccg ttccgttggt gcgtagcgag gcaccgctgg    660
tgggcaccgg gatggaattg cgcgcggcga tcgacgcggc gacgt                    705

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&lt;210&gt; SEQ ID NO 174

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium xenopi

&lt;400&gt; SEQUENCE: 174

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cccaggacgt ggaggcgatc acaccgcaga ccttgatcaa catccgcccc gtggtggccg    60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggatcag aacaaccgc    120
tgtcggggct caccacaag cggcggctct cggcgcttgg tccgggcggg ctgtcgcgcg    180
agcgggcccg gctggaggtc cgtgacgtgc actcgagcca ctacggccgg atgtgccga    240
tcgaaacccc ggagggcccg aacatcggtt tgatcggctc gctgtcggtg tacgcgcggg    300
tcaacccgta cgggttcatt gagacgcctt accgcaaggt ggtcaacggc gtggtcaccg    360
acgagatcgt gtacctgacc gccgacgagg aggaccgcca tgtggtggcg caggccaact    420
cgccgatcga cgaggatggc cgcttcaccg agccgcgggt gctggtgcgc cgcaagggtg    480
gggaggtcga gtacgtgtcc tcctccgagg tggactacat ggacgtctcg ccgcgccaga    540
tggtgtcggg ggccaccgcg atgatcccgt tcctcgagca cgacgacgcc aaccgcgcgt    600
tgatggggcg gaacatgcag cgccaggccg ttccgttggt gcgtagcgag gcaccgctgg    660
tgggcaccgg gatggaattg cgcgcggcga tcgacgcggc gacgt                    705

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&lt;210&gt; SEQ ID NO 175

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium xenopi

&lt;400&gt; SEQUENCE: 175

```

cccaggacgt ggaggcgatc acaccgcaga ccttgatcaa catccgcccc gtggtggccg    60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggatcag aacaaccgc    120
tgtcggggct caccacaag cggcggctct cggcgcttgg tccgggcggg ctgtcgcgcg    180
agcgggcccg gctggaggtc cgtgacgtgc actcgagcca ctacggccgg atgtgccga    240
tcgaaacccc ggagggcccg aacatcggtt tgatcggctc gctgtcggtg tacgcgcggg    300

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tcaaccgta cgggttcatt gagacgcctt accgcaaggt ggtcaacggc gtggtcaccg	360
acgagatcgt gtacctgacc gccgacgagg aggaccgcca tgtggtggcg caggccaact	420
cgccgatcga cgaggatggc cgcttcaccg agccgcgggt gctggtgcgc cgcaaggggtg	480
gggaggtcga gtacgtgtcc tcctccgagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcgggt ggccaccgcg atgatcccgt tcctcgagca cgacgacgcc aaccgcgcgt	600
tgatggggcg gaacatgcag cgccaggccg ttccgttggt gcgtagcgag gcaccgctgg	660
tgggcaccgg gatggaattg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 176  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium xenopi

<400> SEQUENCE: 176

cccaggacgt ggaggcgatc acaccgcaga ccttgatcaa catccgcccc gtggtggccg	60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggatcag aacaaccgc	120
tgtcggggct caccacaag cggcggtctt cggcgcttgg tccgggcgggt ctgtcgcgcg	180
agcgggcccgt gctggaggtc cgtgacgtgc actcgagcca ctacggccgg atgtgcccga	240
tcgaaacccc ggaggggccc aacatcggtt tgatcggctc gctgtcgggtg tacgcgcggg	300
tcaaccgta cgggttcatt gagacgcctt accgcaaggt ggtcaacggc gtggtcaccg	360
acgagatcgt gtacctgacc gccgacgagg aggaccgcca tgtggtggcg caggccaact	420
cgccgatcga cgaggatggc cgcttcaccg agccgcgggt gctggtgcgc cgcaaggggtg	480
gggaggtcga gtacgtgtcc tcctccgagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcgggt ggccaccgcg atgatcccgt tcctcgagca cgacgacgcc aaccgcgcgt	600
tgatggggcg gaacatgcag cgccaggccg ttccgttggt gcgtagcgag gcaccgctgg	660
tgggcaccgg gatggaattg cgcgcggcga tcgacgcggc gacgt	705

<210> SEQ ID NO 177  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Mycobacterium xenopi

<400> SEQUENCE: 177

cccaggacgt ggaggcgatc acaccgcaga ccttgatcaa catccgcccc gtggtggccg	60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggatcag aacaaccgc	120
tgtcggggct caccacaag cggcggtctt cggcgcttgg tccgggcgggt ctgtcgcgcg	180
agcgggcccgt gctggaggtc cgtgacgtgc actcgagcca ctacggccgg atgtgcccga	240
tcgaaacccc ggaggggccc aacatcggtt tgatcggctc gctgtcgggtg tacgcgcggg	300
tcaaccgta cgggttcatt gagacgcctt accgcaaggt ggtcaacggc gtggtcaccg	360
acgagatcgt gtacctgacc gccgacgagg aggaccgcca tgtggtggcg caggccaact	420
cgccgatcga cgaggatggc cgcttcaccg agccgcgggt gctggtgcgc cgcaaggggtg	480
gggaggtcga gtacgtgtcc tcctccgagg tggactacat ggacgtctcg ccgcgccaga	540
tggtgtcgggt ggccaccgcg atgatcccgt tcctcgagca cgacgacgcc aaccgcgcgt	600
tgatggggcg gaacatgcag cgccaggccg ttccgttggt gcgtagcgag gcaccgctgg	660

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tgggcaccgg gatggaattg cgcgcggcga tcgacgcggc gacgt 705

<210> SEQ ID NO 178  
<211> LENGTH: 705  
<212> TYPE: DNA  
<213> ORGANISM: Mycobacterium xenopi

<400> SEQUENCE: 178

cccaggacgt ggaggcgatc acaccgcaga ccttgatcaa catccgcccc gtggtggccg 60  
cgatcaagga gttcttcggc accagccagc tctcgcagtt catggatcag aacaaccgc 120  
tgtcggggct caccacaag cggcggctct cggcgcttgg tccgggcggg ctgtcgcgcg 180  
agcgggccgg gctggaggtc cgtgacgtgc actcgagcca ctacggccgg atgtgcccg 240  
tcgaaacccc ggagggcccg aacatcggtt tgatcggtct gctgtcggtg tacgcgcggg 300  
tcaacccgta cgggttcatt gagacgcctt accgcaaggt ggtcaacggc gtggtcaccg 360  
acgagatcgt gtacctgacc gccgacgagg aggaccgcca tgtggtggcg caggccaact 420  
cgccgatcga cgaggatggc cgcttcaccg agccgcgggt gctggtgcgc cgcaagggtg 480  
gggaggtcga gtacgtgtcc tcctccgagg tggactacat ggacgtctcg ccgcgccaga 540  
tggtgtcggg ggccaccgcg atgatcccg tctcgcagca cgacgacgcc aaccgcgcgt 600  
tgatgggcgc gaacatgcag cgccaggccg ttccgttggt gcgtagcgag gcaccgctgg 660  
tgggcaccgg gatggaattg cgcgcggcga tcgacgcggc gacgt 705

<210> SEQ ID NO 179  
<211> LENGTH: 705  
<212> TYPE: DNA  
<213> ORGANISM: Mycobacterium xenopi

<400> SEQUENCE: 179

cccaggacgt ggaggcgatc acaccgcaga ccttgatcaa catccgcccc gtggtggccg 60  
cgatcaagga gttcttcggc accagccagc tctcgcagtt catggatcag aacaaccgc 120  
tgtcggggct caccacaag cggcggctct cggcgcttgg tccgggcggg ctgtcgcgcg 180  
agcgggccgg gctggaggtc cgtgacgtgc actcgagcca ctacggccgg atgtgcccg 240  
tcgaaacccc ggagggcccg aacatcggtt tgatcggtct gctgtcggtg tacgcgcggg 300  
tcaacccgta cgggttcatt gagacgcctt accgcaaggt ggtcaacggc gtggtcaccg 360  
acgagatcgt gtacctgacc gccgacgagg aggaccgcca tgtggtggcg caggccaact 420  
cgccgatcga cgaggatggc cgcttcaccg agccgcgggt gctggtgcgc cgcaagggtg 480  
gggaggtcga gtacgtgtcc tcctccgagg tggactacat ggacgtctcg ccgcgccaga 540  
tggtgtcggg ggccaccgcg atgatcccg tctcgcagca cgacgacgcc aaccgcgcgt 600  
tgatgggcgc gaacatgcag cgccaggccg ttccgttggt gcgtagcgag gcaccgctgg 660  
tgggcaccgg gatggaattg cgcgcggcga tcgacgcggc gacgt 705

<210> SEQ ID NO 180  
<211> LENGTH: 705  
<212> TYPE: DNA  
<213> ORGANISM: Mycobacterium xenopi

<400> SEQUENCE: 180

cccaggacgt ggaggcgatc acaccgcaga ccttgatcaa catccgcccc gtggtggccg 60

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cgatcaagga gttcttcggc accagccagc tctcgagtt catggatcag aacaaccgc	120
tgtcggggct caccacaag cggcggtctt cggcgcttgg tccggcggt ctgtcgcgcg	180
agcgggccgg gctggaggtc cgtgacgtgc actcgagcca ctacggccgg atgtgcccga	240
tcgaaacccc ggaggcccg aacatcggtt tgatcggttc gctgtcggtg tacgcgcggg	300
tcaaccgta cgggttcatt gagacgctt accgcaaggt ggtcaacggc gtggtcaccg	360
acgagatcgt gtacctgacc gccgacgagg aggaccgcca tgtggtggcg caggccaact	420
cgccgatcga cgaggatggc cgcttcaccg agccgcgggt gctggtgcgc cgcaagggtg	480
gggaggtcga gtacgtgtcc tcctccgagg tggactacat ggacgtctcg ccgcgccaga	540
tgggtgcggt ggccaccgcg atgatcccg tctcagagca cgacgacgcc aaccgcgcgt	600
tgatgggcgc gaacatgcag cgccaggcgg ttccgctggt gcgtagcgag gcaccgctgg	660
tgggcaccgg gatggaattg cgcgcggcga tcgacgcggc gacgt	705

&lt;210&gt; SEQ ID NO 181

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Mycobacterium sp. unique MAC#4

&lt;400&gt; SEQUENCE: 181

cccaggacgt ggaggcgatc acaccgcaga cgctgatcaa catccgtccg gtcgtcgcg	60
cgatcaagga gttcttcggc accagccagc tctcgagtt catggaccag aacaaccgc	120
tgtcggggct gaccacaag cggcgcttgg tccggcggt ctgtcccgtg	180
agcgggccgg cctcgaggtc cgcgacgtgc acccgctcga ctacggccgc atgtgcccga	240
tcgagacccc ggagggtccg aacatcggtc tgatcggttc gctgtcggtg tacgcgaggg	300
tcaaccggtt cggcttcacg gagacgctt accgcaaggt ggtcgacggt gtggtcagcg	360
acgagatcgt gtacctgacc gccgacgagg aggaccgcca cgtggtggcg caggccaact	420
cgccgatcga cgccgacggc cgggttcgtc agggccgcgt cctggtccgc cgcaaggcgg	480
gcgaggtcga gtacgtgccc tcgtccgagg tggactacat ggacgtctcg ccgcgccaga	540
tgggtgcggt ggccaccgcc atgatcccg tctcagagca cgacgacgcc aaccgtgccc	600
tgatgggcgc caacatgcag cgccaggcgg ttccgctggt gcgcagcgag gcgccgctgg	660
tgggcaccgg catggagctg cgcgcggcga tcgacgcggc gacgt	705

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1-19. (canceled)

20. A polynucleotide probe or primer that hybridizes under stringent hybridization conditions to a mycobacterial rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6 and 9 or its complement without hybridizing to the *M. tuberculosis* sequence of SEQ ID NO: 1 or its complement, wherein said stringent hybridization conditions comprise 5×SSPE and a temperature of 25-30° C.

21. The polynucleotide of claim 20 that is a probe.

22. The polynucleotide of claim 21, wherein a central position of the probe aligns with one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6 and 9 which differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.

23. The sequence-specific polynucleotide of claim 20 that is a primer.

24. The polynucleotide of claim 23, wherein the 3' end of the primer aligns with one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6 and 9 which differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.

25. The polynucleotide of claim 20 that hybridizes under stringent hybridization conditions to at least 100 contiguous bases of a mycobacterial rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6 and 9 or its complement without hybridizing to the *M. tuberculosis* sequence of SEQ ID NO:1 or its complement, wherein said stringent hybridization conditions comprise 5×SSPE and a temperature of 25-30° C.

26. A polynucleotide probe or primer that hybridizes under stringent hybridization conditions to at least 100 contiguous bases of a mycobacterial rpoB sequence selected

from the group consisting of SEQ ID NOS: 8 and 10 or its complement without hybridizing to the *M. tuberculosis* sequence of SEQ ID NO:1 or its complement, wherein said stringent hybridization conditions comprise 5×SSPE and a temperature of 25-30° C.

27. The polynucleotide of claim 26, wherein the polynucleotide is a probe, and wherein a central position of the probe aligns with one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 8 and 10 which

differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.

28. The polynucleotide of claim 26, wherein the polynucleotide is a primer, and wherein the 3' end of the primer aligns with one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 8 and 10 which differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.

\* \* \* \* \*