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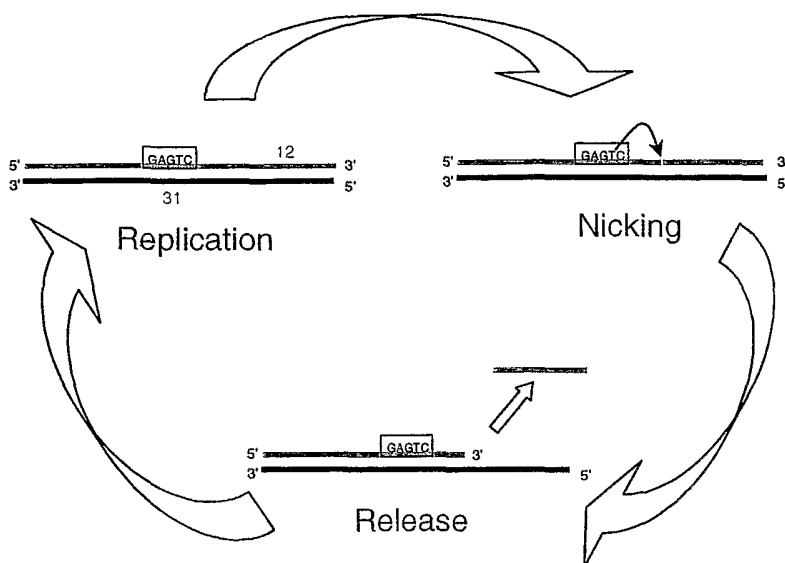
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(54) Title: ORGANISM FINGERPRINTING USING NICKING AGENTS



(57) Abstract: A sample of nucleic acid that is characteristic of a particular source, e.g., a bacterium, can be analyzed to determine whether that particular sample is from a particular source. The analysis protocol subjects the sample to a nicking reaction to produce a family of nicked fragments. In certain embodiments, the nicking reaction is performed in the presence of a polymerase and nucleoside triphosphates to amplify nicked fragments or portions thereof. The nicked fragments or portions thereof may be analyzed to determine the source of the nucleic acid sample.

WO 2004/067765 A2

ORGANISM FINGERPRINTING USING NICKING AGENTS

BACKGROUND OF THE INVENTION

Field of the Invention

The present invention is generally directed to compositions and
5 methods for identifying any type of organism or individual, where the invention
is based on creating and analyzing nucleotide sequence information
characteristic of nucleic acids present in the organism or individual.

Description of the Related Art

Nosocomial (hospital-based) infections have become one of the
10 most serious problems in infectious disease. *Staphylococcus aureus* is
exceeded only by *Escherichia coli* as a leading cause of nosocomial infections.
See, for example, Brumfitt, W. et al., *Drugs Exptl. Clin. Res.* 16:205-214 (1990).
One type of *S. aureus*, methicillin-resistant *S. aureus*, is of a particular interest
because it is resistant to all penicillin-based antibiotics.

15 Patients in the intensive care unit are very susceptible to bacterial
infections, due to interventions such as respiratory tubes and indwelling
catheters. *E. coli* and *S. aureus*, if introduced into surgical wounds, the blood
stream or the urinary tract, cause serious, sometimes life-threatening infections.
There is no easy solution to the problem, but a partial solution in most
20 "nosocomial outbreaks" is simply identifying the source of the infection. That is,
is the infectious agent coming from a common source (e.g., an infected nurse
or doctor, or an instrument such as a respirator) or is there some other reason
for the sudden emergence of a single type of bacterial infection.

Hospital laboratories can quickly identify the infectious agent (e.g.,
25 *S. aureus*), but they do not have the ability to determine whether a single strain
of the organism is causing the outbreak (and therefore a possible common
source) or if several different strains are responsible for the outbreak. At the
present time most outbreaks can only be characterized in retrospect, since the

outbreak is over before the bacterial isolates can be identified. For example, isolates can be identified in a matter of 1 or 2 days, but the strain identification usually takes weeks or even months, because the strains are still analyzed by slow culture-based methods which are labor intensive.

5 Current methods of strain typing bacteria include phage typing, plasmid analysis, and antibiotic susceptibility (biotyping). See, for example, Zuccarelli, A. et al.: *J. Clin. Microbiol.* 28:97-102, 1990; Tokue, Y. et al., *Tohokin J. Exp. Med.* 163:31-37, 1991; Coia, J. et al., *J. Med. Microbiol.* 31:125-132, 1990; Pennington, T. et al., *J. Clin. Microbiol.* 29:390-392, 1991;
10 Tveten, Y. et al., *J. Clin. Microbiol.* 29:110-1105, 1991; Fluit, A. et al., *Eur. J. Clin. Microbiol. Infect. Dis.* 9:605-608, 1990; Thomson-Carter, F. et al., *J. Gen. Microbiol.* 135:2093-2097, 1989; and Preheim, L. et al., *Eur. J. Clin. Microbiol. Infect. Dis.* 10:428-436, 1991. These methods, currently used by the Centers for Disease Control, are laborious, time consuming and often yield inconclusive
15 results.

 A comprehensive understanding of biological systems requires knowledge of the chemical composition of cellular systems, and this understanding is becoming increasingly important in elucidating disease mechanisms (Ban, E., *Anal. Chem.* 70:308A, 1998). Elucidating disease
20 mechanisms requires diagnostic tools for direct DNA sequencing, DNA separation and isolation, and mRNA profiling as well as numerous protein analysis techniques. Analytical methods in this research field must therefore be rapid, accurate, sensitive and robust.

 Interspersed repetitive DNA sequence elements have been
25 characterized extensively in eucaryotes although their function still remains largely unknown. The conserved nature and interspersed distribution of these repetitive sequences have been exploited to amplify unique sequences between repetitive sequences by the polymerase chain reaction. Additionally, species-specific repetitive DNA elements have been used to differentiate
30 between closely related murine species.

Prokaryotic genomes are much smaller than the genomes of mammalian species (approximately 10^6 versus 10^9 base pairs of DNA, respectively). Since these smaller prokaryotic genomes are maintained through selective pressures for rapid DNA replication and cell reproduction the non-coding repetitive DNA should be kept to a minimum unless maintained by other selective forces. For the most part prokaryotes have a high density of transcribed sequences. Nevertheless, families of short intergenic repeated sequences occur in bacteria.

The presence of repetitive sequences has been demonstrated in many different bacterial species. Reports of novel repeated sequences in the eubacterial genera, *Escherichia*, *Salmonella*, *Deinococcus*, *Calothrix*, and *Neisseria*, and the fungi, *Candida albicans* and *Pneumocystis carinii*, illustrate the presence of dispersed extragenic repetitive sequences in many organisms. One such family of repetitive DNA sequences in eubacteria is the Repetitive Extragenic Palindromic (REP) elements. The consensus REP sequence for this family includes a 38-mer sequence containing six totally degenerate positions, including a 5 bp variable loop between each side of the conserved stem of the palindrome.

Previous studies have used repeated rRNA genes as probes in Southern blots to detect restriction fragment length polymorphisms (RFLPs) between strains. Repeated tRNA genes have been used as consensus primer binding sites to directly amplify DNA fragments of different sizes by PCR amplification of different strains. Limitations of both techniques include the use of radioisotope and time-intensive methods such as Southern blotting and polyacrylamide gel electrophoresis to clearly distinguish subtle differences in the sizes of the DNA fragments generated. The latter technique could only distinguish organisms at the species and genus level. The tDNA-PCR fingerprints are generally invariant between strains of a given species and between related species. Other previous studies include the use of species-specific repetitive DNA elements as primer-binding sites for PCR-based bacterial species identification. Though such methods allow species

identification by PCR with picogram amounts of DNA, only single PCR products are generated which precludes the generation of strain-specific genomic fingerprints.

Accordingly, there exists a long-felt need for the development of rapid bacterial strain typing technologies. The present invention fulfills this and other related needs.

BRIEF SUMMARY OF THE INVENTION

The present invention is generally directed to compositions and methods for identifying any type of organism or individual using nucleic acid-based fingerprinting. The method relies on the creation of a family of nucleic acid or oligonucleotide fragments formed by action of nicking agents on a nucleic acid sample. In a preferred embodiment, the nicking reaction is preformed in the presence of a polymerase and one or more (preferably all four of the natural) deoxyribonucleoside triphosphates. Under this preferred embodiment, the nucleic acid or oligonucleotide fragments or portions thereof are created in higher concentration and are therefore more amenable to characterization. According to this method, a family, also referred to herein as a pattern, of nucleic acid or oligonucleotide fragments of known characteristics (e.g., mass/charge ratios) are produced, which identify unambiguously an organism or individual. The readout of the fingerprinting assay is preferably matrix-assisted-laser-desorption ionization (MALDI) or liquid chromatography time-of-flight (LC-TOF) mass spectrometry, however other characterization methods may be used as well.

In a preferred aspect, a method has been devised according to the present invention in which a set of oligonucleotides are linearly amplified from template structures pre-existing in genomic DNA that can be used to initiate their own exponential amplification. By utilizing adjacent, close, nicking agent recognition sequences that occur infrequently in genomic DNA, short oligonucleotides are linearly amplified in the presence of a nicking agent that recognizes the nicking agent recognition sequences. The products from the

linear amplification, referred to herein as "initiating oligonucleotide" or "initiator," can then be coupled to a method for exponentially amplifying the initiating oligonucleotides in true chain reactions. The linear and the exponential amplification reactions can be made into a homogenous assay in which 10^8 -
5 10^9 -fold amplification can be achieved in as little as 3 minutes. In certain embodiments, the linear amplification reaction, the exponential amplification, or both may be performed under isothermal conditions (e.g., at 60°C).

In certain embodiments, the exponential or string reaction is composed of two reaction components: a first amplification reaction that
10 replicates the initiating oligonucleotide and a second amplification reaction that replicates the complement of the initiating oligonucleotide. In the exponential reaction, two template oligonucleotides are used, a first template that comprises a sequence complementary to the initiating oligonucleotide, and a second template that comprises a sequence complementary to the complement of the
15 initiating oligonucleotide. Since the first template may anneal to the complement of the initiating oligonucleotide and be used as a template for amplifying the initiating oligonucleotide, and the second template may anneal to the initiating oligonucleotide and be used as a template for amplifying the complement of the initiating oligonucleotide, once the reaction is initiated, a
20 chain reaction ensues. The reaction has the peculiar property that a very high level of stringency is required in order to trigger the chain amplification.

A useful example is taken from *E. coli* K12 in which 55 unique oligonucleotides can be generated from genomic DNA without the use of pre-synthesized probes or primers. The read-out is ideally done by mass
25 spectrometry (LC-TOF or MALDI) but can also be accomplished by other means, e.g., using real-time fluorimetry or "self-amplifying arrays". Foreknowledge of the sequence of the individual or organism is not necessary as it is possible to generate the fragments *de novo* from genomic DNA. The methods described here permit the creation an assay panel of diagnostic
30 oligonucleotides that can identify any organism or individual.

The present invention is advantageous over previous methods for identifying bacterial species. Although previous studies have demonstrated that species-specific repetitive DNA elements can be used as primer-binding sites for PCR-based bacterial species identification, these methods only generated single PCR products in a single species. The present invention provides a novel approach to using nicking agent recognition sites within a genomic DNA to directly fingerprint bacterial (as well as viral, fungal, in fact, all prokaryotic and eukaryotic genomes). The unique patterns of oligonucleotides generated by a nicking agent recognition sequence identify different bacterial species and strains. In addition, the present invention may produce polymorphic oligonucleotide fragments that contain genetic variations (e.g., single nucleotide polymorphisms, deletions, insertions, variable repeats) from eukaryotic genomes. The characterization of these polymorphic oligonucleotide fragments enables the identification of individual organism from which a nucleic acid sample is obtained.

In one aspect, the present invention provides a method comprising:

- a) providing a nucleic acid sample;
- b) treating the nucleic acid sample with components under nicking conditions, where the components comprise:
 - i) a nicking agent;and the conditions cause the nicking agent to nick the nucleic acid sample to thereby produce a family of initiating oligonucleotide fragments;
- c) subjecting one or more members of the family of initiating oligonucleotide fragments to a characterization process to thereby provide results; and
- d) identifying a source for the nucleic acid sample based on the results of the characterization process.

Optionally, the components of the above method further comprise:

- ii) a polymerase; and
- iii) a deoxyribonucleoside triphosphate.

Optionally, the components of the above methods may further comprise:

iv) a template oligonucleotide comprising from 3' to 5':

(A) a first nucleotide sequence that is at least
5 substantially complementary to a nucleotide sequence present in one or more members of the family of initiating oligonucleotide fragments;

(B) a sequence of one strand of a nicking agent recognition sequence; and

(C) a second nucleotide sequence.
10 Optionally, the template is immobilized.

In certain embodiments, sequence iv)(B) is a sequence of an antisense strand of the nicking agent recognition sequence, and sequence iv)(A) is at least substantially identical to sequence iv)(C).

Optionally, the components of the above methods may further
15 comprising

v) a second template oligonucleotide, comprising, from 3' to 5':

(A) a first nucleotide sequence that is at least substantially identical to a nucleotide sequence present in the one or more
20 members of the family of initiating oligonucleotide fragments;

(B) a sequence of a sense strand of the nicking agent recognition sequence; and

(C) a second nucleotide sequence.
wherein sequence iv)(B) is a sequence of a sense strand of the
25 nicking agent recognition sequence.

Optionally, the 3' terminus of template iv), the 3' termini of template v), or both are blocked. Optionally, sequence iv)(A) is exactly identical to sequence iv)(C). Also optionally, template iv), template v), or both may be immobilized.

30 Optionally, the components may further comprise a restriction endonuclease.

Optionally, the one or more members of the family of initiating oligonucleotide fragments are 6-16 nucleotides in length.

In certain embodiments, the nicking agent is a nicking endonuclease, such as N.BstNB I or N.Alw I.

5 In certain embodiments, the polymerase is *exo*⁻ Vent polymerase, Bst polymerase, or 9°NmTM polymerase.

In certain embodiments, the characterization process is performed at least partially by a technique selected from the group consisting of luminescence spectroscopy or spectrometry, fluorescence spectroscopy or
10 spectrometry, mass spectrometry (such as MALDI or LC-TOF), liquid chromatography, fluorescence polarization, and electrophoresis.

In another aspect, the present invention provides a template oligonucleotide for amplifying a portion of a target nucleic acid, wherein

(i) the portion of the target is 6-16 nucleotides in length and
15 flanked by

(A) a sequence of one strand of a first nicking enzyme recognition sequence, and

(B) a sequence of one strand of a second nicking enzyme recognition sequence, or a sequence of one strand of a restriction
20 enzyme recognition sequence, and

(ii) the template oligonucleotide comprising from 3' to 5':

(A) a first nucleotide sequence that is at least substantially complementary to the portion of the target,

(B) a sequence of an antisense strand of a third nicking
25 enzyme recognition sequence, and

(C) a second nucleotide sequence that is at least substantially identical to the first nucleotide sequence.

Optionally, the first and third nicking enzyme recognition sequences are identical to each other. Optionally, the first, second and third
30 nicking enzyme recognition sequences are identical to each other. In certain

embodiments, some or all of the nicking enzyme recognition sequences are recognizable by N.BstNB I.

Optionally, the 3' terminus of the template oligonucleotide is blocked. Optionally, the 3' terminus of the template oligonucleotide is
5 immobilized.

In certain embodiments, the portion of the target is selected from the products listed in Tables 1, 2, 4, 5, and 9. Optionally, the portion of the target comprises a genetic variation (e.g., single nucleotide polymorphism).

In another aspect, the present invention provides a composition
10 for amplifying a portion of a target nucleic acid, comprising a first template oligonucleotide and a second template oligonucleotide, wherein

(i) the portion of the target is 6-16 nucleotides in length and flanked by

(A) a sequence of one strand of a first nicking enzyme
15 recognition sequence, and

(B) a sequence of one strand of a second nicking enzyme recognition sequence, or a sequence of one strand of a restriction enzyme recognition sequence,

(ii) the first template oligonucleotide comprises from 5' to 3':
20

(A) a first nucleotide sequence,

(B) a sequence of a sense strand of a third nicking agent recognition sequence, and

C) a second nucleotide sequence that is at least substantially complementary to the portion of the target, and

25 (iii) the second template oligonucleotide comprises from 5' to 3':

(A) a first nucleotide sequence,

(B) a sequence of a sense strand of a fourth nicking agent recognition sequence, and

30 (C) a second nucleotide sequence that is at least substantially identical to the portion of the target.

Optionally, the first, third and fourth nicking enzyme recognition sequences are identical to each other. Optionally, the first, second, third and fourth nicking enzyme recognition sequences are identical to each other. In certain embodiments, some or all of the nicking enzyme recognition sequence
5 are recognizable by N.BstNB I.

Optionally, the 3' termini of the first and second templates are blocked. Optionally, the 3' terminus of the first, the 3' terminus of the second, or both termini are immobilized.

Optionally, the portion of the target is selected from the products
10 listed in Tables 1, 2, 4, 5 and 9. Optionally, the portion of the target comprises a genetic variation (e.g., single nucleotide polymorphism).

In another aspect, the present invention provides a composition comprising:

- (1) a nicking agent, and
- 15 (2) at least one fragment selected from the products listed in Tables 1, 2, 4, 5 and 9,

wherein the at least one fragment is produced at least partially by action of the nicking agent.

Optionally, the nicking agent is N.BstNB I or N.Alw I.

20 Optionally, the composition may further comprise a restriction endonuclease selected from Bcl I, Bsa BI, Bsm I, Bsr I and Bsr D1, wherein the at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 50 fragments are selected from the products listed in Table 9.

In another aspect, the present invention provides a kit for
25 identifying the source of a nucleic acid sample, comprising one or two template oligonucleotides as described above for amplifying a portion of a genomic DNA of an organism suspected to be the source of the nucleic acid sample, wherein the portion of the genomic DNA is 6-16 nucleotides in length and flanked by

- (A) a sequence of one strand of a first nicking enzyme
30 recognition sequence, and

(B) a sequence of one strand of a second nicking enzyme recognition sequence, or a sequence of one strand of a restriction enzyme recognition sequence.

Optionally, the kit may further comprise a nicking enzyme that
5 recognizes one or more nicking enzyme recognition sequences in the template(s).

In certain embodiments, the above kits may further comprise a DNA polymerase and/or one or more deoxyribonucleoside triphosphate.

Optionally, the portion of the genomic DNA is selected from the
10 products listed in Tables 1, 2, 4, 5 and 9. Optionally, the portion of the genomic DNA comprises a single nucleotide polymorphism.

In another aspect, the present invention provides an array, comprising

- (a) a substrate having a plurality of distinct areas; and
- 15 (b) the template oligonucleotide of claim A1 or the composition of claim B1 immobilized to at least one of the plurality of distinct areas.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 schematically shows the cycle of the synthesis and release of an amplified short oligonucleotide. On the upper strand is indicated
20 the recognition site for the enzyme N.BstNB I (5'-GAGTC-3') and the specific nicking site four bases downstream on this strand. The oligonucleotide produced is indicated in blue, the primer in green and the template in red. The lengths of the exemplary template and amplified oligonucleotides are shown in the upper left drawing.

25 Figure 2 is a diagram of the reaction scheme for the exponential amplification of oligonucleotides. The segments in red represent the sequence complement of the oligonucleotide sequence to be amplified, the signal sequence (shown in blue). The amplification template, τ , consists of two copies of the signal complement flanking the nicking enzyme recognition site shown as
30 a light blue box, and a spacer sequence, shown as a green segment. The

signal oligonucleotide (labeled σ) is produced in the linear amplification cycle for each amplification template created.

Figure 3 is a schematic representation of a template oligonucleotide used in a replicator type of amplification reactions.

5 Figures 4a and 4b show the time of flight spectra of the multiplexed amplification reaction in the presence of short oligonucleotides generated from the genomic DNA of the E. coli strains K12 and O157, respectively.

10 Figure 5a and 5b show the MALDI spectra of the multiplexed amplification reaction in the presence of short oligonucleotides generated from the genomic DNA of the E. coli strains K12 and O157, respectively.

15 Figure 6 shows real time fluorescence detection of the oligonucleotide amplification by an MJ Opticon I. The time of amplification is plotted on the X axis versus accumulated fluorescence on the Y axis. Each curve from left to right represents a serial dilution of 3-fold. The starting concentration of the trigger was 0.01 picomoles/microliter and the last dilution (far right curve (bottom curve on figure)) was 1.9×10^{-7} picomoles/microliter. This represents a dilution range of about 20,000-fold (3^9).

20 Figure 7 is a schematic diagram showing the ping-pong amplification reaction cycle.

Figure 8 is a schematic diagram showing the application of the ping-pong amplification reaction cycle in discriminating genetic variations.

DETAILED DESCRIPTION OF THE INVENTION

A. Overview

25 The present invention provides methods for identifying any type of organism or individual using polynucleotide-based fingerprinting. The method relies on the creation of a family of polynucleotides formed by action of nicking agents on a nucleic acid sample. For instance, a nucleic acid sample may be nicked by a nicking agent to produce various nicked nucleic acid fragments.

The resulting nicked fragments are then characterized to determine the identity of the organism from which the nucleic acid sample was obtained or derived. Alternatively, a nucleic acid sample may be nicked by a nicking agent in the presence of a DNA polymerase. The presence of the DNA polymerase allows
5 linear amplification of the nicked fragments or portions thereof, thus facilitates the characterization of such fragments. These fragments may be further amplified by coupling the linear amplification reaction with an exponential amplification reaction. Such an exponential amplification greatly increases the speed and the sensitivity of the identification methods.

10 The nicked fragments may be characterized to determine the presence or absence of a particular fragment unique, or characteristic, to a specific species, subspecies, or strain. The conclusion made from the presence or absence of that particular fragment may be further verified by determining the presence or absence of one or more other fragments also
15 unique, or characteristic, to the specific species, subspecies, or strain. In certain embodiments, the presence or absence of particular fragments in a nicking reaction mixture of a nucleic acid sample need not be determined. Rather, the pattern formed by the resulting nicked fragments (*e.g.*, a mass spectrum of the nicked fragments) is characterized and compared with a
20 standard pattern known for a particular species, subspecies, or strain. The standard pattern may be generated by performing the nicking reaction with a nucleic acid sample from the particular species, subspecies or strain under conditions identical to that of the nucleic acid sample. Alternative, the standard pattern may be generated based on the known nucleic acid sequence of the
25 particular species, subspecies, or strain.

 In certain embodiments, the present invention uses the presence of closely located nicking agent recognition sequences. In the presence of a nicking agent that recognizes such sequences, short oligonucleotide fragments (*e.g.*, 6-16 nucleotides long) may be generated or amplified. Short
30 oligonucleotide fragments may also be generated or amplified by the use of a nicking agent in combination with a restriction enzyme if one or more

recognition sequences of the nicking agent are located closely to the recognition sequence(s) of the restriction enzyme. The resulting short oligonucleotide fragments may be easily separated from other larger fragments. Such separation simplifies the pattern generated from the characterization of the nucleic acid fragments in a nicking reaction mixture. In addition, as will be described in detail below, short oligonucleotide fragments may easily be exponentially amplified to increase the speed and sensitivity of the present methods. Short oligonucleotide fragments are also more suitable to certain characterization technologies, such as LC-TOF and MALDI.

10 In some embodiments, the nicked fragments may also contain genetic variations useful to distinguish among individual organisms.

B. Definitions

The following conventions and definition of terms as used herein may be helpful to an understanding of the detailed description of the invention. Additional definitions may be found throughout the description of the present invention.

"Fingerprinting" refers to the identification of a source of nucleic acid based on analysis of the nucleic acid according to the methods described herein. For instance, fingerprinting may be applied to the identification of a bacterial strain from its characteristic pattern of oligonucleotides produced by action of a nicking agent (*e.g.*, N.BstNB I). This characteristic pattern is the strain's genomic "fingerprint", which is determined by the sequence of the strain's genomic DNA.

The terms "3'" and "5'" are used herein to describe the location of a particular site within a single strand of nucleic acid. When a location in a nucleic acid is "3' to" or "3' of" a reference nucleotide or a reference nucleotide sequence, this means that the location is between the 3' terminus of the reference nucleotide or the reference nucleotide sequence and the 3' hydroxyl of that strand of the nucleic acid. Likewise, when a location in a nucleic acid is "5' to" or "5' of" a reference nucleotide or a reference nucleotide sequence, this means that it is between the 5' terminus of the reference nucleotide or the

reference nucleotide sequence and the 5' phosphate of that strand of the nucleic acid. Further, when a nucleotide sequence is "directly 3' to" or "directly 3' of" a reference nucleotide or a reference nucleotide sequence, this means that the nucleotide sequence is immediately next to the 3' terminus of the reference nucleotide or the reference nucleotide sequence. Similarly, when a nucleotide sequence is "directly 5' to" or "directly 5' of" a reference nucleotide or a reference nucleotide sequence, this means that the nucleotide sequence is immediately next to the 5' terminus of the reference nucleotide or the reference nucleotide sequence.

10 As used herein, "nicking" refers to the cleavage of only one strand of a fully double-stranded nucleic acid molecule or a double-stranded portion of a partially double-stranded nucleic acid molecule at a specific position relative to a nucleotide sequence that is recognized by the enzyme that performs the nicking. The specific position where the nucleic acid is nicked is referred to as the "nicking site" (NS).

A "nicking agent" (NA) is an enzyme that recognizes a particular nucleotide sequence of a completely or partially double-stranded nucleic acid molecule and cleaves only one strand of the nucleic acid molecule at a specific position relative to the recognition sequence. Nicking agents include, but are not limited to, a nicking endonuclease (e.g., N.BstNB I) and a restriction endonuclease (e.g., Hinc II) when a completely or partially double-stranded nucleic acid molecule contains a hemimodified recognition/cleavage sequence in which one strand contains at least one derivatized nucleotide(s) that prevents cleavage of that strand (*i.e.*, the strand that contains the derivatized nucleotide(s)) by the restriction endonuclease.

25 A "nicking endonuclease" (NE), as used herein, refers to an endonuclease that recognizes a nucleotide sequence of a completely or partially double-stranded nucleic acid molecule and cleaves only one strand of the nucleic acid molecule at a specific location relative to the recognition sequence. Unlike a restriction endonuclease (RE), which requires its recognition sequence to be modified by containing at least one derivatized nucleotide to prevent cleavage of the derivatized nucleotide-containing strand of a fully or partially double-stranded nucleic acid molecule, a NE typically

recognizes a nucleotide sequence composed of only native nucleotides and cleaves only one strand of a fully or partially double-stranded nucleic acid molecule that contains the nucleotide sequence.

As used herein, "native nucleotide" refers to adenylic acid, guanylic acid, cytidylic acid, thymidylic acid or uridylic acid. A "derivatized nucleotide" is a nucleotide other than a native nucleotide.

The nucleotide sequence of a completely or partially double-stranded nucleic acid molecule that a NA recognizes is referred to as the "nicking agent recognition sequence" (NARS). Likewise, the nucleotide sequence of a completely or partially double-stranded nucleic acid molecule that a NE recognizes is referred to as the "nicking endonuclease recognition sequence" (NERS). The specific sequence that a RE recognizes is referred to as the "restriction endonuclease recognition sequence" (RERS). A "hemimodified RERS," as used herein, refers to a double-stranded RERS in which one strand of the recognition sequence contains at least one derivatized nucleotide (e.g., α -thio deoxynucleotide) that prevents cleavage of that strand (i.e., the strand that contains the derivatized nucleotide within the recognition sequence) by a RE that recognizes the RERS.

In certain embodiments, a NARS is a double-stranded nucleotide sequence where each nucleotide in one strand of the nucleotide is complementary to the nucleotide at its corresponding position in the other strand. In such embodiments, the nucleotide of a NARS in the strand containing a NS nickable by a NA that recognizes the NARS is referred to as a "sequence of the sense strand of the NARS" or a "sequence of the sense strand of the double-stranded NARS," while the nucleotide of the NARS in the strand that does not contain the NS is referred to as a "sequence of the antisense strand of the NARS" or a "sequence of the antisense strand of the double-stranded NARS."

Likewise, in the embodiments where a NERS is a double-stranded nucleotide sequence of which one strand is exactly complementary to the other strand, the nucleotide of a NERS located in the strand containing a NS nickable by a NE that recognizes the NERS is referred to as a "sequence of a sense strand of the NERS" or a "sequence of the sense strand of the double-

stranded NERS," while the nucleotide of the NERS located in the strand that does not contain the NS is referred to a "sequence of the antisense strand of the NERS" or a "sequence of the antisense strand of the double-stranded NERS." For example, the recognition sequence and the nicking site of an
 5 exemplary nicking endonuclease, N.BstNB I, are shown below with "▼" to indicate the cleavage site and N to indicate any nucleotide:



The sequence of the sense strand of the N.BstNB I recognition sequence is 5'-GAGTC-3', whereas that of the antisense strand is 5'-GACTC-3'.

Similarly, the sequence of a hemimodified RERS in the strand
 15 containing a NS nickable by a RE that recognizes the hemimodified RERS (*i.e.*, the strand that does not contain any derivatized nucleotides) is referred to as "the sequence of the sense strand of the hemimodified RERS" and is located in "the sense strand of the hemimodified RERS" of a hemimodified RERS-containing nucleic acid, while the sequence of the hemimodified RERS in the
 20 strand that does not contain the NS (*i.e.*, the strand that contains derivatized nucleotide(s)) is referred to as "the sequence of the antisense strand of the hemimodified RERS" and is located in "the antisense strand of the hemimodified RERS" of a hemimodified RERS-containing nucleic acid.

In certain other embodiments, a NARS is an at most partially
 25 double-stranded nucleotide sequence that has one or more nucleotide mismatches, but contains an intact sense strand of a double-stranded NARS as described above. According to the convention used herein, in the context of describing a NARS, when two nucleic acid molecules anneal to one another so as to form a hybridized product, and the hybridized product includes a NARS,
 30 and there is at least one mismatched base pair within the NARS of the hybridized product, then this NARS is considered to be only partially double-stranded. Such NARSs may be recognized by certain nicking agents (*e.g.*, N.BstNB I) that require only one strand of double-stranded recognition

sequences for their nicking activities. For instance, the NARS of N.BstNB I may contain, in certain embodiments, an intact sense strand, as follows,

5 5'-GAGTC-3'
3'-NNNNN-5'

where N indicates any nucleotide, and N at one position may or may not be identical to N at another position, however there is at least one mismatched base pair within this recognition sequence. In this situation, the NARS will be
10 characterized as having at least one mismatched nucleotide.

In certain other embodiments, a NARS is a partially or completely single-stranded nucleotide sequence that has one or more unmatched nucleotides, but contains an intact sense strand of a double-stranded NARS as described above. According to the convention used herein, in the context of
15 describing a NARS, when two nucleic acid molecules (*i.e.*, a first and a second strand) anneal to one another so as to form a hybridized product, and the hybridized product includes a nucleotide sequence in the first strand that is recognized by a NA, *i.e.*, the hybridized product contains a NARS, and at least one nucleotide in the sequence recognized by the NA does not correspond to,
20 *i.e.*, is not across from, a nucleotide in the second strand when the hybridized product is formed, then there is at least one unmatched nucleotide within the NARS of the hybridized product, and this NARS is considered to be partially or completely single-stranded. Such NARSs may be recognized by certain nicking agents (*e.g.*, N.BstNB I) that require only one strand of double-stranded
25 recognition sequences for their nicking activities. For instance, the NARS of N.BstNB I may contain, in certain embodiments, an intact sense strand, as follows,

30 5'-GAGTC-3'
3'-N₀₋₄-5'

(where "N" indicates any nucleotide, 0-4 indicates the number of the nucleotides "N," a "N" at one position may or may not be identical to a "N" at

another position), which contains the nucleotide of the sense strand of the double-stranded recognition sequence of N.BstNB I. In this instance, at least one of G, A, G, T or C is unmatched, in that there is no corresponding nucleotide in the complementary strand. This situation arises, *e.g.*, when there is a "loop" in the hybridized product, and particularly when the sense sequence is present, completely or in part, within a loop.

As used herein, the phrase "amplifying a nucleic acid molecule" or "amplification of a nucleic acid molecule" refers to the making of two or more copies of the particular nucleic acid molecule.

The term "nucleic acid amplification reaction" refers to the process of making more than one copy of a nucleic acid molecule (A) using a nucleic acid molecule (T) that comprises a sequence complementary to the nucleotide of nucleic acid molecule A as a template.

A first nucleic acid sequence is "at least substantially identical" to a second nucleic acid sequence when the complement of the first sequence is able to anneal to the second sequence to form at least a transient duplex under certain reaction conditions (*e.g.*, conditions for amplifying nucleic acids). In certain preferred embodiments, the first sequence is exactly identical to the second sequence, that is, the nucleotide of the first sequence at each position is identical to the nucleotide of the second sequence at the same position, and the first sequence is of the same length as the second sequence.

A first nucleic acid sequence is "at least substantially complementary" to a second nucleic acid sequence when the first sequence is able to anneal to the second sequence to form at least a transient duplex under certain reaction conditions (*e.g.*, conditions for amplifying nucleic acids). In certain preferred embodiments, the first sequence is exactly or completely complementary to the second sequence, that is, each nucleotide of the first sequence is complementary to the nucleotide of the second sequence at its corresponding position, and the first sequence is of the same length as the second sequence.

A transient duplex between a first nucleic acid sequence and a second nucleic acid sequence is formed when under given reaction conditions, the 3' terminal group of the first nucleic acid sequence (if unblocked) may be

extended by a DNA polymerase using the second nucleic acid sequence as a template; or the 3' terminal group of the second nucleic acid sequence (if unblocked) may be extended by a DNA polymerase using the first nucleic acid sequence as a template. In certain embodiments, at least 80% of the

5 nucleotides of the first nucleic acid in a region of at least 8 nucleotides are complementary to the nucleotides of the second nucleic acid at their corresponding positions. In other embodiments, at least 85%, 90%, 95%, 97%, 98%, or 99% of the nucleotides of the first nucleic acid in a region of at least 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18 nucleotides are complementary to the

10 nucleotides of the second nucleic acid at their corresponding positions.

As used herein, a nucleotide in one strand (referred to as the "first strand") of a double-stranded nucleic acid located at a position "corresponding to" another position (e.g., a defined position) in the other strand (referred to as the "second strand") of a double-stranded nucleic acid refers to the nucleotide

15 in the first strand that is complementary to the nucleotide at the corresponding position in the second strand. Likewise, a position in one strand (referred to as the "first strand") of a double-stranded nucleic acid corresponding to a nicking site within the other strand (referred to as the "second strand") of a double-stranded nucleic acid refers to the position between the two nucleotides in the

20 first strand complementary to those in the second strand between which nicking occurs.

The term "isothermal conditions" refers to a set of reaction conditions where the temperature of the reaction is kept essentially constant (i.e., at the same temperature or within the same narrow temperature range

25 wherein the difference between an upper temperature and a lower temperature is no more than about 20°C) during the course of the amplification. In certain embodiments, a reaction is carried out under conditions where the difference between an upper temperature and a lower temperature is no more than 15°C, 10°C, 5°C, 3°C, 2°C or 1°C. Exemplary temperatures for isothermal

30 amplification include, but are not limited to, any temperature between 50°C to 70°C or the temperature range between 50°C to 70°C, 55°C to 70°C, 60°C to 70°C, 65°C to 70°C, 50°C to 55°C, 50°C to 60°C, or 50°C to 65°C.

The terms "polymorphism" and "genetic variation," as used herein, refer to the occurrence of two or more genetically determined alternative sequences or alleles in a small region (*i.e.*, one to several (*e.g.*, 2, 3, 4, 5, 6, 7, or 8) nucleotides in length) in a population. The allelic form occurring most frequently in a selected population is referred to as the wild type form. Other allelic forms are designated as variant forms. Diploid organisms may be homozygous or heterozygous for allelic forms.

In one aspect of the invention, the genetic variation is a "single-nucleotide polymorphism" (SNP), which refers to any single nucleotide sequence variation, preferably one that is common in a population of organisms and is inherited in a Mendelian fashion. Generally, the SNP is either of two possible bases and there is no possibility of finding a third or fourth nucleotide identity at an SNP site.

C. Sample sources

Biological samples of the present invention include any sample that originates from an organism and that may contain a nucleic acid of interest (*i.e.*, target nucleic acid). They may be provided by obtaining a blood sample, biopsy specimen, tissue explant, organ culture or any other tissue or cell preparation from a subject or a biological source. The subject or biological source may be a human or non-human animal, a plant, a fungus, a bacterium, and virus. In certain preferred embodiments of the invention, the subject or biological source may be suspected of having, or being at risk for having, a genetic disease or a pathogen infection. In other preferred embodiments, the subject or biological source may be a patient that has a genetic disease or a pathogen infection. In certain other embodiments, the subject or biological source may be a control subject that does not have a genetic disease or a pathogen infection.

In certain embodiments, a bacterial sample can be utilized as starting material, provided it contains or is suspected of containing a bacterial genome of interest. Such a sample may be obtained from any source that may potentially be contaminated by bacteria. When looking for bacterial infection or

in distinguishing bacteria from human or animal subjects, the sample to be tested can be selected or extracted from any bodily sample such as blood, urine, spinal fluid, tissue, vaginal swab, stool, amniotic fluid or buccal mouthwash. In other applications, the sample can come from a variety of other
5 sources. For example, in horticulture and agricultural testing, the sample can be from a plant, fertilizer, soil, liquid or other horticultural or agricultural product. In food testing, the sample can be from fresh food or processed food (for example infant formula, seafood, fresh produce and packaged food). In environmental testing, the sample can be from liquid, soil, sewage treatment,
10 sludge and any other sample in the environment considered or suspected of being contaminated by bacteria.

When the sample is a mixture of material for example blood, soil and sludge, it can be treated with an appropriate reagent effective to open the cells and expose or separate the strands of nucleic acids. Although not
15 necessary, this lysing and nucleic acid denaturing step will allow amplification to occur more readily. Further, if desired, the bacteria can be cultured prior to analysis and thus a pure sample obtained.

Although fingerprinting genomic DNA according to the present invention is primarily described herein, the present invention may also be used
20 to characterize other DNA molecules (e.g., cDNA). Thus, the methods according to the present invention may also be applicable to characterize cDNA expression patterns.

D. Nicking Reactions

The nucleic acids isolated from a biological source may be directly
25 used in a nicking reaction. Alternatively, they may be amplified via known methods (such as PCR) prior to being subjected to action of a nicking agent.

As described above, a nicking agent may be a nicking endonuclease (used interchangeably with "nicking enzyme") or a restriction endonuclease (used interchangeably with "restriction enzyme"). A nicking
30 endonuclease (NE) useful in the present invention may or may not have a

nicking site that overlaps with its recognition sequence. An exemplary NE that nicks outside its recognition sequence is N.BstNB I, which recognizes a unique nucleic acid sequence composed of 5'-GAGTC-3', but nicks four nucleotides beyond the 3' terminus of the recognition sequence. The recognition sequence and the nicking site of N.BstNB I are shown below with "▼" to indicate the cleavage site where the letter N denotes any nucleotide:



N.BstNB I may be prepared and isolated as described in U.S. Pat. No. 6,191,267, incorporated herein by reference in its entirety. Buffers and conditions for using this nicking endonuclease are also described in the '267 patent. An additional exemplary NE that nicks outside its recognition sequence is N.AlwI, which recognizes the following double-stranded recognition sequence:



The nicking site of N.AlwI is also indicated by the symbol "▼". Both NEs are available from New England Biolabs (NEB). N.AlwI may also be prepared by mutating a type II_S RE AlwI as described in Xu *et al.* (*Proc. Natl. Acad. Sci. USA* 98:12990-5, 2001).

Exemplary NEs that nick within their NERSs include N.BbvCI-a and N.BbvCI-b. The recognition sequences for the two NEs and the NSs (indicated by the symbol "▼") are shown as follows:

30

N.BbvCI-a

35



N.BbvCI-b



Both NEs are available from NEB.

Additional exemplary nicking endonucleases include, without limitation, N.BstSE I (Abdurashitov *et al.*, *Mol. Biol. (Mosk)* 30: 1261-7, 1996),
 10 an engineered EcoR V (Stahl *et al.*, *Proc. Natl. Acad. Sci. USA* 93: 6175-80, 1996), an engineered Fok I (Kim *et al.*, *Gene* 203: 43-49, 1997), endonuclease V from *Thermotoga maritima* (Huang *et al.*, *Biochem.* 40: 8738-48, 2001), Cvi Nickases (e.g., CviNY2A, CviNYSI, Megabase Research Products, Lincoln, Nebraska) (Zhang *et al.*, *Virology* 240: 366-75, 1998; Nelson *et al.*, *Biol. Chem.*
 15 379: 423-8, 1998; Xia *et al.*, *Nucleic Acids Res.* 16: 9477-87, 1988), and an engineered Mly I (i.e., N.Mly I) (Besnier and Kong, *EMBO Reports* 2: 782-6, 2001). Additional NEs may be obtained by engineering other restriction endonuclease, especially type IIs restriction endonucleases, using methods similar to those for engineering EcoR V, AlwI, Fok I and/or Mly I.

20 A restriction endonuclease useful as a nicking agent can be any restriction endonuclease (RE) that nicks a double-stranded nucleic acid at its hemimodified recognition sequences. Exemplary REs that nick their double-stranded hemimodified recognition sequences include, but are not limited to Ava I, Bsl I, BsmA I, BsoB I, Bsr I, BstN I, BstO I, Fnu4H I, Hinc II, Hind II and
 25 Nci I. Additional REs that nick a hemimodified recognition sequence may be screened by the strand protection assays described in U.S. Pat. No. 5,631,147.

In certain embodiments, a nicking agent may recognize a nucleotide sequence in a DNA-RNA duplex and nicks in one strand of the duplex. In certain other embodiments, a nicking agent may recognize a
 30 nucleotide sequence in a double-stranded RNA and nicks in on strand of the RNA.

Certain nicking agents require only the presence of the sense strand of a double-stranded recognition sequence in an at least partially double-

stranded substrate nucleic acid for their nicking activities. For instance, N.BstNB I is active in nicking a substrate nucleic acid that comprises, in one strand, the sequence of the sense strand of its recognition sequence "5'-GAGTC-3'" of which one or more nucleotides do not form conventional base
5 pairs (e.g., G:C, A:T, or A:U) with nucleotides in the other strand of the substrate nucleic acid. The nicking activity of N.BstNB I decreases with the increase of the number of the nucleotides in the sense strand of its recognition sequence that do not form conventional base pairs with any nucleotides in the other strand of the substrate nucleic acid. However, even if none of the
10 nucleotides of "5'-GAGTC-3'" form conventional base pairs with the nucleotides in the other strand, N.BstNB I may still retain 10-20% of its optimum activity.

Several factors may be considered when choosing a particular nicking agent for a fingerprinting assay according to the present invention. These factors include but not limited to (1) whether the particular nicking agent
15 would produce nicked fragment(s), or a pattern of nicked fragments, unique to the organism from which the nucleic acid sample is suspected to be; (2) the lengths of nicked fragments unique to the organism from which the nucleic acid sample is suspected to be and the characterization technologies; and (3) the optimum temperature of the nicking agent. For instance, if mass spectrometry
20 is chosen as the characterization method, a nicking enzyme that would produce short unique oligonucleotides may be desirable. In the embodiments whether the nicking reaction is performed in the presence of a DNA polymerase, a nicking enzyme with an optimum temperature similar to that of the DNA polymerase may be desirable.

25 The nicking reaction may be simply performed by incubating the nucleic acid sample with a nicking agent under appropriate conditions. Identifying such appropriate conditions are within the ordinary skill in the art. For instance, the nicking reaction may be performed at the optimum temperature of the nicking agent and in a buffer suitable for the nicking agent.

30 The nicking reaction mixture that contains nicked nucleic acid fragments may be directly characterized. The characterization may be

performed by any known applicable methods, including but not limited to, liquid chromatography, electrophoresis, hybridization and mass spectrometry. The use of such methods may indicate the presence or absence of one or more particular fragments unique to a species, subspecies, strain, or individual organism from which the nucleic acid sample is suspected to be. Alternatively, the use of such methods produces a pattern of nicked fragments, which may be compared with the pattern generated from an organism from which the nucleic acid sample is suspected to be.

E. Linear Amplification

10 In certain embodiments, the nicking reaction is performed in the presence of a DNA polymerase so that nicked fragments or portions thereof may be linearly amplified. The amplification produces a larger amount of single-stranded nucleic acid or oligonucleotides, which increases the sensitivity of the fingerprinting assays.

15 In such a nicking reaction, the 3' terminus at the nicking site is extended by a DNA polymerase, preferably being 5'→3' exonuclease deficient and having a strand displacement activity and/or in the presence of a strand displacement facilitator, displacing the strand that contains the 5' terminus produced by the nicking reaction. The resulting extension product having a
20 recreated NARS for the NA is nicked ("re-nicked") by the NA. The 3' terminus produced at the NS by the re-nicking is then extended in the presence of the DNA polymerase, also displacing the strand that contains the 5' terminus produced by the nicking reaction. The nicking-extension cycle is repeated, preferably multiple times, to accumulate/amplify the displaced strand that
25 contains the 5' terminus produced by the nicking reaction.

Various types of DNA polymerase may be used in the present application. For instance, DNA polymerases useful in the present invention may be any DNA polymerase that is 5'→3' exonuclease deficient but has a strand displacement activity. Such DNA polymerases include, but are not
30 limited to, exo⁻ Deep Vent, exo⁻ Bst, exo⁻ Pfu, and exo⁻ Bca. Additional DNA

polymerases useful in the present invention may be screened for or created by the methods described in U.S. Pat. No. 5,631,147, incorporated herein by reference in its entirety. The strand displacement activity may be further enhanced by the presence of a strand displacement facilitator as described

5 below.

Alternatively, in certain embodiments, a DNA polymerase that does not have a strand displacement activity may be used. Such DNA polymerases include, but are not limited to, *exo⁻* Vent, Taq, the Klenow fragment of DNA polymerase I, T5 DNA polymerase, and Phi29 DNA
10 polymerase. In certain embodiments, the use of these DNA polymerases requires the presence of a strand displacement facilitator. A "strand displacement facilitator" is any compound or composition that facilitates strand displacement during nucleic acid extensions from a 3' terminus at a nicking site catalyzed by a DNA polymerase. Exemplary strand displacement facilitators
15 useful in the present invention include, but are not limited to, BMRF1 polymerase accessory subunit (Tsurumi *et al.*, *J. Virology* 67: 7648-53, 1993), adenovirus DNA-binding protein (Zijderveld and van der Vliet, *J. Virology* 68: 1158-64, 1994), herpes simplex viral protein ICP8 (Boehmer and Lehman, *J. Virology* 67: 711-5, 1993; Skaliter and Lehman, *Proc. Natl. Acad. Sci. USA* 91:
20 10665-9, 1994), single-stranded DNA binding protein (Rigler and Romano, *J. Biol. Chem.* 270: 8910-9, 1995), phage T4 gene 32 protein (Villemain and Giedroc, *Biochemistry* 35: 14395-4404, 1996), calf thymus helicase (Siegel *et al.*, *J. Biol. Chem.* 267: 13629-35, 1992) and trehalose. In one embodiment, trehalose is present in the amplification reaction mixture.

25 Additional exemplary DNA polymerases useful in the present invention include, but are not limited to, phage M2 DNA polymerase (Matsumoto *et al.*, *Gene* 84: 247, 1989), phage PhiPRD1 DNA polymerase (Jung *et al.*, *Proc. Natl. Acad. Sci. USA* 84: 8287, 1987), T5 DNA polymerase (Chatterjee *et al.*, *Gene* 97: 13-19, 1991), Sequenase (U.S. Biochemicals),
30 PRD1 DNA polymerase (Zhu and Ito, *Biochim. Biophys. Acta.* 1219: 267-76, 1994), 9°N_mTM DNA polymerase (New England Biolabs) (Southworth *et al.*,

Proc. Natl. Acad. Sci. 93: 5281-5, 1996; Rodriguez *et al.*, *J. Mol. Biol.* 302: 447-62, 2000), and T4 DNA polymerase holoenzyme (Kaboord and Benkovic, *Curr. Biol.* 5: 149-57, 1995).

Alternatively, a DNA polymerase that has a 5'→3' exonuclease
5 activity may be used. For instance, such a DNA polymerase may be useful for
amplifying short nucleic acid fragments that automatically dissociate from the
template nucleic acid after nicking.

In certain embodiments where a nicking agent nicks in the DNA
strand of a RNA-DNA duplex, a RNA-dependent DNA polymerase may be
10 used. In other embodiments where a nicking agent nicks in the RNA strand of
a RNA-DNA duplex, a DNA-dependent DNA polymerase that extends from a
DNA primer, such as Avian Myeloblastosis virus reverse transcriptase
(Promega) may be used. In both instances, a target mRNA need not be
reverse transcribed into cDNA and may be directly mixed with a template
15 nucleic acid molecule that is at least substantially complementary to the target
mRNA.

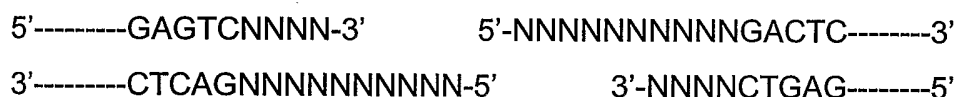
In certain embodiments, it may be desirable to amplify short
oligonucleotide fragments (*e.g.*, 6-20 nucleotides in length). For instance, short
oligonucleotides are more suitable to certain characterization technologies,
20 such as LC-TOF and MALDI. In addition, short fragments may be easily and
more efficiently amplified to increase the speed and sensitivity of the present
methods. Such fragments also allow the use of a DNA polymerase that does
not have a strand displacement activity, or is not 5' to 3' exonuclease deficient.

Generation and amplification of short oligonucleotides is made
25 possible by the presence of one or more pairs of nicking agent recognition
sequences (or one nicking agent recognition sequence and one restriction
enzyme recognition sequence) in close proximity in a nucleic acid sample. In
certain embodiments, the proximity is about 12 to 24 nucleotides. Using
N.BstNB I as an exemplary nicking agent, the structure in the nucleic acid can
30 be visualized as follows:



where N can be any nucleotide, and the number of Ns in the upper strand that is between the sequence of the sense strand of the N.BstNB I recognition sequence (*i.e.*, 5'-GAGTC-3') and the sequence of the antisense strand of the recognition sequence (*i.e.*, 5'-GACTC-3') may be between 12 and 24. After the nicking step that takes place at 55 to 65°C, the duplex dissociates and forms two amplification templates.

10



In the presence of a polymerase, the recessed 3'-hydroxyl of each amplification template is filled in by the polymerase, the nicking enzyme then again cleaves the newly extended strand, the resulting short single-stranded oligonucleotide immediately dissociates, and the cycle of nicking and filling is repeated multiple times, resulting a linear amplification of the short single-stranded oligonucleotides.

The above reaction synthesizes short oligonucleotides whose cycle of reactions depends on the idea that, at the reaction temperature, oligonucleotides above a certain length form stable duplexes, while those below this length form unstable duplexes that dissociate readily. The short oligonucleotide generated in the nicking reaction is below the threshold of stability, and is thereby released from the duplex. The release of the short oligonucleotide from the duplex regenerates a 5' overhang, which may be again used as a template for synthesizing the short oligonucleotide. A schematic representation of a linear amplification of short oligonucleotides using an N.BstNB I as the nicking agent is shown in Figure 1.

The identification of one or more pairs of nicking agent recognition sequence (or one nicking agent recognition sequence and one restriction

enzyme recognition sequence) in close proximity in a genomic DNA with a known sequence may be performed by the use of applicable computer programs. Such identification may facilitate the selection of a nicking agent for fingerprinting a nucleic acid sample suspected to be derived from the genomic DNA, as well as the identification of oligonucleotide fragments or patterns thereof that are unique to the genomic DNA. These unique oligonucleotide fragments or patterns thereof expected to be present in a fingerprinting assay according to the present invention may be used as a standard for those generated from the nucleic acid sample. The comparison of the expected unique oligonucleotide fragments or patterns thereof with those generated from the nucleic acid sample would indicate whether the nucleic acid sample is derived from the genomic DNA.

An exemplary computer program useful in identifying closely located nicking agent recognition sequences, or nicking agent recognition sequences located near restriction enzyme recognition sequences is called Genome Identifier through a Nicking-enzyme generated Unique Mass Spectrum (*GINUMS*). *GINUMS* further predicts the amplified short oligonucleotides of a genomic sequence produced in the linear amplification reactions described herein. When more than one genomic sequence needs to be analyzed, the following process is repeated for each sequence. The search begins with the acquisition of the genomic sequence. The analysis is simplified with "finished" genomic sequence, which is represented by one long sequence, rather than "draft" quality sequence, which is represented by a series of sequences, each a fragment of the overall sequence separated by gaps, although the analysis will work with any sequence or set of sequences. Usually the sequence is stored in FASTA (or Pearson) format, but the program will work with any sequence format. In any case, the sequence is read from either a file or a database, and stored into memory so that it may be searched later. *GINUMS* then searches the genomic sequence for three different patterns, each represented by a regular expression. Regular expressions are simply patterns represented by a string of characters that are used to search text, in this case one long string of

A's, C's, G's and T's representing one strand of the genomic sequence. Using both N.Alw I and N.Bst NBI nicking endonucleases, the three regular expressions (in PERL syntax) are:

- 5 1. GAGTC.{ $\$min$, $\$max$ }GACTC
2. GGATC.{ $\$min$, $\$max$ }GACTC
3. GAGTC.{ $\$min$, $\$max$ }GATCC

where $\$min$ represents the smallest gap between the two DNA restriction
10 endonuclease recognition sequences, and $\$max$ the largest. The default values for both of these variables are 14 and 24, respectively. *GINUMS* searches the genomic sequence with each of the regular expressions one at a time, and then stores all of the matching segments of sequence (termed "hits" for the rest of this document) for each search into separate lists. Thus, all of
15 the hits are composed of the recognition sequences separated by any 14 to 24 base pairs, which are determined by the genomic sequence. The program has three lists of hits in memory, each list the product of searching the genomic sequence with one of the regular expressions. For each hit in all of the lists, *GINUMS* will determine the "product(s)" of the reaction (the sequence that
20 would be amplified), the mass of the product(s) and the starting and ending position of that product in the genomic sequence.

The lists of masses, the products they represent, and the location of those products in the genomic sequence are then written to file or database for permanent storage. Learning to read the regular expressions used in
25 *GINUMS* is trivial, and will be described here. The second regular expression listed in the section above, GGATC.{ $\$min$, $\$max$ }GACTC, where $\$min$ and $\$max$ are integers, will be used as an example for the rest of this section.

The program searches genomic sequence for target sequences (that is, any sequence beginning with GGATC and ending with GACTC,
30 separated by any 14 to 24 nucleotides). In regular expressions, the '.' character represents any one character, in this case any one A, T, C, or G. So, one way

to search for each of these occurrences would be to construct 11 regular expressions and then search the sequence for each, such as:

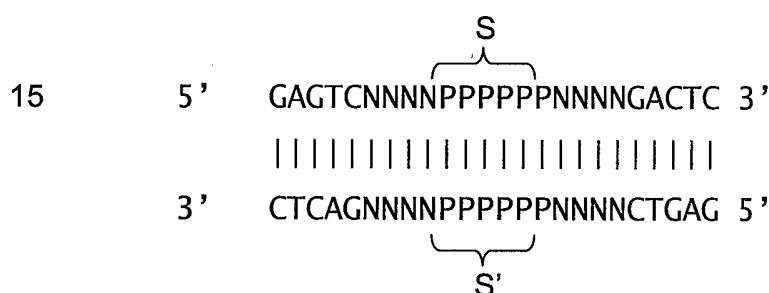
- 1) GGATC.....GACTC (14 .'s)
- 5 2) GGATC.....GACTC (15 .'s)
- .
- .
- .
- 11) GGATC.....GACTC (24 .'s)
- 10

However, to do this for all three search patterns would be cumbersome, and regular expressions provide us with a more elegant solution to the problem. When any character in a regular expression is followed by a number flanked by brackets (e.g., G{6}), then the regular expression represents precisely that number of consecutive characters (so G{6} would represent 6 consecutive G's, or GGGGGG). When there are two numbers (x and y) separated by a ',' (e.g., G{x,y}), the regular expression represents a string of at least x characters and at most y characters. So G{2,4} would represent GG, GGG, and GGGG. When the character preceding the brackets is a '.' (e.g., {2,4}), then the regular expression represents any string of any 2-4 characters. Returning to GGATC.{ $\$min$, $\$max$ }GACTC, it can now be seen that this regular expression represents any string that begins with GGATC, and ends with GACTC, separated by at least $\$min$ characters and at most $\$max$ characters, where $\$min$ and $\$max$ are integers, and $\$min < \max . Because the brackets are preceded by a '.', these can be any characters. Building the profiles for more than one organism is as simple as repeating the process for as many genomic sequences necessary, noting which masses were derived from which organism. *GINUMS* is capable of inputting the genomic sequences of an unlimited number of organisms, each contained within one file, all contained in the same directory, and then returning two outputs. The first output is a set of masses unique to each organism. This can be accomplished by searching for

the existence of each mass in one organism in all of the masses for the other organisms. If that mass is found only in one organism, then it is unique for that organism. *GINUMS* does not do this precisely (it uses the properties of a data structure called a hash), but the process is analogous. The second output is

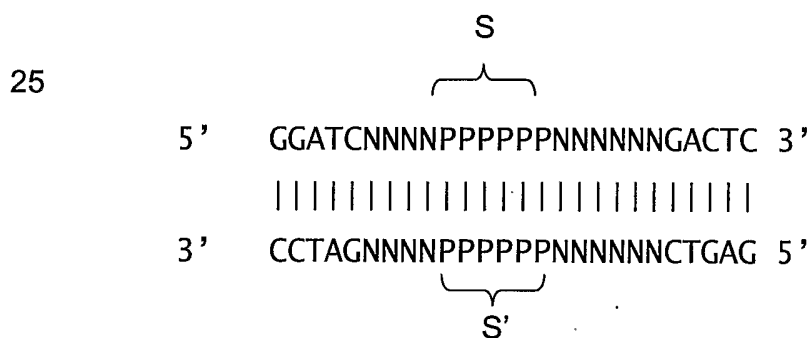
5 the complete list of masses for each organism, and would allow the user to determine if each organism has a distinct "profile" (hence, the name), or set, of masses. These could be written either to file or into a database for permanent storage, so that they may be searched for in experimental data at a later time. *GINUMS* uses the following model to determine the products (and their

10 corresponding masses) of the amplification process on genomic sequence. When two N.BstNB I recognition sequences are present on opposite strands separated by 14 to 24 nucleotides (in the example below, 14 will be used), and oriented as follows:



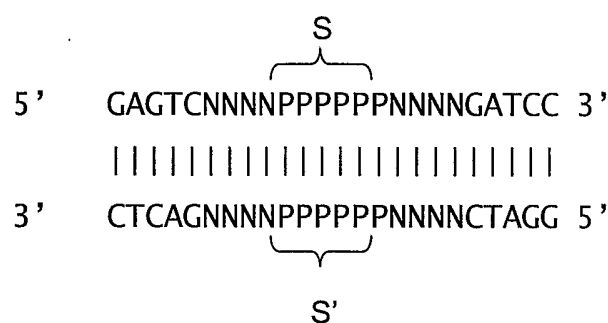
where N represents any nucleotide, and P represents the nucleotides in the

20 product, the products of the reaction are S and S'. When a N.Alw I recognition site is followed by a N.Bst NBI recognition site on the opposite strand separated by the correct number of nucleotides and oriented as follows:



the products are represented by the sequence of P's and is summarized by S and S'. When a N.Bst NBI recognition sequence is followed by a N.Alw I recognition sequence on the opposite strand separated by the correct number of nucleotides and oriented as follows:

5



10

the product sequences are represented by P's, and summarized as S and S'. After finding all of the products predicted by this model in the genomic sequence, the masses of each product is calculated according to the sequence of the product. The results from the use of *GINUMS* on *E. coli* strains K12 and O157 and human chromosome 21 are shown in Tables 1, 2, and 5, respectively.

As one of ordinary skill in the art would appreciate, in addition to the use of N.BstNB I alone or in combination with N.Alw I, short oligonucleotide fragments may also be generated or amplified by the use of a different nicking endonuclease alone or in combination with another nicking endonuclease or restriction endonuclease (e.g., a type IIs restriction endonuclease). In case that two enzymes are used, but have different optimal temperature, a linear amplification reaction may be first performed under the lower optimal temperature and then under the higher optimal temperature.

In certain embodiments, the amplified short fragments may also contain genetic variations. For instance, SNPs in human genomic DNA that are flanked by two N.BstNB I recognition sequences or an N.BstNB I recognition sequence and another restriction enzyme recognition sequence are shown in Table 9. The characterization of such short fragments would identify the SNPs

within these fragments and facilitate the identification of the individual from which a nucleic acid sample is obtained.

F. Exponential Amplification

In certain embodiments, the oligonucleotides linearly amplified as described above may be further exponentially amplified. These oligonucleotides are referred to as "initiating oligonucleotides" or "initiators." Such exponential amplification greatly increases the production rate and amount of the initiating oligonucleotides.

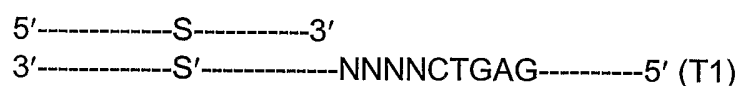
The key idea for exponential amplification is to arrange it so that the oligonucleotide product of the linear reaction serves to create a new primer that in turn anneals to a target template and creates a new primer-template, which in turn produces more of the same oligonucleotide product, creating a chain reaction. A simple scheme for exponentially amplifying a short oligonucleotide (also referred to "direct EXPAR") using N.BstNB I as the nicking agent is depicted in Figure 2. The scheme is based on our observation that even though the product oligonucleotide is unstable as a duplex it will form a transient duplex molecule with its complement and this transient duplex can act as a primer for extension by the DNA polymerase. Once extension of the oligonucleotide has occurred the duplex is stabilized by the additional complementary duplex section and will not readily dissociate. Extending the primer thus creates a stable primer-template that will produce oligonucleotide products in a linear fashion.

To create these new duplexes we need only provide a ready supply of complementary oligonucleotides that we call amplification templates. The key feature of these single-stranded oligonucleotides is that they contain two copies in tandem of the complement of the oligonucleotide product to be amplified, separated by the sequence of the antisense strand of the recognition sequence of N.BstNB I (*i.e.*, 3'-CTCAG-5') and a four base spacer (on the 5' side). When the transient duplex is extended a stable new primer-template is created. This primed template will then continue to produce oligonucleotide

product *via* the linear amplification cycle as described above (nicking after the four base spacer, dissociating the oligonucleotide and re-elongating the primer) as long as the enzymes remain active and dNTPs are available.

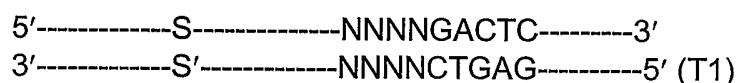
Another scheme for exponentially amplifying short
 5 oligonucleotides (referred to as "the replicator type" or "ping-pong amplification scheme") uses two templates. In this scheme, an initiating oligonucleotide of sequence S primes a first template oligonucleotide T1 (S is about 8 to 16 nucleotides in length) to form the following partially double-stranded nucleic acid molecule. The 3' terminus of T1 may be blocked by a phosphate group.

10



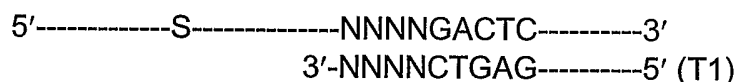
In the presence of a DNA polymerase, the upper strand of the
 15 above partially double-stranded nucleic acid molecule is elongated to form the following fully double-stranded nucleic acid molecule:

20



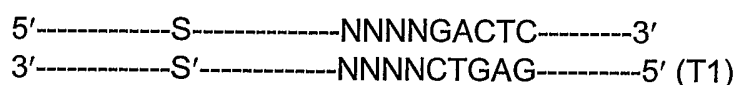
In the presence of a nicking enzyme (*e.g.*, N.BstNB I), the lower strand is nicked to generate a 3' hydroxyl group and release an oligonucleotide blocked at the 3' terminus (un-productive oligonucleotide). The resulting nicked structure is shown below:

25

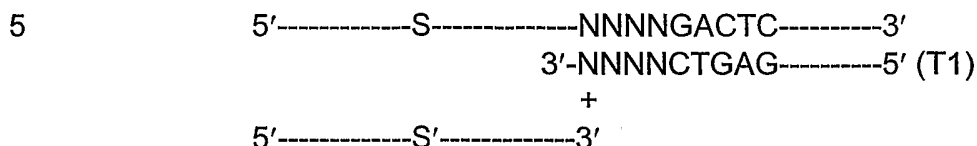


The DNA polymerase uses sequence S as a template and fills in
 30 the recessed 3' hydroxyl group of the lower strand to produce the following double-stranded nucleic acid.

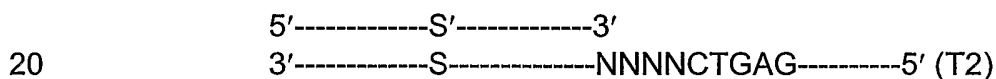
35



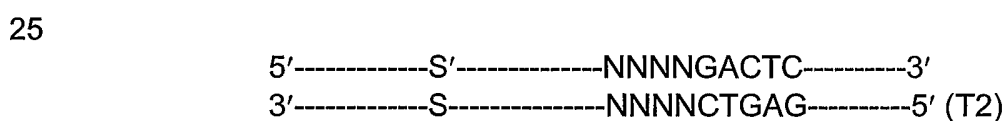
The nicking enzyme cleaves the lower strand, releasing an oligonucleotide having the sequence S' (which is completely complementary to the sequence S) as shown below:



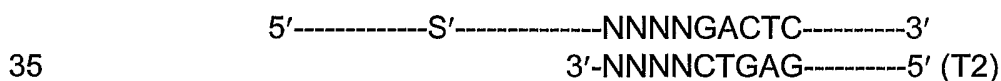
10 The lower strand of the above partially double-stranded nucleic acid may be extended again to produce a fully double-stranded nucleic acid molecule. The lower strand of the fully double-stranded nucleic acid may be nicked again to release another oligonucleotide having the sequence S'. The above extension and nicking cycle may be repeated multiple times, resulting in
15 the amplification of the oligonucleotide having the sequence S'. This oligonucleotide (S') is capable of priming the oligonucleotide template T2 to follow a partially double-stranded nucleic acid molecule as shown below:



In the presence of a DNA polymerase, the upper strand of the above partially double-stranded nucleic acid molecule is elongated to form the following fully double-stranded nucleic acid molecule:



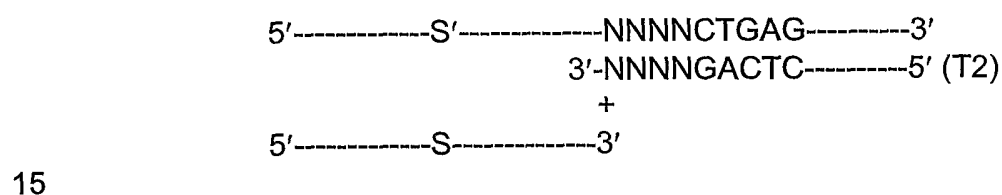
In the presence of a nicking enzyme (e.g., N.BstNB I), the lower
30 strand is nicked to generate a 3' hydroxyl group and release an oligonucleotide
blocked at the 3' terminus (un-productive oligonucleotide). The resulting nicked
structure is shown below:



The DNA polymerase uses S' as a template and fills in the recessed 3' hydroxyl group of the lower strand to produce the following double-stranded nucleic acid:



The nicking enzyme cleaves the lower strand, releasing an oligonucleotide having the sequence S' (which is completely complementary to the sequence S) as shown below:



The lower strand of the above partially double-stranded nucleic acid may be extended again to produce a fully double-stranded nucleic acid molecule. The lower strand of the fully double-stranded nucleic acid may be nicked again to release another oligonucleotide having the sequence S. The above extension and nicking cycle may be repeated multiple times, resulting in the amplification of the oligonucleotide having the sequence S.

The two oligonucleotides having the sequences of S and S' are now capable of priming T1 and T2, respectively, and the exponential amplification is started. It should be noted that S and S' are sufficiently short (e.g., 8-16 nucleotides in length) which prevents the triggers from forming a stable duplex in a reaction mixture under conditions for exponential amplification (e.g., 60°C). This variation of exponential amplification has a substantial advantage of requiring a very high level of stringency of an oligonucleotide priming its template. We have discovered that the oligonucleotide (e.g., an oligonucleotide having the sequence S or S') has to be nearly perfectly base paired with its template for an exponential amplification reaction to start. In many cases, even a single mismatch in the oligonucleotide will inhibit the reaction.

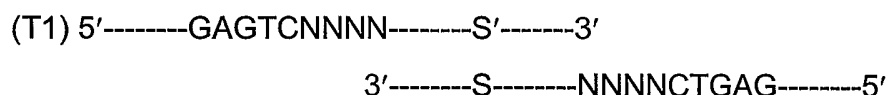
To carry out the exponential reaction, some or all of the following
35 components may be used in certain embodiments.

- 1) The first template oligonucleotide (T1). A schematic representation of T1 is shown in Figure 3. T1 may be 24 to 60 nucleotides (including all the integer values therebetween), preferably 32-36 nucleotides in length. The 3'-end of T1 may be blocked with, for example, a phosphate, an amine, a biotin, a dideoxy group or a fluorophore (that is, there is no free 3'-hydroxyl in T1) to prevent extension by a polymerase. The region from the 3' terminus of T1 to the fifth nucleotide directly 3' to the 3' terminus of the sense strand of a nicking endonuclease recognition sequence (*e.g.*, GAGTC) (*i.e.*, Region I in Figure 6) may be 8, 9, 10, 11, 12, 13, 14, 15 or 16 nucleotides in length and is completely (or at least substantially) complementary to the sequence S. To the 5' side of the above region are 4 nucleotides of any sequence (Region II in Figure 6) over which a nicking endonuclease (*e.g.*, N.BstNB I) reaches to nick. Next in the 5' direction is the sequence 3'-CTGAG-5' which is the sense strand of the recognition sequence for a nicking enzyme (*e.g.*, N.BstNB I). Further in the 5' direction is about 10 to 20 nucleotides of any sequence (Region III in Figure 6). The sequence at the 5' end should not be complementary to any of the sequence at the 3'-end. The concentration of T1 is 0.001 to 1 micromolar if in solution. T1 can also be tethered to a solid support or covalently attached to any type of solid support.
- 2) The second template oligonucleotide (T2). Similar to T1, T2 may be 24 to 60 nucleotides (including all the integer values therebetween), preferably 32-36 nucleotides, in length. The 3'-end of T2 may be blocked with, for example, a phosphate, an amine, a biotin, a dideoxy group or a fluorophore (that is, there is no free 3'-hydroxyl in T2) to prevent extension by a polymerase. The region from the 3' terminus of T2 to the fifth nucleotide directly 3' to the 3' terminus of the sense strand of a nicking endonuclease recognition sequence (*e.g.*, GAGTC) may be 8, 9, 10, 11, 12, 13, 14, 15 or 16 nucleotides in length and is at least substantially complementary to the sequence

- 5' To the 5' side of the above region are 4 nucleotides of any sequence over which a nicking endonuclease (e.g., N.BstNB I) reaches to nick. Next in the 5' direction is the sequence "CTGAG" which is the sense strand of the recognition sequence for a nicking enzyme (e.g., N.BstNB I). Further in the 5' direction is about 10 to 20 nucleotides of any sequence. The sequence at the 5' end should not be complementary to any of the sequence at the 3'-end. The concentration of T2 is 0.001 to 1 micromolar if in solution. T2 can also be tethered to a solid support or covalently attached to any type of solid support.
- 3) A DNA polymerase such as *exo⁻* Vent, 9°N_mTM, Taq, or Bst at a concentration of 0.002 to 20 units per microliter. Preferably the concentration of the polymerase is 0.02 to 0.5 units per microliter. The enzyme is typically available commercially in 100 mM KCl, 0.1 mM EDTA, 10 mM Tris-HCl (pH 7.4), 1 mM DDT, and 50% glycerol.
- 4) A nicking enzyme such as N.BstNB I (from New England Biolabs, (NEB), MA) at a concentration of 0.002 to 20 units per microliter. Preferably the concentration of the nicking enzyme is 0.02 to 0.5 units per microliter. The enzyme is supplied in 50 mM KCl, 10 mM Tris-HCl (pH 7.5), 0.1 mM EDTA, 1 mM DTT, 200 ug/ml BSA and 50% glycerol.
- 5) A salt (e.g., MgCl₂ or MgSO₄) at 0.5 to 10 mM in concentration. Preferably the concentration is 2 to 6 mM.
- 6) A salt (e.g., (NH₄)₂SO₄) in the 5 to 50 mM range, preferably 10 mM.
- 7) A salt (e.g., KCl) at 20 to 200 mM.
- 8) A buffer (e.g., Tris-HCl), pH 7-8, preferably 7.5 in the 10-50 mM range of concentrations, preferably 10 mM.
- 9) A reducing agent (e.g., dithiothreitol (DTT)) in the 0.5 to 5 mM range, preferably 1 mM.
- 10) A detergent (e.g., Triton X-100), in the 0.01% to 1% range (V/V), preferably 0.01% final concentration (V/V).

Because T1 and T2 contain the sequences S' and S, respectively, and these two sequences are complementary to each other, T1 and T2 may anneal to each other to form the following partially double-stranded nucleic acid:

5



(T2)

To prevent the extension of the above partially double-stranded nucleic acid from the 3' terminus of the upper and lower strands, the 3'-termini of T1 and T2 may be blocked so that no free 3'-hydroxyl groups are available for extension. Alternatively, T1 and T2 molecules may be immobilized in different regions of a solid substrate or different solid substrates (e.g., microbeads).

The ping-pong amplification reaction cycle is also schematically described in Figure 7. The use of the ping-pong amplification reaction cycle in discriminating genetic variations is shown in Figure 8.

G. Implementation formats

The fingerprinting assays described above (which may include a nicking, linear amplification, or exponential amplification reaction) may be carried out in various formats. For instance, the reactions may be performed in a mixture where all the components are soluble. Alternatively, one or all of the template(s) can be covalently attached at the 3' end or the 5' end to a solid phase with the use of cross-linkers or spacers. The solid phase includes (without limitation) nylon tip beads, fluted tips, microbeads, microplate wells, membranes, slides, arrays, and the materials of which the solid phase is made include glass, nylon 6/6, silica, plastics like polystyrene, polymers like poly(ethyleneimine), etc.

For example, a replicator type of exponential amplification reaction may be performed using immobilized templates. More specifically, the

first template (T1) molecules may be linked to beads, while the second template (T2) molecules are linked to different beads. The beads linked with T1 molecules may be mixed with the beads linked with T2 molecules in a reaction mixture to amplify two oligonucleotides (*i.e.*, S and S' as described above in the context of the replicator type of amplification reaction). In addition, such a reaction may be carried out to amplify multiple oligonucleotide sequences. Beads linked with template molecules other than T1 and T2 molecules may be included in the reaction mixture so that oligonucleotides other than S and S' may also be amplified.

It is also possible and advantageous to perform amplification reactions (*e.g.*, direct EXPAR as described above) on arrays of immobilized oligonucleotides. The arrays can be composed of elements separated spatially on a 2-dimensional solid support. Suitable solid supports include, but are not limited to, glass slides, wafers, beads, microbeads, rods, ribbons, nylon6/6, nylon parts, polymer-coated solid supports, wells, etc. The arrays can be further assembled on a 3-dimensional solid support.

In such a reaction, the amplification template (*e.g.*, τ in Figure 2) is immobilized to a solid support at its 5' end or its 3' end, preferably at its 3'-end. There may or may not be any spacer between the template oligonucleotide and the solid support. The immobilized template, when annealing to a trigger oligonucleotide, may be used as a template to amplify an oligonucleotide having a sequence identical to the trigger oligonucleotide. The newly synthesized oligonucleotide then primes an adjacent template oligonucleotide in the element on (or in) the array and an exponential amplification reaction takes place. Oligonucleotide amplification is detected by employing a DNA binding dye that preferentially binds to double strand DNA (*e.g.*, SYBR[®] green).

The methods for immobilizing a nucleic acid or an oligonucleotide are known in the art. In certain embodiments, nucleic acids or oligonucleotides of the present invention are immobilized to a substrate to form an array. As used herein, an "array" refers to a collection of nucleic acids or oligonucleotides

that are placed on a solid support in distinct areas. Each area is separated by some distance in which no nucleic acid or oligonucleotide is bound or deposited. In some embodiments, area sizes are 20 to 500 microns and the center to center distances of neighboring areas range from 50 to 1500 microns.

- 5 The array of the present invention may contain 2-9, 10-100, 101-400, 401-1,000, or more than 1,000 distinct areas.

Generally, the nucleic acid or oligonucleotide may be immobilized to a substrate in the following two ways: (1) synthesizing the nucleic acids or the oligonucleotides directly on the substrate (often termed "*in situ* synthesis"),
10 or (2) synthesizing or otherwise preparing the nucleic acid or the oligonucleotides separately and then position and bind them to the substrate (sometimes termed "post-synthetic attachment"). For *in situ* synthesis, the primary technology is photolithography. Briefly, the technology involves modifying the surface of a solid support with photolabile groups that protect, for
15 example, oxygen atoms bound to the substrate through linking elements. This array of protected hydroxyl groups is illuminated through a photolithographic mask, producing reactive hydroxyl groups in the illuminated areas. A 3'-O-phosphoramidite-activated deoxynucleoside protected at the 5'-hydroxyl with the same photolabile group is then presented to the surface and coupling
20 occurs through the hydroxyl group at illuminated areas. Following further chemical reactions, the substrate is rinsed and its surface is illuminated through a second mask to expose additional hydroxyl groups for coupling. A second 5'-protected, 3'-O-phosphoramidite-activated deoxynucleoside is present to the surface. The selective photo-de-protection and coupling cycles are repeated
25 until the desired set of products is obtained. Detailed description of using photolithography in array fabrication may be found in the following patents or published patent applications: U.S. Patent Nos. 5,143,854; 5,424,186; 5,856,101; 5,593,839; 5,908,926; 5,737,257; and Published PCT Patent Application Nos. WO99/40105; WO99/60156; WO00/35931.

30 The post-synthetic attachment approach requires a methodology for attaching pre-existing oligonucleotides to a substrate. One method uses the

biotin-streptavidin interaction. Briefly, it is well known that biotin and streptavidin form a non-covalent, but very strong, interaction that may be considered equivalent in strength to a covalent bond. Alternatively, one may covalently bind pre-synthesized or pre-prepared nucleic acids or

5 oligonucleotides to a substrate. For example, carbodiimides are commonly used in three different approaches to couple DNA to solid supports. In one approach, the support is coated with hydrazide groups that are then treated with carbodiimide and carboxy-modified oligonucleotide. Alternatively, a substrate with multiple carboxylic acid groups may be treated with an amino-

10 modified oligonucleotide and carbodiimide. Epoxide-based chemistries are also used with amine modified oligonucleotides. Detailed descriptions of methods for attaching pre-existing oligonucleotides to a substrate may be found in the following references: U.S. Patent Nos. 6,030,782; 5,760,130; 5,919,626; published PCT Patent Application No. WO00/40593; Stimpson et al. *Proc. Natl.*

15 *Acad. Sci.* 92:6379-6383 (1995); Beattie et al. *Clin. Chem.* 41:700-706 (1995); Lamture et al. *Nucleic Acids Res.* 22:2121-2125 (1994); Chrisey et al. *Nucleic Acids Res.* 24:3031-3039 (1996); and Holmstrom et al., *Anal. Biochem.* 209:278-283 (1993).

The primary post-synthetic attachment technologies include ink

20 jetting and mechanical spotting. Ink jetting involves the dispensing of nucleic acids or oligonucleotides using a dispenser derived from the ink-jet printing industry. The nucleic acid oligonucleotides are withdrawn from the source plate up into the print head and then moved to a location above the substrate. The nucleic acids or oligonucleotides are then forced through a small orifice,

25 causing the ejection of a droplet from the print head onto the surface of the substrate. Detailed description of using ink jetting in array fabrication may be found in the following patents: U.S. Patent Nos: 5,700,637; 6,054,270; 5,658,802; 5,958,342; 6,136,962 and 6,001,309.

Mechanical spotting involves the use of rigid pins. The pins are

30 dipped into a nucleic acid or oligonucleotide solution, thereby transferring a small volume of the solution onto the tip of the pins. Touching the pin tips onto

the substrate leaves spots, the diameters of which are determined by the surface energies of the pins, the nucleic acid or oligonucleotide solution, and the substrate. Mechanical spotting may be used to spot multiple arrays with a single nucleic acid or oligonucleotide loading. Detailed description of using
5 mechanical spotting in array fabrication may be found in the following patents or published patent applications: U.S. Patent Nos. 6,054,270; 6,040,193; 5,429,807; 5,807,522; 6,110,426; 6,063,339; 6,101,946; and published PCT Patent Application Nos. WO99/36760; 99/05308; 00/01859; 00/01798.

One of ordinary skill in the art would appreciate that besides the
10 techniques described above, other methods may also be used in immobilizing nucleic acids or oligonucleotides to a substrate. Descriptions of such methods can be found in, but are not limited to, the following patent or published patent applications: U.S. Patent Nos. 5,677,195; 6,030,782; 5,760,130; and 5,919,626; and published PCT Patent Application Nos. WO98/01221; WO99/41007;
15 WO99/42813; WO99/43688; WO99/63385; WO00/40593; WO99/19341; and WO00/07022.

The substrate to which the nucleic acids or oligonucleotides of the present invention are immobilized to form an array is prepared from a suitable material. The substrate is preferably rigid and has a surface that is
20 substantially flat. In some embodiments, the surface may have raised portions to delineate areas. Such delineation separates the amplification reaction mixtures at distinct areas from each other and allows for the amplification products at distinct areas to be analyzed or characterized individually. The suitable material includes, but is not limited to, silicon, glass, paper, ceramic,
25 metal, metalloid, and plastics. Typical substrates are silicon wafers and borosilicate slides (*e.g.*, microscope glass slides). An example of a particularly useful solid support is a silicon wafer that is usually used in the electronic industry in the construction of semiconductors. The wafers are highly polished and reflective on one side and can be easily coated with various linkers, such
30 as poly(ethyleneimine) using silane chemistry. Wafers are commercially available from companies such as WaferNet, San Jose, CA.

Depending on the contemplated application, one of ordinary skill in the art may vary the composition of immobilized molecules of the present array. For instance, the T1 or T2 molecules of the present invention may or may not be immobilized to every distinct area of the array. Preferably, the

5 nucleic acids or oligonucleotides in a distinct area of an array are homogeneous. More preferably, the nucleic acids or oligonucleotides in every distinct area of an array to which the nucleic acids or oligonucleotides are immobilized are homogeneous. The term "homogeneous," as used herein, indicates that each nucleic acid or oligonucleotide molecule in a distinct area

10 has the same sequence as another nucleic acid or oligonucleotide molecule in the same area. Alternatively, the nucleic acid or oligonucleotide in at least one of the distinct areas of an array are heterogeneous. The term "heterogeneous," as used herein, indicates that at least one nucleic acid or oligonucleotide molecule in a distinct area has a different sequence from another nucleic acid

15 or oligonucleotide molecule in the area. In some embodiments, molecules other than the nucleic acids or oligonucleotides described above may also be present in some or all of distinct areas of an array. For instance, a molecule useful as an internal control for the quality of an array may be attached to some or all of distinct areas of an array. Another example for such a molecule may

20 be a nucleic acid useful as an indicator of hybridization stringency. In other embodiments, the composition of nucleic acids or oligonucleotides in every distinct area of an array is the same. Such an array may be useful in determining genetic variations in a particular gene in a selected population of organisms or in parallel diagnosis of a disease or a disorder associated with

25 mutations in a particular gene.

Depending on the envisioned application, the immobilized nucleic acids or oligonucleotides of the present invention (e.g., the T1 or T2 molecules) may contain oligonucleotide sequences that are at least substantially complementary or identical to various target nucleic acids. Such target nucleic

30 acids include, but are not limited to, genes associated with hereditary diseases in animals, oncogenes, genes related to disease predisposition, genomic DNAs

useful for forensics and/or paternity determination, genes associated with or rendering desirable features in plants or animals, and genomic or episomic DNA of infectious organisms. An array of the present invention may contain nucleic acids or oligonucleotides that are at least substantially complementary or identical to a particular type of target nucleic acids in distinct areas. For example, an array may have a nucleic acid or an oligonucleotide that is at least substantially complementary or identical to a first gene related to disease predisposition in a first distinct area, another nucleic acid or an oligonucleotide that is at least substantially complementary or identical to a second gene also related to disease predisposition in a second distinct area, yet another nucleic acid or an oligonucleotide that is at least substantially complementary or identical to a third gene also related to disease predisposition in a third distinct area, etc. Such an array is useful to determine disease predisposition of an individual animal (including a human) or a plant. Alternatively, an array may have nucleic acids or oligonucleotides that are at least substantially complementary or identical to multiple types of target nucleic acids categorized by the functions of the targets.

In addition, an array may contain nucleic acids or oligonucleotides that are at least substantially complementary or identical to a portion of a target nucleic acid that contains various potential genetic variations. For instance, a first area of the array may contain immobilized nucleic acids or oligonucleotides that are at least substantially complementary or identical to a portion of a target gene that contains a genetic variation of one allele of the target. A second area of the array may contain immobilized nucleic acids or oligonucleotides that are at least substantially complementary or identical to a portion of target gene that contains a genetic variation of another allele of the target. The array may have additional areas that contain immobilized nucleic acids or oligonucleotides that are at least substantially complementary or identical to portions of the target gene that contains genetic variations of additional alleles of the target.

In general, for successful performance in an array environment, the immobilized nucleic acids or oligonucleotides must be stable and not

dissociate during various treatment, such as hybridization, washing or incubation at the temperature at which an amplification reaction is performed. The density of the immobilized nucleic acids or oligonucleotides must be sufficient for the subsequent analysis. For an array suitable for the present methods, typically 1000 to 10^{12} , preferably 1000 to 10^6 , 10^6 to 10^9 , or 10^9 to 10^{12} ODNP molecules are immobilized in at least one distinct area. However, there must be minimal non-specific binding of other nucleic acids to the substrate. The immobilization process should not interfere with the ability of immobilized nucleic acids or oligonucleotides required for exponential nucleic acid amplification.

In certain embodiments, it may be desirable to have the nucleic acids or oligonucleotides of the present invention indirectly bound to the substrate via a linker. The linker (also referred to as a "linking element") comprises a chemical chain that serves to distance the nucleic acids or oligonucleotides from the substrate. In certain embodiments, the linker may be cleavable. There are a number of ways to position a linking element. In one common approach, the substrate is coated with a polymeric layer that provides linking elements with a lot of reactive ends/sites. A common example is glass slides coated with polylysine, which are commercially available. Another example is substrates coated with poly(ethyleneimine) as described in Published PCT Application No. WO99/04896 and U.S. Patent No. 6,150,103.

The array of the present invention enables the high throughput of various analyses to which the present nucleic acid amplification is applicable. For instance, an array of T2 molecules may be used to amplify multiple target nucleic acids. The reaction mixture or the products of an amplification reaction performed in the presence of a target nucleic acid may be pooled together and applied to the array of T2 molecules. Alternatively, the reaction mixtures or the amplification products of different amplification reactions may be applied to distinct areas of the array. Another round ("second round") of amplification reactions may then be performed on the array in the presence of a nicking agent that recognizes the nicking agent recognition sequence of which the antisense

strand is present in the T2 molecules. The amplification products of the second round of reactions performed on the array may be pooled together and analyzed. If the array (e.g., a microwell array) has distinct areas that are delineated by certain physical barriers, the amplification products of the second
5 round of reactions in distinct arrays may be analyzed individually.

For the nucleic acid molecules of the present invention that do not form an array, they may be immobilized via the methods described above that are useful in preparing an array. In addition, any methods known in the art may be used. For instance, a target nucleic acid of the present invention may be
10 immobilized by the use of a fixative or tissue printing. It may also be first isolated or purified and then transferred to a substrate that binds to nucleic acids or oligonucleotides, such as nitrocellulose or nylon membranes.

H. Product Identification

The products of a nicking reaction, a linear amplification reaction
15 or an exponential amplification reaction according to the present invention may be characterized by any applicable known methods. These methods include, but are not limited to mass spectrometry, fluorescence spectrometry, electrophoresis, liquid chromatography, hybridization and radiography. Certain exemplary methods are described in more detail below.

20 In certain embodiments, not all the amplified nucleic acids are characterized. In other words, in these embodiments, only certain amplified nucleic acids that meet a given criterion need be characterized. For instance, the amplified nucleic acid molecules may first be separated by liquid chromatography and only the fractions that contain short nucleic acid fragments
25 are further characterized by, for example, mass chromatography.

Mass Spectrometry

The fingerprinting assays of the present invention can be read out in a number of ways but the most ideal is by mass spectrometry since a series of well-defined and characterized oligonucleotides are generated that have

known mass/charge ratios (m/z). Exemplary mass spectrometric analysis includes Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry (MALDI) and Time-of-Fight (TOF).

Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry (MALDI-MS) is becoming an ever more popular technique for studying biomolecules (Hillenkamp et al., *Anal. Chem.* 63, 1193A-1203A, 1991). This technique ionizes high molecular weight biopolymers with minimal concomitant fragmentation of the sample material. This is typically accomplished via the incorporation of the sample to be analyzed into a matrix that absorbs radiation from an incident UV or IR laser. This energy is then transferred from the matrix to the sample resulting in desorption of the sample into the gas phase with subsequent ionization and minimal fragmentation. One of the advantages of MALDI-MS over ESI-MS is the simplicity of the spectra obtained: MALDI spectra are generally dominated by singly charged species. Typically, the gaseous ions generated by MALDI techniques are detected and analyzed by determining the time-of-flight (TOF) of these ions. While MALDI-TOF MS is not a high resolution technique, resolution can be improved by making modifications to such systems, e.g., by the use of tandem MS techniques, or by the use of other types of analyzers, such as Fourier transform (FT) and quadrupole ion traps.

MALDI techniques have found application for the rapid and straightforward determination of the molecular weight of certain biomolecules (Feng and Konishi, *Anal. Chem.* 64, 2090-2095, 1992; Nelson, Dogruel and Williams, *Rapid Commun. Mass Spectrom.* 8, 627-631, 1994). These techniques have been used to confirm the identity and integrity of certain biomolecules such as peptides, proteins, oligonucleotides, nucleic acids, glycoproteins, oligosaccharides and carbohydrates. Further, these MS techniques have found biochemical applications in the detection and identification of post-translational modifications on proteins. Verification of DNA and RNA sequences that are less than 100 bases in length has also been

accomplished using ESI with FTMS to measure the molecular weight of the nucleic acids (Little et al, *Proc. Natl. Acad. Sci. USA* 92, 2318-2322, 1995).

The matrix is an important feature of MALDI-MS. Typically, analysis of nucleic acids by MALDI can be divided into two steps. The first step
5 involves preparing the sample by mixing the sample to be analyzed with a molar excess of a chemical commonly referred to as the "matrix." See, e.g., Wu et al. *Rapid Commun. Mass Spectrom.* 7:142-146 (1993). The primary purpose of the matrix is to promote ionization of the nucleic acid. Without the matrix, the nucleic acid molecule tends to fragment upon exposure to the laser
10 energy, so that the mass and identity of the nucleic acid is difficult or impossible to determine. In general, the term "matrix" refers to a substance which absorbs radiation at a wavelength substantially corresponding to the pulse of laser energy used in the MALDI method, and where the matrix facilitates desorption and ionization of molecules. A matrix may be any one of several small, light-
15 absorbing chemicals that may be mixed in solution with a nucleic acid in such a manner so that, upon drying on a solid support (e.g., a sample plate or a probe element), the crystalline matrix-embedded analyte molecules are successfully desorbed by laser irradiation and ionized from the solid phase crystals into the vapor phase and accelerate as intact molecular ions. The second step of the
20 MALDI process involves desorption of the bulk portions of the solid sample by a short pulse of laser light.

While this is probably the most commonly employed approach to combining matrix and analyte prior to MALDI-MS analysis, other methods may be used. For instance, according to one aspect of the invention, the analyte-
25 containing sample is added to (e.g., spotted onto) a coating of cationic polyelectrolyte, allowing the analyte (nucleic acid) to bind to the cationic polyelectrolyte. This spot is then washed in order to purify the nucleic acid. The spot is then treated with matrix (when the matrix is a liquid) or a solution of matrix (when the matrix is a solid). When the matrix is a solid, the spot should
30 be allowed to dry in order to remove the solvent that was formerly used to dissolve the matrix in solution. Thereafter, this spot of nucleic acid and matrix

can be subjected to MALDI-MS to provide a very strong signal due to the nucleic acid.

Accordingly, in one aspect, the present invention provides a solid support having a surface, where that surface is at least partially coated with a coating comprising cationic polyelectrolyte, where at least some of the cationic polyelectrolyte is in contact with nucleic acid and the nucleic acid is in contact with matrix. In a preferred embodiment, the solid support is a plate, *e.g.*, a stainless steel plate, and the cationic polyelectrolyte either forms a continuous coating across all or a significant portion of the surface, or is spotted onto the surface in distinct regions. Nucleic acid and matrix is then located in distinct regions on the surface, so as to provide an array-type appearance. For example, the surface may be a 96-well plate, with cationic polyelectrolyte, nucleic acid and matrix located in one, and preferably more than one, of the wells. This array is then subjected to MALDI-MS, where the various regions are sequentially subjected to laser light, and the mass spectrum of the nucleic acid present in the spots is sequentially obtained.

To achieve its purpose, the matrix should meet one or more of the following criteria, and preferably meets many or all of these criteria. The matrix should be able to embed and isolate nucleic acid (*e.g.*, by co-crystallization), it should be soluble in solvents compatible with nucleic acids, it should be stable under the vacuum used in MALDI, it should assist co-desorption of the nucleic acid upon laser irradiation, and it should promote ionization of the nucleic acid. In order to meet these criteria, the matrix should comprise a chromophore that strongly absorbs in the wavelength of light being emitted by the laser. For instance, if the laser is an ultraviolet laser, then the matrix should have a chromophore that absorbs in the ultraviolet region.

The following chemicals have been identified as suitable matrices for nucleic acids, where these as well as other suitable matrix chemicals known in the art may be used in the methods and compositions of the present invention: 6-aza-2-thiothymine (ATT), glycerol, 2,4,6-trihydroxyacetophenone (THAP), picolinic acid (PA), 3-hydroxy picolinic acid (HPA), 2,5-

dihydroxybenzoic acid, anthranilic acid, nicotinic acid, and salicylamide.

Mixtures of these chemicals are also suitable. Typically, the matrix is a solid at room temperature. However, the matrix may be a liquid chemical, where

suitable liquid matrices are substituted or unsubstituted: (1) alcohols, including:

- 5 glycerol, 1,2- or 1,3-propane diol, 1,2-, 1,3- or 1,4-butane diol, triethanolamine; (2) carboxylic acids including: formic acid, lactic acid, acetic acid, propionic acid, butanoic acid, pentanoic acid, hexanoic acid and esters thereof; (3) primary or secondary amides including acetamide, propanamide, butanamide, pentanamide and hexanamide, whether branched or unbranched; (4) primary or
10 secondary amines, including propylamine, butylamine, pentylamine, hexylamine, heptylamine, diethylamine and dipropylamine; (5) nitriles, hydrazine and hydrazide. These liquid matrices are particularly useful when the MALDI laser emits light in the infrared spectrum. It is reported that THAP works best for samples below 10kDa while HPA and PA are more appropriate for
15 oligonucleotides above 10kDa. Acidic matrices, *e.g.*, HPA, are preferred for single-stranded nucleic acids, while neutral matrices, *e.g.*, glycerol and ATT, are preferred for double-stranded nucleic acids.

In certain preferred embodiments of the present invention, another type of mass spectrometry other than MALDI may be employed. MS is
20 particularly advantageous in those applications in which it is desirable to eliminate a size separation step prior to molecular weight determination. Sensitivities of MS may be achieved to at least to 1 amu. The smallest mass differences in nucleic acid bases is between adenine and thymidine which is 9 Daltons.

- 25 Particularly preferred methodologies according to the present invention employ Liquid Chromatography-Time-of-Flight Mass Spectrometry (LC-TOF-MS). LC-TOF-MS is composed of an orthogonal acceleration Time-of-Flight (TOF) MS detector for atmospheric pressure ionization (API) analysis using electrospray (ES) or atmospheric pressure chemical ionization (APCI).
30 LC-TOF-MS provides high mass resolution (5000 FWHM), high mass measurement accuracy (to within 5ppm) and very good sensitivity (ability to

detect femtomolar amount of DNA polymer). TOF instruments are generally more sensitive than quadrupoles, but are correspondingly more expensive.

LC-TOF-MS has a more efficient duty cycle since the current instruments can sequentially analyze one mass at a time while rejecting all others (this is referred to as single ion monitoring (SIM)). LC-TOF-MS samples all of the ions passing into the TOF analyzer at the same time. This results in higher sensitivity, provides quantitative data, which improves the sensitivity between 10 and 100 fold. Enhanced resolution (5000 FWHM) and mass measurement accuracy of better than 5 ppm imply that differences between nucleosides as small as 9 amu (Daltons) can be accurately measured. The TOF mass analyzer performs very high frequency sampling (10 spectra/sec) of all ions simultaneously across the full mass range of interest. The duty cycle of the LC-TOF-MS allows high sensitivity spectra to be recorded in quick succession making the instrument compatible with more efficient separations techniques such as narrow bore LC, capillary chromatography (CE) and capillary electrochromatography (CEC). The ions are pulsed into the analyzer, effectively taking a 'snapshot' of the ions present at any time.

In the first stage the ES or APCI aerosol spray is directed perpendicularly past the sampling cone, which is displaced from the central axis of the instrument. Ions are extracted orthogonally from the spray into the sampling cone aperture leaving large droplets, involatile materials, particulates and other unwanted components to collect in the vent port that is protected with an exchangeable liner. The second orthogonal step enables the volume of gas (and ions) sampled from atmosphere to be increased compared with conventional API sources. Gas at atmospheric pressure sampled through an aperture into a partial vacuum forms a freely expanding jet, which represents a region of high performance compared to the surrounding vacuum. When this jet is directed into the second aperture of a conventional API interface it increases the flow of gas through the second aperture. Maintaining a suitable vacuum in the MS-TOF therefore places a restriction on the maximum diameter of the apertures in such an LC interface. Ions in the partial vacuum of the ion

block are extracted electrostatically into the hexapole ion bridge that efficiently transports ions to the analyzer.

The coupling of the TOF mass analyzers with MUX-technology allows the connection of up to 8 HPLC columns in parallel to a single LC-TOF-MS. (Micromass, Manchester UK). A multiplexed electrospray (ESI) interface is used for on-line LC-MS utilizing an indexed stepper motor to sequentially sample from up to 8 HPLC columns or liquid inlets operated in parallel.

Use of LC-TOF-MS is sometimes preferred over use of MALDI-TOF because LC-TOF-MS is a quantitative method for analysis of the molecular weight of polymers. LC-TOF-MS does not fragment the polymers and it employs a very gentle ionization process compared to matrix-assisted-laser-desorption-ionization (MALDI). Because every MALDI blast is different, the ionization is not quantitative. LC-TOF-MS does, however, produce different m/z values for polymers.

15 High Performance Liquid Chromatography (HPLC)

High-Performance Liquid Chromatography (HPLC) is a chromatographic technique for separation of compounds dissolved in solution. HPLC instruments consist of a reservoir of mobile phase, a pump, an injector, a separation column, and a detector. Compounds are separated by injecting an aliquot of the sample mixture onto the column. The different components in the mixture pass through the column at different rates due to differences in their partitioning behavior between the mobile liquid phase and the stationary phase. The pumps provide a steady high performance with no pulsating, and can be programmed to vary the composition of the solvent during the course of the separation.

Exemplary detectors useful within the methods of present invention include UV-VIS absorption, or fluorescence after excitation with a suitable wavelength, mass spectrometers and IR spectrometers. Recently, IP-RO-HPLC on non-porous PS/DVB particles with chemically bonded alkyl chains have been shown to be rapid alternatives to capillary electrophoresis in the

analysis of both single and double-strand nucleic acids providing similar degrees of resolution. (Huber et al., *Anal. Biochem.* 212:351 (1993); Huber et al., *Nuc. Acids Res.* 21:1061 (1993); Huber et al. *Biotechniques* 16:898 (1993)). In contrast to ion-exchange chromatography, which does not always retain
5 double-strand DNA as a function of strand length (since AT base pairs interact with the positively charged stationary phase, more strongly than GC base-pairs), IP-RP-HPLC enables a strictly size-dependent separation.

A method has been developed using 100 mM triethylammonium acetate as ion-pairing reagent, phosphodiester oligonucleotides could be
10 successfully separated on alkylated non-porous 2.3 μ M poly(styrene-divinylbenzene) particles by means of high performance liquid chromatography. (Oefner et al., *Anal. Biochem.* 223:39 (1994)). The technique described allows the separation of PCR products differing by only 4 to 8 base pairs in length within a size range of 50 to 200 nucleotides.

15 Denaturing HPLC (DHPLC) is an ion-pair reversed-phase high performance liquid chromatography methodology (IP-RP-HPLC) that uses a non-porous C-18 column as the stationary phase. The column is comprised of a polystyrene-divinylbenzene copolymer. The mobile phase is comprised of an ion-pairing agent of triethylammonium acetate (TEAA), which mediates binding
20 of DNA to the stationary phase, and acetonitrile (ACN) as an organic agent to achieve subsequent separation of the DNA from the column. A linear gradient of acetonitrile allows separation DHPLC identifies mutations and polymorphisms based on detection of heteroduplex formation between mismatched nucleotides in double stranded PCR amplified DNA. Sequence
25 variation creates a mixed population of heteroduplexes and homoduplexes during reannealing of wild type and mutant DNA of fragments based on size and/or presence of heteroduplexes (this is the traditional use of the DHPLC technology). When this mixed population is analyzed by HPLC under partially denaturing temperatures, the heteroduplexes elute from the column earlier than
30 the homoduplexes because of their reduced melting temperature. Analysis can

be performed on individual samples to determine heterozygosity, or on mixed samples to identify sequence variation between individuals.

Real-time Fluorescence

The various nicking and amplification reactions described above
5 may also be readout by detectors that measure real-time fluorescence, such as the MJ Opticon from MJ Research (Boston, MA), the ABI Prism 7000 instrument (Foster City, CA), and endpoint plate readers, such as the Ultramark from Biorad (Hercules, CA). Real time monitoring is a very useful method as it enables parameters such as initial rates to be determined with accuracy and
10 ease. The use of double-strand specific fluorescent dyes such as SYBR[®] green from Molecular Probes (Eugene OR) is especially useful when used during the amplification reactions described above. Dyes that bind to single strand nucleic acids can also be used, perhaps at times with slightly less efficacy than double-strand specific dyes. Currently, there are four types of
15 detection chemistries that can be used for real time fluorescence readout: intercalating dyes such as SYBR[®], dual labeled probes, FRET (fluorescent energy transfer) probes and Molecular Beacons. Exemplary fluorescent intercalating agents include, without limitation, those disclosed in U.S. Pat. Nos. 4,119,521; 5,599,932, 5,658,735; 5,734,058; 5,763,162; 5,808,077; 6,015,902;
20 6,255,048 and 6,280,933, those discussed in Glazer and Rye, *Nature* 359: 859-61, 1992, PicoGreen dye, and SYBR[®] dyes such as SYBR[®] Gold, SYBR[®] Green I and SYBR[®] Green II (Molecular Probes, Eugene WA). Fluorescence produced by fluorescent intercalating agents may be detected by various detectors, including PMTs, CCD cameras, fluorescent-based microscopes,
25 fluorescent-based scanners, fluorescent-based microplate readers, fluorescent-based capillary readers.

To increase the signal produced by fluorescent intercalating agents, after the amplification reaction, the nicking agent in the reaction mixture may be inactivated (e.g., by heat) and a fresh DNA polymerase be added. The
30 presence of the active DNA polymerase, but not the nicking agent, allows any

partial duplexes to be extended to completely double-stranded nucleic acid fragments. The generation of such completely double-stranded nucleic acid fragments allow the binding of a greater number of fluorescent intercalating agents, which in turn increase the signal that may be detected.

5 I. Compositions/Kits

In one aspect, the present invention provides a composition or kit comprising polynucleotide, a nicking agent and a polymerase. The inventive compositions have unique properties that render them particularly useful in identifying the source organism of a nucleic acid sample. Such a source
10 organism may be a bacterium, fungus, virus, plant, non-human animal or human.

Such a composition or kit generally comprises the template oligonucleotide(s) useful for amplifying initiating oligonucleotides described above. It may also further comprise at least one, two, several, or each of the
15 following components: (1) a nicking agent (*e.g.*, a NE or a RE) that recognizes the nicking agent recognition sequence of which one strand is present in the template oligonucleotide(s); (2) a suitable buffer for nicking agent (1); (3) a RE that functions in combination with a nicking agent (with may be identical to or different from nicking agent (1); (4) a suitable buffer for RE (3); (5) a DNA
20 polymerase; (6) a suitable buffer for the DNA polymerase (5); (7) dNTPs; (8) a modified dNTP; (9) a strand displacement facilitator (*e.g.*, 1M trehalose); and (10) a fluorescent intercalating agent. Detailed descriptions of many of the above components have been provided above.

J. Applications

25 The present invention alleviates and overcomes many drawbacks of the present state of the art through the discovery of novel methods and kits for rapidly fingerprinting DNA to identify prokaryotic and eukaryotic species, subspecies, and especially strains or individuals of the subspecies. With respect to prokaryotic organisms, the present invention is especially suited for

identifying different bacterial strains involved in, for example, nosocomial infections, since the methods and kits are to be sensitive enough to detect differences between, for example, bacterial isolates of the same species. With respect to eukaryotes, the present invention contemplates identifying, for instance, species, subspecies, and the differences between the individuals of the subspecies, such as pedigrees.

In various aspects of the present invention the method can be used for: (1) diagnosis of bacterial disease, in plants animals and humans; (2) monitoring for bacterial content and/or contamination in the environment; (3) monitoring food for bacterial contamination; (4) monitoring manufacturing processes for bacterial contamination; (5) monitoring quality assurance/quality control of laboratory tests involving microbiological assays; (6) tracing bacterial contamination and/or outbreaks of bacterial infections; (7) genome mapping; (8) monitoring bioremediation sites; and (9) monitoring agricultural sites for test crops, bacteria and recombinant molecules.

The method is useful on pure or isolated cultures as well as actual samples from the test site. Because of the simplicity of the test it can also be automated for rapid and quick assay of samples. A further aspect of the present invention is a machine for automating the identification of bacterial strains, particularly by mass spectrometry.

The present invention affords the medical community with a means to not only identify the infectious agents, but also to rapidly characterize the strain or strains involved so that effective measures may be timely employed.

Another application of this method is in the manufacturing process. A number of manufacturing processes for instance drugs, microorganism-aided synthesis, food manufacturing, chemical manufacturing and fermentation process all rely either on the presence or absence of bacteria. In either case the method of the present invention can be used. It can monitor bacterial contamination or test that strain purity is being maintained.

This method can also be used to test stored blood for bacterial contamination. This would be important in blood banking where bacteria such as *Yersinia enterocolitica* can cause serious infection and death if it is in transfused blood.

5 The procedure can also be used for quality assurance and quality control in monitoring bacterial contamination in laboratory tests. For example the Guthrie bacterial inhibition assay uses a specific strain of bacteria to measure phenylalanine in newborn screening. If this strain changes it could affect test results and thus affect the accuracy of the newborn screening
10 program. This method of the present invention can be used to monitor the strain's purity. Any other laboratory test that uses or relies on bacteria in the assay can be monitored. The laboratory or test environment can also be monitored for bacterial contamination by sampling the lab and testing for specific strains of bacteria.

15 This procedure will also be useful in hospitals for tracing the origin and distribution of bacterial infections. It can show whether or not the infection of the patient is a hospital-specific strain. The type of treatment and specific anti-bacterial agent can depend on the source and nature of the bacteria.

 There are a variety of applications for the fingerprinting
20 technology described here. An immediate need is in rapid pathogen detection and bio-threat. Since short oligonucleotides can be generated and amplified ($10^8 - 10^9$ fold) from a nucleic acid sample in a 3-5 minutes time frame and the amplification of can be achieved in 3 minutes, it is conceivable that 10-15 minutes assay can be constructed. It is certain that clinical utility can be gained
25 from the viral quantification as a tool for disease monitoring and cancer typing. Since the assay is highly quantitative using real-time fluorescence readout, we see rapid real-time molecular diagnostics to aid in the appropriate use of antimicrobials. This type of fingerprinting technology will also speed the development and application of nucleic acid-based technologies for microbial
30 content analyses in foods stock.

The fingerprinting technology described herein may be useful to detect polymorphisms in the human genome, in view of the large number of fragments that can be generated. The methods and compositions of the present invention may be used to interrogate a sample for the presence of

5 fragments that uniquely identify all pathogens, and fragments obtained from the human genome that can be used to uniquely identify individuals.

The following examples are provided for purposes of illustration and not the invention is not limited thereby.

EXAMPLES

EXAMPLE 1COMPUTATIONAL RESULTS FROM GENOMIC DNAs USING N.BstNB I NICKING
ENZYME AND N. AlwI NICKING ENZYME

5

Computer assisted identification of the adjacent nicking enzyme recognition sites of N.BstNB I and/or N.Alw I in E. coli was performed.

Oligonucleotide fragments 6-16 nucleotides in length that would be generated from the genomic DNA of E. coli K12 and O157 are shown in Tables 1 and 2,
10 respectively. A total of 115 oligonucleotides that are 6-16 nucleotides long could be generated from these two strains. Out of the combined 115 oligonucleotides, 70 oligonucleotides have unique masses, whereas each of the remaining fragments has a mass identical to another fragment (see Table 3). Twelve oligonucleotides uniquely identify K12, and 15 oligonucleotides uniquely
15 identify O157 (Table 4). These oligonucleotides unique for distinguishing the two E. coli strains are not found in the oligonucleotides that would be generated in the presence of N.BstNB I from chromosome 21 of the human genome (see Table 5).

Table 6 lists the relative probability of obtaining an overlapping
20 mass (composition) as a function of the length of the trigger in a background of DNA that is as complex as the human genome (4 billion bases).

Table 7 lists the number of oligonucleotides having 6-16 nucleotides that would be generated in the presence of N.BstNB I from 35 bacterial species. The average number of oligonucleotides that would be
25 generated per organism is 19. Greater than 99% of these fragments have a unique mass and sequence, thus virtually every one of the fingerprinting oligonucleotides is unique to the organism from which it is generated.

Table 1: E. coli K12 oligonucleotide fragments.

Position of the first nucleotide of oligo- nucleotide in genomic DNA	Product 5' → 3'	Position of the last nucleotide of oligo- nucleotide in genomic DNA	Base Mass	m/z=2	m/z=3	m/z=4	Mass difference between adjacent fragments
4064758	CACAAC	4064763	1825.2	911.6	607.4	455.3	38.0
2111739	GTCGTC	2111744	1863.2	930.6	620.1	464.8	8.0
765268	GATTCA	765273	1871.2	934.6	622.7	466.8	18.0
4571546	AACAGA	4571551	1889.2	943.6	628.7	471.3	22.0
4549455	GATAGT	4549460	1911.2	954.6	636.1	476.8	7.0
4567093	TGTTGG	4567098	1918.2	958.1	638.4	478.6	169.1
49704	CTCTCTC	49710	2087.3	1042.7	694.8	520.8	9.0
1139368	ACCCTTC	1139374	2096.4	1047.2	697.8	523.1	49.0
1403700	GACATCC	1403706	2145.4	1071.7	714.1	535.3	12.0
3715545	TTCGTTT	3715551	2157.4	1077.7	718.1	538.3	4.0
1274893	GATCCCG	1274899	2161.4	1079.7	719.5	539.3	5.0
2201638	TGTTACT	2201644	2166.4	1082.2	721.1	540.6	3.0
3528528	CCATAGA	3528534	2169.4	1083.7	722.1	541.4	22.0
3528528	TCTATGG	3528534	2191.4	1094.7	729.5	546.9	2.0
2201638	AGTAACA	2201644	2193.4	1095.7	730.1	547.4	7.0
4397983	GATCAGT	4397989	2200.4	1099.2	732.5	549.1	16.0
1403700	GGATGTC	1403706	2216.4	1107.2	737.8	553.1	40.0
3901602	GATGGTG	3901608	2256.5	1127.2	751.2	563.1	18.0
49704	GAGAGAG	49710	2274.5	1136.2	757.2	567.6	144.1
3143034	AACATCCC	3143041	2418.6	1208.3	805.2	603.6	47.0
2638367	TGTCGCCA	2638374	2465.6	1231.8	820.9	615.4	273.2
1156599	TCCACCAGT	1156607	2738.8	1368.4	911.9	683.7	15.0
1325420	TGTACCACT	1325428	2753.8	1375.9	916.9	687.4	33.0
2413336	AAAATCTCG	2413344	2786.8	1392.4	927.9	695.7	32.0

Position of the first nucleotide of oligo- nucleotide in genomic DNA	Product 5'→3'	Position of the last nucleotide of oligo- nucleotide in genomic DNA	Base Mass	m/z=2	m/z=3	m/z=4	Mass difference between adjacent fragments
272636	AACGTGCGT	272644	2818.8	1408.4	938.6	703.7	17.0
2074077	TGAAAAAAG	2074085	2835.9	1416.9	944.3	708.0	287.2
1651695	AACGTGTTGC	1651704	3123.0	1560.5	1040.0	779.8	1.0
3436566	CGCGAGTTGC	3436575	3124.0	1561.0	1040.3	780.0	17.0
1093455	TAAAGCGGCA	1093464	3141.0	1569.5	1046.0	784.3	246.1
1302101	CACTACTTTGG	1302111	3387.2	1692.6	1128.1	845.8	3.0
386112	CGCAGCATCAA	386122	3390.2	1694.1	1129.1	846.6	55.0
1302101	CCAAAGTAGTG	1302111	3445.2	1721.6	1147.4	860.3	258.2
2974219	TGCAGACCACAA	2974230	3703.4	1850.7	1233.5	924.9	40.0
427004	CCAGTGAGCAAA	427015	3743.4	1870.7	1246.8	934.9	13.0
1701613	CGGTATATCGTG	1701624	3756.4	1877.2	1251.1	938.1	42.1
1413750	TGAAGCTAAGGA	1413761	3798.5	1898.2	1265.2	948.6	233.1
2937922	AGTGCGCCGCTGC	2937934	4031.6	2014.8	1342.9	1006.9	29.0
105759	TGCTTGGACAGTT	105771	4060.6	2029.3	1352.5	1014.2	80.0
312061	GGATTGAGTGTG	312073	4140.7	2069.3	1379.2	1034.2	19.0
2275435	GTTGAGCGAGGAG	2275447	4159.7	2078.8	1385.6	1038.9	473.3
2063725	ATAAGCGCCTCTGCG	2063739	4633.0	2315.5	1543.3	1157.2	17.0
3963947	ACCGTAAACAGGCAT	3963961	4650.0	2324.0	1549.0	1161.5	9.0
2273723	TCAGGCCAAACAGAA	2273737	4659.0	2328.5	1552.0	1163.8	14.0
2063725	CGCAGAGCGCTTAT	2063739	4673.0	2335.5	1556.7	1167.3	12.0
412051	CGTGTTTTATGGCTG	412065	4685.0	2341.5	1560.7	1170.3	20.1
198629	TTGAAACGGGCATAA	198643	4705.1	2351.5	1567.4	1175.3	60.0
3408973	AGGGGTTTTTGGGTT	3408987	4765.1	2381.5	1587.4	1190.3	89.1
1097197	TCTCCGCTTTTCCATG	1097212	4854.1	2426.1	1617.0	1212.5	83.1
3826599	CAACCGGTTGCGCATT	3826614	4937.2	2467.6	1644.7	1233.3	4.0

Position of the first nucleotide of oligo- nucleotide in genomic DNA	Product 5'→3'	Position of the last nucleotide of oligo- nucleotide in genomic DNA	Base Mass	m/z=2	m/z=3	m/z=4	Mass difference between adjacent fragments
2524967	TGAAACTTTTTCGTAT	2524982	4941.2	2469.6	1646.1	1234.3	45.0
3826599	AATGCGCAACCGGTTG	3826614	4986.2	2492.1	1661.1	1245.6	20.0
558515	TTCTGGATGAATGTTA	558530	5006.2	2502.1	1667.7	1250.6	4.0
1595241	TACCGTGATGACAGAG	1595256	5010.3	2504.1	1669.1	1251.6	58.1
1097197	CATGGAAAAGCGGAGA	1097212	5068.3	2533.2	1688.4	1266.1	

Table 2: E. coli O157 oligonucleotide fragments.

Start	Product	5'→3'	End	Mass	m/z=2	m/z=3	m/z=4	difference
1095650	CCTCCC		1095655	1768.1	883.1	588.4	441.0	57.1
4862976	CACAAC		4862981	1825.2	911.6	607.4	455.3	38.0
2787876	GTCTGC		2787881	1863.2	930.6	620.1	464.8	48.1
5406708	GATAGT		5406713	1911.2	954.6	636.1	476.8	7.0
5432628	TGTTGG		5432633	1918.2	958.1	638.4	478.6	169.1
54118	CTCTCTC		54124	2087.3	1042.7	694.8	520.8	9.0
1499252	ACCCTTC		1499258	2096.4	1047.2	697.8	523.1	49.0
1915148	GACATCC		1915154	2145.4	1071.7	714.1	535.3	12.0
4465490	TTCGTTT		4465496	2157.4	1077.7	718.1	538.3	9.0
2882357	TGTTACT		2882363	2166.4	1082.2	721.1	540.6	27.0
2882357	AGTAACA		2882363	2193.4	1095.7	730.1	547.4	7.0
5254130	GATCAGT		5254136	2200.4	1099.2	732.5	549.1	16.0
1915148	GGATGTC		1915154	2216.4	1107.2	737.8	553.1	15.0
2914783	GATGGTT		2914789	2231.4	1114.7	742.8	556.9	43.0
54118	GAGAGAG		54124	2274.5	1136.2	757.2	567.6	144.1
3885373	AACATCCC		3885380	2418.6	1208.3	805.2	603.6	28.0
1764961	CTGCTTTT		1764968	2446.6	1222.3	814.5	610.6	9.0
2148971	ATTTCCTG		2148978	2455.6	1226.8	817.5	612.9	10.0
3356488	TGTCGCCA		3356495	2465.6	1231.8	820.9	615.4	0.0
5347073	CTTCGGCA		5347080	2465.6	1231.8	820.9	615.4	49.0
5347073	TGCCGAAG		5347080	2514.6	1256.3	837.2	627.7	8.0
2148971	CAGGAAAT		2148978	2522.7	1260.3	839.9	629.7	216.1
1516471	TCCACCAGT		1516479	2738.8	1368.4	911.9	683.7	15.0
1828106	TGTACCACT		1828114	2753.8	1375.9	916.9	687.4	33.0
3141487	AAAATCTCG		3141495	2786.8	1392.4	927.9	695.7	62.0
368468	TGGAATGTT		368476	2848.8	1423.4	948.6	711.2	266.2
154799	TCAATGTAAA		154808	3115.0	1556.5	1037.3	777.8	9.0
4173941	CGCGAGTTGC		4173950	3124.0	1561.0	1040.3	780.0	263.2
1746921	CACTACTTTGG		1746931	3387.2	1692.6	1128.1	845.8	3.0

Start	Product 5'→3'	End	Mass	m/z=2	m/z=3	m/z=4	difference
447890	CGCAGCATCAA	447900	3390.2	1694.1	1129.1	846.6	6.0
392522	TGGCAATATCC	392532	3396.2	1697.1	1131.1	848.1	49.0
1746921	CCTAAGTAGTG	1746931	3445.2	1721.6	1147.4	860.3	21.0
1660620	GATATTATTGG	1660630	3466.3	1732.1	1154.4	865.6	237.2
3698597	TGCAGACCACAA	3698608	3703.4	1850.7	1233.5	924.9	40.0
491409	CCAGTGAGCAAA	491420	3743.4	1870.7	1246.8	934.9	13.0
2303220	CGGTATATCGTG	2303231	3756.4	1877.2	1251.1	938.1	42.1
1925197	TGAAGCTAAGGA	1925208	3798.5	1898.2	1265.2	948.6	233.1
3662300	AGTGGCCCGCTGC	3662312	4031.6	2014.8	1342.9	1006.9	29.0
110364	TGCTTGACAGTT	110376	4060.6	2029.3	1352.5	1014.2	99.1
3012345	GTTGAGCGAGGAG	3012357	4159.7	2078.8	1385.6	1038.9	134.1
2268011	TTTAACGCCAGTTC	2268024	4293.8	2145.9	1430.3	1072.4	11.0
1856922	CCGCGCGTAATGCC	1856935	4304.8	2151.4	1433.9	1075.2	80.0
1856922	GGCATTACGCGCGG	1856935	4384.8	2191.4	1460.6	1095.2	7.0
2268011	GAACGGCGTTAAA	2268024	4391.9	2194.9	1463.0	1097.0	207.1
2701876	CGGTATTTTCATCCCG	2701890	4599.0	2298.5	1532.0	1148.7	34.0
2735173	ATAAGCGCTCTGCG	2735187	4633.0	2315.5	1543.3	1157.2	17.0
4759738	ACCGTAAACAGGCAT	4759752	4650.0	2324.0	1549.0	1161.5	9.0
3010633	TCAGGCCAAACAGAA	3010647	4659.0	2328.5	1552.0	1163.8	14.0
2735173	CGCAGAGCGCTTAT	2735187	4673.0	2335.5	1556.7	1167.3	12.0
474811	CGTGTTTTATGGCTG	474825	4685.0	2341.5	1560.7	1170.3	21.0
2701876	CGGGATGAAATACCG	2701890	4706.1	2352.0	1567.7	1175.5	59.0
4146296	AGGGTTTTTGGGTT	4146310	4765.1	2381.5	1587.4	1190.3	89.1
1457114	TCTCCGCTTTTCCATG	1457129	4854.1	2426.1	1617.0	1212.5	83.1
4573519	CAACCGGTTGGGCATT	4573534	4937.2	2467.6	1644.7	1233.3	4.0
3251326	TGAAACTTTTTCGTAT	3251341	4941.2	2469.6	1646.1	1234.3	38.0
1785538	ACGGTGCCTGCCCGGG	1785553	4979.2	2488.6	1658.7	1243.8	0.0
1952836	ACGGTGCCTGCCCGGG	1952851	4979.2	2488.6	1658.7	1243.8	0.0
2228257	ACGGTGCCTGCCCGGG	2228272	4979.2	2488.6	1658.7	1243.8	7.0
4573519	AATGCGCAACCGGTTG	4573534	4986.2	2492.1	1661.1	1245.6	24.0
2121139	TACCGTGATGACAGAG	2121154	5010.3	2504.1	1669.1	1251.6	58.1

Start	Product 5'→3'	End	Mass	m/z=2	m/z=3	m/z=4	difference
1457114	CATGGAAAAGCGGAGA	1457129	5068.3	2533.2	1688.4	1266.1	

Table 3. Comparison of the shared and unique fingerprinting fragments between two E. coli strain K12 and O157

Length of fragment	Total number of fragments	Number of fragment per strain K12/O157	Number of fragments with unique masses	Number of fragments without unique masses	Number of fragments unique to strain K12/O157
6	11	6/5	7	4	2/1
7	23	13/10	14	9	3/1
8	9	2/7	6	2	0/3
9	9	5/4	6	3	2/1
10	5	3/2	4	1	2/1
11	8	3/5	5	3	0/2
12	8	4/4	4	4	0/0
13	7	4/3	4	3	1/0
14	4	0/4	4	0	0/2
15	15	7/8	8	7	1/1
16	16	7/9	8	7	1/3
total	115	54/61	70	43 (2 repeats)	12/15
total %		47/53	61	61 (unique)	17/21 (unique)

Table 4. Unique fingerprinting oligonucleotides for *E. coli* strains O157H7 and K12

Sig.	Start	Organism	Product	End	Sequence
5-1-1-3	154799	escherichia_coli_O157H7.fna	TCAATGTAAA	154808	GAGTCATTGTCAATGTAAAAGTTGATCC
2-0-3-4	368468	escherichia_coli_O157H7.fna	TGGAATGTT	368476	GGATCCCCTAACATTCCAGACAGACTC
3-3-2-3	392522	escherichia_coli_O157H7.fna	TGGCAATATCC	392532	GGATCGGGTGGATATTGCCACCATGACTC
1-0-5-0	1095650	escherichia_coli_O157H7.fna	GGAGGG	1095655	GGATACCGGGGAGGGCTGGACTC
3-0-3-5	1660620	escherichia_coli_O157H7.fna	GATATTATTGG	1660630	GGATCAAAATCCAATAATATCCCATGACTC
0-2-1-5	1764961	escherichia_coli_O157H7.fna	CTGCTTTT	1764968	GAGTCCGGGCTGCTTTTTCGGGATCC
1-6-7-2	1785538	escherichia_coli_O157H7.fna	ACGGTGCCTGCCCGGG	1785553	GAGTCGGTGACGGTGCCTGCCCGGGAGGTGATCC
2-4-6-2	1856922	escherichia_coli_O157H7.fna	GGCATTACGCGCGG	1856935	GAGTCGTGCGGCATTACGCGGGCGCAGACTC
1-6-7-2	1952836	escherichia_coli_O157H7.fna	ACGGTGCCTGCCCGGG	1952851	GAGTCGGTGACGGTGCCTGCCCGGGAGGTGATCC
4-1-2-1	2148971	escherichia_coli_O157H7.fna	CAGGAAAT	2148978	GAGTCTCTTCAGGAAATGCGCGACTC
1-6-7-2	2228257	escherichia_coli_O157H7.fna	ACGGTGCCTGCCCGGG	2228272	GGATCACCTCCCGGGCAGGCACCGTCACCGACTC
3-4-2-5	2268011	escherichia_coli_O157H7.fna	TTTAACGCCAGTTC	2268024	GAGTCATCTTTAAGCCAGTTCCTGCGACTC
5-3-5-2	2701876	escherichia_coli_O157H7.fna	CGGGATGAAATACCG	2701890	GAGTCCGAACGGTATTTTCATCCCGTGATGACTC
1-0-3-3	2914783	escherichia_coli_O157H7.fna	GATGGTT	2914789	GGATCAGGTAACCATCCGTGGACTC
2-2-3-1	5347073	escherichia_coli_O157H7.fna	TGCCGAAG	5347080	GAGTCCGGCCTTCGGCACCAAGACTC
6-2-4-3	198629	escherichia_coli_K12.fna	TTGAAACGGGCATAA	198643	GGATCGCGGTTATGCCCGTTTCAACATCGACTC
2-2-3-2	272636	escherichia_coli_K12.fna	AACGTGCGT	272644	GGATCAGTGACGACGTTTCATGACTC
2-0-6-5	312061	escherichia_coli_K12.fna	GGATTGAGTGTTG	312073	GGATCATTTCAACACTCAATCCCTGTGACTC
4-1-4-7	558515	escherichia_coli_K12.fna	TTCTGGATGAATGTTA	558530	GAGTCTCTGTTCTGGATGAATGTTAAGACGATCC
2-1-1-2	765268	escherichia_coli_K12.fna	GATTCA	765273	GGATCATGATGAATCTGACGACTC
4-2-3-1	1093455	escherichia_coli_K12.fna	TAAAGCGGCA	1093464	GAGTCACCATAAAGCGGCATTTTGATCC
1-3-2-1	1274893	escherichia_coli_K12.fna	GATCCCG	1274899	GGATCAGATCGGGATCAAGAGACTC
2-2-3-3	1651695	escherichia_coli_K12.fna	AACGTGTTGC	1651704	GGATCGACAGCAACACGTTCAACCGACTC
5-1-2-1	2074077	escherichia_coli_K12.fna	TGAAAAACG	2074085	GAGTCCGCTGAAAAAACGACCGGATCC
3-2-1-1	3528528	escherichia_coli_K12.fna	CCATAGA	3528534	GAGTCAAAGCCATAGACAATGACTC
1-0-4-2	3901602	escherichia_coli_K12.fna	GATGGTG	3901608	GGATCTCCACACCATCATCTGACTC
4-1-1-0	4571546	escherichia_coli_K12.fna	AACAGA	4571551	GGATCGATGTCTGTTCAGGGACTC

Table 5: oligonucleotide fragments from human chromosome 21. Sig. (signature) indicates the number of As-Cs-Gs-Ts (A-C-T-G). The "sequence" includes the sequence of the sense or antisense strand of the recognition sequence(s) of N.BstNB I and/or N.Alw I

Sig.	Start	Product	End	Sequence
0-0-2-4	21342426	TTTTGG	21342431	GAGTCCCGATTTTGGGCAAGACTC
0-0-2-4	33597518	TTGTGT	33597523	GAGTCAGCCACACAAAGTTAGACTC
0-0-2-4	33598110	TTGTGT	33598115	GAGTCAGCCACACAAAGTTAGACTC
0-0-2-6	3869614	TTGTTGTT	3869621	GAGTCAAGGTTGTTGTTACCAGATCC
0-0-5-2	25071211	GGGTGTG	25071217	GAGTCCCCCACACCCCTCTGGACTC
0-1-0-13	31168454	TCTTTTTTTTTTTT	31168467	GAGTCTCTCTCTTTTTTTTTTTTTTTTGAGATCC
0-1-0-5	24179267	TTTCT	24179272	GGATCCAGCAGAAAAAGAAATGACTC
0-1-1-4	3885471	TCTTG	3885476	GAGTCCAGCCAAAGATTATGACTC
0-1-1-4	8035824	CTGTTT	8035829	GAGTCCCAACTGTTTAGAGGACTC
0-1-2-3	33597444	TTGCGT	33597449	GAGTCAGCCACGCAAGTTAGACTC
0-1-2-3	33597666	TTGCGT	33597671	GAGTCAGCCACGCAAGTTAGACTC
0-1-2-3	33597814	TTGCGT	33597819	GAGTCAGCCACGCAAGTTAGACTC
0-1-2-3	33598036	TTGCGT	33598041	GAGTCAGCCACGCAAGTTAGACTC
0-1-2-3	33598332	TTGCGT	33598337	GAGTCAGCCACGCAAGTTAGACTC
0-1-2-5	15651283	CTGTTTGT	15651290	GAGTCTGAACAAACAGACATGACTC
0-1-3-2	8623105	TGGGTC	8623110	GAGTCTGATTGGGTCTGCAGACTC
0-1-3-3	31857088	GGTGCT	31857094	GAGTCATGTGGTGTCTGTGGGACTC
0-1-3-3	31935633	GGTGCT	31935639	GAGTCCACAGACACACCAGTACTC
0-1-4-2	27397521	GTTGGGC	27397527	GGATCTCAGGCCCCAACCCAGTACTC
0-1-4-2	32790478	GGTCTG	32790484	GAGTCTGCTCAGACCCCTCTGGACTC
0-1-4-4	28501162	GCTGTGTGT	28501170	GAGTCCCTTGCTGTGTGTCATGGATCC
0-2-0-4	12632883	TCTTCT	12632888	GAGTCAGAGTCTTCTTCTGACTC
0-2-0-4	14277246	TCTTTC	14277251	GAGTCAACTGAAAGAGATCGACTC
0-2-0-5	12773697	TCTCTTT	12773703	GAGTCATACAAAGAGACTTAGACTC
0-2-2-2	29443352	GGCTCT	29443357	GGATCCAGAGAGCCCCACGACTC
0-2-2-5	21080027	GTCCCTTTTG	21080035	GAGTCTTGAGTCCCTTTTGATGTGATCC
0-2-2-6	9023054	TCTGGTTTTC	9023063	GAGTCTGCCTCTGGTTTTTCGGAAGATCC

Sig.	Start	Product	End	Sequence
0-2-3-2	18327068	GCTCTGG	18327074	GAGTCAGAGGCTCTGGACTTGACTC
0-2-3-4	24560854	TTTCCGGGT	24560862	GGATCTCCACCCGGAAAAGCAGACTC
0-2-4-0	15389884	CGGGCG	15389889	GAGTCACCGCGCCCGCCGGACTC
0-2-4-0	32334583	GGGGCC	32334588	GAGTCCACAGGGGCCACAAGATCC
0-2-4-2	19442336	TGCCTGGG	19442343	GAGTCAAACTGCCTGGGTTTGGATCC
0-2-4-5	205051	TTGGCCTTGTG	205061	GAGTCAGGCCACAAGGCCAAGCTGACTC
0-2-8-4	262944	GCGTTGGGGCGGTT	262957	GAGTCGT'CAGCGTTGGGGCGGTTGTGGGATCC
0-3-1-2	30154426	CTCTGC	30154431	GAGTCTACCGCAGAGTAATGACTC
0-3-2-2	13784707	CCGTGTC	13784713	GAGTCACACGACACGGTCAAGACTC
0-3-2-2	33520625	GGTCTCC	33520631	GAGTCAGTGGGAGACCCCAAGACTC
0-3-2-3	19126274	CGTCTTG	19126281	GAGTCTGCAGCAAGACGATCTGACTC
0-3-2-4	11217484	CTGCCTGTT	11217492	GAGTCCGCTCTGCCTGTTATTGATCC
0-3-3-0	1106893	GGGGCC	1106898	GAGTCTCAGGGCCCGAGGTGACTC
0-3-3-5	9929406	TGGCTTTGCCT	9929416	GGATCCACTAGGCAAGCCAGGGGGACTC
0-3-4-2	31617757	TGTCCTGGG	31617765	GAGTCACGCCCCGGGACACACGGACTC
0-3-5-4	32203026	TGCTGCGGTGT	32203037	GAGTCTCTCTGCCTGCGGTGTGATGATCC
0-4-0-2	32391382	CCCTTC	32391387	GAGTCTGTCTCCCTTCTTTTGACTC
0-4-0-4	2022002	TCTTCTCC	2022009	GAGTCTAATTCTTCTCTGTTGACTC
0-4-1-3	29987299	CCTCGTTC	29987306	GAGTCTCTCTCTCGTTCACTTGACTC
0-4-2-0	15389884	CGCCCG	15389889	GAGTCACCGCGCCCCCGCCGGACTC
0-4-2-3	29473088	TGCTGTCC	29473096	GAGTCGCTGTGCCTGTCTGCAGACTC
0-4-3-2	27248245	TGCTGGCC	27248253	GAGTCACCATGCCTGGCCCTGAGACTC
0-4-3-3	18383621	TGTGCCCTCG	18383630	GAGTCCCACTGTGCCCTCGGGATGATCC
0-4-3-4	31292411	TGCTTGCCTG	31292421	GAGTCTCTCTGCCTTGCTGTCCCGACTC
0-4-4-1	22220483	CCTGGCCGG	22220491	GAGTCGAGCCGGCCAGGTGGGGACTC
0-4-4-3	27383276	GGCTGTGCCTC	27383286	GAGTCCAGGGCTGTGCCTCCACCGATCC
0-5-0-5	10650004	CCTTCTTCTC	10650013	GGATCTTTGGAGAAGAAGGACGGGACTC
0-5-4-6	21631191	TCTGTTTGGGCCCT	21631205	GAGTCATT'CAGGGGCCCCAACAGATGGGACTC
0-6-3-2	18915782	TGCCCCGCCTC	18915792	GAGTCAGAAGAGCCCGGCACAGTACTC
0-7-0-1	5132291	CCCCCTCC	5132298	GGATCAGGAGAGGGGGAGAGGACTC
0-7-3-1	29842128	CCCCCTCGGGC	29842138	GAGTCCAGCCCCCTCGGGCCTCTGACTC

Sig.	Start	Product	End	Sequence
1-0-2-3	21124548	TTGGAT	21124553	GAGTCTTCTTTGGATTGTGGACTC
1-0-3-4	8622993	GAGTTTGG	8623000	GAGTCAAGGCCAAAACCTCCTGAGACTC
1-0-4-1	29789692	GTGGAG	29789697	GAGTACGGCTCCACTCTGGACTC
1-0-4-2	31022101	GGTGTGA	31022107	GAGTCCAGTGGTGTGATCTCGACTC
1-0-6-6	33647155	GGGTTTGTAGGT	33647167	GAGTCTCCAGGGTTTGTAGGTAACGATCC
1-0-7-2	3807096	GAGTGGGTGG	3807105	GGATCTTCTCCACCCACTCCACCGACTC
1-1-1-3	8943855	CTGATT	8943860	GAGTCAGAGCTGATTCATAGATCC
1-1-1-3	9986275	TTTGCA	9986280	GAGTCTCTTTGCAAAATTGTGACTC
1-1-1-3	13756486	TCGATT	13756491	GAGTCAAGGAATCGAGGATGACTC
1-1-1-4	29197174	CTGATTT	29197180	GGATCTCCGAAATCAGAGGCGACTC
1-1-2-2	11437659	GGATTC	11437664	GAGTCTTGTGAATCCCTTTGACTC
1-1-2-2	21573587	ATCTGG	21573592	GAGTCTGAAATCTGGGATGGATCC
1-1-2-3	8996410	CTTGGTA	8996416	GAGTCCCTTCTTGGTATCAAGACTC
1-1-2-3	11364756	TCAGTTG	11364762	GAGTCATGCCAACTGAAGCAGACTC
1-1-2-4	729516	TGCTGTAT	729523	GGATCTAATATACAGCATGAGGACTC
1-1-2-4	15353782	TGCTGTAT	15353789	GGATCTAATATACAGCATGATGACTC
1-1-2-4	19277839	ATCTTTGG	19277846	GAGTCTTGGATTCTTGGATAGGACTC
1-1-2-4	30112644	TGATGCTT	30112651	GGATCCACCAAGCATCATGCAGACTC
1-1-2-4	30578468	TGTTGACT	30578475	GGATCAGAAAAGTCAACAGCAGGACTC
1-1-3-2	2054154	CTGGAGT	2054160	GGATCCAGAACTCCAGCCTAGACTC
1-1-3-2	25479138	TGCTGGA	25479144	GAGTCTAGGTGCTGGATCCAGACTC
1-1-3-4	13758263	GGCTTAGT	13758271	GGATCAAGGACTAAAGCCTGGAGACTC
1-1-4-4	30620951	ATTGTGGCTG	30620960	GAGTCCACATTTGTGGCTGGGAGACTC
1-1-4-6	7653890	GGTATTTCTGGT	7653901	GAGTCAAATGGTATTTCTGGTCTAGATCC
1-1-5-6	33893597	GAGTTTCTGGGT	33893609	GGATCGTTTACCCAGAAAACCTCTAAAGACTC
1-1-6-3	14180710	TGGGGCTTAG	14180720	GAGTCAAACCTGGGGCTTAGAAATGACTC
1-1-6-3	16393787	GTTCGGTGAG	16393797	GGATCTCGGCTCACCGCAACCTCTGACTC
1-1-7-4	28887813	GCTAGGTGGGCTT	28887825	GAGTCTCTAGGTAGTGGGCTTTAGAGATCC
1-1-8-2	30805916	TGGAGCGTGGG	30805927	GAGTCCCTGTTGGGAGCGTGGGTTGTGATCC
1-2-0-3	13942792	ACTTCT	13942797	GAGTCCAGACTTCTCAGAGATCC
1-2-1-2	6583673	GTACCT	6583678	GAGTCCCATGTACCTCTAAGATCC

Sig.	Start	Product	End	Sequence
1-2-1-2	19177346	CTGACT	19177351	GAGTCTGATCTGACTTTTGGACTC
1-2-1-2	32832241	CAGCTT	32832246	GAGTCACTGAAGCTGAACAGACTC
1-2-1-4	20284976	CTTCTTAG	20284983	GAGTCCCTCCCTTCTTAGCTTGGATCC
1-2-2-2	28989805	CTAGGCT	28989811	GAGTCCGTACGCTAGGTTAGACTC
1-2-2-2	29601185	GCCTTGA	29601191	GAGTCAGGTGCCTTGAATTGGATCC
1-2-2-2	30045931	TCTGGAC	30045937	GAGTCTTTTCTGGACTCCAGATCC
1-2-2-9	17293703	ATGTTTCCCTTGTTT	17293716	GGATCTAGAAAACAAGAAACATTCTTGACTC
1-2-3-1	32584915	CCGGAGT	32584921	GAGTCACTGACTCCGGGGCTGACTC
1-2-3-4	32905734	TTGCTCTGGA	32905743	GAGTCCGTGTCCAGAGCAAGGCTGACTC
1-2-4-1	20619692	GAGGTGCC	20619699	GAGTCCCAGGAGGTGCCAGTGACTC
1-2-4-2	25643851	CGCTGGATG	25643859	GAGTCCAGCCGTGGATGGCCAGACTC
1-2-5-1	32059013	GGATGGGCC	32059021	GGATCAATCGGCCCATCCTGTGGACTC
1-2-5-3	29196098	CTGGTGAGCGT	29196108	GGATCTCTCACGCTCACCAAGGAAAGACTC
1-2-5-6	33752323	GCTTTTAGGGTCTG	33752336	GAGTCAGCACAGACCCCTAAAGCTAAGGACTC
1-2-6-2	30361545	TGGGTGCCAGG	30361555	GAGTCAAGGTGGTGCCAGGGGCTGACTC
1-2-6-4	33917713	TCTGGCTGGAGTG	33917725	GAGTCTCGTTCTGGCTGGAGTGCAGTGACTC
1-2-7-2	10589062	GTTGCAGGGCGG	10589073	GAGTCTGATGTTGCAGGGCGGGAAGGATCC
1-3-0-3	27334605	ACTCTCT	27334611	GAGTCCAGCACTCTCTGGGTGATCC
1-3-2-0	30024200	GGACCC	30024205	GAGTCCCATGGACCCCAAGATCC
1-3-2-1	32584915	ACTCCGG	32584921	GAGTCACTGACTCCGGGGCTGACTC
1-3-2-2	29863514	ATCCTGGC	29863521	GGATCTGGAGCCAGGATTAATGACTC
1-3-2-3	29736871	GTCTCTGAC	29736879	GAGTCCCTTTGTCTCTGACCCAGGACTC
1-3-2-9	5408125	TTTCTGTCTTTGACT	5408139	GAGTCTCTGTTTCTGTCTTTGACTCTCTGACTC
1-3-3-2	23936390	CCATCTGGG	23936398	GAGTCCCCACCATCTGGGGCCAGATCC
1-3-3-3	25598534	CCTATGGGCT	25598543	GAGTCCCCACCTATGGGCTGAGGATCC
1-3-3-6	18506656	CTGAGTGTCTCT	18506668	GAGTCTTACAGAGAACAACACTCAGCATAGACTC
1-3-3-7	28059253	CTTTTCTATGCTGG	28059266	GAGTCTCTGCTTTTCTATGCTGGGTAAGATCC
1-3-4-2	30518999	GAGTGGCTCC	30519008	GAGTCCCTGGGAGTGGCTCCCCCTAGACTC
1-3-5-4	21002027	TCTTGGCTGGGCA	21002039	GAGTCGATGTCTTGGCTGGGCACAGTGACTC
1-3-5-5	19923865	TGCCTGCTGTGGAT	19923878	GGATCTCCCATCCACAGCAGGCAACAGACTC
1-3-6-2	31227003	GGGGGTCTCCAG	31227014	GAGTCCGCGGGGGGTCTCCAGACAGGATCC

Sig.	Start	Product	End	Sequence
1-3-7-0	29842128	GCCCGAGGGG	29842138	GAGTCCAGCCCCCTCGGGCCTCTGACTC
1-3-8-4	19067255	GGTCCCCTTGGGGATG	19067270	GGATCCCTCCATCCCCAAGGACCCACCTGACTC
1-4-0-1	29789692	CTCCAC	29789697	GAGTCACGGCTCCACTCTGGACTC
1-4-0-4	28253771	CCATCCTTT	28253779	GAGTCTACCCCATCCTTTTGTAGATCC
1-4-0-7	8044034	TTTTCTCCTACT	8044045	GAGTCAAGTTTTTCTCCTACTCTTAGATCC
1-4-1-4	3000479	TTTCCCAGTC	3000488	GAGTCAGTGGACTGGGAAAGGCAGACTC
1-4-1-4	6605602	TTTCCCAGTC	6605611	GAGTCTGCCCTTCCCAGTCCACTGACTC
1-4-1-4	16808362	TCTCTCAGTC	16808371	GAGTCTGTCTCTCTCAGTCCACTGACTC
1-4-2-1	20619692	GGCACCTC	20619699	GAGTCCCAGGAGGTGCCCAGTGAATC
1-4-2-2	21527811	CCTGAGCTC	21527819	GGATCACTTGAGCTCAGGAGTGGACTC
1-4-2-4	2636234	TGGCTTCACTT	2636244	GAGTCCAGCTGGCTTCACTAGTGGATCC
1-4-3-2	31957583	CCCATCTGGG	31957592	GAGTCATCCCCCAGATGGGACAGACTC
1-4-3-6	28721600	TCTAGTGTCTCCTG	28721613	GAGTCTGTTCAGGAGACACTAGAGAGGACTC
1-4-4-0	22220483	CCGGCCAGG	22220491	GAGTCGCAGCCGGCCAGGTGGGGACTC
1-4-4-3	12281311	CCTGCTGAGCTG	12281322	GAGTCTGCACAGCTCAGCAGGTAGTGAATC
1-4-4-7	20634452	TGGCTTGTACTTTGCC	20634467	GAGTCAGCCGGCAAGTACAAGCCATGCTGACTC
1-5-0-0	1077004	CCACCC	1077009	GAGTCCATACCAACCCCAAGTGAATC
1-5-1-2	30821736	CCCCTGATC	30821744	GAGTCCAACCCCTGATCTGTGGATCC
1-5-1-3	899804	TCTCCTGACC	899813	GAGTCTTGATCTCCTGACCTCGTGAATC
1-5-1-3	5585769	TCTCCCAGTC	5585778	GAGTCAGTGGACTGGGAGAGGCAGACTC
1-5-2-6	14980846	ATCGTTCTCTTCTG	14980859	GAGTCCATTCAAGGAAGAACGATATGTGACTC
1-5-3-1	15145160	CACGCGGCTC	15145169	GAGTCAGTCCACGCGGCTCTGCAGATCC
1-5-3-1	19767972	GGCCTCCAGC	19767981	GGATCACTAGCTGGAGGCCCTTGGGACTC
1-5-4-3	6529088	CCCAGGTCTGGCT	6529100	GAGTCTGCCCCAGGTCTGGCTAGTGGATCC
1-5-6-3	32610836	GGGTGGCCCTGTCCA	32610850	GAGTCACTGGGTGGCCCTGTCCAGTGTGACTC
1-6-0-1	32926206	CCTCCCCA	32926213	GGATCAATGTGGGAGGTTTCAGACTC
1-6-1-3	2129131	GACTCTCCTCC	2129141	GAGTCAAAATGGAGGAGAGTCCCATGACTC
1-6-4-3	12170409	TGGTGGCCCTGCAC	12170422	GAGTCGAAATGGTGGCCCTGCACCTCCAGACTC
1-6-4-3	26181246	TCCGGAGCCTCTCG	26181259	GAGTCTGATTCGGGAGCCTCTCGGGTGGATCC
1-8-2-1	24027206	CCACCTCCGCGC	24027217	GGATCTTGGGCGGAGGTGGGTCCGACTC
1-9-1-3	33439792	CCCCAGTCTCCCTT	33439805	GAGTCCCCTCCCCAGTCTCCCCCTCCAGACTC

Sig.	Start	Product	End	Sequence
2-0-0-4	9427183	ATTAT	9427188	GAGTCAAGTATAAATCCAGGACTC
2-0-1-3	11180295	ATGTAT	11180300	GAGTCCCTATATACATTCTAGACTC
2-0-2-4	9363911	GGTATTTA	9363918	GAGTCTTAAGGTATTTATCAGGATCC
2-0-3-1	28169212	AGTGA	28169217	GAGTCAAAAAGTGGAGAACGATCC
2-0-3-1	31441095	ATGGGA	31441100	GAGTCTACGATGGGACCGAGATCC
2-0-3-3	28401060	GTTTAGGA	28401067	GGATCCTTGTCTCTAAACATTCCGACTC
2-0-3-4	9409920	TGTGATATG	9409928	GGATCTTTCCATATACAGTCAGACTC
2-0-4-0	32391382	GAAGGG	32391387	GAGTCTGTCCCTTCTTTTGACTC
2-0-6-2	9349292	GGTTGGGAA	9349301	GGATCTTTCTTCCCCAACCCAGTGACTC
2-0-6-6	1506217	GTGGTGTATTGAGT	1506230	GAGTCAACAGTGGTGTATTGAGTGTATGACTC
2-0-7-1	10808696	GGTGGGAA	10808705	GAGTCAGTGGGTGGGAAGGCAGATCC
2-1-0-5	619226	TCATTTAT	619233	GAGTCAGATATAAATGAATCAGACTC
2-1-0-5	15224385	TCATTTAT	15224392	GAGTCAGATATAAATGAGTCAGACTC
2-1-0-7	22190209	ATTTTATTCT	22190218	GGATCAGTCAGAAATAAATTTGATGACTC
2-1-1-2	211515	GAACCT	211520	GGATCTCCCAAGTCTTGATGACTC
2-1-1-2	26774780	TAAGCT	26774785	GAGTCTTCCAGCTTATGGGGACTC
2-1-1-2	27292190	AATTCG	27292195	GGATCTCCGCGAATTTATAGACTC
2-1-1-2	28430669	TAACTG	28430674	GGATCACAGCAGTTACAGAGACTC
2-1-1-3	1437969	AGTCTAT	1437975	GAGTCCCATAGTCTATTTCTGACTC
2-1-1-3	5262945	AGACTTT	5262951	GAGTCTCTAGACTTTTGATTGACTC
2-1-1-4	7980226	TTTTGAAC	7980233	GAGTCAAGGTTTGAACCTCAAGACTC
2-1-1-6	12544191	GTCATTTTAT	12544200	GAGTCCCAAGTCATTTTATATTTGATCC
2-1-1-7	11947722	TTGTCATTAT	11947732	GAGTCTGGAATAATAGACAATGGAGACTC
2-1-2-1	19177346	AGTCAG	19177351	GAGTCTGATCTGACTTTTGACTC
2-1-2-1	32832241	AAGCTG	32832246	GAGTCACTGAAGCTGAACAGACTC
2-1-2-3	12598485	TGTGTCAA	12598492	GAGTCTAAATTGACACACAAGGACTC
2-1-2-3	18502098	ATGTGACT	18502105	GGATCACAGAGTCACATGAGTGACTC
2-1-2-3	21268368	TGAATCTG	21268375	GAGTCTCTCTGAATCTGCCGTGATCC
2-1-2-4	9867805	GTTTAGATC	9867813	GAGTCAAAGGATCTAAACCTATGACTC
2-1-3-0	11386861	GGAAGC	11386866	GGATCAATGGCTTCCCAGTACTC
2-1-3-0	30154426	GCAGAG	30154431	GAGTCTACCGCAGAGTAATGACTC

Sig.	Start	Product	End	Sequence
2-1-3-1	11314754	AAGTGGC	11314760	GGATCTCCTGCCACTTCTCTGACTC
2-1-3-1	30743951	GATGGCA	30743957	GAGTCTCAGATGGCATGGTGATCC
2-1-3-3	7200489	TGCTAAGTG	7200497	GAGTCTGGCTGCTAAGTGGCCTGATCC
2-1-3-3	14978682	GAGGATTCT	14978690	GAGTCTGTGAGAAATCCTCTATTGACTC
2-1-3-6	4549922	GATCTTTGTAG	4549933	GGATCCTAGCTACAAAAGATCCCATGACTC
2-1-3-6	12106378	GGTATTTCTAGT	12106389	GAGTCAAATGGTATTTCTAGTGTAGATCC
2-1-3-6	12365955	GGTATTTCTAGT	12365966	GAGTCAAATGGTATTTCTAGTGTAGATCC
2-1-4-2	28136865	AGATCTGGG	28136873	GAGTCAGAGAGATCTGGGTTTGGATCC
2-1-4-3	14222830	GACTTGGTGA	14222839	GAGTCAGTGGACTTGGTGAGGCAGATCC
2-1-4-5	5975272	GGTATATCTGGT	5975283	GGATCTAGAACCAGATATACCATTTGACTC
2-1-5-4	22052058	GTGAGCTGTGTA	22052069	GAGTCCACAGTGAGCTGTGTAGATGGACTC
2-1-6-1	10781164	GGCTGGGGAA	10781173	GAGTCCGACAGGCTGGGGAAGGCAGATCC
2-1-6-1	14383318	GGCTGGGGAA	14383327	GAGTCAGTGGGCTGGGGAAGGCAGATCC
2-1-6-1	15549307	GGCTGGGGAA	15549316	GGATCTGCCTTCCCCAGCCCCACTGACTC
2-1-6-1	15551718	GGCTGGGGAA	15551727	GGATCTGCCTTCCCCAGCCCCACTGACTC
2-1-6-1	24002408	GGCTGGGGAA	24002417	GAGTCAGTGGGCTGGGGAAGGTAGATCC
2-1-6-2	32080603	GCAGAGTGTGG	32080613	GGATCTTCTCCACACTCTGCACAGGACTC
2-1-8-3	20750485	GTGGGAGTGTGGCA	20750498	GAGTCCCACGTGGGAGTGTGGCATTTGGGACTC
2-2-0-3	12533497	TTTCCAA	12533503	GAGTCAGGATTTCCAAAGAGGACTC
2-2-0-4	30068854	TTAACTCT	30068861	GGATCAGCGAGAGTTAATGCTGACTC
2-2-0-6	18038803	TTTCTTTCATA	18038812	GAGTCAGAGTATGAAGAAAGATTGACTC
2-2-0-7	13894251	ATTTTTCATC	13894261	GAGTCCATCATTTTTTTCATCTTTGGATCC
2-2-1-1	11437659	GAATCC	11437664	GAGTCTTGTGAATCCCTTTGACTC
2-2-1-1	22626704	AGTCAC	22626709	GAGTCCCCCAGTCACTGAAGATCC
2-2-1-3	22498075	ACCTTGAT	22498082	GAGTCCAATATCAAGGTATTGGACTC
2-2-1-4	22683181	TATTGCCCTA	22683189	GAGTCACTGTATTGCCCTAAGGAGACTC
2-2-2-1	28989805	AGCCTAG	28989811	GAGTCCGTCAGCCTAGGTTAGACTC
2-2-2-2	7173254	TCTGCGAA	7173261	GAGTCACCATCTGCGAAAATTTGATCC
2-2-2-2	22855526	ACACTGGT	22855533	GAGTCTGTGACCACTGTTGGAGACTC
2-2-2-3	12738618	TCCTTAAGG	12738626	GAGTCGACTCCTTAAGGCCCTAGACTC
2-2-2-3	15436214	CTATGATGC	15436222	GAGTCTTGGCATCATAGGAGGGACTC

Sig.	Start	Product	End	Sequence
2-2-2-3	18410822	CATGGCTTA	18410830	GGATCCAGCTAAGCCATGCCTGGACTC
2-2-2-3	31131563	TTGTGACAC	31131571	GGATCAACAGTGTACAAAGTCAGACTC
2-2-2-4	22164257	CTGCATTGTA	22164266	GGATCTGGTTACAATGCAGATCTGACTC
2-2-3-0	13784707	GACACGG	13784713	GAGTCACACGACACGGTCAAGACTC
2-2-3-0	33520625	GGAGACC	33520631	GAGTCAGTGGGAGACCCCAAGACTC
2-2-3-4	28815015	TTAACCTTGGG	28815025	GAGTCCCTTCCCAAGTTAAGGCTGACTC
2-2-3-4	32414641	TTCTTGGGACA	32414651	GAGTCAACGTTCTTGGACAATTGGACTC
2-2-3-6	5932904	GTTTAGTTTAGCC	5932916	GAGTCTGTGGTTTAGTTAGCCTTTGGATCC
2-2-3-6	17378613	TGGTTTCAATTGC	17378625	GAGTCAGAGGCAATTGAAACCAGAGTGACTC
2-2-4-1	24532350	AGCGAGTGC	24532358	GAGTCAGTCAGCGAGTGTGGGATCC
2-2-4-1	28237615	GCAGGCTGA	28237623	GGATCCCTGTGAGCCTGCTCAAGACTC
2-2-4-2	24146793	GTGAGCACTG	24146802	GAGTCAGCTGTGAGCACTGCTCAGATCC
2-2-5-1	11221991	CGCTGGGGAA	11222000	GAGTCAGTGCCTGGGAAAGCGGATCC
2-2-5-4	33655118	GTACTGTGGGCTA	33655130	GAGTCTTGGGTACTGTGGGCTAGTAAGACTC
2-2-5-7	33039205	TCAGTGTGTTGATGT	33039220	GAGTCTTTATCAGTGTGTTGATGTTCCAGACTC
2-2-6-1	12966530	AGCGGAGGCT	12966540	GAGTCATTGAGCGGAGGCTGTAAGATCC
2-3-1-0	8623105	GACCCA	8623110	GAGTCTGATTGGGTCTGCAGACTC
2-3-1-0	32976276	CCAGCA	32976281	GAGTCCCCACCAGCAAGAAGATCC
2-3-1-1	25479138	TCCAGCA	25479144	GAGTCTAGGTGCTGGATCCAGACTC
2-3-1-3	23935558	TCCATGCAT	23935566	GAGTCAGGTTCCATGCATTCTCTGATCC
2-3-1-8	4324439	TTCAATCTTCTGTA	4324452	GGATCCATATACAGAAGAAATGAAACTAGACTC
2-3-2-0	12748618	CAGAGCC	12748624	GAGTCTGGTTCAGAGCCAGTGATCC
2-3-2-0	18327068	CCAGAGC	18327074	GAGTCAGAGGCTCTGGACTTGACTC
2-3-2-3	6083987	ACCCGAGTTT	6083996	GAGTCTATGAAACTCGGGTCAATGACTC
2-3-2-6	8878952	TGCATTCTTTGAC	8878964	GAGTCTGCCTGCATTCTTTGACTTATGATCC
2-3-3-1	23435111	CCGCAGATG	23435119	GGATCCTCACATCTGCGGCGATGACTC
2-3-3-1	31671742	CCAGGCATG	31671750	GAGTCTGGGCCAGGCATGGCGGGATCC
2-3-3-4	30387315	CTGGATTCCATG	30387326	GAGTCTTTGCATGGAATCCAGCCTGGACTC
2-3-3-4	31097332	TATGTTGCCCAG	31097343	GAGTCCAGCCTGGGCAACATAGCAAGACTC
2-3-3-8	18319692	CTAATGTCCTTTTGG	18319707	GAGTCTCAACTAATGTCCTTTTGGATTGACTC
2-3-4-0	27248245	GGCCAGGCA	27248253	GAGTCACCATGCCTGGCCCTGAGACTC

Sig.	Start	Product	End	Sequence
2-3-4-1	25770313	AAGCTGCGG	25770322	GAGTCAGCAAAGCCTGCGGATGGGATCC
2-3-4-1	31957583	CCCAGATGGG	31957592	GAGTCATCCCCCAGATGGGGACAGACTC
2-3-4-3	24894356	CAGAGGTTTCGC	24894367	GGATCTGCAGCGAAACCTCTGTGGTGACTC
2-3-4-5	11647570	GTGTAGAGCCTTCT	11647583	GGATCCCGAGAAAGGCTCTACACCCATGACTC
2-3-4-5	23934318	CTCTGAAC TGGGTT	23934331	GAGTCTCAGAAACCCAGTTTACAGAGTCTGGACTC
2-3-6-0	18915782	GAGCCCGGCA	18915792	GAGTCAGAAGAGCCCGGGCACAGTGACTC
2-3-6-2	21787129	CAGCGAGCTGGTG	21787141	GAGTCAGGCCAGCAGCTGGTGAGGAGACTC
2-3-6-4	2368241	GCCTGGTATTCGAGG	2368255	GGATCTGGACCTCGAATACCAAGGCTTTTGACTC
2-4-0-0	1207352	CCAACC	1207357	GAGTCCATACCAACCAAGTGATCC
2-4-0-1	19713320	CCTCACA	19713326	GAGTCCTGTCTCTCACAGACAGATCC
2-4-0-1	31022101	TCACACC	31022107	GAGTCCAGTGGTGTGATCTCGACTC
2-4-0-4	18201500	ATCTCCTATC	18201509	GGATCCTGAGATAGGAGATGGCAGACTC
2-4-1-0	32790478	CAGACCC	32790484	GAGTCTGCTCAGACCCCTCTGGACTC
2-4-1-6	32574843	ATCTGTCTTACT	32574855	GGATCCTCCAGTAAGGACAGATACGTGACTC
2-4-2-1	25643851	CATCCAGCG	25643859	GAGTCCAGCCGCTGGATGGCCAGACTC
2-4-2-2	3443735	AGATGTCCCC	3443744	GAGTCAGTGAGATGTCCCCACAGGATCC
2-4-3-0	31617757	CCCGGGACA	31617765	GAGTCACGCCCCGGGACACACGGACTC
2-4-3-1	30518999	GGAGCCACTC	30519008	GAGTCCCTGGAGTGGCTCCCCCTAGACTC
2-4-3-3	19951433	CCTATGCAGGCT	19951444	GAGTCATCTCCTATGCAGGCTGCCCTGACTC
2-4-3-3	32722468	GCCTTCGGAATC	32722479	GAGTCCCTCGGCCCTTCGGAATCTCCTGACTC
2-4-7-3	33231602	CGAGGTGCAGTGGCCT	33231617	GAGTCCAAACGAGGTGCAGTGGCCTGACTGATCC
2-5-0-0	25071211	CACACCC	25071217	GAGTCCCCCCACACCCCTCTGGACTC
2-5-0-5	26992119	CCATTTCCTACT	26992130	GAGTCAGTAAGTAGGAAATGGGTGCGACTC
2-5-1-1	30264305	GACTCCCCA	30264313	GGATCCAGTGGGGAGTCTCTCGGACTC
2-5-1-3	24033358	ATCCCTGCCAT	24033368	GAGTCTTGAATGGCAGGGATGGAGGACTC
2-5-2-3	8407948	ACTCTGGACCTC	8407959	GGATCACTTGAGGTCCAGAGTTGGAGACTC
2-5-2-4	23901817	CAAGCCCGTTTCT	23901829	GAGTCATTGCAAGCCCGTTTCTTAAGGACTC
2-5-4-5	29781742	CCCTTGGTGCCTTAGA	29781757	GAGTCACATTTCTAAGGCACCAAGGGTGAGGACTC
2-6-1-3	3162555	ACTCCTGACCTC	3162566	GAGTCTTGAACCTCCTGACCTCAGGTGATCC
2-6-2-1	30361545	CCTGGCACCCA	30361555	GAGTCAAGGTGGTGCCAGGGGCTGACTC
2-6-3-2	21787129	CACCAGCTCGCTG	21787141	GAGTCAGGCCAGCGAGCTGGTGAGGAGACTC

Sig.	Start	Product	End	Sequence
2-6-3-3	23945172	AGGCTGCCCCATT	23945185	GAGTCTAGAAGGCTGCCCCATTCTCACGACTC
2-6-3-5	12507913	GCTTTAGCCCCCTATG	12507928	GGATCACAGCATAGGGGCTGAAAGCCCCCTTGACTC
2-6-5-3	30415056	CTCCCTGCAGCAGGTG	30415071	GAGTCCCGCCTCCCTGCAGCAGGTGCTGACTC
2-7-1-5	21169634	AGTCCCATCTCTTCC	21169648	GAGTCTGCAAGTCCCATTCTTCCCAGGATCC
2-7-2-4	2783952	CTGTACCTGCTCCA	2783966	GAGTCAGGATGGAGCAGGTGACAGGGGTGACTC
2-8-2-4	33028162	CTGTCCCCCTCCTGAA	33028177	GAGTCAAGGCTGTCCCCCTCCTGAAGTCAGATCC
3-0-0-3	3350206	ATATTA	3350211	GGATCTATATAATATATGAGACTC
3-0-0-5	1575134	TTTAAATA	1575141	GAGTCTCTTTTTTAATAGAATGACTC
3-0-1-2	21517708	GAAATT	21517713	GAGTCTAAGGAAATTTATGAGATCC
3-0-1-4	23801449	TTTGAATA	23801456	GAGTCCAGATTTGAATAAGGTGACTC
3-0-2-1	2654630	GAGAA	2654635	GGATCATTAATTCTCTCAAGACTC
3-0-2-2	12533497	TTGGAAA	12533503	GAGTCAGGATTTCCAAAGAGGACTC
3-0-2-2	14744550	TGAGATA	14744556	GAGTCCATTGTGAGATAATGTGATCC
3-0-2-3	19462765	AGATTAG	19462772	GAGTCATGCCTAAATCTTTCTGACTC
3-0-2-4	3082986	TTATAAGGT	3082994	GGATCCGTGACCTTATAAAAGGGACTC
3-0-3-1	26717503	ATGAGAG	26717509	GAGTCACAGATGAGAGCGGAGATCC
3-0-3-3	10042155	TGGGAATAT	10042163	GAGTCCCTTGTGGGAATATGAAAGATCC
3-0-4-0	20808976	AAGGGAG	20808982	GAGTCTGAGAAGGGAGATGGGATCC
3-0-4-1	19720180	GGTGAAAG	19720187	GGATCCACACTTTTCAACCATTTGACTC
3-0-5-1	18704652	AGGAGGAT	18704660	GGATCGGATATCCTCCCTCCCTGACTC
3-1-0-2	11180295	ATACAT	11180300	GAGTCTATATACATTTCTAGACTC
3-1-0-2	21654351	TCAAAT	21654356	GAGTCCCTATTCAAATTTTGTGATCC
3-1-1-1	9986275	TGCAAA	9986280	GAGTCTCTTTTGCAAAATTTGTGACTC
3-1-1-1	13756486	AATCGA	13756491	GAGTCAAGGAATCGAGGATGACTC
3-1-1-1	25929627	GATACA	25929632	GAGTCTACAGATACAAGGAGATCC
3-1-1-2	1437969	ATAGACT	1437975	GAGTCCCATAGTCTATTCTGACTC
3-1-1-2	5262945	AAAGTCT	5262951	GAGTCCCTCTAGACTTTGATTGACTC
3-1-1-4	9912776	CTGAATTAT	9912784	GAGTCCATACTGAATTATTCTGACTC
3-1-2-1	28155980	GTCAGA	28155986	GAGTCAGCTGTCAAGAGATAGATCC
3-1-2-2	22498075	ATCAAGGT	22498082	GAGTCCAATATCAAGGTATTGGACTC
3-1-2-5	5331028	GTATATAGTTC	5331038	GAGTCATTGGTATATAGTTCTCAAGATCC

Sig.	Start	Product	End	Sequence
3-1-3-1	23421470	TGGCAAAG	23421477	GGATCCTCTCTTTTGCCAAAGGGGACTC
3-1-3-2	28691310	GCTTGGAAA	28691318	GGATCTGCCTTTTCCAAGCCACTGACTC
3-1-4-0	29987299	GAACGAGG	29987306	GAGTCTCCTCCTCGTTCACTTGACTC
3-1-4-1	28241661	GACTGAGGA	28241669	GAGTCAGTGGACTGAGGAGGGAGATCC
3-1-4-2	9753627	GGCTGTAGAA	9753636	GGATCTGCCTTCTACAGCCCACTGACTC
3-1-4-3	12666387	GTTGCAGTAAG	12666397	GGATCTCGGCTTACTGCAACCTCCGACTC
3-1-4-4	25350996	TCAAGGTGTGA	25351007	GAGTCAGGCTCAAGTTGTGAATGTGACTC
3-1-4-6	14333110	GGGATTTTAGTTCA	14333123	GAGTCAGAAAGGGATTTTAGTTCAATGTGACTC
3-1-4-7	18897789	TTTTTGTAGATGAGC	18897803	GGATCCCTGGCTCATCTACAAAAGCCGAGACTC
3-1-5-1	2994368	GGCTGGGAAA	2994377	GAGTCAGTGGCTGGGAAAGGCAGATCC
3-1-5-1	5585769	GACTGGGAGA	5585778	GAGTCAGTGGACTGGGAGAGGCAGACTC
3-1-5-1	14389987	GGCTGGGAAA	14389996	GAGTCAGTGGCTGGGAAAGGCAGATCC
3-1-5-1	16194477	GGCTGGGAAA	16194486	GAGTCAGTGGCTGGGAAAGGCAGATCC
3-1-5-2	24033358	ATGGCAGGGAT	24033368	GAGTCTTGAATGGCAGGGATGGAGGACTC
3-1-6-1	2129131	GGAGGAGAGTC	2129141	GAGTCAATGGAGGAGAGTCCCATGACTC
3-1-9-1	33439792	AGGGGAGACTGGGG	33439805	GAGTCCCTCCCCAGTCTCCCCCTCCAGACTC
3-2-0-1	21124548	ATCCAA	21124553	GAGTCTTCTTTTGGATTGTGGACTC
3-2-0-3	19462765	CTAAATCT	19462772	GAGTCATGCCTAAATCTTTCTGACTC
3-2-1-0	15857752	CCAAAG	15857757	GAGTCCCTTACCAAAGTCATGATCC
3-2-1-0	33597444	ACGCAA	33597449	GAGTCAGCCACGCAAGTTAGACTC
3-2-1-0	33597666	ACGCAA	33597671	GAGTCAGCCACGCAAGTTAGACTC
3-2-1-0	33597814	ACGCAA	33597819	GAGTCAGCCACGCAAGTTAGACTC
3-2-1-0	33598036	ACGCAA	33598041	GAGTCAGCCACGCAAGTTAGACTC
3-2-1-0	33598332	ACGCAA	33598337	GAGTCAGCCACGCAAGTTAGACTC
3-2-1-1	8996410	TACCAAG	8996416	GAGTCCCTTCTTGGTATCAAGACTC
3-2-1-1	11364756	CAACTGA	11364762	GAGTCATGCCAACTGAAGCAGACTC
3-2-1-1	22714224	TCCAAGA	22714230	GAGTCAGACTCCAAGAGCTGGATCC
3-2-1-2	12598485	TTGACACA	12598492	GAGTCTAAATTGACACACACAAGGACTC
3-2-1-4	25288155	CAAATGCTTT	25288164	GAGTCGTGGCAAATGCTTTTCCAGATCC
3-2-1-5	10431179	ACATTTCTAGT	10431189	GGATCAAAAAC TAGAAATGTTAAGGACTC
3-2-2-1	19159639	AAATGGCC	19159646	GGATCTGAGGGCCATTTTCTGACTC

Sig.	Start	Product	End	Sequence
3-2-2-2	12738618	CCTTAAGGA	12738626	GAGTCGCACTCCTTAAGGCCTAGACTC
3-2-2-2	15436214	GCATCATAG	15436222	GAGTCCTTGGCATCATAGGAGGACTC
3-2-2-2	19716680	AATGACTCG	19716688	GAGTCCTGGCAATGACTCGTCTGGATCC
3-2-2-2	23157997	GTAAGCCAT	23158005	GGATCTCCCATGGCTTACAATGGACTC
3-2-2-3	19474034	ATTCTGGAA	19474043	GGATCCTGGTTCAGGAATCCAAGACTC
3-2-2-4	20638088	ACGGATTACT	20638098	GGATCTTTCAGTAAATCCGTGGCTGACTC
3-2-2-7	33817389	TCTTATGAGTATCT	33817402	GAGTCATTTTCTTATGAGTATCTAATGACTC
3-2-3-0	19126274	GCAAGACG	19126281	GAGTCCTGCAGCAAGACGATCTGACTC
3-2-3-1	29736871	GTCAGAGAC	29736879	GAGTCCTTTGTCTCTGACCCAGGACTC
3-2-3-2	6083987	AAACTCGGGT	6083996	GAGTCATGAAACTCGGGTCAATGACTC
3-2-3-2	12664695	AACCTGGAGT	12664704	GAGTCACATAACCTGGAGTTAAGGATCC
3-2-3-6	1209487	TGCTGTGTGTTCAAA	1209500	GAGTCAGAAATGTCTGTGTTCAAATCCTGACTC
3-2-3-6	33773747	TGAGAACTTTGTCT	33773760	GAGTCCTGATGAGAACTTTGTCTCAGGACTC
3-2-4-0	29473088	GGACAGGCA	29473096	GAGTCGCTGTGCCTGTCTCTGCAGACTC
3-2-4-1	1795301	GACTGGCAGA	1795310	GAGTCAGTGGACTGGCAGAGGCAGATCC
3-2-4-4	4718510	GAATGGTTCACTG	4718522	GAGTCAGCAGAAATGGTTCACTGTTCTGATCC
3-2-5-5	23758787	GTGTGCTGTGAATAC	23758801	GAGTCGAGTGTATTCACAGCACACAGGGGACTC
3-2-6-1	19789414	GACTGAGGCAGG	19789425	GGATCACCTCCTGCCTCAGTCAACAGACTC
3-2-7-4	32820688	GTTCTGTGGAGGACA	32820703	GAGTCATTCTGTTCTGTGGAGGGACAAGTGGACTC
3-3-1-0	9674013	CCCAAAG	9674019	GAGCTTTAACCCAAAGCACAGATCC
3-3-1-0	31857088	AGACACC	31857094	GAGTCATGTGGTGTCTGTGGGACTC
3-3-1-0	31935633	AGACACC	31935639	GAGTCCCACAGACACACCACGTGACTC
3-3-1-2	14978682	AGAAATCCTC	14978690	GAGTCGTGAGAAATCCTCTATTGACTC
3-3-1-7	13563376	TAATAGTCCTTTTC	13563389	GAGTCGTAGAAAAGGACTATTAGAAAAGACTC
3-3-2-1	33424071	AATGCAGCC	33424079	GAGTCCTGGAAATGCAGCCCTGAGATCC
3-3-2-2	13372656	CATCAGTAGC	13372665	GAGTCCATGCATCAGTAGCTTAGGATCC
3-3-4-2	10808838	ATTCAGGGCAG	10808849	GGATCCTTCCTGCCCTGGAATATTGGACTC
3-3-4-2	19951433	AGCCTGCATAGG	19951444	GAGTCATCTCCTATGCAGGCTGCCCTGACTC
3-3-4-2	22284404	GGGATATCCCAG	22284415	GGATCCCTTCTGGGATATCCCTTCTGACTC
3-3-4-2	32722468	GATCCGAAGGC	32722479	GAGTCCTCGGCCCTCGGAATCTCCTGACTC
3-3-5-3	2625867	CGTTCAGGGAATG	2625880	GGATCTTTCACATTCCTCGGAACGTGCAGACTC

Sig.	Start	Product	End	Sequence
3-3-5-4	5024130	GGCTGGATTGAAC	5024144	GGATCTAGGGTTCAAATCCAGGCCACTAGACTC
3-3-6-2	23945172	GAATGGGGCAGCCT	23945185	GAGTCTAGAAGGCTGCCCCATTCTCAGACTC
3-3-6-3	24022606	GCGCGTGGATTGAGA	24022620	GAGTCTCAGCGCGTGGATTTCAGATCAGGACTC
3-3-7-1	14651608	GCCTGAGGGCAGGA	14651621	GAGTCTGATGCCTGAGGGCAGGAAGCTGATCC
3-4-1-1	16409217	CCAAATGCC	16409225	GGATCACAAGGCATTGGCCAAAGACTC
3-4-1-3	8109948	TCAACATGCCT	8109958	GGATCTGGAGGCATGTTGACCAAGACTC
3-4-1-5	20735471	TTTGAACCCATCT	20735483	GAGTCAGACAGATGGGTTCAAATCCTGACTC
3-4-1-6	5084130	ATTCTCATGTCACT	5084143	GAGTCTCAAAGTGACATGAGAAATTTGTGACTC
3-4-2-0	22138172	AGCACCCAGC	22138180	GAGTCAGTCAGCACCCAGCTCTGGATCC
3-4-2-3	18763327	AAGCCTTCCTAG	18763338	GAGTCACCCAAAGCCTTCCTAGATTGATCC
3-4-3-1	30276848	AAGGCCTGACC	30276858	GAGTCAGTCAAGGCCTGACCCACAGATCC
3-4-4-1	12281311	CAGCTCAGCAGG	12281322	GAGTCTGCACAGCTCAGCAGGTAGTGACTC
3-4-4-5	2970865	CTTGCCAAAGGTCTTGA	2970880	GGATCTCTCTCAAGACCTTGCCAAGGCCAGACTC
3-4-5-4	27256725	CTGGTTATCAGGGCCA	27256740	GGATCACTTTGGCCCTGATAACCCAGCGGAGACTC
3-4-6-1	12170409	GTGCAGGGGCACCA	12170422	GAGTCGAAATGGTGGCCCTGCACCTCCAGACTC
3-5-1-1	14190105	GCCACTAACC	14190114	GAGTCAGAAGCCACTAACCCAGATGATCC
3-5-3-4	25320211	AGCCATTGTGCACTC	25320225	GAGTCTGTAGCCATTGTGCACCTCCCTGACTC
3-5-6-2	30415056	CACCTGCTGCAGGGAG	30415071	GAGTCCCGCCTCCCTGCAGCAGGTGTGCTGACTC
3-6-1-1	14180710	CTAAGCCCCCA	14180720	GAGTCAAAC TGGGGCTTAGAAATGACTC
3-6-2-2	32111018	GGACTCCACTACC	32111030	GGATCAAGTGGTAGTGGAGTCCCAGGGACTC
3-6-2-4	13538285	GTCACCTCCCAGATT	13538299	GAGTCCAAAAATCTGGGAGGTGACCATCGACTC
3-6-3-3	24022606	TCTGAATCCACGCGC	24022620	GAGTCTCCAGCGCGTGGATTTCAGATCAGGACTC
3-6-3-4	7083234	CTTTCCCCCATGGAGA	7083249	GAGTCTTTGTCTCCATGGGGGAAAAGGAGAGACTC
3-6-3-4	19756052	GTCCCTAGACAGCTCT	19756067	GAGTCTGGAGTCCCTAGACAGCTCTGAAAAGACTC
3-6-4-3	31232261	TCCCTGCTCAGGCAAG	31232276	GAGTCTCTCTCCCTGCTCAGGCAAGAGAGATCC
3-6-4-3	33866318	GGCCATCTCAGGATCC	33866333	GGATCTGGGGGATCCTGAGATGGCCCCAGGACTC
3-6-5-1	32610836	TGGACAGGGCCACCC	32610850	GAGTCACTGGGGTGGCCCTGTCCAGTCTGACTC
3-7-0-5	29788190	TCATTCTCCACCCAT	29788204	GAGTCTTTGTCAATTCTCCACCCATGTCTGACTC
3-7-2-4	21390645	TCCTGAATCTGCCACC	21390660	GAGTCAAGGTCTCTGAATCTGCCACCAGTAGACTC
3-8-1-2	20750485	TGCCACACTCCCAC	20750498	GAGTCCCACGTGGGAGTGTGGCATTTGGGACTC
4-0-0-2	9427183	ATAAAT	9427188	GAGTCAAGTATAAAATCCAGGACTC

Sig.	Start	Product	End	Sequence
4-0-0-4	31759464	TAAATTTA	31759471	GAGTCTCAATAAAATTTAAAGGATCC
4-0-1-8	27892202	TTTATTTTGTAAA	27892214	GAGTCCCAGTTTATTTGTAAAATTTGGACTC
4-0-2-0	12632883	AGAAAG	12632888	GAGTCAGAGTCTTCTTCTGACTC
4-0-2-0	14277246	GAAAGA	14277251	GAGTCAACTGAAAGAGATCGACTC
4-0-2-1	29472882	ATAAAGG	29472888	GGATCTTTTCCCTTTATCAACGACTC
4-0-3-4	28480979	TTAAAAATGTGG	28480989	GAGTCATGATTAAAAATGTGGTGAGATCC
4-0-4-0	2022002	GGAGAAAG	2022009	GAGTCTAATTCTTCTCCTGTTGACTC
4-0-4-1	8297236	GGAATAGGA	8297244	GAGTCATCGGGAATAGGAATAGGATCC
4-1-0-3	19478130	AACTTTAA	19478137	GAGTCAGTAAACTTTAAGATAGATCC
4-1-0-3	23801449	TATTCAAA	23801456	GAGTCCAGATTTGAATAAGGTGACTC
4-1-1-0	3885471	CAAAGA	3885476	GAGTCCAGCCAAAGATTATGACTC
4-1-1-0	8035824	AAACAG	8035829	GAGTCCCAACTGTTTAGAGGACTC
4-1-1-2	7980226	GTTCAAAA	7980233	GAGTCAAGGTTTTGAACTCAAGACTC
4-1-1-3	9912776	ATAATTGAG	9912784	GAGTCCATACCTGAATTATTTCTGACTC
4-1-2-1	7507460	AGAACTAG	7507467	GGATCTTATCTAGTTCTGTCTGACTC
4-1-2-1	21371940	AGCAAAGT	21371947	GGATCAAAGACTTTGCTGTAAAGACTC
4-1-2-2	22683181	TAGGCAATA	22683189	GAGTCACTGTATTGCCATAAGGAGACTC
4-1-3-0	25895856	AACGAGGA	25895863	GAGTCCTACAAACGAGGATAATGATCC
4-1-3-5	16036924	AAGTTGGACATTT	16036936	GAGTCAGAAAAATGTCCAACITCAAAGACTC
4-1-3-6	30918934	AGATACTGTTTATG	30918947	GGATCTGATCATAAACAGTATCTGAAAGACTC
4-1-4-1	3000479	GAATGGGAAA	3000488	GAGTCAGTGGACTGGGAAAGGCAGACTC
4-1-4-1	6605602	GAATGGGAAA	6605611	GAGTCTGCCTTTCCCACTCCACTGACTC
4-1-4-1	11453935	AACTGGGAGA	11453944	GAGTCAGTGAACCTGGGAGAGGCAGATCC
4-1-4-1	16808362	GACTGAGAGA	16808371	GAGTCTGTCTCTCTCAGTCCACTGACTC
4-1-4-1	33643779	GACTGGGAAA	33643788	GGATCTGCCTTTCCCACTCCATGACTC
4-1-4-2	16149438	GACTTGGGAAA	16149448	GAGTCAGTAGACTTTGGGAAAGGGAGATCC
4-1-4-3	23042578	TGATAAGACTGG	23042589	GAGTCGTTCTGATAAGACTGGGGAAGATCC
4-2-0-0	21342426	CCAAAA	21342431	GAGTCCCAGATTTTGGGCAAGACTC
4-2-0-0	33597518	ACACAA	33597523	GAGTCAGCCACACAAAGTTAGACTC
4-2-0-0	33598110	ACACAA	33598115	GAGTCAGCCACACAAAGTTAGACTC
4-2-1-1	19277839	CCAAGAAT	19277846	GAGTCTTGGATTCTTGGATAGGACTC

Sig.	Start	Product	End	Sequence
4-2-1-2	9867805	GATCTAAAC	9867813	GAGTCAAAGGATCTAAACCTATGACTC
4-2-1-5	25037009	GATTCTCATTA	25037020	GAGTCCAGTGATTCTCATTAATTGAGATCC
4-2-1-6	25734365	TTTAGCTAATACT	25734377	GAGTCACATTTTAGCTAATACTTTGAGATCC
4-2-2-3	17132832	AGCATACTAGT	17132842	GGATCTTCCACTAGTATGCTATATGACTC
4-2-2-6	17159417	AATGTGTATACTC	17159430	GAGTCAGAGAAATGTGTATATCTCCGTGGATCC
4-2-2-8	17813774	GTTTGTAGACTATACTT	17813789	GAGTCTGCAAAAGTATAGTCTAAAACCTGGGACTC
4-2-3-4	27582047	ATCTGAAGTGTC	27582059	GAGTCAGAGATCTGAAGTGTGAGAGGACTC
4-2-3-5	7254161	TCACTGTGTGAAA	7254174	GGATCCTGTGTTTTCAACACACAGTGACTGGGACTC
4-2-4-5	15860691	AGCCTTAGAAGGTTT	15860705	GGATCTCTCAAACCTTCTAAGGCTGAGAGACTC
4-2-5-2	23901817	AGAAACGGGCTTG	23901829	GAGTCATTGCAAGCCCGTTTCTTAAGGACTC
4-2-6-3	13538285	AATCTGGGAGGTGAC	13538299	GAGTCCAAAAATCTGGGAGGTGACCATCGACTC
4-2-7-2	2783952	TGGAGCAGGTGACAG	2783966	GAGTCAGGATGGAGCAGGTGACAGGGGTGACTC
4-2-7-3	21390645	GGTGGCAGATTGAGGA	21390660	GAGTCAAGGTCTCTGAATCTGCCACCCAGTAGACTC
4-3-0-1	86222993	CAAAAATC	8623000	GAGTCAAGGCAAAAATCCTTGAGACTC
4-3-0-4	22096783	TAAATATCCCT	22096793	GAGTCCCTCTAAATATCCCTTATAGATCC
4-3-1-5	3038558	ATCATCTTAAGTG	3038570	GAGTCAAAAATCATCTTAAGTGTAAAGACTC
4-3-1-8	7031187	AAACGTCTTTTCTTTA	7031202	GAGTCAATTAACAGTCTTTTCTTTATATGACTC
4-3-2-1	32905734	TCCAGAGCAA	32905743	GAGTCCGTGTCCAGAGCAAGGGTGACTC
4-3-2-2	28815015	CCCAAGGTAA	28815025	GAGTCCCTTCCCAAGGTTAAGGCTGACTC
4-3-2-2	32414641	TGTCCCAAGAA	32414651	GAGTCAACGTCTCTTGGGACAAATTGGACTC
4-3-2-3	6194815	CACAGATGTATC	6194826	GGATCTGTTGATACATCTGTGCTTTGACTC
4-3-2-3	19520077	TCTACAAAGGTC	19520088	GAGTCTTGGTCTACAAAGGCTTAAGGATCC
4-3-2-4	27582047	TGACACTTCAGAT	27582059	GAGTCAGAGATCTGAAGTGTGAGAAAGGACTC
4-3-2-6	25660391	CGATTCTTAATTCAG	25660405	GAGTCCCATCTGAATTAGAAATCGGGGAGACTC
4-3-3-2	23926326	TCCAGAAGGATC	23926337	GAGTCTTCATCCAGAAGGATCAGGTGATCC
4-3-3-2	30387315	CATGGAATCCAG	30387326	GAGTCTTTGCATGGAATCCAGCCTGGACTC
4-3-3-2	31097332	CTGGGCAACATA	31097343	GAGTCCAGCCTGGGCAACATAGCAAGACTC
4-3-4-0	31292411	CAGGCAAGGCA	31292421	GAGTCTCTCTGCCCTTGCCTGTCCCGACTC
4-3-4-4	33917401	ACTGACGGGCATTTA	33917415	GAGTCTACCAGTACGGGGCATTTAGGTTGACTC
4-3-5-3	25320211	GAGTGCACAAATGGCT	25320225	GAGTCTGTAGCCATTTGTGCACTCCCTGACTC
4-3-6-3	7083234	TCTCCATGGGGAAAG	7083249	GAGTCTTTGTCTCCATGGGGGAAAGGAGAGACTC

Sig.	Start	Product	End	Sequence
4-3-6-3	19756052	AGAGCTGTCTAGGGAC	19756067	GAGTCTGGAGTCCCTAGACAGCTCTGAAAGACTC
4-4-0-7	25875523	TAAACTCTTTCCATA	25875537	GAGTCATCTTTAACTCTTTCCATACCCAGACTC
4-4-1-1	27068556	GACACTAACC	27068565	GGATCATCTGGTTAGTGTCTTCTGACTC
4-4-1-1	30620951	CAGCCACAAT	30620960	GAGTCCACATTTGTGGCTGGGGAGACTC
4-4-1-2	33287291	ACCTTCAGAAC	33287301	GGATCCCACGTTCTGAAGTCCCCGACTC
4-4-1-3	25350996	TCACAACTTGA	25351007	GAGTCAGGCTCAAGTTGTGAATGTGACTC
4-4-3-3	15850177	GACTTAGCCAGATC	15850190	GAGTCATTGGACTTAGCCAGATCTACTGATCC
4-4-3-4	33917401	TAAATGCCCGTCAGT	33917415	GAGTCTACCACTGACGGGCATTTAGGTTGACTC
4-4-3-5	273798	ACAGTTGACTGTCTCA	273813	GAGTCATACACAGTTGACTGTCTCAGTGTGACTC
4-4-5-3	29836317	AGAACTGTGGGTACCC	29836332	GAGTCAGGTAGAACTGTGGGTACCCCTCCGGATCC
4-5-1-2	22052058	TACACAGCTCAC	22052069	GAGTCCACAGTGAGCTGTGTAGATGGACTC
4-5-1-5	7028188	AAACTTTGCCATCTC	7028202	GAGTCATTGGAGATGGCAAAGTTTGTGATGACTC
4-5-2-2	33655118	TAGCCACACAGTAC	33655130	GAGTCTTGGGTACTGTGGGCTAGTAAAGACTC
4-5-3-1	10176900	ACAGAGAGCCCCCT	10176912	GGATCCTCCAGGGGCTCTCTGTAGAAAGACTC
4-5-3-1	21002027	TGCCCAGCCAAGA	21002039	GAGTCGATGTCTTGGCTGGGCACAGTACTC
4-5-3-3	21926110	CTCCACAGATGTGAG	21926124	GGATCAGTGTGACATCTGTGGAGAGTGGACTC
4-6-1-5	18855810	CTATTAAACCCCTGTAC	18855825	GAGTCCATGCTATTAAACCCCTGTACCAGGGACTC
4-6-2-1	33917713	CACTCCAGCCAGA	33917725	GAGTCTCGTTCTGGCTGGAGTGCAGTACTC
4-6-2-3	23841885	ACAGTCAGCACTTCC	23841899	GGATCTCCAGGAAGTGTGACTGTTAATGACTC
4-7-2-3	32820688	TGTCCTCCACAGAAC	32820703	GAGTCATTCTGTTCTGTGGAGGGACAAGTGGACTC
4-8-1-2	31630487	CCAACCCACTCTGAC	31630501	GGATCTGGGGTCAAGTGGGTTGGAGGAGACTC
4-8-1-3	18471550	CTCATCAAGCCCATCC	18471565	GGATCCTCTGGATGGGCTTGATGAGGTACGACTC
5-0-0-3	15751134	TATTAAAA	15751141	GAGTCTCTTTTAAATAGAAATGACTC
5-0-1-2	619226	ATAAATGA	619233	GAGTCAGATATAAATGAATCAGACTC
5-0-1-2	15224385	ATAAATGA	15224392	GAGTCAGATATAAATGAGTCAGACTC
5-0-2-0	12773697	AAAGAGA	12773703	GAGTCATACAAAGAGACTTAGACTC
5-0-5-2	26992119	AGTAGGAAATGG	26992130	GAGTCAGTAAGTAGGAAATGGGTGGGACTC
5-0-7-3	29788190	ATGGGTGGAGAAATGA	29788204	GAGTCTTTGTCACTCTCCACCCATGTCTGACTC
5-1-1-5	24998727	TATAATTTGCAA	24998738	GGATCCTTTTGCATAATTAATACTGACTC
5-1-1-6	23902556	ACTTTGATTTAAA	23902568	GAGTCTGAAACTTTGATTTAAACCTTGACTC
5-1-3-2	25725309	TCAGAAATGAGA	25725319	GGATCAGCTTCTCATTTCTGAAATGAGACTC

Sig.	Start	Product	End	Sequence
5-1-3-4	3038558	CAGTTAAGATGAT	3038570	GAGTCAAAAATCATCTTAAGTCTAAGACTC
5-1-4-3	20735471	AGATGGGTTCAAA	20735483	GAGTCAGACAGATGGGTTCAAAATCCTGACTC
5-1-5-4	7028188	GAGATGGCAAAAGTTT	7028202	GAGTCATTGGAGATGGCAAAAGTTTGTGACTC
5-1-6-4	18855810	GTACAGGGGTTAATAG	18855825	GAGTCCATGCTATTAAACCCCTGTACAGGGACTC
5-1-7-2	27407459	GTGCTGAAAGGAGGA	27407473	GAGTCCCAAGTGTGAAAGGAGGATGCAGATCC
5-2-1-0	15651283	ACAAACAG	15651290	GAGTCCTGAACAAACAGACATGACTC
5-2-1-0	28972460	AGCAAAACA	28972467	GAGTCCTTGAGCAAAACATCTCGATCC
5-2-2-2	27918310	CTAAGGTCAAA	27918320	GGATCTTACTTTTGACCTTAGCCAGGACTC
5-2-3-6	14431981	TCTTATCTTGAGAAGA	14431996	GAGTCGTATCTTATCTTGAGAAGAGTGGGATCC
5-2-3-6	19178433	TAAATATTGCATGAGCT	19178448	GGATCCAGGAGCTCATGCAATATTACCAGGACTC
5-2-5-4	2970818	AAAGCATGTTGGTGCA	2970833	GAGTCATCCAAAGCATGTTGGTGCAACAGGATCC
5-2-5-4	22527477	AATCTGAGAAATGGCTG	22527492	GAGTCATTGAATCTGAGAAATGGCTGTTGGGATCC
5-3-1-3	15850371	CATAGAATTACC	15850382	GAGTCTCCACATAGAAATTACCACATGATCC
5-3-1-4	16036924	AAATGTCCAACCTT	16036936	GAGTCAGAAAAATGTCCAACCTTCAAAGACTC
5-3-2-2	23315455	CAGTTAGACACA	23315466	GAGTCCCAGCAGTTAGACACATATTGATCC
5-3-2-4	24952095	TTCCATAAAGCATG	24952108	GGATCCCACCATGCTTTATGGAATAATGACTC
5-3-2-6	18216247	AAGATGTATCATCCTT	18216262	GAGTCTCCCAAGATGTATCATCCTTCCCTGATCC
5-3-3-1	19850611	AAAGAAAGTGCCC	19850622	GAGTCTTTGAAAAGAAAGTGCCCCACAAAGATCC
5-3-3-2	30711102	TTGAAAGCCCAAGC	30711114	GAGTCCCCCTTTGAAAGCCCAAGCCCTTGATCC
5-3-4-4	273798	TGAGACAGTCAACTGT	273813	GAGTCATACACAGTTGACTGTCTCAGTGTGACTC
5-3-5-3	11255290	TCCAAGATGGGAAC TG	11255305	GGATCCTGACAGTTCCCATCTTGGATGCTGACTC
5-4-2-0	205051	CACAAGGCCAA	205061	GAGTCAGGCCACAAAGGCCCAAGTCTGACTC
5-4-3-2	23934318	AACCCAGTTCAGAG	23934331	GAGTCTCAGAACCCAGTTTCAAGTCTGGACTC
5-4-5-2	29781742	TCTAAGGCACCAAGGG	29781757	GAGTCACATTCTAAGGCACCAAGGTGAGGACTC
5-5-2-3	23758787	GTATTCACAGCACAC	23758801	GAGTCGAGTGTATTACACAGCACACAGGGGACTC
5-6-2-1	245423	CCACAAATCGGCACA	245436	GGATCAGAGTGTCCCGATTGTGGATGAGACTC
6-0-2-2	18038803	TATGAAGAAA	18038812	GAGTCAGAGTATGAAGAAAAGATTGACTC
6-1-1-5	23902556	TTTAAATCAAAGT	23902568	GAGTCTGAAACTTTTGATTTTAAACCTTGACTC
6-1-2-3	3952582	TAAAGTCAAGTA	3952593	GGATCTTAATACTTGACTTTAGCCAGACTC
6-1-4-3	5084130	AGTGACATGAGAAT	5084143	GAGTCTCAAAGTGACATGAGAATTTGTGACTC
6-1-5-2	30028652	GAGTAAGAAGCAGT	30028665	GAGTCCCAGGAGTAAGAAGCAGTCAAGGATCC

Sig.	Start	Product	End	Sequence
6-1-8-1	13897829	GGGAAAGAGAGGCTAA	13897844	GGATCTAAATTAGCCTCTCTTCCCATTAGACTC
6-2-1-3	9172896	TTGTACAACAAA	9172907	GGATCACGTTTTTGTGTACAAAGTCAGACTC
6-2-3-4	25660391	CTGAATTAGAAATCG	25660405	GAGTCCCATCTGAATTAGAAATCGGGAGACTC
6-2-3-4	29780020	GATCAAAGACTTTGA	29780034	GAGTCGTGGGATCAAAGACTTTTGAACCGATCC
6-2-5-1	14980846	CAGGAAGGAACGAT	14980859	GAGTCCATTTCAGGAAGGAACGATATGTGACTC
6-3-1-5	1932974	AGTAAACTCACTTAT	1932988	GAGTCCATAAGTAAACTCACITTAATTATGATCC
6-3-2-2	17378613	GCAATTGAAACCA	17378625	GAGTCAGAGGCAATTGAAACCCAGAGTGACTC
6-3-2-3	1209487	TTTGAACACAGACA	1209500	GAGTCAGAAATGTCTGTGTTCAAATCCTGACTC
6-3-2-3	33773747	AGACAAAAGTTCTCA	33773760	GAGTCCTGATGAGAACTTTGTCTCAAGGACTC
6-3-3-1	18506656	AGAGAACACTCAG	18506668	GAGTCTTACAGAGAACACTCAGCATAGACTC
6-3-3-2	33877374	GTAGACAGCATACA	33877387	GGATCTAACTGTATGCTGTCTCTACAGAGACTC
6-3-4-0	2713672	AAGGAGCAGCAA	2713684	GAGTCTCAAAGGAGCAGCAGCAACCTAGATCC
6-3-4-1	28721600	CAGGAGACACTAGA	28721613	GAGTCTGTTTCAGGAGACACTAGAGAGGGACTC
6-4-1-3	14333110	TGAACTAAAAATCCC	14333123	GAGTCAGAAAGGGATTTTAGTTCATGTAGACTC
6-4-5-0	21631191	AGGGCCCCAACAGA	21631205	GAGTCATTTCAGGGGCCCCAACAGATGGAGACTC
6-5-2-1	33752323	CAGACCTTAAAGC	33752336	GAGTCAGCACAGACCCCTAAAGCTAAGGACTC
6-6-0-2	1506217	ACTCAATACACCAC	1506230	GAGTCAACAGTGGTGTATTGAGTGTATGACTC
7-0-2-4	925974	TAAAAAGATATTG	925986	GAGTCAACATATAAAAGATATTGAAGAGATCC
7-0-4-4	25875523	TATGAAAAGAGTTAA	25875537	GAGTCATCTTTAACTCTTCCATACCCAGACTC
7-1-0-3	21712574	AAAAATATTCA	21712584	GAGTCTCAAAAAAATATTCTATATAGATCC
7-1-1-2	11947722	ATAATAGACAA	11947732	GAGTCTGGAATAATAGACAAATGGAGACTC
7-1-3-3	13563376	GAAAAGGACTATTA	13563389	GAGTCTGTAGAAAAGGACTATTAGAAAAGACTC
7-1-3-4	1572344	AAAATAGTCTGTGAA	1572358	GAGTCTGATAAAATAGTCTGTGAAAGCAAGATCC
7-1-4-4	22768695	GCTTAAAGAGTTGAAA	22768710	GAGTCATTGGCTTAAAGAGTTGAAAAATAGATCC
7-1-5-1	27319856	GAAGGAACAAGGAT	27319869	GAGTCTGAGGAAGGAACAAGGATGCGGGATCC
7-2-2-3	33817389	AGATACTCATAAGA	33817402	GAGTCATTTTCTTATGAGTATCTAACTGACTC
7-3-1-1	10734587	ATAAACAGCACA	10734598	GGATCAGAAATGTGCTGTTTATAATGGACTC
7-4-1-3	2663787	AAATTACACTCAGCA	2663801	GGATCCCCTGTGCTGAGTGTAAATTTCTATGACTC
7-4-4-1	20634452	GGCAAAGTACAAGCCA	20634467	GAGTCAGCCGGCAAAGTACAGCCATGCTGACTC
7-5-2-2	33039205	ACATACACGACACTGA	33039220	GAGTCTTTATCAGTGTCTGTATGTTCAGACTC
8-1-0-4	27892202	TTTACAAAATAAA	27892214	GAGTCCCAGTTTATTTGTAAAAATGGACTC

Sig.	Start	Product	End	Sequence
8-1-3-2	24503746	GACAAGAAGAAATTA	24503759	GAGTCTAAGGACAAGAAGAAATTAGATAGATCC
8-1-3-4	7031187	TAAAGAAAAAGACGTTT	7031202	GAGTCAATTAAACGTCTTTCTTTTATTATGACTC
8-1-4-0	13199929	AAAGAGAGAACGA	13199941	GAGTCTTATAAAGAGAGAACGAATTAGATCC
8-1-5-2	22394971	ATGGAGAAAAACAAGGT	22394986	GGATCATTTACCTTGTCTTCTCCATGCGGGACTC
8-2-2-4	17813774	AAGTATAGTCTAAAAAC	17813789	GAGTCTGCAAAAGTATAGTCTAAAAACCTGGGACTC
8-3-3-2	18319692	CCAAAAAGGACATTAG	18319707	GAGTCTCAACTAATGTCCCTTTTGGATTGACTC
9-2-3-1	5408125	AGTCAAAGACAGAAA	5408139	GAGTCTCTGTCTTCTGTCTTTGACTCTCTGACTC

Table 6. Probability of overlap of any given fragment of specified length with a N.BstNB I-derived oligonucleotide created from a genome the size of the human genome

length of fragment	# possibilities	overlap probability human genome
8	6.5×10^4	0.4
9	2.6×10^5	0.1
10	1.0×10^6	0.03
11	4.1×10^6	6.4×10^{-3}
12	1.7×10^7	1.6×10^{-3}
13	6.7×10^7	4.0×10^{-4}
14	2.7×10^8	1.0×10^{-4}
15	1.1×10^9	2.5×10^{-5}
16	4.3×10^9	6.3×10^{-6}

5

Table 7. Number of N.BstNB I derived oligonucleotides per organism

Organism	Number
aeropyrum_pernix.fna	21
archaeoglobus_fulgidus.fna	6
bacillus_subtilis.fna	21
bacillus_halodurans.fna	38
bacillus_halodurans.fna	3
campylobacter_jejuni.fna	3
caulobacter_crescentus.fna	32
chlamydia_muridarum.fna	7
chlamydia_trachomatis.fna	9
chlamydophila_pneumoniae_AR39.fna	17
halobacterium_sp.fna	29
helicobacter_pylori_26695.fna	7
lactococcus_lactis.fna	3
mesorhizobium_loti.fna	28
methanobacterium_thermoautotrophicum.fna	19
mycobacterium_leprae.fna	46
mycobacterium_tuberculosis_CDC1151.fna	47
mycoplasma_pneumoniae.fna	2
mycoplasma_pulmonis.fna	3
neisseria_meningitidis_MC58.fna	1
pasteurella_multocida.fna	5
pseudomonas_aeruginosa.fna	52
pyrococcus_abyssi.fna	2
pyrococcus_horikoshii.fna	11
rickettsia_prowazekii.fna	2
staphylococcus_aureus_Mu50.fna	1
staphylococcus_aureus_N315.fna	8
streptococcus_pyogenes.fna	5
sulfolobus_solfataricus.fna	8
synechocystis_PCC6803.fna	12
thermoplasma_acidophilum.fna	10
thermoplasma_volcanium.fna	5
thermotoga_maritima.fna	38
treponema_pallidum.fna	7

Organism	Number
xylella_fastidiosa.fna	28

EXAMPLE 2GENERATION OF OLIGONUCLEOTIDE-BASED FINGERPRINTS FROM WHOLE GENOMIC
DNA

5 This example shows oligonucleotide-based fingerprints generated from whole genomic DNA and characterization thereof.

Templates Designed for Detecting E. coli O157 and K12

 The following templates were designed to detect E.coli O157 and
10 K12. The first oligonucleotide in each set is the one that would be generated/amplified from the whole genome of E. coli O157 or K12 in the presence of nicking enzymes N.BstNB I and N.Alw I and a DNA polymerase. The next two oligonucleotides are two template oligonucleotides useful in further amplification of the oligonucleotide generated from the whole genome.
15 The sequence of the sense strand of the recognition sequence of N.BstNB I is underlined.

O157-392522 5'-TGGCAATATCC

O157-1S: 5'-TGAAAACCGAAAGAGTCAATTGGATATTGCCA

20 O157-1SP: 5'-TGAAAACCGAAAGAGTCAATTTGGCAATATCC

O157-1660620 5'-GATATTATTGG

O157-2S: 5'-TGAAAACCGAAAGAGTCAATTCCAATAATATC

O157-2SP: 5'-TGAAAACCGAAAGAGTCAATTGATATTATTGG

25

O157-1856922 5'-GGCATTACGCGCGG

O157-3S: 5'-TGAAAACCGAAAGAGTCAATTCCGCCGCGCGTAAT

O157-3SP: 5'-TGAAAACCGAAAGAGTCAATTGGCATTACGCGCGG

30 O157-2268011 5'-TTTAACGCCAGTTC

O157-4S: 5'-TGAAAACCGAAAGAGTCAATTGAACTGGCGTTAAA

O157-4SP: 5'-TGAAAACCGAAAGAGTCAATTTTAAACGCCAGTTC

K12-198629 5'-TTGAAACGGGCATAA

K12-1S: 5'-TGAAAACCGAAAGAGTCAATTTTATGCCCGTTCAA

K12-1SP: 5'-TGAAAACCGAAAGAGTCAATTTTGAACGGGCATAA

5

K12-312061 5'-GGATTGAGTGTTG

K12-2S: 5'-TGAAAACCGAAAGAGTCAATTCAACACTCAATCC

K12-2SP: 5'-TGAAAACCGAAAGAGTCAATTGGATTGAGTGTTG

10 K12-558515 5'-TTCTGGATGAATGTTA

K12-3S: 5'-TGAAAACCGAAAGAGTCAATTTAACATTCATC

K12-3SP: 5'-TGAAAACCGAAAGAGTCAATTGATGAATGTTA

K12-1093455 5'-TAAAGCGGCA

15 K12-4S: 5'-TGAAAACCGAAAGAGTCAATTTGCCGCTTTA

K12-4SP: 5'-TGAAAACCGAAAGAGTCAATTTAAAGCGGCA

Materials

Oligonucleotides were synthesized by Midland Certified Reagent Company, Inc. (Midland, TX), or MWG Biotech, Inc. (High Point NC). The
20 oligonucleotides were routinely checked by time-of-flight mass spectrometry (using LCT from Micromass, Manchester, UK).

All enzymes were purchased from New England Biolabs. The DNA polymerase used was *exo⁻* Vent. The nicking enzyme (N.BstNB,I) has a specific activity of approximately 10^6 units/mg. All HPLC components (water
25 and acetonitrile) were purchased from Fisher Scientific (Pittsburgh, PA). The dimethyl-butylamine was purchased from Sigma-Aldrich Corp. (St. Louis, MO) and a salt was made by the addition of acetic acid (Sigma Aldrich) to pH 8.4. The 2 molar stock solution was filtered using a 0.2 micron nylon filter.

K12 and O157 DNAs were obtained the Coriell Institute. Purified
30 *E. coli* DNA was obtained from Sigma and human liver mRNA was obtained from Ambion (Austin TX). Nicked *E. coli* DNA was prepared by placing 25

micrograms of DNA in 200 microliters of 1x N.BstNB I buffer (New England Biolabs) and 10 ul of N.BstNB I nicking enzyme (20 units). The solution was incubated at 55°C for 60 minutes, and then heated to 95°C for 5 minutes to inactivate the nicking enzyme and denature the E. coli DNA.

5 DNA isolation from prokaryotic sources.

Isolation and quantitation of genomic DNA from gram-negative and spirochete bacteria were also achieved as follows. Cells were pelleted and washed twice in 1 ml of 1M NaCl by centrifugation in a fixed angle microfuge at 15,000 rpm for 5 min. Cells were washed twice and resuspended in TE (10 mm
10 Tris, 25 mM EDTA, pH 8.0) and incubated in 0.2 mg/ml lysozyme and 0.3 mg/ml RNase A for 20 min at 37°C. If lysis by lysozyme was not visible with refractory pathogenic strains, 0.6% SDS was added. To these suspensions, 1% Sarkosyl and 0.6 mg/ml proteinase K were added, and the cells were incubated for 1 hr at 37°C. Cell lysates were extracted twice with phenol and
15 twice with chloroform. The aqueous phase was precipitated with 0.33M NH₄ acetate and 2.5 volumes of ethanol. Precipitated threads of DNA were removed with a sterile Pasteur pipette tip, and dissolved in TE (10 mM Tris, 1 mM EDTA, pH 8.0).

Isolation of genomic DNA from Gram-positive bacteria was also
20 performed as follows. Concentrated cell pellets were washed twice in 1M NaCl and twice in TE (50 mM Tris, 50 mM EDTA, pH 7.8) and spun in a fixed-angle microfuge for 5 min. Cell pellets were resuspended in TE and incubated with 250 U/ml mutanolysin and 0.3 mg/ml RNase A for 30 min at 37°C. To this reaction, 0.6% SDS and 0.6 mg/ml proteinase K were added, and the mixture
25 was incubated for 1 hr at 37°C, followed by 65°C for 45 min. Lysates were extracted twice with phenol and twice with chloroform. The aqueous phase was precipitated with 0.33M NH₄ acetate and 2.5 volumes of ethanol. Precipitated threads of DNA were removed with a sterile Pasteur pipette tip, and dissolved in TE (10 mM Tris, 1 mM EDTA, pH 8.0).

In both instances the genomic DNA was quantitated by spectrofluorimetry at excitation and emission wavelengths of 365 nm and 460 nm respectively using the DNA-specific dye, Hoechst 33258 and a fluorometer.

5 Generating Oligonucleotides from Genomic DNA

The reaction conditions used to generate oligonucleotides from genomic DNA are: 85 mM KCl, 25 mM Tris-HCl (pH 8.8 at 25°C), 2.0 mM MgSO₄, 5 mM MgCl₂, 10 mM (NH₄)₂SO₄, 0.1% Triton X-100, 0.5 mM DTT, 0.8 units N.BstNB I nicking enzyme (NEB), 0.05 units 9°NmTM polymerase (NEB),
 10 200 micromolar dNTPs, 10 micrograms/ml BSA (NEB), and 0.001 to 500 ng of genomic DNA in ultra-pure water that is nuclease free (Ambion, Austin TX). Incubation is at 60°C for the time as specified.

Exponential Amplification of Oligonucleotide Generated from Genomic DNA

The reaction conditions for exponentially amplifying the
 15 oligonucleotides generated from genomic DNA are: 85 mM KCl, 25 mM Tris-HCl (pH 8.8 at 25°C), 2.0 mM MgSO₄, 5 mM MgCl₂, 10 mM (NH₄)₂SO₄, 0.1% Triton X-100, 0.5 mM DTT, 0.4 units N.BstNB I nicking enzyme (NEB), 0.05 units 9°NmTM polymerase (New England Biolabs, (NEB), MA), 0.2 M trehalose, 200 micromolar dNTPs, 10 micrograms/ml BSA (NEB), 0.1 micromolar of each
 20 template oligonucleotide in ultra-pure water that is nuclease free (Ambion). In the case of fluorescence monitoring, SYBR[®] green (Molecular Probes, Eugene OR) was added to 5x concentration (SYBR[®] green is supplied by the manufacturer at a concentration of 10,000X). Incubation is for times indicated in the text at 55°C to 65°C (as specified).

25 To determine the lower limit of detection, the following reaction mixture was assembled in a 5 ml polypropylene tubes on ice (4°C). 100 ul 10x Thermopol Reaction buffer, 50 ul 10x N.BstNB I buffer, 1 ul of the first template oligonucleotide (T1) at 100 uM stock, 1 ul of the second template oligonucleotide (T2) at 100 uM stock, 24 ul 25 mM dNTPS, 1 ul 10 mg/ml BSA,
 30 40 ul N.BstNB I nicking enzyme at 10 units/ul, 24 ul 9°NmTM polymerase, 760 ul

ultra-pure water. The reaction was mixed to homogeneity with a 1 ml pipetor. In a set of 12 microtubes, 120 ul was added to the first tube, then 80 ul was aliquoted over the remaining 11 tubes. The oligonucleotide(s) generated from genomic DNA or otherwise to be exponentially amplified was diluted 1-1000
5 from the stock concentration of 100 uM, to a final concentration of 0.1 uM. One microliter of the 0.1 uM solution was added to the first tube, then eleven, 3-fold dilutions were made by transferring 40 ul from the first tube and mixing. The serial dilutions were made on ice. The tubes were capped and then incubated at 60°C for the times indicated. The reaction was stopped by placing the tube
10 at 4°C or on ice. In the case of real time fluorescence monitoring, an MJ Opticon was programmed as follows: (1) incubate 10 seconds at 60°C, (2) read plate, then repeat the incubation and reading steps 29 more times.

Chromatography, Time-of-Flight (TOF) Mass Spectrometry

The chromatography system was an Agilent 1100 Series HPLC
15 composed of a binary pump, degasser, a column oven, a diode array detector, and thermostatted microwell plate autoinjector (Agilent Technologies, Palo Alto, CA). The column is a Waters Xterra MS C18, incorporating C18 packing with 3.5 uM particle size, with 125 Angstrom pore size, 2.1 mm x 20 mm (Waters Inc. Milford, MA). The column was run at 30°C with a gradient of acetonitrile in
20 5mM dimethyl-butylamine acetate (DMBAA). As a check on the complete release of the signal oligo during the chromatography and injection we ran the column at 50° after incubating the sample briefly at 95°C. We saw no increase in the oligo yield over our standard conditions. Buffer A is 5mM DMBAA, buffer
25 B is 5mM DMBAA and 50% (V/V) acetonitrile. The gradient begins at 10%B and ramps to 15%B over 0.3 minute, to 30%B over 2 minutes, to 90%B over 0.5 minute, to 10%B over 0.25 minute, then holds at 10%B for 1.25 minutes. The column temperature was held constant at 30°C. The flow rate was 0.25 ml/minute. The injection volume was 10 µl. Flow rate into the mass
30 spectrometer was also 0.25 ml/min. The mass spectrometer is a Micromass LCT Time-of-Flight with an electrospray inlet (Micromass Inc. Manchester UK).

The samples were run in electrospray negative mode with a range from 800 to 2000 amu using a 1 second scan time. Source parameters: Desolvation gas 450 L/hr, Capillary 2225V, Sample cone 30V, RF lens 400V, extraction cone 7V, desolvation temperature 275°C, Source temperature 120°C. Analysis of the
5 LC-mass spectrometry data made use of the software supplied by the manufacturer.

Oligonucleotides are known to exhibit different ionization efficiencies, which in our measurements would be translated into sequence-specific differences in measured oligo concentration. A survey of a range of
10 more than 80 different 12mers indicated that the variation between sequences attributable to this difference is less than 30%. Almost all relevant quantitative comparisons are with the same oligo sequence. It is necessary, however, to calibrate for ionization efficiencies for quantitative comparisons between different sequences.

15 MALDI Mass Spectroscopy

MALDI Mass Spectroscopy reagents are 1% PADMAC from a stock solution of 10% w/v of poly(diallyldimethylammonium chloride) from Polysciences in 0.3x SSPE, diluted to 1% w/v in HPLC water. 3-HPA Matrix is prepared fresh daily by placing 25mg of 3-hydroxypicolinic acid washed once
20 with 1000ul acetonitrile, decanted, dissolved in 500ul acetonitrile and 500ul 0.1%TFA. ammonium citrate is prepared by dissolving in HPLC water to 10mg/ml.

The procedure for manual spotting is as follows: on a clean MALDI card (stainless steel, Micromass), 0.5ul of the 1% PADMAC solution
25 was placed onto the center of the well using a P2 pipetman. The plate was heated on a thermocycling block to 50°C and the drop was allowed to dry completely (3 to 5 minutes). The card is allowed to cool. 0.5ul of sample was placed (oligo standard or assay sample) onto the well in the same spot as the PADMAC. The card was placed on the heating block until the spots are dry.
30 This step is repeated if the sample is dilute. The card is removed, cooled and

washed with 2ul of 10mg/ml ammonium citrate on the wells, 1 minute incubation followed by aspiration of the liquid off using vacuum suction. The wash was repeated followed by two washes with 2 ul HPLC grade water as above. The card was heated to dry (2 to 5 minutes). A small drop (about ½ ul) of matrix was applied to each spot. The matrix was dried, and the application was repeated. The card was dried on the heated block for 1 minute.

Acquisition Details: when a MALDI instrument in positive mode with the neutral density filter removed (Micromass Manchester UK) was used, the following parameters were employed: Source voltage of 15000, Pulse voltage of 1313, MCP detector voltage of 1800, Fine Laser Energy % 75, Matrix suppression (amu) 493.2, TLF delay of 500 ns. ADC settings were: Sample period of 0.5 ns and signal sensitivity of 100. Mass range of acquisition was from 1500 to 15000 amu. The laser firing rate was set to 5 Hz and shots per spectrum was set to 5.

Calibration: The daily calibration was performed using a mixture of oligonucleotides. The sequences and calculated average masses was as follows:

	8mer-1v	ATGATGCA	2433.6
	62100 trigger	TTTATGAACT AT	3634.4
20	ITAtop	CCGATCTAGT GAGTCGCTC	5779.8
	48180p	GAAAATCCCC TGAGATGAGT CAGTG	7715.1
	63180	GGTACTAGCCTTATGCGACTCGGTACTAGCCTT	10095

Real-time Fluorescence Measurement

All fluorescence measurements reported here were made on an MJ Opticon™ instrument (MJ Research Ltd., Waltham, MA) using software supplied by the manufacturer. The real-time measurements on this instrument were made using an isothermal protocol using a 10-30 second interval read beginning 10 seconds after the lid and chamber reached 60°C.

Results

Eight short oligonucleotides (6-16 nucleotides in length) unique to E.coli strain K12 or O157, respectively, were generated by incubating 10^5 cells of each strain in the amplification buffer and incubating with the nicking enzyme

5 N.BstNB I and 9°NmTM polymerase for 10 minutes at 60°C.

A small aliquot of the above-described reaction mixture was then added to a replicator type amplification reaction where a set of two templates (*i.e.*, O157-1S and O157-1SP, O157-2S and O157-2SP, O157-3S and O157-3SP, O157-4S and O157-4SP, K12-1S and K12-1SP, K12-2S and K12-2SP,

10 K12-3S and K12-3SP, or K12-4S and K12-4SP) designed to further amplifying one of the eight short oligonucleotides as described above were present. The resulting reaction mixture was for 3 minutes at 60°C, cooled to 4°C and then subjected to both MALDI and LC-TOF mass spectrometry analysis (see Table 8). All the four oligonucleotides from each of the two strains were amplified,

15 while no oligonucleotides were amplified from the negative controls.

Table 8. Analysis of the fingerprinting reactions for E. coli O157 and K12 strains by LC-TOF and mass spectrometry

Name of template oligonucleotide	Peak area LC-TOF	Peak height height
O157-1S	55	172
O157-2S	25	184
O157-3S	36	122
O157-4S	44	78
K12-1S	56	99
K12-2S	26	123
K12-3S	66	176
K12-4S	37	189
negative control	<0.01	not observed
negative control	<0.01	not observed
positive control	75	125

5

False positives can be greatly reduced when one strand of genomic DNA generates an oligonucleotide that is exactly complementary to another oligonucleotide generated from the other strand of the genomic DNA. Under such circumstances, the possibility of an accidental production of not just one, but two, oligonucleotides with masses identical to those expected from the two complementary oligonucleotides generated from the genomic DNA is much smaller than the possibility of an accidental production of one oligonucleotide with a mass identical to that of an oligonucleotide generated from the genomic DNA.

15

Figures 4a and 4b show the TOF spectra of the multiplexed amplification reaction in the presence of short oligonucleotides generated from the genomic DNA of the E. coli strain K12 and O157, respectively.

Figures 5a and 5b show the MALDI spectra of the multiplexed amplification reaction in the presence of short oligonucleotides generated from

the genomic DNA of the E. coli strain K12 and O157, respectively. The figures show that all the eight amplification products and the oligonucleotide generated by the positive control, but no additional fragments were amplified.

Both MALDI and LC-TOF mass spectrometry methods are highly
5 amenable to multiplexing with respect to the simultaneous measurement of mass/charge ratios. Using current off-the-self instrumentation the level of achievable multiplexing should reach 200-500 fragments for LC-TOF and 20-50 different fragments when using MALDI mass spectrometry.

The readout can also be accomplished by real-time fluorescence
10 although the capability to perform intra-well multiplexing is lost. The lower limit of detection for triggering oligonucleotides from E. coli K12 was determined by serially diluting the oligonucleotide generated from the genomic DNA and measuring the duplex formation and intercalation of SYBR[®] green during the exponential amplification reaction using real-time fluorescence monitoring. The
15 trigger was diluted from a starting concentration of 1×10^{-4} micromolar to 1×10^{-12} micromolar in 3-fold intervals per well. The reaction was monitored every 10 seconds using SYBR[®] green on an MJ Opticon[™] 1. As shown in Figure 6, the rate of accumulation of double-strand material is proportional to the concentration of the oligonucleotide generated from the genomic DNA. At the
20 highest concentration of this oligonucleotide, the reaction was complete in 50 seconds, and there was an approximate 20 second delay in accumulation of fluorescence for each 4-fold dilution of the trigger. The eleventh dilution of trigger was clearly above the values of the no-trigger control indicating the lower limit of detection of about 200 molecules. The level of amplification was
25 about 10^8 -fold. There appears to be no fundamental limitation on the lower limit of detection. By scaling down the volume of amplification via miniaturation or by using solid phase technologies, a lower limit of detection of a few tens of molecules should be achieved.

Another tractable form of multiplexing is to covalently immobilize
30 the template amplification-oligonucleotides in an array format where multiplexing is achieved by spatial separation of elements on the array. Each

element contains two templates (T1 and T2) specific for a particular oligonucleotide generated from a genomic DNA. When the template oligonucleotides are covalently immobilized on a surface coated with 70,000 MW poly(ethyleneimine) (PEI), the nicking enzymes and polymerases are not hindered and amplification is nearly as efficient as in solution. Covalent attachment of the amplification-templates has the added advantage that the annealing between the T1 and T2 templates is prevented.

The 8 sets of amplification templates (for E. coli strains K12 and O157) as described above were immobilized on PEI glass slides using cyanuric chloride as the cross-linker (see above). Trigger oligonucleotides were added to the amplification reaction at 1×10^{-3} femtomolar and the reaction was incubated 60°C for 10 (under a coverslip). All K12 elements were positive with K12 triggers and the O157 elements positive with O157 triggers in which the positive and negative controls also showed the results as expected. During the amplification, the single-stranded amplification templates were converted to double strand and in the presence of SYBR® green, the amplifying elements become fluorescent and the negative elements remain unstained.

EXAMPLE 3

COMPUTER-ASSISTED IDENTIFICATION OF SHORT OLIGONUCLEOTIDES CONTAINING SINGLE NUCLEOTIDE POLYMORPHISM

Certain short oligonucleotide fragments generated from the genomic DNA of an organism may contain single nucleotide polymorphisms. In other words, a short oligonucleotide fragment generated from the genomic DNA from one individual may be different from the corresponding fragment from another individual. Such oligonucleotide fragments may be used to characterize genetic variations and to identify a particular individual. Table 9 shows the short oligonucleotides that would be generated from human genomic DNA in the presence of the nicking enzyme N.BstNB I alone or the nicking enzyme N.BstNB1 in combination with another restriction endonuclease

selected from Bcl I, Bsa BI, Bsm I, Bsr I and Bsr D1. In the enzyme column, "NBstNBI" indicates that the fragment is flanked by two N.BstNB I sites.

BclI_NBstNBI indicates that a fragment is flanked by a BclI site and an N.BstNB I site. This table also shows portions of genomic DNA that contains two closely
5 located sequences of one strand of the N.BstNB I recognition sequence, or the sequence of one strand of the N.BstNB I recognition sequence and that of one strand of the BclI recognition sequence.

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
50805	64145	BsrI_NBstNBI	CGGSAA	A	1905.2473	GACAGCGCTAACTGGCTTSCCGTGCCGAC TCCACGTTCTTT
50805	64145	BsrI_NBstNBI	CGGSAA	C	1881.2223	GACAGCGCTAACTGGCTTSCCGTGCCGAC TCCACGTTCTTT
50805	64145	BsrI_NBstNBI	CGGSAA	G	1921.2467	GACAGCGCTAACTGGCTTSCCGTGCCGAC TCCACGTTCTTT
50805	64145	BsrI_NBstNBI	CGGSAA	T	1896.2339	GACAGCGCTAACTGGCTTSCCGTGCCGAC TCCACGTTCTTT
51751	2671530	BsrI_NBstNBI	ACGCGTCACTGCAS	A	4312.7975	TGTCATCCAGACTGGASTGCAGTGACGCG TTCTTGACTCACTGCAACCT
51751	2671530	BsrI_NBstNBI	ACGCGTCACTGCAS	C	4288.7725	TGTCATCCAGACTGGASTGCAGTGACGCG TTCTTGACTCACTGCAACCT
51751	2671530	BsrI_NBstNBI	ACGCGTCACTGCAS	G	4328.7969	TGTCATCCAGACTGGASTGCAGTGACGCG TTCTTGACTCACTGCAACCT
51751	2671530	BsrI_NBstNBI	ACGCGTCACTGCAS	T	4303.7841	TGTCATCCAGACTGGASTGCAGTGACGCG TTCTTGACTCACTGCAACCT
65222	149559	NBstNBI	GAGGAGSCTAGCTCA	A	4706.056	ATGGAGGGATGAGTCACCATGAGCTAGSC TCCTCGGAAGACTCCAGAACGTTT
65222	149559	NBstNBI	GAGGAGSCTAGCTCA	C	4682.031	ATGGAGGGATGAGTCACCATGAGCTAGSC TCCTCGGAAGACTCCAGAACGTTT
65222	149559	NBstNBI	GAGGAGSCTAGCTCA	G	4722.0554	ATGGAGGGATGAGTCACCATGAGCTAGSC TCCTCGGAAGACTCCAGAACGTTT
65222	149559	NBstNBI	GAGGAGSCTAGCTCA	T	4697.0426	ATGGAGGGATGAGTCACCATGAGCTAGSC TCCTCGGAAGACTCCAGAACGTTT
65222	149559	NBstNBI	TGAGCTAGSCTCCTC	A	4607.9804	ATGGAGGGATGAGTCACCATGAGCTAGSC TCCTCGGAAGACTCCAGAACGTTT
65222	149559	NBstNBI	TGAGCTAGSCTCCTC	C	4583.9554	ATGGAGGGATGAGTCACCATGAGCTAGSC TCCTCGGAAGACTCCAGAACGTTT
65222	149559	NBstNBI	TGAGCTAGSCTCCTC	G	4623.9798	ATGGAGGGATGAGTCACCATGAGCTAGSC TCCTCGGAAGACTCCAGAACGTTT
65222	149559	NBstNBI	TGAGCTAGSCTCCTC	T	4598.967	ATGGAGGGATGAGTCACCATGAGCTAGSC TCCTCGGAAGACTCCAGAACGTTT
65395	149694	BclI_NBstNBI	AATTGCAGSATTGATC	A	4984.2517	TTCTTCTGCTTGATCAATSTGCAATTAAG AGACTCTGGTGTATTC

TSC ID	dbSNP ID	Enzymes	Product	Allele	Mass	Sequence
65395	149694	BclI NBstNBI	AATTGCAGSATTGATC	C	4960.2267	TTCTTCTGCTTGATCAATCTGCAATTAAG AGACTCTGGTGATTC
65395	149694	BclI NBstNBI	AATTGCAGSATTGATC	G	5000.2511	TTCTTCTGCTTGATCAATCTGCAATTAAG AGACTCTGGTGATTC
65395	149694	BclI NBstNBI	AATTGCAGSATTGATC	T	4975.2383	TTCTTCTGCTTGATCAATCTGCAATTAAG AGACTCTGGTGATTC
70647	1399493	NBstNBI	GACAAASA	A	2515.6673	ATAAGAGACAGAGTCAGTGGACAAAASACC CCGACTCCCTTGTCCT
70647	1399493	NBstNBI	GACAAASA	C	2491.6423	ATAAGAGACAGAGTCAGTGGACAAAASACC CCGACTCCCTTGTCCT
70647	1399493	NBstNBI	GACAAASA	G	2531.6667	ATAAGAGACAGAGTCAGTGGACAAAASACC CCGACTCCCTTGTCCT
70647	1399493	NBstNBI	GACAAASA	T	2506.6539	ATAAGAGACAGAGTCAGTGGACAAAASACC CCGACTCCCTTGTCCT
70647	1399493	NBstNBI	TSTTTGTC	A	2470.6003	ATAAGAGACAGAGTCAGTGGACAAAASACC CCGACTCCCTTGTCCT
70647	1399493	NBstNBI	TSTTTGTC	C	2446.5753	ATAAGAGACAGAGTCAGTGGACAAAASACC CCGACTCCCTTGTCCT
70647	1399493	NBstNBI	TSTTTGTC	G	2486.5997	ATAAGAGACAGAGTCAGTGGACAAAASACC CCGACTCCCTTGTCCT
70647	1399493	NBstNBI	TSTTTGTC	T	2461.5869	ATAAGAGACAGAGTCAGTGGACAAAASACC CCGACTCCCTTGTCCT
78726	1465092	NBstNBI	agcctccSttct	A	3636.3525	cgggagtcggagtcctcatgagaaSggaggctgggagacfc actgatgaag
78726	1465092	NBstNBI	agcctccSttct	C	3612.3275	cgggagtcggagtcctcatgagaaSggaggctgggagacfc actgatgaag
78726	1465092	NBstNBI	agcctccSttct	G	3652.3519	cgggagtcggagtcctcatgagaaSggaggctgggagacfc actgatgaag
78726	1465092	NBstNBI	agcctccSttct	T	3627.3391	cgggagtcggagtcctcatgagaaSggaggctgggagacfc actgatgaag
78726	1465092	NBstNBI	agaaSggaggct	A	3823.4903	cgggagtcggagtcctcatgagaaSggaggctgggagacfc actgatgaag
78726	1465092	NBstNBI	agaaSggaggct	C	3799.4653	cgggagtcggagtcctcatgagaaSggaggctgggagacfc actgatgaag

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
78726	1465092	NBstNBI	agaaSggaggct	G	3839.4897	cggagtgctggagtcacatgagaaSggaggctgggagactc actgatgaag
78726	1465092	NBstNBI	agaaSggaggct	T	3814.4769	cggagtgctggagtcacatgagaaSggaggctgggagactc actgatgaag
78915	1465241	BclI_NBstNBI	gcSgtgaic	A	2818.824	gaaatagctactgacacSgcagatgactccacatttaac
78915	1465241	BclI_NBstNBI	gcSgtgaic	C	2794.799	gaaatagctactgacacSgcagatgactccacatttaac
78915	1465241	BclI_NBstNBI	gcSgtgaic	G	2834.8234	gaaatagctactgacacSgcagatgactccacatttaac
78915	1465241	BclI_NBstNBI	gcSgtgaic	T	2809.8106	gaaatagctactgacacSgcagatgactccacatttaac
82246	1467407	NBstNBI_Bsrl	ggccSgcgtactg	A	4055.6116	ccctgcccctgagtcctctggggccSgcgtactggcagcgtg cc
82246	1467407	NBstNBI_Bsrl	ggccSgcgtactg	C	4031.5866	ccctgcccctgagtcctctggggccSgcgtactggcagcgtg cc
82246	1467407	NBstNBI_Bsrl	ggccSgcgtactg	G	4071.611	ccctgcccctgagtcctctggggccSgcgtactggcagcgtg cc
82246	1467407	NBstNBI_Bsrl	ggccSgcgtactg	T	4046.5982	ccctgcccctgagtcctctggggccSgcgtactggcagcgtg cc
82247	1467408	NBstNBI_Bsrl	ggcctScgtactg	A	4030.5988	ccctgcccctgagtcctctggggccSgcgtactggcagcgtg c
82247	1467408	NBstNBI_Bsrl	ggcctScgtactg	C	4006.5738	ccctgcccctgagtcctctggggccSgcgtactggcagcgtg c
82247	1467408	NBstNBI_Bsrl	ggcctScgtactg	G	4046.5982	ccctgcccctgagtcctctggggccSgcgtactggcagcgtg c
82247	1467408	NBstNBI_Bsrl	ggcctScgtactg	T	4021.5854	ccctgcccctgagtcctctggggccSgcgtactggcagcgtg c
101914	129050	NBstNBI_Bsml	TCSGAGTCTGAATG	A	4382.8451	CCTCCATATGGAGTCTCCCTCSGAGTCTG AATGCTGGGTTTTCCA
101914	129050	NBstNBI_Bsml	TCSGAGTCTGAATG	C	4358.8201	CCTCCATATGGAGTCTCCCTCSGAGTCTG AATGCTGGGTTTTCCA
101914	129050	NBstNBI_Bsml	TCSGAGTCTGAATG	G	4398.8445	CCTCCATATGGAGTCTCCCTCSGAGTCTG AATGCTGGGTTTTCCA
101914	129050	NBstNBI_Bsml	TCSGAGTCTGAATG	T	4373.8317	CCTCCATATGGAGTCTCCCTCSGAGTCTG AATGCTGGGTTTTCCA
103161	2922643	Bsml_NBstNBI	TCTGTCAITCCAGSGA	A	4936.2017	AGTGAGCCAAGAAATGCATCCTGGAATGA CAGAGAGAGACTCCGCTCTCAAAA

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103161	2922643	BsmI_NBstNBI	TCTGTCAATCCAGSGA	C	4912.1767	AGTGAGCCCAAGAATGCATCSCCTGGAATGA CAGAGAGAGACTCCGTCTCAAAA
103161	2922643	BsmI_NBstNBI	TCTGTCAATCCAGSGA	G	4952.2011	AGTGAGCCCAAGAATGCATCSCCTGGAATGA CAGAGAGAGACTCCGTCTCAAAA
103161	2922643	BsmI_NBstNBI	TCTGTCAATCCAGSGA	T	4927.1883	AGTGAGCCCAAGAATGCATCSCCTGGAATGA CAGAGAGAGACTCCGTCTCAAAA
105625	131104	NBstNBI_BsmI	CCASTAGAATG	A	3429.244	GGTCATCGAGGAGTCTCTGCCASTAGAAT GCTTGTTGCCCA
105625	131104	NBstNBI_BsmI	CCASTAGAATG	C	3405.219	GGTCATCGAGGAGTCTCTGCCASTAGAAT GCTTGTTGCCCA
105625	131104	NBstNBI_BsmI	CCASTAGAATG	G	3445.2434	GGTCATCGAGGAGTCTCTGCCASTAGAAT GCTTGTTGCCCA
105625	131104	NBstNBI_BsmI	CCASTAGAATG	T	3420.2306	GGTCATCGAGGAGTCTCTGCCASTAGAAT GCTTGTTGCCCA
110927	85736	NBstNBI	TCCTTGGAAGACCCSG	A	4970.2279	ACAGACAAATGAGTCAATCCCSGGTCTTTTC CAAGGACAGGACTCATCTGGCACT
110927	85736	NBstNBI	TCCTTGGAAGACCCSG	C	4946.2029	ACAGACAAATGAGTCAATCCCSGGTCTTTTC CAAGGACAGGACTCATCTGGCACT
110927	85736	NBstNBI	TCCTTGGAAGACCCSG	G	4986.2273	ACAGACAAATGAGTCAATCCCSGGTCTTTTC CAAGGACAGGACTCATCTGGCACT
110927	85736	NBstNBI	TCCTTGGAAGACCCSG	T	4961.2145	ACAGACAAATGAGTCAATCCCSGGTCTTTTC CAAGGACAGGACTCATCTGGCACT
110927	85736	NBstNBI	CSGGTCTTTCCAAAGGA	A	4961.2145	ACAGACAAATGAGTCAATCCCSGGTCTTTTC CAAGGACAGGACTCATCTGGCACT
110927	85736	NBstNBI	CSGGTCTTTCCAAAGGA	C	4937.1895	ACAGACAAATGAGTCAATCCCSGGTCTTTTC CAAGGACAGGACTCATCTGGCACT
110927	85736	NBstNBI	CSGGTCTTTCCAAAGGA	G	4977.2139	ACAGACAAATGAGTCAATCCCSGGTCTTTTC CAAGGACAGGACTCATCTGGCACT
110927	85736	NBstNBI	CSGGTCTTTCCAAAGGA	T	4952.2011	ACAGACAAATGAGTCAATCCCSGGTCTTTTC CAAGGACAGGACTCATCTGGCACT
111150	85784	BsrI_NBstNBI	CACAGGGGCSGTGAA	A	4731.0688	TACAGAGGGAAGTGGCTTACSGGCCCTTG TGCTGGGACTCAGTCCCTCAG
111150	85784	BsrI_NBstNBI	CACAGGGGCSGTGAA	C	4707.0438	TACAGAGGGAAGTGGCTTACSGGCCCTTG TGCTGGGACTCAGTCCCTCAG

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111150	85784	BsrI_NBstNBI	CACAGGGGCSGTGAA	G	4747.0682	TACAGAGGGAACTGGCTTACSGCCCCCTG TGCTGGGACTCAGTCCCTCAG
111150	85784	BsrI_NBstNBI	CACAGGGGCSGTGAA	T	4722.0554	TACAGAGGGAACTGGCTTACSGCCCCCTG TGCTGGGACTCAGTCCCTCAG
114553	135562	BsrI_NBstNBI	GCCCACCCGSTT	A	3646.3537	GCCACAGTGGACTGGAASCGGGTGGGC AGTTGACTCAAAACCAATC
114553	135562	BsrI_NBstNBI	GCCCACCCGSTT	C	3622.3287	GCCACAGTGGACTGGAASCGGGTGGGC AGTTGACTCAAAACCAATC
114553	135562	BsrI_NBstNBI	GCCCACCCGSTT	G	3662.3531	GCCACAGTGGACTGGAASCGGGTGGGC AGTTGACTCAAAACCAATC
114553	135562	BsrI_NBstNBI	GCCCACCCGSTT	T	3637.3403	GCCACAGTGGACTGGAASCGGGTGGGC AGTTGACTCAAAACCAATC
114953	135801	NBstNBI	GA CTGAGASA	A	3165.0721	GATTGAGGGTGAGTCTGTCTSTCTCAGTC CACTGACTCAAATGTTAAT
114953	135801	NBstNBI	GA CTGAGASA	C	3141.0471	GATTGAGGGTGAGTCTGTCTSTCTCAGTC CACTGACTCAAATGTTAAT
101914	129050	NBstNBI_BsmI	TCSGAGTCTGAATG	C	4358.8201	CCTCCATATGGAGTCTCCCTCSGAGTCTG AATGCTGGGTTTTCCA
114953	135801	NBstNBI	GA CTGAGASA	T	3156.0587	GATTGAGGGTGAGTCTGTCTSTCTCAGTC CACTGACTCAAATGTTAAT
114953	135801	NBstNBI	TSTCTCAGTC	A	3057.9831	GATTGAGGGTGAGTCTGTCTSTCTCAGTC CACTGACTCAAATGTTAAT
114953	135801	NBstNBI	TSTCTCAGTC	C	3033.9581	GATTGAGGGTGAGTCTGTCTSTCTCAGTC CACTGACTCAAATGTTAAT
114953	135801	NBstNBI	TSTCTCAGTC	G	3073.9825	GATTGAGGGTGAGTCTGTCTSTCTCAGTC CACTGACTCAAATGTTAAT
114953	135801	NBstNBI	TSTCTCAGTC	T	3048.9697	GATTGAGGGTGAGTCTGTCTSTCTCAGTC CACTGACTCAAATGTTAAT
116962	2923573	BsrDI_NBstNBI	GATATSAAGAAGTTAT	A	5032.3017	GTCTTTCTTGCAATGAAATAACTTCTTSA TATCTCCAGACTCTATGCAGCAA
116962	2923573	BsrDI_NBstNBI	GATATSAAGAAGTTAT	C	5008.2767	GTCTTTCTTGCAATGAAATAACTTCTTSA TATCTCCAGACTCTATGCAGCAA
116962	2923573	BsrDI_NBstNBI	GATATSAAGAAGTTAT	G	5048.3011	GTCTTTCTTGCAATGAAATAACTTCTTSA TATCTCCAGACTCTATGCAGCAA

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116962	2923573	BsrDI_NBstNBI	GATATSAAGAAGTTAT	T	5023.2883	GTCCTTTCTTGCAATGAAATAAAGTTCTTSA TATCTCCAGACTCTATGCAGCAA
152327	2085682	BsrI_NBstNBI	TASAGGTTTAAAACC	A	4664.056	TCCTCCTCCAACCTGGGGTTTAAACCTST ATTGGACTCTGGGCCCTTT
152327	2085682	BsrI_NBstNBI	TASAGGTTTAAAACC	C	4640.031	TCCTCCTCCAACCTGGGGTTTAAACCTST ATTGGACTCTGGGCCCTTT
152327	2085682	BsrI_NBstNBI	TASAGGTTTAAAACC	G	4680.0554	TCCTCCTCCAACCTGGGGTTTAAACCTST ATTGGACTCTGGGCCCTTT
152327	2085682	BsrI_NBstNBI	TASAGGTTTAAAACC	T	4655.0426	TCCTCCTCCAACCTGGGGTTTAAACCTST ATTGGACTCTGGGCCCTTT
163645	1321869	BsrI_NBstNBI	TCSTGGAGGAT	A	3476.2544	GAAAGATCAAACCTGGAATCCTCCASGAGC TGGACTCCACGGTAGAA
163645	1321869	BsrI_NBstNBI	TCSTGGAGGAT	C	3452.2294	GAAAGATCAAACCTGGAATCCTCCASGAGC TGGACTCCACGGTAGAA
163645	1321869	BsrI_NBstNBI	TCSTGGAGGAT	G	3492.2538	GAAAGATCAAACCTGGAATCCTCCASGAGC TGGACTCCACGGTAGAA
163645	1321869	BsrI_NBstNBI	TCSTGGAGGAT	T	3467.241	GAAAGATCAAACCTGGAATCCTCCASGAGC TGGACTCCACGGTAGAA
163767	1321945	NBstNBI_BsmI	STTATGGAATG	A	3475.2666	TAAGTACTATGAGTCAGGCSTTATGGAATG CATTTTACAGAT
163767	1321945	NBstNBI_BsmI	STTATGGAATG	C	3451.2416	TAAGTACTATGAGTCAGGCSTTATGGAATG CATTTTACAGAT
163767	1321945	NBstNBI_BsmI	STTATGGAATG	G	3491.266	TAAGTACTATGAGTCAGGCSTTATGGAATG CATTTTACAGAT
163767	1321945	NBstNBI_BsmI	STTATGGAATG	T	3466.2532	TAAGTACTATGAGTCAGGCSTTATGGAATG CATTTTACAGAT
164846	1322742	BsmI_NBstNBI	CSCCCTCCTTCCC	A	4135.6609	GGTGACAGGGGGAATGCAGGGAAGGAGGG GSGGAGGACTCTAAAGGAATA
164846	1322742	BsmI_NBstNBI	CSCCCTCCTTCCC	C	4111.6359	GGTGACAGGGGGAATGCAGGGAAGGAGGG GSGGAGGACTCTAAAGGAATA
164846	1322742	BsmI_NBstNBI	CSCCCTCCTTCCC	G	4151.6603	GGTGACAGGGGGAATGCAGGGAAGGAGGG GSGGAGGACTCTAAAGGAATA
164846	1322742	BsmI_NBstNBI	CSCCCTCCTTCCC	T	4126.6475	GGTGACAGGGGGAATGCAGGGAAGGAGGG GSGGAGGACTCTAAAGGAATA

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166751	1324350	BsrI_NBstNBI	AAGTTCSCAAAT	A	3717.4409	TTTTGTCACACTGGCATTGSGAACTTTT GGGACTCTTGTGGGAGA
166751	1324350	BsrI_NBstNBI	AAGTTCSCAAAT	C	3693.4159	TTTTGTCACACTGGCATTGSGAACTTTT GGGACTCTTGTGGGAGA
166751	1324350	BsrI_NBstNBI	AAGTTCSCAAAT	G	3733.4403	TTTTGTCACACTGGCATTGSGAACTTTT GGGACTCTTGTGGGAGA
166751	1324350	BsrI_NBstNBI	AAGTTCSCAAAT	T	3708.4275	TTTTGTCACACTGGCATTGSGAACTTTT GGGACTCTTGTGGGAGA
169782	1326805	BsrI_NBstNBI	GGAATCTCASTGATGT	A	4976.2261	ATCTGCAGCAACTGGGACATCASTGAGAG TCCCTGGGACTCCTGCACAGCA
169782	1326805	BsrI_NBstNBI	GGAATCTCASTGATGT	C	4952.2011	ATCTGCAGCAACTGGGACATCASTGAGAG TCCCTGGGACTCCTGCACAGCA
169782	1326805	BsrI_NBstNBI	GGAATCTCASTGATGT	G	4992.2255	ATCTGCAGCAACTGGGACATCASTGAGAG TCCCTGGGACTCCTGCACAGCA
169782	1326805	BsrI_NBstNBI	GGAATCTCASTGATGT	T	4967.2127	ATCTGCAGCAACTGGGACATCASTGAGAG TCCCTGGGACTCCTGCACAGCA
172808	1329241	BsrI_NBstNBI	ACCACCGGCGSGTGG	A	4683.0188	GCGGACCAGTACTGGTCCACSGCCCCGGT GGTCTGGGACTCCTGGTATAGA
172808	1329241	BsrI_NBstNBI	ACCACCGGCGSGTGG	C	4658.9938	GCGGACCAGTACTGGTCCACSGCCCCGGT GGTCTGGGACTCCTGGTATAGA
172808	1329241	BsrI_NBstNBI	ACCACCGGCGSGTGG	G	4699.0182	GCGGACCAGTACTGGTCCACSGCCCCGGT GGTCTGGGACTCCTGGTATAGA
172808	1329241	BsrI_NBstNBI	ACCACCGGCGSGTGG	T	4674.0054	GCGGACCAGTACTGGTCCACSGCCCCGGT GGTCTGGGACTCCTGGTATAGA
174831	1330911	NBstNBI_BclI	GTGGSCCGTGATC	A	4070.6232	CCAGGAGTTTGAGTCTGCAGTGGSCCGTG ATCATGCCATTGCA
174831	1330911	NBstNBI_BclI	GTGGSCCGTGATC	C	4046.5982	CCAGGAGTTTGAGTCTGCAGTGGSCCGTG ATCATGCCATTGCA
174831	1330911	NBstNBI_BclI	GTGGSCCGTGATC	G	4086.6226	CCAGGAGTTTGAGTCTGCAGTGGSCCGTG ATCATGCCATTGCA
174831	1330911	NBstNBI_BclI	GTGGSCCGTGATC	T	4061.6098	CCAGGAGTTTGAGTCTGCAGTGGSCCGTG ATCATGCCATTGCA
175974	2857016	BsrI_NBstNBI	TGTGTACCCASGC	A	4303.7841	ACGCCACTGCACCTGGAGCSTGGGTGACA CAGCGAGACTCTGTCTCAGAA

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175974	2857016	BsrI_NBstNBI	TGTGTCACCCASGC	C	4279.7591	ACGCCACTGCACCTGGAGCSTGGGTGACA CAGCGAGACTCTGTCTCAGAA
175974	2857016	BsrI_NBstNBI	TGTGTCACCCASGC	G	4319.7835	ACGCCACTGCACCTGGAGCSTGGGTGACA CAGCGAGACTCTGTCTCAGAA
175974	2857016	BsrI_NBstNBI	TGTGTCACCCASGC	T	4294.7707	ACGCCACTGCACCTGGAGCSTGGGTGACA CAGCGAGACTCTGTCTCAGAA
177075	1332730	NBstNBI_BsrI	AAATGSACTG	A	3140.0593	GGACTCTGGTGAGTCCTCTAAATGSACTG GGTCGCTTCACG
177075	1332730	NBstNBI_BsrI	AAATGSACTG	C	3116.0343	GGACTCTGGTGAGTCCTCTAAATGSACTG GGTCGCTTCACG
177075	1332730	NBstNBI_BsrI	AAATGSACTG	G	3156.0587	GGACTCTGGTGAGTCCTCTAAATGSACTG GGTCGCTTCACG
177075	1332730	NBstNBI_BsrI	AAATGSACTG	T	3131.0459	GGACTCTGGTGAGTCCTCTAAATGSACTG GGTCGCTTCACG
180710	1335615	NBstNBI	AGGTSTG	A	2240.4546	GAAAAAATTAGAGTCGCAAAAGGTSTGGGA GGACTCAGCCAGTAAA
180710	1335615	NBstNBI	AGGTSTG	C	2216.4296	GAAAAAATTAGAGTCGCAAAAGGTSTGGGA GGACTCAGCCAGTAAA
180710	1335615	NBstNBI	AGGTSTG	G	2256.454	GAAAAAATTAGAGTCGCAAAAGGTSTGGGA GGACTCAGCCAGTAAA
180710	1335615	NBstNBI	AGGTSTG	T	2231.4412	GAAAAAATTAGAGTCGCAAAAGGTSTGGGA GGACTCAGCCAGTAAA
180710	1335615	NBstNBI	CASACCT	A	2129.3948	GAAAAAATTAGAGTCGCAAAAGGTSTGGGA GGACTCAGCCAGTAAA
180710	1335615	NBstNBI	CASACCT	C	2105.3698	GAAAAAATTAGAGTCGCAAAAGGTSTGGGA GGACTCAGCCAGTAAA
180710	1335615	NBstNBI	CASACCT	G	2145.3942	GAAAAAATTAGAGTCGCAAAAGGTSTGGGA GGACTCAGCCAGTAAA
180710	1335615	NBstNBI	CASACCT	T	2120.3814	GAAAAAATTAGAGTCGCAAAAGGTSTGGGA GGACTCAGCCAGTAAA
182558	2857424	NBstNBI_BsrI	TCTSTCACCAGACTG	A	4591.981	TTTTAAGACGGAGTCTCACTCTSTCACCAG ACTGGAGTGCAGTGGT
182558	2857424	NBstNBI_BsrI	TCTSTCACCAGACTG	C	4567.956	TTTTAAGACGGAGTCTCACTCTSTCACCAG ACTGGAGTGCAGTGGT

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182558	2857424	NBstNBI_BsrI	TCTSTCACCAGACTG	G	4607.9804	TTTTAAGACGGAGTCTCACTCTSTCACCAG ACTGGAGTGCAGTGGT
182558	2857424	NBstNBI_BsrI	TCTSTCACCAGACTG	T	4582.9676	TTTTAAGACGGAGTCTCACTCTSTCACCAG ACTGGAGTGCAGTGGT
185065	1339136	BsrI_NBstNBI	GGCCCTGCCCCSCT	A	3951.5378	GCATGGAGGAACTGGCAGSGGGCAGGGC CCTAGGACTCCCAAGATTAT
185065	1339136	BsrI_NBstNBI	GGCCCTGCCCCSCT	C	3927.5128	GCATGGAGGAACTGGCAGSGGGCAGGGC CCTAGGACTCCCAAGATTAT
185065	1339136	BsrI_NBstNBI	GGCCCTGCCCCSCT	G	3967.5372	GCATGGAGGAACTGGCAGSGGGCAGGGC CCTAGGACTCCCAAGATTAT
185065	1339136	BsrI_NBstNBI	GGCCCTGCCCCSCT	T	3942.5244	GCATGGAGGAACTGGCAGSGGGCAGGGC CCTAGGACTCCCAAGATTAT
185157		BsrI_NBstNBI	GSCCCTGCCCCACT	A	3935.5384	GTGTGGAGGCACTGGCAGTGGGCAGGGG CCTAGGACTCCCAAGATTAT
185157		BsrI_NBstNBI	GSCCCTGCCCCACT	C	3911.5134	GTGTGGAGGCACTGGCAGTGGGCAGGGG CCTAGGACTCCCAAGATTAT
185157		BsrI_NBstNBI	GSCCCTGCCCCACT	G	3951.5378	GTGTGGAGGCACTGGCAGTGGGCAGGGG CCTAGGACTCCCAAGATTAT
185157		BsrI_NBstNBI	GSCCCTGCCCCACT	T	3926.525	GTGTGGAGGCACTGGCAGTGGGCAGGGG CCTAGGACTCCCAAGATTAT
188867	1342030	BsrI_NBstNBI	GSAATAAATGGTGG	A	4455.9079	GGTTTGTGTTACTGGGCCACCATTTATTSC TTTCGACTCTTCAACCTAC
188867	1342030	BsrI_NBstNBI	GSAATAAATGGTGG	C	4431.8829	GGTTTGTGTTACTGGGCCACCATTTATTSC TTTCGACTCTTCAACCTAC
188867	1342030	BsrI_NBstNBI	GSAATAAATGGTGG	G	4471.9073	GGTTTGTGTTACTGGGCCACCATTTATTSC TTTCGACTCTTCAACCTAC
188867	1342030	BsrI_NBstNBI	GSAATAAATGGTGG	T	4446.8945	GGTTTGTGTTACTGGGCCACCATTTATTSC TTTCGACTCTTCAACCTAC
190135	1343028	BsrI_NBstNBI	STGGTAITTTAATTCAT	A	4652.0274	ATTTCTGCTAACTGGGATGAATAAATACCA SAATAGACTCACTTCACTTA
190135	1343028	BsrI_NBstNBI	STGGTAITTTAATTCAT	C	4628.0024	ATTTCTGCTAACTGGGATGAATAAATACCA SAATAGACTCACTTCACTTA
190135	1343028	BsrI_NBstNBI	STGGTAITTTAATTCAT	G	4668.0268	ATTTCTGCTAACTGGGATGAATAAATACCA SAATAGACTCACTTCACTTA

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190135	1343028	BsrI_NBstNBI	STGGTATTATTCAT	T	4643.014	ATTTCTGCTAACTGGGATGAATAAATACCA SAATAGACTCACTTCACTTA
193888	1346029	NBstNBI_BsrI	GAGAASGACTG	A	3494.2812	GCCGGCTGGTGAGTCCAGGGGAGAASGAC TGGCAGGGGCTGGG
193888	1346029	NBstNBI_BsrI	GAGAASGACTG	C	3470.2562	GCCGGCTGGTGAGTCCAGGGGAGAASGAC TGGCAGGGGCTGGG
193888	1346029	NBstNBI_BsrI	GAGAASGACTG	G	3510.2806	GCCGGCTGGTGAGTCCAGGGGAGAASGAC TGGCAGGGGCTGGG
193888	1346029	NBstNBI_BsrI	GAGAASGACTG	T	3485.2678	GCCGGCTGGTGAGTCCAGGGGAGAASGAC TGGCAGGGGCTGGG
196636	1348254	NBstNBI_BsrI	TGCTGTSCAGTACTG	A	4663.0164	CATGCATGCTGAGTCACTATGCTGTSCAG TACTGGAAATAATTTT
196636	1348254	NBstNBI_BsrI	TGCTGTSCAGTACTG	C	4638.9914	CATGCATGCTGAGTCACTATGCTGTSCAG TACTGGAAATAATTTT
196636	1348254	NBstNBI_BsrI	TGCTGTSCAGTACTG	G	4679.0158	CATGCATGCTGAGTCACTATGCTGTSCAG TACTGGAAATAATTTT
196636	1348254	NBstNBI_BsrI	TGCTGTSCAGTACTG	T	4654.003	CATGCATGCTGAGTCACTATGCTGTSCAG TACTGGAAATAATTTT
221219	1481900	BsrI_NBstNBI	tcatcattStctctt	A	4547.9536	atttggagatactggcaagagaSaattgatgaccaggactcc ttattagaa
221219	1481900	BsrI_NBstNBI	tcatcattStctctt	C	4523.9286	atttggagatactggcaagagaSaattgatgaccaggactcc ttattagaa
221219	1481900	BsrI_NBstNBI	tcatcattStctctt	G	4563.953	atttggagatactggcaagagaSaattgatgaccaggactcc ttattagaa
221219	1481900	BsrI_NBstNBI	tcatcattStctctt	T	4538.9402	atttggagatactggcaagagaSaattgatgaccaggactcc ttattagaa
222004	1482566	BsrI_NBstNBI	tgScccaagtttgaat	A	4960.2267	aagtagaacaactgggtattcaaacattgggScagttgtactct agaacacgt
222004	1482566	BsrI_NBstNBI	tgScccaagtttgaat	C	4936.2017	aagtagaacaactgggtattcaaacattgggScagttgtactct agaacacgt
222004	1482566	BsrI_NBstNBI	tgScccaagtttgaat	G	4976.2261	aagtagaacaactgggtattcaaacattgggScagttgtactct agaacacgt
222004	1482566	BsrI_NBstNBI	tgScccaagtttgaat	T	4951.2133	aagtagaacaactgggtattcaaacattgggScagttgtactct agaacacgt

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
225349	1485319	NBstNBI	catgcagSttaa	A	3733.4403	gtgggaagtggagtcagagcatgcagSttaaagcttgactct ttgcatgg
225349	1485319	NBstNBI	catgcagSttaa	C	3709.4153	gtgggaagtggagtcagagcatgcagSttaaagcttgactct ttgcatgg
225349	1485319	NBstNBI	catgcagSttaa	G	3749.4397	gtgggaagtggagtcagagcatgcagSttaaagcttgactct ttgcatgg
225349	1485319	NBstNBI	catgcagSttaa	T	3724.4269	gtgggaagtggagtcagagcatgcagSttaaagcttgactct ttgcatgg
225349	1485319	NBstNBI	ttaaScitgcatg	A	3724.4269	gtgggaagtggagtcagagcatgcagSttaaagcttgactct ttgcatgg
225349	1485319	NBstNBI	ttaaScitgcatg	C	3700.4019	gtgggaagtggagtcagagcatgcagSttaaagcttgactct ttgcatgg
225349	1485319	NBstNBI	ttaaScitgcatg	G	3740.4263	gtgggaagtggagtcagagcatgcagSttaaagcttgactct ttgcatgg
225349	1485319	NBstNBI	ttaaScitgcatg	T	3715.4135	gtgggaagtggagtcagagcatgcagSttaaagcttgactct ttgcatgg
227789	1487286	NBstNBI	ggcatgSccc	A	3092.9971	tccggaaggagagtcctctagggScatgccacacaggactctat gctctgt
227789	1487286	NBstNBI	ggcatgSccc	C	3068.9721	tccggaaggagagtcctctagggScatgccacacaggactctat gctctgt
227789	1487286	NBstNBI	ggcatgSccc	G	3108.9965	tccggaaggagagtcctctagggScatgccacacaggactctat gctctgt
227789	1487286	NBstNBI	ggcatgSccc	T	3083.9837	tccggaaggagagtcctctagggScatgccacacaggactctat gctctgt
227789	1487286	NBstNBI	gggScatgcc	A	3133.0215	tccggaaggagagtcctctagggScatgccacacaggactctat gctctgt
227789	1487286	NBstNBI	gggScatgcc	C	3108.9965	tccggaaggagagtcctctagggScatgccacacaggactctat gctctgt
227789	1487286	NBstNBI	gggScatgcc	G	3149.0209	tccggaaggagagtcctctagggScatgccacacaggactctat gctctgt
227789	1487286	NBstNBI	gggScatgcc	T	3124.0081	tccggaaggagagtcctctagggScatgccacacaggactctat gctctgt
235036	1357492	NBstNBI	TSAAAAGCTAGAAG	A	4408.8975	TC TTGTCAAGGAGTCCCCTTCTTAGCTTT TSATATAGACTCTTTCTTCTC

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235036	1357492	NBstNBI	TSAAAAGCTAGAAG	C	4384.8725	TCCTGTCAAGGAGTCCCCTTCTTCTAGCTTT TSATATAGACTCTTTTCTTCTC
235036	1357492	NBstNBI	TSAAAAGCTAGAAG	G	4424.8969	TCCTGTCAAGGAGTCCCCTTCTTCTAGCTTT TSATATAGACTCTTTTCTTCTC
235036	1357492	NBstNBI	TSAAAAGCTAGAAG	T	4399.8841	TCCTGTCAAGGAGTCCCCTTCTTCTAGCTTT TSATATAGACTCTTTTCTTCTC
235036	1357492	NBstNBI	CTTCTAGCTTTTSA	A	4283.7817	TCCTGTCAAGGAGTCCCCTTCTTCTAGCTTT TSATATAGACTCTTTTCTTCTC
235036	1357492	NBstNBI	CTTCTAGCTTTTSA	C	4259.7567	TCCTGTCAAGGAGTCCCCTTCTTCTAGCTTT TSATATAGACTCTTTTCTTCTC
235036	1357492	NBstNBI	CTTCTAGCTTTTSA	G	4299.7811	TCCTGTCAAGGAGTCCCCTTCTTCTAGCTTT TSATATAGACTCTTTTCTTCTC
235036	1357492	NBstNBI	CTTCTAGCTTTTSA	T	4274.7683	TCCTGTCAAGGAGTCCCCTTCTTCTAGCTTT TSATATAGACTCTTTTCTTCTC
237771	2858904	NBstNBI_BsrI	GCSGGAACGTG	A	3157.0465	TGAGCATGGAGAGTCGCGGGGCSGGAAC GGGGCTGCCACA
237771	2858904	NBstNBI_BsrI	GCSGGAACGTG	C	3133.0215	TGAGCATGGAGAGTCGCGGGGCSGGAAC GGGGCTGCCACA
237771	2858904	NBstNBI_BsrI	GCSGGAACGTG	G	3173.0459	TGAGCATGGAGAGTCGCGGGGCSGGAAC GGGGCTGCCACA
237771	2858904	NBstNBI_BsrI	GCSGGAACGTG	T	3148.0331	TGAGCATGGAGAGTCGCGGGGCSGGAAC GGGGCTGCCACA
239554	1361502	BsrDI_NBstNBI	TCSCGCCAA	A	2747.7886	TCACCAGGCTGCAATGCATTGGCGSGACC TCGACTCACTGCAACCT
239554	1361502	BsrDI_NBstNBI	TCSCGCCAA	C	2723.7636	TCACCAGGCTGCAATGCATTGGCGSGACC TCGACTCACTGCAACCT
239554	1361502	BsrDI_NBstNBI	TCSCGCCAA	G	2763.788	TCACCAGGCTGCAATGCATTGGCGSGACC TCGACTCACTGCAACCT
239554	1361502	BsrDI_NBstNBI	TCSCGCCAA	T	2738.7752	TCACCAGGCTGCAATGCATTGGCGSGACC TCGACTCACTGCAACCT
249319	1490595	NBstNBI_BsrI	ttctcScactg	A	3347.1678	gatctgaagtgaagtcagttctcScactggaagaaactca
249319	1490595	NBstNBI_BsrI	ttctcScactg	C	3323.1428	gatctgaagtgaagtcagttctcScactggaagaaactca
249319	1490595	NBstNBI_BsrI	ttctcScactg	G	3363.1672	gatctgaagtgaagtcagttctcScactggaagaaactca
249319	1490595	NBstNBI_BsrI	ttctcScactg	T	3338.1544	gatctgaagtgaagtcagttctcScactggaagaaactca

TSC ID	dbSNP ID	Enzymes	Product	Allele	Mass	Sequence
249995	1491157	BsrI_NBstNBI	tgctgggtScagt	A	4694.0274	aaatgtaaaactgggactgSaaccacagacagtctgactct agagcttgt
249995	1491157	BsrI_NBstNBI	tgctgggtScagt	C	4670.0024	aaatgtaaaactgggactgSaaccacagacagtctgactct agagcttgt
249995	1491157	BsrI_NBstNBI	tgctgggtScagt	G	4710.0268	aaatgtaaaactgggactgSaaccacagacagtctgactct agagcttgt
249995	1491157	BsrI_NBstNBI	tgctgggtScagt	T	4685.014	aaatgtaaaactgggactgSaaccacagacagtctgactct agagcttgt
251571	1492464	NBstNBI_BsrI	ttacaattStgaactg	A	4959.2389	ttttatcctgagctgccttacaattStgaactggacttaagcct C
251571	1492464	NBstNBI_BsrI	ttacaattStgaactg	C	4935.2139	ttttatcctgagctgccttacaattStgaactggacttaagcct C
251571	1492464	NBstNBI_BsrI	ttacaattStgaactg	G	4975.2383	ttttatcctgagctgccttacaattStgaactggacttaagcct C
251571	1492464	NBstNBI_BsrI	ttacaattStgaactg	T	4950.2255	ttttatcctgagctgccttacaattStgaactggacttaagcct C
252685	1493360	NBstNBI_BsmI	Sgatggcagggaatg	A	4786.1048	aagagtcacagagtcacacSgatggcagggaatgaggag ccitggag
252685	1493360	NBstNBI_BsmI	Sgatggcagggaatg	C	4762.0798	aagagtcacagagtcacacSgatggcagggaatgaggag ccitggag
252685	1493360	NBstNBI_BsmI	Sgatggcagggaatg	G	4802.1042	aagagtcacagagtcacacSgatggcagggaatgaggag ccitggag
252685	1493360	NBstNBI_BsmI	Sgatggcagggaatg	T	4777.0914	aagagtcacagagtcacacSgatggcagggaatgaggag ccitggag
253701	2866937	NBstNBI	acagttgacSgtctca	A	4945.2151	atgattattagagtcatacacagttgacSgtctcagtgactc aagaccacaa
253701	2866937	NBstNBI	acagttgacSgtctca	C	4921.1901	atgattattagagtcatacacagttgacSgtctcagtgactc aagaccacaa
253701	2866937	NBstNBI	acagttgacSgtctca	G	4961.2145	atgattattagagtcatacacagttgacSgtctcagtgactc aagaccacaa
253701	2866937	NBstNBI	acagttgacSgtctca	T	4936.2017	atgattattagagtcatacacagttgacSgtctcagtgactc aagaccacaa
253701	2866937	NBstNBI	tgagacSgtcaactgt	A	4985.2395	atgattattagagtcatacacagttgacSgtctcagtgactc aagaccacaa

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
253701	2866937	NBstNBI	tgagacSgtcaactgt	C	4961.2145	atgattattagagtcatacacagttgacSgtctcagtgagctc aagaccacaa
253701	2866937	NBstNBI	tgagacSgtcaactgt	G	5001.2389	atgattattagagtcatacacagttgacSgtctcagtgagctc aagaccacaa
253701	2866937	NBstNBI	tgagacSgtcaactgt	T	4976.2261	atgattattagagtcatacacagttgacSgtctcagtgagctc aagaccacaa
256487	1369311	BsrI_NBstNBI	SGGAAAGGAAGTAGG	A	4819.1432	GGCGTGAGCCCACTGGGCTACTTCCCTTTTC CSTTTAGACTCAAAAATCCAG
256487	1369311	BsrI_NBstNBI	SGGAAAGGAAGTAGG	C	4795.1182	GGCGTGAGCCCACTGGGCTACTTCCCTTTTC CSTTTAGACTCAAAAATCCAG
256487	1369311	BsrI_NBstNBI	SGGAAAGGAAGTAGG	G	4835.1426	GGCGTGAGCCCACTGGGCTACTTCCCTTTTC CSTTTAGACTCAAAAATCCAG
256487	1369311	BsrI_NBstNBI	SGGAAAGGAAGTAGG	T	4810.1298	GGCGTGAGCCCACTGGGCTACTTCCCTTTTC CSTTTAGACTCAAAAATCCAG
275678	2897209	NBstNBI_BsaBI	TSATGATTG	A	2832.8478	TACCATGCCTGAGTCTAGCTSATGATTGG TATCCCTACCAATC
275678	2897209	NBstNBI_BsaBI	TSATGATTG	C	2808.8228	TACCATGCCTGAGTCTAGCTSATGATTGG TATCCCTACCAATC
275678	2897209	NBstNBI_BsaBI	TSATGATTG	G	2848.8472	TACCATGCCTGAGTCTAGCTSATGATTGG TATCCCTACCAATC
275678	2897209	NBstNBI_BsaBI	TSATGATTG	T	2823.8344	TACCATGCCTGAGTCTAGCTSATGATTGG TATCCCTACCAATC
278102	1418777	NBstNBI	CGGGSATG	A	2554.6521	TCCTCCCTAGAGTCCAGCCATSCCCGGC CAGACTCCTCTCCAAC
278102	1418777	NBstNBI	CGGGSATG	C	2530.6271	TCCTCCCTAGAGTCCAGCCATSCCCGGC CAGACTCCTCTCCAAC
278102	1418777	NBstNBI	CGGGSATG	G	2570.6515	TCCTCCCTAGAGTCCAGCCATSCCCGGC CAGACTCCTCTCCAAC
278102	1418777	NBstNBI	CGGGSATG	T	2545.6387	TCCTCCCTAGAGTCCAGCCATSCCCGGC CAGACTCCTCTCCAAC
278102	1418777	NBstNBI	CATSCCCG	A	2434.5789	TCCTCCCTAGAGTCCAGCCATSCCCGGC CAGACTCCTCTCCAAC
278102	1418777	NBstNBI	CATSCCCG	C	2410.5539	TCCTCCCTAGAGTCCAGCCATSCCCGGC CAGACTCCTCTCCAAC

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278102	1418777	NBstNBI	CATSCCCG	G	2450.5783	TCCTCCCTAGAGTCCAGCCATSCCCGGC CAGACTCCTCTCCAACC
278102	1418777	NBstNBI	CATSCCCG	T	2425.5655	TCCTCCCTAGAGTCCAGCCATSCCCGGC CAGACTCCTCTCCAACC
278103	1418778	NBstNBI	CSGGGATG	A	2554.6521	TCCTCCCTAGAGTCCAGCCATCCCSGGC CAGACTCCTCTCCAACC
278103	1418778	NBstNBI	CSGGGATG	C	2530.6271	TCCTCCCTAGAGTCCAGCCATCCCSGGC CAGACTCCTCTCCAACC
278103	1418778	NBstNBI	CSGGGATG	G	2570.6515	TCCTCCCTAGAGTCCAGCCATCCCSGGC CAGACTCCTCTCCAACC
278103	1418778	NBstNBI	CSGGGATG	T	2545.6387	TCCTCCCTAGAGTCCAGCCATCCCSGGC CAGACTCCTCTCCAACC
278103	1418778	NBstNBI	CATCCCSG	A	2434.5789	TCCTCCCTAGAGTCCAGCCATCCCSGGC CAGACTCCTCTCCAACC
278103	1418778	NBstNBI	CATCCCSG	C	2410.5539	TCCTCCCTAGAGTCCAGCCATCCCSGGC CAGACTCCTCTCCAACC
278103	1418778	NBstNBI	CATCCCSG	G	2450.5783	TCCTCCCTAGAGTCCAGCCATCCCSGGC CAGACTCCTCTCCAACC
278103	1418778	NBstNBI	CATCCCSG	T	2425.5655	TCCTCCCTAGAGTCCAGCCATCCCSGGC CAGACTCCTCTCCAACC
282241	1422319	NBstNBI_Bsrl	AACSAATGCACTG	A	4031.6384	GACTCTTTTGGAGTCTCTTAACSAATGCAC TGGTATTTATGAAG
282241	1422319	NBstNBI_Bsrl	AACSAATGCACTG	C	4007.6134	GACTCTTTTGGAGTCTCTTAACSAATGCAC TGGTATTTATGAAG
282241	1422319	NBstNBI_Bsrl	AACSAATGCACTG	G	4047.6378	GACTCTTTTGGAGTCTCTTAACSAATGCAC TGGTATTTATGAAG
282241	1422319	NBstNBI_Bsrl	AACSAATGCACTG	T	4022.625	GACTCTTTTGGAGTCTCTTAACSAATGCAC TGGTATTTATGAAG
285664	1425192	NBstNBI_Bsml	STTCTGTGAAGAATG	A	4711.0664	CATGTGAGTGGAGTCGAGASTTCTGTGAA GAATGCCGAAATAGATT
285664	1425192	NBstNBI_Bsml	STTCTGTGAAGAATG	C	4687.0414	CATGTGAGTGGAGTCGAGASTTCTGTGAA GAATGCCGAAATAGATT
285664	1425192	NBstNBI_Bsml	STTCTGTGAAGAATG	G	4727.0658	CATGTGAGTGGAGTCGAGASTTCTGTGAA GAATGCCGAAATAGATT

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
285664	1425192	NBstNBI_BsmI	STTCTGTGAAGATG	T	4702.053	CATGTGAGTGGAGTCGAGASTTCTGTGAA GAATGCCGAAATAGATT
287266	1426547	NBstNBI_BsrI	TSGCACTG	A	2489.6149	ACGGACAGCCGAGTCGTGCTSGCACTGG GGAGCCGTGCT
287266	1426547	NBstNBI_BsrI	TSGCACTG	C	2465.5899	ACGGACAGCCGAGTCGTGCTSGCACTGG GGAGCCGTGCT
287266	1426547	NBstNBI_BsrI	TSGCACTG	G	2505.6143	ACGGACAGCCGAGTCGTGCTSGCACTGG GGAGCCGTGCT
287266	1426547	NBstNBI_BsrI	TSGCACTG	T	2480.6015	ACGGACAGCCGAGTCGTGCTSGCACTGG GGAGCCGTGCT
297694		BsrI_NBstNBI	CGCCSGGC	A	2475.5911	AAAAATGCAAACTGGGCCSGCGCGGT GACTCAAGCCTGTAA
297694		BsrI_NBstNBI	CGCCSGGC	C	2451.5661	AAAAATGCAAACTGGGCCSGCGCGGT GACTCAAGCCTGTAA
297694		BsrI_NBstNBI	CGCCSGGC	G	2491.5905	AAAAATGCAAACTGGGCCSGCGCGGT GACTCAAGCCTGTAA
297694		BsrI_NBstNBI	CGCCSGGC	T	2466.5777	AAAAATGCAAACTGGGCCSGCGCGGT GACTCAAGCCTGTAA
297766	1435517	NBstNBI	GGCATAGGCAASAA	A	4409.8853	TTGTGGACTTGAGTCAACAGGCATAGGCA ASAAATGCGACTCTACTTGTGTA
297766	1435517	NBstNBI	GGCATAGGCAASAA	C	4385.8603	TTGTGGACTTGAGTCAACAGGCATAGGCA ASAAATGCGACTCTACTTGTGTA
297766	1435517	NBstNBI	GGCATAGGCAASAA	G	4425.8847	TTGTGGACTTGAGTCAACAGGCATAGGCA ASAAATGCGACTCTACTTGTGTA
297766	1435517	NBstNBI	GGCATAGGCAASAA	T	4400.8719	TTGTGGACTTGAGTCAACAGGCATAGGCA ASAAATGCGACTCTACTTGTGTA
297766	1435517	NBstNBI	TTSTTGCCTATGCC	A	4284.7695	TTGTGGACTTGAGTCAACAGGCATAGGCA ASAAATGCGACTCTACTTGTGTA
297766	1435517	NBstNBI	TTSTTGCCTATGCC	C	4260.7445	TTGTGGACTTGAGTCAACAGGCATAGGCA ASAAATGCGACTCTACTTGTGTA
297766	1435517	NBstNBI	TTSTTGCCTATGCC	G	4300.7689	TTGTGGACTTGAGTCAACAGGCATAGGCA ASAAATGCGACTCTACTTGTGTA
297766	1435517	NBstNBI	TTSTTGCCTATGCC	T	4275.7561	TTGTGGACTTGAGTCAACAGGCATAGGCA ASAAATGCGACTCTACTTGTGTA

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303458	1440440	BsrI_NBstNBI	SCTGTCA	A	2160.4058	CTTCTCCTTACTGGGTGACAGSGTGAGA CTCCATCTGAAAA
303458	1440440	BsrI_NBstNBI	SCTGTCA	C	2136.3808	CTTCTCCTTACTGGGTGACAGSGTGAGA CTCCATCTGAAAA
303458	1440440	BsrI_NBstNBI	SCTGTCA	G	2176.4052	CTTCTCCTTACTGGGTGACAGSGTGAGA CTCCATCTGAAAA
303458	1440440	BsrI_NBstNBI	SCTGTCA	T	2151.3924	CTTCTCCTTACTGGGTGACAGSGTGAGA CTCCATCTGAAAA
305836	1442464	BsrI_NBstNBI	GGGAAACCCSGTAG	A	4417.8591	TACAGCCCCTACTGGGTACSGGGTTCCC CACTGGACTCTGGACAGCGC
305836	1442464	BsrI_NBstNBI	GGGAAACCCSGTAG	C	4393.8341	TACAGCCCCTACTGGGTACSGGGTTCCC CACTGGACTCTGGACAGCGC
305836	1442464	BsrI_NBstNBI	GGGAAACCCSGTAG	G	4433.8585	TACAGCCCCTACTGGGTACSGGGTTCCC CACTGGACTCTGGACAGCGC
305836	1442464	BsrI_NBstNBI	GGGAAACCCSGTAG	T	4408.8457	TACAGCCCCTACTGGGTACSGGGTTCCC CACTGGACTCTGGACAGCGC
307252	1443658	BsrI_NBstNBI	ATTGGAATTSCAGA	A	4390.8707	GAACCCCTGCACCTGGGTCTGSAATTCCAA TCATGGACTCTGTCCCCTTG
307252	1443658	BsrI_NBstNBI	ATTGGAATTSCAGA	C	4366.8457	GAACCCCTGCACCTGGGTCTGSAATTCCAA TCATGGACTCTGTCCCCTTG
307252	1443658	BsrI_NBstNBI	ATTGGAATTSCAGA	G	4406.8701	GAACCCCTGCACCTGGGTCTGSAATTCCAA TCATGGACTCTGTCCCCTTG
307252	1443658	BsrI_NBstNBI	ATTGGAATTSCAGA	T	4381.8573	GAACCCCTGCACCTGGGTCTGSAATTCCAA TCATGGACTCTGTCCCCTTG
309710	1445763	NBstNBI	CCATATCSGATTTAG	A	4631.0176	ATTGTTCCCTTGAGTCTCACCCATATCSGAT TTAGATGAGACTCTGGACTTTAG
309710	1445763	NBstNBI	CCATATCSGATTTAG	C	4606.9926	ATTGTTCCCTTGAGTCTCACCCATATCSGAT TTAGATGAGACTCTGGACTTTAG
309710	1445763	NBstNBI	CCATATCSGATTTAG	G	4647.017	ATTGTTCCCTTGAGTCTCACCCATATCSGAT TTAGATGAGACTCTGGACTTTAG
309710	1445763	NBstNBI	CCATATCSGATTTAG	T	4622.0042	ATTGTTCCCTTGAGTCTCACCCATATCSGAT TTAGATGAGACTCTGGACTTTAG
309710	1445763	NBstNBI	CTAAATCSGATATGG	A	4680.0554	ATTGTTCCCTTGAGTCTCACCCATATCSGAT TTAGATGAGACTCTGGACTTTAG

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309710	1445763	NBstNBI	CTAAATCSGATATGG	C	4656.0304	ATTGTTCCCTTGAGTCTACCCATATCSGAT TTAGATGAGACTCTGGACTTTAG
309710	1445763	NBstNBI	CTAAATCSGATATGG	G	4696.0548	ATTGTTCCCTTGAGTCTACCCATATCSGAT TTAGATGAGACTCTGGACTTTAG
309710	1445763	NBstNBI	CTAAATCSGATATGG	T	4671.042	ATTGTTCCCTTGAGTCTACCCATATCSGAT TTAGATGAGACTCTGGACTTTAG
311689	1447423	NBstNBI_Bsrl	TGSGCAGGTAAGT	A	4737.067	TGATCAGAAATGAGTCAGGGTGGSGCAGGT AACTGGAATGAGTCAGG
311689	1447423	NBstNBI_Bsrl	TGSGCAGGTAAGT	C	4713.042	TGATCAGAAATGAGTCAGGGTGGSGCAGGT AACTGGAATGAGTCAGG
311689	1447423	NBstNBI_Bsrl	TGSGCAGGTAAGT	G	4753.0664	TGATCAGAAATGAGTCAGGGTGGSGCAGGT AACTGGAATGAGTCAGG
311689	1447423	NBstNBI_Bsrl	TGSGCAGGTAAGT	T	4728.0536	TGATCAGAAATGAGTCAGGGTGGSGCAGGT AACTGGAATGAGTCAGG
314476	1449738	BsaBI_NBstNBI	CAGAAACTSCAGATTA	A	4962.2541	TTGAGGTAGGGATCTTAATCTGSAGTTTCT GGATAGACTCAACCCCTAGA
314476	1449738	BsaBI_NBstNBI	CAGAAACTSCAGATTA	C	4938.2291	TTGAGGTAGGGATCTTAATCTGSAGTTTCT GGATAGACTCAACCCCTAGA
314476	1449738	BsaBI_NBstNBI	CAGAAACTSCAGATTA	G	4978.2535	TTGAGGTAGGGATCTTAATCTGSAGTTTCT GGATAGACTCAACCCCTAGA
314476	1449738	BsaBI_NBstNBI	CAGAAACTSCAGATTA	T	4953.2407	TTGAGGTAGGGATCTTAATCTGSAGTTTCT GGATAGACTCAACCCCTAGA
317176	2899791	BsmI_NBstNBI	GSTCAAGGGCAGGA	A	4441.8841	CTACCATGCTGAATGCTTCCTGCCCTTGA SCATTGGACTCCAAAATATTC
317176	2899791	BsmI_NBstNBI	GSTCAAGGGCAGGA	C	4417.8591	CTACCATGCTGAATGCTTCCTGCCCTTGA SCATTGGACTCCAAAATATTC
317176	2899791	BsmI_NBstNBI	GSTCAAGGGCAGGA	G	4457.8835	CTACCATGCTGAATGCTTCCTGCCCTTGA SCATTGGACTCCAAAATATTC
317176	2899791	BsmI_NBstNBI	GSTCAAGGGCAGGA	T	4432.8707	CTACCATGCTGAATGCTTCCTGCCCTTGA SCATTGGACTCCAAAATATTC
318459	1453099	Bsrl_NBstNBI	STGGAATTCAAA	A	3757.4653	AACCAGACTAACTGGATTGGAATTCACASTG CAGACTCTTATTAGCTA
318459	1453099	Bsrl_NBstNBI	STGGAATTCAAA	C	3733.4403	AACCAGACTAACTGGATTGGAATTCACASTG CAGACTCTTATTAGCTA

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318459	1453099	BsrI_NBstNBI	STGGAATTCAAA	G	3773.4647	AACCAGACTAACTGGATTGGAATTCACASTG CAGACTCTTATTAGCTA
318459	1453099	BsrI_NBstNBI	STGGAATTCAAA	T	3748.4519	AACCAGACTAACTGGATTGGAATTCACASTG CAGACTCTTATTAGCTA
323661	1559017	BsrI_NBstNBI	ATSTCCTGGCTCAAG	A	4632.0054	TTAGGAACCTACTGGACTTGAGCCAGGAS ATGAGGGACTCATGCAAAAGCT
323661	1559017	BsrI_NBstNBI	ATSTCCTGGCTCAAG	C	4607.9804	TTAGGAACCTACTGGACTTGAGCCAGGAS ATGAGGGACTCATGCAAAAGCT
323661	1559017	BsrI_NBstNBI	ATSTCCTGGCTCAAG	G	4648.0048	TTAGGAACCTACTGGACTTGAGCCAGGAS ATGAGGGACTCATGCAAAAGCT
323661	1559017	BsrI_NBstNBI	ATSTCCTGGCTCAAG	T	4622.992	TTAGGAACCTACTGGACTTGAGCCAGGAS ATGAGGGACTCATGCAAAAGCT
323811	1559152	NBstNBI_BsaBI	CCTTSATTTAGATAA	A	4630.0298	GTGCAAAATGTGAGTCTAATCCTTSATTTAG ATAAGTATCACAAAGTTTGA
323811	1559152	NBstNBI_BsaBI	CCTTSATTTAGATAA	C	4606.0048	GTGCAAAATGTGAGTCTAATCCTTSATTTAG ATAAGTATCACAAAGTTTGA
323811	1559152	NBstNBI_BsaBI	CCTTSATTTAGATAA	G	4646.0292	GTGCAAAATGTGAGTCTAATCCTTSATTTAG ATAAGTATCACAAAGTTTGA
323811	1559152	NBstNBI_BsaBI	CCTTSATTTAGATAA	T	4621.0164	GTGCAAAATGTGAGTCTAATCCTTSATTTAG ATAAGTATCACAAAGTTTGA
333129	1495901	BsrI_NBstNBI	aSatatagtgtaga	A	4414.8957	ggtaacattcacigggcctctacactatatStaccagacictgtgc taaag
333129	1495901	BsrI_NBstNBI	aSatatagtgtaga	C	4390.8707	ggtaacattcacigggcctctacactatatStaccagacictgtgc taaag
333129	1495901	BsrI_NBstNBI	aSatatagtgtaga	G	4430.8951	ggtaacattcacigggcctctacactatatStaccagacictgtgc taaag
333129	1495901	BsrI_NBstNBI	aSatatagtgtaga	T	4405.8823	ggtaacattcacigggcctctacactatatStaccagacictgtgc taaag
334322	1496881	BsrI_NBstNBI	ggttttggaScag	A	4109.6598	tctccagaccactggcctgStocaaaaaccttcagactcctaataat gacag
334322	1496881	BsrI_NBstNBI	ggttttggaScag	C	4085.6348	tctccagaccactggcctgStocaaaaaccttcagactcctaataat gacag
334322	1496881	BsrI_NBstNBI	ggttttggaScag	G	4125.6592	tctccagaccactggcctgStocaaaaaccttcagactcctaataat gacag

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334322	1496881	BsrI_NBstNBI	ggttttgaScag	T	4100.6464	ttccagaccacgtggcctgStocaaaaaccttcagactccta
334661	1497161	NBstNBI_BsrI	gagacScatctacig	A	4641.0188	gacag atagttcttggagtcctaggagacScatctactggaaactccta
334661	1497161	NBstNBI_BsrI	gagacScatctacig	C	4616.9938	tg atagttcttggagtcctaggagacScatctactggaaactccta
334661	1497161	NBstNBI_BsrI	gagacScatctacig	G	4657.0182	tg atagttcttggagtcctaggagacScatctactggaaactccta
334661	1497161	NBstNBI_BsrI	gagacScatctacig	T	4632.0054	tg atagttcttggagtcctaggagacScatctactggaaactccta
338321	1500163	NBstNBI_BclI	Sitgac	A	2175.4174	acttgagtttgagtcctggSittgacagtcacaaaccac
338321	1500163	NBstNBI_BclI	Sitgac	C	2151.3924	acttgagtttgagtcctggSittgacagtcacaaaccac
338321	1500163	NBstNBI_BclI	Sitgac	G	2191.4168	acttgagtttgagtcctggSittgacagtcacaaaccac
338321	1500163	NBstNBI_BclI	Sitgac	T	2166.404	acttgagtttgagtcctggSittgacagtcacaaaccac
341380	1502619	BclI_NBstNBI	gcgccSigtac	A	3397.1934	agccagtgtttgatcaSggcgcttctgactcctcaagcaggg
341380	1502619	BclI_NBstNBI	gcgccSigtac	C	3373.1684	agccagtgtttgatcaSggcgcttctgactcctcaagcaggg
341380	1502619	BclI_NBstNBI	gcgccSigtac	G	3413.1928	agccagtgtttgatcaSggcgcttctgactcctcaagcaggg
341380	1502619	BclI_NBstNBI	gcgccSigtac	T	3388.18	agccagtgtttgatcaSggcgcttctgactcctcaagcaggg
344947	2867950	NBstNBI_BsrI	tcgtctcccaSactg	A	4872.1523	ttttggcgtgagtcgtcgtctgtctcccaSactggagtgcaigtg gc
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347837	1507667	NBstNBI	gagagctgtccSgcc	A	4658.006	ccctatgaaagagtccttcagagagcgtgtccSgccctttgactcc ttttctat
347837	1507667	NBstNBI	gagagctgtccSgcc	C	4633.981	ccctatgaaagagtccttcagagagcgtgtccSgccctttgactcc ttttctat
347837	1507667	NBstNBI	gagagctgtccSgcc	G	4674.0054	ccctatgaaagagtccttcagagagcgtgtccSgccctttgactcc ttttctat
347837	1507667	NBstNBI	gagagctgtccSgcc	T	4648.9926	ccctatgaaagagtccttcagagagcgtgtccSgccctttgactcc ttttctat

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347837	1507667	NBstNBI	ggcSggacagctc	C	4633.981	ccctatgaaagagctcttcagagagctgtccSgccccctttgactcc ttttctat
347837	1507667	NBstNBI	ggcSggacagctc	G	4674.0054	ccctatgaaagagctcttcagagagctgtccSgccccctttgactcc ttttctat
347837	1507667	NBstNBI	ggcSggacagctc	T	4648.9926	ccctatgaaagagctcttcagagagctgtccSgccccctttgactcc ttttctat
365028	1384176	NBstNBI_BsrDI	CSGTGCAATG	A	3132.0337	CTCCGGCACAGAGTCACTGCSGTGCAATG CCAGGCCCTCCAA
365028	1384176	NBstNBI_BsrDI	CSGTGCAATG	C	3108.0087	CTCCGGCACAGAGTCACTGCSGTGCAATG CCAGGCCCTCCAA
365028	1384176	NBstNBI_BsrDI	CSGTGCAATG	G	3148.0331	CTCCGGCACAGAGTCACTGCSGTGCAATG CCAGGCCCTCCAA
365028	1384176	NBstNBI_BsrDI	CSGTGCAATG	T	3123.0203	CTCCGGCACAGAGTCACTGCSGTGCAATG CCAGGCCCTCCAA
365351	1384473	NBstNBI	AAGTATGSACAGACCT	A	4978.2535	GTTTCTCTAAGAGTCTGTGAAGTATGSACA GACCTTGAGAGCTCAATGCAACAT
365351	1384473	NBstNBI	AAGTATGSACAGACCT	C	4954.2285	GTTTCTCTAAGAGTCTGTGAAGTATGSACA GACCTTGAGAGCTCAATGCAACAT
365351	1384473	NBstNBI	AAGTATGSACAGACCT	G	4994.2529	GTTTCTCTAAGAGTCTGTGAAGTATGSACA GACCTTGAGAGCTCAATGCAACAT
365351	1384473	NBstNBI	AAGTATGSACAGACCT	T	4969.2401	GTTTCTCTAAGAGTCTGTGAAGTATGSACA GACCTTGAGAGCTCAATGCAACAT
365351	1384473	NBstNBI	AGGTCTGTSCATACTT	A	4951.2133	GTTTCTCTAAGAGTCTGTGAAGTATGSACA GACCTTGAGAGCTCAATGCAACAT
365351	1384473	NBstNBI	AGGTCTGTSCATACTT	C	4927.1883	GTTTCTCTAAGAGTCTGTGAAGTATGSACA GACCTTGAGAGCTCAATGCAACAT
365351	1384473	NBstNBI	AGGTCTGTSCATACTT	G	4967.2127	GTTTCTCTAAGAGTCTGTGAAGTATGSACA GACCTTGAGAGCTCAATGCAACAT
365351	1384473	NBstNBI	AGGTCTGTSCATACTT	T	4942.1999	GTTTCTCTAAGAGTCTGTGAAGTATGSACA GACCTTGAGAGCTCAATGCAACAT
366009	1385032	NBstNBI	ACSTTCT	A	2135.393	CAAGGAAACTGAGTCTCAGAGAAAGTGAA GGACTCACCAGTGGGC

TSC ID	dbSNP ID	Enzymes	Product	Allele	Mass	Sequence
366009	1385032	NBstNBI	ACSTTCT	C	2111.368	CAAGGAAACTGAGTCTCAGAGAAASGTGAA GGACTCACCAGTGGC
366009	1385032	NBstNBI	ACSTTCT	G	2151.3924	CAAGGAAACTGAGTCTCAGAGAAASGTGAA GGACTCACCAGTGGC
366009	1385032	NBstNBI	ACSTTCT	T	2126.3796	CAAGGAAACTGAGTCTCAGAGAAASGTGAA GGACTCACCAGTGGC
366009	1385032	NBstNBI	AGAASGT	A	2233.4686	CAAGGAAACTGAGTCTCAGAGAAASGTGAA GGACTCACCAGTGGC
366009	1385032	NBstNBI	AGAASGT	C	2209.4436	CAAGGAAACTGAGTCTCAGAGAAASGTGAA GGACTCACCAGTGGC
366009	1385032	NBstNBI	AGAASGT	G	2249.468	CAAGGAAACTGAGTCTCAGAGAAASGTGAA GGACTCACCAGTGGC
366009	1385032	NBstNBI	AGAASGT	T	2224.4552	CAAGGAAACTGAGTCTCAGAGAAASGTGAA GGACTCACCAGTGGC
369157	1387518	NBstNBI_Bsrl	ATSCTTTTACACACTG	A	4895.1895	AAAAAATTCGAGTCCAAACATSCTTTTACA CACTGGGTCCAACCCAGA
369157	1387518	NBstNBI_Bsrl	ATSCTTTTACACACTG	C	4871.1645	AAAAAATTCGAGTCCAAACATSCTTTTACA CACTGGGTCCAACCCAGA
369157	1387518	NBstNBI_Bsrl	ATSCTTTTACACACTG	G	4911.1889	AAAAAATTCGAGTCCAAACATSCTTTTACA CACTGGGTCCAACCCAGA
369157	1387518	NBstNBI_Bsrl	ATSCTTTTACACACTG	T	4886.1761	AAAAAATTCGAGTCCAAACATSCTTTTACA CACTGGGTCCAACCCAGA
370533	1388565	BsaBI_NBstNBI	ASGATCT	A	2184.4308	GCCCCACATGATGGAGATCSTTCCTGAC TCCCTAACCTCC
370533	1388565	BsaBI_NBstNBI	ASGATCT	C	2160.4058	GCCCCACATGATGGAGATCSTTCCTGAC TCCCTAACCTCC
370533	1388565	BsaBI_NBstNBI	ASGATCT	G	2200.4302	GCCCCACATGATGGAGATCSTTCCTGAC TCCCTAACCTCC
370533	1388565	BsaBI_NBstNBI	ASGATCT	T	2175.4174	GCCCCACATGATGGAGATCSTTCCTGAC TCCCTAACCTCC
373731	1391081	BsrDI_NBstNBI	SCAGAGG	A	2234.4564	ACTCACCAGAGCAATGGCCCTCTGSCGTGT GACTCAGTCTCTGCC
373731	1391081	BsrDI_NBstNBI	SCAGAGG	C	2210.4314	ACTCACCAGAGCAATGGCCCTCTGSCGTGT GACTCAGTCTCTGCC

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373731	1391081	BsrDI_NBstNBI	SCAGAGG	T	2225.443	ACTCACCAGAGCAATGGCCCTCTGSCGTGT GACTCAGTCTCTGCC
374288	1391526	NBstNBI_Bsrl	CATGTGGCCCSGACTG	A	4962.2023	TATATAGACAGAGTCTCGCCCATGTGGCCCC SGACTGGTCTCAAACTCC
374288	1391526	NBstNBI_Bsrl	CATGTGGCCCSGACTG	C	4938.1773	TATATAGACAGAGTCTCGCCCATGTGGCCCC SGACTGGTCTCAAACTCC
374288	1391526	NBstNBI_Bsrl	CATGTGGCCCSGACTG	G	4978.2017	TATATAGACAGAGTCTCGCCCATGTGGCCCC SGACTGGTCTCAAACTCC
374288	1391526	NBstNBI_Bsrl	CATGTGGCCCSGACTG	T	4953.1889	TATATAGACAGAGTCTCGCCCATGTGGCCCC SGACTGGTCTCAAACTCC
375301	2681733	BsmI_NBstNBI	CTCATGCATCSCAG	A	4287.7847	GATGGGATGGAATGCTCTGSGATGCATG AGAATGGACTCAGGACTTTTG
375301	2681733	BsmI_NBstNBI	CTCATGCATCSCAG	C	4263.7597	GATGGGATGGAATGCTCTGSGATGCATG AGAATGGACTCAGGACTTTTG
375301	2681733	BsmI_NBstNBI	CTCATGCATCSCAG	G	4303.7841	GATGGGATGGAATGCTCTGSGATGCATG AGAATGGACTCAGGACTTTTG
375301	2681733	BsmI_NBstNBI	CTCATGCATCSCAG	T	4278.7713	GATGGGATGGAATGCTCTGSGATGCATG AGAATGGACTCAGGACTTTTG
377443	2868652	NBstNBI_Bsrl	tctgtcgSccagactg	A	4937.1895	tfttgagacagagtctcactctgtcgSccagactggagtgacag tggc
377443	2868652	NBstNBI_Bsrl	tctgtcgSccagactg	C	4913.1645	tfttgagacagagtctcactctgtcgSccagactggagtgacag tggc
377443	2868652	NBstNBI_Bsrl	tctgtcgSccagactg	G	4953.1889	tfttgagacagagtctcactctgtcgSccagactggagtgacag tggc
377443	2868652	NBstNBI_Bsrl	tctgtcgSccagactg	T	4928.1761	tfttgagacagagtctcactctgtcgSccagactggagtgacag tggc
382817	2287247	NBstNBI	taccaggSt	A	2802.8246	tccaatctgtgagtcgggaaSccctggtagcaggactcttccatc ttg
382817	2287247	NBstNBI	taccaggSt	C	2778.7996	tccaatctgtgagtcgggaaSccctggtagcaggactcttccatc ttg
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382817	2287247	NBstNBI	aScctggta	C	2778.7996	ttaaactgtgagtcgggaaScctggtagcaggactcttcaac ttg
382817	2287247	NBstNBI	aScctggta	G	2818.824	ttaaactgtgagtcgggaaScctggtagcaggactcttcaac ttg
382817	2287247	NBstNBI	aScctggta	T	2793.8112	ttaaactgtgagtcgggaaScctggtagcaggactcttcaac ttg
386338	2870005	NBstNBI	ctaStt	A	1846.2083	cTggagctaggagtcacacctaSttctcagactctctcaac c
386338	2870005	NBstNBI	ctaStt	C	1822.1833	cTggagctaggagtcacacctaSttctcagactctctcaac c
386338	2870005	NBstNBI	ctaStt	G	1862.2077	cTggagctaggagtcacacctaSttctcagactctctcaac c
386338	2870005	NBstNBI	ctaStt	T	1837.1949	cTggagctaggagtcacacctaSttctcagactctctcaac c
386338	2870005	NBstNBI	aaStag	A	1904.2595	cTggagctaggagtcacacctaSttctcagactctctcaac c
386338	2870005	NBstNBI	aaStag	C	1880.2345	cTggagctaggagtcacacctaSttctcagactctctcaac c
386338	2870005	NBstNBI	aaStag	G	1920.2589	cTggagctaggagtcacacctaSttctcagactctctcaac c
386338	2870005	NBstNBI	aaStag	T	1895.2461	cTggagctaggagtcacacctaSttctcagactctctcaac c
386625	2289767	BsmI_NBstNBI	cSttggactctg	A	4349.8067	ccgggacacaagaatgctcagcagtagtaccacSgcagtgact ctccagccc
386625	2289767	BsmI_NBstNBI	cSttggactctg	C	4325.7817	ccgggacacaagaatgctcagcagtagtaccacSgcagtgact ctccagccc
386625	2289767	BsmI_NBstNBI	cSttggactctg	G	4365.8061	ccgggacacaagaatgctcagcagtagtaccacSgcagtgact ctccagccc
386625	2289767	BsmI_NBstNBI	cSttggactctg	T	4340.7933	ccgggacacaagaatgctcagcagtagtaccacSgcagtgact ctccagccc

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390621	2292665	NBstNBI_BsrI	totgtaccSagactg	C	4912.1767	tttgagatgggagtgctcactctgttaccSagactggagtgagcag aggc
390621	2292665	NBstNBI_BsrI	totgtaccSagactg	G	4952.2011	tttgagatgggagtgctcactctgttaccSagactggagtgagcag aggc
390621	2292665	NBstNBI_BsrI	tcigtaccSagactg	T	4927.1883	tttgagatgggagtgctcactctgttaccSagactggagtgagcag aggc
394522	2295370	NBstNBI	gagcagtgagtgS	A	4143.686	ctggccagtgagtgctgccgagcagtgaggagtgSagtgacitc ccgtgggcaa
394522	2295370	NBstNBI	gagcagtgagtgS	C	4119.661	ctggccagtgagtgctgccgagcagtgaggagtgSagtgacitc ccgtgggcaa
394522	2295370	NBstNBI	gagcagtgagtgS	G	4159.6854	ctggccagtgagtgctgccgagcagtgaggagtgSagtgacitc ccgtgggcaa
394522	2295370	NBstNBI	gagcagtgagtgS	T	4134.6726	ctggccagtgagtgctgccgagcagtgaggagtgSagtgacitc ccgtgggcaa
394522	2295370	NBstNBI	Sactccactgctc	A	3934.5506	ctggccagtgagtgctgccgagcagtgaggagtgSagtgacitc ccgtgggcaa
394522	2295370	NBstNBI	Sactccactgctc	C	3910.5256	ctggccagtgagtgctgccgagcagtgaggagtgSagtgacitc ccgtgggcaa
394522	2295370	NBstNBI	Sactccactgctc	G	3950.55	ctggccagtgagtgctgccgagcagtgaggagtgSagtgacitc ccgtgggcaa
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394755	2871312	BsrI_NBstNBI	tgccSg	A	1872.2089	atctccacttaactggccSggcacagtgactcacacctgttaa atctccacttaactggccSggcacagtgactcacacctgttaa
394755	2871312	BsrI_NBstNBI	tgccSg	C	1848.1839	atctccacttaactggccSggcacagtgactcacacctgttaa atctccacttaactggccSggcacagtgactcacacctgttaa
394755	2871312	BsrI_NBstNBI	tgccSg	G	1888.2083	atctccacttaactggccSggcacagtgactcacacctgttaa atctccacttaactggccSggcacagtgactcacacctgttaa
394755	2871312	BsrI_NBstNBI	tgccSg	T	1863.1955	atctccacttaactggccSggcacagtgactcacacctgttaa atctccacttaactggccSggcacagtgactcacacctgttaa
395267	2295852	NBstNBI_BsrI	acaaScitccactg	A	4280.7987	ataggaaaaggagtgcaaggacaaScitccactggtaaaaa caatct
395267	2295852	NBstNBI_BsrI	acaaScitccactg	C	4256.7737	ataggaaaaggagtgcaaggacaaScitccactggtaaaaa caatct
395267	2295852	NBstNBI_BsrI	acaaScitccactg	G	4296.7981	ataggaaaaggagtgcaaggacaaScitccactggtaaaaa caatct

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395825	2296259	BsrI_NBstNBI	ccigaaScatt	A	3380.2062	cgggggaacactggaaatgSittcaggggcggaactccgaa gaccga
395825	2296259	BsrI_NBstNBI	ccigaaScatt	C	3356.1812	cgggggaacactggaaatgSittcaggggcggaactccgaa gaccga
395825	2296259	BsrI_NBstNBI	ccigaaScatt	G	3396.2056	cgggggaacactggaaatgSittcaggggcggaactccgaa gaccga
395825	2296259	BsrI_NBstNBI	ccigaaScatt	T	3371.1928	cgggggaacactggaaatgSittcaggggcggaactccgaa gaccga
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399270	2298667	NBstNBI_BsrI	tSggaactg	A	2842.849	gaattcagtagagtgcaaaatgSggaactggactgaagtccag gaattcagtagagtgcaaaatgSggaactggactgaagtccag
399270	2298667	NBstNBI_BsrI	tSggaactg	C	2818.824	gaattcagtagagtgcaaaatgSggaactggactgaagtccag gaattcagtagagtgcaaaatgSggaactggactgaagtccag
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399270	2298667	NBstNBI_BsrI	tSggaactg	T	2833.8356	gaattcagtagagtgcaaaatgSggaactggactgaagtccag gct
409306		NBstNBI	ctgccSc	A	2121.3692	agcagtgaggaggagtgcttcacigccScctgagactctctcag gct
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409306		NBstNBI	ctgccSc	T	2112.3558	agcagtgaggaggagtgcttcacigccScctgagactctctcag gct
409306		NBstNBI	gSggcag	A	2250.4558	agcagtgaggaggagtgcttcacigccScctgagactctctcag gct
409306		NBstNBI	gSggcag	C	2226.4308	agcagtgaggaggagtgcttcacigccScctgagactctctcag gct

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409306		NBstNBI	gSggcag	G	2266.4552	agcagtgaggaggagcttcactgcgccccttgagactctcaccg gct
409306		NBstNBI	gSggcag	T	2241.4424	agcagtgaggaggagcttcactgcgccccttgagactctcaccg gct
420577	2384119	NBstNBI_BsrI	tcagagtccaSactg	A	4641.0188	aatctcaagagagagcttcacttcagagtccaSactggaagaac actta
420577	2384119	NBstNBI_BsrI	tcagagtccaSactg	C	4616.9938	aatctcaagagagagcttcacttcagagtccaSactggaagaac actta
420577	2384119	NBstNBI_BsrI	tcagagtccaSactg	G	4657.0182	aatctcaagagagagcttcacttcagagtccaSactggaagaac actta
420577	2384119	NBstNBI_BsrI	tcagagtccaSactg	T	4632.0054	aatctcaagagagagcttcacttcagagtccaSactggaagaac actta
421069	2384475	BsrDI_NBstNBI	cctgSaatacaaccc	A	4256.7737	agagttggaggaggaatgttggtgattScaggctgggactca agtatgtct
421069	2384475	BsrDI_NBstNBI	cctgSaatacaaccc	C	4232.7487	agagttggaggaggaatgttggtgattScaggctgggactca agtatgtct
421069	2384475	BsrDI_NBstNBI	cctgSaatacaaccc	G	4272.7731	agagttggaggaggaatgttggtgattScaggctgggactca agtatgtct
421069	2384475	BsrDI_NBstNBI	cctgSaatacaaccc	T	4247.7603	agagttggaggaggaatgttggtgattScaggctgggactca agtatgtct
422936	2385767	BsrDI_NBstNBI	glatgS	A	1911.2455	ggaatgagaggaggaatgtcScatacataagacicaagagoc aag
422936	2385767	BsrDI_NBstNBI	glatgS	C	1887.2205	ggaatgagaggaggaatgtcScatacataagacicaagagoc aag
422936	2385767	BsrDI_NBstNBI	glatgS	G	1927.2449	ggaatgagaggaggaatgtcScatacataagacicaagagoc aag
422936	2385767	BsrDI_NBstNBI	glatgS	T	1902.2321	ggaatgagaggaggaatgtcScatacataagacicaagagoc aag
424869	2387118	BsrI_NBstNBI	cScataat	A	2457.6161	atgagaatgaactgggattatgSgttgagactctaaatacccc c
424869	2387118	BsrI_NBstNBI	cScataat	C	2433.5911	atgagaatgaactgggattatgSgttgagactctaaatacccc c
424869	2387118	BsrI_NBstNBI	cScataat	G	2473.6155	atgagaatgaactgggattatgSgttgagactctaaatacccc c

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
424869	2387118	BsrI_NBstNBI	cScataat	T	2448.6027	atgagaatgaactgggattatgSgttgagactaaataccc c
431298	2391567	BsrI_NBstNBI	Stocccaaca	A	3020.9739	cgctgcctccactgggtgttggggaStggggactccagagga aaa
431298	2391567	BsrI_NBstNBI	Stocccaaca	C	2996.9489	cgctgcctccactgggtgttggggaStggggactccagagga aaa
431298	2391567	BsrI_NBstNBI	Stocccaaca	G	3036.9733	cgctgcctccactgggtgttggggaStggggactccagagga aaa
431298	2391567	BsrI_NBstNBI	Stocccaaca	T	3011.9605	cgctgcctccactgggtgttggggaStggggactccagagga aaa
433187	2877209	NBstNBI_BsmI	cgSccagccgggaatg	A	4996.2285	ttacaggcgtagtcaccgcgSccagccgggaatgcattgct tttagg
433187	2877209	NBstNBI_BsmI	cgSccagccgggaatg	C	4972.2035	ttacaggcgtagtcaccgcgSccagccgggaatgcattgct tttagg
433187	2877209	NBstNBI_BsmI	cgSccagccgggaatg	G	5012.2279	ttacaggcgtagtcaccgcgSccagccgggaatgcattgct tttagg
433187	2877209	NBstNBI_BsmI	cgSccagccgggaatg	T	4987.2151	ttacaggcgtagtcaccgcgSccagccgggaatgcattgct tttagg
439799	2397537	NBstNBI_BsrDI	aaSaattggagcaatg	A	4738.1066	tgaagacatggagtcaccaaaaaSaattggagcaatgttcttaa ggtgg
439799	2397537	NBstNBI_BsrDI	aaSaattggagcaatg	C	4714.0816	tgaagacatggagtcaccaaaaaSaattggagcaatgttcttaa ggtgg
439799	2397537	NBstNBI_BsrDI	aaSaattggagcaatg	G	4754.106	tgaagacatggagtcaccaaaaaSaattggagcaatgttcttaa ggtgg
439799	2397537	NBstNBI_BsrDI	aaSaattggagcaatg	T	4729.0932	tgaagacatggagtcaccaaaaaSaattggagcaatgttcttaa ggtgg
452874	2880325	BsrI_NBstNBI	gagatcaS	A	2522.6533	gctggagtcactggcStgatctggcgtgactccaacatcca c
452874	2880325	BsrI_NBstNBI	gagatcaS	C	2498.6283	gctggagtcactggcStgatctggcgtgactccaacatcca c
452874	2880325	BsrI_NBstNBI	gagatcaS	G	2538.6527	gctggagtcactggcStgatctggcgtgactccaacatcca c
452874	2880325	BsrI_NBstNBI	gagatcaS	T	2513.6399	gctggagtcactggcStgatctggcgtgactccaacatcca c

TSC ID	dbSNP ID	Enzymes	Product	Allele	Mass	Sequence
454203	2407398	BsrI_NBstNBI	cactcttSt	A	2728.774	atctggcaccacttggaSaagagtgacttgactctgcaagtg
454203	2407398	BsrI_NBstNBI	cactcttSt	C	2704.749	gg atctggcaccacttggaSaagagtgacttgactctgcaagtg
454203	2407398	BsrI_NBstNBI	cactcttSt	G	2744.7734	gg atctggcaccacttggaSaagagtgacttgactctgcaagtg
454203	2407398	BsrI_NBstNBI	cactcttSt	T	2719.7606	gg atctggcaccacttggaSaagagtgacttgactctgcaagtg
459051	2881236	NBstNBI	gfScag	A	1896.2339	ctcccaataagagtccttggtScagccttgactctcttaatt
459051	2881236	NBstNBI	gfScag	C	1872.2089	ctcccaataagagtccttggtScagccttgactctcttaatt
459051	2881236	NBstNBI	gfScag	G	1912.2333	ctcccaataagagtccttggtScagccttgactctcttaatt
459051	2881236	NBstNBI	gfScag	T	1887.2205	ctcccaataagagtccttggtScagccttgactctcttaatt
459051	2881236	NBstNBI	ctfSac	A	1856.2095	ctcccaataagagtccttggtScagccttgactctcttaatt
459051	2881236	NBstNBI	ctfSac	C	1832.1845	ctcccaataagagtccttggtScagccttgactctcttaatt
459051	2881236	NBstNBI	ctfSac	G	1872.2089	ctcccaataagagtccttggtScagccttgactctcttaatt
459051	2881236	NBstNBI	ctfSac	T	1847.1961	ctcccaataagagtccttggtScagccttgactctcttaatt
459810	2411265	BsrI_NBstNBI	cctccctSc	A	2963.9105	attctgaggactgggSagggaggtaggactcttaacat
459810	2411265	BsrI_NBstNBI	cctccctSc	C	2939.8855	attt attctgaggactgggSagggaggtaggactcttaacat
459810	2411265	BsrI_NBstNBI	cctccctSc	G	2979.9099	attt attctgaggactgggSagggaggtaggactcttaacat
459810	2411265	BsrI_NBstNBI	cctccctSc	T	2954.8971	attt attctgaggactgggSagggaggtaggactcttaacat
463159	2413537	NBstNBI_BclI	aSaaagtgtgac	A	4086.6744	tagcacctagagtcaggtaSaaagtgtgacaaagcttctta
463159	2413537	NBstNBI_BclI	aSaaagtgtgac	C	4062.6494	tagcacctagagtcaggtaSaaagtgtgacaaagcttctta
463159	2413537	NBstNBI_BclI	aSaaagtgtgac	G	4102.6738	tagcacctagagtcaggtaSaaagtgtgacaaagcttctta
463159	2413537	NBstNBI_BclI	aSaaagtgtgac	T	4077.661	tagcacctagagtcaggtaSaaagtgtgacaaagcttctta
463425	2881888	NBstNBI_BsrDI	agtagatgcSgcaatg	A	5034.2773	gcctcttggagtcagtagatgcSgcaatggggccc ccctcc
463425	2881888	NBstNBI_BsrDI	agtagatgcSgcaatg	C	5010.2523	gcctcttggagtcagtagatgcSgcaatggggccc ccctcc
463425	2881888	NBstNBI_BsrDI	agtagatgcSgcaatg	G	5050.2767	gcctcttggagtcagtagatgcSgcaatggggccc ccctcc

TSC ID	dbSNP ID	Enzymes	Product	Allele	Mass	Sequence
463425	2881888	NBstNBI_BsrDI	agtagatgcSgcaatg	T	5025.2639	gtctcttgggagtcctagaagtagatgcSgcaatggtggccc cctcc
467301	2882466	BsrI_NBstNBI	tStttct	A	2141.3912	tgcactccagactcgggagaaaaSagcgagactcigtctcaaa a
467301	2882466	BsrI_NBstNBI	tStttct	C	2117.3662	tgcactccagactcgggagaaaaSagcgagactcigtctcaaa a
467301	2882466	BsrI_NBstNBI	tStttct	G	2157.3906	tgcactccagactcgggagaaaaSagcgagactcigtctcaaa a
467301	2882466	BsrI_NBstNBI	tStttct	T	2132.3778	tgcactccagactcgggagaaaaSagcgagactcigtctcaaa a
468775	2882681	NBstNBI	gtaaacccctSct	A	3669.3909	tgcattgcaggagtcagtggtgtaaacccctSctaaaggactcag tcagtgc
468775	2882681	NBstNBI	gtaaacccctSct	C	3645.3659	tgcattgcaggagtcagtggtgtaaacccctSctaaaggactcag tcagtgc
468775	2882681	NBstNBI	gtaaacccctSct	G	3685.3903	tgcattgcaggagtcagtggtgtaaacccctSctaaaggactcag tcagtgc
468775	2882681	NBstNBI	gtaaacccctSct	T	3660.3775	tgcattgcaggagtcagtggtgtaaacccctSctaaaggactcag tcagtgc
468775	2882681	NBstNBI	agSaggggtttac	A	3789.4641	tgcattgcaggagtcagtggtgtaaacccctSctaaaggactcag tcagtgc
468775	2882681	NBstNBI	agSaggggtttac	C	3765.4391	tgcattgcaggagtcagtggtgtaaacccctSctaaaggactcag tcagtgc
468775	2882681	NBstNBI	agSaggggtttac	G	3805.4635	tgcattgcaggagtcagtggtgtaaacccctSctaaaggactcag tcagtgc
468775	2882681	NBstNBI	agSaggggtttac	T	3780.4507	tgcattgcaggagtcagtggtgtaaacccctSctaaaggactcag tcagtgc
471326	2122618	BsrI_NBstNBI	AAAAACSTGGGGGAA	A	4763.1194	GGCCCGAGTCACTGGGTTCCTCCCCASGTTT TTGTGTGACTCTCTCTCTCTG
471326	2122618	BsrI_NBstNBI	AAAAACSTGGGGGAA	C	4739.0944	GGCCCGAGTCACTGGGTTCCTCCCCASGTTT TTGTGTGACTCTCTCTCTCTG
471326	2122618	BsrI_NBstNBI	AAAAACSTGGGGGAA	G	4779.1188	GGCCCGAGTCACTGGGTTCCTCCCCASGTTT TTGTGTGACTCTCTCTCTCTG
471326	2122618	BsrI_NBstNBI	AAAAACSTGGGGGAA	T	4754.106	GGCCCGAGTCACTGGGTTCCTCCCCASGTTT TTGTGTGACTCTCTCTCTCTG

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
471877	2123010	NBstNBI_BsrDI	GAAGACSTGCAATG	A	4400.8719	GAATGTGAGAGAGTCAGAAAGACSTGC AATGCCACTTGAGGCT
471877	2123010	NBstNBI_BsrDI	GAAGACSTGCAATG	C	4376.8469	GAATGTGAGAGAGTCAGAAAGACSTGC AATGCCACTTGAGGCT
471877	2123010	NBstNBI_BsrDI	GAAGACSTGCAATG	G	4416.8713	GAATGTGAGAGAGTCAGAAAGACSTGC AATGCCACTTGAGGCT
471877	2123010	NBstNBI_BsrDI	GAAGACSTGCAATG	T	4391.8585	GAATGTGAGAGAGTCAGAAAGACSTGC AATGCCACTTGAGGCT
473724	2124270	NBstNBI_BsrI	TGACSACACTACTG	A	4311.8097	GCCTGAGTTTGAGTCCTGATGACSACACT ACTGGCTGGCTAGCTT
473724	2124270	NBstNBI_BsrI	TGACSACACTACTG	C	4287.7847	GCCTGAGTTTGAGTCCTGATGACSACACT ACTGGCTGGCTAGCTT
473724	2124270	NBstNBI_BsrI	TGACSACACTACTG	G	4327.8091	GCCTGAGTTTGAGTCCTGATGACSACACT ACTGGCTGGCTAGCTT
473724	2124270	NBstNBI_BsrI	TGACSACACTACTG	T	4302.7963	GCCTGAGTTTGAGTCCTGATGACSACACT ACTGGCTGGCTAGCTT
476388	2682668	NBstNBI_BclI	AACAGCAGAASTGATC	A	4987.2669	GAGTGCATCAGAGTCTCTCAACAGCAGAA STGATCAAGCAGAAGAA
476388	2682668	NBstNBI_BclI	AACAGCAGAASTGATC	C	4963.2419	GAGTGCATCAGAGTCTCTCAACAGCAGAA STGATCAAGCAGAAGAA
476388	2682668	NBstNBI_BclI	AACAGCAGAASTGATC	G	5003.2663	GAGTGCATCAGAGTCTCTCAACAGCAGAA STGATCAAGCAGAAGAA
476388	2682668	NBstNBI_BclI	AACAGCAGAASTGATC	T	4978.2535	GAGTGCATCAGAGTCTCTCAACAGCAGAA STGATCAAGCAGAAGAA
477695	2126919	BsrI_NBstNBI	CAGACSCAAGTG	A	3743.4415	TAAGGCAACCACTGGACACTTGGTCTGC TCTGACTCAATCTTAACA
477695	2126919	BsrI_NBstNBI	CAGACSCAAGTG	C	3719.4165	TAAGGCAACCACTGGACACTTGGTCTGC TCTGACTCAATCTTAACA
477695	2126919	BsrI_NBstNBI	CAGACSCAAGTG	G	3759.4409	TAAGGCAACCACTGGACACTTGGTCTGC TCTGACTCAATCTTAACA
477695	2126919	BsrI_NBstNBI	CAGACSCAAGTG	T	3734.4281	TAAGGCAACCACTGGACACTTGGTCTGC TCTGACTCAATCTTAACA
480376	2128815	BsrI_NBstNBI	STGAGTTATGATGGT	A	4742.0774	AGCTGAGGGCACTGGCACCATCATAAATC ASTGAAGACTCCACAGCAATC

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
480376	2128815	BsrI_NBstNBI	STGAGTTATGATGGT	C	4718.0524	AGCTGAGGGGCACTGGCACCATCATAACTC ASTGAAGACTCCACAGCAATC
480376	2128815	BsrI_NBstNBI	STGAGTTATGATGGT	G	4758.0768	AGCTGAGGGGCACTGGCACCATCATAACTC ASTGAAGACTCCACAGCAATC
480376	2128815	BsrI_NBstNBI	STGAGTTATGATGGT	T	4733.064	AGCTGAGGGGCACTGGCACCATCATAACTC ASTGAAGACTCCACAGCAATC
485434	2132423	NBstNBI_BclI	GSCTGTGATGATC	A	4069.6354	TGAGTGCAGTGAGTCAGTTGTSCTGTGATG ATCATTCCATATGT
485434	2132423	NBstNBI_BclI	GSCTGTGATGATC	C	4045.6104	TGAGTGCAGTGAGTCAGTTGTSCTGTGATG ATCATTCCATATGT
485434	2132423	NBstNBI_BclI	GSCTGTGATGATC	G	4085.6348	TGAGTGCAGTGAGTCAGTTGTSCTGTGATG ATCATTCCATATGT
485434	2132423	NBstNBI_BclI	GSCTGTGATGATC	T	4060.622	TGAGTGCAGTGAGTCAGTTGTSCTGTGATG ATCATTCCATATGT
485999	2132781	NBstNBI	AGSCTGG	A	2225.443	AAGTCAAGCAGAGTCTTGCAGSCTGGATT TGACTCATTGCACAGG
485999	2132781	NBstNBI	AGSCTGG	C	2201.418	AAGTCAAGCAGAGTCTTGCAGSCTGGATT TGACTCATTGCACAGG
485999	2132781	NBstNBI	AGSCTGG	G	2241.4424	AAGTCAAGCAGAGTCTTGCAGSCTGGATT TGACTCATTGCACAGG
485999	2132781	NBstNBI	AGSCTGG	T	2216.4296	AAGTCAAGCAGAGTCTTGCAGSCTGGATT TGACTCATTGCACAGG
485999	2132781	NBstNBI	CCAGSCT	A	2145.3942	AAGTCAAGCAGAGTCTTGCAGSCTGGATT TGACTCATTGCACAGG
485999	2132781	NBstNBI	CCAGSCT	C	2121.3692	AAGTCAAGCAGAGTCTTGCAGSCTGGATT TGACTCATTGCACAGG
485999	2132781	NBstNBI	CCAGSCT	G	2161.3936	AAGTCAAGCAGAGTCTTGCAGSCTGGATT TGACTCATTGCACAGG
485999	2132781	NBstNBI	CCAGSCT	T	2136.3808	AAGTCAAGCAGAGTCTTGCAGSCTGGATT TGACTCATTGCACAGG
487914	2134048	BsrI_NBstNBI	GGCGSGCCCTGCAGTG	A	5003.2145	CAAGCTCCAGACTGGTCACTGCAGGGGCS GCCCCAGGGACTCCCTAAGCTCC
487914	2134048	BsrI_NBstNBI	GGCGSGCCCTGCAGTG	C	4979.1895	CAAGCTCCAGACTGGTCACTGCAGGGGCS GCCCCAGGGACTCCCTAAGCTCC

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
487914	2134048	BsrI_NBstNBI	GGGCGCCCTGCAGTG	G	5019.2139	CAAGCTCCAGACTGGTCACTGCAGGGCS GCCCCAGGGACTCCCTAAGCTCC
487914	2134048	BsrI_NBstNBI	GGGCGCCCTGCAGTG	T	4994.2011	CAAGCTCCAGACTGGTCACTGCAGGGCS GCCCCAGGGACTCCCTAAGCTCC
494470	2138245	BsrDI_NBstNBI	ACSAACAAA	A	2788.8526	ATTGAAGATGCAATGTATTTGTTSGTCGC TGACTCTATCTTGAAA
494470	2138245	BsrDI_NBstNBI	ACSAACAAA	C	2764.8276	ATTGAAGATGCAATGTATTTGTTSGTCGC TGACTCTATCTTGAAA
494470	2138245	BsrDI_NBstNBI	ACSAACAAA	G	2804.852	ATTGAAGATGCAATGTATTTGTTSGTCGC TGACTCTATCTTGAAA
494470	2138245	BsrDI_NBstNBI	ACSAACAAA	T	2779.8392	ATTGAAGATGCAATGTATTTGTTSGTCGC TGACTCTATCTTGAAA
497278	2140285	BsmI_NBstNBI	CACASTTTAATG	A	3708.4275	CAGGAGCTCTGAATGCACATTAATASTGTG CCGAGACTCTCCTGCTCTT
497278	2140285	BsmI_NBstNBI	CACASTTTAATG	C	3684.4025	CAGGAGCTCTGAATGCACATTAATASTGTG CCGAGACTCTCCTGCTCTT
497278	2140285	BsmI_NBstNBI	CACASTTTAATG	G	3724.4269	CAGGAGCTCTGAATGCACATTAATASTGTG CCGAGACTCTCCTGCTCTT
497278	2140285	BsmI_NBstNBI	CACASTTTAATG	T	3699.4141	CAGGAGCTCTGAATGCACATTAATASTGTG CCGAGACTCTCCTGCTCTT
501758	2143426	BsrDI_NBstNBI	ASGGCTA	A	2209.4436	GGCTGTTCCAGCAATGCTTAGCCSTGCCT GACTCCGCAAAATTAC
501758	2143426	BsrDI_NBstNBI	ASGGCTA	C	2185.4186	GGCTGTTCCAGCAATGCTTAGCCSTGCCT GACTCCGCAAAATTAC
501758	2143426	BsrDI_NBstNBI	ASGGCTA	G	2225.443	GGCTGTTCCAGCAATGCTTAGCCSTGCCT GACTCCGCAAAATTAC
501758	2143426	BsrDI_NBstNBI	ASGGCTA	T	2200.4302	GGCTGTTCCAGCAATGCTTAGCCSTGCCT GACTCCGCAAAATTAC
503331	2144488	NBstNBI	STAATT	A	1870.2333	TGTTGTTATCGAGTCAGTTAATTASGCTGG ACTCTACTCTCAAT
503331	2144488	NBstNBI	STAATT	C	1846.2083	TGTTGTTATCGAGTCAGTTAATTASGCTGG ACTCTACTCTCAAT
503331	2144488	NBstNBI	STAATT	G	1886.2327	TGTTGTTATCGAGTCAGTTAATTASGCTGG ACTCTACTCTCAAT

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
503331	2144488	NBstNBI	STAATT	T	1861.2199	TGTTGTTATCGAGTCAGTTAAATTASGCTGG ACTCTACTCTCAAT
503331	2144488	NBstNBI	AATTAS	A	1879.2467	TGTTGTTATCGAGTCAGTTAAATTASGCTGG ACTCTACTCTCAAT
503331	2144488	NBstNBI	AATTAS	C	1855.2217	TGTTGTTATCGAGTCAGTTAAATTASGCTGG ACTCTACTCTCAAT
503331	2144488	NBstNBI	AATTAS	G	1895.2461	TGTTGTTATCGAGTCAGTTAAATTASGCTGG ACTCTACTCTCAAT
503331	2144488	NBstNBI	AATTAS	T	1870.2333	TGTTGTTATCGAGTCAGTTAAATTASGCTGG ACTCTACTCTCAAT
505419	2145924	NBstNBI_BsrDI	SGTGCAATG	A	2842.849	ACCATCTTGGGAGTCACGGSGTGCAATGC ATGAAATTTCAT
505419	2145924	NBstNBI_BsrDI	SGTGCAATG	C	2818.824	ACCATCTTGGGAGTCACGGSGTGCAATGC ATGAAATTTCAT
505419	2145924	NBstNBI_BsrDI	SGTGCAATG	G	2858.8484	ACCATCTTGGGAGTCACGGSGTGCAATGC ATGAAATTTCAT
505419	2145924	NBstNBI_BsrDI	SGTGCAATG	T	2833.8356	ACCATCTTGGGAGTCACGGSGTGCAATGC ATGAAATTTCAT
506439	2146633	BsrI_NBstNBI	CTGAATTSCCAGCAAA	A	4938.2291	AAATTGGCTCACTGGCTTTGCTGGSAAATT CAGTGGTGACTCCACTGCTGGT
506439	2146633	BsrI_NBstNBI	CTGAATTSCCAGCAAA	C	4914.2041	AAATTGGCTCACTGGCTTTGCTGGSAAATT CAGTGGTGACTCCACTGCTGGT
506439	2146633	BsrI_NBstNBI	CTGAATTSCCAGCAAA	G	4954.2285	AAATTGGCTCACTGGCTTTGCTGGSAAATT CAGTGGTGACTCCACTGCTGGT
506439	2146633	BsrI_NBstNBI	CTGAATTSCCAGCAAA	T	4929.2157	AAATTGGCTCACTGGCTTTGCTGGSAAATT CAGTGGTGACTCCACTGCTGGT
510265	2686969	NBstNBI_BsmI	TCSGAATG	A	2513.6399	GCATGGATTGAGTCATTTTCSGAATGCAT TTACAAAGTC
510265	2686969	NBstNBI_BsmI	TCSGAATG	C	2489.6149	GCATGGATTGAGTCATTTTCSGAATGCAT TTACAAAGTC
510265	2686969	NBstNBI_BsmI	TCSGAATG	G	2529.6393	GCATGGATTGAGTCATTTTCSGAATGCAT TTACAAAGTC
510265	2686969	NBstNBI_BsmI	TCSGAATG	T	2504.6265	GCATGGATTGAGTCATTTTCSGAATGCAT TTACAAAGTC

TSC ID	dbSNP ID	Enzymes	Product	Allele	Mass	Sequence
510743	2149652	NBstNBI_BsrDI	GTCTACTSGGCAATG	A	4672.0298	GAAATTTGTTGAGTCCAGGGTCTACTSGG CAATGATGATGAGCCTA
510743	2149652	NBstNBI_BsrDI	GTCTACTSGGCAATG	C	4648.0048	GAAATTTGTTGAGTCCAGGGTCTACTSGG CAATGATGATGAGCCTA
510743	2149652	NBstNBI_BsrDI	GTCTACTSGGCAATG	G	4688.0292	GAAATTTGTTGAGTCCAGGGTCTACTSGG CAATGATGATGAGCCTA
510743	2149652	NBstNBI_BsrDI	GTCTACTSGGCAATG	T	4663.0164	GAAATTTGTTGAGTCCAGGGTCTACTSGG CAATGATGATGAGCCTA
517617	2688087	NBstNBI_BsmI	SGAATG	A	1920.2589	TCCAGAATGAGAGTCTCAGSGAATGCTTG TTGGCTGC
517617	2688087	NBstNBI_BsmI	SGAATG	C	1896.2339	TCCAGAATGAGAGTCTCAGSGAATGCTTG TTGGCTGC
517617	2688087	NBstNBI_BsmI	SGAATG	G	1936.2583	TCCAGAATGAGAGTCTCAGSGAATGCTTG TTGGCTGC
517617	2688087	NBstNBI_BsmI	SGAATG	T	1911.2455	TCCAGAATGAGAGTCTCAGSGAATGCTTG TTGGCTGC
522055	2688761	NBstNBI_BsrDI	GGTTTSGGGGGCAATG	A	5097.2871	GTGGGTAAGTGAGTCCCAGGGTTTSGGG GGCAATGCGACCTGGTGGG
522055	2688761	NBstNBI_BsrDI	GGTTTSGGGGGCAATG	C	5073.2621	GTGGGTAAGTGAGTCCCAGGGTTTSGGG GGCAATGCGACCTGGTGGG
522055	2688761	NBstNBI_BsrDI	GGTTTSGGGGGCAATG	G	5113.2865	GTGGGTAAGTGAGTCCCAGGGTTTSGGG GGCAATGCGACCTGGTGGG
522055	2688761	NBstNBI_BsrDI	GGTTTSGGGGGCAATG	T	5088.2737	GTGGGTAAGTGAGTCCCAGGGTTTSGGG GGCAATGCGACCTGGTGGG
527539	2689685	BsrI_NBstNBI	SAAACACCTT	A	3373.2202	TTATCCACACACTGGGAAGGTGTTTTSATA AGACTCCTGATTTTGC
527539	2689685	BsrI_NBstNBI	SAAACACCTT	C	3349.1952	TTATCCACACACTGGGAAGGTGTTTTSATA AGACTCCTGATTTTGC
527539	2689685	BsrI_NBstNBI	SAAACACCTT	G	3389.2196	TTATCCACACACTGGGAAGGTGTTTTSATA AGACTCCTGATTTTGC
527539	2689685	BsrI_NBstNBI	SAAACACCTT	T	3364.2068	TTATCCACACACTGGGAAGGTGTTTTSATA AGACTCCTGATTTTGC
528687	2690068	BsrI_NBstNBI	GAGTCSCCTTGAA	A	3749.4397	ACCTCTACCTACTGGGTTTCAAGSGACTCT CCTGACTCAGCCTCCCGA

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
528687	2690068	BsrI_NBstNBI	GAGTCSCTTGAA	C	3725.4147	ACCTCTACCTACTGGTTCAAGSGACTCT CCTGACTCAGCCTCCCCGA
528687	2690068	BsrI_NBstNBI	GAGTCSCTTGAA	G	3765.4391	ACCTCTACCTACTGGTTCAAGSGACTCT CCTGACTCAGCCTCCCCGA
528687	2690068	BsrI_NBstNBI	GAGTCSCTTGAA	T	3740.4263	ACCTCTACCTACTGGTTCAAGSGACTCT CCTGACTCAGCCTCCCCGA
529711	2162319	NBstNBI_BsrI	ASGCTGTGAGTCACTG	A	5001.2389	GACCAAGAGTGAGTCCATCASCCTGTGAG TCACCTGGTCAAGGTTGC
529711	2162319	NBstNBI_BsrI	ASGCTGTGAGTCACTG	C	4977.2139	GACCAAGAGTGAGTCCATCASCCTGTGAG TCACCTGGTCAAGGTTGC
529711	2162319	NBstNBI_BsrI	ASGCTGTGAGTCACTG	G	5017.2383	GACCAAGAGTGAGTCCATCASCCTGTGAG TCACCTGGTCAAGGTTGC
529711	2162319	NBstNBI_BsrI	ASGCTGTGAGTCACTG	T	4992.2255	GACCAAGAGTGAGTCCATCASCCTGTGAG TCACCTGGTCAAGGTTGC
530328	2162759	NBstNBI_BsrDI	CTTCASAAAGCAATG	A	4335.8347	GGCCAGGCCTGAGTCAGGCCCTTCASAAAG CAATGCAGACTGCATAG
530328	2162759	NBstNBI_BsrDI	CTTCASAAAGCAATG	C	4311.8097	GGCCAGGCCTGAGTCAGGCCCTTCASAAAG CAATGCAGACTGCATAG
530328	2162759	NBstNBI_BsrDI	CTTCASAAAGCAATG	G	4351.8341	GGCCAGGCCTGAGTCAGGCCCTTCASAAAG CAATGCAGACTGCATAG
530328	2162759	NBstNBI_BsrDI	CTTCASAAAGCAATG	T	4326.8213	GGCCAGGCCTGAGTCAGGCCCTTCASAAAG CAATGCAGACTGCATAG
533292	2164979	NBstNBI_BsrI	GA CTAGAGASGACTG	A	4730.081	GCCTATGATTGAGTCTGATGACTAGAGAS GACTGGATGGAAGGTGA
533292	2164979	NBstNBI_BsrI	GA CTAGAGASGACTG	C	4706.056	GCCTATGATTGAGTCTGATGACTAGAGAS GACTGGATGGAAGGTGA
533292	2164979	NBstNBI_BsrI	GA CTAGAGASGACTG	G	4746.0804	GCCTATGATTGAGTCTGATGACTAGAGAS GACTGGATGGAAGGTGA
533292	2164979	NBstNBI_BsrI	GA CTAGAGASGACTG	T	4721.0676	GCCTATGATTGAGTCTGATGACTAGAGAS GACTGGATGGAAGGTGA
534503		BclI_NBstNBI	ACTATSTACCTTGATC	A	4895.1895	AGGACACCTCTGATCAAGGTASATAGTAG CTGACTCTTTGAGCATG
534503		BclI_NBstNBI	ACTATSTACCTTGATC	C	4871.1645	AGGACACCTCTGATCAAGGTASATAGTAG CTGACTCTTTGAGCATG

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534503		BclI_NBstNBI	ACTATSTACCTTGATC	G	4911.1889	AGGACACCTCTGTGATCAAGGTASATAGTAG CTGACTCTTTGAGCATG
534503		BclI_NBstNBI	ACTATSTACCTTGATC	T	4886.1761	AGGACACCTCTGTGATCAAGGTASATAGTAG CTGACTCTTTGAGCATG
541826	2171132	BsaBI_NBstNBI	SAAAAATCAGGATGA	A	4722.1072	GATAGTTTTGATTTTCATCCTGATTTTSC TTTGACTCATTTGGTTTT
541826	2171132	BsaBI_NBstNBI	SAAAAATCAGGATGA	C	4698.0822	GATAGTTTTGATTTTCATCCTGATTTTSC TTTGACTCATTTGGTTTT
541826	2171132	BsaBI_NBstNBI	SAAAAATCAGGATGA	G	4738.1066	GATAGTTTTGATTTTCATCCTGATTTTSC TTTGACTCATTTGGTTTT
541826	2171132	BsaBI_NBstNBI	SAAAAATCAGGATGA	T	4713.0938	GATAGTTTTGATTTTCATCCTGATTTTSC TTTGACTCATTTGGTTTT
544581	2692216	BclI_NBstNBI	ACCTSGGTGATC	A	3725.4147	ATCTCTGCACGTGATCACCSAGGTGACGGA CTCCTGTCTTGTA
544581	2692216	BclI_NBstNBI	ACCTSGGTGATC	C	3701.3897	ATCTCTGCACGTGATCACCSAGGTGACGGA CTCCTGTCTTGTA
544581	2692216	BclI_NBstNBI	ACCTSGGTGATC	G	3741.4141	ATCTCTGCACGTGATCACCSAGGTGACGGA CTCCTGTCTTGTA
544581	2692216	BclI_NBstNBI	ACCTSGGTGATC	T	3716.4013	ATCTCTGCACGTGATCACCSAGGTGACGGA CTCCTGTCTTGTA
546320	2174405	NBstNBI_BsaBI	ATCAGSAGATAA	A	3766.4787	CACAGTGAGAGAGTCAACCAATCAGSAGAT AATTATCAAGTGTGAC
546320	2174405	NBstNBI_BsaBI	ATCAGSAGATAA	C	3742.4537	CACAGTGAGAGAGTCAACCAATCAGSAGAT AATTATCAAGTGTGAC
546320	2174405	NBstNBI_BsaBI	ATCAGSAGATAA	G	3782.4781	CACAGTGAGAGAGTCAACCAATCAGSAGAT AATTATCAAGTGTGAC
546320	2174405	NBstNBI_BsaBI	ATCAGSAGATAA	T	3757.4653	CACAGTGAGAGAGTCAACCAATCAGSAGAT AATTATCAAGTGTGAC
548450	2175994	NBstNBI	AAGAATCASGGC	A	3767.4665	CCTGTGGCAGGAGTCTGGGAAGAATCAS GGCCACGGACTCCAAGGGTGC
548450	2175994	NBstNBI	AAGAATCASGGC	C	3743.4415	CCTGTGGCAGGAGTCTGGGAAGAATCAS GGCCACGGACTCCAAGGGTGC
548450	2175994	NBstNBI	AAGAATCASGGC	G	3783.4659	CCTGTGGCAGGAGTCTGGGAAGAATCAS GGCCACGGACTCCAAGGGTGC

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548450	2175994	NBstNBI	AAGAATCASGGC	T	3758.4531	CCTGTGGCAGGAGTCTGGGAAGAATCAS GGCCACGGACTCCAAGGGTGTC
548450	2175994	NBstNBI	GCCSTGATTCTT	A	3691.3885	CCTGTGGCAGGAGTCTGGGAAGAATCAS GGCCACGGACTCCAAGGGTGTC
548450	2175994	NBstNBI	GCCSTGATTCTT	C	3667.3635	CCTGTGGCAGGAGTCTGGGAAGAATCAS GGCCACGGACTCCAAGGGTGTC
548450	2175994	NBstNBI	GCCSTGATTCTT	G	3707.3879	CCTGTGGCAGGAGTCTGGGAAGAATCAS GGCCACGGACTCCAAGGGTGTC
548450	2175994	NBstNBI	GCCSTGATTCTT	T	3682.3751	CCTGTGGCAGGAGTCTGGGAAGAATCAS GGCCACGGACTCCAAGGGTGTC
552419		NBstNBI	GGAASTGTTG	A	3187.0697	TCATCAAATGGAGTCGAATGGAASTGTTG AATGGACTCCAATGGAGTC
552419		NBstNBI	GGAASTGTTG	C	3163.0447	TCATCAAATGGAGTCGAATGGAASTGTTG AATGGACTCCAATGGAGTC
552419		NBstNBI	GGAASTGTTG	G	3203.0691	TCATCAAATGGAGTCGAATGGAASTGTTG AATGGACTCCAATGGAGTC
552419		NBstNBI	GGAASTGTTG	T	3178.0563	TCATCAAATGGAGTCGAATGGAASTGTTG AATGGACTCCAATGGAGTC
552419		NBstNBI	CAACASTTCC	A	3035.9855	TCATCAAATGGAGTCGAATGGAASTGTTG AATGGACTCCAATGGAGTC
552419		NBstNBI	CAACASTTCC	C	3011.9605	TCATCAAATGGAGTCGAATGGAASTGTTG AATGGACTCCAATGGAGTC
552419		NBstNBI	CAACASTTCC	G	3051.9849	TCATCAAATGGAGTCGAATGGAASTGTTG AATGGACTCCAATGGAGTC
552419		NBstNBI	CAACASTTCC	T	3026.9721	TCATCAAATGGAGTCGAATGGAASTGTTG AATGGACTCCAATGGAGTC
560341	2694475	NBstNBI BclI	AATSGCAGAAATTGATC	A	4993.2651	GAATGCATTAGAGTCTTTTAATSGCAGAAAT TGATCAAGCAGAAATGA
560341	2694475	NBstNBI BclI	AATSGCAGAAATTGATC	C	4969.2401	GAATGCATTAGAGTCTTTTAATSGCAGAAAT TGATCAAGCAGAAATGA
560341	2694475	NBstNBI BclI	AATSGCAGAAATTGATC	G	5009.2645	GAATGCATTAGAGTCTTTTAATSGCAGAAAT TGATCAAGCAGAAATGA
560341	2694475	NBstNBI BclI	AATSGCAGAAATTGATC	T	4984.2517	GAATGCATTAGAGTCTTTTAATSGCAGAAAT TGATCAAGCAGAAATGA

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
564555	2186676	NBstNBI	ATCTTGATGAGAGSGA	A	5049.2889	GGGAGACTGAGAGTCTGCCATCTTGATGA GAGSAACTTGACTCCTAAGCTTGA
564555	2186676	NBstNBI	ATCTTGATGAGAGSGA	C	5025.2639	GGGAGACTGAGAGTCTGCCATCTTGATGA GAGSAACTTGACTCCTAAGCTTGA
564555	2186676	NBstNBI	ATCTTGATGAGAGSGA	G	5065.2883	GGGAGACTGAGAGTCTGCCATCTTGATGA GAGSAACTTGACTCCTAAGCTTGA
564555	2186676	NBstNBI	ATCTTGATGAGAGSGA	T	5040.2755	GGGAGACTGAGAGTCTGCCATCTTGATGA GAGSAACTTGACTCCTAAGCTTGA
564555	2186676	NBstNBI	TCSCTCTCATCAAGAT	A	4880.1779	GGGAGACTGAGAGTCTGCCATCTTGATGA GAGSAACTTGACTCCTAAGCTTGA
564555	2186676	NBstNBI	TCSCTCTCATCAAGAT	C	4856.1529	GGGAGACTGAGAGTCTGCCATCTTGATGA GAGSAACTTGACTCCTAAGCTTGA
564555	2186676	NBstNBI	TCSCTCTCATCAAGAT	G	4896.1773	GGGAGACTGAGAGTCTGCCATCTTGATGA GAGSAACTTGACTCCTAAGCTTGA
564555	2186676	NBstNBI	TCSCTCTCATCAAGAT	T	4871.1645	GGGAGACTGAGAGTCTGCCATCTTGATGA GAGSAACTTGACTCCTAAGCTTGA
564936	2186959	NBstNBI_BsmI	TAAATTASTGAATG	A	4389.8829	TATTTGGTAAGAGTCTAAATAAATTASTGA ATGCATGCCCTTGATG
564936	2186959	NBstNBI_BsmI	TAAATTASTGAATG	C	4365.8579	TATTTGGTAAGAGTCTAAATAAATTASTGA ATGCATGCCCTTGATG
564936	2186959	NBstNBI_BsmI	TAAATTASTGAATG	G	4405.8823	TATTTGGTAAGAGTCTAAATAAATTASTGA ATGCATGCCCTTGATG
564936	2186959	NBstNBI_BsmI	TAAATTASTGAATG	T	4380.8695	TATTTGGTAAGAGTCTAAATAAATTASTGA ATGCATGCCCTTGATG
568847	2189668	NBstNBI_Bsrl	TSCAGAGACTG	A	3445.2434	ATAAAAGTAAGAGTCTCTATSCAGAGACTG GCAATTTGTTCT
568847	2189668	NBstNBI_Bsrl	TSCAGAGACTG	C	3421.2184	ATAAAAGTAAGAGTCTCTATSCAGAGACTG GCAATTTGTTCT
568847	2189668	NBstNBI_Bsrl	TSCAGAGACTG	G	3461.2428	ATAAAAGTAAGAGTCTCTATSCAGAGACTG GCAATTTGTTCT
568847	2189668	NBstNBI_Bsrl	TSCAGAGACTG	T	3436.23	ATAAAAGTAAGAGTCTCTATSCAGAGACTG GCAATTTGTTCT
584421	2199416	BclI_NBstNBI	AAACCTATSTTGATC	A	4615.0182	GGATAATTTATGATCAASATAGGTTTAATT GACTCACAGTCTTGC

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584421	2199416	BclI_NBstNBI	AAACCTATSTTGATC	C	4590.9932	GGATAAATTTATGATCAASATAGGTTTAATT GACTCACAGTCTTGC
584421	2199416	BclI_NBstNBI	AAACCTATSTTGATC	G	4631.0176	GGATAAATTTATGATCAASATAGGTTTAATT GACTCACAGTCTTGC
584421	2199416	BclI_NBstNBI	AAACCTATSTTGATC	T	4606.0048	GGATAAATTTATGATCAASATAGGTTTAATT GACTCACAGTCTTGC
585197		NBstNBI_Bsrl	TCSGTCACCAGACTG	A	4616.9938	TTTTGAGATGGAGTCTCACTCSGTCACCA GACTGGAGTGCAGTGGT
585197		NBstNBI_Bsrl	TCSGTCACCAGACTG	C	4592.9688	TTTTGAGATGGAGTCTCACTCSGTCACCA GACTGGAGTGCAGTGGT
585197		NBstNBI_Bsrl	TCSGTCACCAGACTG	G	4632.9932	TTTTGAGATGGAGTCTCACTCSGTCACCA GACTGGAGTGCAGTGGT
585197		NBstNBI_Bsrl	TCSGTCACCAGACTG	T	4607.9804	TTTTGAGATGGAGTCTCACTCSGTCACCA GACTGGAGTGCAGTGGT
589525	2203013	Bsrl_NBstNBI	GACSAGGGTTCCAG	A	4392.8463	GCAAGGAAGGACTGGACTGGAACCCCTSG TCGACAGACTCTTAACCATTT
589525	2203013	Bsrl_NBstNBI	GACSAGGGTTCCAG	C	4368.8213	GCAAGGAAGGACTGGACTGGAACCCCTSG TCGACAGACTCTTAACCATTT
589525	2203013	Bsrl_NBstNBI	GACSAGGGTTCCAG	G	4408.8457	GCAAGGAAGGACTGGACTGGAACCCCTSG TCGACAGACTCTTAACCATTT
589525	2203013	Bsrl_NBstNBI	GACSAGGGTTCCAG	T	4383.8329	GCAAGGAAGGACTGGACTGGAACCCCTSG TCGACAGACTCTTAACCATTT
594644	2206511	NBstNBI	GCCCTAGAAAAGCS	A	4345.8359	AGGACATTATGAGTCTGGAGCCCTAGAAA AGCSTTCTGACTCTGCCACTAGC
594644	2206511	NBstNBI	GCCCTAGAAAAGCS	C	4321.8109	AGGACATTATGAGTCTGGAGCCCTAGAAA AGCSTTCTGACTCTGCCACTAGC
594644	2206511	NBstNBI	GCCCTAGAAAAGCS	G	4361.8353	AGGACATTATGAGTCTGGAGCCCTAGAAA AGCSTTCTGACTCTGCCACTAGC
594644	2206511	NBstNBI	GCCCTAGAAAAGCS	T	4336.8225	AGGACATTATGAGTCTGGAGCCCTAGAAA AGCSTTCTGACTCTGCCACTAGC
594644	2206511	NBstNBI	SGCTTTTCTAGGGC	A	4349.8067	AGGACATTATGAGTCTGGAGCCCTAGAAA AGCSTTCTGACTCTGCCACTAGC
594644	2206511	NBstNBI	SGCTTTTCTAGGGC	C	4325.7817	AGGACATTATGAGTCTGGAGCCCTAGAAA AGCSTTCTGACTCTGCCACTAGC

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
594644	2206511	NBstNBI	SGCTTTTCTAGGGC	G	4365.8061	AGGACATTATGAGTCTGGAGCCCTAGAAA AGCSTTCTGACTCTGCCACTAGC
594644	2206511	NBstNBI	SGCTTTTCTAGGGC	T	4340.7933	AGGACATTATGAGTCTGGAGCCCTAGAAA AGCSTTCTGACTCTGCCACTAGC
594840	2206613	NBstNBI_BsaBI	TSATTTTGATTA	A	3729.4373	AGACTGTTGTGAGTCACTGTSATTTTGATT AGTATCAATTGTAGTG
594840	2206613	NBstNBI_BsaBI	TSATTTTGATTA	C	3705.4123	AGACTGTTGTGAGTCACTGTSATTTTGATT AGTATCAATTGTAGTG
594840	2206613	NBstNBI_BsaBI	TSATTTTGATTA	G	3745.4367	AGACTGTTGTGAGTCACTGTSATTTTGATT AGTATCAATTGTAGTG
594840	2206613	NBstNBI_BsaBI	TSATTTTGATTA	T	3720.4239	AGACTGTTGTGAGTCACTGTSATTTTGATT AGTATCAATTGTAGTG
596205	2207561	BsrI_NBstNBI	STTTTCCATCTTAA	A	4267.7823	AAAGAATACAACTGGATTAAAGATGGAAAAS CAGCGACTCATCTTGGACC
596205	2207561	BsrI_NBstNBI	STTTTCCATCTTAA	C	4243.7573	AAAGAATACAACTGGATTAAAGATGGAAAAS CAGCGACTCATCTTGGACC
596205	2207561	BsrI_NBstNBI	STTTTCCATCTTAA	G	4283.7817	AAAGAATACAACTGGATTAAAGATGGAAAAS CAGCGACTCATCTTGGACC
596205	2207561	BsrI_NBstNBI	STTTTCCATCTTAA	T	4258.7689	AAAGAATACAACTGGATTAAAGATGGAAAAS CAGCGACTCATCTTGGACC
604428	2700096	NBstNBI_BsrI	TCTGCSGCCAGACTG	A	4632.9932	TTTTGAGACGGAGTCTCGCTCTGCSGCCA GACTGGAGTGCAGTGGC
604428	2700096	NBstNBI_BsrI	TCTGCSGCCAGACTG	C	4608.9682	TTTTGAGACGGAGTCTCGCTCTGCSGCCA GACTGGAGTGCAGTGGC
604428	2700096	NBstNBI_BsrI	TCTGCSGCCAGACTG	G	4648.9926	TTTTGAGACGGAGTCTCGCTCTGCSGCCA GACTGGAGTGCAGTGGC
604428	2700096	NBstNBI_BsrI	TCTGCSGCCAGACTG	T	4623.9798	TTTTGAGACGGAGTCTCGCTCTGCSGCCA GACTGGAGTGCAGTGGC
610312	2700890	NBstNBI	GGTTSAATCTTAAT	A	4356.8445	CTACAAGTTTGAGTCATTAGGTTSAATCTT AATCTCTGACTCTTCACTGAGT
610312	2700890	NBstNBI	GGTTSAATCTTAAT	C	4332.8195	CTACAAGTTTGAGTCATTAGGTTSAATCTT AATCTCTGACTCTTCACTGAGT
610312	2700890	NBstNBI	GGTTSAATCTTAAT	G	4372.8439	CTACAAGTTTGAGTCATTAGGTTSAATCTT AATCTCTGACTCTTCACTGAGT

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
610312	2700890	NBstNBI	GGTTSAATCTTAAT	T	4347.8311	CTACAAAGTTTGAGTCATTAGGTTTSAATCTT AATCTCTGACTCTTCACTGAGT
610312	2700890	NBstNBI	ATTAAGATTSAACC	A	4334.8469	CTACAAAGTTTGAGTCATTAGGTTTSAATCTT AATCTCTGACTCTTCACTGAGT
610312	2700890	NBstNBI	ATTAAGATTSAACC	C	4310.8219	CTACAAAGTTTGAGTCATTAGGTTTSAATCTT AATCTCTGACTCTTCACTGAGT
610312	2700890	NBstNBI	ATTAAGATTSAACC	G	4350.8463	CTACAAAGTTTGAGTCATTAGGTTTSAATCTT AATCTCTGACTCTTCACTGAGT
610312	2700890	NBstNBI	ATTAAGATTSAACC	T	4325.8335	CTACAAAGTTTGAGTCATTAGGTTTSAATCTT AATCTCTGACTCTTCACTGAGT
613861	2219487	NBstNBI_Bsrl	AGTGSTACTCAACTG	A	4656.0304	GCAGTCAACTGAGTCTCTAAGTGSTACTC AACTGGTAGTGGACTG
613861	2219487	NBstNBI_Bsrl	AGTGSTACTCAACTG	C	4632.0054	GCAGTCAACTGAGTCTCTAAGTGSTACTC AACTGGTAGTGGACTG
613861	2219487	NBstNBI_Bsrl	AGTGSTACTCAACTG	G	4672.0298	GCAGTCAACTGAGTCTCTAAGTGSTACTC AACTGGTAGTGGACTG
613861	2219487	NBstNBI_Bsrl	AGTGSTACTCAACTG	T	4647.017	GCAGTCAACTGAGTCTCTAAGTGSTACTC AACTGGTAGTGGACTG
620056		Bsrl_NBstNBI	GCTTGCASCA	A	3092.0093	CCCTGAGCACACTGGCTGCTGCAAGCAAT GGACTCACAATGCCAT
620056		Bsrl_NBstNBI	GCTTGCASCA	C	3067.9843	CCCTGAGCACACTGGCTGCTGCAAGCAAT GGACTCACAATGCCAT
620056		Bsrl_NBstNBI	GCTTGCASCA	G	3108.0087	CCCTGAGCACACTGGCTGCTGCAAGCAAT GGACTCACAATGCCAT
620056		Bsrl_NBstNBI	GCTTGCASCA	T	3082.9959	CCCTGAGCACACTGGCTGCTGCAAGCAAT GGACTCACAATGCCAT
625163	2227526	Bsrl_NBstNBI	GGTCAAAGGAGS	A	3823.4903	ATCCTGAATCACTGGGSCCTCCTTTGACCC TCAGACTCTGGAAAAACA
625163	2227526	Bsrl_NBstNBI	GGTCAAAGGAGS	C	3799.4653	ATCCTGAATCACTGGGSCCTCCTTTGACCC TCAGACTCTGGAAAAACA
625163	2227526	Bsrl_NBstNBI	GGTCAAAGGAGS	G	3839.4897	ATCCTGAATCACTGGGSCCTCCTTTGACCC TCAGACTCTGGAAAAACA
625163	2227526	Bsrl_NBstNBI	GGTCAAAGGAGS	T	3814.4769	ATCCTGAATCACTGGGSCCTCCTTTGACCC TCAGACTCTGGAAAAACA

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
625652	2227910	NBstNBI_BsrI	GCTGTTTCASAACTG	A	4647.017	CCGAAAATAGAGTCCAGAGCTGTTTCAS AACTGGCTTTAATGTTG
625652	2227910	NBstNBI_BsrI	GCTGTTTCASAACTG	C	4622.992	CCGAAAATAGAGTCCAGAGCTGTTTCAS AACTGGCTTTAATGTTG
625652	2227910	NBstNBI_BsrI	GCTGTTTCASAACTG	G	4663.0164	CCGAAAATAGAGTCCAGAGCTGTTTCAS AACTGGCTTTAATGTTG
625652	2227910	NBstNBI_BsrI	GCTGTTTCASAACTG	T	4638.0036	CCGAAAATAGAGTCCAGAGCTGTTTCAS AACTGGCTTTAATGTTG
630371	2231205	NBstNBI	TCTGTSTCA	A	2768.7984	CCAGATCATGAGTCCCACACTCTGTSTCAA TGTGACTCATTAGAAAAA
630371	2231205	NBstNBI	TCTGTSTCA	C	2744.7734	CCAGATCATGAGTCCCACACTCTGTSTCAA TGTGACTCATTAGAAAAA
630371	2231205	NBstNBI	TCTGTSTCA	G	2784.7978	CCAGATCATGAGTCCCACACTCTGTSTCAA TGTGACTCATTAGAAAAA
630371	2231205	NBstNBI	TCTGTSTCA	T	2759.785	CCAGATCATGAGTCCCACACTCTGTSTCAA TGTGACTCATTAGAAAAA
630371	2231205	NBstNBI	TGASACAGA	A	2835.863	CCAGATCATGAGTCCCACACTCTGTSTCAA TGTGACTCATTAGAAAAA
630371	2231205	NBstNBI	TGASACAGA	C	2811.838	CCAGATCATGAGTCCCACACTCTGTSTCAA TGTGACTCATTAGAAAAA
630371	2231205	NBstNBI	TGASACAGA	G	2851.8624	CCAGATCATGAGTCCCACACTCTGTSTCAA TGTGACTCATTAGAAAAA
630371	2231205	NBstNBI	TGASACAGA	T	2826.8496	CCAGATCATGAGTCCCACACTCTGTSTCAA TGTGACTCATTAGAAAAA
634111	2234036	BsrI_NBstNBI	TCTSTCG	A	2151.3924	TGCACTCCAGACTGGCGGASAGAGCGGAG ACTCTGTCTCAAAA
634111	2234036	BsrI_NBstNBI	TCTSTCG	C	2127.3674	TGCACTCCAGACTGGCGGASAGAGCGGAG ACTCTGTCTCAAAA
634111	2234036	BsrI_NBstNBI	TCTSTCG	G	2167.3918	TGCACTCCAGACTGGCGGASAGAGCGGAG ACTCTGTCTCAAAA
634111	2234036	BsrI_NBstNBI	TCTSTCG	T	2142.379	TGCACTCCAGACTGGCGGASAGAGCGGAG ACTCTGTCTCAAAA
638671	2237281	BsrDI_NBstNBI	GGACGGGGCCCTGG	A	4409.8335	GCTTTATCTTGCAATGTCCCAGGGCSCCG TCCTTGGGACTCCCACTCTGGGA

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
638671	2237281	BsrDI_NBstNBI	GGACGGGGCCCTGG	C	4385.8085	GCTTTATCTTGCAATGTCCAGGGCSCCG TCCTTGGGACTCCACTCTGGGA
638671	2237281	BsrDI_NBstNBI	GGACGGGGCCCTGG	G	4425.8329	GCTTTATCTTGCAATGTCCAGGGCSCCG TCCTTGGGACTCCACTCTGGGA
638671	2237281	BsrDI_NBstNBI	GGACGGGGCCCTGG	T	4400.8201	GCTTTATCTTGCAATGTCCAGGGCSCCG TCCTTGGGACTCCACTCTGGGA
638755	2237350	NBstNBI	CTGSCAAAAAGA	A	3751.4671	ATTGAGAGAAAGAGTCTCCACTGSCAAAA GATTATGACTCACTGAAAGCT
638755	2237350	NBstNBI	CTGSCAAAAAGA	C	3727.4421	ATTGAGAGAAAGAGTCTCCACTGSCAAAA GATTATGACTCACTGAAAGCT
638755	2237350	NBstNBI	CTGSCAAAAAGA	G	3767.4665	ATTGAGAGAAAGAGTCTCCACTGSCAAAA GATTATGACTCACTGAAAGCT
638755	2237350	NBstNBI	CTGSCAAAAAGA	T	3742.4537	ATTGAGAGAAAGAGTCTCCACTGSCAAAA GATTATGACTCACTGAAAGCT
638755	2237350	NBstNBI	TCTTTTTGSCAG	A	3706.4001	ATTGAGAGAAAGAGTCTCCACTGSCAAAA GATTATGACTCACTGAAAGCT
638755	2237350	NBstNBI	TCTTTTTGSCAG	C	3682.3751	ATTGAGAGAAAGAGTCTCCACTGSCAAAA GATTATGACTCACTGAAAGCT
638755	2237350	NBstNBI	TCTTTTTGSCAG	G	3722.3995	ATTGAGAGAAAGAGTCTCCACTGSCAAAA GATTATGACTCACTGAAAGCT
638755	2237350	NBstNBI	TCTTTTTGSCAG	T	3697.3867	ATTGAGAGAAAGAGTCTCCACTGSCAAAA GATTATGACTCACTGAAAGCT
647097	2243494	BsrI_NBstNBI	CACCTGGGTGSTAGG	A	4728.0536	GTGACATATCACTGGGCCTASCACCCAAG TGATATGACTCCTGTCTTGTG
647097	2243494	BsrI_NBstNBI	CACCTGGGTGSTAGG	C	4704.0286	GTGACATATCACTGGGCCTASCACCCAAG TGATATGACTCCTGTCTTGTG
647097	2243494	BsrI_NBstNBI	CACCTGGGTGSTAGG	G	4744.053	GTGACATATCACTGGGCCTASCACCCAAG TGATATGACTCCTGTCTTGTG
647097	2243494	BsrI_NBstNBI	CACCTGGGTGSTAGG	T	4719.0402	GTGACATATCACTGGGCCTASCACCCAAG TGATATGACTCCTGTCTTGTG
649462	2244951	NBstNBI	AAAGTCCSGA	A	3125.0477	CTTGCTGATGGAGTCTGAGAAAAGTCCSGA GAAAGACTCAGATTACTAC
649462	2244951	NBstNBI	AAAGTCCSGA	C	3101.0227	CTTGCTGATGGAGTCTGAGAAAAGTCCSGA GAAAGACTCAGATTACTAC

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649462	2244951	NBstNBI	AAAGTCCSGA	G	3141.0471	CTTGCTGATGGAGTCTGAGAAAGTCCSGA GAAAGACTCAGATTACTAC
649462	2244951	NBstNBI	AAAGTCCSGA	T	3116.0343	CTTGCTGATGGAGTCTGAGAAAGTCCSGA GAAAGACTCAGATTACTAC
649462	2244951	NBstNBI	TCSGGACTTT	A	3098.0075	CTTGCTGATGGAGTCTGAGAAAGTCCSGA GAAAGACTCAGATTACTAC
649462	2244951	NBstNBI	TCSGGACTTT	C	3073.9825	CTTGCTGATGGAGTCTGAGAAAGTCCSGA GAAAGACTCAGATTACTAC
649462	2244951	NBstNBI	TCSGGACTTT	G	3114.0069	CTTGCTGATGGAGTCTGAGAAAGTCCSGA GAAAGACTCAGATTACTAC
649462	2244951	NBstNBI	TCSGGACTTT	T	3088.9941	CTTGCTGATGGAGTCTGAGAAAGTCCSGA GAAAGACTCAGATTACTAC
652879	2247385	NBstNBI_BsrI	ACSGCTAACTG	A	3405.219	TGTGAGTCAGGAGTCTGGCACSGCTAACT GGGTCCCTGTGCTC
652879	2247385	NBstNBI_BsrI	ACSGCTAACTG	C	3381.194	TGTGAGTCAGGAGTCTGGCACSGCTAACT GGGTCCCTGTGCTC
652879	2247385	NBstNBI_BsrI	ACSGCTAACTG	G	3421.2184	TGTGAGTCAGGAGTCTGGCACSGCTAACT GGGTCCCTGTGCTC
652879	2247385	NBstNBI_BsrI	ACSGCTAACTG	T	3396.2056	TGTGAGTCAGGAGTCTGGCACSGCTAACT GGGTCCCTGTGCTC
654037	2248275	BsrI_NBstNBI	GAAGTGAGGAGSC	A	4152.6994	GCCGACCTGTACTGGTGSCTCCTCACTTC CCTTGACTCCAATGCCATC
654037	2248275	BsrI_NBstNBI	GAAGTGAGGAGSC	C	4128.6744	GCCGACCTGTACTGGTGSCTCCTCACTTC CCTTGACTCCAATGCCATC
654037	2248275	BsrI_NBstNBI	GAAGTGAGGAGSC	G	4168.6988	GCCGACCTGTACTGGTGSCTCCTCACTTC CCTTGACTCCAATGCCATC
654037	2248275	BsrI_NBstNBI	GAAGTGAGGAGSC	T	4143.686	GCCGACCTGTACTGGTGSCTCCTCACTTC CCTTGACTCCAATGCCATC
662593	2254817	NBstNBI	SAGGTAACAAGCTGA	A	4714.0816	CTAGCATGCTGAGTCACCGTCAGCTTGTT ACCTSTTAGGACTCCACGGTCTAG
662593	2254817	NBstNBI	SAGGTAACAAGCTGA	C	4690.0566	CTAGCATGCTGAGTCACCGTCAGCTTGTT ACCTSTTAGGACTCCACGGTCTAG
662593	2254817	NBstNBI	SAGGTAACAAGCTGA	G	4730.081	CTAGCATGCTGAGTCACCGTCAGCTTGTT ACCTSTTAGGACTCCACGGTCTAG

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662593	2254817	NBstNBI	SAGGTAACAAGCTGA	T	4705.0682	CTAGCATGCTGAGTCACCGTCAGCTTGTT ACCTSTTAGGACTCCACGGTCTAG
662593	2254817	NBstNBI	TCAGCTTGTTACCTS	A	4597.9792	CTAGCATGCTGAGTCACCGTCAGCTTGTT ACCTSTTAGGACTCCACGGTCTAG
662593	2254817	NBstNBI	TCAGCTTGTTACCTS	C	4573.9542	CTAGCATGCTGAGTCACCGTCAGCTTGTT ACCTSTTAGGACTCCACGGTCTAG
662593	2254817	NBstNBI	TCAGCTTGTTACCTS	G	4613.9786	CTAGCATGCTGAGTCACCGTCAGCTTGTT ACCTSTTAGGACTCCACGGTCTAG
662593	2254817	NBstNBI	TCAGCTTGTTACCTS	T	4588.9658	CTAGCATGCTGAGTCACCGTCAGCTTGTT ACCTSTTAGGACTCCACGGTCTAG
667387	2258351	NBstNBI	TSGCTGCATGA	A	3436.23	CAAGAGGTATGAGTCCTCATCATGCAGCS ATGAAGACTCCAACAAACAT
667387	2258351	NBstNBI	TSGCTGCATGA	C	3412.205	CAAGAGGTATGAGTCCTCATCATGCAGCS ATGAAGACTCCAACAAACAT
667387	2258351	NBstNBI	TSGCTGCATGA	G	3452.2294	CAAGAGGTATGAGTCCTCATCATGCAGCS ATGAAGACTCCAACAAACAT
667387	2258351	NBstNBI	TSGCTGCATGA	T	3427.2166	CAAGAGGTATGAGTCCTCATCATGCAGCS ATGAAGACTCCAACAAACAT
667387	2258351	NBstNBI	TCATGCAGCSA	A	3405.219	CAAGAGGTATGAGTCCTCATCATGCAGCS ATGAAGACTCCAACAAACAT
667387	2258351	NBstNBI	TCATGCAGCSA	C	3381.194	CAAGAGGTATGAGTCCTCATCATGCAGCS ATGAAGACTCCAACAAACAT
667387	2258351	NBstNBI	TCATGCAGCSA	G	3421.2184	CAAGAGGTATGAGTCCTCATCATGCAGCS ATGAAGACTCCAACAAACAT
667387	2258351	NBstNBI	TCATGCAGCSA	T	3396.2056	CAAGAGGTATGAGTCCTCATCATGCAGCS ATGAAGACTCCAACAAACAT
667720	2708415	NBstNBI_Bsrl	AATAATTSAAGTG	A	4045.6622	ACATTTATTTGAGTCATGAAATAATTSAACT GGCTGATTCCTTT
667720	2708415	NBstNBI_Bsrl	AATAATTSAAGTG	C	4021.6372	ACATTTATTTGAGTCATGAAATAATTSAACT GGCTGATTCCTTT
667720	2708415	NBstNBI_Bsrl	AATAATTSAAGTG	G	4061.6616	ACATTTATTTGAGTCATGAAATAATTSAACT GGCTGATTCCTTT
667720	2708415	NBstNBI_Bsrl	AATAATTSAAGTG	T	4036.6488	ACATTTATTTGAGTCATGAAATAATTSAACT GGCTGATTCCTTT

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671818	2261564	Bsrl_NBstNBI	ASACTCTCTCTC	A	3620.3531	TAGATCAGAAACTGGGAGAGAGAGTSTA TGAGACTCTCAAGGTAGA
671818	2261564	Bsrl_NBstNBI	ASACTCTCTCTC	C	3596.3281	TAGATCAGAAACTGGGAGAGAGAGTSTA TGAGACTCTCAAGGTAGA
671818	2261564	Bsrl_NBstNBI	ASACTCTCTCTC	G	3636.3525	TAGATCAGAAACTGGGAGAGAGAGTSTA TGAGACTCTCAAGGTAGA
671818	2261564	Bsrl_NBstNBI	ASACTCTCTCTC	T	3611.3397	TAGATCAGAAACTGGGAGAGAGAGTSTA TGAGACTCTCAAGGTAGA
672322	2261983	NBstNBI_Bsrl	CAGAGTASTCACTG	A	4351.8341	TGAGTATCGGAGTCCAAACCAGAGTASTC ACTGGATGTAGTATCT
672322	2261983	NBstNBI_Bsrl	CAGAGTASTCACTG	C	4327.8091	TGAGTATCGGAGTCCAAACCAGAGTASTC ACTGGATGTAGTATCT
672322	2261983	NBstNBI_Bsrl	CAGAGTASTCACTG	G	4367.8335	TGAGTATCGGAGTCCAAACCAGAGTASTC ACTGGATGTAGTATCT
672322	2261983	NBstNBI_Bsrl	CAGAGTASTCACTG	T	4342.8207	TGAGTATCGGAGTCCAAACCAGAGTASTC ACTGGATGTAGTATCT
677385	2266029	NBstNBI	SGAAGATTGCA	A	3469.2684	ACTTATGTCTGAGTCAGGTTGCAATCTTCS TGAGGACTCGGTGTACAGAG
677385	2266029	NBstNBI	SGAAGATTGCA	C	3445.2434	ACTTATGTCTGAGTCAGGTTGCAATCTTCS TGAGGACTCGGTGTACAGAG
677385	2266029	NBstNBI	SGAAGATTGCA	G	3485.2678	ACTTATGTCTGAGTCAGGTTGCAATCTTCS TGAGGACTCGGTGTACAGAG
677385	2266029	NBstNBI	SGAAGATTGCA	T	3460.255	ACTTATGTCTGAGTCAGGTTGCAATCTTCS TGAGGACTCGGTGTACAGAG
677385	2266029	NBstNBI	TGCAATCTTCS	A	3371.1928	ACTTATGTCTGAGTCAGGTTGCAATCTTCS TGAGGACTCGGTGTACAGAG
677385	2266029	NBstNBI	TGCAATCTTCS	C	3347.1678	ACTTATGTCTGAGTCAGGTTGCAATCTTCS TGAGGACTCGGTGTACAGAG
677385	2266029	NBstNBI	TGCAATCTTCS	G	3387.1922	ACTTATGTCTGAGTCAGGTTGCAATCTTCS TGAGGACTCGGTGTACAGAG
677385	2266029	NBstNBI	TGCAATCTTCS	T	3362.1794	ACTTATGTCTGAGTCAGGTTGCAATCTTCS TGAGGACTCGGTGTACAGAG
677616	2709587	NBstNBI_Bsrl	TCTGSCACCCAGACTG	A	4906.1785	TTTTGAGATGGAGTCTCACTCTGSCACCC AGACTGGAGGGCAGTGGT

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677616	2709587	NBstNBI_BsrI	TCTGSCACCCAGACTG	C	4882.1535	TTTGGAGATGGAGTCTCACTCTGSCACCC AGACTGGAGGGCAGTGGT
677616	2709587	NBstNBI_BsrI	TCTGSCACCCAGACTG	G	4922.1779	TTTGGAGATGGAGTCTCACTCTGSCACCC AGACTGGAGGGCAGTGGT
677616	2709587	NBstNBI_BsrI	TCTGSCACCCAGACTG	T	4897.1651	TTTGGAGATGGAGTCTCACTCTGSCACCC AGACTGGAGGGCAGTGGT
681161	2268574	BsrI_NBstNBI	CSTTGCA	A	2160.4058	ATCAGGACATACCTGGCTGCAASGGTATGA CTCTCATTATGGA
681161	2268574	BsrI_NBstNBI	CSTTGCA	C	2136.3808	ATCAGGACATACCTGGCTGCAASGGTATGA CTCTCATTATGGA
681161	2268574	BsrI_NBstNBI	CSTTGCA	G	2176.4052	ATCAGGACATACCTGGCTGCAASGGTATGA CTCTCATTATGGA
681161	2268574	BsrI_NBstNBI	CSTTGCA	T	2151.3924	ATCAGGACATACCTGGCTGCAASGGTATGA CTCTCATTATGGA
684154	2270806	BsrDI_NBstNBI	SAGACATTTCCTC	A	3669.3909	AGGCTCCAGGGCAATGCTGAGGAATGTCT SCAAGGACTCTAGTGATGTG
684154	2270806	BsrDI_NBstNBI	SAGACATTTCCTC	C	3645.3659	AGGCTCCAGGGCAATGCTGAGGAATGTCT SCAAGGACTCTAGTGATGTG
684154	2270806	BsrDI_NBstNBI	SAGACATTTCCTC	G	3685.3903	AGGCTCCAGGGCAATGCTGAGGAATGTCT SCAAGGACTCTAGTGATGTG
684154	2270806	BsrDI_NBstNBI	SAGACATTTCCTC	T	3660.3775	AGGCTCCAGGGCAATGCTGAGGAATGTCT SCAAGGACTCTAGTGATGTG
684484	2271065	NBstNBI_BsrI	CATTSAATTGACTG	A	4332.8195	TTAATCTTGTGAGTCTCTTCAATTSATTGTA CTGGGGTGGGAGGAA
684484	2271065	NBstNBI_BsrI	CATTSAATTGACTG	C	4308.7945	TTAATCTTGTGAGTCTCTTCAATTSATTGTA CTGGGGTGGGAGGAA
684484	2271065	NBstNBI_BsrI	CATTSAATTGACTG	G	4348.8189	TTAATCTTGTGAGTCTCTTCAATTSATTGTA CTGGGGTGGGAGGAA
684484	2271065	NBstNBI_BsrI	CATTSAATTGACTG	T	4323.8061	TTAATCTTGTGAGTCTCTTCAATTSATTGTA CTGGGGTGGGAGGAA
684696	2271224	NBstNBI_BsrI	CCSTGCAATGACTG	A	4327.8091	GGTGGGGCTGAGTCTATGCCSTGCAATG ACTGGACAGTAAATCA
684696	2271224	NBstNBI_BsrI	CCSTGCAATGACTG	C	4303.7841	GGTGGGGCTGAGTCTATGCCSTGCAATG ACTGGACAGTAAATCA

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
684696	2271224	NBstNBI_BsrI	CCSTGCAATGACTG	G	4343.8085	GGTGGGGCTGAGTCTATGCCSTGCAATG ACTGGACAGTAAATCA
684696	2271224	NBstNBI_BsrI	CCSTGCAATGACTG	T	4318.7957	GGTGGGGCTGAGTCTATGCCSTGCAATG ACTGGACAGTAAATCA
684696	2271224	NBstNBI_BsrDI	CCSTGCAATG	A	3092.0093	GGTGGGGCTGAGTCTATGCCSTGCAATG ACTGGACAGTAA
684696	2271224	NBstNBI_BsrDI	CCSTGCAATG	C	3067.9843	GGTGGGGCTGAGTCTATGCCSTGCAATG ACTGGACAGTAA
684696	2271224	NBstNBI_BsrDI	CCSTGCAATG	G	3108.0087	GGTGGGGCTGAGTCTATGCCSTGCAATG ACTGGACAGTAA
684696	2271224	NBstNBI_BsrDI	CCSTGCAATG	T	3082.9959	GGTGGGGCTGAGTCTATGCCSTGCAATG ACTGGACAGTAA
685798	2272083	BsrI_NBstNBI	STCAGGTGGCCCTG	A	4359.8079	AATTCTCATCACTGGCAGGGCCACCTGA SCTGGACTCCAGCAAACT
685798	2272083	BsrI_NBstNBI	STCAGGTGGCCCTG	C	4335.7829	AATTCTCATCACTGGCAGGGCCACCTGA SCTGGACTCCAGCAAACT
685798	2272083	BsrI_NBstNBI	STCAGGTGGCCCTG	G	4375.8073	AATTCTCATCACTGGCAGGGCCACCTGA SCTGGACTCCAGCAAACT
685798	2272083	BsrI_NBstNBI	STCAGGTGGCCCTG	T	4350.7945	AATTCTCATCACTGGCAGGGCCACCTGA SCTGGACTCCAGCAAACT
688013	2273742	BsaBI_NBstNBI	TTAGTAGASAGGATTC	A	5024.2761	AAATAAGTGTGATGAGAATCCTSTCTACTA AGAGAGACTCAAATGATGAC
688013	2273742	BsaBI_NBstNBI	TTAGTAGASAGGATTC	C	5000.2511	AAATAAGTGTGATGAGAATCCTSTCTACTA AGAGAGACTCAAATGATGAC
688013	2273742	BsaBI_NBstNBI	TTAGTAGASAGGATTC	G	5040.2755	AAATAAGTGTGATGAGAATCCTSTCTACTA AGAGAGACTCAAATGATGAC
688013	2273742	BsaBI_NBstNBI	TTAGTAGASAGGATTC	T	5015.2627	AAATAAGTGTGATGAGAATCCTSTCTACTA AGAGAGACTCAAATGATGAC
689193	2274693	BsrI_NBstNBI	SCGCGGCTGGCGGGCG	A	5044.2267	TCAGCTGGACACTGGCGCCCGCCAGGCC GCGSCGACACTCCCAAGCCGCC
689193	2274693	BsrI_NBstNBI	SCGCGGCTGGCGGGCG	C	5020.2017	TCAGCTGGACACTGGCGCCCGCCAGGCC GCGSCGACACTCCCAAGCCGCC
689193	2274693	BsrI_NBstNBI	SCGCGGCTGGCGGGCG	G	5060.2261	TCAGCTGGACACTGGCGCCCGCCAGGCC GCGSCGACACTCCCAAGCCGCC

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689193	2274693	BsrI_NBstNBI	SCGCGGCTGGCGGGCGG	T	5035.2133	TCAGCTGGACACTGGGCGCCCGCCAGCC GCGSCGCAGACTCCCAAGCCGCC
696672	2280461	BsrI_NBstNBI	TASGAGC	A	2209.4436	CACCCAAGGAACTGGGGCTCSTAGCCTGA CTCACAACTCTTG
696672	2280461	BsrI_NBstNBI	TASGAGC	C	2185.4186	CACCCAAGGAACTGGGGCTCSTAGCCTGA CTCACAACTCTTG
696672	2280461	BsrI_NBstNBI	TASGAGC	G	2225.443	CACCCAAGGAACTGGGGCTCSTAGCCTGA CTCACAACTCTTG
696672	2280461	BsrI_NBstNBI	TASGAGC	T	2200.4302	CACCCAAGGAACTGGGGCTCSTAGCCTGA CTCACAACTCTTG
703180	2301566	BsaBI_NBstNBI	TSAAGCTTAGAGATTA	A	5008.2767	CTTTATTTTCAGATCATATCTCTAAGCTTSA AGTGGACTCACAAACAATTT
703180	2301566	BsaBI_NBstNBI	TSAAGCTTAGAGATTA	C	4984.2517	CTTTATTTTCAGATCATATCTCTAAGCTTSA AGTGGACTCACAAACAATTT
703180	2301566	BsaBI_NBstNBI	TSAAGCTTAGAGATTA	G	5024.2761	CTTTATTTTCAGATCATATCTCTAAGCTTSA AGTGGACTCACAAACAATTT
703180	2301566	BsaBI_NBstNBI	TSAAGCTTAGAGATTA	T	4999.2633	CTTTATTTTCAGATCATATCTCTAAGCTTSA AGTGGACTCACAAACAATTT
706993		NBstNBI_BclI	AACSGCAAAGTTGATC	A	4978.2535	AAATGCATCAGAGTCTCTTAAACSGCAAAGT TGATCAAAACAGAAGAA
706993		NBstNBI_BclI	AACSGCAAAGTTGATC	C	4954.2285	AAATGCATCAGAGTCTCTTAAACSGCAAAGT TGATCAAAACAGAAGAA
706993		NBstNBI_BclI	AACSGCAAAGTTGATC	G	4994.2529	AAATGCATCAGAGTCTCTTAAACSGCAAAGT TGATCAAAACAGAAGAA
706993		NBstNBI_BclI	AACSGCAAAGTTGATC	T	4969.2401	AAATGCATCAGAGTCTCTTAAACSGCAAAGT TGATCAAAACAGAAGAA
708716	2305783	NBstNBI_BsmI	TAGSAAAGAATG	A	3806.5031	TAGAAAGGCAGAGTCCAGATAGSAAAGAA TGCCTCAGTTAAGT
708716	2305783	NBstNBI_BsmI	TAGSAAAGAATG	C	3782.4781	TAGAAAGGCAGAGTCCAGATAGSAAAGAA TGCCTCAGTTAAGT
708716	2305783	NBstNBI_BsmI	TAGSAAAGAATG	G	3822.5025	TAGAAAGGCAGAGTCCAGATAGSAAAGAA TGCCTCAGTTAAGT
708716	2305783	NBstNBI_BsmI	TAGSAAAGAATG	T	3797.4897	TAGAAAGGCAGAGTCCAGATAGSAAAGAA TGCCTCAGTTAAGT

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713146	2713966	BsrDI_NBstNBI	CCCATTTSCCCAAAC	A	4520.9456	GATATAGAGAGCAATGTTGTTTGGGSAAG TGGGCACAGACTCCATGCTAAAG
713146	2713966	BsrDI_NBstNBI	CCCATTTSCCCAAAC	C	4496.9206	GATATAGAGAGCAATGTTGTTTGGGSAAG TGGGCACAGACTCCATGCTAAAG
713146	2713966	BsrDI_NBstNBI	CCCATTTSCCCAAAC	G	4536.945	GATATAGAGAGCAATGTTGTTTGGGSAAG TGGGCACAGACTCCATGCTAAAG
713146	2713966	BsrDI_NBstNBI	CCCATTTSCCCAAAC	T	4511.9322	GATATAGAGAGCAATGTTGTTTGGGSAAG TGGGCACAGACTCCATGCTAAAG
713961	2309690	NBstNBI_BsrDI	SGCCATAGCAATG	A	4047.6378	GTGCCCAGTAGAGTCTAAASGCCATAGCA ATGTGAAACTCCATC
713961	2309690	NBstNBI_BsrDI	SGCCATAGCAATG	C	4023.6128	GTGCCCAGTAGAGTCTAAASGCCATAGCA ATGTGAAACTCCATC
713961	2309690	NBstNBI_BsrDI	SGCCATAGCAATG	G	4063.6372	GTGCCCAGTAGAGTCTAAASGCCATAGCA ATGTGAAACTCCATC
713961	2309690	NBstNBI_BsrDI	SGCCATAGCAATG	T	4038.6244	GTGCCCAGTAGAGTCTAAASGCCATAGCA ATGTGAAACTCCATC
714626	2310176	NBstNBI	SAGGTGACAGA	A	3494.2812	CTTTTGTGAGAGTCCGCGTCTGTACCT SGTGTGACTCATCCATTCTC
714626	2310176	NBstNBI	SAGGTGACAGA	C	3470.2562	CTTTTGTGAGAGTCCGCGTCTGTACCT SGTGTGACTCATCCATTCTC
714626	2310176	NBstNBI	SAGGTGACAGA	G	3510.2806	CTTTTGTGAGAGTCCGCGTCTGTACCT SGTGTGACTCATCCATTCTC
714626	2310176	NBstNBI	SAGGTGACAGA	T	3485.2678	CTTTTGTGAGAGTCCGCGTCTGTACCT SGTGTGACTCATCCATTCTC
714626	2310176	NBstNBI	TCTGTACACTS	A	3347.1678	CTTTTGTGAGAGTCCGCGTCTGTACCT SGTGTGACTCATCCATTCTC
714626	2310176	NBstNBI	TCTGTACACTS	C	3323.1428	CTTTTGTGAGAGTCCGCGTCTGTACCT SGTGTGACTCATCCATTCTC
714626	2310176	NBstNBI	TCTGTACACTS	G	3363.1672	CTTTTGTGAGAGTCCGCGTCTGTACCT SGTGTGACTCATCCATTCTC
714626	2310176	NBstNBI	TCTGTACACTS	T	3338.1544	CTTTTGTGAGAGTCCGCGTCTGTACCT SGTGTGACTCATCCATTCTC
718101	2312477	NBstNBI_BsrI	GASTAGAGGACTG	A	4127.6866	TTGTAGATATGAGTCTTTAGASTAGAGGAC TGGATGGCTAAAGA

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
718101	2312477	NBstNBI_BsrI	GASTAGAGGACTG	C	4103.6616	TTGTAGATATGAGTCTTTAGASTAGAGGAC TGGATGGCTAAAGA
718101	2312477	NBstNBI_BsrI	GASTAGAGGACTG	G	4143.686	TTGTAGATATGAGTCTTTAGASTAGAGGAC TGGATGGCTAAAGA
718101	2312477	NBstNBI_BsrI	GASTAGAGGACTG	T	4118.6732	TTGTAGATATGAGTCTTTAGASTAGAGGAC TGGATGGCTAAAGA
719650	2313537	NBstNBI_BsrI	GSGTACCACCTG	A	3710.4031	ATTGTTCTGGGAGTCAGATGSGCTACCAC TGGCCACAAGATC
719650	2313537	NBstNBI_BsrI	GSGTACCACCTG	C	3686.3781	ATTGTTCTGGGAGTCAGATGSGCTACCAC TGGCCACAAGATC
719650	2313537	NBstNBI_BsrI	GSGTACCACCTG	G	3726.4025	ATTGTTCTGGGAGTCAGATGSGCTACCAC TGGCCACAAGATC
719650	2313537	NBstNBI_BsrI	GSGTACCACCTG	T	3701.3897	ATTGTTCTGGGAGTCAGATGSGCTACCAC TGGCCACAAGATC
729092	2320006	BsmI_NBstNBI	ATCSCAGG	A	2498.6283	TTTTATTGGGGAATGCTCCTGSGATCAATG ACTCACCTATTGTG
729092	2320006	BsmI_NBstNBI	ATCSCAGG	C	2474.6033	TTTTATTGGGGAATGCTCCTGSGATCAATG ACTCACCTATTGTG
729092	2320006	BsmI_NBstNBI	ATCSCAGG	G	2514.6277	TTTTATTGGGGAATGCTCCTGSGATCAATG ACTCACCTATTGTG
729092	2320006	BsmI_NBstNBI	ATCSCAGG	T	2489.6149	TTTTATTGGGGAATGCTCCTGSGATCAATG ACTCACCTATTGTG
732525	2322391	BsrDI_NBstNBI	GGCSAGGTGCTACAG	A	4722.0554	CCCTTGCCATGCAATGCCCTGTAGCACCT SGCCCTGGGACTCCCCCGAGTC
732525	2322391	BsrDI_NBstNBI	GGCSAGGTGCTACAG	C	4698.0304	CCCTTGCCATGCAATGCCCTGTAGCACCT SGCCCTGGGACTCCCCCGAGTC
732525	2322391	BsrDI_NBstNBI	GGCSAGGTGCTACAG	G	4738.0548	CCCTTGCCATGCAATGCCCTGTAGCACCT SGCCCTGGGACTCCCCCGAGTC
732525	2322391	BsrDI_NBstNBI	GGCSAGGTGCTACAG	T	4713.042	CCCTTGCCATGCAATGCCCTGTAGCACCT SGCCCTGGGACTCCCCCGAGTC
738172	2326616	NBstNBI_BsrI	TCTGTACCCASACTG	A	4881.1657	TTTTGAACCAGAGTCTCACTCTGTACACCA SACTGGAGTGAATGGC
738172	2326616	NBstNBI_BsrI	TCTGTACCCASACTG	C	4857.1407	TTTTGAACCAGAGTCTCACTCTGTACACCA SACTGGAGTGAATGGC

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738172	2326616	NBstNBI_Bsrl	TCTGTCACCCASACTG	G	4897.1651	TTTTGAACCAGAGTCTCACTCTGTCAACCCA SACTGGAGTGAATGGC
738172	2326616	NBstNBI_Bsrl	TCTGTCACCCASACTG	T	4872.1523	TTTTGAACCAGAGTCTCACTCTGTCAACCCA SACTGGAGTGAATGGC
738335	2326753	NBstNBI_Bsrl	SAGGAACACTG	A	3454.2568	GAGAGTTGGGAGTCACTCTSAGGAACACT GGAGAATGGATGC
738335	2326753	NBstNBI_Bsrl	SAGGAACACTG	C	3430.2318	GAGAGTTGGGAGTCACTCTSAGGAACACT GGAGAATGGATGC
738335	2326753	NBstNBI_Bsrl	SAGGAACACTG	G	3470.2562	GAGAGTTGGGAGTCACTCTSAGGAACACT GGAGAATGGATGC
738335	2326753	NBstNBI_Bsrl	SAGGAACACTG	T	3445.2434	GAGAGTTGGGAGTCACTCTSAGGAACACT GGAGAATGGATGC
739215	2327318	BsmI_NBstNBI	GSGCTTAATACAGCA	A	4665.0438	AGTGGTTTTGAATGCCCTGCTGTATTAAGC SCAAACGACTCTATCTAGCTT
739215	2327318	BsmI_NBstNBI	GSGCTTAATACAGCA	C	4641.0188	AGTGGTTTTGAATGCCCTGCTGTATTAAGC SCAAACGACTCTATCTAGCTT
739215	2327318	BsmI_NBstNBI	GSGCTTAATACAGCA	G	4681.0432	AGTGGTTTTGAATGCCCTGCTGTATTAAGC SCAAACGACTCTATCTAGCTT
739215	2327318	BsmI_NBstNBI	GSGCTTAATACAGCA	T	4656.0304	AGTGGTTTTGAATGCCCTGCTGTATTAAGC SCAAACGACTCTATCTAGCTT
739413	2327470	NBstNBI	AGACTTGSTGCCA	A	4038.6244	CTCTATACTAGAGTCTATAAGACTTGSTGC CAAATAGACTCACITTTGGTA
739413	2327470	NBstNBI	AGACTTGSTGCCA	C	4014.5994	CTCTATACTAGAGTCTATAAGACTTGSTGC CAAATAGACTCACITTTGGTA
739413	2327470	NBstNBI	AGACTTGSTGCCA	G	4054.6238	CTCTATACTAGAGTCTATAAGACTTGSTGC CAAATAGACTCACITTTGGTA
739413	2327470	NBstNBI	AGACTTGSTGCCA	T	4029.611	CTCTATACTAGAGTCTATAAGACTTGSTGC CAAATAGACTCACITTTGGTA
739413	2327470	NBstNBI	TGGCASCAGTCT	A	4038.6244	CTCTATACTAGAGTCTATAAGACTTGSTGC CAAATAGACTCACITTTGGTA
739413	2327470	NBstNBI	TGGCASCAGTCT	C	4014.5994	CTCTATACTAGAGTCTATAAGACTTGSTGC CAAATAGACTCACITTTGGTA
739413	2327470	NBstNBI	TGGCASCAGTCT	G	4054.6238	CTCTATACTAGAGTCTATAAGACTTGSTGC CAAATAGACTCACITTTGGTA

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739413	2327470	NBstNBI	TGGCASCAGTCT	T	4029.611	CTCTATAGAGTCTATAAGACTTGSTGC CAATAGACTCACITTTGGTA
739432	2327486	Bsrl_NBstNBI	AGAGCATCTGTTTGGSC	A	4976.2261	GTTGAAGGAAGTGGGSCAAACAGATGC TCTGCCGACTCCCTGACTCCT
739432	2327486	Bsrl_NBstNBI	AGAGCATCTGTTTGGSC	C	4952.2011	GTTGAAGGAAGTGGGSCAAACAGATGC TCTGCCGACTCCCTGACTCCT
739432	2327486	Bsrl_NBstNBI	AGAGCATCTGTTTGGSC	G	4992.2255	GTTGAAGGAAGTGGGSCAAACAGATGC TCTGCCGACTCCCTGACTCCT
739432	2327486	Bsrl_NBstNBI	AGAGCATCTGTTTGGSC	T	4967.2127	GTTGAAGGAAGTGGGSCAAACAGATGC TCTGCCGACTCCCTGACTCCT
742229	2329246	BsaBI_NBstNBI	TTTGCSGATAT	A	3426.2288	CTTTATTCGGATTAAATATCSGCAAAAGTAT GACTCAGATAAAGCC
742229	2329246	BsaBI_NBstNBI	TTTGCSGATAT	C	3402.2038	CTTTATTCGGATTAAATATCSGCAAAAGTAT GACTCAGATAAAGCC
742229	2329246	BsaBI_NBstNBI	TTTGCSGATAT	G	3442.2282	CTTTATTCGGATTAAATATCSGCAAAAGTAT GACTCAGATAAAGCC
742229	2329246	BsaBI_NBstNBI	TTTGCSGATAT	T	3417.2154	CTTTATTCGGATTAAATATCSGCAAAAGTAT GACTCAGATAAAGCC
742347	2717951	Bsrl_NBstNBI	ASAGCTGTTTGG	A	3780.4507	TGTTGGCCAGACTGGTCCAAACAGCTSTT CTTGACTCCCATTGTGAG
742347	2717951	Bsrl_NBstNBI	ASAGCTGTTTGG	C	3756.4257	TGTTGGCCAGACTGGTCCAAACAGCTSTT CTTGACTCCCATTGTGAG
742347	2717951	Bsrl_NBstNBI	ASAGCTGTTTGG	G	3796.4501	TGTTGGCCAGACTGGTCCAAACAGCTSTT CTTGACTCCCATTGTGAG
742347	2717951	Bsrl_NBstNBI	ASAGCTGTTTGG	T	3771.4373	TGTTGGCCAGACTGGTCCAAACAGCTSTT CTTGACTCCCATTGTGAG
748333	2333641	NBstNBI_Bsrl	AATSTGGAACCTG	A	3773.4647	CCCTGACCATGAGTCCCTGAAATSTGGAAC TGGAATATCTTGAT
748333	2333641	NBstNBI_Bsrl	AATSTGGAACCTG	C	3749.4397	CCCTGACCATGAGTCCCTGAAATSTGGAAC TGGAATATCTTGAT
748333	2333641	NBstNBI_Bsrl	AATSTGGAACCTG	G	3789.4641	CCCTGACCATGAGTCCCTGAAATSTGGAAC TGGAATATCTTGAT
748333	2333641	NBstNBI_Bsrl	AATSTGGAACCTG	T	3764.4513	CCCTGACCATGAGTCCCTGAAATSTGGAAC TGGAATATCTTGAT

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752262	2336642	BsrDI_NBstNBI	SATGTGGCAAGC	A	3774.4525	AAATAAGACTGCAATGATGCTTGCCACATS GATTGACTCTTCCITTCGC
752262	2336642	BsrDI_NBstNBI	SATGTGGCAAGC	C	3750.4275	AAATAAGACTGCAATGATGCTTGCCACATS GATTGACTCTTCCITTCGC
752262	2336642	BsrDI_NBstNBI	SATGTGGCAAGC	G	3790.4519	AAATAAGACTGCAATGATGCTTGCCACATS GATTGACTCTTCCITTCGC
752262	2336642	BsrDI_NBstNBI	SATGTGGCAAGC	T	3765.4391	AAATAAGACTGCAATGATGCTTGCCACATS GATTGACTCTTCCITTCGC
752564	2336851	NBstNBI	CATGACAGCSGTTGAC	A	4970.2279	GGCAGATCTAGAGTCCCAAGTCAACSGCT GTCATGGCCTGACTCGTGGTACAGG
752564	2336851	NBstNBI	CATGACAGCSGTTGAC	C	4946.2029	GGCAGATCTAGAGTCCCAAGTCAACSGCT GTCATGGCCTGACTCGTGGTACAGG
752564	2336851	NBstNBI	CATGACAGCSGTTGAC	G	4986.2273	GGCAGATCTAGAGTCCCAAGTCAACSGCT GTCATGGCCTGACTCGTGGTACAGG
752564	2336851	NBstNBI	CATGACAGCSGTTGAC	T	4961.2145	GGCAGATCTAGAGTCCCAAGTCAACSGCT GTCATGGCCTGACTCGTGGTACAGG
752564	2336851	NBstNBI	GTC AACSGCTGTCATG	A	4961.2145	GGCAGATCTAGAGTCCCAAGTCAACSGCT GTCATGGCCTGACTCGTGGTACAGG
752564	2336851	NBstNBI	GTC AACSGCTGTCATG	C	4937.1895	GGCAGATCTAGAGTCCCAAGTCAACSGCT GTCATGGCCTGACTCGTGGTACAGG
752564	2336851	NBstNBI	GTC AACSGCTGTCATG	G	4977.2139	GGCAGATCTAGAGTCCCAAGTCAACSGCT GTCATGGCCTGACTCGTGGTACAGG
752564	2336851	NBstNBI	GTC AACSGCTGTCATG	T	4952.2011	GGCAGATCTAGAGTCCCAAGTCAACSGCT GTCATGGCCTGACTCGTGGTACAGG
753522	2337575	Bsrl_NBstNBI	TGGGGAS	A	2265.4674	CCTGTACCTCACTGGGSTCCCCAGACGGA CTCAGCTCCAGGT
753522	2337575	Bsrl_NBstNBI	TGGGGAS	C	2241.4424	CCTGTACCTCACTGGGSTCCCCAGACGGA CTCAGCTCCAGGT
753522	2337575	Bsrl_NBstNBI	TGGGGAS	G	2281.4668	CCTGTACCTCACTGGGSTCCCCAGACGGA CTCAGCTCCAGGT
753522	2337575	Bsrl_NBstNBI	TGGGGAS	T	2256.454	CCTGTACCTCACTGGGSTCCCCAGACGGA CTCAGCTCCAGGT
758510		Bsrl_NBstNBI	GATGATTAAS	A	3155.0709	TCTTATGCCAACTGGTSTTAATCATCAAAAT GACTCCATAGTAAGA

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758510		BsrI_NBstNBI	GATGATTAAS	C	3131.0459	TCTTATGCCAACTGGTSTTAATCATCAAAT GACTCCATAGTAAGA
758510		BsrI_NBstNBI	GATGATTAAS	G	3171.0703	TCTTATGCCAACTGGTSTTAATCATCAAAT GACTCCATAGTAAGA
758510		BsrI_NBstNBI	GATGATTAAS	T	3146.0575	TCTTATGCCAACTGGTSTTAATCATCAAAT GACTCCATAGTAAGA
765000	2344993	NBstNBI	CAAGCAAGCASATCA	A	4643.0462	TGAAATATCTGAGTCTGGTTGATSTGCTTG CTTGACCTGACTCTTCAAACCTGT
765000	2344993	NBstNBI	CAAGCAAGCASATCA	C	4619.0212	TGAAATATCTGAGTCTGGTTGATSTGCTTG CTTGACCTGACTCTTCAAACCTGT
765000	2344993	NBstNBI	CAAGCAAGCASATCA	G	4659.0456	TGAAATATCTGAGTCTGGTTGATSTGCTTG CTTGACCTGACTCTTCAAACCTGT
765000	2344993	NBstNBI	CAAGCAAGCASATCA	T	4634.0328	TGAAATATCTGAGTCTGGTTGATSTGCTTG CTTGACCTGACTCTTCAAACCTGT
765000	2344993	NBstNBI	TGATSTGCTTGCTTG	A	4669.0146	TGAAATATCTGAGTCTGGTTGATSTGCTTG CTTGACCTGACTCTTCAAACCTGT
765000	2344993	NBstNBI	TGATSTGCTTGCTTG	C	4644.9896	TGAAATATCTGAGTCTGGTTGATSTGCTTG CTTGACCTGACTCTTCAAACCTGT
765000	2344993	NBstNBI	TGATSTGCTTGCTTG	G	4685.014	TGAAATATCTGAGTCTGGTTGATSTGCTTG CTTGACCTGACTCTTCAAACCTGT
765000	2344993	NBstNBI	TGATSTGCTTGCTTG	T	4660.0012	TGAAATATCTGAGTCTGGTTGATSTGCTTG CTTGACCTGACTCTTCAAACCTGT
786866	2360458	NBstNBI_BsmI	GGTTGCCSGAATG	A	4094.6482	GGTCTGAGTAGAGTCAGTCGGTTGCCSGA ATGCAAAAAGTCTGAA
786866	2360458	NBstNBI_BsmI	GGTTGCCSGAATG	C	4070.6232	GGTCTGAGTAGAGTCAGTCGGTTGCCSGA ATGCAAAAAGTCTGAA
786866	2360458	NBstNBI_BsmI	GGTTGCCSGAATG	G	4110.6476	GGTCTGAGTAGAGTCAGTCGGTTGCCSGA ATGCAAAAAGTCTGAA
786866	2360458	NBstNBI_BsmI	GGTTGCCSGAATG	T	4085.6348	GGTCTGAGTAGAGTCAGTCGGTTGCCSGA ATGCAAAAAGTCTGAA
787454	2360842	BclI_NBstNBI	GSTGATC	A	2200.4302	CTCAGGACACTGATCASCCTTAAGACTCAAT TCTGATA
787454	2360842	BclI_NBstNBI	GSTGATC	C	2176.4052	CTCAGGACACTGATCASCCTTAAGACTCAAT TCTGATA

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787454	2360842	BclI_NBstNBI	GSTGATC	G	2216.4296	CTCAGGACACTGATCASCCTTAAGACTCAAT TCTGATA
787454	2360842	BclI_NBstNBI	GSTGATC	T	2191.4168	CTCAGGACACTGATCASCCTTAAGACTCAAT TCTGATA
803810	2091896	BclI_NBstNBI	AATAGCASAATTGATC	A	4977.2657	GCTCACTAATTGATCAATTSTGCTATTAAAG AGACTCTGATCCATTC
803810	2091896	BclI_NBstNBI	AATAGCASAATTGATC	C	4953.2407	GCTCACTAATTGATCAATTSTGCTATTAAAG AGACTCTGATCCATTC
803810	2091896	BclI_NBstNBI	AATAGCASAATTGATC	G	4993.2651	GCTCACTAATTGATCAATTSTGCTATTAAAG AGACTCTGATCCATTC
803810	2091896	BclI_NBstNBI	AATAGCASAATTGATC	T	4968.2523	GCTCACTAATTGATCAATTSTGCTATTAAAG AGACTCTGATCCATTC
805425		BsmI_NBstNBI	AATAACATGTATTTTS	A	4958.2511	TTTTTTTTGAATGCASAAAATACATGTTA TTCCCTGACTCTCCTTTTGAT
805425		BsmI_NBstNBI	AATAACATGTATTTTS	C	4934.2261	TTTTTTTTGAATGCASAAAATACATGTTA TTCCCTGACTCTCCTTTTGAT
805425		BsmI_NBstNBI	AATAACATGTATTTTS	G	4974.2505	TTTTTTTTGAATGCASAAAATACATGTTA TTCCCTGACTCTCCTTTTGAT
805425		BsmI_NBstNBI	AATAACATGTATTTTS	T	4949.2377	TTTTTTTTGAATGCASAAAATACATGTTA TTCCCTGACTCTCCTTTTGAT
810718	2096899	NBstNBI	CTSGGGAG	A	2554.6521	CAGGCTGCCGGAGTCTCCACTSGGGAGA TTGGACTCTAACAGAGTA
810718	2096899	NBstNBI	CTSGGGAG	C	2530.6271	CAGGCTGCCGGAGTCTCCACTSGGGAGA TTGGACTCTAACAGAGTA
810718	2096899	NBstNBI	CTSGGGAG	G	2570.6515	CAGGCTGCCGGAGTCTCCACTSGGGAGA TTGGACTCTAACAGAGTA
810718	2096899	NBstNBI	CTSGGGAG	T	2545.6387	CAGGCTGCCGGAGTCTCCACTSGGGAGA TTGGACTCTAACAGAGTA
810718	2096899	NBstNBI	CTCCCSAG	A	2434.5789	CAGGCTGCCGGAGTCTCCACTSGGGAGA TTGGACTCTAACAGAGTA
810718	2096899	NBstNBI	CTCCCSAG	C	2410.5539	CAGGCTGCCGGAGTCTCCACTSGGGAGA TTGGACTCTAACAGAGTA
810718	2096899	NBstNBI	CTCCCSAG	G	2450.5783	CAGGCTGCCGGAGTCTCCACTSGGGAGA TTGGACTCTAACAGAGTA

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810718	2096899	NBstNBI	CTCCCSAG	T	2425.5655	CAGGCTGCCGGAGTCTCCACTSGGGAGA TTGGACTCTAACAGAGTA
811250	2097340	NBstNBI_BsrI	STGTTCACTG	A	3098.0075	ACAATAATTGGAGTCAGCASTGTTCACTG GACAAAAGTCAG
811250	2097340	NBstNBI_BsrI	STGTTCACTG	C	3073.9825	ACAATAATTGGAGTCAGCASTGTTCACTG GACAAAAGTCAG
811250	2097340	NBstNBI_BsrI	STGTTCACTG	G	3114.0069	ACAATAATTGGAGTCAGCASTGTTCACTG GACAAAAGTCAG
811250	2097340	NBstNBI_BsrI	STGTTCACTG	T	3088.9941	ACAATAATTGGAGTCAGCASTGTTCACTG GACAAAAGTCAG
811617	2097599	NBstNBI	ACSCATTGGATT	A	4028.6232	TGTGCTGTAAGAGTCATGTACSCATTGGA TTTTGAAGACTCAGAAATTTTAA
811617	2097599	NBstNBI	ACSCATTGGATT	C	4004.5982	TGTGCTGTAAGAGTCATGTACSCATTGGA TTTTGAAGACTCAGAAATTTTAA
811617	2097599	NBstNBI	ACSCATTGGATT	G	4044.6226	TGTGCTGTAAGAGTCATGTACSCATTGGA TTTTGAAGACTCAGAAATTTTAA
811617	2097599	NBstNBI	ACSCATTGGATT	T	4019.6098	TGTGCTGTAAGAGTCATGTACSCATTGGA TTTTGAAGACTCAGAAATTTTAA
811617	2097599	NBstNBI	AAATCCAATGSGT	A	4046.65	TGTGCTGTAAGAGTCATGTACSCATTGGA TTTTGAAGACTCAGAAATTTTAA
811617	2097599	NBstNBI	AAATCCAATGSGT	C	4022.625	TGTGCTGTAAGAGTCATGTACSCATTGGA TTTTGAAGACTCAGAAATTTTAA
811617	2097599	NBstNBI	AAATCCAATGSGT	G	4062.6494	TGTGCTGTAAGAGTCATGTACSCATTGGA TTTTGAAGACTCAGAAATTTTAA
811617	2097599	NBstNBI	AAATCCAATGSGT	T	4037.6366	TGTGCTGTAAGAGTCATGTACSCATTGGA TTTTGAAGACTCAGAAATTTTAA
816768	2101338	NBstNBI	TATTCTSATAGTTG	A	4347.8311	TAGGCCTGTGGAGTCAGACTATTCTSATA GTTGCTTTGACTCTGCTGCCCAT
816768	2101338	NBstNBI	TATTCTSATAGTTG	C	4323.8061	TAGGCCTGTGGAGTCAGACTATTCTSATA GTTGCTTTGACTCTGCTGCCCAT
816768	2101338	NBstNBI	TATTCTSATAGTTG	G	4363.8305	TAGGCCTGTGGAGTCAGACTATTCTSATA GTTGCTTTGACTCTGCTGCCCAT
816768	2101338	NBstNBI	TATTCTSATAGTTG	T	4338.8177	TAGGCCTGTGGAGTCAGACTATTCTSATA GTTGCTTTGACTCTGCTGCCCAT

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816768	2101338	NBstNBI	CAACTATSAGAATA	A	4343.8603	TAGGCCCTGTGGAGTCAGACTATTCTTSATA GTTGCTTTGACTCTGCTGCCCAT
816768	2101338	NBstNBI	CAACTATSAGAATA	C	4319.8353	TAGGCCCTGTGGAGTCAGACTATTCTTSATA GTTGCTTTGACTCTGCTGCCCAT
816768	2101338	NBstNBI	CAACTATSAGAATA	G	4359.8597	TAGGCCCTGTGGAGTCAGACTATTCTTSATA GTTGCTTTGACTCTGCTGCCCAT
816768	2101338	NBstNBI	CAACTATSAGAATA	T	4334.8469	TAGGCCCTGTGGAGTCAGACTATTCTTSATA GTTGCTTTGACTCTGCTGCCCAT
819731	2103431	NBstNBI_BsrI	GSGGATGAAACTG	A	4127.6866	TGGCATACTTGAGTCCTGAGSGGATGAAA CTGGACCAGCAGACA
819731	2103431	NBstNBI_BsrI	GSGGATGAAACTG	C	4103.6616	TGGCATACTTGAGTCCTGAGSGGATGAAA CTGGACCAGCAGACA
819731	2103431	NBstNBI_BsrI	GSGGATGAAACTG	G	4143.686	TGGCATACTTGAGTCCTGAGSGGATGAAA CTGGACCAGCAGACA
819731	2103431	NBstNBI_BsrI	GSGGATGAAACTG	T	4118.6732	TGGCATACTTGAGTCCTGAGSGGATGAAA CTGGACCAGCAGACA
823530	2106023	BsrDI_NBstNBI	TCTGAGAGGGS	A	3501.2672	GGACCTTGACAGCAATGTTSCCCTCTCAGA CAGAGACTCAATTTTACACA
823530	2106023	BsrDI_NBstNBI	TCTGAGAGGGS	C	3477.2422	GGACCTTGACAGCAATGTTSCCCTCTCAGA CAGAGACTCAATTTTACACA
823530	2106023	BsrDI_NBstNBI	TCTGAGAGGGS	G	3517.2666	GGACCTTGACAGCAATGTTSCCCTCTCAGA CAGAGACTCAATTTTACACA
823530	2106023	BsrDI_NBstNBI	TCTGAGAGGGS	T	3492.2538	GGACCTTGACAGCAATGTTSCCCTCTCAGA CAGAGACTCAATTTTACACA
823980	2728133	BsrI_NBstNBI	CTCCTATCCAS	A	3316.1568	AGATAACAACACACTGGASTGGATAGGAGTA CGGACTCTTCTACAAGA
823980	2728133	BsrI_NBstNBI	CTCCTATCCAS	C	3292.1318	AGATAACAACACACTGGASTGGATAGGAGTA CGGACTCTTCTACAAGA
823980	2728133	BsrI_NBstNBI	CTCCTATCCAS	G	3332.1562	AGATAACAACACACTGGASTGGATAGGAGTA CGGACTCTTCTACAAGA
823980	2728133	BsrI_NBstNBI	CTCCTATCCAS	T	3307.1434	AGATAACAACACACTGGASTGGATAGGAGTA CGGACTCTTCTACAAGA
825600	2728342	NBstNBI_BsrI	ATCAGAGCTSACTG	A	4351.8341	ACCTGGAGTGAGTCTAGAAATCAGAGGCTS ACTGGAGATGATCAGA

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825600	2728342	NBstNBI_BsrI	ATCAGAGCTSACTG	C	4327.8091	ACCTGGGAGTGAGTCTAGAATCAGAGGCTS ACTGGAGATGATCAGA
825600	2728342	NBstNBI_BsrI	ATCAGAGCTSACTG	G	4367.8335	ACCTGGGAGTGAGTCTAGAATCAGAGGCTS ACTGGAGATGATCAGA
825600	2728342	NBstNBI_BsrI	ATCAGAGCTSACTG	T	4342.8207	ACCTGGGAGTGAGTCTAGAATCAGAGGCTS ACTGGAGATGATCAGA
827614	2108862	NBstNBI_BclI	AATAGCAGAASTGATC	A	5002.2785	GAATGCATTAGAGTCTCCTAATAGCAGAA STGATCAAGTAGAAGAA
827614	2108862	NBstNBI_BclI	AATAGCAGAASTGATC	C	4978.2535	GAATGCATTAGAGTCTCCTAATAGCAGAA STGATCAAGTAGAAGAA
827614	2108862	NBstNBI_BclI	AATAGCAGAASTGATC	G	5018.2779	GAATGCATTAGAGTCTCCTAATAGCAGAA STGATCAAGTAGAAGAA
827614	2108862	NBstNBI_BclI	AATAGCAGAASTGATC	T	4993.2651	GAATGCATTAGAGTCTCCTAATAGCAGAA STGATCAAGTAGAAGAA
829117	2109646	BsrI_NBstNBI	TSTGTGC	A	2191.4168	ATTGATCACCACCTGGAGCACASAGAAAGA CTCTTAATCCAAA
829117	2109646	BsrI_NBstNBI	TSTGTGC	C	2167.3918	ATTGATCACCACCTGGAGCACASAGAAAGA CTCTTAATCCAAA
829117	2109646	BsrI_NBstNBI	TSTGTGC	G	2207.4162	ATTGATCACCACCTGGAGCACASAGAAAGA CTCTTAATCCAAA
829117	2109646	BsrI_NBstNBI	TSTGTGC	T	2182.4034	ATTGATCACCACCTGGAGCACASAGAAAGA CTCTTAATCCAAA
829757	2110124	NBstNBI	STCAGGGGCTGTGAA	A	4737.067	GAAGAAGCGGAGTCAGAAATTCACAGCC CCTGASGTCTGACTCTGAATCCTGG
829757	2110124	NBstNBI	STCAGGGGCTGTGAA	C	4713.042	GAAGAAGCGGAGTCAGAAATTCACAGCC CCTGASGTCTGACTCTGAATCCTGG
829757	2110124	NBstNBI	STCAGGGGCTGTGAA	G	4753.0664	GAAGAAGCGGAGTCAGAAATTCACAGCC CCTGASGTCTGACTCTGAATCCTGG
829757	2110124	NBstNBI	STCAGGGGCTGTGAA	T	4728.0536	GAAGAAGCGGAGTCAGAAATTCACAGCC CCTGASGTCTGACTCTGAATCCTGG
829757	2110124	NBstNBI	TTCACAGCCCCTGAS	A	4576.9694	GAAGAAGCGGAGTCAGAAATTCACAGCC CCTGASGTCTGACTCTGAATCCTGG
829757	2110124	NBstNBI	TTCACAGCCCCTGAS	C	4552.9444	GAAGAAGCGGAGTCAGAAATTCACAGCC CCTGASGTCTGACTCTGAATCCTGG

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
829757	2110124	NBstNBI	TTCACAGCCCCCTGAS	G	4592.9688	GAAGAAAGCGGAGTCCAGATTCAGAACATTCACAGCC CCTGASGTCGTGACTCTGAAATCCTGG
829757	2110124	NBstNBI	TTCACAGCCCCCTGAS	T	4567.956	GAAGAAAGCGGAGTCCAGATTCAGAACATTCACAGCC CCTGASGTCGTGACTCTGAAATCCTGG
833650	2112937	NBstNBI	GGSGTGA	A	2265.4674	ACCCAAGCTGGAGTCCAGTGGSGTGATCT CGACTCACTGTGACTT
833650	2112937	NBstNBI	GGSGTGA	C	2241.4424	ACCCAAGCTGGAGTCCAGTGGSGTGATCT CGACTCACTGTGACTT
833650	2112937	NBstNBI	GGSGTGA	G	2281.4668	ACCCAAGCTGGAGTCCAGTGGSGTGATCT CGACTCACTGTGACTT
833650	2112937	NBstNBI	GGSGTGA	T	2256.454	ACCCAAGCTGGAGTCCAGTGGSGTGATCT CGACTCACTGTGACTT
833650	2112937	NBstNBI	TCACSCC	A	2105.3698	ACCCAAGCTGGAGTCCAGTGGSGTGATCT CGACTCACTGTGACTT
833650	2112937	NBstNBI	TCACSCC	C	2081.3448	ACCCAAGCTGGAGTCCAGTGGSGTGATCT CGACTCACTGTGACTT
833650	2112937	NBstNBI	TCACSCC	G	2121.3692	ACCCAAGCTGGAGTCCAGTGGSGTGATCT CGACTCACTGTGACTT
833650	2112937	NBstNBI	TCACSCC	T	2096.3564	ACCCAAGCTGGAGTCCAGTGGSGTGATCT CGACTCACTGTGACTT
835985	2114686	NBstNBI	ACASTC	A	1840.2101	CTAAGAAGTGGAGTCCAGCCACASTCATCT GACTCCAAAGCCCCAC
835985	2114686	NBstNBI	ACASTC	C	1816.1851	CTAAGAAGTGGAGTCCAGCCACASTCATCT GACTCCAAAGCCCCAC
835985	2114686	NBstNBI	ACASTC	G	1856.2095	CTAAGAAGTGGAGTCCAGCCACASTCATCT GACTCCAAAGCCCCAC
835985	2114686	NBstNBI	ACASTC	T	1831.1967	CTAAGAAGTGGAGTCCAGCCACASTCATCT GACTCCAAAGCCCCAC
835985	2114686	NBstNBI	GASTGT	A	1911.2455	CTAAGAAGTGGAGTCCAGCCACASTCATCT GACTCCAAAGCCCCAC
835985	2114686	NBstNBI	GASTGT	C	1887.2205	CTAAGAAGTGGAGTCCAGCCACASTCATCT GACTCCAAAGCCCCAC
835985	2114686	NBstNBI	GASTGT	G	1927.2449	CTAAGAAGTGGAGTCCAGCCACASTCATCT GACTCCAAAGCCCCAC

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835985	2114686	NBstNBI	GASTGT	T	1902.2321	CTAAGAAAGTGGAGTCAGCCACASTCATCT GACTCCAAAGCCAC
843054	2119636	BsaBI_NBstNBI	CTSTCATGGATT	A	4019.6098	ATAGGCTTCAGATGTAAATCCATGASAGTC TGGACTCATGAATGTTG
843054	2119636	BsaBI_NBstNBI	CTSTCATGGATT	C	3995.5848	ATAGGCTTCAGATGTAAATCCATGASAGTC TGGACTCATGAATGTTG
843054	2119636	BsaBI_NBstNBI	CTSTCATGGATT	G	4035.6092	ATAGGCTTCAGATGTAAATCCATGASAGTC TGGACTCATGAATGTTG
843054	2119636	BsaBI_NBstNBI	CTSTCATGGATT	T	4010.5964	ATAGGCTTCAGATGTAAATCCATGASAGTC TGGACTCATGAATGTTG
846056	2732155	NBstNBI_Bsrl	CTTGAASGGGGACTG	A	4737.067	TGTTGTGCTGGAGTCAAGACTTGAASGGG GACTGGAGGAAGAGGAA
846056	2732155	NBstNBI_Bsrl	CTTGAASGGGGACTG	C	4713.042	TGTTGTGCTGGAGTCAAGACTTGAASGGG GACTGGAGGAAGAGGAA
846056	2732155	NBstNBI_Bsrl	CTTGAASGGGGACTG	G	4753.0664	TGTTGTGCTGGAGTCAAGACTTGAASGGG GACTGGAGGAAGAGGAA
846056	2732155	NBstNBI_Bsrl	CTTGAASGGGGACTG	T	4728.0536	TGTTGTGCTGGAGTCAAGACTTGAASGGG GACTGGAGGAAGAGGAA
848035	2733257	Bsrl_NBstNBI	AGGAASGCCAAGTTCT	A	4994.2529	CAGGTTACTGACTGGGAGAACTTGGCSTT CCTCCAGACTCCAGATATGAG
848035	2733257	Bsrl_NBstNBI	AGGAASGCCAAGTTCT	C	4970.2279	CAGGTTACTGACTGGGAGAACTTGGCSTT CCTCCAGACTCCAGATATGAG
848035	2733257	Bsrl_NBstNBI	AGGAASGCCAAGTTCT	G	5010.2523	CAGGTTACTGACTGGGAGAACTTGGCSTT CCTCCAGACTCCAGATATGAG
848035	2733257	Bsrl_NBstNBI	AGGAASGCCAAGTTCT	T	4985.2395	CAGGTTACTGACTGGGAGAACTTGGCSTT CCTCCAGACTCCAGATATGAG
853300	2736465	NBstNBI	TGGGCS	A	1912.2333	CAAGGAGAGAGAGTCACCTTGGGCSAGC TGACTCCCACCCACCC
853300	2736465	NBstNBI	TGGGCS	C	1888.2083	CAAGGAGAGAGAGTCACCTTGGGCSAGC TGACTCCCACCCACCC
853300	2736465	NBstNBI	TGGGCS	G	1928.2327	CAAGGAGAGAGAGTCACCTTGGGCSAGC TGACTCCCACCCACCC
853300	2736465	NBstNBI	TGGGCS	T	1903.2199	CAAGGAGAGAGAGTCACCTTGGGCSAGC TGACTCCCACCCACCC

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853300	2736465	NBstNBI	SGCCCA	A	1841.1979	CAAGGAGAGAGAGTCACCTTGGGCSAGC TGACTCCCACCCACCC
853300	2736465	NBstNBI	SGCCCA	C	1817.1729	CAAGGAGAGAGAGTCACCTTGGGCSAGC TGACTCCCACCCACCC
853300	2736465	NBstNBI	SGCCCA	G	1857.1973	CAAGGAGAGAGAGTCACCTTGGGCSAGC TGACTCCCACCCACCC
853300	2736465	NBstNBI	SGCCCA	T	1832.1845	CAAGGAGAGAGAGTCACCTTGGGCSAGC TGACTCCCACCCACCC
855271	2737580	NBstNBI	TTCSTT	A	1837.1949	ACCAGGATTTGAGTCTGTAAASGAAAAGTG GACTCATGGCTTCCT
855271	2737580	NBstNBI	TTCSTT	C	1813.1699	ACCAGGATTTGAGTCTGTAAASGAAAAGTG GACTCATGGCTTCCT
855271	2737580	NBstNBI	TTCSTT	G	1853.1943	ACCAGGATTTGAGTCTGTAAASGAAAAGTG GACTCATGGCTTCCT
855271	2737580	NBstNBI	TTCSTT	T	1828.1815	ACCAGGATTTGAGTCTGTAAASGAAAAGTG GACTCATGGCTTCCT
855271	2737580	NBstNBI	AASGAA	A	1913.2729	ACCAGGATTTGAGTCTGTAAASGAAAAGTG GACTCATGGCTTCCT
855271	2737580	NBstNBI	AASGAA	C	1889.2479	ACCAGGATTTGAGTCTGTAAASGAAAAGTG GACTCATGGCTTCCT
855271	2737580	NBstNBI	AASGAA	G	1929.2723	ACCAGGATTTGAGTCTGTAAASGAAAAGTG GACTCATGGCTTCCT
855271	2737580	NBstNBI	AASGAA	T	1904.2595	ACCAGGATTTGAGTCTGTAAASGAAAAGTG GACTCATGGCTTCCT
855686	2737852	NBstNBI_Bsrl	AAGASGGGTTAACTG	A	4745.0926	TGAGGTTGGGGAGTCTGGAAGASGGGT TAACTGGCTATGATATTG
855686	2737852	NBstNBI_Bsrl	AAGASGGGTTAACTG	C	4721.0676	TGAGGTTGGGGAGTCTGGAAGASGGGT TAACTGGCTATGATATTG
855686	2737852	NBstNBI_Bsrl	AAGASGGGTTAACTG	G	4761.092	TGAGGTTGGGGAGTCTGGAAGASGGGT TAACTGGCTATGATATTG
855686	2737852	NBstNBI_Bsrl	AAGASGGGTTAACTG	T	4736.0792	TGAGGTTGGGGAGTCTGGAAGASGGGT TAACTGGCTATGATATTG
855734	2737884	BsmI_NBstNBI	TCTTGCCACCATACS	A	4551.9566	GAAGTCTGGGAATGCASGTATGTTGGCA AGACTCTGACTCCAAATAGTAA

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855734	2737884	BsmI_NBstNBI	TCTTGCCACCATAACS	C	4527.9316	GAAGTGTGGGAATGCASGTATGGTGGCA AGACTCTGACTCCAAATAGTAA
855734	2737884	BsmI_NBstNBI	TCTTGCCACCATAACS	G	4567.956	GAAGTGTGGGAATGCASGTATGGTGGCA AGACTCTGACTCCAAATAGTAA
855734	2737884	BsmI_NBstNBI	TCTTGCCACCATAACS	T	4542.9432	GAAGTGTGGGAATGCASGTATGGTGGCA AGACTCTGACTCCAAATAGTAA
855778	2737901	NBstNBI_BsrI	TAGTSTTGTAAGT	A	4059.6342	TTGAGATTGAGAGTCTCTGTAGTSTTGTA TGGGAAAATATACA
855778	2737901	NBstNBI_BsrI	TAGTSTTGTAAGT	C	4035.6092	TTGAGATTGAGAGTCTCTGTAGTSTTGTA TGGGAAAATATACA
855778	2737901	NBstNBI_BsrI	TAGTSTTGTAAGT	G	4075.6336	TTGAGATTGAGAGTCTCTGTAGTSTTGTA TGGGAAAATATACA
855778	2737901	NBstNBI_BsrI	TAGTSTTGTAAGT	T	4050.6208	TTGAGATTGAGAGTCTCTGTAGTSTTGTA TGGGAAAATATACA
856356	2903380	NBstNBI_BsrI	CGSGCAAAGGCACTG	A	4691.0444	AAGGCCAAAAGAGTCATTTTCGSGCAAAGG CACTGGGATGCTCTATT
856356	2903380	NBstNBI_BsrI	CGSGCAAAGGCACTG	C	4667.0194	AAGGCCAAAAGAGTCATTTTCGSGCAAAGG CACTGGGATGCTCTATT
856356	2903380	NBstNBI_BsrI	CGSGCAAAGGCACTG	G	4707.0438	AAGGCCAAAAGAGTCATTTTCGSGCAAAGG CACTGGGATGCTCTATT
856356	2903380	NBstNBI_BsrI	CGSGCAAAGGCACTG	T	4682.031	AAGGCCAAAAGAGTCATTTTCGSGCAAAGG CACTGGGATGCTCTATT
864016	2904887	BsrI_NBstNBI	AGTTTGSG	A	2544.6509	TGTTGTCCAGACTGGTCSCAAACCTCCTAG ACTCAAGCAATACA
864016	2904887	BsrI_NBstNBI	AGTTTGSG	C	2520.6259	TGTTGTCCAGACTGGTCSCAAACCTCCTAG ACTCAAGCAATACA
864016	2904887	BsrI_NBstNBI	AGTTTGSG	G	2560.6503	TGTTGTCCAGACTGGTCSCAAACCTCCTAG ACTCAAGCAATACA
864016	2904887	BsrI_NBstNBI	AGTTTGSG	T	2535.6375	TGTTGTCCAGACTGGTCSCAAACCTCCTAG ACTCAAGCAATACA
866087	2743875	BsrI_NBstNBI	TTTATTTSCGAAGTTC	A	4941.2121	CTGGGGCAAAAAGTGGGGAACCTTCGSAAT AAAGGCTGACTCAACCACAGAG
866087	2743875	BsrI_NBstNBI	TTTATTTSCGAAGTTC	C	4917.1871	CTGGGGCAAAAAGTGGGGAACCTTCGSAAT AAAGGCTGACTCAACCACAGAG

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866087	2743875	Bsrl_NBstNBI	TTTATTTSCGAAGTTC	G	4957.2115	CTGGGCAAACTGGGAACTTCGSAAT AAAGCTGACTCAACCACAGAG
866087	2743875	Bsrl_NBstNBI	TTTATTTSCGAAGTTC	T	4932.1987	CTGGGCAAACTGGGAACTTCGSAAT AAAGCTGACTCAACCACAGAG
868183	2745127	NBstNBI_Bsrl	TCSTCTGGAGACTG	A	4358.8201	CATGAAAGTTGAGTCTCCTTCSTCTGGAG ACTGGACAGTGTGGAT
868183	2745127	NBstNBI_Bsrl	TCSTCTGGAGACTG	C	4334.7951	CATGAAAGTTGAGTCTCCTTCSTCTGGAG ACTGGACAGTGTGGAT
868183	2745127	NBstNBI_Bsrl	TCSTCTGGAGACTG	G	4374.8195	CATGAAAGTTGAGTCTCCTTCSTCTGGAG ACTGGACAGTGTGGAT
868183	2745127	NBstNBI_Bsrl	TCSTCTGGAGACTG	T	4349.8067	CATGAAAGTTGAGTCTCCTTCSTCTGGAG ACTGGACAGTGTGGAT
872489		NBstNBI_Bsml	AAGCASGAATG	A	3478.2818	TAAATTTCCAGAGTCCATTAAGCASCAGATG CAGGTCATCAGT
872489		NBstNBI_Bsml	AAGCASGAATG	C	3454.2568	TAAATTTCCAGAGTCCATTAAGCASCAGATG CAGGTCATCAGT
872489		NBstNBI_Bsml	AAGCASGAATG	G	3494.2812	TAAATTTCCAGAGTCCATTAAGCASCAGATG CAGGTCATCAGT
872489		NBstNBI_Bsml	AAGCASGAATG	T	3469.2684	TAAATTTCCAGAGTCCATTAAGCASCAGATG CAGGTCATCAGT
883307	2753825	NBstNBI	TTGTGSGATCTCAG	A	4703.0408	TGAGGTTCTAGAGTCTCCTTTGTGSGAT CTCAGCCCCGACTCCACCTCTGCG
883307	2753825	NBstNBI	TTGTGSGATCTCAG	C	4679.0158	TGAGGTTCTAGAGTCTCCTTTGTGSGAT CTCAGCCCCGACTCCACCTCTGCG
883307	2753825	NBstNBI	TTGTGSGATCTCAG	G	4719.0402	TGAGGTTCTAGAGTCTCCTTTGTGSGAT CTCAGCCCCGACTCCACCTCTGCG
883307	2753825	NBstNBI	TTGTGSGATCTCAG	T	4694.0274	TGAGGTTCTAGAGTCTCCTTTGTGSGAT CTCAGCCCCGACTCCACCTCTGCG
883307	2753825	NBstNBI	CTGAGATCSCCACAA	A	4610.0078	TGAGGTTCTAGAGTCTCCTTTGTGSGAT CTCAGCCCCGACTCCACCTCTGCG
883307	2753825	NBstNBI	CTGAGATCSCCACAA	C	4585.9828	TGAGGTTCTAGAGTCTCCTTTGTGSGAT CTCAGCCCCGACTCCACCTCTGCG
883307	2753825	NBstNBI	CTGAGATCSCCACAA	G	4626.0072	TGAGGTTCTAGAGTCTCCTTTGTGSGAT CTCAGCCCCGACTCCACCTCTGCG

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883307	2753825	NBstNBI	CTGAGATCSCCACA	T	4600.9944	TGAGGTTCTAGAGTCTCCTTTGTGGSGAT CTCAGCCCCGACTCCACCTCTGCG
886509	2755591	NBstNBI	CSGCTGAGGACCCCCA	A	4916.1797	GTTACCTGGTGAGTCTGATGGGGTCTCT CAGCSGTGCTGACTCCACATTTTCC
886509	2755591	NBstNBI	CSGCTGAGGACCCCCA	C	4892.1547	GTTACCTGGTGAGTCTGATGGGGTCTCT CAGCSGTGCTGACTCCACATTTTCC
886509	2755591	NBstNBI	CSGCTGAGGACCCCCA	G	4932.1791	GTTACCTGGTGAGTCTGATGGGGTCTCT CAGCSGTGCTGACTCCACATTTTCC
886509	2755591	NBstNBI	CSGCTGAGGACCCCCA	T	4907.1663	GTTACCTGGTGAGTCTGATGGGGTCTCT CAGCSGTGCTGACTCCACATTTTCC
886509	2755591	NBstNBI	TGGGGTCTCAGCSG	A	5018.2261	GTTACCTGGTGAGTCTGATGGGGTCTCT CAGCSGTGCTGACTCCACATTTTCC
886509	2755591	NBstNBI	TGGGGTCTCAGCSG	C	4994.2011	GTTACCTGGTGAGTCTGATGGGGTCTCT CAGCSGTGCTGACTCCACATTTTCC
886509	2755591	NBstNBI	TGGGGTCTCAGCSG	G	5034.2255	GTTACCTGGTGAGTCTGATGGGGTCTCT CAGCSGTGCTGACTCCACATTTTCC
886509	2755591	NBstNBI	TGGGGTCTCAGCSG	T	5009.2127	GTTACCTGGTGAGTCTGATGGGGTCTCT CAGCSGTGCTGACTCCACATTTTCC
893284	2759454	BsrDI_NBstNBI	GGCTTCSACTGGG	A	4070.6232	GAGGCTGCCAGCAATGAACCCAGTSGAA GCCAGTAGACTCCTGGCTTTCA
893284	2759454	BsrDI_NBstNBI	GGCTTCSACTGGG	C	4046.5982	GAGGCTGCCAGCAATGAACCCAGTSGAA GCCAGTAGACTCCTGGCTTTCA
893284	2759454	BsrDI_NBstNBI	GGCTTCSACTGGG	G	4086.6226	GAGGCTGCCAGCAATGAACCCAGTSGAA GCCAGTAGACTCCTGGCTTTCA
893284	2759454	BsrDI_NBstNBI	GGCTTCSACTGGG	T	4061.6098	GAGGCTGCCAGCAATGAACCCAGTSGAA GCCAGTAGACTCCTGGCTTTCA
894113	2760001	BsrI_NBstNBI	SGGCTTTG	A	2520.6259	GGGACCCAGCACTGGACAAAAGCCSGTTG GACTCCCTCCCCTAT
894113	2760001	BsrI_NBstNBI	SGGCTTTG	C	2496.6009	GGGACCCAGCACTGGACAAAAGCCSGTTG GACTCCCTCCCCTAT
894113	2760001	BsrI_NBstNBI	SGGCTTTG	G	2536.6253	GGGACCCAGCACTGGACAAAAGCCSGTTG GACTCCCTCCCCTAT
894113	2760001	BsrI_NBstNBI	SGGCTTTG	T	2511.6125	GGGACCCAGCACTGGACAAAAGCCSGTTG GACTCCCTCCCCTAT

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894349	2760153	NBstNBI_Bsrl	TTGCSGGGACTG	A	3781.4385	TTTTCAGCAGAGTCCACTTTTGCSGGGAC TGCCCGGCCCGGC
894349	2760153	NBstNBI_Bsrl	TTGCSGGGACTG	C	3757.4135	TTTTCAGCAGAGTCCACTTTTGCSGGGAC TGCCCGGCCCGGC
894349	2760153	NBstNBI_Bsrl	TTGCSGGGACTG	G	3797.4379	TTTTCAGCAGAGTCCACTTTTGCSGGGAC TGCCCGGCCCGGC
894349	2760153	NBstNBI_Bsrl	TTGCSGGGACTG	T	3772.4251	TTTTCAGCAGAGTCCACTTTTGCSGGGAC TGCCCGGCCCGGC
903968	2912352	NBstNBI	TGTTCCCTGSCCCCTCT	A	4839.1139	TAAAGACCTGGAGTCATGGTGTTCCTGSC CCCTCTAGTGGACTCTCAAGGAGGT
903968	2912352	NBstNBI	TGTTCCCTGSCCCCTCT	C	4815.0889	TAAAGACCTGGAGTCATGGTGTTCCTGSC CCCTCTAGTGGACTCTCAAGGAGGT
903968	2912352	NBstNBI	TGTTCCCTGSCCCCTCT	G	4855.1133	TAAAGACCTGGAGTCATGGTGTTCCTGSC CCCTCTAGTGGACTCTCAAGGAGGT
903968	2912352	NBstNBI	TGTTCCCTGSCCCCTCT	T	4830.1005	TAAAGACCTGGAGTCATGGTGTTCCTGSC CCCTCTAGTGGACTCTCAAGGAGGT
903968	2912352	NBstNBI	AGAGGGGSCAGGAACA	A	5093.3163	TAAAGACCTGGAGTCATGGTGTTCCTGSC CCCTCTAGTGGACTCTCAAGGAGGT
903968	2912352	NBstNBI	AGAGGGGSCAGGAACA	C	5069.2913	TAAAGACCTGGAGTCATGGTGTTCCTGSC CCCTCTAGTGGACTCTCAAGGAGGT
903968	2912352	NBstNBI	AGAGGGGSCAGGAACA	G	5109.3157	TAAAGACCTGGAGTCATGGTGTTCCTGSC CCCTCTAGTGGACTCTCAAGGAGGT
903968	2912352	NBstNBI	AGAGGGGSCAGGAACA	T	5084.3029	TAAAGACCTGGAGTCATGGTGTTCCTGSC CCCTCTAGTGGACTCTCAAGGAGGT
906867	2767545	BsmI_NBstNBI	GAGGSCCT	A	2514.6277	ACTTGTGTCAGAAATGCAAGGSCCTCATCT GACTCATAACTGGCT
906867	2767545	BsmI_NBstNBI	GAGGSCCT	C	2490.6027	ACTTGTGTCAGAAATGCAAGGSCCTCATCT GACTCATAACTGGCT
906867	2767545	BsmI_NBstNBI	GAGGSCCT	G	2530.6271	ACTTGTGTCAGAAATGCAAGGSCCTCATCT GACTCATAACTGGCT
906867	2767545	BsmI_NBstNBI	GAGGSCCT	T	2505.6143	ACTTGTGTCAGAAATGCAAGGSCCTCATCT GACTCATAACTGGCT
918421	2773873	NBstNBI_Bsrl	AGSAATTACTG	A	3444.2556	CACAGATCTGGAGTCATAGAGSAATTACT GGTGTGGTGTCAA

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918421	2773873	NBstNBI_Bsrl	AGSAATTACTG	C	3420.2306	CACAGATCTGGAGTCATAGAGSAATTACT GGTGTGGTGCAA
918421	2773873	NBstNBI_Bsrl	AGSAATTACTG	G	3460.255	CACAGATCTGGAGTCATAGAGSAATTACT GGTGTGGTGCAA
918421	2773873	NBstNBI_Bsrl	AGSAATTACTG	T	3435.2422	CACAGATCTGGAGTCATAGAGSAATTACT GGTGTGGTGCAA
922074	2775964	NBstNBI_Bsrl	CCTAGCTTCSAAACTG	A	4905.1907	CTAATATTCTGAGTCATCTCCTAGCTTCSA AACTGGCCTCTTCCAAG
922074	2775964	NBstNBI_Bsrl	CCTAGCTTCSAAACTG	C	4881.1657	CTAATATTCTGAGTCATCTCCTAGCTTCSA AACTGGCCTCTTCCAAG
922074	2775964	NBstNBI_Bsrl	CCTAGCTTCSAAACTG	G	4921.1901	CTAATATTCTGAGTCATCTCCTAGCTTCSA AACTGGCCTCTTCCAAG
922074	2775964	NBstNBI_Bsrl	CCTAGCTTCSAAACTG	T	4896.1773	CTAATATTCTGAGTCATCTCCTAGCTTCSA AACTGGCCTCTTCCAAG
937317	2780135	Bsrl_NBstNBI	CATGCSATTG	A	3107.0209	CTAGTGGCTAACTGGGCAATSGCATGGTT GGACTCACITTTGCCA
937317	2780135	Bsrl_NBstNBI	CATGCSATTG	C	3082.9959	CTAGTGGCTAACTGGGCAATSGCATGGTT GGACTCACITTTGCCA
937317	2780135	Bsrl_NBstNBI	CATGCSATTG	G	3123.0203	CTAGTGGCTAACTGGGCAATSGCATGGTT GGACTCACITTTGCCA
937317	2780135	Bsrl_NBstNBI	CATGCSATTG	T	3098.0075	CTAGTGGCTAACTGGGCAATSGCATGGTT GGACTCACITTTGCCA
941300	2782964	NBstNBI	CATTCTGCCCAS	A	3949.5622	GCAGAGGGATGAGTCAAAGSTGGGCAGA AATGTCATGACTCCTACTCTCCC
941300	2782964	NBstNBI	CATTCTGCCCAS	C	3925.5372	GCAGAGGGATGAGTCAAAGSTGGGCAGA AATGTCATGACTCCTACTCTCCC
941300	2782964	NBstNBI	CATTCTGCCCAS	G	3965.5616	GCAGAGGGATGAGTCAAAGSTGGGCAGA AATGTCATGACTCCTACTCTCCC
941300	2782964	NBstNBI	CATTCTGCCCAS	T	3940.5488	GCAGAGGGATGAGTCAAAGSTGGGCAGA AATGTCATGACTCCTACTCTCCC
941300	2782964	NBstNBI	STGGGCAGAAATG	A	4127.6866	GCAGAGGGATGAGTCAAAGSTGGGCAGA AATGTCATGACTCCTACTCTCCC
941300	2782964	NBstNBI	STGGGCAGAAATG	C	4103.6616	GCAGAGGGATGAGTCAAAGSTGGGCAGA AATGTCATGACTCCTACTCTCCC

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941300	2782964	NBstNBI	STGGGCAGAAATG	G	4143.686	GCAGAGGGATGAGTCAAAGSTGGGCAGA AATGTCATGACTCCTACTCTCCC
941300	2782964	NBstNBI	STGGGCAGAAATG	T	4118.6732	GCAGAGGGATGAGTCAAAGSTGGGCAGA AATGTCATGACTCCTACTCTCCC
948237	2788078	BsrDI_NBstNBI	AAAGTCTTAS	A	3115.0465	GACTAATGCTGCAATGAATAAGACTTTG GGGACTCTTGGGAAGGC
948237	2788078	BsrDI_NBstNBI	AAAGTCTTAS	C	3091.0215	GACTAATGCTGCAATGAATAAGACTTTG GGGACTCTTGGGAAGGC
948237	2788078	BsrDI_NBstNBI	AAAGTCTTAS	G	3131.0459	GACTAATGCTGCAATGAATAAGACTTTG GGGACTCTTGGGAAGGC
948237	2788078	BsrDI_NBstNBI	AAAGTCTTAS	T	3106.0331	GACTAATGCTGCAATGAATAAGACTTTG GGGACTCTTGGGAAGGC
948318	2788152	NBstNBI_BclI	CSCAGTGATC	A	3092.0093	TGCTAGTAATGAGTCCTTTTCSAGTGATCA GAGAAGTTTG
948318	2788152	NBstNBI_BclI	CSCAGTGATC	C	3067.9843	TGCTAGTAATGAGTCCTTTTCSAGTGATCA GAGAAGTTTG
948318	2788152	NBstNBI_BclI	CSCAGTGATC	G	3108.0087	TGCTAGTAATGAGTCCTTTTCSAGTGATCA GAGAAGTTTG
948318	2788152	NBstNBI_BclI	CSCAGTGATC	T	3082.9959	TGCTAGTAATGAGTCCTTTTCSAGTGATCA GAGAAGTTTG
952794	2791396	NBstNBI	GCAAGGGAGSTGGGA	A	4811.1176	TGGTCCAGGCGGAGTCACCTTGCAAGGGAG STGGGATGGTGACTCTAGGGTAGGG
952794	2791396	NBstNBI	GCAAGGGAGSTGGGA	C	4787.0926	TGGTCCAGGCGGAGTCACCTTGCAAGGGAG STGGGATGGTGACTCTAGGGTAGGG
952794	2791396	NBstNBI	GCAAGGGAGSTGGGA	G	4827.117	TGGTCCAGGCGGAGTCACCTTGCAAGGGAG STGGGATGGTGACTCTAGGGTAGGG
952794	2791396	NBstNBI	GCAAGGGAGSTGGGA	T	4802.1042	TGGTCCAGGCGGAGTCACCTTGCAAGGGAG STGGGATGGTGACTCTAGGGTAGGG
952794	2791396	NBstNBI	TCCCASCTCCCTTGC	A	4503.9066	TGGTCCAGGCGGAGTCACCTTGCAAGGGAG STGGGATGGTGACTCTAGGGTAGGG
952794	2791396	NBstNBI	TCCCASCTCCCTTGC	C	4479.8816	TGGTCCAGGCGGAGTCACCTTGCAAGGGAG STGGGATGGTGACTCTAGGGTAGGG
952794	2791396	NBstNBI	TCCCASCTCCCTTGC	G	4519.906	TGGTCCAGGCGGAGTCACCTTGCAAGGGAG STGGGATGGTGACTCTAGGGTAGGG

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952794	2791396	NBstNBI	TCCASCCTCCCTTGC	T	4494.8932	TGGTCCAGGCGAGTCACCTTGCAAGGGAG STGGGATGGTGACTCTAGGGTAGGG
953718	2792013	BsrDI_NBstNBI	AASGTGGCAAGC	A	3783.4659	AAATAAGACTGCAATGATGCTTGCCACSTT GATTGACTCTTCCCTTCGC
953718	2792013	BsrDI_NBstNBI	AASGTGGCAAGC	C	3759.4409	AAATAAGACTGCAATGATGCTTGCCACSTT GATTGACTCTTCCCTTCGC
953718	2792013	BsrDI_NBstNBI	AASGTGGCAAGC	G	3799.4653	AAATAAGACTGCAATGATGCTTGCCACSTT GATTGACTCTTCCCTTCGC
953718	2792013	BsrDI_NBstNBI	AASGTGGCAAGC	T	3774.4525	AAATAAGACTGCAATGATGCTTGCCACSTT GATTGACTCTTCCCTTCGC
955074	2792900	BsrI_NBstNBI	CTTSTTG	A	2166.404	AGATTTACAAACTGGCCAAASAAGGCCTGA CTCCTTCACAAAC
955074	2792900	BsrI_NBstNBI	CTTSTTG	C	2142.379	AGATTTACAAACTGGCCAAASAAGGCCTGA CTCCTTCACAAAC
955074	2792900	BsrI_NBstNBI	CTTSTTG	G	2182.4034	AGATTTACAAACTGGCCAAASAAGGCCTGA CTCCTTCACAAAC
955074	2792900	BsrI_NBstNBI	CTTSTTG	T	2157.3906	AGATTTACAAACTGGCCAAASAAGGCCTGA CTCCTTCACAAAC
957541	2794458	BsmI_NBstNBI	SATCAGCTAGTTGAA	A	4680.0554	CAGAGATAAAGAATGCCCTTCAACTAGCTG ATSGAGAGACTCAACAAGCCAA
957541	2794458	BsmI_NBstNBI	SATCAGCTAGTTGAA	C	4656.0304	CAGAGATAAAGAATGCCCTTCAACTAGCTG ATSGAGAGACTCAACAAGCCAA
957541	2794458	BsmI_NBstNBI	SATCAGCTAGTTGAA	G	4696.0548	CAGAGATAAAGAATGCCCTTCAACTAGCTG ATSGAGAGACTCAACAAGCCAA
957541	2794458	BsmI_NBstNBI	SATCAGCTAGTTGAA	T	4671.042	CAGAGATAAAGAATGCCCTTCAACTAGCTG ATSGAGAGACTCAACAAGCCAA
966513	2800247	BsrI_NBstNBI	CAGTTASGTGCTAGG	A	4712.0542	GTGATGCATCACTGGTCTCTAGCACSTAAC TGATGTGACTCTCCTCTCCTT
966513	2800247	BsrI_NBstNBI	CAGTTASGTGCTAGG	C	4688.0292	GTGATGCATCACTGGTCTCTAGCACSTAAC TGATGTGACTCTCCTCTCCTT
966513	2800247	BsrI_NBstNBI	CAGTTASGTGCTAGG	G	4728.0536	GTGATGCATCACTGGTCTCTAGCACSTAAC TGATGTGACTCTCCTCTCCTT
966513	2800247	BsrI_NBstNBI	CAGTTASGTGCTAGG	T	4703.0408	GTGATGCATCACTGGTCTCTAGCACSTAAC TGATGTGACTCTCCTCTCCTT

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968388	2801537	NBstNBI_BsrI	GGSGTGGTGCACTG	A	4439.8567	TTGATTTAAGAGTCGCAGGGSGTGGTGC ACTGGCTCATACCTGT
968388	2801537	NBstNBI_BsrI	GGSGTGGTGCACTG	C	4415.8317	TTGATTTAAGAGTCGCAGGGSGTGGTGC ACTGGCTCATACCTGT
968388	2801537	NBstNBI_BsrI	GGSGTGGTGCACTG	G	4455.8561	TTGATTTAAGAGTCGCAGGGSGTGGTGC ACTGGCTCATACCTGT
968388	2801537	NBstNBI_BsrI	GGSGTGGTGCACTG	T	4430.8433	TTGATTTAAGAGTCGCAGGGSGTGGTGC ACTGGCTCATACCTGT
971822	2803967	BsrI_NBstNBI	TGACAACSCCA	A	3374.208	CTGCTGTACACACTGGTGGSGTTGTCAGG GTGACTCACGTGGACAC
971822	2803967	BsrI_NBstNBI	TGACAACSCCA	C	3350.183	CTGCTGTACACACTGGTGGSGTTGTCAGG GTGACTCACGTGGACAC
971822	2803967	BsrI_NBstNBI	TGACAACSCCA	G	3390.2074	CTGCTGTACACACTGGTGGSGTTGTCAGG GTGACTCACGTGGACAC
971822	2803967	BsrI_NBstNBI	TGACAACSCCA	T	3365.1946	CTGCTGTACACACTGGTGGSGTTGTCAGG GTGACTCACGTGGACAC
973481	2805318	BsrI_NBstNBI	CCCSGAAGAA	A	3110.0361	TCCCTTCTCCACTGGCTTCTTCSGGGAGA TGACTCACTCTCACA
973481	2805318	BsrI_NBstNBI	CCCSGAAGAA	C	3086.0111	TCCCTTCTCCACTGGCTTCTTCSGGGAGA TGACTCACTCTCACA
973481	2805318	BsrI_NBstNBI	CCCSGAAGAA	G	3126.0355	TCCCTTCTCCACTGGCTTCTTCSGGGAGA TGACTCACTCTCACA
973481	2805318	BsrI_NBstNBI	CCCSGAAGAA	T	3101.0227	TCCCTTCTCCACTGGCTTCTTCSGGGAGA TGACTCACTCTCACA
974124	2805750	NBstNBI	TGATTCASGTGA	A	4068.6476	TAAGGTAGAAGAGTCGGAGTGATTCASTG TGAGAAGGACTCAATCCTTCCCT
974124	2805750	NBstNBI	TGATTCASGTGA	C	4044.6226	TAAGGTAGAAGAGTCGGAGTGATTCASTG TGAGAAGGACTCAATCCTTCCCT
974124	2805750	NBstNBI	TGATTCASGTGA	G	4084.647	TAAGGTAGAAGAGTCGGAGTGATTCASTG TGAGAAGGACTCAATCCTTCCCT
974124	2805750	NBstNBI	TGATTCASGTGA	T	4059.6342	TAAGGTAGAAGAGTCGGAGTGATTCASTG TGAGAAGGACTCAATCCTTCCCT
974124	2805750	NBstNBI	TCACASTGAATCA	A	4006.6256	TAAGGTAGAAGAGTCGGAGTGATTCASTG TGAGAAGGACTCAATCCTTCCCT

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
974124	2805750	NBstNBI	TCACASTGAATCA	C	3982.6006	TAAGGTAGAAGAGTCGGAGTGATTCASTG TGAGAAAGGACTCAATCCTTCCT
974124	2805750	NBstNBI	TCACASTGAATCA	G	4022.625	TAAGGTAGAAGAGTCGGAGTGATTCASTG TGAGAAAGGACTCAATCCTTCCT
974124	2805750	NBstNBI	TCACASTGAATCA	T	3997.6122	TAAGGTAGAAGAGTCGGAGTGATTCASTG TGAGAAAGGACTCAATCCTTCCT
974890	2806301	BclI_NBstNBI	CASCAGAACTGATC	A	4320.8231	TTCATTGTTTGATCAGTTCTGTTGAG ACTCTAATGCATTT
974890	2806301	BclI_NBstNBI	CASCAGAACTGATC	C	4296.7981	TTCATTGTTTGATCAGTTCTGTTGAG ACTCTAATGCATTT
974890	2806301	BclI_NBstNBI	CASCAGAACTGATC	G	4336.8225	TTCATTGTTTGATCAGTTCTGTTGAG ACTCTAATGCATTT
974890	2806301	BclI_NBstNBI	CASCAGAACTGATC	T	4311.8097	TTCATTGTTTGATCAGTTCTGTTGAG ACTCTAATGCATTT
982277	2811467	BsrI_NBstNBI	AAATCCSTGGAGGAA	A	4714.0816	TCTCAGACTTACTGGTTTCTCCASGGATT TGCTTGACTCTAAATTATTGG
982277	2811467	BsrI_NBstNBI	AAATCCSTGGAGGAA	C	4690.0566	TCTCAGACTTACTGGTTTCTCCASGGATT TGCTTGACTCTAAATTATTGG
982277	2811467	BsrI_NBstNBI	AAATCCSTGGAGGAA	G	4730.081	TCTCAGACTTACTGGTTTCTCCASGGATT TGCTTGACTCTAAATTATTGG
982277	2811467	BsrI_NBstNBI	AAATCCSTGGAGGAA	T	4705.0682	TCTCAGACTTACTGGTTTCTCCASGGATT TGCTTGACTCTAAATTATTGG
982820	2811828	NBstNBI_BsrI	AASAGACTG	A	2835.863	TTTTGAGACAGAGTCCCAAAASAGACTGG AGTGCAGTGGC
982820	2811828	NBstNBI_BsrI	AASAGACTG	C	2811.838	TTTTGAGACAGAGTCCCAAAASAGACTGG AGTGCAGTGGC
982820	2811828	NBstNBI_BsrI	AASAGACTG	G	2851.8624	TTTTGAGACAGAGTCCCAAAASAGACTGG AGTGCAGTGGC
982820	2811828	NBstNBI_BsrI	AASAGACTG	T	2826.8496	TTTTGAGACAGAGTCCCAAAASAGACTGG AGTGCAGTGGC
983859	2812569	NBstNBI	ATTAAGCCCTAGSC	A	4311.8097	AGGGCAAAAAGAGTCTGAGSCTAGGGCT TAATTTCTGACTCTGCTTCCTCA
983859	2812569	NBstNBI	ATTAAGCCCTAGSC	C	4287.7847	AGGGCAAAAAGAGTCTGAGSCTAGGGCT TAATTTCTGACTCTGCTTCCTCA

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983859	2812569	NBstNBI	ATTAAGCCCTAGSC	G	4327.8091	AGGCAAAAAGAGTCTCTGAGSCTAGGGCT TAATTTCTGACTCTGCTTCTCA
983859	2812569	NBstNBI	ATTAAGCCCTAGSC	T	4302.7963	AGGCAAAAAGAGTCTCTGAGSCTAGGGCT TAATTTCTGACTCTGCTTCTCA
983859	2812569	NBstNBI	GSCTAGGGCTTAAT	A	4382.8451	AGGCAAAAAGAGTCTCTGAGSCTAGGGCT TAATTTCTGACTCTGCTTCTCA
983859	2812569	NBstNBI	GSCTAGGGCTTAAT	C	4358.8201	AGGCAAAAAGAGTCTCTGAGSCTAGGGCT TAATTTCTGACTCTGCTTCTCA
983859	2812569	NBstNBI	GSCTAGGGCTTAAT	G	4398.8445	AGGCAAAAAGAGTCTCTGAGSCTAGGGCT TAATTTCTGACTCTGCTTCTCA
983859	2812569	NBstNBI	GSCTAGGGCTTAAT	T	4373.8317	AGGCAAAAAGAGTCTCTGAGSCTAGGGCT TAATTTCTGACTCTGCTTCTCA
984558	2813139	NBstNBI_BsmI	CCTSTTGAATG	A	3411.2172	AACCTGCCAGGAGTCTCTCCCTSTTGAAT GCCTGGAGTTGCC
984558	2813139	NBstNBI_BsmI	CCTSTTGAATG	C	3387.1922	AACCTGCCAGGAGTCTCTCCCTSTTGAAT GCCTGGAGTTGCC
984558	2813139	NBstNBI_BsmI	CCTSTTGAATG	G	3427.2166	AACCTGCCAGGAGTCTCTCCCTSTTGAAT GCCTGGAGTTGCC
984558	2813139	NBstNBI_BsmI	CCTSTTGAATG	T	3402.2038	AACCTGCCAGGAGTCTCTCCCTSTTGAAT GCCTGGAGTTGCC
986183	2814465	BsrI_NBstNBI	GACACSA	A	2178.4326	GGTCTTCAGACTGGCTSGTGTGTCAGTGGA CTCATTGAAATGC
986183	2814465	BsrI_NBstNBI	GACACSA	C	2154.4076	GGTCTTCAGACTGGCTSGTGTGTCAGTGGA CTCATTGAAATGC
986183	2814465	BsrI_NBstNBI	GACACSA	G	2194.432	GGTCTTCAGACTGGCTSGTGTGTCAGTGGA CTCATTGAAATGC
986183	2814465	BsrI_NBstNBI	GACACSA	T	2169.4192	GGTCTTCAGACTGGCTSGTGTGTCAGTGGA CTCATTGAAATGC
986406	2814608	BsrI_NBstNBI	AAACSTATTITTTCTT	A	4596.0036	TATACCTGAGACTGGGAAGAAAAATASGT TTAATGGACTCCCAATTCCAT
986406	2814608	BsrI_NBstNBI	AAACSTATTITTTCTT	C	4571.9786	TATACCTGAGACTGGGAAGAAAAATASGT TTAATGGACTCCCAATTCCAT
986406	2814608	BsrI_NBstNBI	AAACSTATTITTTCTT	G	4612.003	TATACCTGAGACTGGGAAGAAAAATASGT TTAATGGACTCCCAATTCCAT

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986406	2814608	BsrI_NBstNBI	AAACSTATTTTCTT	T	4586.9902	TATACCTGAGACTGGGAAGAAAAATASGT TTAATGGACTCCCAATTCCAT
990835	2817602	BsrI_NBstNBI	GACTTCSCATG	A	3396.2056	ACCACATTGAACCTGGCCATGSGAAGTCTC AGGACTCCCATGAGTCAG
990835	2817602	BsrI_NBstNBI	GACTTCSCATG	C	3372.1806	ACCACATTGAACCTGGCCATGSGAAGTCTC AGGACTCCCATGAGTCAG
990835	2817602	BsrI_NBstNBI	GACTTCSCATG	G	3412.205	ACCACATTGAACCTGGCCATGSGAAGTCTC AGGACTCCCATGAGTCAG
990835	2817602	BsrI_NBstNBI	GACTTCSCATG	T	3387.1922	ACCACATTGAACCTGGCCATGSGAAGTCTC AGGACTCCCATGAGTCAG
999475	2823307	NBstNBI_BclI	AATAGCAGAASTGATC	A	5002.2785	GAATGCAACAGAGTCTCTTAATAGCAGAA STGATCAAGCAATTGAT
999475	2823307	NBstNBI_BclI	AATAGCAGAASTGATC	C	4978.2535	GAATGCAACAGAGTCTCTTAATAGCAGAA STGATCAAGCAATTGAT
999475	2823307	NBstNBI_BclI	AATAGCAGAASTGATC	G	5018.2779	GAATGCAACAGAGTCTCTTAATAGCAGAA STGATCAAGCAATTGAT
999475	2823307	NBstNBI_BclI	AATAGCAGAASTGATC	T	4993.2651	GAATGCAACAGAGTCTCTTAATAGCAGAA STGATCAAGCAATTGAT
1016144	2836177	BsrDI_NBstNBI	ATGGSAA	A	2233.4686	TCGCAGAGCTGCAATGGGTTSCCATAAAT GACTCAAGGTGACAA
1016144	2836177	BsrDI_NBstNBI	ATGGSAA	C	2209.4436	TCGCAGAGCTGCAATGGGTTSCCATAAAT GACTCAAGGTGACAA
1016144	2836177	BsrDI_NBstNBI	ATGGSAA	G	2249.468	TCGCAGAGCTGCAATGGGTTSCCATAAAT GACTCAAGGTGACAA
1016144	2836177	BsrDI_NBstNBI	ATGGSAA	T	2224.4552	TCGCAGAGCTGCAATGGGTTSCCATAAAT GACTCAAGGTGACAA
1021484	2840139	BsrDI_NBstNBI	AAATCATAST	A	3099.0471	CTTTCTACCAGCAATGTAATATGATTTAT GTGACTCCTCCAGCTA
1021484	2840139	BsrDI_NBstNBI	AAATCATAST	C	3075.0221	CTTTCTACCAGCAATGTAATATGATTTAT GTGACTCCTCCAGCTA
1021484	2840139	BsrDI_NBstNBI	AAATCATAST	G	3115.0465	CTTTCTACCAGCAATGTAATATGATTTAT GTGACTCCTCCAGCTA
1021484	2840139	BsrDI_NBstNBI	AAATCATAST	T	3090.0337	CTTTCTACCAGCAATGTAATATGATTTAT GTGACTCCTCCAGCTA

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1021661	2840255	BsrI_NBstNBI	STACAGCAAGATGGGC	A	5019.2657	GAGGCACAGAACTGGGGCCCATCTTGCT GTASGTTAGACTCTCCACTCTGC
1021661	2840255	BsrI_NBstNBI	STACAGCAAGATGGGC	C	4995.2407	GAGGCACAGAACTGGGGCCCATCTTGCT GTASGTTAGACTCTCCACTCTGC
1021661	2840255	BsrI_NBstNBI	STACAGCAAGATGGGC	G	5035.2651	GAGGCACAGAACTGGGGCCCATCTTGCT GTASGTTAGACTCTCCACTCTGC
1021661	2840255	BsrI_NBstNBI	STACAGCAAGATGGGC	T	5010.2523	GAGGCACAGAACTGGGGCCCATCTTGCT GTASGTTAGACTCTCCACTCTGC
1029438	2845078	NBstNBI_BsmI	AATCAGSTGAATG	A	4086.6744	ATGTCAGTGGGAGTCATCCAATCAGSTGA ATGCCTACATAGAAC
1029438	2845078	NBstNBI_BsmI	AATCAGSTGAATG	C	4062.6494	ATGTCAGTGGGAGTCATCCAATCAGSTGA ATGCCTACATAGAAC
1029438	2845078	NBstNBI_BsmI	AATCAGSTGAATG	G	4102.6738	ATGTCAGTGGGAGTCATCCAATCAGSTGA ATGCCTACATAGAAC
1029438	2845078	NBstNBI_BsmI	AATCAGSTGAATG	T	4077.661	ATGTCAGTGGGAGTCATCCAATCAGSTGA ATGCCTACATAGAAC
1031273	2846485	NBstNBI	TTACCCGGTAGC	A	3685.3903	ACATACTCTGGAGTCAAAAAGCTASCGGGT AAATTTGACTCAGAAAAATAA
1031273	2846485	NBstNBI	TTACCCGGTAGC	C	3661.3653	ACATACTCTGGAGTCAAAAAGCTASCGGGT AAATTTGACTCAGAAAAATAA
1031273	2846485	NBstNBI	TTACCCGGTAGC	G	3701.3897	ACATACTCTGGAGTCAAAAAGCTASCGGGT AAATTTGACTCAGAAAAATAA
1031273	2846485	NBstNBI	TTACCCGGTAGC	T	3676.3769	ACATACTCTGGAGTCAAAAAGCTASCGGGT AAATTTGACTCAGAAAAATAA
1031273	2846485	NBstNBI	GCTASCGGGTAA	A	3774.4525	ACATACTCTGGAGTCAAAAAGCTASCGGGT AAATTTGACTCAGAAAAATAA
1031273	2846485	NBstNBI	GCTASCGGGTAA	C	3750.4275	ACATACTCTGGAGTCAAAAAGCTASCGGGT AAATTTGACTCAGAAAAATAA
1031273	2846485	NBstNBI	GCTASCGGGTAA	G	3790.4519	ACATACTCTGGAGTCAAAAAGCTASCGGGT AAATTTGACTCAGAAAAATAA
1031273	2846485	NBstNBI	GCTASCGGGTAA	T	3765.4391	ACATACTCTGGAGTCAAAAAGCTASCGGGT AAATTTGACTCAGAAAAATAA
1050534	2945301	BsrI_NBstNBI	ctccccStggca	A	3646.3537	gttcagcagcactggctgcccaSggggaggacagactcttga caccat

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1050534	2945301	BsrI_NBstNBI	ctcccStggca	C	3622.3287	gttcagcagcactggctgcccaSggggaggacagactcttga caccat
1050534	2945301	BsrI_NBstNBI	ctcccStggca	G	3662.3531	gttcagcagcactggctgcccaSggggaggacagactcttga caccat
1050534	2945301	BsrI_NBstNBI	ctcccStggca	T	3637.3403	gttcagcagcactggctgcccaSggggaggacagactcttga caccat
1057869	2950805	NBstNBI_BsrI	Scigtgccagactg	A	4632.9932	ttfngtgcggagctcctcacScigtgccagactggagtgacgt ggt
1057869	2950805	NBstNBI_BsrI	Scigtgccagactg	C	4608.9682	ttfngtgcggagctcctcacScigtgccagactggagtgacgt ggt
1057869	2950805	NBstNBI_BsrI	Scigtgccagactg	G	4648.9926	ttfngtgcggagctcctcacScigtgccagactggagtgacgt ggt
1057869	2950805	NBstNBI_BsrI	Scigtgccagactg	T	4623.9798	ttfngtgcggagctcctcacScigtgccagactggagtgacgt ggt
1060531	2952875	BsmI_NBstNBI	tggggtttaSaga	A	4133.6848	ccaagttttgaatgctcttStaaccaccccaaaaggactcattag gcttg
1060531	2952875	BsmI_NBstNBI	tggggtttaSaga	C	4109.6598	ccaagttttgaatgctcttStaaccaccccaaaaggactcattag gcttg
1060531	2952875	BsmI_NBstNBI	tggggtttaSaga	G	4149.6842	ccaagttttgaatgctcttStaaccaccccaaaaggactcattag gcttg
1060531	2952875	BsmI_NBstNBI	tggggtttaSaga	T	4124.6714	ccaagttttgaatgctcttStaaccaccccaaaaggactcattag gcttg
1085531	2935538	BsrI_NBstNBI	Stcaaaagagg	A	3165.0721	cigacacccctactggggcctcttftgaScccagactcaccctgtag aa
1085531	2935538	BsrI_NBstNBI	Stcaaaagagg	C	3141.0471	cigacacccctactggggcctcttftgaScccagactcaccctgtag aa
1085531	2935538	BsrI_NBstNBI	Stcaaaagagg	G	3181.0715	cigacacccctactggggcctcttftgaScccagactcaccctgtag aa
1085531	2935538	BsrI_NBstNBI	Stcaaaagagg	T	3156.0587	cigacacccctactggggcctcttftgaScccagactcaccctgtag aa
1085971	2935853	BsrDI_NBstNBI	Ssttaataactcag	A	4639.0432	acttagaatagcaatgaactgagttatttaaSacaggactct gcatgaaat
1085971	2935853	BsrDI_NBstNBI	Ssttaataactcag	C	4615.0182	acttagaatagcaatgaactgagttatttaaSacaggactct gcatgaaat

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1085971	2935853	BsrDI_NBstNBI	Stttaataactcag	G	4655.0426	acttagaatagaatgaactgagttatttaaSacaggactct gcatgaaat
1085971	2935853	BsrDI_NBstNBI	Stttaataactcag	T	4630.0298	acttagaatagaatgaactgagttatttaaSacaggactct gcatgaaat
1086251	2936064	NBstNBI_BsrI	cStagtgcactg	A	3725.4147	cttgccctgctgagtcactgcStagtgcactggggcaggagg a
1086251	2936064	NBstNBI_BsrI	cStagtgcactg	C	3701.3897	cttgccctgctgagtcactgcStagtgcactggggcaggagg a
1086251	2936064	NBstNBI_BsrI	cStagtgcactg	G	3741.4141	cttgccctgctgagtcactgcStagtgcactggggcaggagg a
1086251	2936064	NBstNBI_BsrI	cStagtgcactg	T	3716.4013	cttgccctgctgagtcactgcStagtgcactggggcaggagg a
1092249	2937488	BsrI_NBstNBI	Stggatgacatggag	A	4761.092	tctgaagagactggcctccatgtcatccaSagctgactctg tcccagg
1092249	2937488	BsrI_NBstNBI	Stggatgacatggag	C	4737.067	tctgaagagactggcctccatgtcatccaSagctgactctg tcccagg
1092249	2937488	BsrI_NBstNBI	Stggatgacatggag	G	4777.0914	tctgaagagactggcctccatgtcatccaSagctgactctg tcccagg
1092249	2937488	BsrI_NBstNBI	Stggatgacatggag	T	4752.0786	tctgaagagactggcctccatgtcatccaSagctgactctg tcccagg
1094518	2973097	BsrI_NBstNBI	acatSa	A	1864.2351	ccccacacagactggttSaigtgccagactcagccagcggg tcccagg
1094518	2973097	BsrI_NBstNBI	acatSa	C	1840.2101	ccccacacagactggttSaigtgccagactcagccagcggg tcccagg
1094518	2973097	BsrI_NBstNBI	acatSa	G	1880.2345	ccccacacagactggttSaigtgccagactcagccagcggg tcccagg
1094518	2973097	BsrI_NBstNBI	acatSa	T	1855.2217	ccccacacagactggttSaigtgccagactcagccagcggg tcccagg
1101294	2976009	BsrDI_NBstNBI	ctttcagaaSag	A	3733.4403	aagggaggagcagaatgagctSttctgaaagggcagactcc agaaaaggga
1101294	2976009	BsrDI_NBstNBI	ctttcagaaSag	C	3709.4153	aagggaggagcagaatgagctSttctgaaagggcagactcc agaaaaggga
1101294	2976009	BsrDI_NBstNBI	ctttcagaaSag	G	3749.4397	aagggaggagcagaatgagctSttctgaaagggcagactcc agaaaaggga
1101294	2976009	BsrDI_NBstNBI	ctttcagaaSag	T	3724.4269	aagggaggagcagaatgagctSttctgaaagggcagactcc agaaaaggga
1110561	3029079	NBstNBI_BsrI	TCTGTCATSTAGACTG	A	4951.2133	TTTGGACAGAGTCTAACTCTGTGTCATSTA GACTGGAGTGCAGTGGC

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
1110561	3029079	NBstNBI_Bsrl	TCTGTCATSTAGACTG	C	4927.1883	TTTGTAGACAGAGTCTAACTCTGTCTATSTA GACTGGAGTGCAGTGGC
1110561	3029079	NBstNBI_Bsrl	TCTGTCATSTAGACTG	G	4967.2127	TTTGTAGACAGAGTCTAACTCTGTCTATSTA GACTGGAGTGCAGTGGC
1110561	3029079	NBstNBI_Bsrl	TCTGTCATSTAGACTG	T	4942.1999	TTTGTAGACAGAGTCTAACTCTGTCTATSTA GACTGGAGTGCAGTGGC
1111780	3030229	NBstNBI_Bsrl	TCTGTSGCCCAGACTG	A	4937.1895	TTTGTAGACAGAGTCTTGTCTGTCTGTSGCCC AGACTGGAGTGCAGTGGT
1111780	3030229	NBstNBI_Bsrl	TCTGTSGCCCAGACTG	C	4913.1645	TTTGTAGACAGAGTCTTGTCTGTCTGTSGCCC AGACTGGAGTGCAGTGGT
1111780	3030229	NBstNBI_Bsrl	TCTGTSGCCCAGACTG	G	4953.1889	TTTGTAGACAGAGTCTTGTCTGTCTGTSGCCC AGACTGGAGTGCAGTGGT
1111780	3030229	NBstNBI_Bsrl	TCTGTSGCCCAGACTG	T	4928.1761	TTTGTAGACAGAGTCTTGTCTGTCTGTSGCCC AGACTGGAGTGCAGTGGT
1113635	3031951	Bsrl_NBstNBI	TATSATCG	A	2488.6271	CCTATCTTAACTGGCGGATSATAAGGGG ACTCTCTGAGGAGG
1113635	3031951	Bsrl_NBstNBI	TATSATCG	C	2464.6021	CCTATCTTAACTGGCGGATSATAAGGGG ACTCTCTGAGGAGG
1113635	3031951	Bsrl_NBstNBI	TATSATCG	G	2504.6265	CCTATCTTAACTGGCGGATSATAAGGGG ACTCTCTGAGGAGG
1113635	3031951	Bsrl_NBstNBI	TATSATCG	T	2479.6137	CCTATCTTAACTGGCGGATSATAAGGGG ACTCTCTGAGGAGG
1116657	3034617	BclI_NBstNBI	SATAGCAGAACTGATC	A	4978.2535	TTCTTCTGCTTGATCAGTTCTGCTATSAAG AGACTCTGATGCAGCC
1116657	3034617	BclI_NBstNBI	SATAGCAGAACTGATC	C	4954.2285	TTCTTCTGCTTGATCAGTTCTGCTATSAAG AGACTCTGATGCAGCC
1116657	3034617	BclI_NBstNBI	SATAGCAGAACTGATC	G	4994.2529	TTCTTCTGCTTGATCAGTTCTGCTATSAAG AGACTCTGATGCAGCC
1116657	3034617	BclI_NBstNBI	SATAGCAGAACTGATC	T	4969.2401	TTCTTCTGCTTGATCAGTTCTGCTATSAAG AGACTCTGATGCAGCC
1117282	3035206	BsrDI_NBstNBI	CATAGCTTSCCT	A	3371.1928	ATCAAGCTCAGCAATGTGAGSAAGCTATG CACTGACTCAAGAACAGTG
1117282	3035206	BsrDI_NBstNBI	CATAGCTTSCCT	C	3347.1678	ATCAAGCTCAGCAATGTGAGSAAGCTATG CACTGACTCAAGAACAGTG

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1117282	3035206	BsrDI_NBstNBI	CATAGCTTCT	G	3387.1922	ATCAAGCTCAGCAATGTGAGSAAGCTATG CACTGACTCAAGAACAGTG
1117282	3035206	BsrDI_NBstNBI	CATAGCTTCT	T	3362.1794	ATCAAGCTCAGCAATGTGAGSAAGCTATG CACTGACTCAAGAACAGTG
1120496	3038034	Bsrl_NBstNBI	CSAGCCCTGGCAC	A	3984.5762	GTACCAACACACTGGTGTGCCAGGGCTSG TACTGACTCAGAGCTGCAG
1120496	3038034	Bsrl_NBstNBI	CSAGCCCTGGCAC	C	3960.5512	GTACCAACACACTGGTGTGCCAGGGCTSG TACTGACTCAGAGCTGCAG
1120496	3038034	Bsrl_NBstNBI	CSAGCCCTGGCAC	G	4000.5756	GTACCAACACACTGGTGTGCCAGGGCTSG TACTGACTCAGAGCTGCAG
1120496	3038034	Bsrl_NBstNBI	CSAGCCCTGGCAC	T	3975.5628	GTACCAACACACTGGTGTGCCAGGGCTSG TACTGACTCAGAGCTGCAG
1124023	3041176	NBstNBI_Bsrl	TCTGTTGSCCAGACTG	A	4952.2011	TTTTAGATGGAGTCTTAGTCTGTTGSCCA GACTGGAGTGCAGTGAC
1124023	3041176	NBstNBI_Bsrl	TCTGTTGSCCAGACTG	C	4928.1761	TTTTAGATGGAGTCTTAGTCTGTTGSCCA GACTGGAGTGCAGTGAC
1124023	3041176	NBstNBI_Bsrl	TCTGTTGSCCAGACTG	G	4968.2005	TTTTAGATGGAGTCTTAGTCTGTTGSCCA GACTGGAGTGCAGTGAC
1124023	3041176	NBstNBI_Bsrl	TCTGTTGSCCAGACTG	T	4943.1877	TTTTAGATGGAGTCTTAGTCTGTTGSCCA GACTGGAGTGCAGTGAC
1134459	3050211	Bsrl_NBstNBI	TATCCTCCTCSCCTCC	A	4768.0785	TTAGCAGAAAGACTGGAGGAGGSGAGGAG GATAGAGAGACTCGTATAGCAGG
1134459	3050211	Bsrl_NBstNBI	TATCCTCCTCSCCTCC	C	4744.0535	TTAGCAGAAAGACTGGAGGAGGSGAGGAG GATAGAGAGACTCGTATAGCAGG
1134459	3050211	Bsrl_NBstNBI	TATCCTCCTCSCCTCC	G	4784.0779	TTAGCAGAAAGACTGGAGGAGGSGAGGAG GATAGAGAGACTCGTATAGCAGG
1134459	3050211	Bsrl_NBstNBI	TATCCTCCTCSCCTCC	T	4759.0651	TTAGCAGAAAGACTGGAGGAGGSGAGGAG GATAGAGAGACTCGTATAGCAGG
1139564	3053650	NBstNBI	GGCTCGAACCACATTT	A	4921.1901	GAAGTTAAAAGAGTCAATGGGCTCGAACC CASTTTTCTGACTCCAGGCCAGAG
1139564	3053650	NBstNBI	GGCTCGAACCACATTT	C	4897.1651	GAAGTTAAAAGAGTCAATGGGCTCGAACC CASTTTTCTGACTCCAGGCCAGAG
1139564	3053650	NBstNBI	GGCTCGAACCACATTT	G	4937.1895	GAAGTTAAAAGAGTCAATGGGCTCGAACC CASTTTTCTGACTCCAGGCCAGAG

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1139564	3053650	NBstNBI	GGCTCGAACCCTTT	T	4912.1767	GAAGTTAAAAGAGTCAATGGGCTCGAACC CASTTTTCTGACTCCAGGCCAGAG
1139564	3053650	NBstNBI	AAASTGGGTTTCGAGCC	A	5010.2523	GAAGTTAAAAGAGTCAATGGGCTCGAACC CASTTTTCTGACTCCAGGCCAGAG
1139564	3053650	NBstNBI	AAASTGGGTTTCGAGCC	C	4986.2273	GAAGTTAAAAGAGTCAATGGGCTCGAACC CASTTTTCTGACTCCAGGCCAGAG
1139564	3053650	NBstNBI	AAASTGGGTTTCGAGCC	G	5026.2517	GAAGTTAAAAGAGTCAATGGGCTCGAACC CASTTTTCTGACTCCAGGCCAGAG
1139564	3053650	NBstNBI	AAASTGGGTTTCGAGCC	T	5001.2389	GAAGTTAAAAGAGTCAATGGGCTCGAACC CASTTTTCTGACTCCAGGCCAGAG
1139885	3053912	NBstNBI_Bsrl	AASGTCAGAACTG	A	4071.6628	CTCCCCAGTAGAGTCTGTCAASGTCAGAA CTGGCCAAACATTAC
1139885	3053912	NBstNBI_Bsrl	AASGTCAGAACTG	C	4047.6378	CTCCCCAGTAGAGTCTGTCAASGTCAGAA CTGGCCAAACATTAC
1139885	3053912	NBstNBI_Bsrl	AASGTCAGAACTG	G	4087.6622	CTCCCCAGTAGAGTCTGTCAASGTCAGAA CTGGCCAAACATTAC
1139885	3053912	NBstNBI_Bsrl	AASGTCAGAACTG	T	4062.6494	CTCCCCAGTAGAGTCTGTCAASGTCAGAA CTGGCCAAACATTAC
1142455	3056067	Bsrl_NBstNBI	ACACCASATAGACACA	A	4916.2315	CTCTCCTCTTACTGGGTGTGTCTATSTGGT GTGTGCGACTCCGTTGGGTGG
1142455	3056067	Bsrl_NBstNBI	ACACCASATAGACACA	C	4892.2065	CTCTCCTCTTACTGGGTGTGTCTATSTGGT GTGTGCGACTCCGTTGGGTGG
1142455	3056067	Bsrl_NBstNBI	ACACCASATAGACACA	G	4932.2309	CTCTCCTCTTACTGGGTGTGTCTATSTGGT GTGTGCGACTCCGTTGGGTGG
1142455	3056067	Bsrl_NBstNBI	ACACCASATAGACACA	T	4907.2181	CTCTCCTCTTACTGGGTGTGTCTATSTGGT GTGTGCGACTCCGTTGGGTGG
1142573	3056159	NBstNBI_Bsrl	CGTGATGCCCCASACTG	A	4946.2029	TTTTGAGATAGAGTCTCGCCGTGATGCCCC ASACTGGAGTGCAATGGT
1142573	3056159	NBstNBI_Bsrl	CGTGATGCCCCASACTG	C	4922.1779	TTTTGAGATAGAGTCTCGCCGTGATGCCCC ASACTGGAGTGCAATGGT
1142573	3056159	NBstNBI_Bsrl	CGTGATGCCCCASACTG	G	4962.2023	TTTTGAGATAGAGTCTCGCCGTGATGCCCC ASACTGGAGTGCAATGGT
1142573	3056159	NBstNBI_Bsrl	CGTGATGCCCCASACTG	T	4937.1895	TTTTGAGATAGAGTCTCGCCGTGATGCCCC ASACTGGAGTGCAATGGT

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1143207	3056673	NBstNBI_BsaBI	GACTCSATTGATTG	A	4357.8323	TATTATTTTCAGAGTCAATTGACTCSATTGA TTGAGATCACCAAACCTCC
1143207	3056673	NBstNBI_BsaBI	GACTCSATTGATTG	C	4333.8073	TATTATTTTCAGAGTCAATTGACTCSATTGA TTGAGATCACCAAACCTCC
1143207	3056673	NBstNBI_BsaBI	GACTCSATTGATTG	G	4373.8317	TATTATTTTCAGAGTCAATTGACTCSATTGA TTGAGATCACCAAACCTCC
1143207	3056673	NBstNBI_BsaBI	GACTCSATTGATTG	T	4348.8189	TATTATTTTCAGAGTCAATTGACTCSATTGA TTGAGATCACCAAACCTCC
1144880	3058055	BsmI_NBstNBI	CASTGAT	A	2184.4308	AAGAGGACTTGAATGCAATCASTGAATGG ACTCGAATGAAATC
1144880	3058055	BsmI_NBstNBI	CASTGAT	C	2160.4058	AAGAGGACTTGAATGCAATCASTGAATGG ACTCGAATGAAATC
1144880	3058055	BsmI_NBstNBI	CASTGAT	G	2200.4302	AAGAGGACTTGAATGCAATCASTGAATGG ACTCGAATGAAATC
1144880	3058055	BsmI_NBstNBI	CASTGAT	T	2175.4174	AAGAGGACTTGAATGCAATCASTGAATGG ACTCGAATGAAATC
1158090	3067733	BsrI_NBstNBI	CSAGAT	A	1880.2345	AAAATTTTCCTACTGGGATCTSGCAGAGAC TCCACAAGGCAT
1158090	3067733	BsrI_NBstNBI	CSAGAT	C	1856.2095	AAAATTTTCCTACTGGGATCTSGCAGAGAC TCCACAAGGCAT
1158090	3067733	BsrI_NBstNBI	CSAGAT	G	1896.2339	AAAATTTTCCTACTGGGATCTSGCAGAGAC TCCACAAGGCAT
1158090	3067733	BsrI_NBstNBI	CSAGAT	T	1871.2211	AAAATTTTCCTACTGGGATCTSGCAGAGAC TCCACAAGGCAT
1160170	3069090	NBstNBI	CCCAGGAGCCSC	A	3680.3799	CAGGATATTTGAGTCTCTGSGGGCTCCTG GGTAAAGACTCCAATGTAGCA
1160170	3069090	NBstNBI	CCCAGGAGCCSC	C	3656.3549	CAGGATATTTGAGTCTCTGSGGGCTCCTG GGTAAAGACTCCAATGTAGCA
1160170	3069090	NBstNBI	CCCAGGAGCCSC	G	3696.3793	CAGGATATTTGAGTCTCTGSGGGCTCCTG GGTAAAGACTCCAATGTAGCA
1160170	3069090	NBstNBI	CCCAGGAGCCSC	T	3671.3665	CAGGATATTTGAGTCTCTGSGGGCTCCTG GGTAAAGACTCCAATGTAGCA
1160170	3069090	NBstNBI	GSGGCTCCTGGG	A	3782.4263	CAGGATATTTGAGTCTCTGSGGGCTCCTG GGTAAAGACTCCAATGTAGCA

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1160170	3069090	NBstNBI	GSGGCTCCTGGG	C	3758.4013	CAGGATATTTGAGTCCTCTGSGGCTCCTG GGTAAAGACTCCAATGTAGCA
1160170	3069090	NBstNBI	GSGGCTCCTGGG	G	3798.4257	CAGGATATTTGAGTCCTCTGSGGCTCCTG GGTAAAGACTCCAATGTAGCA
1160170	3069090	NBstNBI	GSGGCTCCTGGG	T	3773.4129	CAGGATATTTGAGTCCTCTGSGGCTCCTG GGTAAAGACTCCAATGTAGCA
1162597	3071173	BsrI_NBstNBI	TCCTAGGCCSGTAT	A	4318.7957	TAAAGGGAGAACTGGGATACSGGCCTAG GAATATGACTCACCATGCTGT
1162597	3071173	BsrI_NBstNBI	TCCTAGGCCSGTAT	C	4294.7707	TAAAGGGAGAACTGGGATACSGGCCTAG GAATATGACTCACCATGCTGT
1162597	3071173	BsrI_NBstNBI	TCCTAGGCCSGTAT	G	4334.7951	TAAAGGGAGAACTGGGATACSGGCCTAG GAATATGACTCACCATGCTGT
1162597	3071173	BsrI_NBstNBI	TCCTAGGCCSGTAT	T	4309.7823	TAAAGGGAGAACTGGGATACSGGCCTAG GAATATGACTCACCATGCTGT
1165236	3073412	NBstNBI_BsrI	CCACSCACTG	A	3036.9733	ATCGAGCACTGAGTCTGGGCCACSCACTG GTGAGCTGTTCA
1165236	3073412	NBstNBI_BsrI	CCACSCACTG	C	3012.9483	ATCGAGCACTGAGTCTGGGCCACSCACTG GTGAGCTGTTCA
1165236	3073412	NBstNBI_BsrI	CCACSCACTG	G	3052.9727	ATCGAGCACTGAGTCTGGGCCACSCACTG GTGAGCTGTTCA
1165236	3073412	NBstNBI_BsrI	CCACSCACTG	T	3027.9599	ATCGAGCACTGAGTCTGGGCCACSCACTG GTGAGCTGTTCA
1174608	3080461	NBstNBI_BsrI	TGSTACTG	A	2504.6265	GAAGGTATCAGAGTCCTCCTGSTACTGGT TTGAAGCTAA
1174608	3080461	NBstNBI_BsrI	TGSTACTG	C	2480.6015	GAAGGTATCAGAGTCCTCCTGSTACTGGT TTGAAGCTAA
1174608	3080461	NBstNBI_BsrI	TGSTACTG	G	2520.6259	GAAGGTATCAGAGTCCTCCTGSTACTGGT TTGAAGCTAA
1174608	3080461	NBstNBI_BsrI	TGSTACTG	T	2495.6131	GAAGGTATCAGAGTCCTCCTGSTACTGGT TTGAAGCTAA
1181912	3085170	BsrI_NBstNBI	SGTGCAGTCCCTC	A	3990.5744	CTTGGCCAGAACTGGGAGGGGACTGCAC STGAGGACTCCAGGGTCTCT
1181912	3085170	BsrI_NBstNBI	SGTGCAGTCCCTC	C	3966.5494	CTTGGCCAGAACTGGGAGGGGACTGCAC STGAGGACTCCAGGGTCTCT

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1181912	3085170	Bsrl_NBstNBI	SGTGACGTCCCTC	G	4006.5738	CTTGGCCAGAACTGGGAGGGGACTGCAC STGAGGACTCCAGGGGTCTT
1181912	3085170	Bsrl_NBstNBI	SGTGACGTCCCTC	T	3981.561	CTTGGCCAGAACTGGGAGGGGACTGCAC STGAGGACTCCAGGGGTCTT
1184657	3086984	Bsml_NBstNBI	TTGCGCCSC	A	2754.7746	CCCAGGCGTGGAATGCAGSGGCGCAATC TTGACTCACTGCAACCT
1184657	3086984	Bsml_NBstNBI	TTGCGCCSC	C	2730.7496	CCCAGGCGTGGAATGCAGSGGCGCAATC TTGACTCACTGCAACCT
1184657	3086984	Bsml_NBstNBI	TTGCGCCSC	G	2770.774	CCCAGGCGTGGAATGCAGSGGCGCAATC TTGACTCACTGCAACCT
1184657	3086984	Bsml_NBstNBI	TTGCGCCSC	T	2745.7612	CCCAGGCGTGGAATGCAGSGGCGCAATC TTGACTCACTGCAACCT
1191246	3091881	NBstNBI_Bsrl	SGGGACTG	A	2554.6521	GACCCACCTGGAGTCCCACSGGGACTGG ACAGCCCCAC
1191246	3091881	NBstNBI_Bsrl	SGGGACTG	C	2530.6271	GACCCACCTGGAGTCCCACSGGGACTGG ACAGCCCCAC
1191246	3091881	NBstNBI_Bsrl	SGGGACTG	G	2570.6515	GACCCACCTGGAGTCCCACSGGGACTGG ACAGCCCCAC
1191246	3091881	NBstNBI_Bsrl	SGGGACTG	T	2545.6387	GACCCACCTGGAGTCCCACSGGGACTGG ACAGCCCCAC
1205938	3104174	NBstNBI	AGTGAACCCST	A	3445.2434	GTAATGCACTGAGTCATTTASGGTTCCACT CTGGGACTCAGTTTCCTAG
1205938	3104174	NBstNBI	AGTGAACCCST	C	3421.2184	GTAATGCACTGAGTCATTTASGGTTCCACT CTGGGACTCAGTTTCCTAG
1205938	3104174	NBstNBI	AGTGAACCCST	G	3461.2428	GTAATGCACTGAGTCATTTASGGTTCCACT CTGGGACTCAGTTTCCTAG
1205938	3104174	NBstNBI	AGTGAACCCST	T	3436.23	GTAATGCACTGAGTCATTTASGGTTCCACT CTGGGACTCAGTTTCCTAG
1205938	3104174	NBstNBI	ASGGTTCCACT	A	3396.2056	GTAATGCACTGAGTCATTTASGGTTCCACT CTGGGACTCAGTTTCCTAG
1205938	3104174	NBstNBI	ASGGTTCCACT	C	3372.1806	GTAATGCACTGAGTCATTTASGGTTCCACT CTGGGACTCAGTTTCCTAG
1205938	3104174	NBstNBI	ASGGTTCCACT	G	3412.205	GTAATGCACTGAGTCATTTASGGTTCCACT CTGGGACTCAGTTTCCTAG

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1205938	3104174	NBstNBI	ASGGTTCCACT	T	3387.1922	GTAATGCACTGAGTCATTTASGGTCCACT CTGGGACTCAGTTTCCTAG
1207612	3105504	NBstNBI_BsrI	CCSGGGTTGGACTG	A	4399.8323	CAGACTGATTGAGTCAGATCCSGGGTTGG ACTGGACAGCAAAGCG
1207612	3105504	NBstNBI_BsrI	CCSGGGTTGGACTG	C	4375.8073	CAGACTGATTGAGTCAGATCCSGGGTTGG ACTGGACAGCAAAGCG
1207612	3105504	NBstNBI_BsrI	CCSGGGTTGGACTG	G	4415.8317	CAGACTGATTGAGTCAGATCCSGGGTTGG ACTGGACAGCAAAGCG
1207612	3105504	NBstNBI_BsrI	CCSGGGTTGGACTG	T	4390.8189	CAGACTGATTGAGTCAGATCCSGGGTTGG ACTGGACAGCAAAGCG
1211753	3108706	BsmI_NBstNBI	TSGTGCCAT	A	2793.8112	GCTCAAGCTGGAATGCAATGGCACSATCT CGACTCACTGCAACCT
1211753	3108706	BsmI_NBstNBI	TSGTGCCAT	C	2769.7862	GCTCAAGCTGGAATGCAATGGCACSATCT CGACTCACTGCAACCT
1211753	3108706	BsmI_NBstNBI	TSGTGCCAT	G	2809.8106	GCTCAAGCTGGAATGCAATGGCACSATCT CGACTCACTGCAACCT
1211753	3108706	BsmI_NBstNBI	TSGTGCCAT	T	2784.7978	GCTCAAGCTGGAATGCAATGGCACSATCT CGACTCACTGCAACCT
1215261	3111178	BsrI_NBstNBI	TCAGTCS	A	2160.4058	TGCACTCCAGACTGGGSGACTGAGTGAGA CTCTCTCAAAAAA
1215261	3111178	BsrI_NBstNBI	TCAGTCS	C	2136.3808	TGCACTCCAGACTGGGSGACTGAGTGAGA CTCTCTCAAAAAA
1215261	3111178	BsrI_NBstNBI	TCAGTCS	G	2176.4052	TGCACTCCAGACTGGGSGACTGAGTGAGA CTCTCTCAAAAAA
1215261	3111178	BsrI_NBstNBI	TCAGTCS	T	2151.3924	TGCACTCCAGACTGGGSGACTGAGTGAGA CTCTCTCAAAAAA
1216262	3111877	NBstNBI_BsrDI	CCTSGCAATG	A	3092.0093	GTAATTATGTGAGTCAGTTCTCGCAATGA ATTGCTTTCTT
1216262	3111877	NBstNBI_BsrDI	CCTSGCAATG	C	3067.9843	GTAATTATGTGAGTCAGTTCTCGCAATGA ATTGCTTTCTT
1216262	3111877	NBstNBI_BsrDI	CCTSGCAATG	G	3108.0087	GTAATTATGTGAGTCAGTTCTCGCAATGA ATTGCTTTCTT
1216262	3111877	NBstNBI_BsrDI	CCTSGCAATG	T	3082.9959	GTAATTATGTGAGTCAGTTCTCGCAATGA ATTGCTTTCTT

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1218414	3113311	NBstNBI_BsrI	TSTGTCACCCAGACTG	A	4921.1901	TTTTTGACAGAGTCTTGCTSTGTACCCCA GACTGGGTGCAATGGC
1218414	3113311	NBstNBI_BsrI	TSTGTCACCCAGACTG	C	4897.1651	TTTTTGACAGAGTCTTGCTSTGTACCCCA GACTGGGTGCAATGGC
1218414	3113311	NBstNBI_BsrI	TSTGTCACCCAGACTG	G	4937.1895	TTTTTGACAGAGTCTTGCTSTGTACCCCA GACTGGGTGCAATGGC
1218414	3113311	NBstNBI_BsrI	TSTGTCACCCAGACTG	T	4912.1767	TTTTTGACAGAGTCTTGCTSTGTACCCCA GACTGGGTGCAATGGC
1221473	3115313	BsrI_NBstNBI	GGGCTGGAGCTGTAS	A	4753.0664	CTCTAGGGCCACTGGCSTACAGCTCCAGC CCGCAGGACTCTGCCCTCACT
1221473	3115313	BsrI_NBstNBI	GGGCTGGAGCTGTAS	C	4729.0414	CTCTAGGGCCACTGGCSTACAGCTCCAGC CCGCAGGACTCTGCCCTCACT
1221473	3115313	BsrI_NBstNBI	GGGCTGGAGCTGTAS	G	4769.0658	CTCTAGGGCCACTGGCSTACAGCTCCAGC CCGCAGGACTCTGCCCTCACT
1221473	3115313	BsrI_NBstNBI	GGGCTGGAGCTGTAS	T	4744.053	CTCTAGGGCCACTGGCSTACAGCTCCAGC CCGCAGGACTCTGCCCTCACT
1229187	3121202	BclI_NBstNBI	ASCAGTCTGATC	A	3709.4153	TTCACCATGTTGATCAGACTGSTCTGGGA CTCCTGGGCTTAA
1229187	3121202	BclI_NBstNBI	ASCAGTCTGATC	C	3685.3903	TTCACCATGTTGATCAGACTGSTCTGGGA CTCCTGGGCTTAA
1229187	3121202	BclI_NBstNBI	ASCAGTCTGATC	G	3725.4147	TTCACCATGTTGATCAGACTGSTCTGGGA CTCCTGGGCTTAA
1229187	3121202	BclI_NBstNBI	ASCAGTCTGATC	T	3700.4019	TTCACCATGTTGATCAGACTGSTCTGGGA CTCCTGGGCTTAA
1231042	3122411	NBstNBI	TAGGGGGSGTCA	A	3830.4763	TCCCTAAAAAGAGTCAGTCTAGGGGGSGT CACAGTGACTCACACCTCTAA
1231042	3122411	NBstNBI	TAGGGGGSGTCA	C	3806.4513	TCCCTAAAAAGAGTCAGTCTAGGGGGSGT CACAGTGACTCACACCTCTAA
1231042	3122411	NBstNBI	TAGGGGGSGTCA	G	3846.4757	TCCCTAAAAAGAGTCAGTCTAGGGGGSGT CACAGTGACTCACACCTCTAA
1231042	3122411	NBstNBI	TAGGGGGSGTCA	T	3821.4629	TCCCTAAAAAGAGTCAGTCTAGGGGGSGT CACAGTGACTCACACCTCTAA
1231042	3122411	NBstNBI	TGACSCCCCCTA	A	3630.3543	TCCCTAAAAAGAGTCAGTCTAGGGGGSGT CACAGTGACTCACACCTCTAA

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
1231042	3122411	NBstNBI	TGACSCCCCTA	C	3606.3293	TCCCTAAAAAGAGTCAGTCTAGGGGGSGT CACAGTGACTCACACCTCTAA
1231042	3122411	NBstNBI	TGACSCCCCTA	G	3646.3537	TCCCTAAAAAGAGTCAGTCTAGGGGGSGT CACAGTGACTCACACCTCTAA
1231042	3122411	NBstNBI	TGACSCCCCTA	T	3621.3409	TCCCTAAAAAGAGTCAGTCTAGGGGGSGT CACAGTGACTCACACCTCTAA
1235334	3124985	BsrI_NBstNBI	TTCAGSIT	A	2768.7984	GCCGGAATACACTGGGAASCTGGAACATA GACTCAACTCCTTCT
1235334	3124985	BsrI_NBstNBI	TTCAGSIT	C	2744.7734	GCCGGAATACACTGGGAASCTGGAACATA GACTCAACTCCTTCT
1235334	3124985	BsrI_NBstNBI	TTCAGSIT	G	2784.7978	GCCGGAATACACTGGGAASCTGGAACATA GACTCAACTCCTTCT
1235334	3124985	BsrI_NBstNBI	TTCAGSIT	T	2759.785	GCCGGAATACACTGGGAASCTGGAACATA GACTCAACTCCTTCT
1238033	3126387	NBstNBI_BsrI	CCCSGCACTG	A	3052.9727	TGGAAGAGCAGAGTCACAGCCCCSGCACT GGGACCTAACAG
1238033	3126387	NBstNBI_BsrI	CCCSGCACTG	C	3028.9477	TGGAAGAGCAGAGTCACAGCCCCSGCACT GGGACCTAACAG
1238033	3126387	NBstNBI_BsrI	CCCSGCACTG	G	3068.9721	TGGAAGAGCAGAGTCACAGCCCCSGCACT GGGACCTAACAG
1238033	3126387	NBstNBI_BsrI	CCCSGCACTG	T	3043.9593	TGGAAGAGCAGAGTCACAGCCCCSGCACT GGGACCTAACAG
1243265	3131276	NBstNBI_BclI	AACAGCAGASGTGATC	A	5003.2663	GAATGGATTAGAGTCTCTCAACAGCAGAS GTGATCAAGCAGAAGAA
1243265	3131276	NBstNBI_BclI	AACAGCAGASGTGATC	C	4979.2413	GAATGGATTAGAGTCTCTCAACAGCAGAS GTGATCAAGCAGAAGAA
1243265	3131276	NBstNBI_BclI	AACAGCAGASGTGATC	G	5019.2657	GAATGGATTAGAGTCTCTCTCAACAGCAGAS GTGATCAAGCAGAAGAA
1243265	3131276	NBstNBI_BclI	AACAGCAGASGTGATC	T	4994.2529	GAATGGATTAGAGTCTCTCTCAACAGCAGAS GTGATCAAGCAGAAGAA
1244959	3132899	NBstNBI_BsmI	ATSAGAATG	A	2850.8746	GGGAGGGAAGGAGTCTAACATSAGAATGC ATTATGAACATA
1244959	3132899	NBstNBI_BsmI	ATSAGAATG	C	2826.8496	GGGAGGGAAGGAGTCTAACATSAGAATGC ATTATGAACATA

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1244959	3132899	NBstNBI_BsmI	ATSAGAAATG	G	2866.874	GGGAGGGAAGGAGTCTAACATSAGAATGC ATTATGAACTA
1244959	3132899	NBstNBI_BsmI	ATSAGAAATG	T	2841.8612	GGGAGGGAAGGAGTCTAACATSAGAATGC ATTATGAACTA
1250566	3137907	BsrI_NBstNBI	ACGTGTAATTTASGTT	A	4981.2365	GTTTGGGTACTGTGAAACSTAAATACA CGTGTAGACTCTTCTTTAA
1250566	3137907	BsrI_NBstNBI	ACGTGTAATTTASGTT	C	4957.2115	GTTTGGGTACTGTGAAACSTAAATACA CGTGTAGACTCTTCTTTAA
1250566	3137907	BsrI_NBstNBI	ACGTGTAATTTASGTT	G	4997.2359	GTTTGGGTACTGTGAAACSTAAATACA CGTGTAGACTCTTCTTTAA
1250566	3137907	BsrI_NBstNBI	ACGTGTAATTTASGTT	T	4972.2231	GTTTGGGTACTGTGAAACSTAAATACA CGTGTAGACTCTTCTTTAA
1251133	3138418	NBstNBI_BsrI	STAAGTGTAAGT	A	4077.661	GCATTAGCAGAGTCTGGASTAAGTGTA CTGGATTAGTCAAT
1251133	3138418	NBstNBI_BsrI	STAAGTGTAAGT	C	4053.636	GCATTAGCAGAGTCTGGASTAAGTGTA CTGGATTAGTCAAT
1251133	3138418	NBstNBI_BsrI	STAAGTGTAAGT	G	4093.6604	GCATTAGCAGAGTCTGGASTAAGTGTA CTGGATTAGTCAAT
1251133	3138418	NBstNBI_BsrI	STAAGTGTAAGT	T	4068.6476	GCATTAGCAGAGTCTGGASTAAGTGTA CTGGATTAGTCAAT
1252963	3139977	NBstNBI_BsrI	TGTGTGCCTAGACTG	A	4992.2255	TTTGAGATGGAGTCCCCTGTGTSGCCT AGACTGGAGTGCAGTGGC
1252963	3139977	NBstNBI_BsrI	TGTGTGCCTAGACTG	C	4968.2005	TTTGAGATGGAGTCCCCTGTGTSGCCT AGACTGGAGTGCAGTGGC
1252963	3139977	NBstNBI_BsrI	TGTGTGCCTAGACTG	G	5008.2249	TTTGAGATGGAGTCCCCTGTGTSGCCT AGACTGGAGTGCAGTGGC
1252963	3139977	NBstNBI_BsrI	TGTGTGCCTAGACTG	T	4983.2121	TTTGAGATGGAGTCCCCTGTGTSGCCT AGACTGGAGTGCAGTGGC
1255536	3142048	NBstNBI_BclI	AAATSTGATC	A	3115.0465	AATTATACCAGAGTCAAAGAAATSTGATCA TGCAAAACCAC
1255536	3142048	NBstNBI_BclI	AAATSTGATC	C	3091.0215	AATTATACCAGAGTCAAAGAAATSTGATCA TGCAAAACCAC
1255536	3142048	NBstNBI_BclI	AAATSTGATC	G	3131.0459	AATTATACCAGAGTCAAAGAAATSTGATCA TGCAAAACCAC

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1255536	3142048	NBstNBI_BclI	AAATSTGATC	T	3106.0331	AATTATACCAGAGTCAAAGAAATSTGATCA TGCAAAACCAC
1261252	3146203	NBstNBI_BsmI	STAATGAATG	A	3155.0709	ACTAGGGCCAGAGTCGTACSTAATGAATG CTTACAAAATTA
1261252	3146203	NBstNBI_BsmI	STAATGAATG	C	3131.0459	ACTAGGGCCAGAGTCGTACSTAATGAATG CTTACAAAATTA
1261252	3146203	NBstNBI_BsmI	STAATGAATG	G	3171.0703	ACTAGGGCCAGAGTCGTACSTAATGAATG CTTACAAAATTA
1261252	3146203	NBstNBI_BsmI	STAATGAATG	T	3146.0575	ACTAGGGCCAGAGTCGTACSTAATGAATG CTTACAAAATTA
1261397	3146322	BsrI_NBstNBI	STCCCCTAAGATGC	A	4287.7847	CAACATGGAAACTGGGCATCTTAGGGGA SAGAAGACTCCAAGAGTCC
1261397	3146322	BsrI_NBstNBI	STCCCCTAAGATGC	C	4263.7597	CAACATGGAAACTGGGCATCTTAGGGGA SAGAAGACTCCAAGAGTCC
1261397	3146322	BsrI_NBstNBI	STCCCCTAAGATGC	G	4303.7841	CAACATGGAAACTGGGCATCTTAGGGGA SAGAAGACTCCAAGAGTCC
1261397	3146322	BsrI_NBstNBI	STCCCCTAAGATGC	T	4278.7713	CAACATGGAAACTGGGCATCTTAGGGGA SAGAAGACTCCAAGAGTCC
1261493	3146410	BsrI_NBstNBI	CTGASC	A	1856.2095	CCGGAAGAGAACTGGGGSTCAGTTCAGA CTCAGATGCTTCA
1261493	3146410	BsrI_NBstNBI	CTGASC	C	1832.1845	CCGGAAGAGAACTGGGGSTCAGTTCAGA CTCAGATGCTTCA
1261493	3146410	BsrI_NBstNBI	CTGASC	G	1872.2089	CCGGAAGAGAACTGGGGSTCAGTTCAGA CTCAGATGCTTCA
1261493	3146410	BsrI_NBstNBI	CTGASC	T	1847.1961	CCGGAAGAGAACTGGGGSTCAGTTCAGA CTCAGATGCTTCA
1261799	3146671	BclI_NBstNBI	SAATAAATGATC	A	3741.4659	CACTCAGGTTTGATCATTTATTSGAAGGAC TCACAGGGATCA
1261799	3146671	BclI_NBstNBI	SAATAAATGATC	C	3717.4409	CACTCAGGTTTGATCATTTATTSGAAGGAC TCACAGGGATCA
1261799	3146671	BclI_NBstNBI	SAATAAATGATC	G	3757.4653	CACTCAGGTTTGATCATTTATTSGAAGGAC TCACAGGGATCA
1261799	3146671	BclI_NBstNBI	SAATAAATGATC	T	3732.4525	CACTCAGGTTTGATCATTTATTSGAAGGAC TCACAGGGATCA

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1263932	3148644	BsrI_NBstNBI	TSTAAAGTGAAATAA	A	4712.106	TCCTTCTGTGACTGGCTTATTTCACTTTAS ATAATGACTCTGGTTTTATC
1263932	3148644	BsrI_NBstNBI	TSTAAAGTGAAATAA	C	4688.081	TCCTTCTGTGACTGGCTTATTTCACTTTAS ATAATGACTCTGGTTTTATC
1263932	3148644	BsrI_NBstNBI	TSTAAAGTGAAATAA	G	4728.1054	TCCTTCTGTGACTGGCTTATTTCACTTTAS ATAATGACTCTGGTTTTATC
1263932	3148644	BsrI_NBstNBI	TSTAAAGTGAAATAA	T	4703.0926	TCCTTCTGTGACTGGCTTATTTCACTTTAS ATAATGACTCTGGTTTTATC
1268715	3152397	NBstNBI	AGGTAGAACASGTGTG	A	5074.3017	CACCAGGGCTGAGTCCCAGCACACACSTGTT CTACCTGTGTGACTCCGAGCCTTAC
1268715	3152397	NBstNBI	AGGTAGAACASGTGTG	C	5050.2767	CACCAGGGCTGAGTCCCAGCACACACSTGTT CTACCTGTGTGACTCCGAGCCTTAC
1268715	3152397	NBstNBI	AGGTAGAACASGTGTG	G	5090.3011	CACCAGGGCTGAGTCCCAGCACACACSTGTT CTACCTGTGTGACTCCGAGCCTTAC
1268715	3152397	NBstNBI	AGGTAGAACASGTGTG	T	5065.2883	CACCAGGGCTGAGTCCCAGCACACACSTGTT CTACCTGTGTGACTCCGAGCCTTAC
1268715	3152397	NBstNBI	CACACSTGTTCTACCT	A	4856.1529	CACCAGGGCTGAGTCCCAGCACACACSTGTT CTACCTGTGTGACTCCGAGCCTTAC
1268715	3152397	NBstNBI	CACACSTGTTCTACCT	C	4832.1279	CACCAGGGCTGAGTCCCAGCACACACSTGTT CTACCTGTGTGACTCCGAGCCTTAC
1268715	3152397	NBstNBI	CACACSTGTTCTACCT	G	4872.1523	CACCAGGGCTGAGTCCCAGCACACACSTGTT CTACCTGTGTGACTCCGAGCCTTAC
1268715	3152397	NBstNBI	CACACSTGTTCTACCT	T	4847.1395	CACCAGGGCTGAGTCCCAGCACACACSTGTT CTACCTGTGTGACTCCGAGCCTTAC
1276972	3158124	BsrI_NBstNBI	GGATTGCTTCG	A	3756.4257	GTCTTGAACACTACTGGCCSAGCAATCCA TCCGACTCAGCCTCCCAA
1276972	3158124	BsrI_NBstNBI	GGATTGCTTCG	C	3732.4007	GTCTTGAACACTACTGGCCSAGCAATCCA TCCGACTCAGCCTCCCAA
1276972	3158124	BsrI_NBstNBI	GGATTGCTTCG	G	3772.4251	GTCTTGAACACTACTGGCCSAGCAATCCA TCCGACTCAGCCTCCCAA
1276972	3158124	BsrI_NBstNBI	GGATTGCTTCG	T	3747.4123	GTCTTGAACACTACTGGCCSAGCAATCCA TCCGACTCAGCCTCCCAA
1280135	3160903	BsmI_NBstNBI	SCCTGGC	A	2161.3936	AGCTTGTGGTGAATGCTGCCAGGSGCTGG GACTCTCTCTTCAGG

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1280135	3160903	BsmI_NBstNBI	SCCTGGC	C	2137.3686	AGCTTGGTGAATGCTGCCAGGSGCTGG GACTCTCTTTCAGG
1280135	3160903	BsmI_NBstNBI	SCCTGGC	G	2177.393	AGCTTGGTGAATGCTGCCAGGSGCTGG GACTCTCTTTCAGG
1280135	3160903	BsmI_NBstNBI	SCCTGGC	T	2152.3802	AGCTTGGTGAATGCTGCCAGGSGCTGG GACTCTCTTTCAGG
1282543	3162854	BsmI_NBstNBI	CTGCAAACTSGGGA	A	4376.8469	CCACGGTATGGAATGCTTCCCSAGTTTGC AGTAGAGACTCCTGGATGCTC
1282543	3162854	BsmI_NBstNBI	CTGCAAACTSGGGA	C	4352.8219	CCACGGTATGGAATGCTTCCCSAGTTTGC AGTAGAGACTCCTGGATGCTC
1282543	3162854	BsmI_NBstNBI	CTGCAAACTSGGGA	G	4392.8463	CCACGGTATGGAATGCTTCCCSAGTTTGC AGTAGAGACTCCTGGATGCTC
1282543	3162854	BsmI_NBstNBI	CTGCAAACTSGGGA	T	4367.8335	CCACGGTATGGAATGCTTCCCSAGTTTGC AGTAGAGACTCCTGGATGCTC
1288772	3167242	BsrI_NBstNBI	TTTTTGTAS	A	2798.8216	CAGAAACAAGACTGGASTACAAAAATAGA GACTCAAAGAAATTG
1288772	3167242	BsrI_NBstNBI	TTTTTGTAS	C	2774.7966	CAGAAACAAGACTGGASTACAAAAATAGA GACTCAAAGAAATTG
1288772	3167242	BsrI_NBstNBI	TTTTTGTAS	G	2814.821	CAGAAACAAGACTGGASTACAAAAATAGA GACTCAAAGAAATTG
1288772	3167242	BsrI_NBstNBI	TTTTTGTAS	T	2789.8082	CAGAAACAAGACTGGASTACAAAAATAGA GACTCAAAGAAATTG
1290522	3168768	BsrI_NBstNBI	CSGTAGT	A	2200.4302	CTGCCCTTCAGACTGGAACTACSGTTTTGA CTCTTCTTGGGTC
1290522	3168768	BsrI_NBstNBI	CSGTAGT	C	2176.4052	CTGCCCTTCAGACTGGAACTACSGTTTTGA CTCTTCTTGGGTC
1290522	3168768	BsrI_NBstNBI	CSGTAGT	G	2216.4296	CTGCCCTTCAGACTGGAACTACSGTTTTGA CTCTTCTTGGGTC
1290522	3168768	BsrI_NBstNBI	CSGTAGT	T	2191.4168	CTGCCCTTCAGACTGGAACTACSGTTTTGA CTCTTCTTGGGTC
1293566	3170645	NBstNBI_BsrDI	CCCCSGCAATG	A	3366.1824	TAGTATACAAGAGTCCCTCCCCCGCAAT GCAATTCTTCAC
1293566	3170645	NBstNBI_BsrDI	CCCCSGCAATG	C	3342.1574	TAGTATACAAGAGTCCCTCCCCCGCAAT GCAATTCTTCAC

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1293566	3170645	NBstNBI_BsrDI	CCCCSGCAATG	G	3382.1818	TAGTATACAAGAGTCTTCCCCCSGCAAT GCAATTTCTTAC
1293566	3170645	NBstNBI_BsrDI	CCCCSGCAATG	T	3357.169	TAGTATACAAGAGTCTTCCCCCSGCAAT GCAATTTCTTAC
1303750	3001591	NBstNBI_BsrI	SGCCCCTACTG	A	3357.169	CCTGTATAAGGAGTCTGTCSGCCCCCTACT GGGAGGTGTCTCC
1303750	3001591	NBstNBI_BsrI	SGCCCCTACTG	C	3333.144	CCTGTATAAGGAGTCTGTCSGCCCCCTACT GGGAGGTGTCTCC
1303750	3001591	NBstNBI_BsrI	SGCCCCTACTG	G	3373.1684	CCTGTATAAGGAGTCTGTCSGCCCCCTACT GGGAGGTGTCTCC
1303750	3001591	NBstNBI_BsrI	SGCCCCTACTG	T	3348.1556	CCTGTATAAGGAGTCTGTCSGCCCCCTACT GGGAGGTGTCTCC
1305026	3002659	BclI_NBstNBI	TAGACCCCTGATC	A	4287.7847	GCTTCTGCTTGATCAGGGGGTCTACTGG GACTCTCTTTGTGAT
1305026	3002659	BclI_NBstNBI	TAGACCCCTGATC	C	4263.7597	GCTTCTGCTTGATCAGGGGGTCTACTGG GACTCTCTTTGTGAT
1305026	3002659	BclI_NBstNBI	TAGACCCCTGATC	G	4303.7841	GCTTCTGCTTGATCAGGGGGTCTACTGG GACTCTCTTTGTGAT
1305026	3002659	BclI_NBstNBI	TAGACCCCTGATC	T	4278.7713	GCTTCTGCTTGATCAGGGGGTCTACTGG GACTCTCTTTGTGAT
1305457	3003023	BsrDI_NBstNBI	GAAGTSACAGA	A	3478.2818	AGGGTCTCTGGCAATGTTTCTGTSACTTC CCTTGACTCTAGACACTTC
1305457	3003023	BsrDI_NBstNBI	GAAGTSACAGA	C	3454.2568	AGGGTCTCTGGCAATGTTTCTGTSACTTC CCTTGACTCTAGACACTTC
1305457	3003023	BsrDI_NBstNBI	GAAGTSACAGA	G	3494.2812	AGGGTCTCTGGCAATGTTTCTGTSACTTC CCTTGACTCTAGACACTTC
1305457	3003023	BsrDI_NBstNBI	GAAGTSACAGA	T	3469.2684	AGGGTCTCTGGCAATGTTTCTGTSACTTC CCTTGACTCTAGACACTTC
1305510	3003072	NBstNBI_BsrI	TSTGTCACCGAAACTG	A	4945.2151	TTCGGAGATGGAGTCTTGCTSTGTACCCG AAACTGGAGTGCAGTGGC
1305510	3003072	NBstNBI_BsrI	TSTGTCACCGAAACTG	C	4921.1901	TTCGGAGATGGAGTCTTGCTSTGTACCCG AAACTGGAGTGCAGTGGC
1305510	3003072	NBstNBI_BsrI	TSTGTCACCGAAACTG	G	4961.2145	TTCGGAGATGGAGTCTTGCTSTGTACCCG AAACTGGAGTGCAGTGGC

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1305510	3003072	NBstNBI_BsrI	TSTGTCACCGAACTG	T	4936.2017	TTCGGAGATGGAGTCTTGCTSTGTCAACCG AAACTGGAGTGCAGTGCC
1305511	3003073	NBstNBI_BsrI	TGTGTCACSGAACTG	A	4985.2395	TTCGGAGATGGAGTCTTGCTGTGTCAACSG AAACTGGAGTGCAGTGCC
1305511	3003073	NBstNBI_BsrI	TGTGTCACSGAACTG	C	4961.2145	TTCGGAGATGGAGTCTTGCTGTGTCAACSG AAACTGGAGTGCAGTGCC
1305511	3003073	NBstNBI_BsrI	TGTGTCACSGAACTG	G	5001.2389	TTCGGAGATGGAGTCTTGCTGTGTCAACSG AAACTGGAGTGCAGTGCC
1305511	3003073	NBstNBI_BsrI	TGTGTCACSGAACTG	T	4976.2261	TTCGGAGATGGAGTCTTGCTGTGTCAACSG AAACTGGAGTGCAGTGCC
1308637	3005532	NBstNBI_BsrI	AATGTSTGTAACTG	A	4695.067	TCACTGCCAAGAGTCATATAATGTSTGTAA ACTGGCTTAAAAAGCA
1308637	3005532	NBstNBI_BsrI	AATGTSTGTAACTG	C	4671.042	TCACTGCCAAGAGTCATATAATGTSTGTAA ACTGGCTTAAAAAGCA
1308637	3005532	NBstNBI_BsrI	AATGTSTGTAACTG	G	4711.0664	TCACTGCCAAGAGTCATATAATGTSTGTAA ACTGGCTTAAAAAGCA
1308637	3005532	NBstNBI_BsrI	AATGTSTGTAACTG	T	4686.0536	TCACTGCCAAGAGTCATATAATGTSTGTAA ACTGGCTTAAAAAGCA
1321227	3014338	BsrI_NBstNBI	STCATGG	A	2200.4302	TCAGATAGCCACTGGCCCATGASCAGTGA CTCAAAAATTTCT
1321227	3014338	BsrI_NBstNBI	STCATGG	C	2176.4052	TCAGATAGCCACTGGCCCATGASCAGTGA CTCAAAAATTTCT
1321227	3014338	BsrI_NBstNBI	STCATGG	G	2216.4296	TCAGATAGCCACTGGCCCATGASCAGTGA CTCAAAAATTTCT
1321227	3014338	BsrI_NBstNBI	STCATGG	T	2191.4168	TCAGATAGCCACTGGCCCATGASCAGTGA CTCAAAAATTTCT
1327055	3018765	NBstNBI	CSGCCAGTG	A	2803.8124	TCTTCCCCTGGAGTCAGGCCSGCCAGTG GCTGGACTCTCTCCGACT
1327055	3018765	NBstNBI	CSGCCAGTG	C	2779.7874	TCTTCCCCTGGAGTCAGGCCSGCCAGTG GCTGGACTCTCTCCGACT
1327055	3018765	NBstNBI	CSGCCAGTG	G	2819.8118	TCTTCCCCTGGAGTCAGGCCSGCCAGTG GCTGGACTCTCTCCGACT
1327055	3018765	NBstNBI	CSGCCAGTG	T	2794.799	TCTTCCCCTGGAGTCAGGCCSGCCAGTG GCTGGACTCTCTCCGACT

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1327055	3018765	NBstNBI	CACTGGCSG	A	2803.8124	TCITCCCCTGGAGTCAGGCCSGCCAGTG GCTGGACTCTCTCCGACT
1327055	3018765	NBstNBI	CACTGGCSG	C	2779.7874	TCITCCCCTGGAGTCAGGCCSGCCAGTG GCTGGACTCTCTCCGACT
1327055	3018765	NBstNBI	CACTGGCSG	G	2819.8118	TCITCCCCTGGAGTCAGGCCSGCCAGTG GCTGGACTCTCTCCGACT
1327055	3018765	NBstNBI	CACTGGCSG	T	2794.799	TCITCCCCTGGAGTCAGGCCSGCCAGTG GCTGGACTCTCTCCGACT
1332591	3022894	NBstNBI_BclI	GGTASGTGTTGTGATC	A	5047.2615	CAGATTCTGAGAGTCTTCAGGTASGTGTT GTGATCAGAACAAATTT
1332591	3022894	NBstNBI_BclI	GGTASGTGTTGTGATC	C	5023.2365	CAGATTCTGAGAGTCTTCAGGTASGTGTT GTGATCAGAACAAATTT
1332591	3022894	NBstNBI_BclI	GGTASGTGTTGTGATC	G	5063.2609	CAGATTCTGAGAGTCTTCAGGTASGTGTT GTGATCAGAACAAATTT
1332591	3022894	NBstNBI_BclI	GGTASGTGTTGTGATC	T	5038.2481	CAGATTCTGAGAGTCTTCAGGTASGTGTT GTGATCAGAACAAATTT
1339841		BsrI_NBstNBI	GCCTGGCASCATTG	A	4303.7841	GGGCTCTTCCACTGGTGAATGSTGCCAGG CCTGGGACTCAACCTTCAGA
1339841		BsrI_NBstNBI	GCCTGGCASCATTG	C	4279.7591	GGGCTCTTCCACTGGTGAATGSTGCCAGG CCTGGGACTCAACCTTCAGA
1339841		BsrI_NBstNBI	GCCTGGCASCATTG	G	4319.7835	GGGCTCTTCCACTGGTGAATGSTGCCAGG CCTGGGACTCAACCTTCAGA
1339841		BsrI_NBstNBI	GCCTGGCASCATTG	T	4294.7707	GGGCTCTTCCACTGGTGAATGSTGCCAGG CCTGGGACTCAACCTTCAGA
1345732		NBstNBI	CCCATSGGC	A	2763.788	TTCTGTTTTTGAGTCATCGCCCATSGGCAT TTGACTCTTCGTGCTC
1345732		NBstNBI	CCCATSGGC	C	2739.763	TTCTGTTTTTGAGTCATCGCCCATSGGCAT TTGACTCTTCGTGCTC
1345732		NBstNBI	CCCATSGGC	G	2779.7874	TTCTGTTTTTGAGTCATCGCCCATSGGCAT TTGACTCTTCGTGCTC
1345732		NBstNBI	CCCATSGGC	T	2754.7746	TTCTGTTTTTGAGTCATCGCCCATSGGCAT TTGACTCTTCGTGCTC
1345732		NBstNBI	GCCSATGGG	A	2843.8368	TTCTGTTTTTGAGTCATCGCCCATSGGCAT TTGACTCTTCGTGCTC

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1345732		NBstNBI	GCCSATGGG	C	2819.8118	TTCTGTTTTTGGATCATGCCCCATSGGCAT TTGACTCTTCGTGTC
1345732		NBstNBI	GCCSATGGG	G	2859.8362	TTCTGTTTTTGGATCATGCCCCATSGGCAT TTGACTCTTCGTGTC
1345732		NBstNBI	GCCSATGGG	T	2834.8234	TTCTGTTTTTGGATCATGCCCCATSGGCAT TTGACTCTTCGTGTC
1358854		NBstNBI_Bsrl	TGCACSTGGGGTACTG	A	5017.2383	GTAGACAAAGTGAGTCTGTATGCACSTGGG GTACTGGATGAAATACTT
1358854		NBstNBI_Bsrl	TGCACSTGGGGTACTG	C	4993.2133	GTAGACAAAGTGAGTCTGTATGCACSTGGG GTACTGGATGAAATACTT
1358854		NBstNBI_Bsrl	TGCACSTGGGGTACTG	G	5033.2377	GTAGACAAAGTGAGTCTGTATGCACSTGGG GTACTGGATGAAATACTT
1358854		NBstNBI_Bsrl	TGCACSTGGGGTACTG	T	5008.2249	GTAGACAAAGTGAGTCTGTATGCACSTGGG GTACTGGATGAAATACTT
1359449		Bsrl_NBstNBI	TGCCTTTGST	A	3088.9941	AGGCAGAACAACTGGAASCAAAAGGCAGG AAGACTCAAAGCTGGGA
1359449		Bsrl_NBstNBI	TGCCTTTGST	C	3064.9691	AGGCAGAACAACTGGAASCAAAAGGCAGG AAGACTCAAAGCTGGGA
1359449		Bsrl_NBstNBI	TGCCTTTGST	G	3104.9935	AGGCAGAACAACTGGAASCAAAAGGCAGG AAGACTCAAAGCTGGGA
1359449		Bsrl_NBstNBI	TGCCTTTGST	T	3079.9807	AGGCAGAACAACTGGAASCAAAAGGCAGG AAGACTCAAAGCTGGGA
1385515		NBstNBI_Bsrl	TCTGSCACCCAGACTG	A	4906.1785	TTTGAGACACAGTCTTGCTCTGSCACCC AGACTGGAGTGCAGTGGC
1385515		NBstNBI_Bsrl	TCTGSCACCCAGACTG	C	4882.1535	TTTGAGACACAGTCTTGCTCTGSCACCC AGACTGGAGTGCAGTGGC
1385515		NBstNBI_Bsrl	TCTGSCACCCAGACTG	G	4922.1779	TTTGAGACACAGTCTTGCTCTGSCACCC AGACTGGAGTGCAGTGGC
1385515		NBstNBI_Bsrl	TCTGSCACCCAGACTG	T	4897.1651	TTTGAGACACAGTCTTGCTCTGSCACCC AGACTGGAGTGCAGTGGC
1389331		NBstNBI_Bsrl	GCSSGAGAATCACTG	A	4706.056	AGCTACTCGAGAGTCTGAGGCSGGAGAAT CACTGGAATCTGGGAGG
1389331		NBstNBI_Bsrl	GCSSGAGAATCACTG	C	4682.031	AGCTACTCGAGAGTCTGAGGCSGGAGAAT CACTGGAATCTGGGAGG

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
1389331		NBstNBI_BsrI	GCSGGAGAATCACTG	G	4722.0554	AGCTACTCGAGAGTCTGAGGCSGGAGAAT CACTGGAATCTGGAGG
1389331		NBstNBI_BsrI	GCSGGAGAATCACTG	T	4697.0426	AGCTACTCGAGAGTCTGAGGCSGGAGAAT CACTGGAATCTGGAGG
1389340		NBstNBI_BclI	TASTGATC	A	2488.6271	TTGGCAGTAGAGTCAATTTTASTGATCATA ATTCTTCC
1389340		NBstNBI_BclI	TASTGATC	C	2464.6021	TTGGCAGTAGAGTCAATTTTASTGATCATA ATTCTTCC
1389340		NBstNBI_BclI	TASTGATC	G	2504.6265	TTGGCAGTAGAGTCAATTTTASTGATCATA ATTCTTCC
1389340		NBstNBI_BclI	TASTGATC	T	2479.6137	TTGGCAGTAGAGTCAATTTTASTGATCATA ATTCTTCC
1393794		BsrI_NBstNBI	ATAGTATCTCCTSTG	A	4622.0042	GCCAATCTATACTGGTCASAGGAGATACT ATGTGTGACTCAGAAGCTCAA
1393794		BsrI_NBstNBI	ATAGTATCTCCTSTG	C	4597.9792	GCCAATCTATACTGGTCASAGGAGATACT ATGTGTGACTCAGAAGCTCAA
1393794		BsrI_NBstNBI	ATAGTATCTCCTSTG	G	4638.0036	GCCAATCTATACTGGTCASAGGAGATACT ATGTGTGACTCAGAAGCTCAA
1393794		BsrI_NBstNBI	ATAGTATCTCCTSTG	T	4612.9908	GCCAATCTATACTGGTCASAGGAGATACT ATGTGTGACTCAGAAGCTCAA
1402797		NBstNBI_BsrI	SACAGTTACTG	A	3420.2306	CATGGATCAGGAGTCAGGASACAGTTACT GGATCCTCTACTT
1402797		NBstNBI_BsrI	SACAGTTACTG	C	3396.2056	CATGGATCAGGAGTCAGGASACAGTTACT GGATCCTCTACTT
1402797		NBstNBI_BsrI	SACAGTTACTG	G	3436.23	CATGGATCAGGAGTCAGGASACAGTTACT GGATCCTCTACTT
1402797		NBstNBI_BsrI	SACAGTTACTG	T	3411.2172	CATGGATCAGGAGTCAGGASACAGTTACT GGATCCTCTACTT
1407259		NBstNBI_BsrI	SCAGGAGAATCACTG	A	4690.0566	AGCTACTCTGGAGTCTGAGSCAGGAGAAT CACTGGAGCCCAAGAGT
1407259		NBstNBI_BsrI	SCAGGAGAATCACTG	C	4666.0316	AGCTACTCTGGAGTCTGAGSCAGGAGAAT CACTGGAGCCCAAGAGT
1407259		NBstNBI_BsrI	SCAGGAGAATCACTG	G	4706.056	AGCTACTCTGGAGTCTGAGSCAGGAGAAT CACTGGAGCCCAAGAGT

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1407259		NBstNBI_BsrI	SCAGAGAATCACTG	T	4681.0432	AGCTACTCTGGAGTCTGAGSCAGGAGAAT CACTGGAGCCCAAGAGT
1408058		NBstNBI_BsrI	AAGCSCACTG	A	3101.0227	TTTGCCCTTTGAGTACCAAAAGCSCACTG GGGACAAAAAAG
1408058		NBstNBI_BsrI	AAGCSCACTG	C	3076.9977	TTTGCCCTTTGAGTACCAAAAGCSCACTG GGGACAAAAAAG
1408058		NBstNBI_BsrI	AAGCSCACTG	G	3117.0221	TTTGCCCTTTGAGTACCAAAAGCSCACTG GGGACAAAAAAG
1408058		NBstNBI_BsrI	AAGCSCACTG	T	3092.0093	TTTGCCCTTTGAGTACCAAAAGCSCACTG GGGACAAAAAAG
1412922		BsrI_NBstNBI	GAGATCAACTSG	A	3758.4531	AGCTGAGTTGACTGGCCSAGTTGATCTCT AGAGACTCAATGTGATAA
1412922		BsrI_NBstNBI	GAGATCAACTSG	C	3734.4281	AGCTGAGTTGACTGGCCSAGTTGATCTCT AGAGACTCAATGTGATAA
1412922		BsrI_NBstNBI	GAGATCAACTSG	G	3774.4525	AGCTGAGTTGACTGGCCSAGTTGATCTCT AGAGACTCAATGTGATAA
1412922		BsrI_NBstNBI	GAGATCAACTSG	T	3749.4397	AGCTGAGTTGACTGGCCSAGTTGATCTCT AGAGACTCAATGTGATAA
1425866		NBstNBI_BsrI	TCTSTCGCCCAGACTG	A	4897.1651	TTTTGAGACAGAGTCTCGCTCTSTCGCCC AGACTGGAGTGCAGTGGT
1425866		NBstNBI_BsrI	TCTSTCGCCCAGACTG	C	4873.1401	TTTTGAGACAGAGTCTCGCTCTSTCGCCC AGACTGGAGTGCAGTGGT
1425866		NBstNBI_BsrI	TCTSTCGCCCAGACTG	G	4913.1645	TTTTGAGACAGAGTCTCGCTCTSTCGCCC AGACTGGAGTGCAGTGGT
1425866		NBstNBI_BsrI	TCTSTCGCCCAGACTG	T	4888.1517	TTTTGAGACAGAGTCTCGCTCTSTCGCCC AGACTGGAGTGCAGTGGT
1439483		BsmI_NBstNBI	TAATTTT	A	2174.4296	GAATGGACACGGAATGCTSAAAATTAATGG ACTCGAATGGAATG
1439483		BsmI_NBstNBI	TAATTTT	C	2150.4046	GAATGGACACGGAATGCTSAAAATTAATGG ACTCGAATGGAATG
1439483		BsmI_NBstNBI	TAATTTT	G	2190.429	GAATGGACACGGAATGCTSAAAATTAATGG ACTCGAATGGAATG
1439483		BsmI_NBstNBI	TAATTTT	T	2165.4162	GAATGGACACGGAATGCTSAAAATTAATGG ACTCGAATGGAATG

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
1439484		BsmI_NBstNBI	TAASTTG	A	2199.4424	GAATGGACACGGAATGCTCAASTTAAATGG ACTCGAATGGAATG
1439484		BsmI_NBstNBI	TAASTTG	C	2175.4174	GAATGGACACGGAATGCTCAASTTAAATGG ACTCGAATGGAATG
1439484		BsmI_NBstNBI	TAASTTG	G	2215.4418	GAATGGACACGGAATGCTCAASTTAAATGG ACTCGAATGGAATG
1439484		BsmI_NBstNBI	TAASTTG	T	2190.429	GAATGGACACGGAATGCTCAASTTAAATGG ACTCGAATGGAATG
1439485		BsmI_NBstNBI	SAATTTG	A	2199.4424	GAATGGACACGGAATGCTCAAAATTTAAATGG ACTCGAATGGAATG
1439485		BsmI_NBstNBI	SAATTTG	C	2175.4174	GAATGGACACGGAATGCTCAAAATTTAAATGG ACTCGAATGGAATG
1439485		BsmI_NBstNBI	SAATTTG	G	2215.4418	GAATGGACACGGAATGCTCAAAATTTAAATGG ACTCGAATGGAATG
1439485		BsmI_NBstNBI	SAATTTG	T	2190.429	GAATGGACACGGAATGCTCAAAATTTAAATGG ACTCGAATGGAATG
1439907		NBstNBI	GTSAAAAATATT	A	3443.2678	CTACTTTAGTGAGTCTGACAAATATTTTSAC TTTAGACTCAAACGCAATA
1439907		NBstNBI	GTSAAAAATATT	C	3419.2428	CTACTTTAGTGAGTCTGACAAATATTTTSAC TTTAGACTCAAACGCAATA
1439907		NBstNBI	GTSAAAAATATT	G	3459.2672	CTACTTTAGTGAGTCTGACAAATATTTTSAC TTTAGACTCAAACGCAATA
1439907		NBstNBI	GTSAAAAATATT	T	3434.2544	CTACTTTAGTGAGTCTGACAAATATTTTSAC TTTAGACTCAAACGCAATA
1439907		NBstNBI	AATATTTTSAC	A	3394.23	CTACTTTAGTGAGTCTGACAAATATTTTSAC TTTAGACTCAAACGCAATA
1439907		NBstNBI	AATATTTTSAC	C	3370.205	CTACTTTAGTGAGTCTGACAAATATTTTSAC TTTAGACTCAAACGCAATA
1439907		NBstNBI	AATATTTTSAC	G	3410.2294	CTACTTTAGTGAGTCTGACAAATATTTTSAC TTTAGACTCAAACGCAATA
1439907		NBstNBI	AATATTTTSAC	T	3385.2166	CTACTTTAGTGAGTCTGACAAATATTTTSAC TTTAGACTCAAACGCAATA
1454640		NBstNBI	TTCSTTGGA	A	2808.8228	TGAAAAGACTGAGTCTCCCATCCAASGAAT GAAGACTCAGAAATGAAGC

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1454640		NBstNBI	TTCSTTGGA	C	2784.7978	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454640		NBstNBI	TTCSTTGGA	G	2824.8222	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454640		NBstNBI	TTCSTTGGA	T	2799.8094	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454640		NBstNBI	TCCAASGAA	A	2795.8386	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454640		NBstNBI	TCCAASGAA	C	2771.8136	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454640		NBstNBI	TCCAASGAA	G	2811.838	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454640		NBstNBI	TCCAASGAA	T	2786.8252	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454641		NBstNBI	TTSCSTTGGA	A	2808.8228	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454641		NBstNBI	TTSCSTTGGA	C	2784.7978	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454641		NBstNBI	TTSCSTTGGA	G	2824.8222	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454641		NBstNBI	TTSCSTTGGA	T	2799.8094	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454641		NBstNBI	TCCAAGSAA	A	2795.8386	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454641		NBstNBI	TCCAAGSAA	C	2771.8136	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454641		NBstNBI	TCCAAGSAA	G	2811.838	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454641		NBstNBI	TCCAAGSAA	T	2786.8252	TGAAAAGACTGAGTCTCCATCCAASGAAT GAAGACTCAGAATGAAGC
1454642		NBstNBI	TCCAAGGSA	A	2811.838	TGAAAAGACTGAGTCTCCATCCAAGGSAT GAAGACTCAGAATGAAGC
1454642		NBstNBI	TCCAAGGSA	C	2787.813	TGAAAAGACTGAGTCTCCATCCAAGGSAT GAAGACTCAGAATGAAGC

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
1454642		NBstNBI	TCCAAGGSA	G	2827.8374	TGAAAAGACTGAGTCTCCATCCAAGGSAT GAAGACTCAGAATGAAGC
1454642		NBstNBI	TCCAAGGSA	T	2802.8246	TGAAAAGACTGAGTCTCCATCCAAGGSAT GAAGACTCAGAATGAAGC
1454642		NBstNBI	TSCCTTGA	A	2793.8112	TGAAAAGACTGAGTCTCCATCCAAGGSAT GAAGACTCAGAATGAAGC
1454642		NBstNBI	TSCCTTGA	C	2769.7862	TGAAAAGACTGAGTCTCCATCCAAGGSAT GAAGACTCAGAATGAAGC
1454642		NBstNBI	TSCCTTGA	G	2809.8106	TGAAAAGACTGAGTCTCCATCCAAGGSAT GAAGACTCAGAATGAAGC
1454642		NBstNBI	TSCCTTGA	T	2784.7978	TGAAAAGACTGAGTCTCCATCCAAGGSAT GAAGACTCAGAATGAAGC
1468852		NBstNBI_BsrI	ATATASACTG	A	3115.0465	GTAACTAGAGAGTCAGTCATATASACTG GAATTCAGAAG
1468852		NBstNBI_BsrI	ATATASACTG	C	3091.0215	GTAACTAGAGAGTCAGTCATATASACTG GAATTCAGAAG
1468852		NBstNBI_BsrI	ATATASACTG	G	3131.0459	GTAACTAGAGAGTCAGTCATATASACTG GAATTCAGAAG
1468852		NBstNBI_BsrI	ATATASACTG	T	3106.0331	GTAACTAGAGAGTCAGTCATATASACTG GAATTCAGAAG
1471203		NBstNBI_BclI	ASATAAGAAATGTGATC	A	5017.2901	AACTGAGATGGAGTCTTATASATAAAGAATG TGATCATGGGAGTGAC
1471203		NBstNBI_BclI	ASATAAGAAATGTGATC	C	4993.2651	AACTGAGATGGAGTCTTATASATAAAGAATG TGATCATGGGAGTGAC
1471203		NBstNBI_BclI	ASATAAGAAATGTGATC	G	5033.2895	AACTGAGATGGAGTCTTATASATAAAGAATG TGATCATGGGAGTGAC
1471203		NBstNBI_BclI	ASATAAGAAATGTGATC	T	5008.2767	AACTGAGATGGAGTCTTATASATAAAGAATG TGATCATGGGAGTGAC
1479523		NBstNBI	GGTGACACSTCGCC	A	4328.7969	CCGCAGCTCTGAGTCTCCAGGCCGASGTGT CACCACAGGACTCGTTTCCCGT
1479523		NBstNBI	GGTGACACSTCGCC	C	4304.7719	CCGCAGCTCTGAGTCTCCAGGCCGASGTGT CACCACAGGACTCGTTTCCCGT
1479523		NBstNBI	GGTGACACSTCGCC	G	4344.7963	CCGCAGCTCTGAGTCTCCAGGCCGASGTGT CACCACAGGACTCGTTTCCCGT

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
1479523		NBstNBI	GGTGACACSTCGCC	T	4319.7835	CCGCAGCTCTGAGTCTCCAGGCGASGTGT CACACAGGACTCGTTTCCCGT
1479523		NBstNBI	GGCGASGTGTCACC	A	4368.8213	CCGCAGCTCTGAGTCTCCAGGCGASGTGT CACACAGGACTCGTTTCCCGT
1479523		NBstNBI	GGCGASGTGTCACC	C	4344.7963	CCGCAGCTCTGAGTCTCCAGGCGASGTGT CACACAGGACTCGTTTCCCGT
1479523		NBstNBI	GGCGASGTGTCACC	G	4384.8207	CCGCAGCTCTGAGTCTCCAGGCGASGTGT CACACAGGACTCGTTTCCCGT
1479523		NBstNBI	GGCGASGTGTCACC	T	4359.8079	CCGCAGCTCTGAGTCTCCAGGCGASGTGT CACACAGGACTCGTTTCCCGT
1513534		BsrI_NBstNBI	CCTTTCGGA	A	3082.9959	CATCCCTCGCACTGGTCCSAAAAGGCCT AGACTCGAAAATTGAG
1513534		BsrI_NBstNBI	CCTTTCGGA	C	3058.9709	CATCCCTCGCACTGGTCCSAAAAGGCCT AGACTCGAAAATTGAG
1513534		BsrI_NBstNBI	CCTTTCGGA	G	3098.9953	CATCCCTCGCACTGGTCCSAAAAGGCCT AGACTCGAAAATTGAG
1513534		BsrI_NBstNBI	CCTTTCGGA	T	3073.9825	CATCCCTCGCACTGGTCCSAAAAGGCCT AGACTCGAAAATTGAG
1515262		NBstNBI_BsaBI	STTGTGATGG	A	3178.0563	ACCCAGCCTTGAGTCCCTAASTTGTGATGG GAATCTTTAGAGAAA
1515262		NBstNBI_BsaBI	STTGTGATGG	C	3154.0313	ACCCAGCCTTGAGTCCCTAASTTGTGATGG GAATCTTTAGAGAAA
1515262		NBstNBI_BsaBI	STTGTGATGG	G	3194.0557	ACCCAGCCTTGAGTCCCTAASTTGTGATGG GAATCTTTAGAGAAA
1515262		NBstNBI_BsaBI	STTGTGATGG	T	3169.0429	ACCCAGCCTTGAGTCCCTAASTTGTGATGG GAATCTTTAGAGAAA
1531777		BclI_NBstNBI	ACSTGTAAGATGATC	A	4680.0554	TTTAAGGAGCTGATCATCTTACASGTCATT GACTCAGTGGGGAAG
1531777		BclI_NBstNBI	ACSTGTAAGATGATC	C	4656.0304	TTTAAGGAGCTGATCATCTTACASGTCATT GACTCAGTGGGGAAG
1531777		BclI_NBstNBI	ACSTGTAAGATGATC	G	4696.0548	TTTAAGGAGCTGATCATCTTACASGTCATT GACTCAGTGGGGAAG
1531777		BclI_NBstNBI	ACSTGTAAGATGATC	T	4671.042	TTTAAGGAGCTGATCATCTTACASGTCATT GACTCAGTGGGGAAG

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
1532351		BsrI_NBstNBI	AACSGGT	A	2209.4436	CAATGTCCAGACTGGAACCSGTTTGCAGA CTCAGAACCCTT
1532351		BsrI_NBstNBI	AACSGGT	C	2185.4186	CAATGTCCAGACTGGAACCSGTTTGCAGA CTCAGAACCCTT
1532351		BsrI_NBstNBI	AACSGGT	G	2225.443	CAATGTCCAGACTGGAACCSGTTTGCAGA CTCAGAACCCTT
1532351		BsrI_NBstNBI	AACSGGT	T	2200.4302	CAATGTCCAGACTGGAACCSGTTTGCAGA CTCAGAACCCTT
1551407		BclI_NBstNBI	CTAASGAACCTTGATC	A	4640.031	GCTAAGGGTTTGATCAAGTTCSTTAGGGT TGACTCATGGTAAGCA
1551407		BclI_NBstNBI	CTAASGAACCTTGATC	C	4616.006	GCTAAGGGTTTGATCAAGTTCSTTAGGGT TGACTCATGGTAAGCA
1551407		BclI_NBstNBI	CTAASGAACCTTGATC	G	4656.0304	GCTAAGGGTTTGATCAAGTTCSTTAGGGT TGACTCATGGTAAGCA
1551407		BclI_NBstNBI	CTAASGAACCTTGATC	T	4631.0176	GCTAAGGGTTTGATCAAGTTCSTTAGGGT TGACTCATGGTAAGCA
1565170		BsrI_NBstNBI	TGAGGGGSGGAATGTG	A	5146.3249	TCCAGCTGCATGGGCACATTCSCCCCC TCACCCCTGACTCACAAGGTGT
1565170		BsrI_NBstNBI	TGAGGGGSGGAATGTG	C	5122.2999	TCCAGCTGCATGGGCACATTCSCCCCC TCACCCCTGACTCACAAGGTGT
1565170		BsrI_NBstNBI	TGAGGGGSGGAATGTG	G	5162.3243	TCCAGCTGCATGGGCACATTCSCCCCC TCACCCCTGACTCACAAGGTGT
1565170		BsrI_NBstNBI	TGAGGGGSGGAATGTG	T	5137.3115	TCCAGCTGCATGGGCACATTCSCCCCC TCACCCCTGACTCACAAGGTGT
1566573		BsrI_NBstNBI	AASAGAACCATGGAA	A	4707.0956	AACACTAGTCACTGGGTCCCATGGTTCTST TCCGTGACTCATGGCTTCTA
1566573		BsrI_NBstNBI	AASAGAACCATGGAA	C	4683.0706	AACACTAGTCACTGGGTCCCATGGTTCTST TCCGTGACTCATGGCTTCTA
1566573		BsrI_NBstNBI	AASAGAACCATGGAA	G	4723.095	AACACTAGTCACTGGGTCCCATGGTTCTST TCCGTGACTCATGGCTTCTA
1566573		BsrI_NBstNBI	AASAGAACCATGGAA	T	4698.0822	AACACTAGTCACTGGGTCCCATGGTTCTST TCCGTGACTCATGGCTTCTA
1567397		BsrI_NBstNBI	AGTTCAAGSC	A	3116.0343	ATCATAGCTCACTGGAGSCTTGAACCTCT GGACTCAAGCAATCCT

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1567397		BsrI_NBstNBI	AGTTCAGGSC	C	3092.0093	ATCATAGCTCACTGGAGSCTTGAACCTTCT GGACTCAAGCAATCCT
1567397		BsrI_NBstNBI	AGTTCAGGSC	G	3132.0337	ATCATAGCTCACTGGAGSCTTGAACCTTCT GGACTCAAGCAATCCT
1567397		BsrI_NBstNBI	AGTTCAGGSC	T	3107.0209	ATCATAGCTCACTGGAGSCTTGAACCTTCT GGACTCAAGCAATCCT
1576428		NBstNBI	TACCCSCCAG	A	2996.9489	GACCTGGCAGAGTCTGCGTACCCSCCA CTAGCGACTCTTCAGCCCTC
1576428		NBstNBI	TACCCSCCAG	C	2972.9239	GACCTGGCAGAGTCTGCGTACCCSCCA CTAGCGACTCTTCAGCCCTC
1576428		NBstNBI	TACCCSCCAG	G	3012.9483	GACCTGGCAGAGTCTGCGTACCCSCCA CTAGCGACTCTTCAGCCCTC
1576428		NBstNBI	TACCCSCCAG	T	2987.9355	GACCTGGCAGAGTCTGCGTACCCSCCA CTAGCGACTCTTCAGCCCTC
1576428		NBstNBI	GTGGSGGGTA	A	3228.0819	GACCTGGCAGAGTCTGCGTACCCSCCA CTAGCGACTCTTCAGCCCTC
1576428		NBstNBI	GTGGSGGGTA	C	3204.0569	GACCTGGCAGAGTCTGCGTACCCSCCA CTAGCGACTCTTCAGCCCTC
1576428		NBstNBI	GTGGSGGGTA	G	3244.0813	GACCTGGCAGAGTCTGCGTACCCSCCA CTAGCGACTCTTCAGCCCTC
1576428		NBstNBI	GTGGSGGGTA	T	3219.0685	GACCTGGCAGAGTCTGCGTACCCSCCA CTAGCGACTCTTCAGCCCTC
1577648		NBstNBI_BsrI	SGGAACTG	A	2538.6527	GTTTACTGGAGAGTCAGAAASGGAACTGGG TATGACTAGA
1577648		NBstNBI_BsrI	SGGAACTG	C	2514.6277	GTTTACTGGAGAGTCAGAAASGGAACTGGG TATGACTAGA
1577648		NBstNBI_BsrI	SGGAACTG	G	2554.6521	GTTTACTGGAGAGTCAGAAASGGAACTGGG TATGACTAGA
1577648		NBstNBI_BsrI	SGGAACTG	T	2529.6393	GTTTACTGGAGAGTCAGAAASGGAACTGGG TATGACTAGA
1581386		NBstNBI	GTSATTTC	A	2768.7984	GATGGAGACTGAGTCATCTGGAATTSACA TCTGACTCCTGGACATA
1581386		NBstNBI	GTSATTTC	C	2744.7734	GATGGAGACTGAGTCATCTGGAATTSACA TCTGACTCCTGGACATA

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
1581386		NBstNBI	GTSATTTCC	G	2784.7978	GATGGAGACTGAGTCATCTGGAAATSACA TCTGACTCCTGGGACATA
1581386		NBstNBI	GTSATTTCC	T	2759.785	GATGGAGACTGAGTCATCTGGAAATSACA TCTGACTCCTGGGACATA
1581386		NBstNBI	GGAAATSAC	A	2835.863	GATGGAGACTGAGTCATCTGGAAATSACA TCTGACTCCTGGGACATA
1581386		NBstNBI	GGAAATSAC	C	2811.838	GATGGAGACTGAGTCATCTGGAAATSACA TCTGACTCCTGGGACATA
1581386		NBstNBI	GGAAATSAC	G	2851.8624	GATGGAGACTGAGTCATCTGGAAATSACA TCTGACTCCTGGGACATA
1581386		NBstNBI	GGAAATSAC	T	2826.8496	GATGGAGACTGAGTCATCTGGAAATSACA TCTGACTCCTGGGACATA
1594830		NBstNBI	TTTTSTTGCCCAG	A	3691.3885	CCAGGAGTTTGAGTCCAGCCTGGGCAASA AAGTGAGACTCCCATCTGTAA
1594830		NBstNBI	TTTTSTTGCCCAG	C	3667.3635	CCAGGAGTTTGAGTCCAGCCTGGGCAASA AAGTGAGACTCCCATCTGTAA
1594830		NBstNBI	TTTTSTTGCCCAG	G	3707.3879	CCAGGAGTTTGAGTCCAGCCTGGGCAASA AAGTGAGACTCCCATCTGTAA
1594830		NBstNBI	TTTTSTTGCCCAG	T	3682.3751	CCAGGAGTTTGAGTCCAGCCTGGGCAASA AAGTGAGACTCCCATCTGTAA
1594830		NBstNBI	CTGGGCAASAAA	A	3767.4665	CCAGGAGTTTGAGTCCAGCCTGGGCAASA AAGTGAGACTCCCATCTGTAA
1594830		NBstNBI	CTGGGCAASAAA	C	3743.4415	CCAGGAGTTTGAGTCCAGCCTGGGCAASA AAGTGAGACTCCCATCTGTAA
1594830		NBstNBI	CTGGGCAASAAA	G	3783.4659	CCAGGAGTTTGAGTCCAGCCTGGGCAASA AAGTGAGACTCCCATCTGTAA
1594830		NBstNBI	CTGGGCAASAAA	T	3758.4531	CCAGGAGTTTGAGTCCAGCCTGGGCAASA AAGTGAGACTCCCATCTGTAA
1598049		NBstNBI	CSCTCGACACCTCTGC	A	4842.1291	TCCAGCCCCGAGTCCCACGCAGAGGTG TCGAGSGTGGGACTCTGTCTGAGT
1598049		NBstNBI	CSCTCGACACCTCTGC	C	4818.1041	TCCAGCCCCGAGTCCCACGCAGAGGTG TCGAGSGTGGGACTCTGTCTGAGT
1598049		NBstNBI	CSCTCGACACCTCTGC	G	4858.1285	TCCAGCCCCGAGTCCCACGCAGAGGTG TCGAGSGTGGGACTCTGTCTGAGT

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1598049		NBstNBI	CSCTCGACACCTCTGC	T	4833.1157	TCCAGCCCCGAGTCCCACGCAGAGGTG TCGAGSGTGGGACTCTGTGCTGAGT
1598049		NBstNBI	GCAGAGGTGTCGAGSG	A	5091.2889	TCCAGCCCCGAGTCCCACGCAGAGGTG TCGAGSGTGGGACTCTGTGCTGAGT
1598049		NBstNBI	GCAGAGGTGTCGAGSG	C	5067.2639	TCCAGCCCCGAGTCCCACGCAGAGGTG TCGAGSGTGGGACTCTGTGCTGAGT
1598049		NBstNBI	GCAGAGGTGTCGAGSG	G	5107.2883	TCCAGCCCCGAGTCCCACGCAGAGGTG TCGAGSGTGGGACTCTGTGCTGAGT
1598049		NBstNBI	GCAGAGGTGTCGAGSG	T	5082.2755	TCCAGCCCCGAGTCCCACGCAGAGGTG TCGAGSGTGGGACTCTGTGCTGAGT
1605424		NBstNBI_BsrI	ATTCSTCACTG	A	3371.1928	CTGCTAGTTGGAGTCTTCATTCSTCACTG GCTATTGGCTGG
1605424		NBstNBI_BsrI	ATTCSTCACTG	C	3347.1678	CTGCTAGTTGGAGTCTTCATTCSTCACTG GCTATTGGCTGG
1605424		NBstNBI_BsrI	ATTCSTCACTG	G	3387.1922	CTGCTAGTTGGAGTCTTCATTCSTCACTG GCTATTGGCTGG
1605424		NBstNBI_BsrI	ATTCSTCACTG	T	3362.1794	CTGCTAGTTGGAGTCTTCATTCSTCACTG GCTATTGGCTGG
1607860		NBstNBI_BclI	SGTGAGGACTGATC	A	4407.8579	TTGGCTCCCAGAGTCCCCCSGTGAGGACT GATCACGAACTCCAT
1607860		NBstNBI_BclI	SGTGAGGACTGATC	C	4383.8329	TTGGCTCCCAGAGTCCCCCSGTGAGGACT GATCACGAACTCCAT
1607860		NBstNBI_BclI	SGTGAGGACTGATC	G	4423.8573	TTGGCTCCCAGAGTCCCCCSGTGAGGACT GATCACGAACTCCAT
1607860		NBstNBI_BclI	SGTGAGGACTGATC	T	4398.8445	TTGGCTCCCAGAGTCCCCCSGTGAGGACT GATCACGAACTCCAT
1611299		BsrDI_NBstNBI	GGCGCAATCTSAG	A	4063.6372	GGCAGAGGTTGCAATGAGCTSAGATTGCG CCACTGGACTCCAGCTTGGGT
1611299		BsrDI_NBstNBI	GGCGCAATCTSAG	C	4039.6122	GGCAGAGGTTGCAATGAGCTSAGATTGCG CCACTGGACTCCAGCTTGGGT
1611299		BsrDI_NBstNBI	GGCGCAATCTSAG	G	4079.6366	GGCAGAGGTTGCAATGAGCTSAGATTGCG CCACTGGACTCCAGCTTGGGT
1611299		BsrDI_NBstNBI	GGCGCAATCTSAG	T	4054.6238	GGCAGAGGTTGCAATGAGCTSAGATTGCG CCACTGGACTCCAGCTTGGGT

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1612845		NBstNBI	AGCAACGACTST	A	3718.4287	ACATTTCTTAGAGTCCAGAAASAGTCGTTGC TTAAAGACTCTGAAGGCCTA
1612845		NBstNBI	AGCAACGACTST	C	3694.4037	ACATTTCTTAGAGTCCAGAAASAGTCGTTGC TTAAAGACTCTGAAGGCCTA
1612845		NBstNBI	AGCAACGACTST	G	3734.4281	ACATTTCTTAGAGTCCAGAAASAGTCGTTGC TTAAAGACTCTGAAGGCCTA
1612845		NBstNBI	AGCAACGACTST	T	3709.4153	ACATTTCTTAGAGTCCAGAAASAGTCGTTGC TTAAAGACTCTGAAGGCCTA
1612845		NBstNBI	ASAGTCGTTGCT	A	3740.4263	ACATTTCTTAGAGTCCAGAAASAGTCGTTGC TTAAAGACTCTGAAGGCCTA
1612845		NBstNBI	ASAGTCGTTGCT	C	3716.4013	ACATTTCTTAGAGTCCAGAAASAGTCGTTGC TTAAAGACTCTGAAGGCCTA
1612845		NBstNBI	ASAGTCGTTGCT	G	3756.4257	ACATTTCTTAGAGTCCAGAAASAGTCGTTGC TTAAAGACTCTGAAGGCCTA
1612845		NBstNBI	ASAGTCGTTGCT	T	3731.4129	ACATTTCTTAGAGTCCAGAAASAGTCGTTGC TTAAAGACTCTGAAGGCCTA
1617320		NBstNBI_BsaBI	CTGSAGGATGG	A	3501.2672	TTATCTTATGGAGTCACGCCTGSAGGATG GTGATCCCATCAGATT
1617320		NBstNBI_BsaBI	CTGSAGGATGG	C	3477.2422	TTATCTTATGGAGTCACGCCTGSAGGATG GTGATCCCATCAGATT
1617320		NBstNBI_BsaBI	CTGSAGGATGG	G	3517.2666	TTATCTTATGGAGTCACGCCTGSAGGATG GTGATCCCATCAGATT
1617320		NBstNBI_BsaBI	CTGSAGGATGG	T	3492.2538	TTATCTTATGGAGTCACGCCTGSAGGATG GTGATCCCATCAGATT
1618470		NBstNBI_BclI	CACSCTGATC	A	3051.9849	TTATCCCTTGGAGTCAGCCCACSCCTGATC AAATTCGAAAAG
1618470		NBstNBI_BclI	CACSCTGATC	C	3027.9599	TTATCCCTTGGAGTCAGCCCACSCCTGATC AAATTCGAAAAG
1618470		NBstNBI_BclI	CACSCTGATC	G	3067.9843	TTATCCCTTGGAGTCAGCCCACSCCTGATC AAATTCGAAAAG
1618470		NBstNBI_BclI	CACSCTGATC	T	3042.9715	TTATCCCTTGGAGTCAGCCCACSCCTGATC AAATTCGAAAAG
1619791		NBstNBI	ATGACCTCCTTCS	A	3949.5622	AATGTTTTTATAGATCAGCCSGAAGGAGGT CATTAAATGACTCAAGGAAGGGG

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1619791		NBstNBI	ATGACCTCCTTCS	C	3925.5372	AATGTTTTTAGAGTCAGCCSGAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1619791		NBstNBI	ATGACCTCCTTCS	G	3965.5616	AATGTTTTTAGAGTCAGCCSGAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1619791		NBstNBI	ATGACCTCCTTCS	T	3940.5488	AATGTTTTTAGAGTCAGCCSGAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1619791		NBstNBI	SGAAGGAGGTCAT	A	4127.6866	AATGTTTTTAGAGTCAGCCSGAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1619791		NBstNBI	SGAAGGAGGTCAT	C	4103.6616	AATGTTTTTAGAGTCAGCCSGAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1619791		NBstNBI	SGAAGGAGGTCAT	G	4143.686	AATGTTTTTAGAGTCAGCCSGAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1619791		NBstNBI	SGAAGGAGGTCAT	T	4118.6732	AATGTTTTTAGAGTCAGCCSGAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1619792		NBstNBI	ASAAGGAGGTCAT	A	4111.6872	AATGTTTTTAGAGTCAGCCSAAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1619792		NBstNBI	ASAAGGAGGTCAT	C	4087.6622	AATGTTTTTAGAGTCAGCCSAAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1619792		NBstNBI	ASAAGGAGGTCAT	G	4127.6866	AATGTTTTTAGAGTCAGCCSAAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1619792		NBstNBI	ASAAGGAGGTCAT	T	4102.6738	AATGTTTTTAGAGTCAGCCSAAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1619792		NBstNBI	ATGACCTCCTTST	A	3964.5738	AATGTTTTTAGAGTCAGCCSAAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1619792		NBstNBI	ATGACCTCCTTST	C	3940.5488	AATGTTTTTAGAGTCAGCCSAAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1619792		NBstNBI	ATGACCTCCTTST	G	3980.5732	AATGTTTTTAGAGTCAGCCSAAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1619792		NBstNBI	ATGACCTCCTTST	T	3955.5604	AATGTTTTTAGAGTCAGCCSAAAGGAGGT CATTAACTGACTCAAGGAAGGGG
1625696		NBstNBI	ACSCAT	A	1840.2101	TCATATTGAGAGTCACAGATGSGTTGATG ACTCTCAGATCATG
1625696		NBstNBI	ACSCAT	C	1816.1851	TCATATTGAGAGTCACAGATGSGTTGATG ACTCTCAGATCATG

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1625696		NBstNBI	ACSCAT	G	1856.2095	TCATATTTGAGAGTCACAGATGSGTTGATG ACTCTCAGATCATG
1625696		NBstNBI	ACSCAT	T	1831.1967	TCATATTTGAGAGTCACAGATGSGTTGATG ACTCTCAGATCATG
1625696		NBstNBI	ATGSGT	A	1911.2455	TCATATTTGAGAGTCACAGATGSGTTGATG ACTCTCAGATCATG
1625696		NBstNBI	ATGSGT	C	1887.2205	TCATATTTGAGAGTCACAGATGSGTTGATG ACTCTCAGATCATG
1625696		NBstNBI	ATGSGT	G	1927.2449	TCATATTTGAGAGTCACAGATGSGTTGATG ACTCTCAGATCATG
1625696		NBstNBI	ATGSGT	T	1902.2321	TCATATTTGAGAGTCACAGATGSGTTGATG ACTCTCAGATCATG
1633504		BsrI_NBstNBI	TGTTSATCCA	A	3082.0081	GTAACAAAAGACTGGCTGGGATSAACATTTT GACTCTCTTTTGACA
1633504		BsrI_NBstNBI	TGTTSATCCA	C	3057.9831	GTAACAAAAGACTGGCTGGGATSAACATTTT GACTCTCTTTTGACA
1633504		BsrI_NBstNBI	TGTTSATCCA	G	3098.0075	GTAACAAAAGACTGGCTGGGATSAACATTTT GACTCTCTTTTGACA
1633504		BsrI_NBstNBI	TGTTSATCCA	T	3072.9947	GTAACAAAAGACTGGCTGGGATSAACATTTT GACTCTCTTTTGACA
1640696		NBstNBI_BsrI	CCCSACTG	A	2434.5789	CAGATGCCATGAGTCTATCCCCSACTGGT GGGGTGAAGT
1640696		NBstNBI_BsrI	CCCSACTG	C	2410.5539	CAGATGCCATGAGTCTATCCCCSACTGGT GGGGTGAAGT
1640696		NBstNBI_BsrI	CCCSACTG	G	2450.5783	CAGATGCCATGAGTCTATCCCCSACTGGT GGGGTGAAGT
1640696		NBstNBI_BsrI	CCCSACTG	T	2425.5655	CAGATGCCATGAGTCTATCCCCSACTGGT GGGGTGAAGT
1642816		NBstNBI_BsrI	SCCGATACTG	A	3092.0093	GTGAGCCTGAGAGTCCGGCGSCCGATACT GGATGCACCTCTG
1642816		NBstNBI_BsrI	SCCGATACTG	C	3067.9843	GTGAGCCTGAGAGTCCGGCGSCCGATACT GGATGCACCTCTG
1642816		NBstNBI_BsrI	SCCGATACTG	G	3108.0087	GTGAGCCTGAGAGTCCGGCGSCCGATACT GGATGCACCTCTG

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1642816		NBstNBI_BsrI	SCCGATACTG	T	3082.9959	GTGAGCCTGAGAGTCCGGSCCGGATCTG GGATGCACCTTCTG
1654562		NBstNBI_BclI	CASCTGTGATC	A	3396.2056	GGCCTCCTGTGAGTCAGAACASCTGTGAT CACTCCAGGAGG
1654562		NBstNBI_BclI	CASCTGTGATC	C	3372.1806	GGCCTCCTGTGAGTCAGAACASCTGTGAT CACTCCAGGAGG
1654562		NBstNBI_BclI	CASCTGTGATC	G	3412.205	GGCCTCCTGTGAGTCAGAACASCTGTGAT CACTCCAGGAGG
1654562		NBstNBI_BclI	CASCTGTGATC	T	3387.1922	GGCCTCCTGTGAGTCAGAACASCTGTGAT CACTCCAGGAGG
1660005		BsaBI_NBstNBI	SGATGG	A	1936.2583	TTGGATCAGGGATCCCCATCSGTCTGACT CACGTGTCTAT
1660005		BsaBI_NBstNBI	SGATGG	C	1912.2333	TTGGATCAGGGATCCCCATCSGTCTGACT CACGTGTCTAT
1660005		BsaBI_NBstNBI	SGATGG	G	1952.2577	TTGGATCAGGGATCCCCATCSGTCTGACT CACGTGTCTAT
1660005		BsaBI_NBstNBI	SGATGG	T	1927.2449	TTGGATCAGGGATCCCCATCSGTCTGACT CACGTGTCTAT
1681922		BsrI_NBstNBI	AGAGCGSTGGG	A	3526.28	GGACTGTCCAACTGGCCCCASCCTCTGA CTGACTCCTTCCCAGAC
1681922		BsrI_NBstNBI	AGAGCGSTGGG	C	3502.255	GGACTGTCCAACTGGCCCCASCCTCTGA CTGACTCCTTCCCAGAC
1681922		BsrI_NBstNBI	AGAGCGSTGGG	G	3542.2794	GGACTGTCCAACTGGCCCCASCCTCTGA CTGACTCCTTCCCAGAC
1681922		BsrI_NBstNBI	AGAGCGSTGGG	T	3517.2666	GGACTGTCCAACTGGCCCCASCCTCTGA CTGACTCCTTCCCAGAC
1681923		BsrI_NBstNBI	AGAGCSTTGGG	A	3501.2672	GGACTGTCCAACTGGCCCCAASGCTCTGA CTGACTCCTTCCCAGAC
1681923		BsrI_NBstNBI	AGAGCSTTGGG	C	3477.2422	GGACTGTCCAACTGGCCCCAASGCTCTGA CTGACTCCTTCCCAGAC
1681923		BsrI_NBstNBI	AGAGCSTTGGG	G	3517.2666	GGACTGTCCAACTGGCCCCAASGCTCTGA CTGACTCCTTCCCAGAC
1681923		BsrI_NBstNBI	AGAGCSTTGGG	T	3492.2538	GGACTGTCCAACTGGCCCCAASGCTCTGA CTGACTCCTTCCCAGAC

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1690112		NBstNBI	ASTGATTAC	A	2801.8368	CTGGCCAGGTGAGTCAACAGTAATCASTG TTTGACTCTTCATGACAA
1690112		NBstNBI	ASTGATTAC	C	2777.8118	CTGGCCAGGTGAGTCAACAGTAATCASTG TTTGACTCTTCATGACAA
1690112		NBstNBI	ASTGATTAC	G	2817.8362	CTGGCCAGGTGAGTCAACAGTAATCASTG TTTGACTCTTCATGACAA
1690112		NBstNBI	ASTGATTAC	T	2792.8234	CTGGCCAGGTGAGTCAACAGTAATCASTG TTTGACTCTTCATGACAA
1690112		NBstNBI	GTAATCAST	A	2801.8368	CTGGCCAGGTGAGTCAACAGTAATCASTG TTTGACTCTTCATGACAA
1690112		NBstNBI	GTAATCAST	C	2777.8118	CTGGCCAGGTGAGTCAACAGTAATCASTG TTTGACTCTTCATGACAA
1690112		NBstNBI	GTAATCAST	G	2817.8362	CTGGCCAGGTGAGTCAACAGTAATCASTG TTTGACTCTTCATGACAA
1690112		NBstNBI	GTAATCAST	T	2792.8234	CTGGCCAGGTGAGTCAACAGTAATCASTG TTTGACTCTTCATGACAA
1703345		BsrI_NBstNBI	CTCCTAGGTCCASCT	A	4567.956	CCCCCTGGAGACTGGAAGSTGGACCTAG GAGTGGAGACTCATATTGCTGC
1703345		BsrI_NBstNBI	CTCCTAGGTCCASCT	C	4543.931	CCCCCTGGAGACTGGAAGSTGGACCTAG GAGTGGAGACTCATATTGCTGC
1703345		BsrI_NBstNBI	CTCCTAGGTCCASCT	G	4583.9554	CCCCCTGGAGACTGGAAGSTGGACCTAG GAGTGGAGACTCATATTGCTGC
1703345		BsrI_NBstNBI	CTCCTAGGTCCASCT	T	4558.9426	CCCCCTGGAGACTGGAAGSTGGACCTAG GAGTGGAGACTCATATTGCTGC
1704439		NBstNBI	TCCSCACCTCCC	A	3566.3049	ACCTCTGACAGAGTCTCTGGGGGAGGTGS GGACACAGACTCAGGGGAGAGA
1704439		NBstNBI	TCCSCACCTCCC	C	3542.2799	ACCTCTGACAGAGTCTCTGGGGGAGGTGS GGACACAGACTCAGGGGAGAGA
1704439		NBstNBI	TCCSCACCTCCC	G	3582.3043	ACCTCTGACAGAGTCTCTGGGGGAGGTGS GGACACAGACTCAGGGGAGAGA
1704439		NBstNBI	TCCSCACCTCCC	T	3557.2915	ACCTCTGACAGAGTCTCTGGGGGAGGTGS GGACACAGACTCAGGGGAGAGA
1704439		NBstNBI	GGGAGGTGSGGA	A	3895.5135	ACCTCTGACAGAGTCTCTGGGGGAGGTGS GGACACAGACTCAGGGGAGAGA

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1704439		NBstNBI	GGGAGGTGSGGA	C	3871.4885	ACCTCTGACAGAGTCCTGGGGGAGGTGS GGACACAGACTCAGGGGAGAGA
1704439		NBstNBI	GGGAGGTGSGGA	G	3911.5129	ACCTCTGACAGAGTCCTGGGGGAGGTGS GGACACAGACTCAGGGGAGAGA
1704439		NBstNBI	GGGAGGTGSGGA	T	3886.5001	ACCTCTGACAGAGTCCTGGGGGAGGTGS GGACACAGACTCAGGGGAGAGA
1713191		BsrI_NBstNBI	TCTGTCS	A	2151.3924	TTCACCTCCAGACTGGGSGACAGAGCAAGA CTCCATCTCAAAA
1713191		BsrI_NBstNBI	TCTGTCS	C	2127.3674	TTCACCTCCAGACTGGGSGACAGAGCAAGA CTCCATCTCAAAA
1713191		BsrI_NBstNBI	TCTGTCS	G	2167.3918	TTCACCTCCAGACTGGGSGACAGAGCAAGA CTCCATCTCAAAA
1713191		BsrI_NBstNBI	TCTGTCS	T	2142.379	TTCACCTCCAGACTGGGSGACAGAGCAAGA CTCCATCTCAAAA
1722938		NBstNBI_BsrI	CGCAGCTGCSTCACTG	A	4922.1779	ATGTGTCCAGGAGTCGCATCGCAGCTGCS TCACTGGTGGATTAAGAT
1722938		NBstNBI_BsrI	CGCAGCTGCSTCACTG	C	4898.1529	ATGTGTCCAGGAGTCGCATCGCAGCTGCS TCACTGGTGGATTAAGAT
1722938		NBstNBI_BsrI	CGCAGCTGCSTCACTG	G	4938.1773	ATGTGTCCAGGAGTCGCATCGCAGCTGCS TCACTGGTGGATTAAGAT
1722938		NBstNBI_BsrI	CGCAGCTGCSTCACTG	T	4913.1645	ATGTGTCCAGGAGTCGCATCGCAGCTGCS TCACTGGTGGATTAAGAT
1738930		NBstNBI_BclI	CACCTGSGTGATC	A	4014.5994	GCCAGACAAGAGTCCCACATCACCTGSGTG ATCAGTGCAGAGTT
1738930		NBstNBI_BclI	CACCTGSGTGATC	C	3990.5744	GCCAGACAAGAGTCCCACATCACCTGSGTG ATCAGTGCAGAGTT
1738930		NBstNBI_BclI	CACCTGSGTGATC	G	4030.5988	GCCAGACAAGAGTCCCACATCACCTGSGTG ATCAGTGCAGAGTT
1738930		NBstNBI_BclI	CACCTGSGTGATC	T	4005.586	GCCAGACAAGAGTCCCACATCACCTGSGTG ATCAGTGCAGAGTT
1741191		NBstNBI_BsrI	CTAASGGACTG	A	3445.2434	GAATGCAATGGAGTCGAAACTAASGGACT GGAATAGAAATGGA
1741191		NBstNBI_BsrI	CTAASGGACTG	C	3421.2184	GAATGCAATGGAGTCGAAACTAASGGACT GGAATAGAAATGGA

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1741191		NBstNBI_BsrI	CTAASGGACTG	G	3461.2428	GAATGCAATGGAGTCGAAACTAASGGACT GGAATAGAAATGGA
1741191		NBstNBI_BsrI	CTAASGGACTG	T	3436.23	GAATGCAATGGAGTCGAAACTAASGGACT GGAATAGAAATGGA
1741545		BsrI_NBstNBI	TCCTAAGSTCCATTT	A	4581.9798	TATGCAAAAAAAGCTGGAAAAATGGASCTTAG GATGGTGACTCGACTTTAAAAA
1741545		BsrI_NBstNBI	TCCTAAGSTCCATTT	C	4557.9548	TATGCAAAAAAAGCTGGAAAAATGGASCTTAG GATGGTGACTCGACTTTAAAAA
1741545		BsrI_NBstNBI	TCCTAAGSTCCATTT	G	4597.9792	TATGCAAAAAAAGCTGGAAAAATGGASCTTAG GATGGTGACTCGACTTTAAAAA
1741545		BsrI_NBstNBI	TCCTAAGSTCCATTT	T	4572.9664	TATGCAAAAAAAGCTGGAAAAATGGASCTTAG GATGGTGACTCGACTTTAAAAA
1746878		BsrI_NBstNBI	TTSCCATAGAT	A	3395.2178	CCTGAATAAAAACTGGAAATCTATGGSAAATAC TGACTCTAAAAATTTTC
1746878		BsrI_NBstNBI	TTSCCATAGAT	C	3371.1928	CCTGAATAAAAACTGGAAATCTATGGSAAATAC TGACTCTAAAAATTTTC
1746878		BsrI_NBstNBI	TTSCCATAGAT	G	3411.2172	CCTGAATAAAAACTGGAAATCTATGGSAAATAC TGACTCTAAAAATTTTC
1746878		BsrI_NBstNBI	TTSCCATAGAT	T	3386.2044	CCTGAATAAAAACTGGAAATCTATGGSAAATAC TGACTCTAAAAATTTTC
1750588		BsrI_NBstNBI	STGATG	A	1911.2455	TTGAAAGTGAAACTGGACATCASA AAAAGAC TCAGTTGCTTTA
1750588		BsrI_NBstNBI	STGATG	C	1887.2205	TTGAAAGTGAAACTGGACATCASA AAAAGAC TCAGTTGCTTTA
1750588		BsrI_NBstNBI	STGATG	G	1927.2449	TTGAAAGTGAAACTGGACATCASA AAAAGAC TCAGTTGCTTTA
1750588		BsrI_NBstNBI	STGATG	T	1902.2321	TTGAAAGTGAAACTGGACATCASA AAAAGAC TCAGTTGCTTTA
1751415		NBstNBI_BsrI	GCSCACTG	A	2474.6033	AGCCTTTCCTGAGTCTCCAGCSCACTGGC CTCCCCCAT
1751415		NBstNBI_BsrI	GCSCACTG	C	2450.5783	AGCCTTTCCTGAGTCTCCAGCSCACTGGC CTCCCCCAT
1751415		NBstNBI_BsrI	GCSCACTG	G	2490.6027	AGCCTTTCCTGAGTCTCCAGCSCACTGGC CTCCCCCAT

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1751415		NBstNBI BsrI	GCSCACTG	T	2465.5899	AGCCTTTCCTGAGTCTCCAGCSCACTGGC CTCCCCCAT
1753631		BsrI_NBstNBI	AGTATCCCCCAS	A	3654.3793	GTCTGTTCTGACTGGTSTGGGGGATACTA AAGGACTCATGAAAGGCT
1753631		BsrI_NBstNBI	AGTATCCCCCAS	C	3630.3543	GTCTGTTCTGACTGGTSTGGGGGATACTA AAGGACTCATGAAAGGCT
1753631		BsrI_NBstNBI	AGTATCCCCCAS	G	3670.3787	GTCTGTTCTGACTGGTSTGGGGGATACTA AAGGACTCATGAAAGGCT
1753631		BsrI_NBstNBI	AGTATCCCCCAS	T	3645.3659	GTCTGTTCTGACTGGTSTGGGGGATACTA AAGGACTCATGAAAGGCT
1762242		NBstNBI	ACAACATTS	A	2770.8258	GAGAAGGAGAGAGTCCGGGSAATGTTGTT ACTGACTCCATTTTACC
1762242		NBstNBI	ACAACATTS	C	2746.8008	GAGAAGGAGAGAGTCCGGGSAATGTTGTT ACTGACTCCATTTTACC
1762242		NBstNBI	ACAACATTS	G	2786.8252	GAGAAGGAGAGAGTCCGGGSAATGTTGTT ACTGACTCCATTTTACC
1762242		NBstNBI	ACAACATTS	T	2761.8124	GAGAAGGAGAGAGTCCGGGSAATGTTGTT ACTGACTCCATTTTACC
1762242		NBstNBI	SAATGTTGT	A	2832.8478	GAGAAGGAGAGAGTCCGGGSAATGTTGTT ACTGACTCCATTTTACC
1762242		NBstNBI	SAATGTTGT	C	2808.8228	GAGAAGGAGAGAGTCCGGGSAATGTTGTT ACTGACTCCATTTTACC
1762242		NBstNBI	SAATGTTGT	G	2848.8472	GAGAAGGAGAGAGTCCGGGSAATGTTGTT ACTGACTCCATTTTACC
1762242		NBstNBI	SAATGTTGT	T	2823.8344	GAGAAGGAGAGAGTCCGGGSAATGTTGTT ACTGACTCCATTTTACC
1765021		BsrI_NBstNBI	TGAGGGGGGAATGTG	A	5146.3249	TTCCAGCTGTACTGGGCACATTCSCCCCC TCACCCCTGACTCAGAAGGTGTT
1765021		BsrI_NBstNBI	TGAGGGGGGAATGTG	C	5122.2999	TTCCAGCTGTACTGGGCACATTCSCCCCC TCACCCCTGACTCAGAAGGTGTT
1765021		BsrI_NBstNBI	TGAGGGGGGAATGTG	G	5162.3243	TTCCAGCTGTACTGGGCACATTCSCCCCC TCACCCCTGACTCAGAAGGTGTT
1765021		BsrI_NBstNBI	TGAGGGGGGAATGTG	T	5137.3115	TTCCAGCTGTACTGGGCACATTCSCCCCC TCACCCCTGACTCAGAAGGTGTT

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
1765346		BsrI_NBstNBI	TGACTCTTGGSTTC	A	4324.7939	AGATCAATAAACTGGTGAASCCAAAGAGTC AAACTGACTCCAAAGTTGAA
1765346		BsrI_NBstNBI	TGACTCTTGGSTTC	C	4300.7689	AGATCAATAAACTGGTGAASCCAAAGAGTC AAACTGACTCCAAAGTTGAA
1765346		BsrI_NBstNBI	TGACTCTTGGSTTC	G	4340.7933	AGATCAATAAACTGGTGAASCCAAAGAGTC AAACTGACTCCAAAGTTGAA
1765346		BsrI_NBstNBI	TGACTCTTGGSTTC	T	4315.7805	AGATCAATAAACTGGTGAASCCAAAGAGTC AAACTGACTCCAAAGTTGAA
1768549		NBstNBI	AGCCTGCATAGS	A	3734.4281	AGAGACGTCTGAGTCAGGCAGCCTGCATA GSAGATGACTCTGCTGTGAGA
1768549		NBstNBI	AGCCTGCATAGS	C	3710.4031	AGAGACGTCTGAGTCAGGCAGCCTGCATA GSAGATGACTCTGCTGTGAGA
1768549		NBstNBI	AGCCTGCATAGS	G	3750.4275	AGAGACGTCTGAGTCAGGCAGCCTGCATA GSAGATGACTCTGCTGTGAGA
1768549		NBstNBI	AGCCTGCATAGS	T	3725.4147	AGAGACGTCTGAGTCAGGCAGCCTGCATA GSAGATGACTCTGCTGTGAGA
1768549		NBstNBI	SCTATGCAGGCT	A	3725.4147	AGAGACGTCTGAGTCAGGCAGCCTGCATA GSAGATGACTCTGCTGTGAGA
1768549		NBstNBI	SCTATGCAGGCT	C	3701.3897	AGAGACGTCTGAGTCAGGCAGCCTGCATA GSAGATGACTCTGCTGTGAGA
1768549		NBstNBI	SCTATGCAGGCT	G	3741.4141	AGAGACGTCTGAGTCAGGCAGCCTGCATA GSAGATGACTCTGCTGTGAGA
1768549		NBstNBI	SCTATGCAGGCT	T	3716.4013	AGAGACGTCTGAGTCAGGCAGCCTGCATA GSAGATGACTCTGCTGTGAGA
1777645		NBstNBI_BsrI	TTCAGASGGGAACTG	A	4721.0676	CCTCTCAACAGAGTCCCCCTTCAGASGGG AACTGGCTTTTGAGGTG
1777645		NBstNBI_BsrI	TTCAGASGGGAACTG	C	4697.0426	CCTCTCAACAGAGTCCCCCTTCAGASGGG AACTGGCTTTTGAGGTG
1777645		NBstNBI_BsrI	TTCAGASGGGAACTG	G	4737.067	CCTCTCAACAGAGTCCCCCTTCAGASGGG AACTGGCTTTTGAGGTG
1777645		NBstNBI_BsrI	TTCAGASGGGAACTG	T	4712.0542	CCTCTCAACAGAGTCCCCCTTCAGASGGG AACTGGCTTTTGAGGTG
1778373		BsrI_NBstNBI	TCTGASGCA	A	2802.8246	TGGGACAGGACTGGGTGCSTCAGATGT GGACTCCATCTGCCCT

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
1778373		BsrI_NBstNBI	TCTGASGCA	C	2778.7996	TGGGACAGGACTGGGTGCSTCAGATGT GGACTCCATCTGCCCT
1778373		BsrI_NBstNBI	TCTGASGCA	G	2818.824	TGGGACAGGACTGGGTGCSTCAGATGT GGACTCCATCTGCCCT
1778373		BsrI_NBstNBI	TCTGASGCA	T	2793.8112	TGGGACAGGACTGGGTGCSTCAGATGT GGACTCCATCTGCCCT
1783062		NBstNBI	AGTTATCCATGSCG	A	4342.8207	TGAAAAAGTTGAGTCAGGCCGSCATGGAT AACTGAGAGACTCAAGACCCGAG
1783062		NBstNBI	AGTTATCCATGSCG	C	4318.7957	TGAAAAAGTTGAGTCAGGCCGSCATGGAT AACTGAGAGACTCAAGACCCGAG
1783062		NBstNBI	AGTTATCCATGSCG	G	4358.8201	TGAAAAAGTTGAGTCAGGCCGSCATGGAT AACTGAGAGACTCAAGACCCGAG
1783062		NBstNBI	AGTTATCCATGSCG	T	4333.8073	TGAAAAAGTTGAGTCAGGCCGSCATGGAT AACTGAGAGACTCAAGACCCGAG
1783062		NBstNBI	CGSCATGGATAACT	A	4351.8341	TGAAAAAGTTGAGTCAGGCCGSCATGGAT AACTGAGAGACTCAAGACCCGAG
1783062		NBstNBI	CGSCATGGATAACT	C	4327.8091	TGAAAAAGTTGAGTCAGGCCGSCATGGAT AACTGAGAGACTCAAGACCCGAG
1783062		NBstNBI	CGSCATGGATAACT	G	4367.8335	TGAAAAAGTTGAGTCAGGCCGSCATGGAT AACTGAGAGACTCAAGACCCGAG
1783062		NBstNBI	CGSCATGGATAACT	T	4342.8207	TGAAAAAGTTGAGTCAGGCCGSCATGGAT AACTGAGAGACTCAAGACCCGAG
1789527		NBstNBI_BsrI	AAASACACTG	A	3109.0483	GAGTAAAGGTGAGTCTTGCAAAASACACTG GTGGCATTTTGC
1789527		NBstNBI_BsrI	AAASACACTG	C	3085.0233	GAGTAAAGGTGAGTCTTGCAAAASACACTG GTGGCATTTTGC
1789527		NBstNBI_BsrI	AAASACACTG	G	3125.0477	GAGTAAAGGTGAGTCTTGCAAAASACACTG GTGGCATTTTGC
1789527		NBstNBI_BsrI	AAASACACTG	T	3100.0349	GAGTAAAGGTGAGTCTTGCAAAASACACTG GTGGCATTTTGC
1790529		BsrI_NBstNBI	TCTGTCS	A	2151.3924	TGCACTCCAGACTGGGSGACAGAGTAAGA CTCTGTCTCAAAA
1790529		BsrI_NBstNBI	TCTGTCS	C	2127.3674	TGCACTCCAGACTGGGSGACAGAGTAAGA CTCTGTCTCAAAA

TSC_ID	dbSNP_ID	Enzymes	Product	Allele	Mass	Sequence
1790529		BsrI_NBstNBI	TCTGTCS	G	2167.3918	TGCACTCCAGACTGGGSGACAGAGTAAGA CTCTGTCTCAAAA
1790529		BsrI_NBstNBI	TCTGTCS	T	2142.379	TGCACTCCAGACTGGGSGACAGAGTAAGA CTCTGTCTCAAAA

All of the above U.S. patents, U.S. patent application publications, U.S. patent applications, foreign patents, foreign patent applications and non-
5 patent publications referred to in this specification and/or listed in the Application Data Sheet, are incorporated herein by reference, in their entirety.

From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit
10 and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

1. A method comprising:
 - a) providing a nucleic acid sample;
 - b) treating the nucleic acid sample with components under nicking conditions, where the components comprise:
 - i) a nicking agent;and the conditions cause the nicking agent to nick the nucleic acid sample to thereby produce a family of initiating oligonucleotide fragments;
 - c) subjecting one or more members of the family of initiating oligonucleotide fragments to a characterization process to thereby provide results; and
 - d) identifying a source for the nucleic acid sample based on the results of the characterization process.
2. The method of claim 1 wherein the components further comprise:
 - ii) a polymerase; and
 - iii) a deoxyribonucleoside triphosphate.
3. The method of claim 2 wherein the components further comprise:
 - iv) a template oligonucleotide comprising from 3' to 5':
 - (A) a first nucleotide sequence that is at least substantially complementary to a nucleotide sequence present in one or more members of the family of initiating oligonucleotide fragments;
 - (B) a sequence of one strand of a nicking agent recognition sequence; and
 - (C) a second nucleotide sequence.

4. The method of claim 3 wherein sequence iv)(B) is a sequence of an antisense strand of the nicking agent recognition sequence, and sequence iv)(A) is at least substantially identical to sequence iv)(C).

5. The method of claim 3 wherein the components further comprising

v) a second template oligonucleotide, comprising, from 3' to 5':

(A) a first nucleotide sequence that is at least substantially identical to a nucleotide sequence present in the one or more members of the family of initiating oligonucleotide fragments;

(B) a sequence of a sense strand of the nicking agent recognition sequence; and

(C) a second nucleotide sequence.

wherein sequence iv)(B) is a sequence of a sense strand of the nicking agent recognition sequence.

6. The method of claim 1 wherein the components further comprises a restriction endonuclease.

7. The method of claim 1 wherein the one or more members of the family of initiating oligonucleotide fragments are 6-16 nucleotides in length.

8. The method of claim 1 wherein the nicking agent is a nicking endonuclease.

9. The method of claim 1 wherein the nicking agent is N.BstNB I.

10. The method of claim 2 wherein the polymerase is selected from *exo*⁻ Vent polymerase, Bst polymerase, and 9°NmTM polymerase.

11. The method of claim 3 wherein the 3' terminus of template iv) is blocked.
12. The method of claim 4 wherein sequence iv)(A) is exactly identical to sequence iv)(C).
13. The method of claim 5 wherein the 3' termini of template iv) and v) are blocked.
14. The method of claim 3 wherein the template is immobilized.
15. The method of claim 5 wherein templates iv) and v) are immobilized.
16. The method of claim 1 wherein the characterization process is performed at least partially by a technique selected from the group consisting of luminescence spectroscopy or spectrometry, fluorescence spectroscopy or spectrometry, mass spectrometry, liquid chromatography, fluorescence polarization, and electrophoresis.
17. The method of claim 16 wherein the characterization process is performed at least partially by mass spectrometry.
18. The method of claim 17 wherein the mass spectrometry is MALDI or LC-TOF.
19. A template oligonucleotide for amplifying a portion of a target nucleic acid, wherein
 - (i) the portion of the target is 6-16 nucleotides in length and flanked by

- (A) a sequence of one strand of a first nicking enzyme recognition sequence, and
- (B) a sequence of one strand of a second nicking enzyme recognition sequence, or a sequence of one strand of a restriction enzyme recognition sequence, and
- (ii) the template oligonucleotide comprising from 3' to 5':
 - (A) a first nucleotide sequence that is at least substantially complementary to the portion of the target,
 - (B) a sequence of an antisense strand of a third nicking enzyme recognition sequence, and
 - (C) a second nucleotide sequence that is at least substantially identical to the first nucleotide sequence.

20. The template oligonucleotide of claim 19 wherein the first and third nicking enzyme recognition sequences are identical to each other.

21. The template oligonucleotide of claim 19 wherein the first, second and third nicking enzyme recognition sequences are identical to each other.

22. The template oligonucleotide of claim 21 wherein the first, second and third nicking enzyme recognition sequences are recognizable by N.BstNB I.

23. The template oligonucleotide of claim 19 wherein the 3' terminus of the template oligonucleotide is blocked.

24. The template oligonucleotide of claim 19 wherein the 3' terminus of the template oligonucleotide is immobilized.

25. The template oligonucleotide of claim 19, wherein the portion of the target is selected from the products listed in Tables 1, 2, 4, 5, and 9.

26. The template oligonucleotide of claim 19 wherein the portion of the target comprises a genetic variation.

27. The template oligonucleotide of claim 26 wherein the genetic variation is a single nucleotide polymorphism.

28. A composition for amplifying a portion of a target nucleic acid, comprising a first template oligonucleotide and a second template oligonucleotide, wherein

(i) the portion of the target is 6-16 nucleotides in length and flanked by

(A) a sequence of one strand of a first nicking enzyme recognition sequence, and

(B) a sequence of one strand of a second nicking enzyme recognition sequence, or a sequence of one strand of a restriction enzyme recognition sequence,

(ii) the first template oligonucleotide comprises from 5' to 3':

(A) a first nucleotide sequence,

(B) a sequence of a sense strand of a third nicking agent recognition sequence, and

(C) a second nucleotide sequence that is at least substantially complementary to the portion of the target, and

(iii) the second template oligonucleotide comprises from 5' to 3':

(A) a first nucleotide sequence,

(B) a sequence of a sense strand of a fourth nicking agent recognition sequence, and

(C) a second nucleotide sequence that is at least substantially identical to the portion of the target.

29. The composition of claim 28 wherein the first, third and fourth nicking enzyme recognition sequences are identical to each other.

30. The composition of claim 28 wherein the first, second, third and fourth nicking enzyme recognition sequences are identical to each other.

31. The composition of claim 29 wherein the first, third and fourth nicking enzyme recognition sequences are recognizable by N.BstNB I.

32. The composition of claim 28 wherein the 3' termini of the first and second templates are blocked.

33. The composition of claim 28 wherein the 3' termini of the first and second templates are immobilized.

34. The composition of claim 28 wherein the portion of the target is selected from the products listed in Tables 1, 2, 4, 5 and 9.

35. The composition of claim 28 wherein the portion of the target comprises a genetic variation.

36. The composition of claim 35 wherein the genetic variation is a single nucleotide polymorphism.

37. A composition comprising:
(1) a nicking agent, and
(2) at least one fragment selected from the products listed in Tables 1, 2, 4, 5 and 9,

wherein the at least one fragment is produced at least partially by action of the nicking agent.

38. The composition of claim 37, wherein the nicking agent is N.BstNB I.

39. The composition of claim 38, wherein the nicking agent is N.Alw I.

40. The composition of claim 37 further comprising a restriction endonuclease selected from Bcl I, Bsa BI, Bsm I, Bsr I and Bsr D1, wherein the at least one fragment is selected from the products listed in Table 9.

41. The composition of claim 37 comprising at least two fragments selected from the products listed in Tables 1, 2, 4, 5 and 9.

42. The composition of claim 37 comprising at least three fragments selected from the products listed in Tables 1, 2, 4, 5 and 9.

43. The composition of claim 37 comprising at least five fragments selected from the products listed in Tables 1, 2, 4, 5 and 9.

44. A kit for identifying the source of a nucleic acid sample, comprising one or two template oligonucleotides for amplifying a portion of a genomic DNA of an organism suspected to be the source of the nucleic acid sample, wherein the portion of the genomic DNA is 6-16 nucleotides in length and flanked by

(A) a sequence of one strand of a first nicking enzyme recognition sequence, and

(B) a sequence of one strand of a second nicking enzyme recognition sequence, or a sequence of one strand of a restriction enzyme recognition sequence.

45. The kit of claim 44 wherein the one or two template oligonucleotides is the template oligonucleotide of claim 19.

46. The kit of claim 44 wherein the one or two template oligonucleotides is the template oligonucleotide of claim 20.

47. The kit of claim 46 further comprising a nicking enzyme that recognizes the first and third nicking enzyme recognition sequences.

48. The kit of claim 44 wherein the one or two template oligonucleotides is the first and second template oligonucleotides of claim 28.

49. The kit of claim 44 wherein the one or two template oligonucleotides is the first and second template oligonucleotides of claim 29.

50. The kit of claim 49 further comprising a nicking enzyme that recognizes the first, third and fourth nicking enzyme recognition sequences.

51. The kit of claim 44 further comprising a DNA polymerase.

52. The kit of claim 51 further comprising one or more deoxyribonucleoside triphosphate.

53. The kit of claim 44 wherein the portion of the genomic DNA is selected from the products listed in Tables 1, 2, 4, 5 and 9.

54. The kit of claim 44 wherein the portion of the genomic DNA comprises a single nucleotide polymorphism.

55. An array, comprising

- (a) a substrate having a plurality of distinct areas; and
- (b) the template oligonucleotide of claim A1 or the composition of claim B1 immobilized to at least one of the plurality of distinct areas.

Figure 1

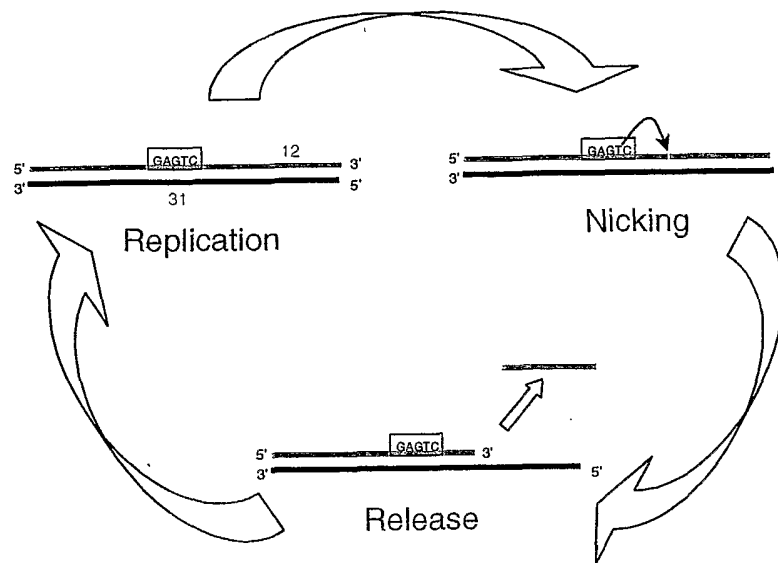
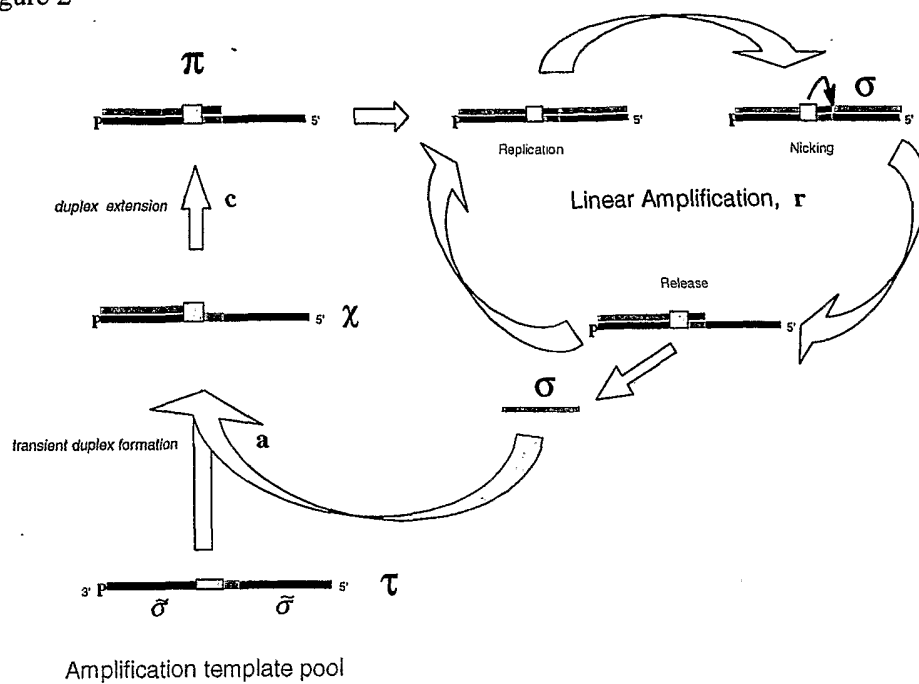


Figure 2



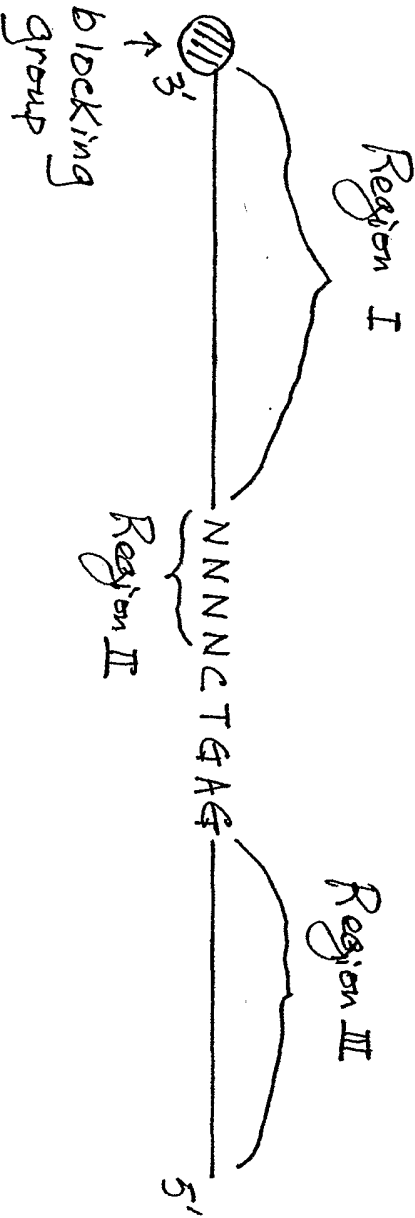


Figure 3

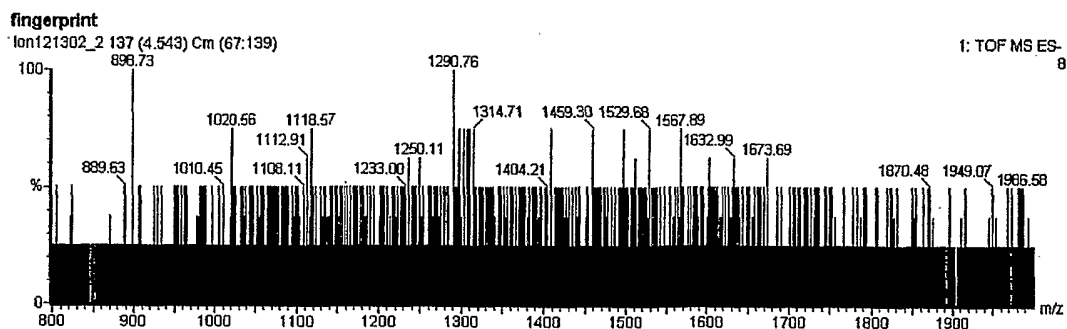


Figure 4a
Fingerprint of K12 (TOF)

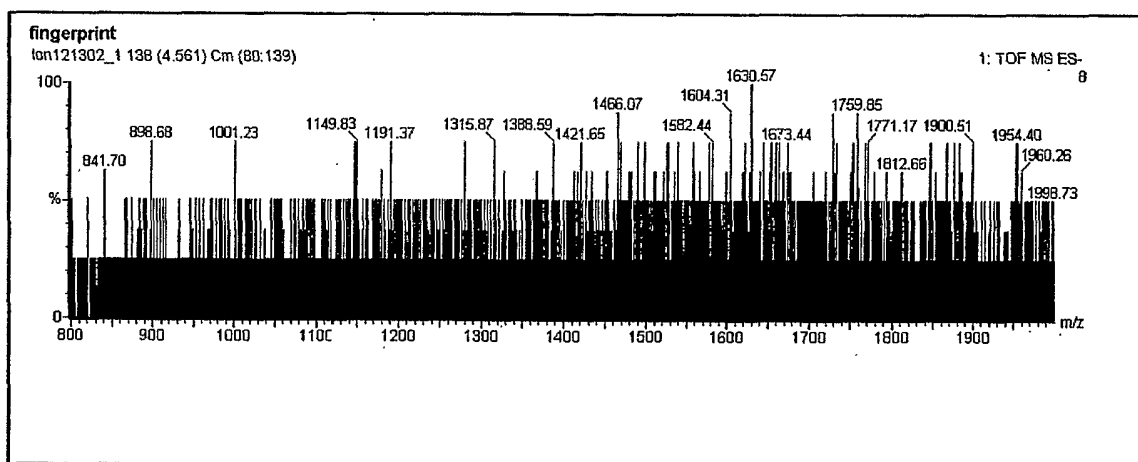


Figure 4b
Fingerprint of O157 (TOF)

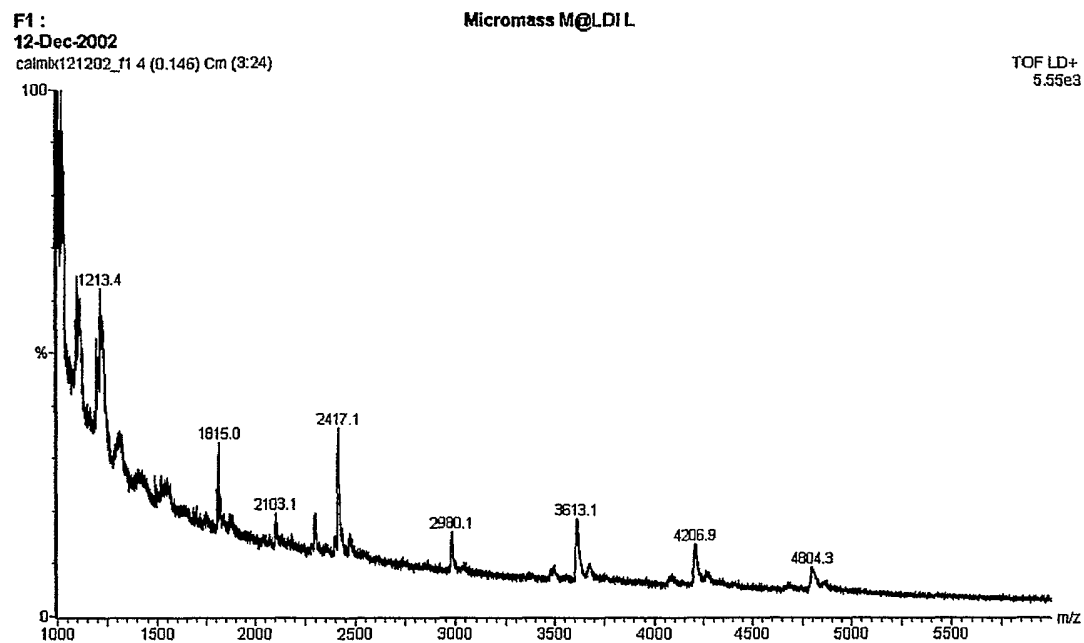


Figure 5a
K12 MALDI

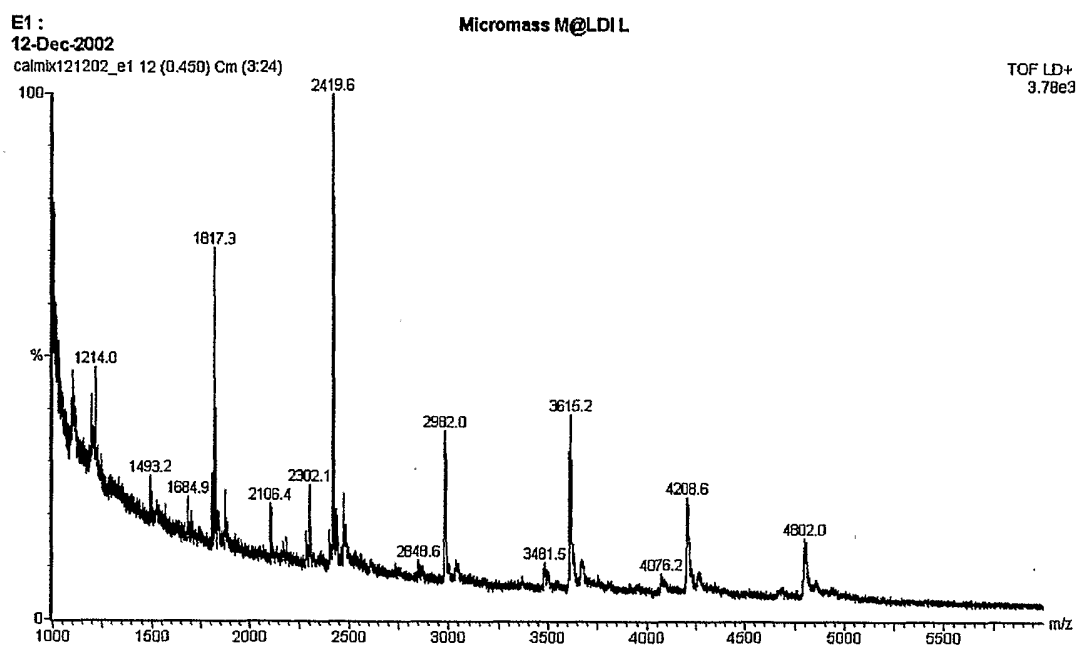
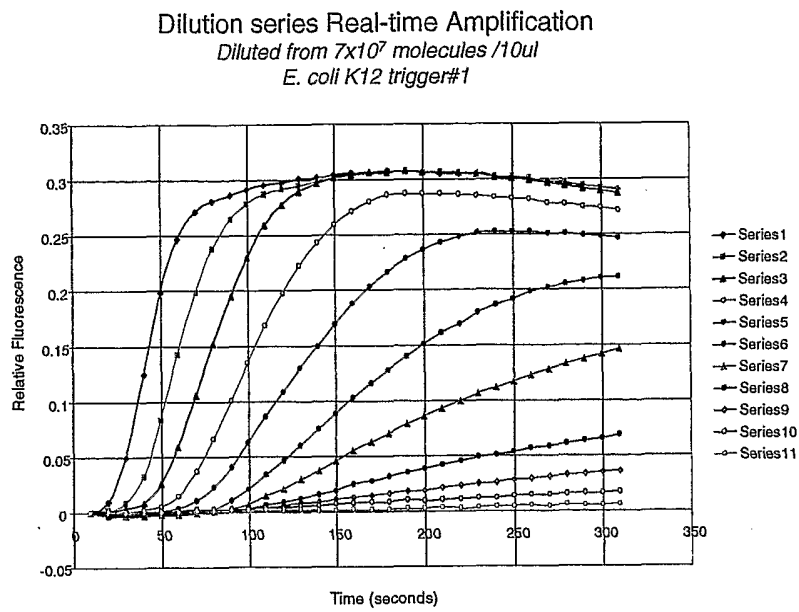


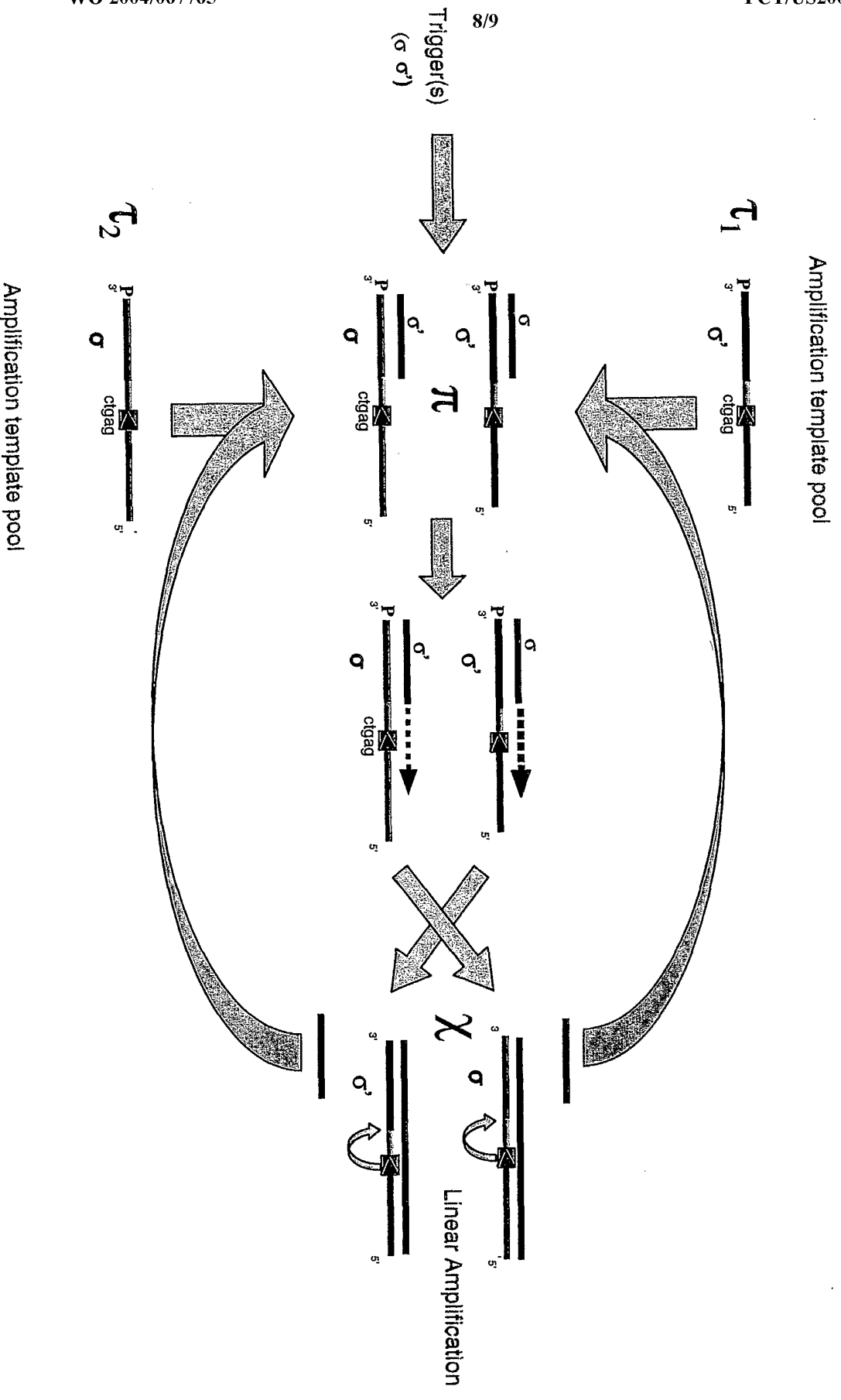
Figure 5b
O157 MALDI



6

Figure 6

The Ping-Pong Amplification Reaction Cycle



17:01:15 67

Another view of Ping-Pong Reaction

How the specificity is achieved: 2 discrimination steps in every cycle

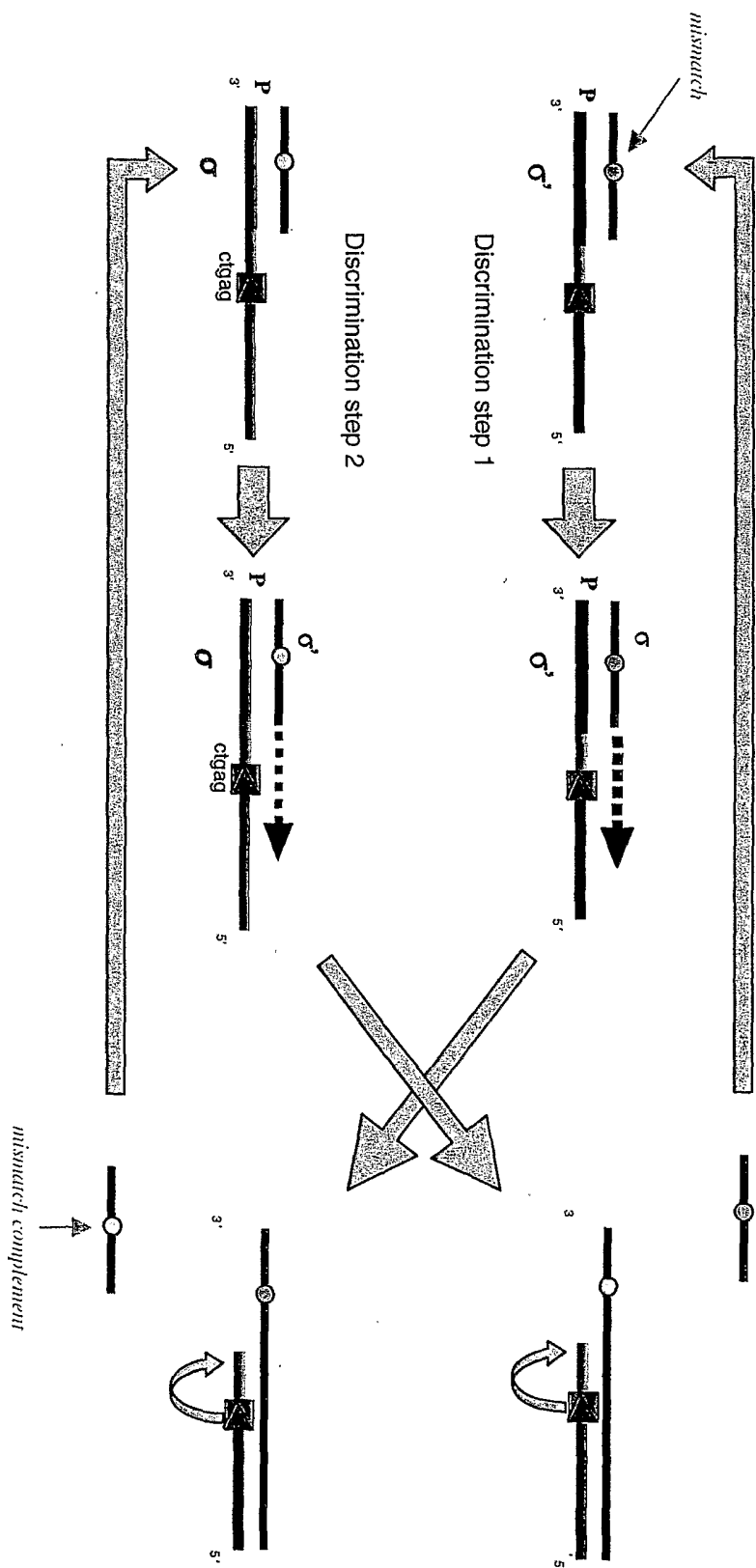


Figure 8