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Hamady et al.(10) **Pub. No.: US 2010/0323348 A1**(43) **Pub. Date: Dec. 23, 2010**(54) **METHODS AND COMPOSITIONS FOR
USING ERROR-DETECTING AND/OR
ERROR-CORRECTING BARCODES IN
NUCLEIC ACID AMPLIFICATION PROCESS**(75) Inventors: **Micah L. Hamady**, Berkeley, CA
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Denver, CO (US)(21) Appl. No.: **12/693,612**(22) Filed: **Jan. 26, 2010****Related U.S. Application Data**(60) Provisional application No. 61/148,931, filed on Jan.
31, 2009.**Publication Classification**(51) **Int. Cl.**
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C07H 21/00 (2006.01)(52) **U.S. Cl.** **435/6; 536/24.33**(57) **ABSTRACT**

The present invention provides methods and compositions for detecting and correcting errors in nucleic acid amplification processes, and methods for using the same. In particular, barcode amplification errors are detected and corrected such that integrity in sample assignment is maintained. The methods are compatible with high throughput sequencing techniques as some of the barcodes are based upon Hamming codes, thereby allowing self-correction for single bit errors. Some methods and compositions of the invention allow characterization (e.g., sequencing) of a plurality of nucleic acid samples simultaneously within a single sequencing reaction.

(a)

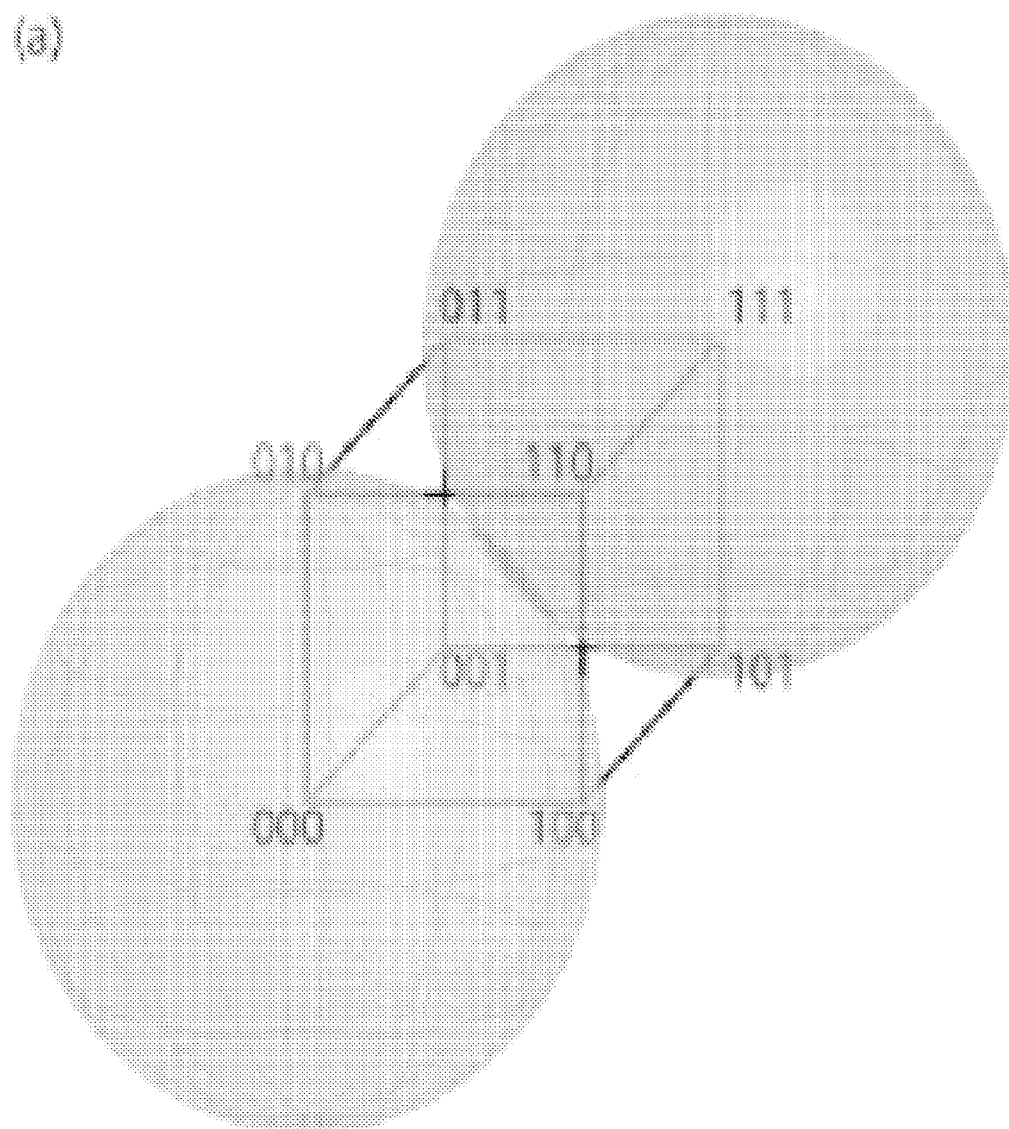


FIGURE 1A

(b) 0: [1111111111111111...]
 1: [1010101010101010...]
 2: [-110011001100110...]
 4: [---1111000011110...]

(c)

$$\begin{bmatrix} 0 & 0 & 0 & 1 & 1 & 1 & 1 \\ 0 & 1 & 1 & 0 & 0 & 1 & 1 \\ 1 & 0 & 1 & 0 & 1 & 0 & 1 \end{bmatrix} \times \begin{bmatrix} 1 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 1 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix} \begin{array}{l} = 0, \text{so no} \\ \text{error: remove} \\ \text{parity bits} \end{array} \begin{bmatrix} x \\ x \\ 0 \\ x \\ 0 \\ 1 \\ 1 \end{bmatrix} = 0011 = 3$$

$$\begin{bmatrix} 0 & 0 & 0 & 1 & 1 & 1 & 1 \\ 0 & 1 & 1 & 0 & 0 & 1 & 1 \\ 1 & 0 & 1 & 0 & 1 & 0 & 1 \end{bmatrix} \times \begin{bmatrix} 1 \\ 1 \\ 0 \\ 0 \\ 0 \\ 0 \\ 1 \end{bmatrix} = \begin{bmatrix} 1 \\ 1 \\ 0 \end{bmatrix} \begin{array}{l} = 6, \text{so error} \\ \text{at position 6:} \\ \text{flip bit and} \\ \text{remove} \\ \text{parity bits} \end{array} \begin{bmatrix} x \\ x \\ 0 \\ x \\ 0 \\ 1 \\ 1 \end{bmatrix} = 0011 = 3$$

FIGURE 1B and FIGURE 1C

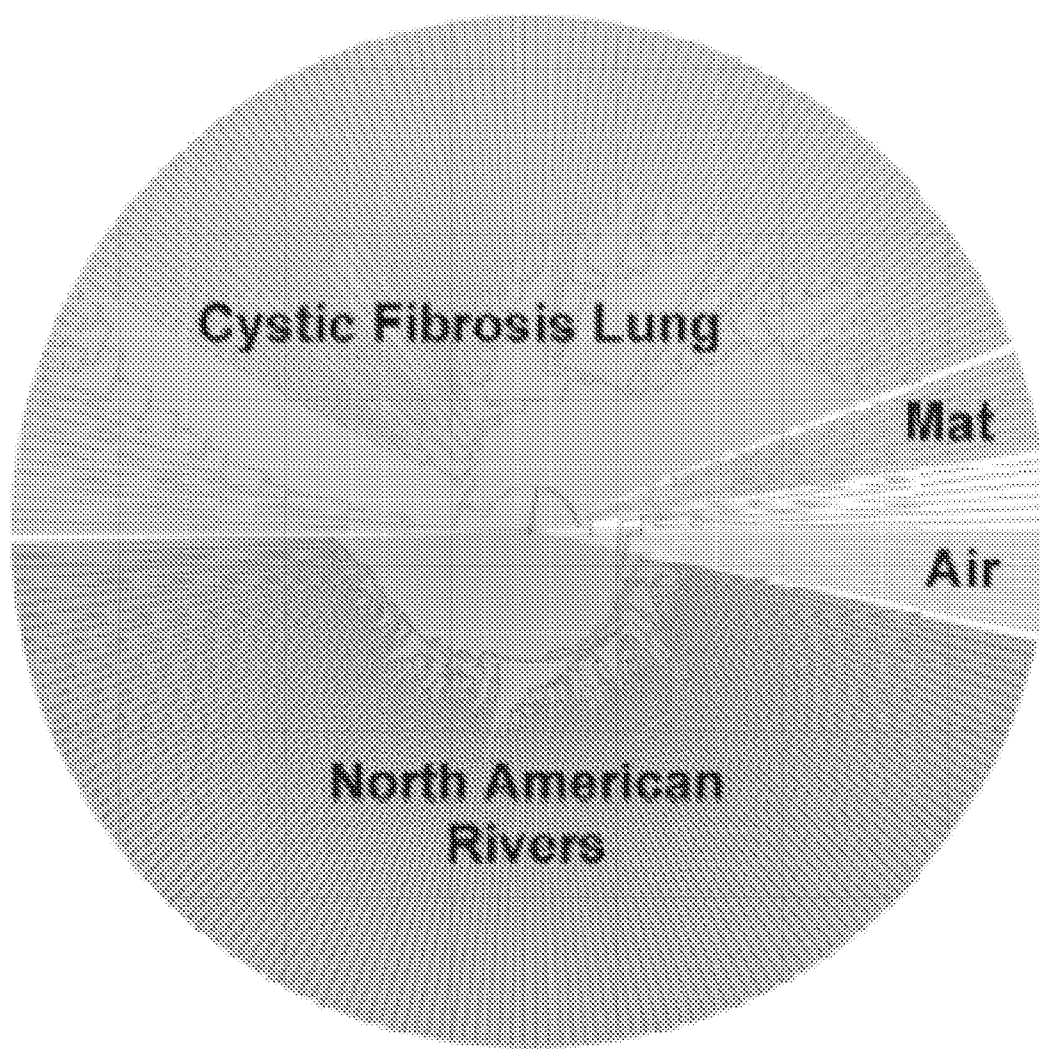
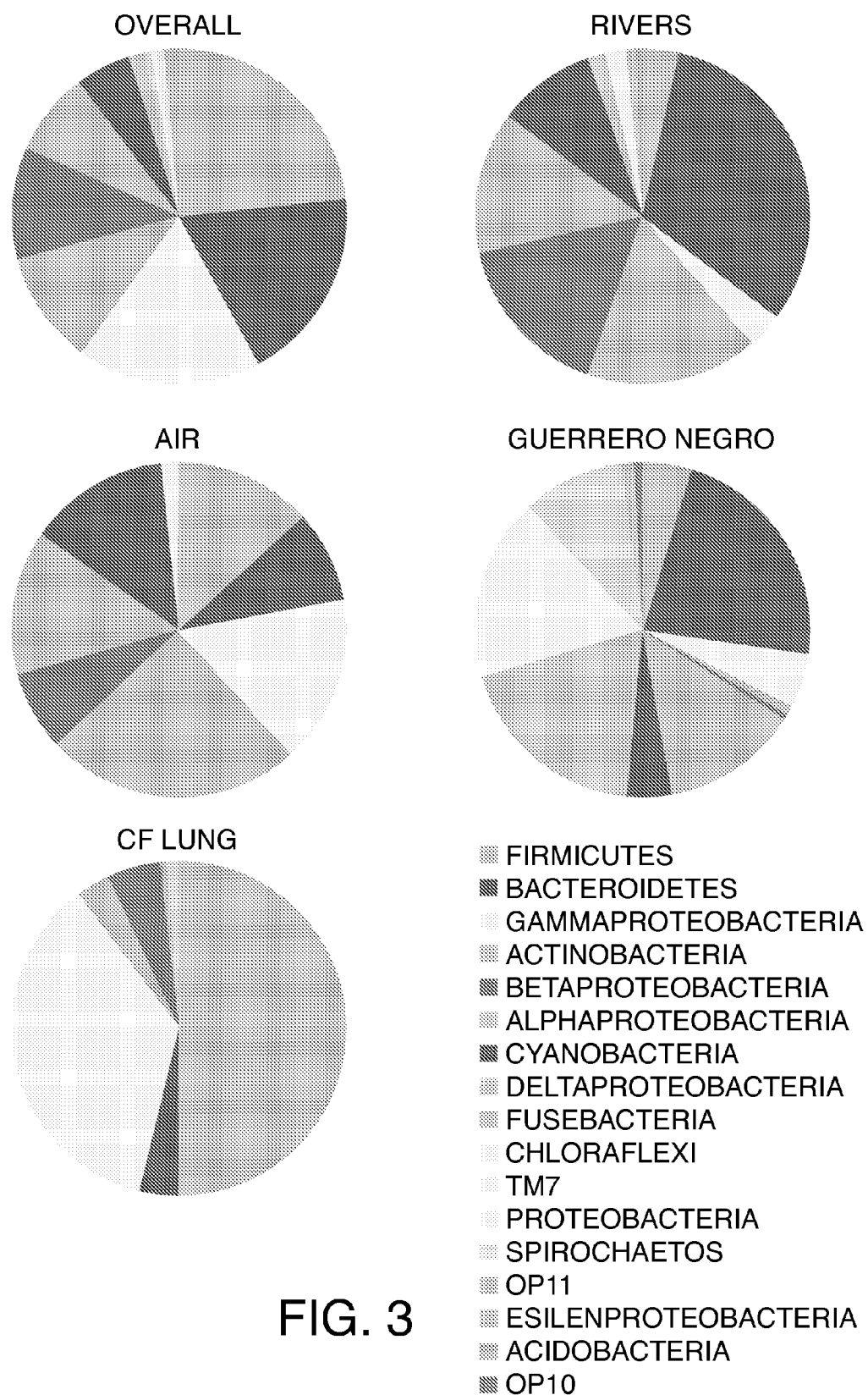


FIGURE 2



METHODS AND COMPOSITIONS FOR USING ERROR-DETECTING AND/OR ERROR-CORRECTING BARCODES IN NUCLEIC ACID AMPLIFICATION PROCESS

**STATEMENT REGARDING FEDERALLY
FUNDED RESEARCH** This invention was made
with government support under Grant Nos.
T32GM065103 and P01DK078669 awarded by the
National Institutes of Health. The government has
certain rights in the invention.

FIELD OF THE INVENTION

[0001] The present invention relates to nucleic acid sequencing. In particular, the invention relates to methods and compositions for detecting errors and correcting such errors during nucleic acid amplification such that accurate sample identification may be maintained. The combination of the methods and compositions described herein allow characterization of a plurality of nucleic acid samples simultaneously when using high throughput amplification and/or sequencing technologies.

BACKGROUND OF THE INVENTION

[0002] DNA barcodes were first developed as a tool for species-level identifications. Consequently, there is a rapidly growing database of these short sequences from a wide variety of taxa. Correlations have also been drawn between the nucleotide content of the short DNA barcode sequences and the genomes from which they are derived. Consequently, short nucleotide sequences can reliably track information about the composition of the entire genome. Min et al., "DNA barcodes provide a quick preview of mitochondrial genome composition" *PLoS One* 2(3):e325 (2007).

[0003] In the past several years, microarray technologies based on whole genome analysis have been applied to the study of gene expression and/or amplification. Microarrays arose out of the development of large-scale sequencing approaches and generate a far greater volume of data than the data representing the sequences themselves. Ghosh D., "High throughput and global approaches to gene expression" *Comb Chem High Throughput Screen* 3:411-20 (2000). The current state of development of microarray expression and/or amplification has overshadowed conventional sequencing methods and the associated approaches to manage and analyze the information they generate.

[0004] What is needed in the art is an efficient, low cost method for tracking and identifying specific nucleic acids during polymerase chain reaction amplification that is compatible with conventional high throughput data generation technology.

SUMMARY OF THE INVENTION

[0005] The present invention relates to nucleic acid sequencing. In particular, the invention relates to methods and compositions for detecting errors and correcting such errors during nucleic acid amplification such that accurate sample identification may be maintained. The combination of the methods and compositions described herein allow characterization of a plurality of nucleic acid samples simultaneously when using high throughput amplification and/or sequencing technologies.

[0006] In one embodiment, the present invention contemplates methods and compositions comprising primers encoding error-correcting sequence tags and/or error-detecting sequence tags (i.e., for example, error-correcting barcodes and/or error-detecting barcodes).

[0007] In one embodiment, the present invention contemplates a pyrosequencing compatible primer comprising a first region containing a unique error-detecting/correcting hamming barcode. In one embodiment, the primer further comprises a second region complementary to a bacterial 16S rRNA gene. In one embodiment, the barcode is attached to the 3' end of the primer. In one embodiment, the barcode is attached to the 5' end of the primer. In one embodiment, the barcode is attached to the 3' end and the 5' end of the primer.

[0008] In one embodiment, the present invention contemplates a method of assigning sequence data to individual samples from a mixture of samples, comprising: a) providing: i) a pyrosequencing compatible primer comprising a first region containing a unique error-detecting/correcting barcode and a second region complementary to a target nucleic acid molecule and, and ii) a target nucleic acid molecule, b) amplifying said target nucleic acid molecule with said primer, c) pooling a plurality of said amplification product, and d) pyrosequencing said pooled amplification products to determine their respective nucleotide sequences. In one embodiment, the plurality of amplification products are pooled in equimolar ratios. In one embodiment, the unique error-detecting/correcting barcode is a Hamming code. In one embodiment, the target nucleic acid molecule comprises a portion of the 16S rRNA gene. In one embodiment, the barcode is attached to the 3' end of the primer. In one embodiment, the barcode is attached to the 5' end of the primer. In one embodiment, the barcode is attached to the 3' end and the 5' end of the primer. In one embodiment, the method further comprises identifying amplification products with unique barcode sequence errors. In one embodiment, the compositions are used in parallel sequencing runs, wherein a plurality of sequencing assays are performed simultaneously. In one embodiment, the sequencing assay comprises pyrosequencing wherein nucleic acid sequences from many samples may be characterized simultaneously in a nucleic acid amplification process. In one embodiment, the method further comprising correcting the unique barcode sequence of amplification products containing correctable unique barcode sequence errors. In one embodiment, the method further comprises discarding the nucleotide sequence of amplification products containing non-correctable unique barcode sequence errors. In one embodiment, the method further comprises aligning the nucleotide sequences of said amplification products to generate a phylogenetic tree.

[0009] In one embodiment, the present invention contemplates a method comprising: a) providing: i) a plurality of samples comprising nucleic acid sequences; i) a plurality of primers error correcting and/or error-detecting sequence tags (i.e., for example, 'barcodes'), wherein said primers are at least partially complementary to said nucleic acid sequences; ii) a parallel sequencing technique (i.e., for example, pyrosequencing) capable of simultaneously characterizing said nucleic acid sequences from said plurality of samples; b) amplifying said plurality of nucleic acid samples using said plurality of primers; and c) analyzing said sequence tags of said amplified nucleic acids. In one embodiment, the sequence tag identifies a sample assignment thereby identifying one of said samples from which said nucleic acid was

derived. In one embodiment, the sequence tag identifies the presence of an error in said nucleic acid, thereby establishing a probability that said sample assignment is incorrect. In one embodiment, the sequence tag identifies the absence of any error in said nucleic acid, thereby establishing a probability that said sample assignment is correct.

DEFINITIONS

[0010] The term “parity bit” as used herein, refers to any bit that is added to a bit-coded string (i.e., for example, a series of “ones” and zeros”) to ensure that the number of bits with the value one in a set of bits is even or odd. Parity bits are used as the simplest form of error detecting code. For example, two variants of parity bits may include, but are not limited to, an even parity bit and an odd parity bit. When using even parity, the parity bit is set to 1 if the number of ones in a given set of bits (not including the parity bit) is odd, making the entire set of bits (including the parity bit) even. When using odd parity, the parity bit is set to 1 if the number of ones in a given set of bits (not including the parity bit) is even, making the entire set of bits (including the parity bit) odd. In other words, an even parity bit will be set to “1” if the number of 1’s+1 is even, and an odd parity bit will be set to “1” if the number of 1’s+1 is odd.

[0011] The term “parallel sequencing technique” as used herein, refers to any method capable of sequencing multiple templates at one time (i.e., for example, simultaneously). Usually, such techniques are performed by immobilizing either a template or primer on a solid support (i.e., for example, a microarray) configured to support a high throughput process. Pyrosequencing is compatible with most parallel, or massively parallel, sequencing technologies. Fuller C. W., “Rapid parallel nucleic acid analysis” U.S. Pat. No. 7,264,934 (herein incorporated by reference).

[0012] The term “pyrosequencing” as used herein, refers to any pyrophosphate-based nucleic acid sequencing method. Hyman U.S. Pat. No. 4,971,903 (herein incorporated by reference). This technique is based on the observation that pyrophosphate (PPi) is released upon incorporation of the next correct nucleotide 3’ of the primer sequence. For example, when only one of the four nucleotides (i.e., for example, A, T, G, C) is introduced into the reaction at a time, PPi is generated only when the correct nucleotide is introduced. Thus, the production of PPi reveals the identity of the next correct base. Using this process in an iterative fashion results in the identification of the template nucleotide sequence. Pyrosequencing is compatible with most high throughput sequencing techniques, such as using template carrying microbeads deposited in microfabricated picoliter-sized reaction wells. Margulies et al., *Nature E-Pub* 31 Jul. 2005.

[0013] The term “simultaneously” as used herein refers to any two or more processes that are occurring more or less at the same time. It is not intended that each process begin and end precisely together, but only that their respective durations overlap.

[0014] The term “pyrosequencing compatible primer” as used herein, refers to any primer, or primer pair, that is capable of supporting nucleic acid amplification using any pyrosequencing technology.

[0015] The term “unique error-detecting/correcting Hamming barcode” or “Hamming sequence tag” as used herein, refers to any nucleic acid barcode having a unique sequence identified by the concepts and algorithms associated with Hamming codes (infra).

[0016] The term “Hamming code” as used herein, refers an arithmetic process that identifies unique binary codes based upon inherent redundancy that are capable of correcting single bit errors. For example, a Hamming code can be matched with a nucleic acid barcode in order to screen for single nucleotide errors occurring during nucleic acid amplification. The identification of a single nucleotide error by using a Hamming code, thereby allows for the correction of the nucleic acid barcode.

[0017] The term “sample assignment” as used herein, refers to any established relationship between the source of a specific nucleotide and an attached barcode. For example, when a unique barcode is cross-referenced with a specific geographic location as to where the nucleotide was obtained, the nucleotide has a sample assignment of that specific geographic location.

[0018] The term “equimolar ratios” as used herein, refers to any mixture comprising at least two components, wherein the concentration of each component is the same.

[0019] The term “amplification products” as used herein, refers to any nucleotide produced by the replication and/or amplification of DNA or RNA. For example, mRNA may be amplified into cDNA by reverse transcriptase. Alternative, a DNA template may undergo amplification of at least one of its strands during a polymerase chain reaction (PCR) thereby producing amplification products whose composition is dependent upon the primer pair.

[0020] The term “unique barcode sequence error” as used herein, refers to any alteration in a barcode nucleic acid sequence occurring during amplification.

[0021] The term “correctable unique barcode sequence error” as used herein, refers to any single bit error occurring in a barcode nucleic acid sequence during amplification.

[0022] The term “uncorrectable unique barcode sequence error” as used herein, refers to any bit error that is greater than an single bit error (i.e., for example, a two bit, three bit, four bit etc) error occurring during amplification.

[0023] The term “discarding” as used herein, refers to any process that does not rely on a barcode nucleic acid sequence comprising an uncorrectable unique barcode sequence error. Such an error results in an improper sample assignment for the coded nucleic acid thereby resulting in a mis-classification.

[0024] The term “phylogenetic tree” as used herein, refers to any diagram or other similar representation showing the evolutionary relationships among various biological species or other entities that are known to have a common ancestor. For example, a phylogenetic tree may comprise nodes with descendants representing the most recent common ancestor of the descendants, and the edge lengths in some trees may correspond to time estimates.

[0025] The term “sample” as used herein is used in its broadest sense and includes environmental and biological samples. Environmental samples include material from the environment such as soil and water. Biological samples may be animal, including, human, fluid (e.g., blood, plasma and serum), solid (e.g., stool), tissue, liquid foods (e.g., milk), and solid foods (e.g., vegetables). For example, a pulmonary sample may be collected by bronchoalveolar lavage (BAL) which comprises fluid and cells derived from lung tissues. A biological sample may comprise a cell, tissue extract, body fluid, chromosomes or extrachromosomal elements isolated from a cell, genomic DNA (in solution or bound to a solid support such as for Southern blot analysis), RNA (in solution

or bound to a solid support such as for Northern blot analysis), cDNA (in solution or bound to a solid support) and the like.

[0026] The term “affinity” as used herein, refers to any attractive force between substances or particles that causes them to enter into and remain in chemical combination. For example, an inhibitor compound that has a high affinity for a receptor will provide greater efficacy in preventing the receptor from interacting with its natural ligands, than an inhibitor with a low affinity.

[0027] The term “derived from” as used herein, refers to the source of a compound or sequence. In one respect, a compound or sequence may be derived from an organism or particular species. In another respect, a compound or sequence may be derived from a larger complex or sequence. “Nucleic acid sequence” and “nucleotide sequence” as used herein refer to an oligonucleotide or polynucleotide, and fragments or portions thereof, and to DNA or RNA of genomic or synthetic origin which may be single- or double-stranded, and represent the sense or antisense strand.

[0028] The term “an isolated nucleic acid”, as used herein, refers to any nucleic acid molecule that has been removed from its natural state (e.g., removed from a cell and is, in a preferred embodiment, free of other genomic nucleic acid).

[0029] The terms “amino acid sequence” and “polypeptide sequence” as used herein, are interchangeable and to refer to a sequence of amino acids.

[0030] As used herein the term “portion” or “region” when in reference to a protein (as in “a portion or region of a given protein”) refers to fragments of that protein. The fragments may range in size from four amino acid residues to the entire amino acid sequence minus one amino acid.

[0031] The term “portion” or “region” when used in reference to a nucleotide sequence refers to fragments of that nucleotide sequence. The fragments may range in size from 5 nucleotide residues to the entire nucleotide sequence minus one nucleic acid residue.

[0032] The term “functionally equivalent codon”, as used herein, refers to different codons that encode the same amino acid. This phenomenon is often referred to as “degeneracy” of the genetic code. For example, six different codons encode the amino acid arginine.

[0033] A “variant” of a protein is defined as an amino acid sequence which differs by one or more amino acids from a polypeptide sequence or any homolog of the polypeptide sequence. The variant may have “conservative” changes, wherein a substituted amino acid has similar structural or chemical properties, e.g., replacement of leucine with isoleucine. More rarely, a variant may have “nonconservative” changes, e.g., replacement of a glycine with a tryptophan. Similar minor variations may also include amino acid deletions or insertions (i.e., additions), or both. Guidance in determining which and how many amino acid residues may be substituted, inserted or deleted without abolishing biological or immunological activity may be found using computer programs including, but not limited to, DNASTar® software.

[0034] A “variant” of a nucleotide is defined as a novel nucleotide sequence which differs from a reference oligonucleotide by having deletions, insertions and substitutions. These may be detected using a variety of methods (e.g., sequencing, hybridization assays etc.).

[0035] A “deletion” is defined as a change in either nucleotide or amino acid sequence in which one or more nucleotides or amino acid residues, respectively, are absent.

[0036] An “insertion” or “addition” is that change in a nucleotide or amino acid sequence which has resulted in the addition of one or more nucleotides or amino acid residues.

[0037] A “substitution” results from the replacement of one or more nucleotides or amino acids by different nucleotides or amino acids, respectively.

[0038] The term “derivative” as used herein, refers to any chemical modification of a nucleic acid or an amino acid. Illustrative of such modifications would be replacement of hydrogen by an alkyl, acyl, or amino group. For example, a nucleic acid derivative would encode a polypeptide which retains essential biological characteristics.

[0039] As used herein, the terms “complementary” or “complementarity” are used in reference to “polynucleotides” and “oligonucleotides” (which are interchangeable terms that refer to a sequence of nucleotides) related by the base-pairing rules. For example, the sequence “C-A-G-T,” is complementary to the sequence “G-T-C-A.” Complementarity can be “partial” or “total.” “Partial” complementarity is where one or more nucleic acid bases is not matched according to the base pairing rules. “Total” or “complete” complementarity between nucleic acids is where each and every nucleic acid base is matched with another base under the base pairing rules. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, as well as detection methods which depend upon binding between nucleic acids.

[0040] The terms “homology” and “homologous” as used herein in reference to nucleotide sequences refer to a degree of complementarity with other nucleotide sequences. There may be partial homology or complete homology (i.e., identity). A nucleotide sequence which is partially complementary, i.e., “substantially homologous,” to a nucleic acid sequence is one that at least partially inhibits a completely complementary sequence from hybridizing to a target nucleic acid sequence. The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or Northern blot, solution hybridization and the like) under conditions of low stringency. A substantially homologous sequence or probe will compete for and inhibit the binding (i.e., the hybridization) of a completely homologous sequence to a target sequence under conditions of low stringency. This is not to say that conditions of low stringency are such that non-specific binding is permitted; low stringency conditions require that the binding of two sequences to one another be a specific (i.e., selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of complementarity (e.g., less than about 30% identity); in the absence of non-specific binding the probe will not hybridize to the second non-complementary target.

[0041] The terms “homology” and “homologous” as used herein in reference to amino acid sequences refer to the degree of identity of the primary structure between two amino acid sequences. Such a degree of identity may be directed a portion of each amino acid sequence, or to the entire length of the amino acid sequence. Two or more amino acid sequences that are “substantially homologous” may have at least 50% identity, preferably at least 75% identity, more preferably at least 85% identity, most preferably at least 95%, or 100% identity.

[0042] An oligonucleotide sequence which is a “homolog” is defined herein as an oligonucleotide sequence which exhibits greater than or equal to 50% identity to a sequence, when sequences having a length of 100 bp or larger are compared.

[0043] Low stringency conditions comprise conditions equivalent to binding or hybridization at 42° C. in a solution consisting of 5×SSPE (43.8 g/l NaCl, 6.9 g/l NaH₂PO₄·H₂O and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.1% SDS, 5×Denhardt’s reagent {50×Denhardt’s contains per 500 ml: 5 g Ficoll (Type 400, Pharmacia), 5 g BSA (Fraction V; Sigma)} and 100 µg/ml denatured salmon sperm DNA followed by washing in a solution comprising 5×SSPE, 0.1% SDS at 42° C. when a probe of about 500 nucleotides in length is employed. Numerous equivalent conditions may also be employed to comprise low stringency conditions; factors such as the length and nature (DNA, RNA, base composition) of the probe and nature of the target (DNA, RNA, base composition, present in solution or immobilized, etc.) and the concentration of the salts and other components (e.g., the presence or absence of formamide, dextran sulfate, polyethylene glycol), as well as components of the hybridization solution may be varied to generate conditions of low stringency hybridization different from, but equivalent to, the above listed conditions. In addition, conditions which promote hybridization under conditions of high stringency (e.g., increasing the temperature of the hybridization and/or wash steps, the use of formamide in the hybridization solution, etc.) may also be used.

[0044] As used herein, the term “hybridization” is used in reference to the pairing of complementary nucleic acids using any process by which a strand of nucleic acid joins with a complementary strand through base pairing to form a hybridization complex. Hybridization and the strength of hybridization (i.e., the strength of the association between the nucleic acids) is impacted by such factors as the degree of complementarity between the nucleic acids, stringency of the conditions involved, the T_m of the formed hybrid, and the G:C ratio within the nucleic acids.

[0045] As used herein the term “hybridization complex” refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary G and C bases and between complementary A and T bases; these hydrogen bonds may be further stabilized by base stacking interactions. The two complementary nucleic acid sequences hydrogen bond in an antiparallel configuration. A hybridization complex may be formed in solution (e.g., C₀ t or R₀ t analysis) or between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized to a solid support (e.g., a nylon membrane or a nitrocellulose filter as employed in Southern and Northern blotting, dot blotting or a glass slide as employed in situ hybridization, including FISH (fluorescent in situ hybridization)).

[0046] As used herein, the term “ T_m ” is used in reference to the “melting temperature.” The melting temperature is the temperature at which a population of double-stranded nucleic acid molecules becomes half dissociated into single strands. As indicated by standard references, a simple estimate of the T_m value may be calculated by the equation: $T_m = 81.5 + 0.41 (\% G+C)$, when a nucleic acid is in aqueous solution at 1M NaCl. Anderson et al., “Quantitative Filter Hybridization” In: *Nucleic Acid Hybridization* (1985). More sophisticated computations take structural, as well as sequence characteristics, into account for the calculation of T_m .

[0047] As used herein, the term “stringency” is used in reference to the conditions of temperature, ionic strength, and the presence of other compounds such as organic solvents, under which nucleic acid hybridizations are conducted. “Stringency” typically occurs in a range from about T_m to about 20° C. to 25° C. below T_m . A “stringent hybridization” can be used to identify or detect identical polynucleotide sequences or to identify or detect similar or related polynucleotide sequences. For example, when fragments are employed in hybridization reactions under stringent conditions the hybridization of fragments which contain unique sequences (i.e., regions which are either non-homologous to or which contain less than about 50% homology or complementarity are favored. Alternatively, when conditions of “weak” or “low” stringency are used hybridization may occur with nucleic acids that are derived from organisms that are genetically diverse (i.e., for example, the frequency of complementary sequences is usually low between such organisms).

[0048] As used herein, the term “amplifiable nucleic acid” is used in reference to nucleic acids which may be amplified by any amplification method. It is contemplated that “amplifiable nucleic acid” will usually comprise “sample template.”

[0049] As used herein, the term “sample template” refers to nucleic acid originating from a sample which is analyzed for the presence of a target sequence of interest. In contrast, “background template” is used in reference to nucleic acid other than sample template which may or may not be present in a sample. Background template is most often inadvertent. It may be the result of carryover, or it may be due to the presence of nucleic acid contaminants sought to be purified away from the sample. For example, nucleic acids from organisms other than those to be detected may be present as background in a test sample.

[0050] “Amplification” is defined as the production of additional copies of a nucleic acid sequence and is generally carried out using polymerase chain reaction. Dieffenbach C. W. and G. S. Dveksler (1995) In: *PCR Primer, a Laboratory Manual*, Cold Spring Harbor Press, Plainview, N.Y.

[0051] As used herein, the term “polymerase chain reaction” (“PCR”) refers to the method of K. B. Mullis U.S. Pat. Nos. 4,683,195 and 4,683,202, herein incorporated by reference, which describe a method for increasing the concentration of a segment of a target sequence in a mixture of genomic DNA without cloning or purification. The length of the amplified segment of the desired target sequence is determined by the relative positions of two oligonucleotide primers with respect to each other, and therefore, this length is a controllable parameter. By virtue of the repeating aspect of the process, the method is referred to as the “polymerase chain reaction” (hereinafter “PCR”). Because the desired amplified segments of the target sequence become the predominant sequences (in terms of concentration) in the mixture, they are said to be “PCR amplified”. With PCR, it is possible to amplify a single copy of a specific target sequence in genomic DNA to a level detectable by several different methodologies (e.g., hybridization with a labeled probe; incorporation of biotinylated primers followed by avidin-enzyme conjugate detection; incorporation of ³²P-labeled deoxynucleotide triphosphates, such as dCTP or dATP, into the amplified segment). In addition to genomic DNA, any oligonucleotide sequence can be amplified with the appropriate set of primer molecules. In particular, the amplified segments created by the PCR process itself are, themselves, efficient templates for subsequent PCR amplifications.

[0052] As used herein, the term “primer” refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product which is complementary to a nucleic acid strand is induced, (i.e., in the presence of nucleotides and an inducing agent such as DNA polymerase and at a suitable temperature and pH). The primer is preferably single stranded for maximum efficiency in amplification, but may alternatively be double stranded. If double stranded, the primer is first treated to separate its strands before being used to prepare extension products. Preferably, the primer is an oligodeoxy-ribonucleotide. The primer must be sufficiently long to prime the synthesis of extension products in the presence of the inducing agent. The exact lengths of the primers will depend on many factors, including temperature, source of primer and the use of the method.

[0053] As used herein, the term “probe” refers; to an oligonucleotide (i.e., a sequence of nucleotides), whether occurring naturally as in a purified restriction digest or produced synthetically, recombinantly or by PCR amplification, which is capable of hybridizing to another oligonucleotide of interest. A probe may be single-stranded or double-stranded. Probes are useful in the detection, identification and isolation of particular gene sequences. It is contemplated that any probe used in the present invention will be labeled with any “reporter molecule,” so that is detectable in any detection system, including, but not limited to enzyme (e.g., ELISA, as well as enzyme-based histochemical assays), fluorescent, radioactive, and luminescent systems. It is not intended that the present invention be limited to any particular detection system or label.

[0054] As used herein, the terms “restriction endonucleases” and “restriction enzymes” refer to bacterial enzymes, each of which cut double-stranded DNA at or near a specific nucleotide sequence.

[0055] DNA molecules are said to have “5' ends” and “3' ends” because mononucleotides are reacted to make oligonucleotides in a manner such that the 5' phosphate of one mononucleotide pentose ring is attached to the 3' oxygen of its neighbor in one direction via a phosphodiester linkage. Therefore, an end of an oligonucleotide is referred to as the “5' end” if its 5' phosphate is not linked to the 3' oxygen of a mononucleotide pentose ring. An end of an oligonucleotide is referred to as the “3' end” if its 3' oxygen is not linked to a 5' phosphate of another mononucleotide pentose ring. As used herein, a nucleic acid sequence, even if internal to a larger oligonucleotide, also may be said to have 5' and 3' ends. In either a linear or circular DNA molecule, discrete elements are referred to as being “upstream” or 5' of the “downstream” or 3' elements. This terminology reflects the fact that transcription proceeds in a 5' to 3' fashion along the DNA strand. The promoter and enhancer elements which direct transcription of a linked gene are generally located 5' or upstream of the coding region. However, enhancer elements can exert their effect even when located 3' of the promoter element and the coding region. Transcription termination and polyadenylation signals are located 3' or downstream of the coding region.

[0056] As used herein, the term “an oligonucleotide having a nucleotide sequence encoding a gene” means a nucleic acid sequence comprising the coding region of a gene, i.e. the nucleic acid sequence which encodes a gene product. The

coding region may be present in a cDNA, genomic DNA or RNA form. When present in a DNA form, the oligonucleotide may be single-stranded (i.e., the sense strand) or double-stranded. Suitable control elements such as enhancers/promoters, splice junctions, polyadenylation signals, etc. may be placed in close proximity to the coding region of the gene if needed to permit proper initiation of transcription and/or correct processing of the primary RNA transcript. Alternatively, the coding region utilized in the expression vectors of the present invention may contain endogenous enhancers/promoters, splice junctions, intervening sequences, polyadenylation signals, etc. or a combination of both endogenous and exogenous control elements.

[0057] As used herein, the term “regulatory element” refers to a genetic element which controls some aspect of the expression of nucleic acid sequences. For example, a promoter is a regulatory element which facilitates the initiation of transcription of an operably linked coding region. Other regulatory elements are splicing signals, polyadenylation signals, termination signals, etc.

[0058] Transcriptional control signals in eukaryotes comprise “promoter” and “enhancer” elements. Promoters and enhancers consist of short arrays of DNA sequences that interact specifically with cellular proteins involved in transcription. Maniatis, T. et al., *Science* 236:1237 (1987). Promoter and enhancer elements have been isolated from a variety of eukaryotic sources including genes in plant, yeast, insect and mammalian cells and viruses (analogous control elements, i.e., promoters, are also found in prokaryotes). The selection of a particular promoter and enhancer depends on what cell type is to be used to express the protein of interest.

[0059] The presence of “splicing signals” on an expression vector often results in higher levels of expression of the recombinant transcript. Splicing signals mediate the removal of introns from the primary RNA transcript and consist of a splice donor and acceptor site. Sambrook, J. et al., In: *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor laboratory Press, New York (1989) pp. 16.7-16.8. A commonly used splice donor and acceptor site is the splice junction from the 16S RNA of SV40.

[0060] The term “poly A site” or “poly A sequence” as used herein denotes a DNA sequence which directs both the termination and polyadenylation of the nascent RNA transcript. Efficient polyadenylation of the recombinant transcript is desirable as transcripts lacking a poly A tail are unstable and are rapidly degraded. The poly A signal utilized in an expression vector may be “heterologous” or “endogenous.” An endogenous poly A signal is one that is found naturally at the 3' end of the coding region of a given gene in the genome. A heterologous poly A signal is one which is isolated from one gene and placed 3' of another gene. Efficient expression of recombinant DNA sequences in eukaryotic cells involves expression of signals directing the efficient termination and polyadenylation of the resulting transcript. Transcription termination signals are generally found downstream of the polyadenylation signal and are a few hundred nucleotides in length.

[0061] The term “transfection” or “transfected” refers to the introduction of foreign DNA into a cell.

[0062] As used herein, the terms “nucleic acid molecule encoding”, “DNA sequence encoding,” and “DNA encoding” refer to the order or sequence of deoxyribonucleotides along a strand of deoxyribonucleic acid. The order of these deoxyribonucleotides determines the order of amino acids along

the polypeptide (protein) chain. The DNA sequence thus codes for the amino acid sequence.

[0063] The term “Southern blot” refers to the analysis of DNA on agarose or acrylamide gels to fractionate the DNA according to size, followed by transfer and immobilization of the DNA from the gel to a solid support, such as nitrocellulose or a nylon membrane. The immobilized DNA is then probed with a labeled oligodeoxyribonucleotide probe or DNA probe to detect DNA species complementary to the probe used. The DNA may be cleaved with restriction enzymes prior to electrophoresis. Following electrophoresis, the DNA may be partially depurinated and denatured prior to or during transfer to the solid support. Southern blots are a standard tool of molecular biologists. J. Sambrook et al. (1989) In: *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, NY, pp 9.31-9.58.

[0064] The term “Northern blot” as used herein refers to the analysis of RNA by electrophoresis of RNA on agarose gels to fractionate the RNA according to size followed by transfer of the RNA from the gel to a solid support, such as nitrocellulose or a nylon membrane. The immobilized RNA is then probed with a labeled oligodeoxyribonucleotide probe or DNA probe to detect RNA species complementary to the probe used. Northern blots are a standard tool of molecular biologists. J. Sambrook, J. et al. (1989) supra, pp 7.39-7.52.

[0065] The term “reverse Northern blot” as used herein refers to the analysis of DNA by electrophoresis of DNA on agarose gels to fractionate the DNA on the basis of size followed by transfer of the fractionated DNA from the gel to a solid support, such as nitrocellulose or a nylon membrane. The immobilized DNA is then probed with a labeled oligoribonucleotide probe or RNA probe to detect DNA species complementary to the ribo probe used.

[0066] As used herein the term “coding region” when used in reference to a structural gene refers to the nucleotide sequences which encode the amino acids found in the nascent polypeptide as a result of translation of a mRNA molecule. The coding region is bounded, in eukaryotes, on the 5' side by the nucleotide triplet “ATG” which encodes the initiator methionine and on the 3' side by one of the three triplets which specify stop codons (i.e., TAA, TAG, TGA).

[0067] As used herein, the term “structural gene” refers to a DNA sequence coding for RNA or a protein. In contrast, “regulatory genes” are structural genes which encode products which control the expression of other genes (e.g., transcription factors).

[0068] As used herein, the term “gene” means the deoxyribonucleotide sequences comprising the coding region of a structural gene and including sequences located adjacent to the coding region on both the 5' and 3' ends for a distance of about 1 kb on either end such that the gene corresponds to the length of the full-length mRNA. The sequences which are located 5' of the coding region and which are present on the mRNA are referred to as 5' non-translated sequences. The sequences which are located 3' or downstream of the coding region and which are present on the mRNA are referred to as 3' non-translated sequences. The term “gene” encompasses both cDNA and genomic forms of a gene. A genomic form or clone of a gene contains the coding region interrupted with non-coding sequences termed “introns” or “intervening regions” or “intervening sequences.” Introns are segments of a gene which are transcribed into heterogeneous nuclear RNA (hnRNA); introns may contain regulatory elements such as enhancers. Introns are removed or “spliced out” from the

nuclear or primary transcript; introns therefore are absent in the messenger RNA (mRNA) transcript. The mRNA functions during translation to specify the sequence or order of amino acids in a nascent polypeptide.

[0069] In addition to containing introns, genomic forms of a gene may also include sequences located on both the 5' and 3' end of the sequences which are present on the RNA transcript. These sequences are referred to as “flanking” sequences or regions (these flanking sequences are located 5' or 3' to the non-translated sequences present on the mRNA transcript). The 5' flanking region may contain regulatory sequences such as promoters and enhancers which control or influence the transcription of the gene. The 3' flanking region may contain sequences which direct the termination of transcription, posttranscriptional cleavage and polyadenylation.

[0070] The term “label” or “detectable label” are used herein, to refer to any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Such labels include biotin for staining with labeled streptavidin conjugate, magnetic beads (e.g., Dynabeads®), fluorescent dyes (e.g., fluorescein, texas red, rhodamine, green fluorescent protein, and the like), radiolabels (e.g., ³H, ¹²⁵I, ³⁵S, ¹⁴C, or ³²P), enzymes (e.g., horse radish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and calorimetric labels such as colloidal gold or colored glass or plastic (e.g., polystyrene, polypropylene, latex, etc.) beads. Patents teaching the use of such labels include, but are not limited to, U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241 (all herein incorporated by reference). The labels contemplated in the present invention may be detected by many methods. For example, radiolabels may be detected using photographic film or scintillation counters, fluorescent markers may be detected using a photodetector to detect emitted light. Enzymatic labels are typically detected by providing the enzyme with a substrate and detecting, the reaction product produced by the action of the enzyme on the substrate, and calorimetric labels are detected by simply visualizing the colored label.

[0071] The term “binding” as used herein, refers to any interaction between an infection control composition and a surface. Such as surface is defined as a “binding surface”. Binding may be reversible or irreversible. Such binding may be, but is not limited to, non-covalent binding, covalent bonding, ionic bonding, Van de Waal forces or friction, and the like. An infection control composition is bound to a surface if it is impregnated, incorporated, coated, in suspension with, in solution with, mixed with, etc.

BRIEF DESCRIPTION OF THE DRAWINGS

[0072] The file of this patent contains at least one drawing executed in color. Copies of this patent with color drawings will be provided by the Patent and Trademark Office upon request and payment of the necessary fee.

[0073] FIG. 1 presents one embodiment of the concept of creating Hamming barcodes

[0074] FIG. 1A: Two representative Hamming hyperspheres (blue: center coordinates=(0, 0, 0); red: center coordinates=(1, 1, 1)).

[0075] FIG. 1B: Codeword regions comprising a length of 16 (or longer) checked by parity bits at positions 0, 1, 2, and 4; bits that are checked by each position are marked with 1.

[0076] FIG. 1C: Decoding a “received” codeword containing the binary value of 3 (0011) ($n=7, k=4$): Case 1: No errors. Case 2: Single-bit error at position 6 that is detected and corrected.

[0077] FIG. 2 presents exemplary data showing UniFrac clustering of samples from a cystic fibrosis lung, a Guerrero Negro microbial mat, air, and North American rivers obtained by pyrosequencing with barcodes.

[0078] FIG. 3 shows taxonomic distributions of bacteria in each of the major sample types in FIG. 2.

DETAILED DESCRIPTION OF THE INVENTION

[0079] The present invention relates to nucleic acid sequencing. In particular, the invention relates to methods and compositions for detecting errors and correcting such errors during nucleic acid amplification (i.e., for example, a nucleic acid barcode) such that accurate sample identification may be maintained. The combination of the methods and compositions described herein allow characterization of a plurality of nucleic acid samples simultaneously when using high throughput amplification and/or sequencing technologies.

[0080] In one embodiment, the present invention contemplates a composition comprising a tagged (i.e., for example, a Hamming barcode) nucleotide sequence, wherein the nucleotide averages between approximately 270 nucleotides and 1500 nucleotides. In one embodiment, the nucleotide sequence is derived from the 16S rRNA gene. Other embodiments provide a tagged nucleotide sequence wherein the tag is attached to the 3' or 5' end of the nucleotide sequence. Alternatively, some embodiments of the present invention contemplate a tagged nucleotide sequence wherein the tag is attached to both the 3' and 5' ends of the nucleotide sequence. Although it is not necessary to understand the mechanism of an invention, it is believed that single end tags may be advantageous for sequencing because variation in the length of variable regions in different species may preclude the second tag from being read.

[0081] In one embodiment, the present invention contemplates a method comprising: a) amplifying a nucleic acid sample using a primer comprising a barcode; and b) using the barcodes to provide sample assignments to a sample from which the nucleic acid was obtained. Although it is not necessary to understand the mechanism of an invention, it is believed that such sample assignments can be done with high confidence because of the unique error-detecting/correcting barcodes that correct amplification mistakes in each respective sample, thereby maintaining the integrity of the sample assignment information.

I. Conventional Error-Correcting Coding

[0082] The use of error-correction codes has been implemented in many different fields of art. For example, not only in biotechnology, but in information media such as cell phones and/or compact disks. R H Morelos-Zaragoza, *The Art of Error-Correcting Coding*. (John Wiley & Sons, Hoboken, N.J., (2006). As discussed below, these conventional techniques did not recognize, or employ, the advantages of Hamming barcodes (infra).

[0083] A. Cell Culture Assays

[0084] Quantitative and highly parallel methods for analyzing deletion mutants using barcodes in *Saccharomyces cerevisiae* have been reported. Shoemaker et al., “Quantitative Phenotypic Analysis of Yeast Deletion Mutants Using a

Highly Parallel Molecular Bar-Coding Strategy” *Nature Genetics* 14(4): 450-456 (1996). This approach uses a PCR targeting strategy to generate large numbers of deletion strains that are individually labeled with a unique 20-base tag sequence that can be detected by hybridization to a high-density oligonucleotide array. The tags serve as unique identifiers (molecular barcodes) that allow analysis of large numbers of deletion strains simultaneously through selective growth conditions.

[0085] B. Vector Analysis Assays

[0086] Methods for identifying an mRNA source pool from which individual cDNAs were derived have been tried by adding unique 6-nucleotide “bar codes” to the 3'-end of each mRNA during first-strand cDNA synthesis. Qiu et al., “DNA Sequence-Based “Bar Codes” for Tracking the Origins of Expressed Sequence Tags From a Maize Library Constructed Using Multiple mRNA Sources” *Plant Physiology* 133: 475-481 (2003). This method utilized an error-correcting decoding algorithm that identified a source mRNA pool for more than 97% of the expressed sequence tags (ESTs) examined. Of the 3,684 sequences examined with this decoding algorithm, 3,531 (95.8%) had exact bar code matches, 70 (1.9%) had errors in their bar codes that were decodable, and 83 (2.3%) were not decodable.

[0087] This prior method relies upon a natural metric for designing DNA bar codes known as an “edit metric” where the minimal distance between two strands of bar code DNA sequences is a single base insertion, deletion, or substitution required to transform one strand into the other. (Gusfield, 1997). This method produces a higher rate of uncorrectable errors than other barcoded libraries, thus requiring bar codes that allow for the correction of two errors (i.e., for example, being at least five edits apart). To address this problem, it is pointed out that lengthening the bar codes by just 2 by (to 8 bp) would provide 34 unique bar codes (Ashlock et al., 2002). Unlike the present invention, these bar codes are located within an EST sequence by identifying the vector and poly(T) sequences and then determining whether the bases at the approximate location of the bar code match any of the bar codes used in the construction of the library.

[0088] C. Pyrosequencing Assays

[0089] Methods of labeling and amplifying nucleic acid molecules with primers comprising unique five-nucleotide barcodes have been identified following amplification by methods that include pyrosequencing. Ronaghi et al. “Methods and Compositions for Clonal Amplification of Nucleic Acid” United States Patent Application Number 2006/008, 824 (herein incorporated by reference). The described bar-coded primers are attached to a solid surface (i.e., for example, a bead) such that specific nucleic acid targets may be isolated/immobilized prior to amplification with other (non-barcoded) primers. While the resulting PCR product(s) include the unique barcode sequence the barcoded PCR primer(s) are not amplified.

[0090] DNA bar codes and pyro sequencing have been used to detect minor drug resistance mutations in multidrug-resistant HIV populations. Each primer consisted of the conventional 454 A and 454 B sequences at the 5' ends and the HIV-complementary regions at the 3' end separated by a 4-nucleotide DNA bar code sequence. The results identified a variety of minor drug resistance alleles in patient samples and demonstrated the feasibility of using pyrosequencing for efficient HIV genotyping. Several controls were included in these experiments to allow estimations of the background

error rate associated with pyrosequencing. Hoffmann et al., "DNA Barcoding and Pyrosequencing to Identify Rare HIV Drug Resistance Mutations" *Nucleic Acids Research* 35(13): e91 (2007).

[0091] Pyrosequencing-tailored barcoding approaches have been reported that utilize 48 reverse-forward barcode pairs that are separated by a cloning linker, and are unique with respect to at least 4 nucleotide positions. Such a configuration was believed to provide uniquely barcoded libraries from up to 48 different samples. The barcoded primers were each 45-46 nucleotides long and consisted of: i) a forward or reverse 454 sequencing primer, ii) a forward or reverse barcode and iii) a forward or reverse cloning-linker. Lengthening the barcodes and/or increasing the variation(s) in the fixed forward and reverse linkers may expand the multiplexing capacity of this approach. Parameswaran et al., "A Pyrosequencing-Tailored Nucleotide Barcode Design Unveils Opportunities For Large-Scale Sample Multiplexing" *Nucleic Acids Research* 35(19): e130 (2007).

[0092] Conventional PCR with 5'-nucleotide tagged primers can generate homologous DNA amplification products from multiple specimens that are then subjected to pyrosequencing. Each DNA sequence is subsequently traced back to its individual source through 5'tag-analysis. This approach enables the assignment of virtually all the generated DNA sequences to the correct source once sequencing anomalies are accounted for. Binladen et al., "The Use of Coded PCR Primers Enables High-Throughput Sequencing of Multiple Homolog Amplification Products By 454 Parallel Sequencing" *PloS ONE* 2: e197 (2007). Conventional primers specific for 16S mammalian mitochondrial DNA (mtDNA) were modified into sixteen unique forward, and sixteen reverse primers through the addition of 5'-dinucleotide tags. The results indicated a bias in the distribution of the differently tagged primers that is dependent on the 5' nucleotide of the tag. Specifically, primers 5'-labeled with a cytosine were heavily overrepresented among the final sequences, while those 5'-labeled with a thymine were strongly underrepresented. A weaker bias was also reported for the distribution of sequences sorted by the second nucleotide of the dinucleotide tags. In comparison to the dinucleotide tags, the performance of tetranucleotide tagged primers was less efficient than predicted. Although the small number of tetranucleotide tagged primers tested renders statistically supported comparisons difficult, data indicate that overall the rate of sequence misassignment for these primers was lower than for the dinucleotide tags.

[0093] Characterization of 141,000 sequences of 16S rRNA genes obtained from 100 uncultured gastrointestinal bacterial samples from rhesus macaques was performed using primers marked with a "unique DNA bar code". These bar codes were represented by distinctive 4 base sequences between the 16S rRNA gene complementarity region and the pyrosequencing primer binding site. McKenna et al., "The Macaque Gut Microbiome In Health, Lentiviral Infection, and Chronic Enterocolitis" *PloS Pathog.* 4(2): e20 (2008). The resulting error rate for the barcoding procedure was estimated by cataloging all those sequences reads with bar codes that were not among those used for labeling. The analysis indicated that only 0.01% of sequences were likely to be miscataloged due to errors parsing the bar codes.

[0094] Integration site populations have been characterized from gene transfer studies using DNA barcoding and pyrosequencing. To sequence all the samples in a single sequencing

experiment, primers that contain unique 4-bp barcodes were used in the second PCR step. The PCR products were gel purified and pooled prior to pyrosequencing. Wang et al., "DNA Barcoding and Pyrosequencing to Analyze Adverse Events In Therapeutic Gene Transfer" *Nucleic Acids Research* 36(9): e49 (2008).

[0095] 454-pyrosequencing based methods have been reported for monitoring microbial communities in which the hyper-variable region of the 16S rRNA gene is amplified using primers that target adjacent conserved regions followed by direct sequencing of individual PCR products. Andersson et al., "Comparative Analysis of Human Gut Microbiota by Barcoded Pyrosequencing, *PloS ONE* 3(7): e2836 (2008). Including a sample-specific four nucleotide barcode sequence on one of the primers allows multiple samples to be analyzed in parallel on a single 454-pyrosequencing plate. It was suggested that the recognized pyrosequencing error rate might potentially disturb taxonomic classifications but offered not suggestions for using error correcting and/or detecting Hamming barcodes.

[0096] Methods that couple multiplex PCR with sample-specific DNA barcodes and "next-generation sequencing" (i.e., for example, pyrosequencing) have been reported to enable mutation discovery in candidate genes for multiple samples in parallel. The final amplification step of this method relies on universal PCR primers tailed with 454 Life Sciences A or B at the 5' end, followed by a sample-specific DNA sequence and 454 sequencing primers such that the first few bases indicate from which sample each read originated. Varley et al., "Nested Patch PCR Enables Highly Multiplexed Mutation Discovery In Candidate Genes" *Genome Res.* 18:1844-1850 (2008). While the method was admittedly error-prone due to the nature of 454 sequencing, there was no suggestions to use error-correcting and/or detecting Hamming barcodes.

II. Calculation Of Hamming Code Resolution

[0097] One class of error-correcting codes that use redundancy and standard linear algebra techniques has been referred to as a Hamming code. Hamming R. W., *Bell System Technical Journal* 29:147 (1950). Other encoding schemes similar to Hamming codes include Golay codes. Briefly, Hamming codes, like other error-correcting codes, are based on the principle of redundancy and are constructed by adding redundant parity bits to data that is to be transmitted over a noisy medium. Such error-correcting codes encode sample identifiers with redundant parity bits, and "transmit" these sample identifiers as codewords. Although it is not necessary to understand the mechanism of an invention, it is believed that if each nucleotide base is encoded by two (2) bits, then an eight (8) nucleotide base codeword would comprise sixteen (16) bits of information for transmission.

[0098] Hamming codes may be represented by a subset of the possible codewords that are chosen from the center of multidimensional spheres (i.e., for example, hyperspheres) in a binary subspace. Single bit errors may fall within hyperspheres associated with a specific codeword and can thus be corrected. On the other hand, double bit errors that do not associate with a specific codeword can be detected, but not corrected. Consider a first hypersphere centered at coordinates (0, 0, 0) (i.e., for example, using an x-y-z coordinate system), wherein any single-bit error can be corrected by falling within a radius of 1 from the center coordinates; i.e., for example, single bit errors having the coordinates of (0, 0,

0); (0, 1, 0); (0, 0, 1); (1, 0, 0), or (1, 1, 0). Likewise, a second hypersphere may be constructed wherein single-bit errors can be corrected by falling within a radius of 1 of its center coordinates (1, 1, 1) (i.e., for example, (1,1,1); (1, 0, 1); (0, 1, 0); or (0, 1, 1). See, FIG. 1A (first hypersphere-blue; second hypersphere-red).

[0099] Codeword regions comprising a length of 16 or more bits may be checked by parity bits at positions 0, 1, 2, and 4, wherein the bits that are checked by each position are marked with 1. See, FIG. 1B. Consequently, a “received” codeword containing a binary value of 3 (0011) ($n=7$, $k=4$) may be decoded for possible correction. The first case contains no errors; the second contains a single-bit error at position 6 that is detected and corrected. See, FIG. 3. Note that this is an example of a Hamming error-correcting code: the method claims all error-detecting and error-correcting codes.

[0100] For example, let n be the total number of bits in the codeword being transmitted, and k be the number of bits of information to be transmitted. Hamming codes use $n-k$ bits of redundancy, and because not all 2^n possible codewords are used, there are 2^k valid, error-correcting codewords is 2^k that form a k -dimensional subspace. The Hamming distance is defined as the number of bits that differ between two vectors in this subspace, and the relevant parameter for error-correction is the minimum Hamming distance. Next, let t be the radius of a sphere in this subspace where any change within this sphere can be corrected. The error-correcting capability is the largest radius such that all Hamming spheres are disjoint: $t = \text{floor}((d_{\min} - 1)/2)$, where $d_{\min}$ is the minimum Hamming distance. Thus, the minimum Hamming distance between codewords needed to correct a single error is 3.

[0101] In one embodiment, the present invention contemplates a barcode that uses Hamming codes to encode sample identifiers as DNA translations of each binary codeword using 2 bits/base. For example, 8-base codewords ($n=16$) use 11 bits for sample identifiers ($k=11$), and 5 bits of redundancy ($n-k=5$). There are thus $2^{11}=2048$ possible 8-base codewords. Alternatively, a 4-base barcodes can encode up to 16 codewords, thereby generating 67 million 16-base codewords. One can easily use increasing base lengths to provide ready scalability.

III. Error-Correction Hamming Codes in Pyrosequencing

[0102] Pyrosequencing may improve sequencing by eliminating the laborious step of producing clone libraries and generating hundreds of thousands of sequences in a single run. Margulies et al., *Nature* 437(7057):376 (2005). These improvements may include, for example, the ability to assess global microbial community diversity Huber et al., *Science* 318(5847):97 (2007); Roesch et al., *ISME J* 1:283 (2007); Sogin et al., *Proc Natl Acad Sci USA* 103:12115 (2006). In one embodiment, the present invention contemplates a method comprising pyrosequencing amplified nucleic acids containing Hamming barcoded error-correcting and/or error-detecting primers. In one embodiment, the method further comprises estimating the total sequencing error rate. In one embodiment, the method further comprises eliminating sample mis-assignment of the nucleic acid.

[0103] In one embodiment, the present invention contemplates a method comprising amplifying nucleic acids. In one embodiment, the amplification method may further comprise steps including, but not limited to, sequencing genes, detecting alleles, or diagnosing a medical condition. Further, a nucleic acid amplification method may comprise detecting

and/or correcting nucleotide sequence errors as a research tool for understanding of microbial habitats.

[0104] The presently disclosed methods have several advantages over conventionally used pyrosequencing methods currently in use including, but not limited to: 1) the ability to detect and correct errors in the barcodes to eliminate possible mis-assignment; 2) the barcodes only require 8 nucleotides, which is important when read lengths are limited; and 3) the ability to tag only one end of the sequence (i.e., for example, tagging the reverse primer) is useful since variation in the length of variable regions in different species may preclude a second tag from being read.

[0105] Conventional culture-independent 16S rRNA-based analysis of microbial community composition through pyrosequencing has been limited by the expense of each individual run, and by the difficulty of splitting a single plate across multiple runs. N. R. Pace, *Science* 276(5313): 734 (1997). Several reports have suggested that a barcode (i.e., a unique tag) may be added to each primer before PCR amplification. Binladen et al., *PLoS ONE* 2 (2), e197 (2007); Hoffmann et al., *Nucleic Acids Res* 35 (13), e91 (2007); and Parameswaran et al., *Nucleic Acids Res* 35 (19), e130 (2007). In one embodiment, the present invention contemplates a method comprising amplifying each sample with a known tagged primer, wherein the subsequent sequencing can be performed on an equimolar mixture of PCR-amplified DNA from each sample, thereby allowing the sequences to be assigned to samples based on the unique barcode.

[0106] Disadvantages of such conventional pyrosequencing barcoding methods (supra) include, but are not limited to: i) sequencing only twenty-five samples in a single pyrosequencing run; ii) a limited number of usable unique barcodes; or iii) an ability to detect sequencing errors that change sample assignment and/or identification. Although it is not necessary to understand the mechanism of an invention, it is believed that overcoming these disadvantages by using pyrosequencing in conjunction with Hamming barcodes will create a highly robust method that maintains an error-free sample assignment code. For example, because the 5' end of the read is generally considered more error-prone than other nucleotide regions the presently disclosed invention is believed to solve this problem. Huse et al., *Genome Biol* 8:R143 (2007).

[0107] A. Identifying Nucleic Acid Sequences Tagged with Bar Codes

[0108] In one embodiment, the present invention contemplates an improved method for culture-independent 16S rRNA pyrosequencing analysis that reduces both cost and error rate by processing more than 25 samples in a single pyrosequencing run. PCR amplification of each sample with unique barcode tagged primers prior to pyrosequencing permits an assignment of sequence data to individual samples from equimolar mixtures of PCR-amplified DNA.

[0109] In one embodiment, the present invention contemplates a barcode based on error-correcting Hamming codes that use a minimum amount of redundancy and are implemented using standard linear algebraic techniques. In addition to increasing the numbers of unique barcodes available, error-correcting barcodes are able to detect and/or correct sequencing errors. Although it is not necessary to understand the mechanism of an invention, it is believed that such sequencing errors occurring within a barcode are sufficient to change sample identification assignments. This technique is readily scalable, for example while an 8-base barcode upon

which the present primers were created provide 2,048 possible combinations, a 4-base barcode would provide 16 possible combinations, and a 16-base barcode would provide 67 million possible combinations.

[0110] In one embodiment, the present invention contemplates using a Hamming code analysis to identify an 8-base barcode scheme using the nucleotides including but not limited to, adenosine (A), thymidine (T), cytosine (C), or guanosine (G) (i.e., for example, at least 1544 barcodes). See, Table 1.

TABLE 1

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
AACCAACC SEQ ID NO: 1	GCTCCCTCGCGCCATCAGAACCAACCCATGCTC GCCTCCCGTAGGAGT SEQ ID NO: 2
AACCAAGG SEQ ID NO: 3	GCCTCCCTCGCGCCATCAGAACCAAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 4
AACCATCG SEQ ID NO: 5	GCCTCCCTCGCGCCATCAGAACCATCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 6
AACCATGC SEQ ID NO: 7	GCCTCCCTCGCGCCATCAGAACCATGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 8
AACCGCAT SEQ ID NO: 9	GCCTCCCTCGCGCCATCAGAACCGCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 10
AACCGCTA SEQ ID NO: 11	GCCTCCCTCGCGCCATCAGAACCGCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 12
AACCGGAA SEQ ID NO: 13	GCCTCCCTCGCGCCATCAGAACCGGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 14
AACCGGTT SEQ ID NO: 15	GCCTCCCTCGCGCCATCAGAACCGGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 16
AACCTACG SEQ ID NO: 17	GCCTCCCTCGCGCCATCAGAACCTACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 18
AACCTAGC SEQ ID NO: 19	GCCTCCCTCGCGCCATCAGAACCTAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 20
AACCTTCC SEQ ID NO: 21	GCCTCCCTCGCGCCATCAGAACCTTCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 22
AACCTTGG SEQ ID NO: 23	GCCTCCCTCGCGCCATCAGAACCTTGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 24
AACGAACG SEQ ID NO: 25	GCCTCCCTCGCGCCATCAGAACGAACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 26
AACGAAGC SEQ ID NO: 27	GCCTCCCTCGCGCCATCAGAACGAAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 28
AACGATCC	GCCTCCCTCGCGCCATCAGAACGATCCCATGCT

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
SEQ ID NO: 29	GCCTCCCGTAGGAGT SEQ ID NO: 30
AACGATGG SEQ ID NO: 31	GCCTCCCTCGCGCCATCAGAACGATGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 32
AACGCCAT SEQ ID NO: 33	GCCTCCCTCGCGCCATCAGAACGCCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 34
AACGCCTA SEQ ID NO: 35	GCCTCCCTCGCGCCATCAGAACGCCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 36
AACGCGAA SEQ ID NO: 37	GCCTCCCTCGCGCCATCAGAACGCGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 38
AACGCGTT SEQ ID NO: 39	GCCTCCCTCGCGCCATCAGAACGCGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 40
AACGCAA SEQ ID NO: 41	GCCTCCCTCGCGCCATCAGAACGGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 42
AACGGCTT SEQ ID NO: 43	GCCTCCCTCGCGCCATCAGAACGGCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 44
AACGTACC SEQ ID NO: 45	GCCTCCCTCGCGCCATCAGAACGTACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 46
AACGTAGG SEQ ID NO: 47	GCCTCCCTCGCGCCATCAGAACGTAGGCATGCT CTCCCGTAGGAGT SEQ ID NO: 48
AACGTTCG SEQ ID NO: 49	GCCTCCCTCGCGCCATCAGAACGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 50
AACGTTGC SEQ ID NO: 51	GCCTCCCTCGCGCCATCAGAACGTTGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 52
AAGCAACG SEQ ID NO: 53	GCCTCCCTCGCGCCATCAGAAAGCAACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 54
AAGCAAGC SEQ ID NO: 55	GCCTCCCTCGCGCCATCAGAAAGCAAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 56
AAGCATCC SEQ ID NO: 57	GCCTCCCTCGCGCCATCAGAAAGCATCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 58
AAGCATGG SEQ ID NO: 59	GCCTCCCTCGCGCCATCAGAAAGCATGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 60
AAGCCGAA SEQ ID NO: 61	GCCTCCCTCGCGCCATCAGAAAGCCGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 62
AAGCCGTT SEQ ID NO: 63	GCCTCCCTCGCGCCATCAGAAAGCCGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 64

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
AAGCGCAA SEQ ID NO: 65	GCCTCCCTCGCGCCATCAGAAGCGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 66
AAGCGCTT SEQ ID NO: 67	GCCTCCCTCGCGCCATCAGAAGCGCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 68
AAGCGGAT SEQ ID NO: 69	GCCTCCCTCGCGCCATCAGAAGCGGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 70
AAGCGGTA SEQ ID NO: 71	GCCTCCCTCGCGCCATCAGAAGCGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 72
AAGCTACC SEQ ID NO: 73	GCCTCCCTCGCGCCATCAGAAGCTACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 74
AAGCTAGG SEQ ID NO: 75	GCCTCCCTCGCGCCATCAGAAGCTAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 76
AAGCTTCG SEQ ID NO: 77	GCCTCCCTCGCGCCATCAGAAGCTTCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 78
AAGCTTGC SEQ ID NO: 79	GCCTCCCTCGCGCCATCAGAAGCTTGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 80
AAGGAACC SEQ ID NO: 81	GCCTCCCTCGCGCCATCAGAAGGAACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 82
AAGGAAGG SEQ ID NO: 83	GCCTCCCTCGCGCCATCAGAAGGAAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 84
AAGGATCG SEQ ID NO: 85	GCCTCCCTCGCGCCATCAGAAGGATCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 86
AAGGATGC SEQ ID NO: 87	GCCTCCCTCGCGCCATCAGAAGGATGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 88
AAGGCCAA SEQ ID NO: 89	GCCTCCCTCGCGCCATCAGAAGGCCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 90
AAGGCCTT SEQ ID NO: 91	GCCTCCCTCGCGCCATCAGAAGGCCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 92
AAGGCGAT SEQ ID NO: 93	GCCTCCCTCGCGCCATCAGAAGGCGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 94
AAGGCGTA SEQ ID NO: 95	GCCTCCCTCGCGCCATCAGAAGGCGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 96
AAGGTACG SEQ ID NO: 97	GCCTCCCTCGCGCCATCAGAAGGTACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 98

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
AAGGTAGC SEQ ID NO: 99	GCCTCCCTCGCGCCATCAGAAGGTAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 100
AAGGTTCC SEQ ID NO: 101	GCCTCCCTCGCGCCATCAGAAGGTTCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 102
AAGGTTGG SEQ ID NO: 103	GCCTCCCTCGCGCCATCAGAAGGTTGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 104
AATACCGC SEQ ID NO: 104	GCCTCCCTCGCGCCATCAGAATACCGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 106
AATACGCC SEQ ID NO: 107	GCCTCCCTCGCGCCATCAGAATACGCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 108
AATAGCGG SEQ ID NO: 109	GCCTCCCTCGCGCCATCAGAATAGCGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 110
AATAGGCG SEQ ID NO: 111	GCCTCCCTCGCGCCATCAGAATAGGCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 112
AATTCCGG SEQ ID NO: 113	GCCTCCCTCGCGCCATCAGAATTCCGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 114
AATTCGCG SEQ ID NO: 115	GCCTCCCTCGCGCCATCAGAATTGCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 116
AATTCGGC SEQ ID NO: 117	GCCTCCCTCGCGCCATCAGAATTGCGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 118
AATTGCCG SEQ ID NO: 119	GCCTCCCTCGCGCCATCAGAATTGCCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 120
AATTGCGC SEQ ID NO: 121	GCCTCCCTCGCGCCATCAGAATTGCGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 122
AATTGGCC SEQ ID NO: 123	GCCTCCCTCGCGCCATCAGAATTGGCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 124
ACACACAC SEQ ID NO: 125	GCCTCCCTCGCGCCATCAGACACACACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 126
ACACACTG SEQ ID NO: 127	GCCTCCCTCGCGCCATCAGACACACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 128
ACACAGAG SEQ ID NO: 129	GCCTCCCTCGCGCCATCAGACACAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 130
ACACAGTC SEQ ID NO: 131	GCCTCCCTCGCGCCATCAGACACAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 132

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
ACACCACA SEQ ID NO: 133	GCCTCCCTCGCGCCATCAGACACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 134
ACACCAGT SEQ ID NO: 135	GCCTCCCTCGCGCCATCAGACACCAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 136
ACACCTCT SEQ ID NO: 137	GCCTCCCTCGCGCCATCAGACACCTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 138
ACACCTGA SEQ ID NO: 139	GCCTCCCTCGCGCCATCAGACACCTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 140
ACACGACT SEQ ID NO: 141	GCCTCCCTCGCGCCATCAGACACGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 142
ACACGAGA SEQ ID NO: 143	GCCTCCCTCGCGCCATCAGACACGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 144
ACACGTCA SEQ ID NO: 145	GCCTCCCTCGCGCCATCAGACACGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 146
ACACGTGT SEQ ID NO: 147	GCCTCCCTCGCGCCATCAGACACGTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 148
ACACTCAG SEQ ID NO: 149	GCCTCCCTCGCGCCATCAGACACTCAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 150
ACACTCTC SEQ ID NO: 151	GCCTCCCTCGCGCCATCAGACACTCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 152
ACACTGAC SEQ ID NO: 153	GCCTCCCTCGCGCCATCAGACACTGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 154
ACACTGTG SEQ ID NO: 155	GCCTCCCTCGCGCCATCAGACACTGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 156
ACAGACAG SEQ ID NO: 157	GCCTCCCTCGCGCCATCAGACAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 158
ACAGACTC SEQ ID NO: 159	GCCTCCCTCGCGCCATCAGACAGACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 160
ACAGAGAC SEQ ID NO: 161	GCCTCCCTCGCGCCATCAGACAGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 162
ACAGAGTG SEQ ID NO: 163	GCCTCCCTCGCGCCATCAGACAGAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 164
ACAGCACT SEQ ID NO: 165	GCCTCCCTCGCGCCATCAGACAGCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 166

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
ACAGCAGA SEQ ID NO: 167	GCCTCCCTCGCGCCATCAGACAGCAGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 168
ACAGCTCA SEQ ID NO: 169	GCCTCCCTCGCGCCATCAGACAGCTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 170
ACAGCTGT SEQ ID NO: 171	GCCTCCCTCGCGCCATCAGACAGCTGTCTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 172
ACAGGACA SEQ ID NO: 173	GCCTCCCTCGCGCCATCAGACAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 174
ACAGGAGT SEQ ID NO: 175	GCCTCCCTCGCGCCATCAGACAGGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 176
ACAGGTCT SEQ ID NO: 177	GCCTCCCTCGCGCCATCAGACAGGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 178
ACAGGTGA SEQ ID NO: 179	GCCTCCCTCGCGCCATCAGACAGGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 180
ACAGTCAC SEQ ID NO: 181	GCCTCCCTCGCGCCATCAGACAGTCACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 182
ACAGTCTG SEQ ID NO: 183	GCCTCCCTCGCGCCATCAGACAGTCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 184
ACAGTGAG SEQ ID NO: 185	GCCTCCCTCGCGCCATCAGACAGTGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 186
ACAGTGTC SEQ ID NO: 187	GCCTCCCTCGCGCCATCAGACAGTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 188
ACCAACCA SEQ ID NO: 189	GCCTCCCTCGCGCCATCAGACCAACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 190
ACCAACGT SEQ ID NO: 191	GCCTCCCTCGCGCCATCAGACCAACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 192
ACCAAGCT SEQ ID NO: 193	GCCTCCCTCGCGCCATCAGACCAAGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 194
ACCAAGGA SEQ ID NO: 195	GCCTCCCTCGCGCCATCAGACCAAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 196
ACCACAAC SEQ ID NO: 197	GCCTCCCTCGCGCCATCAGACCACAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 198
ACCACATG SEQ ID NO: 199	GCCTCCCTCGCGCCATCAGACCACATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 200

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
ACCACTAG SEQ ID NO: 201	GCCTCCCTCGCGCCATCAGACCACTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 202
ACCACTTC SEQ ID NO: 203	GCCTCCCTCGCGCCATCAGACCACTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 204
ACCAGAAG SEQ ID NO: 205	GCCTCCCTCGCGCCATCAGACCAGAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 206
ACCAGATC SEQ ID NO: 207	GCCTCCCTCGCGCCATCAGACCAGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 208
ACCAGTAC SEQ ID NO: 209	GCCTCCCTCGCGCCATCAGACCAGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 210
ACCAGTTG SEQ ID NO: 211	GCCTCCCTCGCGCCATCAGACCAGTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 212
ACCATCCT SEQ ID NO: 213	GCCTCCCTCGCGCCATCAGACCATCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 214
ACCATCGA SEQ ID NO: 215	GCCTCCCTCGCGCCATCAGACCATCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 216
ACCATGCA SEQ ID NO: 217	GCCTCCCTCGCGCCATCAGACCATGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 218
ACCATGGT SEQ ID NO: 219	GCCTCCCTCGCGCCATCAGACCATGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 220
ACCTACCT SEQ ID NO: 221	GCCTCCCTCGCGCCATCAGACCTACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 222
ACCTACGA SEQ ID NO: 223	GCCTCCCTCGCGCCATCAGACCTACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 224
ACCTAGCA SEQ ID NO: 225	GCCTCCCTCGCGCCATCAGACCTAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 226
ACCTAGGT SEQ ID NO: 227	GCCTCCCTCGCGCCATCAGACCTAGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 228
ACCTCAAG SEQ ID NO: 229	GCCTCCCTCGCGCCATCAGACCTCAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 230
ACCTCATC SEQ ID NO: 231	GCCTCCCTCGCGCCATCAGACCTCATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 232
ACCTCTAC SEQ ID NO: 233	GCCTCCCTCGCGCCATCAGACCTCTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 234

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
ACCTCTTG SEQ ID NO: 235	GCCTCCCTCGCGCCATCAGACCTCTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 236
ACCTGAAC SEQ ID NO: 237	GCCTCCCTCGCGCCATCAGACCTGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 238
ACCTGATG SEQ ID NO: 239	GCCTCCCTCGCGCCATCAGACCTGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 240
ACCTGTAG SEQ ID NO: 241	GCCTCCCTCGCGCCATCAGACCTGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 242
ACCTGTTT SEQ ID NO: 243	GCCTCCCTCGCGCCATCAGACCTGTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 244
ACCTTCCA SEQ ID NO: 245	GCCTCCCTCGCGCCATCAGACCTTCCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 246
ACCTTCGT SEQ ID NO: 247	GCCTCCCTCGCGCCATCAGACCTTCGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 248
ACCTTGCT SEQ ID NO: 249	GCCTCCCTCGCGCCATCAGACCTTGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 250
ACCTTGGA SEQ ID NO: 251	GCCTCCCTCGCGCCATCAGACCTTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 252
ACGAACCT SEQ ID NO: 253	GCCTCCCTCGCGCCATCAGACGAACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 254
ACGAACGA SEQ ID NO: 255	GCCTCCCTCGCGCCATCAGACGAACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 256
ACGAAGCA SEQ ID NO: 257	GCCTCCCTCGCGCCATCAGACGAAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 258
ACGAAGGT SEQ ID NO: 259	GCCTCCCTCGCGCCATCAGACGAAGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 260
ACGACAAG SEQ ID NO: 261	GCCTCCCTCGCGCCATCAGACGACAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 262
ACGACATC SEQ ID NO: 263	GCCTCCCTCGCGCCATCAGACGACATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 264
ACGACTAC SEQ ID NO: 265	GCCTCCCTCGCGCCATCAGACGACTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 266
ACGACTTG SEQ ID NO: 267	GCCTCCCTCGCGCCATCAGACGACTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 268

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
ACGAGAAC SEQ ID NO: 269	GCCTCCCTCGCGCCATCAGACGAGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 270
ACGAGATG SEQ ID NO: 271	GCCTCCCTCGCGCCATCAGACGAGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 272
ACGAGTAG SEQ ID NO: 273	GCCTCCCTCGCGCCATCAGACGAGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 274
ACGAGTTC SEQ ID NO: 275	GCCTCCCTCGCGCCATCAGACGAGTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 276
ACGATCCA SEQ ID NO: 277	GCCTCCCTCGCGCCATCAGACGATCCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 278
ACGATCGT SEQ ID NO: 279	GCCTCCCTCGCGCCATCAGACGATCGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 280
ACGATGCT SEQ ID NO: 281	GCCTCCCTCGCGCCATCAGACGATGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 282
ACGATGGA SEQ ID NO: 283	GCCTCCCTCGCGCCATCAGACGATGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 284
ACGTACCA SEQ ID NO: 285	GCCTCCCTCGCGCCATCAGACGTACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 286
ACGTACGT SEQ ID NO: 287	GCCTCCCTCGCGCCATCAGACGTACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 288
ACGTAGCT SEQ ID NO: 289	GCCTCCCTCGCGCCATCAGACGTAGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 290
ACGTAGGA SEQ ID NO: 291	GCCTCCCTCGCGCCATCAGACGTAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 292
ACGTCAAC SEQ ID NO: 293	GCCTCCCTCGCGCCATCAGACGTCAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 294
ACGTCATG SEQ ID NO: 295	GCCTCCCTCGCGCCATCAGACGTATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 296
ACGTCTAG SEQ ID NO: 297	GCCTCCCTCGCGCCATCAGACGTCTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 298
ACGTCTTC SEQ ID NO: 299	GCCTCCCTCGCGCCATCAGACGTCTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 300
ACGTGAAG SEQ ID NO: 301	GCCTCCCTCGCGCCATCAGACGTGAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 302

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
ACGTGATC SEQ ID NO: 303	GCCTCCCTCGCGCCATCAGACGTGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 304
ACGTGTAC SEQ ID NO: 305	GCCTCCCTCGCGCCATCAGACGTGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 306
ACGTGTTG SEQ ID NO: 307	GCCTCCCTCGCGCCATCAGACGTGTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 308
ACGTTCTT SEQ ID NO: 309	GCCTCCCTCGCGCCATCAGACGTTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 310
ACGTTCTGA SEQ ID NO: 311	GCCTCCCTCGCGCCATCAGACGTTCTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 312
ACGTTGCA SEQ ID NO: 313	GCCTCCCTCGCGCCATCAGACGTTGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 314
ACGTTGGT SEQ ID NO: 315	GCCTCCCTCGCGCCATCAGACGTTGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 316
ACTCACAG SEQ ID NO: 317	GCCTCCCTCGCGCCATCAGACTCACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 318
ACTCACTC SEQ ID NO: 319	GCCTCCCTCGCGCCATCAGACTCACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 320
ACTCAGAC SEQ ID NO: 321	GCCTCCCTCGCGCCATCAGACTCAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 322
ACTCAGTG SEQ ID NO: 323	GCCTCCCTCGCGCCATCAGACTCAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 324
ACTCCACT SEQ ID NO: 325	GCCTCCCTCGCGCCATCAGACTCCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 326
ACTCCAGA SEQ ID NO: 327	GCCTCCCTCGCGCCATCAGACTCCAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 328
ACTCCTCA SEQ ID NO: 329	GCCTCCCTCGCGCCATCAGACTCCTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 330
ACTCCTGT SEQ ID NO: 331	GCCTCCCTCGCGCCATCAGACTCCTGTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 332
ACTCGACA SEQ ID NO: 333	GCCTCCCTCGCGCCATCAGACTCGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 334
ACTCGAGT SEQ ID NO: 335	GCCTCCCTCGCGCCATCAGACTCGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 336

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
ACTCGTCT SEQ ID NO: 337	GCCTCCCTCGCGCCATCAGACTCGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 338
ACTCGTGA SEQ ID NO: 339	GCCTCCCTCGCGCCATCAGACTCGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 340
ACTCTCAC SEQ ID NO: 341	GCCTCCCTCGCGCCATCAGACTCTCACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 342
ACTCTCTG SEQ ID NO: 343	GCCTCCCTCGCGCCATCAGACTCTCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 344
ACTCTGAG SEQ ID NO: 345	GCCTCCCTCGCGCCATCAGACTCTGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 346
ACTCTGTC SEQ ID NO: 347	GCCTCCCTCGCGCCATCAGACTCTGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 348
ACTGACAC SEQ ID NO: 349	GCCTCCCTCGCGCCATCAGACTGACACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 350
ACTGACTG SEQ ID NO: 351	GCCTCCCTCGCGCCATCAGACTGACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 352
ACTGAGAG SEQ ID NO: 353	GCCTCCCTCGCGCCATCAGACTGAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 354
ACTGAGTC SEQ ID NO: 355	GCCTCCCTCGCGCCATCAGACTGAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 356
ACTGCACA SEQ ID NO: 357	GCCTCCCTCGCGCCATCAGACTGCACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 358
ACTGCAGT SEQ ID NO: 359	GCCTCCCTCGCGCCATCAGACTGCAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 360
ACTGCTCT SEQ ID NO: 361	GCCTCCCTCGCGCCATCAGACTGCTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 362
ACTGCTGA SEQ ID NO: 363	GCCTCCCTCGCGCCATCAGACTGCTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 364
ACTGGACT SEQ ID NO: 365	GCCTCCCTCGCGCCATCAGACTGGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 366
ACTGGAGA SEQ ID NO: 367	GCCTCCCTCGCGCCATCAGACTGGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 368
ACTGGTCA SEQ ID NO: 369	GCCTCCCTCGCGCCATCAGACTGGTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 370

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
ACTGGTGT SEQ ID NO: 371	GCCTCCCTCGCGCCATCAGACTGGTGTCTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 372
ACTGTGAG SEQ ID NO: 373	GCCTCCCTCGCGCCATCAGACTGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 374
ACTGTCTC SEQ ID NO: 375	GCCTCCCTCGCGCCATCAGACTGTCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 376
ACTGTGAC SEQ ID NO: 377	GCCTCCCTCGCGCCATCAGACTGTGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 378
ACTGTGTG SEQ ID NO: 379	GCCTCCCTCGCGCCATCAGACTGTGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 380
AGACACAG SEQ ID NO: 381	GCCTCCCTCGCGCCATCAGAGACACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 382
AGACACTC SEQ ID NO: 383	GCCTCCCTCGCGCCATCAGAGACACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 384
AGACAGAC SEQ ID NO: 385	GCCTCCCTCGCGCCATCAGAGACAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 386
AGACAGTG SEQ ID NO: 387	GCCTCCCTCGCGCCATCAGAGACAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 388
AGACCACT SEQ ID NO: 389	GCCTCCCTCGCGCCATCAGAGACCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 390
AGACCAGA SEQ ID NO: 391	GCCTCCCTCGCGCCATCAGAGACCAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 392
AGACCTCA SEQ ID NO: 393	GCCTCCCTCGCGCCATCAGAGACCTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 394
AGACCTGT SEQ ID NO: 395	GCCTCCCTCGCGCCATCAGAGACCTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 396
AGACGACA SEQ ID NO: 397	GCCTCCCTCGCGCCATCAGAGACGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 398
AGACGAGT SEQ ID NO: 399	GCCTCCCTCGCGCCATCAGAGACGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 400
AGACGTCT SEQ ID NO: 401	GCCTCCCTCGCGCCATCAGAGACGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 402
AGACGTGA SEQ ID NO: 403	GCCTCCCTCGCGCCATCAGAGACGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 404

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
AGACTCAC SEQ ID NO: 405	GCCTCCCTCGCGCCATCAGAGACTCACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 406
AGACTCTG SEQ ID NO: 407	GCCTCCCTCGCGCCATCAGAGACTCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 408
AGACTGAG SEQ ID NO: 409	GCCTCCCTCGCGCCATCAGAGACTGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 410
AGACTGTC SEQ ID NO: 411	GCCTCCCTCGCGCCATCAGAGACTGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 412
AGAGACAC SEQ ID NO: 413	GCCTCCCTCGCGCCATCAGAGAGACACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 414
AGAGACTG SEQ ID NO: 415	GCCTCCCTCGCGCCATCAGAGAGACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 416
AGAGAGAG SEQ ID NO: 417	GCCTCCCTCGCGCCATCAGAGAGAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 418
AGAGAGTC SEQ ID NO: 419	GCCTCCCTCGCGCCATCAGAGAGAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 420
AGAGCACA SEQ ID NO: 421	GCCTCCCTCGCGCCATCAGAGAGCACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 422
AGAGCAGT SEQ ID NO: 423	GCCTCCCTCGCGCCATCAGAGAGCAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 424
AGAGCTCT SEQ ID NO: 425	GCCTCCCTCGCGCCATCAGAGAGCTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 426
AGAGCTGA SEQ ID NO: 427	GCCTCCCTCGCGCCATCAGAGAGCTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 428
AGAGGACT SEQ ID NO: 429	GCCTCCCTCGCGCCATCAGAGAGGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 430
AGAGGAGA SEQ ID NO: 431	GCCTCCCTCGCGCCATCAGAGAGGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 432
AGAGGTCA SEQ ID NO: 433	GCCTCCCTCGCGCCATCAGAGAGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 434
AGAGGTGT SEQ ID NO: 435	GCCTCCCTCGCGCCATCAGAGAGGTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 436
AGAGTCAG SEQ ID NO: 437	GCCTCCCTCGCGCCATCAGAGAGTCAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 438

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
AGAGTCTC SEQ ID NO: 439	GCCTCCCTCGCGCCATCAGAGAGTCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 440
AGAGTGAC SEQ ID NO: 441	GCCTCCCTCGCGCCATCAGAGAGTGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 442
AGAGTGTG SEQ ID NO: 443	GCCTCCCTCGCGCCATCAGAGAGTGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 444
AGCAACCT SEQ ID NO: 445	GCCTCCCTCGCGCCATCAGAGCAACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 446
AGCAACGA SEQ ID NO: 447	GCCTCCCTCGCGCCATCAGAGCAACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 448
AGCAAGCA SEQ ID NO: 449	GCCTCCCTCGCGCCATCAGAGCAAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 450
AGCAAGGT SEQ ID NO: 451	GCCTCCCTCGCGCCATCAGAGCAAGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 452
AGCACAAAG SEQ ID NO: 453	GCCTCCCTCGCGCCATCAGAGCACAAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 454
AGCACATC SEQ ID NO: 455	GCCTCCCTCGCGCCATCAGAGCACATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 456
AGCACTAC SEQ ID NO: 457	GCCTCCCTCGCGCCATCAGAGCACTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 458
AGCACTTG SEQ ID NO: 459	GCCTCCCTCGCGCCATCAGAGCACTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 460
AGCAGAAC SEQ ID NO: 461	GCCTCCCTCGCGCCATCAGAGCAGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 462
AGCAGATG SEQ ID NO: 463	GCCTCCCTCGCGCCATCAGAGCAGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 464
AGCAGTAG SEQ ID NO: 465	GCCTCCCTCGCGCCATCAGAGCAGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 466
AGCAGTTC SEQ ID NO: 467	GCCTCCCTCGCGCCATCAGAGCAGTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 468
AGCATCCA SEQ ID NO: 469	GCCTCCCTCGCGCCATCAGAGCATCCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 470
AGCATCGT SEQ ID NO: 471	GCCTCCCTCGCGCCATCAGAGCATCGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 472

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
AGCATGCT SEQ ID NO: 473	GCCTCCCTCGCGCCATCAGAGCATGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 474
AGCATGGA SEQ ID NO: 475	GCCTCCCTCGCGCCATCAGAGCATGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 476
AGCTACCA SEQ ID NO: 477	GCCTCCCTCGCGCCATCAGAGCTACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 478
AGCTACGT SEQ ID NO: 479	GCCTCCCTCGCGCCATCAGAGCTACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 480
AGCTAGCT SEQ ID NO: 481	GCCTCCCTCGCGCCATCAGAGCTAGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 482
AGCTAGGA SEQ ID NO: 483	GCCTCCCTCGCGCCATCAGAGCTAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 484
AGCTCAAC SEQ ID NO: 485	GCCTCCCTCGCGCCATCAGAGCTCAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 486
AGCTCATG SEQ ID NO: 487	GCCTCCCTCGCGCCATCAGAGCTCATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 488
AGCTCTAG SEQ ID NO: 489	GCCTCCCTCGCGCCATCAGAGCTCTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 490
AGCTCTTC SEQ ID NO: 491	GCCTCCCTCGCGCCATCAGAGCTCTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 492
AGCTGAAG SEQ ID NO: 493	GCCTCCCTCGCGCCATCAGAGCTGAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 494
AGCTGATC SEQ ID NO: 495	GCCTCCCTCGCGCCATCAGAGCTGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 496
AGCTGTAC SEQ ID NO: 497	GCCTCCCTCGCGCCATCAGAGCTGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 498
AGCTGTTG SEQ ID NO: 499	GCCTCCCTCGCGCCATCAGAGCTGTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 500
AGCTTCCT SEQ ID NO: 501	GCCTCCCTCGCGCCATCAGAGCTTCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 502
AGCTTCGA SEQ ID NO: 503	GCCTCCCTCGCGCCATCAGAGCTTCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 504
AGCTTGCA SEQ ID NO: 505	GCCTCCCTCGCGCCATCAGAGCTTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 506

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
AGCTTGGT SEQ ID NO: 507	GCCTCCCTCGCGCCATCAGAGCTTGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 508
AGGAACCA SEQ ID NO: 509	GCCTCCCTCGCGCCATCAGAGGAACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 510
AGGAACGT SEQ ID NO: 511	GCCTCCCTCGCGCCATCAGAGGAACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 512
AGGAAGCT SEQ ID NO: 513	GCCTCCCTCGCGCCATCAGAGGAAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 514
AGGAAGGA SEQ ID NO: 515	GCCTCCCTCGCGCCATCAGAGGAAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 516
AGGACAAC SEQ ID NO: 517	GCCTCCCTCGCGCCATCAGAGGACAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 518
AGGACATG SEQ ID NO: 519	GCCTCCCTCGCGCCATCAGAGGACATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 520
AGGACTAG SEQ ID NO: 521	GCCTCCCTCGCGCCATCAGAGGACTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 522
AGGACTTC SEQ ID NO: 523	GCCTCCCTCGCGCCATCAGAGGACTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 524
AGGAGAAG SEQ ID NO: 525	GCCTCCCTCGCGCCATCAGAGGAGAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 526
AGGAGATC SEQ ID NO: 527	GCCTCCCTCGCGCCATCAGAGGAGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 528
AGGAGTAC SEQ ID NO: 529	GCCTCCCTCGCGCCATCAGAGGAGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 530
AGGAGTTG SEQ ID NO: 531	GCCTCCCTCGCGCCATCAGAGGAGTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 532
AGGATCCT SEQ ID NO: 533	GCCTCCCTCGCGCCATCAGAGGATCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 534
AGGATCGA SEQ ID NO: 535	GCCTCCCTCGCGCCATCAGAGGATCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 536
AGGATGCA SEQ ID NO: 537	GCCTCCCTCGCGCCATCAGAGGATGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 538
AGGATGGT SEQ ID NO: 539	GCCTCCCTCGCGCCATCAGAGGATGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 540

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
AGGTACCT SEQ ID NO: 541	GCCTCCCTCGCGCCATCAGAGGTACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 542
AGGTACGA SEQ ID NO: 543	GCCTCCCTCGCGCCATCAGAGGTACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 544
AGGTAGCA SEQ ID NO: 545	GCCTCCCTCGCGCCATCAGAGGTAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 546
AGGTAGGT SEQ ID NO: 547	GCCTCCCTCGCGCCATCAGAGGTAGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 548
AGGTCAAG SEQ ID NO: 549	GCCTCCCTCGCGCCATCAGAGGTCAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 550
AGGTCATC SEQ ID NO: 551	GCCTCCCTCGCGCCATCAGAGGTCATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 552
AGGTCTAC SEQ ID NO: 553	GCCTCCCTCGCGCCATCAGAGGTCTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 554
AGGTCTTG SEQ ID NO: 555	GCCTCCCTCGCGCCATCAGAGGTCTTGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 556
AGGTGAAC SEQ ID NO: 557	GCCTCCCTCGCGCCATCAGAGGTGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 558
AGGTGATG SEQ ID NO: 559	GCCTCCCTCGCGCCATCAGAGGTGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 560
AGGTGTAG SEQ ID NO: 561	GCCTCCCTCGCGCCATCAGAGGTGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 562
AGGTGTTC SEQ ID NO: 563	GCCTCCCTCGCGCCATCAGAGGTGTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 564
AGGTTCCA SEQ ID NO: 565	GCCTCCCTCGCGCCATCAGAGGTTCCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 566
AGGTTCGT SEQ ID NO: 567	GCCTCCCTCGCGCCATCAGAGGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 568
AGGTTGCT SEQ ID NO: 569	GCCTCCCTCGCGCCATCAGAGGTGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 570
AGGTTGGA SEQ ID NO: 571	GCCTCCCTCGCGCCATCAGAGGTTGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 572
AGTCACAC SEQ ID NO: 573	GCCTCCCTCGCGCCATCAGAGTCACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 574

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
AGTCACTG SEQ ID NO: 575	GCCTCCCTCGCGCCATCAGAGTCACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 576
AGTCAGAG SEQ ID NO: 577	GCCTCCCTCGCGCCATCAGAGTCAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 578
AGTCAGTC SEQ ID NO: 579	GCCTCCCTCGCGCCATCAGAGTCAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 580
AGTCCACA SEQ ID NO: 581	GCCTCCCTCGCGCCATCAGAGTCCACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 582
AGTCCAGT SEQ ID NO: 583	GCCTCCCTCGCGCCATCAGAGTCCAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 584
AGTCCTCT SEQ ID NO: 585	GCCTCCCTCGCGCCATCAGAGTCCTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 586
AGTCCTGA SEQ ID NO: 587	GCCTCCCTCGCGCCATCAGAGTCCTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 588
AGTCGACT SEQ ID NO: 589	GCCTCCCTCGCGCCATCAGAGTCGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 590
AGTCGAGA SEQ ID NO: 591	GCCTCCCTCGCGCCATCAGAGTCGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 592
AGTCGTCA SEQ ID NO: 593	GCCTCCCTCGCGCCATCAGAGTCGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 594
AGTCGTGT SEQ ID NO: 595	GCCTCCCTCGCGCCATCAGAGTCGTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 596
AGTCTCAG SEQ ID NO: 597	GCCTCCCTCGCGCCATCAGAGTCTCAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 598
AGTCTCTC SEQ ID NO: 599	GCCTCCCTCGCGCCATCAGAGTCTCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 600
AGTCTGAC SEQ ID NO: 601	GCCTCCCTCGCGCCATCAGAGTCTGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 602
AGTCTGTG SEQ ID NO: 603	GCCTCCCTCGCGCCATCAGAGTCTGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 604
AGTGACAG SEQ ID NO: 605	GCCTCCCTCGCGCCATCAGAGTGACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 606
AGTGACTC SEQ ID NO: 607	GCCTCCCTCGCGCCATCAGAGTGACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 608

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
AGTGAGAC SEQ ID NO: 609	GCCTCCCTCGCGCCATCAGAGTGAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 610
AGTGAGTG SEQ ID NO: 611	GCCTCCCTCGCGCCATCAGAGTGAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 612
AGTGCACT SEQ ID NO: 613	GCCTCCCTCGCGCCATCAGAGTGCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 614
AGTGCAGA SEQ ID NO: 615	GCCTCCCTCGCGCCATCAGAGTGCAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 616
AGTGCTCA SEQ ID NO: 617	GCCTCCCTCGCGCCATCAGAGTGCTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 618
AGTGCTGT SEQ ID NO: 619	GCCTCCCTCGCGCCATCAGAGTGCTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 620
AGTGGACA SEQ ID NO: 621	GCCTCCCTCGCGCCATCAGAGTGGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 622
AGTGGAGT SEQ ID NO: 623	GCCTCCCTCGCGCCATCAGAGTGGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 624
AGTGGTCT SEQ ID NO: 625	GCCTCCCTCGCGCCATCAGAGTGGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 626
AGTGGTGA SEQ ID NO: 627	GCCTCCCTCGCGCCATCAGAGTGGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 628
AGTGTAC SEQ ID NO: 629	GCCTCCCTCGCGCCATCAGAGTGTCACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 630
AGTGTCTG SEQ ID NO: 631	GCCTCCCTCGCGCCATCAGAGTGTCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 632
AGTGTGAG SEQ ID NO: 633	GCCTCCCTCGCGCCATCAGAGTGTGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 634
AGTGTGTC SEQ ID NO: 635	GCCTCCCTCGCGCCATCAGAGTGTGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 636
ATAACCGC SEQ ID NO: 637	GCCTCCCTCGCGCCATCAGATAACCGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 638
ATAACGCC SEQ ID NO: 639	GCCTCCCTCGCGCCATCAGATAACGCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 640
ATAAGCGG SEQ ID NO: 641	GCCTCCCTCGCGCCATCAGATAAGCGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 642

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
ATAAGGCG SEQ ID NO: 643	GCCTCCCTCGCGCCATCAGATAAGGCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 644
ATATCCGG SEQ ID NO: 645	GCCTCCCTCGCGCCATCAGATATCCGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 646
ATATCGCG SEQ ID NO: 647	GCCTCCCTCGCGCCATCAGATATCGCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 648
ATATCGGC SEQ ID NO: 649	GCCTCCCTCGCGCCATCAGATATCGGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 650
ATATGCCG SEQ ID NO: 651	GCCTCCCTCGCGCCATCAGATATGCCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 652
ATATGCGC SEQ ID NO: 653	GCCTCCCTCGCGCCATCAGATATGCGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 654
ATATGGCC SEQ ID NO: 655	GCCTCCCTCGCGCCATCAGATATGGCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 656
ATCCAACG SEQ ID NO: 657	GCCTCCCTCGCGCCATCAGATCCAACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 658
ATCCAAGC SEQ ID NO: 659	GCCTCCCTCGCGCCATCAGATCCAAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 660
ATCCATCC SEQ ID NO: 661	GCCTCCCTCGCGCCATCAGATCCATCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 662
ATCCATGG SEQ ID NO: 663	GCCTCCCTCGCGCCATCAGATCCATGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 664
ATCCGCAA SEQ ID NO: 665	GCCTCCCTCGCGCCATCAGATCCGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 666
ATCCGCTT SEQ ID NO: 667	GCCTCCCTCGCGCCATCAGATCCGCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 668
ATCCGGAT SEQ ID NO: 669	GCCTCCCTCGCGCCATCAGATCCGGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 670
ATCCGGTA SEQ ID NO: 671	GCCTCCCTCGCGCCATCAGATCCGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 672
ATCCTACC SEQ ID NO: 673	GCCTCCCTCGCGCCATCAGATCCTACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 674
ATCCTAGG SEQ ID NO: 675	GCCTCCCTCGCGCCATCAGATCCTAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 676

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
ATCCTTCG SEQ ID NO: 677	GCCTCCCTCGCGCCATCAGATCCTTCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 678
ATCCTTGC SEQ ID NO: 679	GCCTCCCTCGCGCCATCAGATCCTTGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 680
ATCGAACC SEQ ID NO: 681	GCCTCCCTCGCGCCATCAGATCGAAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 682
ATCGAAGG SEQ ID NO: 683	GCCTCCCTCGCGCCATCAGATCGAAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 684
ATCGATCG SEQ ID NO: 685	GCCTCCCTCGCGCCATCAGATCGATCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 686
ATCGATGC SEQ ID NO: 687	GCCTCCCTCGCGCCATCAGATCGATGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 688
ATCGCCAA SEQ ID NO: 689	GCCTCCCTCGCGCCATCAGATCGCCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 690
ATCGCCTT SEQ ID NO: 691	GCCTCCCTCGCGCCATCAGATCGCCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 692
ATCGCGAT SEQ ID NO: 693	GCCTCCCTCGCGCCATCAGATCGCGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 694
ATCGCGTA SEQ ID NO: 695	GCCTCCCTCGCGCCATCAGATCGCGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 696
ATCGGCAT SEQ ID NO: 697	GCCTCCCTCGCGCCATCAGATCGGCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 698
ATCGGCTA SEQ ID NO: 699	GCCTCCCTCGCGCCATCAGATCGGCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 700
ATCGTACG SEQ ID NO: 701	GCCTCCCTCGCGCCATCAGATCGTACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 702
ATCGTAGC SEQ ID NO: 703	GCCTCCCTCGCGCCATCAGATCGTAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 704
ATCGTTCC SEQ ID NO: 705	GCCTCCCTCGCGCCATCAGATCGTTCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 706
ATCGTTGG SEQ ID NO: 707	GCCTCCCTCGCGCCATCAGATCGTTGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 708
ATGCAACC SEQ ID NO: 709	GCCTCCCTCGCGCCATCAGATGCAAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 710

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
ATGCAAGG SEQ ID NO: 711	GCCTCCCTCGCGCCATCAGATGCAAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 712
ATGCATCG SEQ ID NO: 713	GCCTCCCTCGCGCCATCAGATGCATCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 714
ATGCATGC SEQ ID NO: 715	GCCTCCCTCGCGCCATCAGATGCATGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 716
ATGCCGAT SEQ ID NO: 717	GCCTCCCTCGCGCCATCAGATGCCGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 718
ATGCCGTA SEQ ID NO: 719	GCCTCCCTCGCGCCATCAGATGCCGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 720
ATGCGCAT SEQ ID NO: 721	GCCTCCCTCGCGCCATCAGATGCGCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 722
ATGCGCTA SEQ ID NO: 723	GCCTCCCTCGCGCCATCAGATGCGCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 724
ATGCGGAA SEQ ID NO: 725	GCCTCCCTCGCGCCATCAGATGCGGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 726
ATGCGGTT SEQ ID NO: 727	GCCTCCCTCGCGCCATCAGATGCGGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 728
ATGCTACG SEQ ID NO: 729	GCCTCCCTCGCGCCATCAGATGCTACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 730
ATGCTAGC SEQ ID NO: 731	GCCTCCCTCGCGCCATCAGATGCTAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 732
ATGCTTCC SEQ ID NO: 733	GCCTCCCTCGCGCCATCAGATGCTTCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 734
ATGCTTGG SEQ ID NO: 735	GCCTCCCTCGCGCCATCAGATGCTTGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 736
ATGGAACG SEQ ID NO: 737	GCCTCCCTCGCGCCATCAGATGGAACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 738
ATGGAAGC SEQ ID NO: 739	GCCTCCCTCGCGCCATCAGATGGAAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 740
ATGGATCC SEQ ID NO: 741	GCCTCCCTCGCGCCATCAGATGGATCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 742
ATGGATGG SEQ ID NO: 743	GCCTCCCTCGCGCCATCAGATGGATGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 744

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
ATGGCCAT SEQ ID NO: 745	GCCTCCCTCGCGCCATCAGATGGCCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 746
ATGGCCTA SEQ ID NO: 747	GCCTCCCTCGCGCCATCAGATGGCCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 748
ATGGCGAA SEQ ID NO: 749	GCCTCCCTCGCGCCATCAGATGGCGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 750
ATGGCGTT SEQ ID NO: 751	GCCTCCCTCGCGCCATCAGATGGCGTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 752
ATGGTACC SEQ ID NO: 753	GCCTCCCTCGCGCCATCAGATGGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 754
ATGGTAGG SEQ ID NO: 755	GCCTCCCTCGCGCCATCAGATGGTAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 756
ATGGTTCG SEQ ID NO: 757	GCCTCCCTCGCGCCATCAGATGGTTCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 758
ATGGTTGC SEQ ID NO: 759	GCCTCCCTCGCGCCATCAGATGGTTGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 760
ATTACCGG SEQ ID NO: 761	GCCTCCCTCGCGCCATCAGATTACCGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 762
ATTACGCG SEQ ID NO: 763	GCCTCCCTCGCGCCATCAGATTACGCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 764
ATTACGGC SEQ ID NO: 765	GCCTCCCTCGCGCCATCAGATTACGGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 766
ATTAGCCG SEQ ID NO: 767	GCCTCCCTCGCGCCATCAGATTAGCCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 768
ATTAGCGC SEQ ID NO: 769	GCCTCCCTCGCGCCATCAGATTAGCGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 770
ATTAGGCC SEQ ID NO: 771	GCCTCCCTCGCGCCATCAGATTAGGCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 772
CAACACCA SEQ ID NO: 773	GCCTCCCTCGCGCCATCAGCAACACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 774
CAACACGT SEQ ID NO: 775	GCCTCCCTCGCGCCATCAGCAACACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 776
CAACAGCT SEQ ID NO: 777	GCCTCCCTCGCGCCATCAGCAACAGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 778

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CAACAGGA SEQ ID NO: 779	GCCTCCCTCGCGCCATCAGCAACAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 780
CAACCAAC SEQ ID NO: 781	GCCTCCCTCGCGCCATCAGCAACCAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 782
CAACCATG SEQ ID NO: 783	GCCTCCCTCGCGCCATCAGCAACCATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 784
CAACCTAG SEQ ID NO: 785	GCCTCCCTCGCGCCATCAGCAACCTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 786
CAACCTTC SEQ ID NO: 787	GCCTCCCTCGCGCCATCAGCAACCTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 788
CAACGAAG SEQ ID NO: 789	GCCTCCCTCGCGCCATCAGCAACGAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 790
CAACGATC SEQ ID NO: 791	GCCTCCCTCGCGCCATCAGCAACGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 792
CAACGTAC SEQ ID NO: 793	GCCTCCCTCGCGCCATCAGCAACGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 794
CAACGTTG SEQ ID NO: 795	GCCTCCCTCGCGCCATCAGCAACGTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 796
CAACTCCT SEQ ID NO: 797	GCCTCCCTCGCGCCATCAGCAACTCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 798
CAACTCGA SEQ ID NO: 799	GCCTCCCTCGCGCCATCAGCAACTCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 800
CAACTGCA SEQ ID NO: 801	GCCTCCCTCGCGCCATCAGCAACTGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 802
CAACTGGT SEQ ID NO: 803	GCCTCCCTCGCGCCATCAGCAACTGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 804
CAAGACCT SEQ ID NO: 805	GCCTCCCTCGCGCCATCAGCAAGACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 806
CAAGACGA SEQ ID NO: 807	GCCTCCCTCGCGCCATCAGCAAGACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 808
CAAGAGCA SEQ ID NO: 809	GCCTCCCTCGCGCCATCAGCAAGAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 810
CAAGAGGT SEQ ID NO: 811	GCCTCCCTCGCGCCATCAGCAAGAGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 812

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CAAGCAAG SEQ ID NO: 813	GCCTCCCTCGCGCCATCAGCAAGCAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 814
CAAGCATC SEQ ID NO: 815	GCCTCCCTCGCGCCATCAGCAAGCATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 816
CAAGCTAC SEQ ID NO: 817	GCCTCCCTCGCGCCATCAGCAAGCTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 818
CAAGCTTG SEQ ID NO: 819	GCCTCCCTCGCGCCATCAGCAAGCTTGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 820
CAAGGAAC SEQ ID NO: 821	GCCTCCCTCGCGCCATCAGCAAGGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 822
CAAGGATG SEQ ID NO: 823	GCCTCCCTCGCGCCATCAGCAAGGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 824
CAAGGTAG SEQ ID NO: 825	GCCTCCCTCGCGCCATCAGCAAGGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 826
CAAGGTTT SEQ ID NO: 827	GCCTCCCTCGCGCCATCAGCAAGGTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 828
CAAGTCCA SEQ ID NO: 829	GCCTCCCTCGCGCCATCAGCAAGTCCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 830
CAAGTCGT SEQ ID NO: 831	GCCTCCCTCGCGCCATCAGCAAGTCGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 832
CAAGTGCT SEQ ID NO: 833	GCCTCCCTCGCGCCATCAGCAAGTGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 834
CAAGTGGA SEQ ID NO: 835	GCCTCCCTCGCGCCATCAGCAAGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 836
CACAACAC SEQ ID NO: 837	GCCTCCCTCGCGCCATCAGCACAAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 838
CACAACTG SEQ ID NO: 839	GCCTCCCTCGCGCCATCAGCACAACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 840
CACAAGAG SEQ ID NO: 841	GCCTCCCTCGCGCCATCAGCACAAAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 842
CACAAGTC SEQ ID NO: 843	GCCTCCCTCGCGCCATCAGCACAAAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 844
CACACACA SEQ ID NO: 845	GCCTCCCTCGCGCCATCAGCACACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 846

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CACACAGT SEQ ID NO: 847	GCCTCCCTCGCGCCATCAGCACACAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 848
CACACTCT SEQ ID NO: 849	GCCTCCCTCGCGCCATCAGCACACTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 850
CACACTGA SEQ ID NO: 851	GCCTCCCTCGCGCCATCAGCACACTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 852
CACAGACT SEQ ID NO: 853	GCCTCCCTCGCGCCATCAGCACAGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 854
CACAGAGA SEQ ID NO: 855	GCCTCCCTCGCGCCATCAGCACAGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 856
CACAGTCA SEQ ID NO: 857	GCCTCCCTCGCGCCATCAGCACAGTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 858
CACAGTGT SEQ ID NO: 859	GCCTCCCTCGCGCCATCAGCACAGTGTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 860
CACATCAG SEQ ID NO: 861	GCCTCCCTCGCGCCATCAGCACATCAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 862
CACATCTC SEQ ID NO: 863	GCCTCCCTCGCGCCATCAGCACATCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 864
CACATGAC SEQ ID NO: 865	GCCTCCCTCGCGCCATCAGCACATGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 866
CACATGTG SEQ ID NO: 867	GCCTCCCTCGCGCCATCAGCACATGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 868
CACTACAG SEQ ID NO: 869	GCCTCCCTCGCGCCATCAGCACTACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 870
CACTACTC SEQ ID NO: 871	GCCTCCCTCGCGCCATCAGCACTACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 872
CACTAGAC SEQ ID NO: 873	GCCTCCCTCGCGCCATCAGCACTAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 874
CACTAGTG SEQ ID NO: 875	GCCTCCCTCGCGCCATCAGCACTAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 876
CACTCACT SEQ ID NO: 877	GCCTCCCTCGCGCCATCAGCACTCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 878
CACTCAGA SEQ ID NO: 879	GCCTCCCTCGCGCCATCAGCACTCAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 880

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CACTCTCA SEQ ID NO: 881	GCCTCCCTCGCGCCATCAGCACTCTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 882
CACTCTGT SEQ ID NO: 883	GCCTCCCTCGCGCCATCAGCACTCTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 884
CACTGACA SEQ ID NO: 885	GCCTCCCTCGCGCCATCAGCACTGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 886
CACTGAGT SEQ ID NO: 887	GCCTCCCTCGCGCCATCAGCACTGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 888
CACTGTCT SEQ ID NO: 889	GCCTCCCTCGCGCCATCAGCACTGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 890
CACTGTGA SEQ ID NO: 891	GCCTCCCTCGCGCCATCAGCACTGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 892
CACTTCAC SEQ ID NO: 893	GCCTCCCTCGCGCCATCAGCACTTCACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 894
CACTTCTG SEQ ID NO: 895	GCCTCCCTCGCGCCATCAGCACTTCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 896
CACTTGAG SEQ ID NO: 897	GCCTCCCTCGCGCCATCAGCACTTGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 898
CACTTGTC SEQ ID NO: 899	GCCTCCCTCGCGCCATCAGCACTTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 900
CAGAACAG SEQ ID NO: 901	GCCTCCCTCGCGCCATCAGCAGAACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 902
CAGAACTC SEQ ID NO: 903	GCCTCCCTCGCGCCATCAGCAGAACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 904
CAGAAGAC SEQ ID NO: 905	GCCTCCCTCGCGCCATCAGCAGAAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 906
CAGAAGTG SEQ ID NO: 907	GCCTCCCTCGCGCCATCAGCAGAAGTGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 908
CAGACACT SEQ ID NO: 909	GCCTCCCTCGCGCCATCAGCAGACACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 910
CAGACAGA SEQ ID NO: 911	GCCTCCCTCGCGCCATCAGCAGACAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 912
CAGACTCA SEQ ID NO: 913	GCCTCCCTCGCGCCATCAGCAGACTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 914

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CAGACTGT SEQ ID NO: 915	GCCTCCCTCGCGCCATCAGCAGACTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 916
CAGAGACA SEQ ID NO: 917	GCCTCCCTCGCGCCATCAGCAGAGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 918
CAGAGAGT SEQ ID NO: 919	GCCTCCCTCGCGCCATCAGCAGAGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 920
CAGAGTCT SEQ ID NO: 921	GCCTCCCTCGCGCCATCAGCAGAGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 922
CAGAGTGA SEQ ID NO: 923	GCCTCCCTCGCGCCATCAGCAGAGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 924
CAGATCAC SEQ ID NO: 925	GCCTCCCTCGCGCCATCAGCAGATCACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 926
CAGATCTG SEQ ID NO: 927	GCCTCCCTCGCGCCATCAGCAGATCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 928
CAGATGAG SEQ ID NO: 929	GCCTCCCTCGCGCCATCAGCAGATGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 930
CAGATGTC SEQ ID NO: 931	GCCTCCCTCGCGCCATCAGCAGATGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 932
CAGTACAC SEQ ID NO: 933	GCCTCCCTCGCGCCATCAGCAGTACACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 934
CAGTACTG SEQ ID NO: 935	GCCTCCCTCGCGCCATCAGCAGTACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 936
CAGTAGAG SEQ ID NO: 937	GCCTCCCTCGCGCCATCAGCAGTAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 938
CAGTAGTC SEQ ID NO: 939	GCCTCCCTCGCGCCATCAGCAGTAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 940
CAGTCACA SEQ ID NO: 941	GCCTCCCTCGCGCCATCAGCAGTCACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 942
CAGTCAGT SEQ ID NO: 943	GCCTCCCTCGCGCCATCAGCAGTCAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 944
CAGTCTCT SEQ ID NO: 945	GCCTCCCTCGCGCCATCAGCAGTCTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 946
CAGTCTGA SEQ ID NO: 947	GCCTCCCTCGCGCCATCAGCAGTCTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 948

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CAGTGACT SEQ ID NO: 949	GCCTCCCTCGCGCCATCAGCAGTGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 950
CAGTGAGA SEQ ID NO: 951	GCCTCCCTCGCGCCATCAGCAGTGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 952
CAGTGTCA SEQ ID NO: 953	GCCTCCCTCGCGCCATCAGCAGTGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 954
CAGTGTGT SEQ ID NO: 955	GCCTCCCTCGCGCCATCAGCAGTGTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 956
CAGTTCAG SEQ ID NO: 957	GCCTCCCTCGCGCCATCAGCAGTTCAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 958
CAGTTCTC SEQ ID NO: 959	GCCTCCCTCGCGCCATCAGCAGTTCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 960
CAGTTGAC SEQ ID NO: 961	GCCTCCCTCGCGCCATCAGCAGTTGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 962
CAGTTGTG SEQ ID NO: 963	GCCTCCCTCGCGCCATCAGCAGTTGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 964
CATCACCT SEQ ID NO: 965	GCCTCCCTCGCGCCATCAGCATCACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 966
CATCACGA SEQ ID NO: 967	GCCTCCCTCGCGCCATCAGCATCACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 968
CATCAGCA SEQ ID NO: 969	GCCTCCCTCGCGCCATCAGCATCAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 970
CATCAGGT SEQ ID NO: 971	GCCTCCCTCGCGCCATCAGCATCAGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 972
CATCCAAG SEQ ID NO: 973	GCCTCCCTCGCGCCATCAGCATCCAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 974
CATCCATC SEQ ID NO: 975	GCCTCCCTCGCGCCATCAGCATCCATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 976
CATCCTAC SEQ ID NO: 977	GCCTCCCTCGCGCCATCAGCATCCTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 978
CATCCTTG SEQ ID NO: 979	GCCTCCCTCGCGCCATCAGCATCCTTGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 980
CATCGAAC SEQ ID NO: 981	GCCTCCCTCGCGCCATCAGCATCGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 982

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CATCGATG SEQ ID NO: 983	GCCTCCCTCGCGCCATCAGCATCGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 984
CATCGTAG SEQ ID NO: 985	GCCTCCCTCGCGCCATCAGCATCGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 986
CATCGTTC SEQ ID NO: 987	GCCTCCCTCGCGCCATCAGCATCGTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 988
CATCTCCA SEQ ID NO: 989	GCCTCCCTCGCGCCATCAGCATCTCCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 990
CATCTCGT SEQ ID NO: 991	GCCTCCCTCGCGCCATCAGCATCTCGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 992
CATCTGCT SEQ ID NO: 993	GCCTCCCTCGCGCCATCAGCATCTGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 994
CATCTGGA SEQ ID NO: 995	GCCTCCCTCGCGCCATCAGCATCTGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 996
CATGACCA SEQ ID NO: 997	GCCTCCCTCGCGCCATCAGCATGACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 998
CATGACGT SEQ ID NO: 999	GCCTCCCTCGCGCCATCAGCATGACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1000
CATGAGCT SEQ ID NO: 1001	GCCTCCCTCGCGCCATCAGCATGAGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1002
CATGAGGA SEQ ID NO: 1003	GCCTCCCTCGCGCCATCAGCATGAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1004
CATGAAC SEQ ID NO: 1005	GCCTCCCTCGCGCCATCAGCATGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1006
CATGCATG SEQ ID NO: 1007	GCCTCCCTCGCGCCATCAGCATGCATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1008
CATGCTAG SEQ ID NO: 1009	GCCTCCCTCGCGCCATCAGCATGCTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1010
CATGCTTC SEQ ID NO: 1011	GCCTCCCTCGCGCCATCAGCATGCTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1012
CATGGAAG SEQ ID NO: 1013	GCCTCCCTCGCGCCATCAGCATGGAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1014
CATGGATC SEQ ID NO: 1015	GCCTCCCTCGCGCCATCAGCATGGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1016

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CATGGTAC SEQ ID NO: 1017	GCCTCCCTCGCGCCATCAGCATGGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1018
CATGGTTG SEQ ID NO: 1019	GCCTCCCTCGCGCCATCAGCATGGTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1020
CATGTCCT SEQ ID NO: 1021	GCCTCCCTCGCGCCATCAGCATGTCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1022
CATGTCGA SEQ ID NO: 1023	GCCTCCCTCGCGCCATCAGCATGTCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1024
CATGTGCA SEQ ID NO: 1025	GCCTCCCTCGCGCCATCAGCATGTGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1026
CATGTGGT SEQ ID NO: 1027	GCCTCCCTCGCGCCATCAGCATGTGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1028
CCAACCAA SEQ ID NO: 1029	GCCTCCCTCGCGCCATCAGCCAACCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1030
CCAACCTT SEQ ID NO: 1031	GCCTCCCTCGCGCCATCAGCCAACCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1032
CCAACGAT SEQ ID NO: 1033	GCCTCCCTCGCGCCATCAGCCAACGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1034
CCAACGTA SEQ ID NO: 1035	GCCTCCCTCGCGCCATCAGCCAACGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1036
CCAAGCAT SEQ ID NO: 1037	GCCTCCCTCGCGCCATCAGCCAAGCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1038
CCAAGCTA SEQ ID NO: 1039	GCCTCCCTCGCGCCATCAGCCAAGCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1040
CCAAGGAA SEQ ID NO: 1041	GCCTCCCTCGCGCCATCAGCCAAGGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1042
CCAAGGTT SEQ ID NO: 1043	GCCTCCCTCGCGCCATCAGCCAAGGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1044
CCAATACG SEQ ID NO: 1045	GCCTCCCTCGCGCCATCAGCCAATACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1046
CCAATAGC SEQ ID NO: 1047	GCCTCCCTCGCGCCATCAGCCAATAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1048
CCAATTCC SEQ ID NO: 1049	GCCTCCCTCGCGCCATCAGCCAATTCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1050

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CCAATTGG SEQ ID NO: 1051	GCCTCCCTCGCGCCATCAGCCAATTGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1052
CCATAACG SEQ ID NO: 1053	GCCTCCCTCGCGCCATCAGCCATAACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1054
CCATAAGC SEQ ID NO: 1055	GCCTCCCTCGCGCCATCAGCCATAAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1056
CCATATCC SEQ ID NO: 1057	GCCTCCCTCGCGCCATCAGCCATATCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1058
CCATATGG SEQ ID NO: 1059	GCCTCCCTCGCGCCATCAGCCATATGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1060
CCATCCAT SEQ ID NO: 1061	GCCTCCCTCGCGCCATCAGCCATCCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1062
CCATCCTA SEQ ID NO: 1063	GCCTCCCTCGCGCCATCAGCCATCCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1064
CCATCGAA SEQ ID NO: 1065	GCCTCCCTCGCGCCATCAGCCATCGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1066
CCATCGTT SEQ ID NO: 1067	GCCTCCCTCGCGCCATCAGCCATCGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1068
CCATGCAA SEQ ID NO: 1069	GCCTCCCTCGCGCCATCAGCCATGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1070
CCATGCTT SEQ ID NO: 1071	GCCTCCCTCGCGCCATCAGCCATGCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1072
CCATGGAT SEQ ID NO: 1073	GCCTCCCTCGCGCCATCAGCCATGGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1074
CCATGGTA SEQ ID NO: 1075	GCCTCCCTCGCGCCATCAGCCATGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1076
CCATTACC SEQ ID NO: 1077	GCCTCCCTCGCGCCATCAGCCATTACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1078
CCATTAGG SEQ ID NO: 1079	GCCTCCCTCGCGCCATCAGCCATTAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1080
CCGCAATA SEQ ID NO: 1081	GCCTCCCTCGCGCCATCAGCCGCAATACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1082
CCGCATAA SEQ ID NO: 1083	GCCTCCCTCGCGCCATCAGCCGCATAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1084

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CCGCTATT SEQ ID NO: 1085	GCCTCCCTCGCGCCATCAGCCGCTATTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1086
CCGCTTAT SEQ ID NO: 1087	GCCTCCCTCGCGCCATCAGCCGCTTATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1088
CCGGAATT SEQ ID NO: 1089	GCCTCCCTCGCGCCATCAGCCGGAATTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1090
CCGATAT SEQ ID NO: 1091	GCCTCCCTCGCGCCATCAGCCGATATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1092
CCGATTA SEQ ID NO: 1093	GCCTCCCTCGCGCCATCAGCCGATTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1094
CCGTAAT SEQ ID NO: 1095	GCCTCCCTCGCGCCATCAGCCGTAATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1096
CCGTATA SEQ ID NO: 1097	GCCTCCCTCGCGCCATCAGCCGTATACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1098
CCGTATA SEQ ID NO: 1099	GCCTCCCTCGCGCCATCAGCCGTAAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1100
CCTAATCC SEQ ID NO: 1101	GCCTCCCTCGCGCCATCAGCCTAATCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1102
CCTAATGG SEQ ID NO: 1103	GCCTCCCTCGCGCCATCAGCCTAATGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1104
CCTACCAT SEQ ID NO: 1105	GCCTCCCTCGCGCCATCAGCCTACCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1106
CCTACCTA SEQ ID NO: 1107	GCCTCCCTCGCGCCATCAGCCTACCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1108
CCTACGAA SEQ ID NO: 1109	GCCTCCCTCGCGCCATCAGCCTACGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1110
CCTACGTT SEQ ID NO: 1111	GCCTCCCTCGCGCCATCAGCCTACGTTTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1112
CCTAGCAA SEQ ID NO: 1113	GCCTCCCTCGCGCCATCAGCCTAGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1114
CCTAGCTT SEQ ID NO: 1115	GCCTCCCTCGCGCCATCAGCCTAGCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1116
CCTAGGAT SEQ ID NO: 1117	GCCTCCCTCGCGCCATCAGCCTAGGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1118

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CCTAGGTA SEQ ID NO: 1119	GCCTCCCTCGCGCCATCAGCCTAGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1120
CCTATACC SEQ ID NO: 1121	GCCTCCCTCGCGCCATCAGCCTATACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1122
CCTATAGG SEQ ID NO: 1123	GCCTCCCTCGCGCCATCAGCCTATAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1124
CCTATTCG SEQ ID NO: 1125	GCCTCCCTCGCGCCATCAGCCTATTCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1126
CCTATTGC SEQ ID NO: 1127	GCCTCCCTCGCGCCATCAGCCTATTGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1128
CCTTAACC SEQ ID NO: 1129	GCCTCCCTCGCGCCATCAGCCTTAACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1130
CCTTAAGG SEQ ID NO: 1131	GCCTCCCTCGCGCCATCAGCCTTAAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1132
CCTTATCG SEQ ID NO: 1133	GCCTCCCTCGCGCCATCAGCCTTATCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1134
CCTTATGC SEQ ID NO: 1135	GCCTCCCTCGCGCCATCAGCCTTATGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1136
CCTTCCAA SEQ ID NO: 1137	GCCTCCCTCGCGCCATCAGCCTTCCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1138
CCTTCCTT SEQ ID NO: 1139	GCCTCCCTCGCGCCATCAGCCTTCCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1140
CCTTCGAT SEQ ID NO: 1141	GCCTCCCTCGCGCCATCAGCCTTCGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1142
CCTTCGTA SEQ ID NO: 1143	GCCTCCCTCGCGCCATCAGCCTTCGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1144
CCTTGCA SEQ ID NO: 1145	GCCTCCCTCGCGCCATCAGCCTTGCAATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1146
CCTTGCTA SEQ ID NO: 1147	GCCTCCCTCGCGCCATCAGCCTTGCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1148
CCTTGGA SEQ ID NO: 1149	GCCTCCCTCGCGCCATCAGCCTTGGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1150
CCTTGTT SEQ ID NO: 1151	GCCTCCCTCGCGCCATCAGCCTTGTTTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1152

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CGAACCAT SEQ ID NO: 1153	GCCTCCCTCGCGCCATCAGCGAACCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1154
CGAACCTA SEQ ID NO: 1155	GCCTCCCTCGCGCCATCAGCGAACCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1156
CGAACGAA SEQ ID NO: 1157	GCCTCCCTCGCGCCATCAGCGAACGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1158
CGAACGTT SEQ ID NO: 1159	GCCTCCCTCGCGCCATCAGCGAACGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1160
CGAAGCAA SEQ ID NO: 1161	GCCTCCCTCGCGCCATCAGCGAAGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1162
CGAAGCTT SEQ ID NO: 1163	GCCTCCCTCGCGCCATCAGCGAAGCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1164
CGAAGGAT SEQ ID NO: 1165	GCCTCCCTCGCGCCATCAGCGAAGGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1166
CGAAGGTA SEQ ID NO: 1167	GCCTCCCTCGCGCCATCAGCGAAGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1168
CGAATACC SEQ ID NO: 1169	GCCTCCCTCGCGCCATCAGCGAATACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1170
CGAATAGG SEQ ID NO: 1171	GCCTCCCTCGCGCCATCAGCGAATAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1172
CGAATTCG SEQ ID NO: 1173	GCCTCCCTCGCGCCATCAGCGAATTGCGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1174
CGAATTGC SEQ ID NO: 1175	GCCTCCCTCGCGCCATCAGCGAATTGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1176
CGATAACC SEQ ID NO: 1177	GCCTCCCTCGCGCCATCAGCGATAAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1178
CGATAAGG SEQ ID NO: 1179	GCCTCCCTCGCGCCATCAGCGATAAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1180
CGATATCG SEQ ID NO: 1181	GCCTCCCTCGCGCCATCAGCGATATCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1182
CGATATGC SEQ ID NO: 1183	GCCTCCCTCGCGCCATCAGCGATATGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1184
CGATCAA SEQ ID NO: 1185	GCCTCCCTCGCGCCATCAGCGATCCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1186

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CGATCCTT SEQ ID NO: 1187	GCCTCCCTCGCGCCATCAGCGATCCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1188
CGATCGAT SEQ ID NO: 1189	GCCTCCCTCGCGCCATCAGCGATCGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1190
CGATCGTA SEQ ID NO: 1191	GCCTCCCTCGCGCCATCAGCGATCGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1192
CGATGCAT SEQ ID NO: 1193	GCCTCCCTCGCGCCATCAGCGATGCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1194
CGATGCTA SEQ ID NO: 1195	GCCTCCCTCGCGCCATCAGCGATGCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1196
CGATGGAA SEQ ID NO: 1197	GCCTCCCTCGCGCCATCAGCGATGGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1198
CGATGGTT SEQ ID NO: 1199	GCCTCCCTCGCGCCATCAGCGATGGTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1200
CGATTACG SEQ ID NO: 1201	GCCTCCCTCGCGCCATCAGCGATTACGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1202
CGATTAGC SEQ ID NO: 1203	GCCTCCCTCGCGCCATCAGCGATTAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1204
CGCCAATA SEQ ID NO: 1205	GCCTCCCTCGCGCCATCAGCGCCAATACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1206
CGCCATAA SEQ ID NO: 1207	GCCTCCCTCGCGCCATCAGCGCCATAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1208
CGCCTATT SEQ ID NO: 1209	GCCTCCCTCGCGCCATCAGCGCCTATTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1210
CGCCTTAT SEQ ID NO: 1211	GCCTCCCTCGCGCCATCAGCGCCTTATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1212
CGCGAATT SEQ ID NO: 1213	GCCTCCCTCGCGCCATCAGCGCGAATTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1214
CGCGATAT SEQ ID NO: 1215	GCCTCCCTCGCGCCATCAGCGCGATATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1216
CGCGATTA SEQ ID NO: 1217	GCCTCCCTCGCGCCATCAGCGCGATTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1218
CGCGTAAT SEQ ID NO: 1219	GCCTCCCTCGCGCCATCAGCGCGTAATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1220

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CGCGTATA SEQ ID NO: 1221	GCCTCCCTCGCGCCATCAGCGGTATACATGCT SEQ ID NO: 1222
CGCGTTAA SEQ ID NO: 1223	GCCTCCCTCGCGCCATCAGCGGTTAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1224
CGGCAATT SEQ ID NO: 1225	GCCTCCCTCGCGCCATCAGCGCAATTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1226
CGGCATAT SEQ ID NO: 1227	GCCTCCCTCGCGCCATCAGCGGCATATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1228
CGGCATTA SEQ ID NO: 1229	GCCTCCCTCGCGCCATCAGCGGCATTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1230
CGGCTAAT SEQ ID NO: 1231	GCCTCCCTCGCGCCATCAGCGGCTAATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1232
CGGCTATA SEQ ID NO: 1233	GCCTCCCTCGCGCCATCAGCGGTATACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1234
CGGCTTAA SEQ ID NO: 1235	GCCTCCCTCGCGCCATCAGCGGTTAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1236
CGTAATCG SEQ ID NO: 1237	GCCTCCCTCGCGCCATCAGCGTAATCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1238
CGTAATGC SEQ ID NO: 1239	GCCTCCCTCGCGCCATCAGCGTAATGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1240
CGTACCAA SEQ ID NO: 1241	GCCTCCCTCGCGCCATCAGCGTACCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1242
CGTACCTT SEQ ID NO: 1243	GCCTCCCTCGCGCCATCAGCGTACCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1244
CGTACGAT SEQ ID NO: 1245	GCCTCCCTCGCGCCATCAGCGTACGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1246
CGTACGTA SEQ ID NO: 1247	GCCTCCCTCGCGCCATCAGCGTACGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1248
CGTAGCAT SEQ ID NO: 1249	GCCTCCCTCGCGCCATCAGCGTAGCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1250
CGTAGCTA SEQ ID NO: 1251	GCCTCCCTCGCGCCATCAGCGTAGCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1252
CGTAGGAA SEQ ID NO: 1253	GCCTCCCTCGCGCCATCAGCGTAGGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1254

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CGTAGGTT SEQ ID NO: 1255	GCCTCCCTCGCGCCATCAGCGTAGGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1256
CGTATACG SEQ ID NO: 1257	GCCTCCCTCGCGCCATCAGCGTATACGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1258
CGTATAGC SEQ ID NO: 1259	GCCTCCCTCGCGCCATCAGCGTATAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1260
CGTATTCC SEQ ID NO: 1261	GCCTCCCTCGCGCCATCAGCGTATTCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1262
CGTATTGG SEQ ID NO: 1263	GCCTCCCTCGCGCCATCAGCGTATTGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1264
CGTTAACG SEQ ID NO: 1265	GCCTCCCTCGCGCCATCAGCGTTAACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1266
CGTTAAGC SEQ ID NO: 1267	GCCTCCCTCGCGCCATCAGCGTTAAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1268
CGTTATCC SEQ ID NO: 1269	GCCTCCCTCGCGCCATCAGCGTTATCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1270
CGTTATGG SEQ ID NO: 1271	GCCTCCCTCGCGCCATCAGCGTTATGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1272
CGTTCCAT SEQ ID NO: 1273	GCCTCCCTCGCGCCATCAGCGTTCCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1274
CGTTCCTA SEQ ID NO: 1275	GCCTCCCTCGCGCCATCAGCGTTCCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1276
CGTTCGAA SEQ ID NO: 1277	GCCTCCCTCGCGCCATCAGCGTTCGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1278
CGTTCGTT SEQ ID NO: 1279	GCCTCCCTCGCGCCATCAGCGTTCGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1280
CGTTGCAA SEQ ID NO: 1281	GCCTCCCTCGCGCCATCAGCGTTGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1282
CGTTGCTT SEQ ID NO: 1283	GCCTCCCTCGCGCCATCAGCGTTGCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1284
CGTTGGAT SEQ ID NO: 1285	GCCTCCCTCGCGCCATCAGCGTTGGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1286
CGTTGGTA SEQ ID NO: 1287	GCCTCCCTCGCGCCATCAGCGTTGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1288

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CTACACCT SEQ ID NO: 1289	GCCTCCCTCGCGCCATCAGCTACACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1290
CTACACGA SEQ ID NO: 1291	GCCTCCCTCGCGCCATCAGCTACACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1292
CTACAGCA SEQ ID NO: 1293	GCCTCCCTCGCGCCATCAGCTACAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1294
CTACAGGT SEQ ID NO: 1295	GCCTCCCTCGCGCCATCAGCTACAGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1296
CTACCAAG SEQ ID NO: 1297	GCCTCCCTCGCGCCATCAGCTACCAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1298
CTACCATC SEQ ID NO: 1299	GCCTCCCTCGCGCCATCAGCTACCATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1300
CTACCTAC SEQ ID NO: 1301	GCCTCCCTCGCGCCATCAGCTACCTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1302
CTACCTTG SEQ ID NO: 1303	GCCTCCCTCGCGCCATCAGCTACCTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1304
CTACGAAC SEQ ID NO: 1305	GCCTCCCTCGCGCCATCAGCTACGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1306
CTACGATG SEQ ID NO: 1307	GCCTCCCTCGCGCCATCAGCTACGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1308
CTACGTAG SEQ ID NO: 1309	GCCTCCCTCGCGCCATCAGCTACGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1310
CTACGTTT SEQ ID NO: 1311	GCCTCCCTCGCGCCATCAGCTACGTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1312
CTACTCCA SEQ ID NO: 1313	GCCTCCCTCGCGCCATCAGCTACTCCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1314
CTACTCGT SEQ ID NO: 1315	GCCTCCCTCGCGCCATCAGCTACTCGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1316
CTACTGCT SEQ ID NO: 1317	GCCTCCCTCGCGCCATCAGCTACTGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1318
CTACTGGA SEQ ID NO: 1319	GCCTCCCTCGCGCCATCAGCTACTGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1320
CTAGACCA SEQ ID NO: 1321	GCCTCCCTCGCGCCATCAGCTAGACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1322

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CTAGACGT SEQ ID NO: 1323	GCCTCCCTCGCGCCATCAGCTAGACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1324
CTAGAGCT SEQ ID NO: 1325	GCCTCCCTCGCGCCATCAGCTAGAGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1326
CTAGAGGA SEQ ID NO: 1327	GCCTCCCTCGCGCCATCAGCTAGAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1328
CTAGCAAC SEQ ID NO: 1329	GCCTCCCTCGCGCCATCAGCTAGCAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1330
CTAGCATG SEQ ID NO: 1331	GCCTCCCTCGCGCCATCAGCTAGCATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1332
CTAGCTAG SEQ ID NO: 1333	GCCTCCCTCGCGCCATCAGCTAGCTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1334
CTAGCTTC SEQ ID NO: 1335	GCCTCCCTCGCGCCATCAGCTAGCTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1336
CTAGGAAG SEQ ID NO: 1337	GCCTCCCTCGCGCCATCAGCTAGGAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1338
CTAGGATC SEQ ID NO: 1339	GCCTCCCTCGCGCCATCAGCTAGGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1340
CTAGGTAC SEQ ID NO: 1341	GCCTCCCTCGCGCCATCAGCTAGGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1342
CTAGGTTG SEQ ID NO: 1343	GCCTCCCTCGCGCCATCAGCTAGGTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1344
CTAGTCCT SEQ ID NO: 1345	GCCTCCCTCGCGCCATCAGCTAGTCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1346
CTAGTCGA SEQ ID NO: 1347	GCCTCCCTCGCGCCATCAGCTAGTCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1348
CTAGTGCA SEQ ID NO: 1349	GCCTCCCTCGCGCCATCAGCTAGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1350
CTAGTGGT SEQ ID NO: 1351	GCCTCCCTCGCGCCATCAGCTAGTGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1352
CTCAACAG SEQ ID NO: 1353	GCCTCCCTCGCGCCATCAGCTCAACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1354
CTCAACTC SEQ ID NO: 1355	GCCTCCCTCGCGCCATCAGCTCAACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1356

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CTCAAGAC SEQ ID NO: 1357	GCCTCCCTCGCGCCATCAGCTCAAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1358
CTCAAGTG SEQ ID NO: 1359	GCCTCCCTCGCGCCATCAGCTCAAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1360
CTCACACT SEQ ID NO: 1361	GCCTCCCTCGCGCCATCAGCTCACACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1362
CTCACAGA SEQ ID NO: 1363	GCCTCCCTCGCGCCATCAGCTCACAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1364
CTCACTCA SEQ ID NO: 1365	GCCTCCCTCGCGCCATCAGCTCACTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1366
CTCACTGT SEQ ID NO: 1367	GCCTCCCTCGCGCCATCAGCTCACTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1368
CTCAGACA SEQ ID NO: 1369	GCCTCCCTCGCGCCATCAGCTCAGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1370
CTCAGAGT SEQ ID NO: 1371	GCCTCCCTCGCGCCATCAGCTCAGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1372
CTCAGTCT SEQ ID NO: 1373	GCCTCCCTCGCGCCATCAGCTCAGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1374
CTCAGTGA SEQ ID NO: 1375	GCCTCCCTCGCGCCATCAGCTCAGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1376
CTCATCAC SEQ ID NO: 1377	GCCTCCCTCGCGCCATCAGCTCATCACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1378
CTCATCTG SEQ ID NO: 1379	GCCTCCCTCGCGCCATCAGCTCATCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1380
CTCATGAG SEQ ID NO: 1381	GCCTCCCTCGCGCCATCAGCTCATGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1382
CTCATGTC SEQ ID NO: 1383	GCCTCCCTCGCGCCATCAGCTCATGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1384
CTCTACAC SEQ ID NO: 1385	GCCTCCCTCGCGCCATCAGCTCTACACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1386
CTCTACTG SEQ ID NO: 1387	GCCTCCCTCGCGCCATCAGCTCTACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1388
CTCTAGAG SEQ ID NO: 1389	GCCTCCCTCGCGCCATCAGCTCTAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1390

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CTCTAGTC SEQ ID NO: 1391	GCCTCCCTCGCGCCATCAGCTCTAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1392
CTCTACA SEQ ID NO: 1393	GCCTCCCTCGCGCCATCAGCTCTCACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1394
CTCTCAGT SEQ ID NO: 1395	GCCTCCCTCGCGCCATCAGCTCTCAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1396
CTCTCTCT SEQ ID NO: 1397	GCCTCCCTCGCGCCATCAGCTCTCTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1398
CTCTCTGA SEQ ID NO: 1399	GCCTCCCTCGCGCCATCAGCTCTCTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1400
CTCTGACT SEQ ID NO: 1401	GCCTCCCTCGCGCCATCAGCTCTGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1402
CTCTGAGA SEQ ID NO: 1403	GCCTCCCTCGCGCCATCAGCTCTGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1404
CTCTGTCA SEQ ID NO: 1405	GCCTCCCTCGCGCCATCAGCTCTGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1406
CTCTGTGT SEQ ID NO: 1407	GCCTCCCTCGCGCCATCAGCTCTGTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1408
CTCTTCAG SEQ ID NO: 1409	GCCTCCCTCGCGCCATCAGCTCTTCAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1410
CTCTTCTC SEQ ID NO: 1411	GCCTCCCTCGCGCCATCAGCTCTTCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1412
CTCTTGAC SEQ ID NO: 1413	GCCTCCCTCGCGCCATCAGCTCTTGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1414
CTCTTGTG SEQ ID NO: 1415	GCCTCCCTCGCGCCATCAGCTCTTGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1416
CTGAACAC SEQ ID NO: 1417	GCCTCCCTCGCGCCATCAGCTGAACACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1418
CTGAAGTG SEQ ID NO: 1419	GCCTCCCTCGCGCCATCAGCTGAAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1420
CTGAAGAG SEQ ID NO: 1421	GCCTCCCTCGCGCCATCAGCTGAAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1422
CTGAAGTC SEQ ID NO: 1423	GCCTCCCTCGCGCCATCAGCTGAAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1424

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CTGACACA SEQ ID NO: 1425	GCCTCCCTCGCGCCATCAGCTGACACACATGCT SEQ ID NO: 1426
CTGACAGT SEQ ID NO: 1427	GCCTCCCTCGCGCCATCAGCTGACAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1428
CTGACTCT SEQ ID NO: 1429	GCCTCCCTCGCGCCATCAGCTGACTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1430
CTGACTGA SEQ ID NO: 1431	GCCTCCCTCGCGCCATCAGCTGACTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1432
CTGAGACT SEQ ID NO: 1433	GCCTCCCTCGCGCCATCAGCTGAGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1434
CTGAGAGA SEQ ID NO: 1435	GCCTCCCTCGCGCCATCAGCTGAGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1436
CTGAGTCA SEQ ID NO: 1437	GCCTCCCTCGCGCCATCAGCTGAGTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1438
CTGAGTGT SEQ ID NO: 1439	GCCTCCCTCGCGCCATCAGCTGAGTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1440
CTGATCAG SEQ ID NO: 1441	GCCTCCCTCGCGCCATCAGCTGATCAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1142
CTGATCTC SEQ ID NO: 1143	GCCTCCCTCGCGCCATCAGCTGATCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1144
CTGATGAC SEQ ID NO: 1145	GCCTCCCTCGCGCCATCAGCTGATGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1146
CTGATGTG SEQ ID NO: 1147	GCCTCCCTCGCGCCATCAGCTGATGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1148
CTGTACAG SEQ ID NO: 1149	GCCTCCCTCGCGCCATCAGCTGTACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1150
CTGTACTC SEQ ID NO: 1151	GCCTCCCTCGCGCCATCAGCTGTACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1152
CTGTAGAC SEQ ID NO: 1153	GCCTCCCTCGCGCCATCAGCTGTAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1154
CTGTAGTG SEQ ID NO: 1155	GCCTCCCTCGCGCCATCAGCTGTAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1156
CTGTCACT SEQ ID NO: 1157	GCCTCCCTCGCGCCATCAGCTGTCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1158

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CTGTCAGA SEQ ID NO: 1159	GCCTCCCTCGCGCCATCAGCTGTCAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1160
CTGTCTCA SEQ ID NO: 1161	GCCTCCCTCGCGCCATCAGCTGTCTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1162
CTGTCTGT SEQ ID NO: 1163	GCCTCCCTCGCGCCATCAGCTGTCTGTCTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1164
CTGTGACA SEQ ID NO: 1165	GCCTCCCTCGCGCCATCAGCTGTGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1166
CTGTGAGT SEQ ID NO: 1167	GCCTCCCTCGCGCCATCAGCTGTGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1168
CTGTGTCT SEQ ID NO: 1169	GCCTCCCTCGCGCCATCAGCTGTGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1170
CTGTGTGA SEQ ID NO: 1171	GCCTCCCTCGCGCCATCAGCTGTGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1172
CTGTTTAC SEQ ID NO: 1173	GCCTCCCTCGCGCCATCAGCTGTTTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1174
CTGTTCTG SEQ ID NO: 1175	GCCTCCCTCGCGCCATCAGCTGTTCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1176
CTGTTGAG SEQ ID NO: 1177	GCCTCCCTCGCGCCATCAGCTGTTGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1178
CTGTTGTC SEQ ID NO: 1179	GCCTCCCTCGCGCCATCAGCTGTTGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1180
CTTCACCA SEQ ID NO: 1181	GCCTCCCTCGCGCCATCAGCTTCACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1182
CTTCACGT SEQ ID NO: 1183	GCCTCCCTCGCGCCATCAGCTTCACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1184
CTTCAGCT SEQ ID NO: 1185	GCCTCCCTCGCGCCATCAGCTTCAGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1186
CTTCAGGA SEQ ID NO: 1187	GCCTCCCTCGCGCCATCAGCTTCAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1188
CTTCAAC SEQ ID NO: 1189	GCCTCCCTCGCGCCATCAGCTTCAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1190
CTTCCATG SEQ ID NO: 1191	GCCTCCCTCGCGCCATCAGCTTCCATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1192

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CTTCCTAG SEQ ID NO: 1193	GCCTCCCTCGCGCCATCAGCTTCCTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1194
CTTCCTTC SEQ ID NO: 1195	GCCTCCCTCGCGCCATCAGCTTCCTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1196
CTTCGAAG SEQ ID NO: 1197	GCCTCCCTCGCGCCATCAGCTTCGAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1198
CTTCGATC SEQ ID NO: 1199	GCCTCCCTCGCGCCATCAGCTTCGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1200
CTTCGTAC SEQ ID NO: 1201	GCCTCCCTCGCGCCATCAGCTTCGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1202
CTTCGTTG SEQ ID NO: 1203	GCCTCCCTCGCGCCATCAGCTTCGTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1204
CTTCTCCT SEQ ID NO: 1205	GCCTCCCTCGCGCCATCAGCTTCTCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1206
CTTCTCGA SEQ ID NO: 1207	GCCTCCCTCGCGCCATCAGCTTCTCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1208
CTTCTGCA SEQ ID NO: 1209	GCCTCCCTCGCGCCATCAGCTTCTGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1210
CTTCTGGT SEQ ID NO: 1211	GCCTCCCTCGCGCCATCAGCTTCTGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1212
CTTGACCT SEQ ID NO: 1213	GCCTCCCTCGCGCCATCAGCTTGACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1214
CTTGACGA SEQ ID NO: 1215	GCCTCCCTCGCGCCATCAGCTTGACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1216
CTTGAGCA SEQ ID NO: 1217	GCCTCCCTCGCGCCATCAGCTTGAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1218
CTTGAGGT SEQ ID NO: 1219	GCCTCCCTCGCGCCATCAGCTTGAGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1220
CTTGCAAG SEQ ID NO: 1221	GCCTCCCTCGCGCCATCAGCTTGCAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1222
CTTGCAATC SEQ ID NO: 1223	GCCTCCCTCGCGCCATCAGCTTGCAATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1224
CTTGCTAC SEQ ID NO: 1225	GCCTCCCTCGCGCCATCAGCTTGCTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1226

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
CTTGCTTG SEQ ID NO: 1227	GCCTCCCTCGCGCCATCAGCTTGCTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1228
CTTGAAC SEQ ID NO: 1229	GCCTCCCTCGCGCCATCAGCTTGGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1230
CTTGATG SEQ ID NO: 1231	GCCTCCCTCGCGCCATCAGCTTGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1232
CTTGGTAG SEQ ID NO: 1233	GCCTCCCTCGCGCCATCAGCTTGGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1234
CTTGTTT SEQ ID NO: 1235	GCCTCCCTCGCGCCATCAGCTTGTTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1236
CTTGTCCA SEQ ID NO: 1237	GCCTCCCTCGCGCCATCAGCTTGTCCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1238
CTTGTCTG SEQ ID NO: 1239	GCCTCCCTCGCGCCATCAGCTTGTCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1240
CTTGTGCT SEQ ID NO: 1241	GCCTCCCTCGCGCCATCAGCTTGTGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1242
CTTGTGGA SEQ ID NO: 1243	GCCTCCCTCGCGCCATCAGCTTGTGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1244
GAACACCT SEQ ID NO: 1245	GCCTCCCTCGCGCCATCAGGAACACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1246
GAACACGA SEQ ID NO: 1247	GCCTCCCTCGCGCCATCAGGAACACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1248
GAACAGCA SEQ ID NO: 1249	GCCTCCCTCGCGCCATCAGGAACAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1250
GAACAGGT SEQ ID NO: 1251	GCCTCCCTCGCGCCATCAGGAACAGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1252
GAACCAAG SEQ ID NO: 1253	GCCTCCCTCGCGCCATCAGGAACCAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1254
GAACCATC SEQ ID NO: 1255	GCCTCCCTCGCGCCATCAGGAACCATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1256
GAACCTAC SEQ ID NO: 1257	GCCTCCCTCGCGCCATCAGGAACCTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1258
GAACCTTG SEQ ID NO: 1259	GCCTCCCTCGCGCCATCAGGAACCTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1260

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GAACGAAC SEQ ID NO: 1261	GCCTCCCTCGCGCCATCAGGAACGAACCATGCT SEQ ID NO: 1262
GAACGATG SEQ ID NO: 1263	GCCTCCCTCGCGCCATCAGGAACGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1264
GAACGTAG SEQ ID NO: 1265	GCCTCCCTCGCGCCATCAGGAACGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1266
GAACGTTC SEQ ID NO: 1267	GCCTCCCTCGCGCCATCAGGAACGTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1268
GAACTCCA SEQ ID NO: 1269	GCCTCCCTCGCGCCATCAGGAACCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1270
GAACTCGT SEQ ID NO: 1271	GCCTCCCTCGCGCCATCAGGAACCTCGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1272
GAACTGCT SEQ ID NO: 1273	GCCTCCCTCGCGCCATCAGGAACCTGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1274
GAACTGGA SEQ ID NO: 1275	GCCTCCCTCGCGCCATCAGGAACCTGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1276
GAAGACCA SEQ ID NO: 1277	GCCTCCCTCGCGCCATCAGGAAGACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1278
GAAGACGT SEQ ID NO: 1279	GCCTCCCTCGCGCCATCAGGAAGACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1280
GAAGAGCT SEQ ID NO: 1281	GCCTCCCTCGCGCCATCAGGAAGAGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1282
GAAGAGGA SEQ ID NO: 1283	GCCTCCCTCGCGCCATCAGGAAGAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1284
GAAGCAAC SEQ ID NO: 1285	GCCTCCCTCGCGCCATCAGGAAGCAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1286
GAAGCATG SEQ ID NO: 1287	GCCTCCCTCGCGCCATCAGGAAGCATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1288
GAAGCTAG SEQ ID NO: 1289	GCCTCCCTCGCGCCATCAGGAAGCTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1290
GAAGCTTC SEQ ID NO: 1291	GCCTCCCTCGCGCCATCAGGAAGCTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1292
GAAGGAAG SEQ ID NO: 1293	GCCTCCCTCGCGCCATCAGGAAGGAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1294

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GAAGGATC SEQ ID NO: 1295	GCCTCCCTCGCGCCATCAGGAAGGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1296
GAAGGTAC SEQ ID NO: 1297	GCCTCCCTCGCGCCATCAGGAAGGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1298
GAAGGTTG SEQ ID NO: 1299	GCCTCCCTCGCGCCATCAGGAAGGTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1300
GAAGTCCT SEQ ID NO: 1301	GCCTCCCTCGCGCCATCAGGAAGTCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1302
GAAGTCGA SEQ ID NO: 1303	GCCTCCCTCGCGCCATCAGGAAGTCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1304
GAAGTGCA SEQ ID NO: 1305	GCCTCCCTCGCGCCATCAGGAAGTGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1306
GAAGTGGT SEQ ID NO: 1307	GCCTCCCTCGCGCCATCAGGAAGTGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1308
GACAACAG SEQ ID NO: 1309	GCCTCCCTCGCGCCATCAGGACAACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1310
GACAATC SEQ ID NO: 1311	GCCTCCCTCGCGCCATCAGGACAATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1312
GACAAGAC SEQ ID NO: 1313	GCCTCCCTCGCGCCATCAGGACAAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1314
GACAAGTG SEQ ID NO: 1315	GCCTCCCTCGCGCCATCAGGACAAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1316
GACAACT SEQ ID NO: 1317	GCCTCCCTCGCGCCATCAGGACAACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1318
GACACAGA SEQ ID NO: 1319	GCCTCCCTCGCGCCATCAGGACACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1320
GACACTCA SEQ ID NO: 1321	GCCTCCCTCGCGCCATCAGGACACTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1322
GACACTGT SEQ ID NO: 1323	GCCTCCCTCGCGCCATCAGGACACTGTCTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1324
GACAGACA SEQ ID NO: 1325	GCCTCCCTCGCGCCATCAGGACAGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1326
GACAGAGT SEQ ID NO: 1327	GCCTCCCTCGCGCCATCAGGACAGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1328

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GACAGTCT SEQ ID NO: 1329	GCCTCCCTCGCGCCATCAGGACAGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1330
GACAGTGA SEQ ID NO: 1331	GCCTCCCTCGCGCCATCAGGACAGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1332
GACATCAC SEQ ID NO: 1333	GCCTCCCTCGCGCCATCAGGACATCACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1334
GACATCTG SEQ ID NO: 1335	GCCTCCCTCGCGCCATCAGGACATCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1336
GACATGAG SEQ ID NO: 1337	GCCTCCCTCGCGCCATCAGGACATGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1338
GACATGTC SEQ ID NO: 1339	GCCTCCCTCGCGCCATCAGGACATGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1340
GACTACAC SEQ ID NO: 1341	GCCTCCCTCGCGCCATCAGGACTACACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1342
GACTACTG SEQ ID NO: 1343	GCCTCCCTCGCGCCATCAGGACTACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1344
GACTAGAG SEQ ID NO: 1345	GCCTCCCTCGCGCCATCAGGACTAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1346
GACTAGTC SEQ ID NO: 1347	GCCTCCCTCGCGCCATCAGGACTAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1348
GACTACAA SEQ ID NO: 1349	GCCTCCCTCGCGCCATCAGGACTCACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1350
GACTCAGT SEQ ID NO: 1351	GCCTCCCTCGCGCCATCAGGACTCAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1352
GACTCTCT SEQ ID NO: 1353	GCCTCCCTCGCGCCATCAGGACTCTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1354
GACTCTGA SEQ ID NO: 1355	GCCTCCCTCGCGCCATCAGGACTCTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1356
GACTGACT SEQ ID NO: 1357	GCCTCCCTCGCGCCATCAGGACTGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1358
GACTGAGA SEQ ID NO: 1359	GCCTCCCTCGCGCCATCAGGACTGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1360
GACTGTCA SEQ ID NO: 1361	GCCTCCCTCGCGCCATCAGGACTGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1362

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GACTGTGT SEQ ID NO: 1363	GCCTCCCTCGCGCCATCAGGACTGTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1364
GACTTCAG SEQ ID NO: 1365	GCCTCCCTCGCGCCATCAGGACTTCAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1366
GACTTCTC SEQ ID NO: 1367	GCCTCCCTCGCGCCATCAGGACTTCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1368
GACTTGAC SEQ ID NO: 1369	GCCTCCCTCGCGCCATCAGGACTTGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1370
GACTTGTG SEQ ID NO: 1371	GCCTCCCTCGCGCCATCAGGACTTGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1372
GAGAACAC SEQ ID NO: 1373	GCCTCCCTCGCGCCATCAGGAGAACACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1374
GAGAACTG SEQ ID NO: 1375	GCCTCCCTCGCGCCATCAGGAGAACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1376
GAGAAGAG SEQ ID NO: 1377	GCCTCCCTCGCGCCATCAGGAGAAAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1378
GAGAAGTC SEQ ID NO: 1379	GCCTCCCTCGCGCCATCAGGAGAAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1380
GAGACACA SEQ ID NO: 1381	GCCTCCCTCGCGCCATCAGGAGACACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1382
GAGACAGT SEQ ID NO: 1383	GCCTCCCTCGCGCCATCAGGAGACAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1384
GAGACTCT SEQ ID NO: 1385	GCCTCCCTCGCGCCATCAGGAGACTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1386
GAGACTGA SEQ ID NO: 1387	GCCTCCCTCGCGCCATCAGGAGACTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1388
GAGAGACT SEQ ID NO: 1389	GCCTCCCTCGCGCCATCAGGAGAGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1390
GAGAGAGA SEQ ID NO: 1391	GCCTCCCTCGCGCCATCAGGAGAGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1392
GAGAGTCA SEQ ID NO: 1393	GCCTCCCTCGCGCCATCAGGAGAGTCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1394
GAGAGTGT SEQ ID NO: 1395	GCCTCCCTCGCGCCATCAGGAGAGTGTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1396

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GAGATCAG SEQ ID NO: 1397	GCCTCCCTCGCGCCATCAGGAGATCAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1398
GAGATCTC SEQ ID NO: 1399	GCCTCCCTCGCGCCATCAGGAGATCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1400
GAGATGAC SEQ ID NO: 1401	GCCTCCCTCGCGCCATCAGGAGATGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1402
GAGATGTG SEQ ID NO: 1403	GCCTCCCTCGCGCCATCAGGAGATGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1404
GAGTACAG SEQ ID NO: 1405	GCCTCCCTCGCGCCATCAGGAGTACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1406
GAGTACTC SEQ ID NO: 1407	GCCTCCCTCGCGCCATCAGGAGTACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1408
GAGTAGAC SEQ ID NO: 1409	GCCTCCCTCGCGCCATCAGGAGTAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1410
GAGTAGTG SEQ ID NO: 1411	GCCTCCCTCGCGCCATCAGGAGTAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1412
GAGTCACT SEQ ID NO: 1413	GCCTCCCTCGCGCCATCAGGAGTCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1414
GAGTCAGA SEQ ID NO: 1415	GCCTCCCTCGCGCCATCAGGAGTCAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1416
GAGTCTCA SEQ ID NO: 1417	GCCTCCCTCGCGCCATCAGGAGTCTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1418
GAGTCTGT SEQ ID NO: 1419	GCCTCCCTCGCGCCATCAGGAGTCTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1420
GAGTGACA SEQ ID NO: 1421	GCCTCCCTCGCGCCATCAGGAGTGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1422
GAGTGAGT SEQ ID NO: 1423	GCCTCCCTCGCGCCATCAGGAGTGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1424
GAGTGTCT SEQ ID NO: 1425	GCCTCCCTCGCGCCATCAGGAGTGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1426
GAGTGTGA SEQ ID NO: 1427	GCCTCCCTCGCGCCATCAGGAGTGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1428
GAGTTCAC SEQ ID NO: 1429	GCCTCCCTCGCGCCATCAGGAGTTCACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1430

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GAGTTCTG SEQ ID NO: 1431	GCCTCCCTCGCGCCATCAGGAGTTCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1432
GAGTTGAG SEQ ID NO: 1433	GCCTCCCTCGCGCCATCAGGAGTTGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1434
GAGTTGTC SEQ ID NO: 1435	GCCTCCCTCGCGCCATCAGGAGTTGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1436
GATCACCA SEQ ID NO: 1437	GCCTCCCTCGCGCCATCAGGATCACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1438
GATCACGT SEQ ID NO: 1439	GCCTCCCTCGCGCCATCAGGATCACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1440
GATCAGCT SEQ ID NO: 1441	GCCTCCCTCGCGCCATCAGGATCAGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1442
GATCAGGA SEQ ID NO: 1443	GCCTCCCTCGCGCCATCAGGATCAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1444
GATCAAC SEQ ID NO: 1445	GCCTCCCTCGCGCCATCAGGATCAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1446
GATCCATG SEQ ID NO: 1447	GCCTCCCTCGCGCCATCAGGATCCATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1448
GATCCTAG SEQ ID NO: 1449	GCCTCCCTCGCGCCATCAGGATCCTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1450
GATCCTTC SEQ ID NO: 1451	GCCTCCCTCGCGCCATCAGGATCCTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1452
GATCGAAG SEQ ID NO: 1453	GCCTCCCTCGCGCCATCAGGATCGAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1454
GATCGATC SEQ ID NO: 1455	GCCTCCCTCGCGCCATCAGGATCGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1456
GATCGTAC SEQ ID NO: 1457	GCCTCCCTCGCGCCATCAGGATCGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1458
GATCGTTG SEQ ID NO: 1459	GCCTCCCTCGCGCCATCAGGATCGTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1460
GATCTCCT SEQ ID NO: 1461	GCCTCCCTCGCGCCATCAGGATCTCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1462
GATCTCGA SEQ ID NO: 1463	GCCTCCCTCGCGCCATCAGGATCTCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1464

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GATCTGCA SEQ ID NO: 1465	GCCTCCCTCGCGCCATCAGGATCTGCACATGCT SEQ ID NO: 1466
GATCTGGT SEQ ID NO: 1467	GCCTCCCTCGCGCCATCAGGATCTGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1468
GATGACCT SEQ ID NO: 1469	GCCTCCCTCGCGCCATCAGGATGACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1470
GATGACGA SEQ ID NO: 1471	GCCTCCCTCGCGCCATCAGGATGACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1472
GATGAGCA SEQ ID NO: 1473	GCCTCCCTCGCGCCATCAGGATGAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1474
GATGAGGT SEQ ID NO: 1475	GCCTCCCTCGCGCCATCAGGATGAGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1476
GATGCAAG SEQ ID NO: 1477	GCCTCCCTCGCGCCATCAGGATGCAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1478
GATGCATC SEQ ID NO: 1479	GCCTCCCTCGCGCCATCAGGATGCATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1480
GATGCTAC SEQ ID NO: 1481	GCCTCCCTCGCGCCATCAGGATGCTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1482
GATGCTTG SEQ ID NO: 1483	GCCTCCCTCGCGCCATCAGGATGCTTGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1484
GATGGAAC SEQ ID NO: 1485	GCCTCCCTCGCGCCATCAGGATGGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1486
GATGGATG SEQ ID NO: 1487	GCCTCCCTCGCGCCATCAGGATGGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1488
GATGGTAG SEQ ID NO: 1489	GCCTCCCTCGCGCCATCAGGATGGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1490
GATGGTTC SEQ ID NO: 1491	GCCTCCCTCGCGCCATCAGGATGGTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1492
GATGTCCA SEQ ID NO: 1493	GCCTCCCTCGCGCCATCAGGATGTCCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1494
GATGTCGT SEQ ID NO: 1495	GCCTCCCTCGCGCCATCAGGATGTCGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1496
GATGTGCT SEQ ID NO: 1497	GCCTCCCTCGCGCCATCAGGATGTGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1498

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GATGTGGA SEQ ID NO: 1499	GCCTCCCTCGCGCCATCAGGATGTGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1500
GCAACCAT SEQ ID NO: 1501	GCCTCCCTCGCGCCATCAGGCAACCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1502
GCAACCTA SEQ ID NO: 1503	GCCTCCCTCGCGCCATCAGGCAACCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1504
GCAACGAA SEQ ID NO: 1505	GCCTCCCTCGCGCCATCAGGCAACGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1506
GCAACGTT SEQ ID NO: 1507	GCCTCCCTCGCGCCATCAGGCAACGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1508
GCAAGCAA SEQ ID NO: 1509	GCCTCCCTCGCGCCATCAGGCAAGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1510
GCAAGCTT SEQ ID NO: 1511	GCCTCCCTCGCGCCATCAGGCAAGCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1512
GCAAGGAT SEQ ID NO: 1513	GCCTCCCTCGCGCCATCAGGCAAGGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1514
GCAAGGTA SEQ ID NO: 1515	GCCTCCCTCGCGCCATCAGGCAAGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1516
GCAATACC SEQ ID NO: 1517	GCCTCCCTCGCGCCATCAGGCAATACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1518
GCAATAGG SEQ ID NO: 1519	GCCTCCCTCGCGCCATCAGGCAATAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1520
GCAATTCG SEQ ID NO: 1521	GCCTCCCTCGCGCCATCAGGCAATTGCGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1522
GCAATTGC SEQ ID NO: 1523	GCCTCCCTCGCGCCATCAGGCAATTGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1524
GCATAACC SEQ ID NO: 1525	GCCTCCCTCGCGCCATCAGGCATAACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1526
GCATAAGG SEQ ID NO: 1527	GCCTCCCTCGCGCCATCAGGCATAAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1528
GCATATCG SEQ ID NO: 1529	GCCTCCCTCGCGCCATCAGGCATATCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1530
GCATATGC SEQ ID NO: 1531	GCCTCCCTCGCGCCATCAGGCATATGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1532

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GCATCCAA SEQ ID NO: 1533	GCCTCCCTCGCGCCATCAGGCATCCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1534
GCATCCTT SEQ ID NO: 1535	GCCTCCCTCGCGCCATCAGGCATCCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1536
GCATCGAT SEQ ID NO: 1537	GCCTCCCTCGCGCCATCAGGCATCGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1538
GCATCGTA SEQ ID NO: 1539	GCCTCCCTCGCGCCATCAGGCATCGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1540
GCATGCAT SEQ ID NO: 1541	GCCTCCCTCGCGCCATCAGGCATGCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1542
GCATGCTA SEQ ID NO: 1543	GCCTCCCTCGCGCCATCAGGCATGCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1544
GCATGGAA SEQ ID NO: 1545	GCCTCCCTCGCGCCATCAGGCATGGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1546
GCATGGTT SEQ ID NO: 1547	GCCTCCCTCGCGCCATCAGGCATGGTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1548
GCATTACG SEQ ID NO: 1549	GCCTCCCTCGCGCCATCAGGCATTACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1550
GCATTAGC SEQ ID NO: 1551	GCCTCCCTCGCGCCATCAGGCATTAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1552
GCCGAATT SEQ ID NO: 1553	GCCTCCCTCGCGCCATCAGGCCGAATTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1554
GCCGATAT SEQ ID NO: 1555	GCCTCCCTCGCGCCATCAGGCCGATATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1556
GCCGATTA SEQ ID NO: 1557	GCCTCCCTCGCGCCATCAGGCCGATTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1558
GCCGTAAT SEQ ID NO: 1559	GCCTCCCTCGCGCCATCAGGCCGTAATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1560
GCCGTATA SEQ ID NO: 1561	GCCTCCCTCGCGCCATCAGGCCGTATACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1562
GCCGTAA SEQ ID NO: 1563	GCCTCCCTCGCGCCATCAGGCCGTTAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1564
GCGCAATT SEQ ID NO: 1565	GCCTCCCTCGCGCCATCAGGCCGAATTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1566

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GCGCATAT SEQ ID NO: 1567	GCCTCCCTCGCGCCATCAGGCGCATATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1568
GCGCATT SEQ ID NO: 1569	GCCTCCCTCGCGCCATCAGGCGCATTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1570
GCGCTAAT SEQ ID NO: 1571	GCCTCCCTCGCGCCATCAGGCGCTAATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1572
GCGCTATA SEQ ID NO: 1573	GCCTCCCTCGCGCCATCAGGCGCTATACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1574
GCGCTTAA SEQ ID NO: 1575	GCCTCCCTCGCGCCATCAGGCGCTTAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1576
GCGGAATA SEQ ID NO: 1577	GCCTCCCTCGCGCCATCAGGCGGAATACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1578
GCGGATAA SEQ ID NO: 1579	GCCTCCCTCGCGCCATCAGGCGGATAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1580
GCGGTATT SEQ ID NO: 1581	GCCTCCCTCGCGCCATCAGGCGGTATTATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1582
GCGGTAT SEQ ID NO: 1583	GCCTCCCTCGCGCCATCAGGCGGTATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1584
GCTAATCG SEQ ID NO: 1585	GCCTCCCTCGCGCCATCAGGCTAATCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1586
GCTAATGC SEQ ID NO: 1587	GCCTCCCTCGCGCCATCAGGCTAATGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1588
GCTACCAA SEQ ID NO: 1589	GCCTCCCTCGCGCCATCAGGCTACCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1590
GCTACCTT SEQ ID NO: 1591	GCCTCCCTCGCGCCATCAGGCTACCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1592
GCTACGAT SEQ ID NO: 1593	GCCTCCCTCGCGCCATCAGGCTACGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1594
GCTACGTA SEQ ID NO: 1595	GCCTCCCTCGCGCCATCAGGCTACGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1596
GCTAGCAT SEQ ID NO: 1597	GCCTCCCTCGCGCCATCAGGCTAGCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1598
GCTAGCTA SEQ ID NO: 1599	GCCTCCCTCGCGCCATCAGGCTAGCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1600

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GCTAGGAA SEQ ID NO: 1601	GCCTCCCTCGCGCCATCAGGCTAGGAACATGCT SEQ ID NO: 1602
GCTAGGTT SEQ ID NO: 1603	GCCTCCCTCGCGCCATCAGGCTAGGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1604
GCTATACG SEQ ID NO: 1605	GCCTCCCTCGCGCCATCAGGCTATACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1606
GCTATAGC SEQ ID NO: 1607	GCCTCCCTCGCGCCATCAGGCTATAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1608
GCTATTCC SEQ ID NO: 1609	GCCTCCCTCGCGCCATCAGGCTATTCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1610
GCTATTGG SEQ ID NO: 1611	GCCTCCCTCGCGCCATCAGGCTATTGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1612
GCTTAACG SEQ ID NO: 1613	GCCTCCCTCGCGCCATCAGGCTTAACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1614
GCTTAAGC SEQ ID NO: 1615	GCCTCCCTCGCGCCATCAGGCTTAAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1616
GCTTATCC SEQ ID NO: 1617	GCCTCCCTCGCGCCATCAGGCTTATCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1618
GCTTATGG SEQ ID NO: 1619	GCCTCCCTCGCGCCATCAGGCTTATGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1620
GCTTCCAT SEQ ID NO: 1621	GCCTCCCTCGCGCCATCAGGCTTCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1622
GCTTCTTA SEQ ID NO: 1623	GCCTCCCTCGCGCCATCAGGCTTCTTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1624
GCTTCGAA SEQ ID NO: 1625	GCCTCCCTCGCGCCATCAGGCTTCGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1626
GCTTCGTT SEQ ID NO: 1627	GCCTCCCTCGCGCCATCAGGCTTCGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1628
GCTTGCAA SEQ ID NO: 1629	GCCTCCCTCGCGCCATCAGGCTTGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1630
GCTTGCTT SEQ ID NO: 1631	GCCTCCCTCGCGCCATCAGGCTTGCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1632
GCTTGGAT SEQ ID NO: 1633	GCCTCCCTCGCGCCATCAGGCTTGGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1634

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GCTTGTA SEQ ID NO: 1635	GCCTCCCTCGCGCCATCAGGCTTGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1636
GGAACCAA SEQ ID NO: 1637	GCCTCCCTCGCGCCATCAGGGAACCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1638
GGAACCTT SEQ ID NO: 1639	GCCTCCCTCGCGCCATCAGGGAACCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1640
GGAACGAT SEQ ID NO: 1641	GCCTCCCTCGCGCCATCAGGGAACGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1642
GGAACGTA SEQ ID NO: 1643	GCCTCCCTCGCGCCATCAGGGAACGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1644
GGAAGCAT SEQ ID NO: 1645	GCCTCCCTCGCGCCATCAGGGAAGCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1646
GGAAGCTA SEQ ID NO: 1647	GCCTCCCTCGCGCCATCAGGGAAGCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1648
GGAAGGAA SEQ ID NO: 1649	GCCTCCCTCGCGCCATCAGGGAAGGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1650
GGAAGGTT SEQ ID NO: 1651	GCCTCCCTCGCGCCATCAGGGAAGGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1652
GGAATACG SEQ ID NO: 1653	GCCTCCCTCGCGCCATCAGGGAATACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1654
GGAATAGC SEQ ID NO: 1655	GCCTCCCTCGCGCCATCAGGGAATAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1656
GGAATTCC SEQ ID NO: 1657	GCCTCCCTCGCGCCATCAGGGAATTCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1658
GGAATTGG SEQ ID NO: 1659	GCCTCCCTCGCGCCATCAGGGAATTGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1660
GGATAACG SEQ ID NO: 1661	GCCTCCCTCGCGCCATCAGGGATAACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1662
GGATAAGC SEQ ID NO: 1663	GCCTCCCTCGCGCCATCAGGGATAAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1664
GGATATCC SEQ ID NO: 1665	GCCTCCCTCGCGCCATCAGGGATATCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1666
GGATATGG SEQ ID NO: 1667	GCCTCCCTCGCGCCATCAGGGATATGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1668

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GGATCCAT SEQ ID NO: 1669	GCCTCCCTCGCGCCATCAGGGATCCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1670
GGATCCTA SEQ ID NO: 1671	GCCTCCCTCGCGCCATCAGGGATCCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1672
GGATCGAA SEQ ID NO: 1673	GCCTCCCTCGCGCCATCAGGGATCGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1674
GGATCGTT SEQ ID NO: 1675	GCCTCCCTCGCGCCATCAGGGATCGTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1676
GGATGCAA SEQ ID NO: 1677	GCCTCCCTCGCGCCATCAGGGATGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1678
GGATGCTT SEQ ID NO: 1679	GCCTCCCTCGCGCCATCAGGGATGCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1680
GGATGGAT SEQ ID NO: 1681	GCCTCCCTCGCGCCATCAGGGATGGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1682
GGATGGTA SEQ ID NO: 1683	GCCTCCCTCGCGCCATCAGGGATGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1684
GGATTACC SEQ ID NO: 1685	GCCTCCCTCGCGCCATCAGGGATTACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1686
GGATTAGG SEQ ID NO: 1687	GCCTCCCTCGCGCCATCAGGGATTAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1688
GGCCAATT SEQ ID NO: 1689	GCCTCCCTCGCGCCATCAGGGCCAATTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1690
GGCCATAT SEQ ID NO: 1691	GCCTCCCTCGCGCCATCAGGGCCATATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1692
GGCCATTA SEQ ID NO: 1693	GCCTCCCTCGCGCCATCAGGGCCATTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1694
GGCCTAAT SEQ ID NO: 1695	GCCTCCCTCGCGCCATCAGGGCCTAATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1696
GGCCTATA SEQ ID NO: 1697	GCCTCCCTCGCGCCATCAGGGCCTATACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1698
GGCCTTAA SEQ ID NO: 1699	GCCTCCCTCGCGCCATCAGGGCCTTAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1700
GGCGAATA SEQ ID NO: 1701	GCCTCCCTCGCGCCATCAGGGCGAATACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1702

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GGCGATAA SEQ ID NO: 1703	GCCTCCCTCGCGCCATCAGGGCGATAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1704
GGCGTATT SEQ ID NO: 1705	GCCTCCCTCGCGCCATCAGGGCGTATTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1706
GGCGTTAT SEQ ID NO: 1707	GCCTCCCTCGCGCCATCAGGGCGTTATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1708
GGTAATCC SEQ ID NO: 1709	GCCTCCCTCGCGCCATCAGGGTAATCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1710
GGTAATGG SEQ ID NO: 1711	GCCTCCCTCGCGCCATCAGGGTAATGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1712
GGTACCAT SEQ ID NO: 1713	GCCTCCCTCGCGCCATCAGGGTACCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1714
GGTACCTA SEQ ID NO: 1715	GCCTCCCTCGCGCCATCAGGGTACCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1716
GGTACGAA SEQ ID NO: 1717	GCCTCCCTCGCGCCATCAGGGTACGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1718
GGTACGTT SEQ ID NO: 1719	GCCTCCCTCGCGCCATCAGGGTACGTTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1720
GGTAGCAA SEQ ID NO: 1721	GCCTCCCTCGCGCCATCAGGGTAGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1722
GGTAGCTT SEQ ID NO: 1723	GCCTCCCTCGCGCCATCAGGGTAGCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1724
GGTAGGAT SEQ ID NO: 1725	GCCTCCCTCGCGCCATCAGGGTAGGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1726
GGTAGGTA SEQ ID NO: 1727	GCCTCCCTCGCGCCATCAGGGTAGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1728
GGTATACC SEQ ID NO: 1729	GCCTCCCTCGCGCCATCAGGGTATACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1730
GGTATAGG SEQ ID NO: 1731	GCCTCCCTCGCGCCATCAGGGTATAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1732
GGTATTCG SEQ ID NO: 1733	GCCTCCCTCGCGCCATCAGGGTATTCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1734
GGTATTGC SEQ ID NO: 1735	GCCTCCCTCGCGCCATCAGGGTATTGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1736

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GGTTAACC SEQ ID NO: 1737	GCCTCCCTCGCGCCATCAGGGTTAACCCATGCT SEQ ID NO: 1738
GGTTAAGG SEQ ID NO: 1739	GCCTCCCTCGCGCCATCAGGGTTAAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1740
GGTTATCG SEQ ID NO: 1741	GCCTCCCTCGCGCCATCAGGGTTATCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1742
GGTTATGC SEQ ID NO: 1743	GCCTCCCTCGCGCCATCAGGGTTATGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1744
GGTTCCAA SEQ ID NO: 1745	GCCTCCCTCGCGCCATCAGGGTTCCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1746
GGTTCCTT SEQ ID NO: 1747	GCCTCCCTCGCGCCATCAGGGTTCCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1748
GGTTCGAT SEQ ID NO: 1749	GCCTCCCTCGCGCCATCAGGGTTCGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1750
GGTTCGTA SEQ ID NO: 1751	GCCTCCCTCGCGCCATCAGGGTTCGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1752
GGTTGCAT SEQ ID NO: 1753	GCCTCCCTCGCGCCATCAGGGTTGCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1754
GGTTGCTA SEQ ID NO: 1755	GCCTCCCTCGCGCCATCAGGGTTGCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1756
GGTTGGAA SEQ ID NO: 1757	GCCTCCCTCGCGCCATCAGGGTTGGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1758
GGTTGGTT SEQ ID NO: 1759	GCCTCCCTCGCGCCATCAGGGTTGGTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1760
GTACACCA SEQ ID NO: 1761	GCCTCCCTCGCGCCATCAGGTACACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1762
GTACACGT SEQ ID NO: 1763	GCCTCCCTCGCGCCATCAGGTACACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1764
GTACAGCT SEQ ID NO: 1765	GCCTCCCTCGCGCCATCAGGTACAGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1766
GTACAGGA SEQ ID NO: 1767	GCCTCCCTCGCGCCATCAGGTACAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1768
GTACCAAC SEQ ID NO: 1769	GCCTCCCTCGCGCCATCAGGTACCAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1770

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GTACCATG SEQ ID NO: 1771	GCCTCCCTCGCGCCATCAGGTACCATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1772
GTACCTAG SEQ ID NO: 1773	GCCTCCCTCGCGCCATCAGGTACCTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1774
GTACCTTC SEQ ID NO: 1775	GCCTCCCTCGCGCCATCAGGTACCTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1776
GTACGAAG SEQ ID NO: 1777	GCCTCCCTCGCGCCATCAGGTACGAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1778
GTACGATC SEQ ID NO: 1779	GCCTCCCTCGCGCCATCAGGTACGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1780
GTACGTAC SEQ ID NO: 1781	GCCTCCCTCGCGCCATCAGGTACGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1782
GTACGTTG SEQ ID NO: 1783	GCCTCCCTCGCGCCATCAGGTACGTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1784
GTACTCCT SEQ ID NO: 1785	GCCTCCCTCGCGCCATCAGGTACTCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1786
GTACTCGA SEQ ID NO: 1787	GCCTCCCTCGCGCCATCAGGTACTCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1788
GTACTGCA SEQ ID NO: 1789	GCCTCCCTCGCGCCATCAGGTACTGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1790
GTACTGGT SEQ ID NO: 1791	GCCTCCCTCGCGCCATCAGGTACTGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1792
GTAGACCT SEQ ID NO: 1793	GCCTCCCTCGCGCCATCAGGTAGACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1794
GTAGACGA SEQ ID NO: 1795	GCCTCCCTCGCGCCATCAGGTAGACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1796
GTAGAGCA SEQ ID NO: 1797	GCCTCCCTCGCGCCATCAGGTAGAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1798
GTAGAGGT SEQ ID NO: 1799	GCCTCCCTCGCGCCATCAGGTAGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1800
GTAGCAAG SEQ ID NO: 1801	GCCTCCCTCGCGCCATCAGGTAGCAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1802
GTAGCATC SEQ ID NO: 1803	GCCTCCCTCGCGCCATCAGGTAGCATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1804

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GTAGCTAC SEQ ID NO: 1805	GCCTCCCTCGCGCCATCAGGTAGCTACCATGCT SEQ ID NO: 1806
GTAGCTTG SEQ ID NO: 1807	GCCTCCCTCGCGCCATCAGGTAGCTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1808
GTAGGAAC SEQ ID NO: 1809	GCCTCCCTCGCGCCATCAGGTAGGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1810
GTAGGATG SEQ ID NO: 1811	GCCTCCCTCGCGCCATCAGGTAGGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1812
GTAGGTAG SEQ ID NO: 1813	GCCTCCCTCGCGCCATCAGGTAGGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1814
GTAGGTTT SEQ ID NO: 1815	GCCTCCCTCGCGCCATCAGGTAGGTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1816
GTAGTCCA SEQ ID NO: 1817	GCCTCCCTCGCGCCATCAGGTAGTCCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1818
GTAGTCGT SEQ ID NO: 1819	GCCTCCCTCGCGCCATCAGGTAGTCGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1820
GTAGTGCT SEQ ID NO: 1821	GCCTCCCTCGCGCCATCAGGTAGTGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1822
GTAGTGGA SEQ ID NO: 1823	GCCTCCCTCGCGCCATCAGGTAGTGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1824
GTCAACAC SEQ ID NO: 1825	GCCTCCCTCGCGCCATCAGGTCAACACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1826
GTCAACTG SEQ ID NO: 1827	GCCTCCCTCGCGCCATCAGGTCAACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1828
GTCAAGAG SEQ ID NO: 1829	GCCTCCCTCGCGCCATCAGGTCAAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1830
GTCAAGTC SEQ ID NO: 1831	GCCTCCCTCGCGCCATCAGGTCAAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1832
GTCACACA SEQ ID NO: 1833	GCCTCCCTCGCGCCATCAGGTCACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1834
GTCACAGT SEQ ID NO: 1835	GCCTCCCTCGCGCCATCAGGTCACAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1836
GTCACTCT SEQ ID NO: 1837	GCCTCCCTCGCGCCATCAGGTCACTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1838

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GTCCTGA SEQ ID NO: 1839	GCCTCCCTCGCGCCATCAGGTCACTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1840
GTCAGACT SEQ ID NO: 1841	GCCTCCCTCGCGCCATCAGGTCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1842
GTCAGAGA SEQ ID NO: 1843	GCCTCCCTCGCGCCATCAGGTCAAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1844
GTCAGTCA SEQ ID NO: 1845	GCCTCCCTCGCGCCATCAGGTCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1846
GTCAGTGT SEQ ID NO: 1847	GCCTCCCTCGCGCCATCAGGTCACTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1848
GTCATCAG SEQ ID NO: 1849	GCCTCCCTCGCGCCATCAGGTCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1850
GTCATCTC SEQ ID NO: 1851	GCCTCCCTCGCGCCATCAGGTCACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1852
GTCATGAC SEQ ID NO: 1853	GCCTCCCTCGCGCCATCAGGTCACTGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1854
GTCATGTG SEQ ID NO: 1855	GCCTCCCTCGCGCCATCAGGTCACTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1856
GTCTACAG SEQ ID NO: 1857	GCCTCCCTCGCGCCATCAGGTCTACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1858
GTCTACTC SEQ ID NO: 1859	GCCTCCCTCGCGCCATCAGGTCTACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1860
GTCTAGAC SEQ ID NO: 1861	GCCTCCCTCGCGCCATCAGGTCTAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1862
GTCTAGTG SEQ ID NO: 1863	GCCTCCCTCGCGCCATCAGGTCTAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1864
GTCTCACT SEQ ID NO: 1865	GCCTCCCTCGCGCCATCAGGTCTCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1866
GTCTCAGA SEQ ID NO: 1867	GCCTCCCTCGCGCCATCAGGTCTCAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1868
GTCTCTCA SEQ ID NO: 1869	GCCTCCCTCGCGCCATCAGGTCTCTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1870
GTCTCTGT SEQ ID NO: 1871	GCCTCCCTCGCGCCATCAGGTCTGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1872

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GTCTGACA SEQ ID NO: 1873	GCCTCCCTCGCGCCATCAGGTCTGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1874
GTCTGAGT SEQ ID NO: 1875	GCCTCCCTCGCGCCATCAGGTCTGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1876
GTCTGTCT SEQ ID NO: 1877	GCCTCCCTCGCGCCATCAGGTCTGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1878
GTCTGTGA SEQ ID NO: 1879	GCCTCCCTCGCGCCATCAGGTCTGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1880
GTCTTCAC SEQ ID NO: 1881	GCCTCCCTCGCGCCATCAGGTCTTCACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1882
GTCTTCTG SEQ ID NO: 1883	GCCTCCCTCGCGCCATCAGGTCTTCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1884
GTCTTGAG SEQ ID NO: 1885	GCCTCCCTCGCGCCATCAGGTCTTGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1886
GTCTTGTC SEQ ID NO: 1887	GCCTCCCTCGCGCCATCAGGTCTTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1888
GTGAACAG SEQ ID NO: 1889	GCCTCCCTCGCGCCATCAGGTGAACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1890
GTGAACTC SEQ ID NO: 1891	GCCTCCCTCGCGCCATCAGGTGAACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1892
GTGAAGAC SEQ ID NO: 1893	GCCTCCCTCGCGCCATCAGGTGAAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1894
GTGAAGTG SEQ ID NO: 1895	GCCTCCCTCGCGCCATCAGGTGAAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1896
GTGACACT SEQ ID NO: 1897	GCCTCCCTCGCGCCATCAGGTGACACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1898
GTGACAGA SEQ ID NO: 1899	GCCTCCCTCGCGCCATCAGGTGACAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1900
GTGACTCA SEQ ID NO: 1901	GCCTCCCTCGCGCCATCAGGTGACTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1902
GTGACTGT SEQ ID NO: 1903	GCCTCCCTCGCGCCATCAGGTGACTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1904
GTGAGACA SEQ ID NO: 1905	GCCTCCCTCGCGCCATCAGGTGAGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1906

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GTGAGAGT SEQ ID NO: 1907	GCCTCCCTCGCGCCATCAGGTGAGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1908
GTGAGTCT SEQ ID NO: 1909	GCCTCCCTCGCGCCATCAGGTGAGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1910
GTGAGTGA SEQ ID NO: 1911	GCCTCCCTCGCGCCATCAGGTGAGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1912
GTGATCAC SEQ ID NO: 1913	GCCTCCCTCGCGCCATCAGGTGATCACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1914
GTGATCTG SEQ ID NO: 1915	GCCTCCCTCGCGCCATCAGGTGATCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1916
GTGATGAG SEQ ID NO: 1917	GCCTCCCTCGCGCCATCAGGTGATGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1918
GTGATGTC SEQ ID NO: 1919	GCCTCCCTCGCGCCATCAGGTGATGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1920
GTGTACAC SEQ ID NO: 1921	GCCTCCCTCGCGCCATCAGGTGTACACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1922
GTGTACTG SEQ ID NO: 1923	GCCTCCCTCGCGCCATCAGGTGTACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1924
GTGTAGAG SEQ ID NO: 1925	GCCTCCCTCGCGCCATCAGGTGTAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1926
GTGTAGTC SEQ ID NO: 1927	GCCTCCCTCGCGCCATCAGGTGTAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1928
GTGTACAA SEQ ID NO: 1929	GCCTCCCTCGCGCCATCAGGTGTACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1930
GTGTCAGT SEQ ID NO: 1931	GCCTCCCTCGCGCCATCAGGTGTCAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1932
GTGTCTCT SEQ ID NO: 1933	GCCTCCCTCGCGCCATCAGGTGTCTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1934
GTGTCTGA SEQ ID NO: 1935	GCCTCCCTCGCGCCATCAGGTGTCTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1936
GTGTGACT SEQ ID NO: 1937	GCCTCCCTCGCGCCATCAGGTGTGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1938
GTGTGAGA SEQ ID NO: 1939	GCCTCCCTCGCGCCATCAGGTGTGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1940

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GTGTGTCA SEQ ID NO: 1941	GCCTCCCTCGCGCCATCAGGTGTGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1942
GTGTGTGT SEQ ID NO: 1943	GCCTCCCTCGCGCCATCAGGTGTGTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1944
GTGTTTCA SEQ ID NO: 1945	GCCTCCCTCGCGCCATCAGGTGTTTCAATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1946
GTGTTCTC SEQ ID NO: 1947	GCCTCCCTCGCGCCATCAGGTGTTCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1948
GTGTTGAC SEQ ID NO: 1949	GCCTCCCTCGCGCCATCAGGTGTTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1950
GTGTTGTG SEQ ID NO: 1951	GCCTCCCTCGCGCCATCAGGTGTTGTGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1952
GTTACCT SEQ ID NO: 1953	GCCTCCCTCGCGCCATCAGGTTACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1954
GTTACGA SEQ ID NO: 1955	GCCTCCCTCGCGCCATCAGGTTACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1956
GTTACGA SEQ ID NO: 1957	GCCTCCCTCGCGCCATCAGGTTACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1958
GTTACAGT SEQ ID NO: 1959	GCCTCCCTCGCGCCATCAGGTTACAGTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1960
GTTCAAG SEQ ID NO: 1961	GCCTCCCTCGCGCCATCAGGTTCAAGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1962
GTTCCATC SEQ ID NO: 1963	GCCTCCCTCGCGCCATCAGGTTCCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1964
GTTCCATC SEQ ID NO: 1965	GCCTCCCTCGCGCCATCAGGTTCCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1966
GTTCCCTG SEQ ID NO: 1967	GCCTCCCTCGCGCCATCAGGTTCCCTGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1968
GTTGGAAC SEQ ID NO: 1969	GCCTCCCTCGCGCCATCAGGTTGGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1970
GTTGATG SEQ ID NO: 1971	GCCTCCCTCGCGCCATCAGGTTGATGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1972
GTTGCTAG SEQ ID NO: 1973	GCCTCCCTCGCGCCATCAGGTTGCTAGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1974

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GTTCTTC SEQ ID NO: 1975	GCCTCCCTCGCGCCATCAGGTTCTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1976
GTTCTCCA SEQ ID NO: 1977	GCCTCCCTCGCGCCATCAGGTTCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1978
GTTCTCGT SEQ ID NO: 1979	GCCTCCCTCGCGCCATCAGGTTCTCGTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1980
GTTCTGCT SEQ ID NO: 1981	GCCTCCCTCGCGCCATCAGGTTCTGCTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1982
GTTCTGGA SEQ ID NO: 1983	GCCTCCCTCGCGCCATCAGGTTCTGGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1984
GTTGACCA SEQ ID NO: 1985	GCCTCCCTCGCGCCATCAGGTTGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1986
GTTGACGT SEQ ID NO: 1987	GCCTCCCTCGCGCCATCAGGTTGACGTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1988
GTTGAGCT SEQ ID NO: 1989	GCCTCCCTCGCGCCATCAGGTTGAGCTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1990
GTTGAGGA SEQ ID NO: 1991	GCCTCCCTCGCGCCATCAGGTTGAGGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1992
GTTGCAAC SEQ ID NO: 1993	GCCTCCCTCGCGCCATCAGGTTGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1994
GTTGCATG SEQ ID NO: 1995	GCCTCCCTCGCGCCATCAGGTTGCATGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1996
GTTGCTAG SEQ ID NO: 1997	GCCTCCCTCGCGCCATCAGGTTGCTAGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 1998
GTTGCTTC SEQ ID NO: 1999	GCCTCCCTCGCGCCATCAGGTTGCTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2000
GTTGGAAG SEQ ID NO: 2001	GCCTCCCTCGCGCCATCAGGTTGGAAGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2002
GTTGGATC SEQ ID NO: 2003	GCCTCCCTCGCGCCATCAGGTTGGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2004
GTTGGTAC SEQ ID NO: 2005	GCCTCCCTCGCGCCATCAGGTTGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2006
GTTGGTTG SEQ ID NO: 2007	GCCTCCCTCGCGCCATCAGGTTGGTTGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2008

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
GTTGTCCT SEQ ID NO: 2009	GCCTCCCTCGCGCCATCAGGTTGTCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2010
GTTGTCGA SEQ ID NO: 2011	GCCTCCCTCGCGCCATCAGGTTGTCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2012
GTTGTGCA SEQ ID NO: 2013	GCCTCCCTCGCGCCATCAGGTTGTGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2014
GTTGTGGT SEQ ID NO: 2015	GCCTCCCTCGCGCCATCAGGTTGTGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2016
TAATCCGG SEQ ID NO: 2017	GCCTCCCTCGCGCCATCAGTAATCCGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2018
TAATCGCG SEQ ID NO: 2019	GCCTCCCTCGCGCCATCAGTAATCGCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2020
TAATCGGC SEQ ID NO: 2021	GCCTCCCTCGCGCCATCAGTAATCGGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2022
TAATGCCG SEQ ID NO: 2023	GCCTCCCTCGCGCCATCAGTAATGCCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2034
TAATGCGC SEQ ID NO: 2035	GCCTCCCTCGCGCCATCAGTAATGCGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2036
TAATGGCC SEQ ID NO: 2037	GCCTCCCTCGCGCCATCAGTAATGGCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2038
TACCAACG SEQ ID NO: 2039	GCCTCCCTCGCGCCATCAGTACCAACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2040
TACCAAGC SEQ ID NO: 2041	GCCTCCCTCGCGCCATCAGTACCAAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2042
TACCATCC SEQ ID NO: 2043	GCCTCCCTCGCGCCATCAGTACCATCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2044
TACCATGG SEQ ID NO: 2045	GCCTCCCTCGCGCCATCAGTACCATGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2046
TACCGCAA SEQ ID NO: 2047	GCCTCCCTCGCGCCATCAGTACCGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2048
TACCGCTT SEQ ID NO: 2049	GCCTCCCTCGCGCCATCAGTACCGCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2050
TACCGGAT SEQ ID NO: 2051	GCCTCCCTCGCGCCATCAGTACCGGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2052

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TACCGGTA SEQ ID NO: 2053	GCCTCCCTCGCGCCATCAGTACCGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2054
TACCTACC SEQ ID NO: 2055	GCCTCCCTCGCGCCATCAGTACCTACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2056
TACCTAGG SEQ ID NO: 2057	GCCTCCCTCGCGCCATCAGTACCTAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2058
TACCTTCG SEQ ID NO: 2059	GCCTCCCTCGCGCCATCAGTACCTTCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2060
TACCTTGC SEQ ID NO: 2061	GCCTCCCTCGCGCCATCAGTACCTTGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2062
TACGAACC SEQ ID NO: 2063	GCCTCCCTCGCGCCATCAGTACGAACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2064
TACGAAGG SEQ ID NO: 2065	GCCTCCCTCGCGCCATCAGTACGAAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2066
TACGATCG SEQ ID NO: 2067	GCCTCCCTCGCGCCATCAGTACGATCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2068
TACGATGC SEQ ID NO: 2069	GCCTCCCTCGCGCCATCAGTACGATGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2070
TACGCCAA SEQ ID NO: 2071	GCCTCCCTCGCGCCATCAGTACGCCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2072
TACGCCTT SEQ ID NO: 2073	GCCTCCCTCGCGCCATCAGTACGCCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2074
TACGCGAT SEQ ID NO: 2075	GCCTCCCTCGCGCCATCAGTACGCGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2076
TACGCGTA SEQ ID NO: 2077	GCCTCCCTCGCGCCATCAGTACGCGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2078
TACGGCAT SEQ ID NO: 2079	GCCTCCCTCGCGCCATCAGTACGGCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2080
TACGGCTA SEQ ID NO: 2081	GCCTCCCTCGCGCCATCAGTACGGCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2082
TACGTACG SEQ ID NO: 2083	GCCTCCCTCGCGCCATCAGTACGTACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2084
TACGTAGC SEQ ID NO: 2085	GCCTCCCTCGCGCCATCAGTACGTAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2086

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TACGTTCC SEQ ID NO: 2087	GCCTCCCTCGCGCCATCAGTACGTTCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2088
TACGTTGG SEQ ID NO: 2089	GCCTCCCTCGCGCCATCAGTACGTTGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2090
TAGCAACC SEQ ID NO: 2091	GCCTCCCTCGCGCCATCAGTAGCAACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2092
TAGCAAGG SEQ ID NO: 2093	GCCTCCCTCGCGCCATCAGTAGCAAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2094
TAGCATCG SEQ ID NO: 2095	GCCTCCCTCGCGCCATCAGTAGCATCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2096
TAGCATGC SEQ ID NO: 2097	GCCTCCCTCGCGCCATCAGTAGCATGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2098
TAGCCGAT SEQ ID NO: 2099	GCCTCCCTCGCGCCATCAGTAGCCGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2100
TAGCCGTA SEQ ID NO: 2101	GCCTCCCTCGCGCCATCAGTAGCCGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2102
TAGCGCAT SEQ ID NO: 2103	GCCTCCCTCGCGCCATCAGTAGCGCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2104
TAGCGCTA SEQ ID NO: 2105	GCCTCCCTCGCGCCATCAGTAGCGCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2106
TAGCGGAA SEQ ID NO: 2107	GCCTCCCTCGCGCCATCAGTAGCGGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2108
TAGCGGTT SEQ ID NO: 2109	GCCTCCCTCGCGCCATCAGTAGCGGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2110
TAGCTACG SEQ ID NO: 2111	GCCTCCCTCGCGCCATCAGTAGCTACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2112
TAGCTAGC SEQ ID NO: 2113	GCCTCCCTCGCGCCATCAGTAGCTAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2114
TAGCTTCC SEQ ID NO: 2115	GCCTCCCTCGCGCCATCAGTAGCTTCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2116
TAGCTTGG SEQ ID NO: 2117	GCCTCCCTCGCGCCATCAGTAGCTTGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2118
TAGGAACG SEQ ID NO: 2119	GCCTCCCTCGCGCCATCAGTAGGAACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2120

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TAGGAAGC SEQ ID NO: 2121	GCCTCCCTCGCGCCATCAGTAGGAAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2122
TAGGATCC SEQ ID NO: 2123	GCCTCCCTCGCGCCATCAGTAGGATCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2134
TAGGATGG SEQ ID NO: 2135	GCCTCCCTCGCGCCATCAGTAGGATGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2136
TAGGCCAT SEQ ID NO: 2137	GCCTCCCTCGCGCCATCAGTAGGCCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2138
TAGGCCTA SEQ ID NO: 2139	GCCTCCCTCGCGCCATCAGTAGGCCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2140
TAGGCGAA SEQ ID NO: 2141	GCCTCCCTCGCGCCATCAGTAGGCGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2142
TAGGCGTT SEQ ID NO: 2143	GCCTCCCTCGCGCCATCAGTAGGCGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2144
TAGGTACC SEQ ID NO: 2145	GCCTCCCTCGCGCCATCAGTAGGTACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2146
TAGGTAGG SEQ ID NO: 2147	GCCTCCCTCGCGCCATCAGTAGGTAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2148
TAGGTTCG SEQ ID NO: 2149	GCCTCCCTCGCGCCATCAGTAGGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2150
TAGGTTGC SEQ ID NO: 2151	GCCTCCCTCGCGCCATCAGTAGGTTGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2152
TATACCGG SEQ ID NO: 2153	GCCTCCCTCGCGCCATCAGTATACCGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2154
TATACGCG SEQ ID NO: 2155	GCCTCCCTCGCGCCATCAGTATACGCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2156
TATACGGC SEQ ID NO: 2157	GCCTCCCTCGCGCCATCAGTATACGGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2158
TATAGCCG SEQ ID NO: 2159	GCCTCCCTCGCGCCATCAGTATAGCCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2160
TATAGCGC SEQ ID NO: 2161	GCCTCCCTCGCGCCATCAGTATAGCGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2162
TATAGGCC SEQ ID NO: 2163	GCCTCCCTCGCGCCATCAGTATAGGCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2164

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TATTCGCG SEQ ID NO: 2165	GCCTCCCTCGCGCCATCAGTATTCCGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2166
TATTCGCC SEQ ID NO: 2167	GCCTCCCTCGCGCCATCAGTATTGCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2168
TATTGCGG SEQ ID NO: 2169	GCCTCCCTCGCGCCATCAGTATTGCGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2170
TATTGGCG SEQ ID NO: 2171	GCCTCCCTCGCGCCATCAGTATTGGCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2172
TCACACAG SEQ ID NO: 2173	GCCTCCCTCGCGCCATCAGTCACACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2174
TCACACTC SEQ ID NO: 2175	GCCTCCCTCGCGCCATCAGTCACACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2176
TCACAGAC SEQ ID NO: 2177	GCCTCCCTCGCGCCATCAGTCACAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2178
TCACAGTG SEQ ID NO: 2179	GCCTCCCTCGCGCCATCAGTCACAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2180
TCACCACT SEQ ID NO: 2181	GCCTCCCTCGCGCCATCAGTCACCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2182
TCACCAGA SEQ ID NO: 2183	GCCTCCCTCGCGCCATCAGTCACCAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2184
TCACCTCA SEQ ID NO: 2185	GCCTCCCTCGCGCCATCAGTCACCTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2186
TCACCTGT SEQ ID NO: 2187	GCCTCCCTCGCGCCATCAGTCACCTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2188
TCACGACA SEQ ID NO: 2189	GCCTCCCTCGCGCCATCAGTCACGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2190
TCACGAGT SEQ ID NO: 2191	GCCTCCCTCGCGCCATCAGTCACGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2192
TCAGTCT SEQ ID NO: 2193	GCCTCCCTCGCGCCATCAGTCAGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2194
TCAGTGTA SEQ ID NO: 2195	GCCTCCCTCGCGCCATCAGTCAGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2196
TCACTCAC SEQ ID NO: 2197	GCCTCCCTCGCGCCATCAGTCACTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2198

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TCACTCTG SEQ ID NO: 2199	GCCTCCCTCGCGCCATCAGTCACTCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2200
TCACTGAG SEQ ID NO: 2201	GCCTCCCTCGCGCCATCAGTCACTGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2202
TCACTGTC SEQ ID NO: 2203	GCCTCCCTCGCGCCATCAGTCACTGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2204
TCAGACAC SEQ ID NO: 2205	GCCTCCCTCGCGCCATCAGTCAGACACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2206
TCAGACTG SEQ ID NO: 2207	GCCTCCCTCGCGCCATCAGTCAGACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2208
TCAGAGAG SEQ ID NO: 2209	GCCTCCCTCGCGCCATCAGTCAGAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2210
TCAGAGTC SEQ ID NO: 2211	GCCTCCCTCGCGCCATCAGTCAGAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2212
TCAGACA SEQ ID NO: 2213	GCCTCCCTCGCGCCATCAGTCAGCACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2214
TCAGCAGT SEQ ID NO: 2215	GCCTCCCTCGCGCCATCAGTCAGCAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2216
TCAGTCT SEQ ID NO: 2217	GCCTCCCTCGCGCCATCAGTCAGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2218
TCAGTGTA SEQ ID NO: 2219	GCCTCCCTCGCGCCATCAGTCAGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2220
TCAGGACT SEQ ID NO: 2221	GCCTCCCTCGCGCCATCAGTCAGGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2222
TCAGGAGA SEQ ID NO: 2223	GCCTCCCTCGCGCCATCAGTCAGGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2224
TCAGGTCA SEQ ID NO: 2225	GCCTCCCTCGCGCCATCAGTCAGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2226
TCAGGTGT SEQ ID NO: 2227	GCCTCCCTCGCGCCATCAGTCAGGTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2228
TCAGTCAG SEQ ID NO: 2229	GCCTCCCTCGCGCCATCAGTCAGTCAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2230
TCAGTCTC SEQ ID NO: 2231	GCCTCCCTCGCGCCATCAGTCAGTCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2232

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TCAGTGAC SEQ ID NO: 2233	GCCTCCCTCGCGCCATCAGTCAGTGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2234
TCAGTGTG SEQ ID NO: 2235	GCCTCCCTCGCGCCATCAGTCAGTGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2236
TCCAACCT SEQ ID NO: 2237	GCCTCCCTCGCGCCATCAGTCCAACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2238
TCCAACGA SEQ ID NO: 2239	GCCTCCCTCGCGCCATCAGTCCAACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2240
TCCAAGCA SEQ ID NO: 2241	GCCTCCCTCGCGCCATCAGTCCAAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2242
TCCAAGGT SEQ ID NO: 2243	GCCTCCCTCGCGCCATCAGTCCAAGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2244
TCCACAAG SEQ ID NO: 2245	GCCTCCCTCGCGCCATCAGTCCACAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2246
TCCACATC SEQ ID NO: 2247	GCCTCCCTCGCGCCATCAGTCCACATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2248
TCCACTAC SEQ ID NO: 2249	GCCTCCCTCGCGCCATCAGTCCACTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2250
TCCACTTG SEQ ID NO: 2251	GCCTCCCTCGCGCCATCAGTCCACTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2252
TCCAGAAC SEQ ID NO: 2253	GCCTCCCTCGCGCCATCAGTCCAGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2254
TCCAGATG SEQ ID NO: 2255	GCCTCCCTCGCGCCATCAGTCCAGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2256
TCCAGTAG SEQ ID NO: 2257	GCCTCCCTCGCGCCATCAGTCCAGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2258
TCCAGTTC SEQ ID NO: 2259	GCCTCCCTCGCGCCATCAGTCCAGTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2260
TCCATCCA SEQ ID NO: 2261	GCCTCCCTCGCGCCATCAGTCCATCCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2262
TCCATCGT SEQ ID NO: 2263	GCCTCCCTCGCGCCATCAGTCCATCGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2264
TCCATGCT SEQ ID NO: 2265	GCCTCCCTCGCGCCATCAGTCCATGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2266

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TCCATGGA SEQ ID NO: 2267	GCCTCCCTCGCGCCATCAGTCCATGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2268
TCCTACCA SEQ ID NO: 2269	GCCTCCCTCGCGCCATCAGTTCCTACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2270
TCCTACGT SEQ ID NO: 2271	GCCTCCCTCGCGCCATCAGTTCCTACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2272
TCCTAGCT SEQ ID NO: 2273	GCCTCCCTCGCGCCATCAGTTCCTAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2274
TCCTAGGA SEQ ID NO: 2275	GCCTCCCTCGCGCCATCAGTTCCTAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2276
TCCTCAAC SEQ ID NO: 2277	GCCTCCCTCGCGCCATCAGTTCCTCAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2278
TCCTCATG SEQ ID NO: 2279	GCCTCCCTCGCGCCATCAGTTCCTCATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2280
TCCTCTAG SEQ ID NO: 2281	GCCTCCCTCGCGCCATCAGTTCCTCTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2282
TCCTCTTC SEQ ID NO: 2283	GCCTCCCTCGCGCCATCAGTTCCTCTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2284
TCCTGAAG SEQ ID NO: 2285	GCCTCCCTCGCGCCATCAGTTCCTGAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2286
TCCTGATC SEQ ID NO: 2287	GCCTCCCTCGCGCCATCAGTTCCTGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2288
TCCTGTAC SEQ ID NO: 2289	GCCTCCCTCGCGCCATCAGTTCCTGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2290
TCCTGTTG SEQ ID NO: 2291	GCCTCCCTCGCGCCATCAGTTCCTGTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2292
TCCTTCCT SEQ ID NO: 2293	GCCTCCCTCGCGCCATCAGTTCCTTCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2294
TCCTTCGA SEQ ID NO: 2295	GCCTCCCTCGCGCCATCAGTTCCTTCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2296
TCCTTGCA SEQ ID NO: 2297	GCCTCCCTCGCGCCATCAGTTCCTTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2298
TCCTTGGT SEQ ID NO: 2299	GCCTCCCTCGCGCCATCAGTTCCTTGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2700

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TCGAACCA SEQ ID NO: 2701	GCCTCCCTCGCGCCATCAGTCGAACCACATGCT SEQ ID NO: 2702
TCGAACGT SEQ ID NO: 2703	GCCTCCCTCGCGCCATCAGTCGAACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2704
TCGAAGCT SEQ ID NO: 2705	GCCTCCCTCGCGCCATCAGTCGAAGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2706
TCGAAGGA SEQ ID NO: 2707	GCCTCCCTCGCGCCATCAGTCGAAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2708
TCGACAAC SEQ ID NO: 2709	GCCTCCCTCGCGCCATCAGTCGACAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2710
TCGACATG SEQ ID NO: 2711	GCCTCCCTCGCGCCATCAGTCGACATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2712
TCGACTAG SEQ ID NO: 2713	GCCTCCCTCGCGCCATCAGTCGACTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2714
TCGACTTC SEQ ID NO: 2715	GCCTCCCTCGCGCCATCAGTCGACTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2716
TCGAGAAG SEQ ID NO: 2717	GCCTCCCTCGCGCCATCAGTCGAGAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2718
TCGAGATC SEQ ID NO: 2719	GCCTCCCTCGCGCCATCAGTCGAGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2720
TCGAGTAC SEQ ID NO: 2721	GCCTCCCTCGCGCCATCAGTCGAGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2722
TCGAGTTG SEQ ID NO: 2723	GCCTCCCTCGCGCCATCAGTCGAGTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2724
TCGATCCT SEQ ID NO: 2725	GCCTCCCTCGCGCCATCAGTCGATCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2726
TCGATCGA SEQ ID NO: 2727	GCCTCCCTCGCGCCATCAGTCGATCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2728
TCGATGCA SEQ ID NO: 2729	GCCTCCCTCGCGCCATCAGTCGATGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2730
TCGATGGT SEQ ID NO: 2731	GCCTCCCTCGCGCCATCAGTCGATGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2732
TCGTACCT SEQ ID NO: 2733	GCCTCCCTCGCGCCATCAGTCGTACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2734

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TCGTACGA SEQ ID NO: 2735	GCCTCCCTCGCGCCATCAGTCGTACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2736
TCGTAGCA SEQ ID NO: 2737	GCCTCCCTCGCGCCATCAGTCGTAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2738
TCGTAGGT SEQ ID NO: 2739	GCCTCCCTCGCGCCATCAGTCGTAGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2740
TCGTCAAG SEQ ID NO: 2741	GCCTCCCTCGCGCCATCAGTCGTCAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2742
TCGTATC SEQ ID NO: 2743	GCCTCCCTCGCGCCATCAGTCGTATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2744
TCGTCTAC SEQ ID NO: 2745	GCCTCCCTCGCGCCATCAGTCGTCTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2746
TCGTCTTG SEQ ID NO: 2747	GCCTCCCTCGCGCCATCAGTCGTCTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2748
TCGTGAAC SEQ ID NO: 2749	GCCTCCCTCGCGCCATCAGTCGTGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2750
TCGTGATG SEQ ID NO: 2751	GCCTCCCTCGCGCCATCAGTCGTGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2752
TCGTGTAG SEQ ID NO: 2753	GCCTCCCTCGCGCCATCAGTCGTGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2754
TCGTGTTT SEQ ID NO: 2755	GCCTCCCTCGCGCCATCAGTCGTGTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2756
TCGTGCCA SEQ ID NO: 2757	GCCTCCCTCGCGCCATCAGTCGTTCCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2758
TCGTTCGT SEQ ID NO: 2759	GCCTCCCTCGCGCCATCAGTCGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2760
TCGTTGCT SEQ ID NO: 2761	GCCTCCCTCGCGCCATCAGTCGTTGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2762
TCGTTGGA SEQ ID NO: 2763	GCCTCCCTCGCGCCATCAGTCGTTGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2764
TCTCACAC SEQ ID NO: 2765	GCCTCCCTCGCGCCATCAGTCTCACACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2766
TCTCACTG SEQ ID NO: 2767	GCCTCCCTCGCGCCATCAGTCTCACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2768

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TCTCAGAG SEQ ID NO: 2769	GCCTCCCTCGCGCCATCAGTCTCAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2770
TCTCAGTC SEQ ID NO: 2771	GCCTCCCTCGCGCCATCAGTCTCAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2772
TCTCCACA SEQ ID NO: 2773	GCCTCCCTCGCGCCATCAGTCTCCACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2774
TCTCCAGT SEQ ID NO: 2775	GCCTCCCTCGCGCCATCAGTCTCCAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2776
TCTCCTCT SEQ ID NO: 2777	GCCTCCCTCGCGCCATCAGTCTCCTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2778
TCTCCTGA SEQ ID NO: 2779	GCCTCCCTCGCGCCATCAGTCTCCTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2780
TCTCGACT SEQ ID NO: 2781	GCCTCCCTCGCGCCATCAGTCTCGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2782
TCTCGAGA SEQ ID NO: 2783	GCCTCCCTCGCGCCATCAGTCTCGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2784
TCTCGTCA SEQ ID NO: 2785	GCCTCCCTCGCGCCATCAGTCTCGTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2786
TCTCGTGT SEQ ID NO: 2787	GCCTCCCTCGCGCCATCAGTCTCGTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2788
TCTCTCAG SEQ ID NO: 2789	GCCTCCCTCGCGCCATCAGTCTCTCAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2790
TCTCTCTC SEQ ID NO: 2791	GCCTCCCTCGCGCCATCAGTCTCTCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2792
TCTCTGAC SEQ ID NO: 2793	GCCTCCCTCGCGCCATCAGTCTCTGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2794
TCTCTGTG SEQ ID NO: 2795	GCCTCCCTCGCGCCATCAGTCTCTGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2796
TCTGACAG SEQ ID NO: 2797	GCCTCCCTCGCGCCATCAGTCTGACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2798
TCTGACTC SEQ ID NO: 2799	GCCTCCCTCGCGCCATCAGTCTGACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2800
TCTGAGAC SEQ ID NO: 2801	GCCTCCCTCGCGCCATCAGTCTGAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2802

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TCTGAGTG SEQ ID NO: 2803	GCCTCCCTCGCGCCATCAGTCTGAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2804
TCTGCACT SEQ ID NO: 2805	GCCTCCCTCGCGCCATCAGTCTGCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2806
TCTGCAGA SEQ ID NO: 2807	GCCTCCCTCGCGCCATCAGTCTGCAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2808
TCTGCTCA SEQ ID NO: 2809	GCCTCCCTCGCGCCATCAGTCTGCTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2810
TCTGTGT SEQ ID NO: 2811	GCCTCCCTCGCGCCATCAGTCTGTGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2812
TCTGGACA SEQ ID NO: 2813	GCCTCCCTCGCGCCATCAGTCTGGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2814
TCTGGAGT SEQ ID NO: 2815	GCCTCCCTCGCGCCATCAGTCTGGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2816
TCTGGTCT SEQ ID NO: 2817	GCCTCCCTCGCGCCATCAGTCTGGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2818
TCTGGTGA SEQ ID NO: 2819	GCCTCCCTCGCGCCATCAGTCTGGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2820
TCTGTAC SEQ ID NO: 2821	GCCTCCCTCGCGCCATCAGTCTGTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2822
TCTGTCTG SEQ ID NO: 2823	GCCTCCCTCGCGCCATCAGTCTGTCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2824
TCTGTGAG SEQ ID NO: 2825	GCCTCCCTCGCGCCATCAGTCTGTGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2826
TCTGTGTC SEQ ID NO: 2827	GCCTCCCTCGCGCCATCAGTCTGTGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2828
TGACACAC SEQ ID NO: 2829	GCCTCCCTCGCGCCATCAGTGACACACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2830
TGACACTG SEQ ID NO: 2831	GCCTCCCTCGCGCCATCAGTGACACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2832
TGACAGAG SEQ ID NO: 2833	GCCTCCCTCGCGCCATCAGTGACAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2834
TGACAGTC SEQ ID NO: 2835	GCCTCCCTCGCGCCATCAGTGACAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2836

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TGACCACA SEQ ID NO: 2837	GCCTCCCTCGCGCCATCAGTGACCACACATGCT SEQ ID NO: 2838
TGACCAGT SEQ ID NO: 2839	GCCTCCCTCGCGCCATCAGTGACCAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2840
TGACCTCT SEQ ID NO: 2841	GCCTCCCTCGCGCCATCAGTGACCTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2842
TGACCTGA SEQ ID NO: 2843	GCCTCCCTCGCGCCATCAGTGACCTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2844
TGACGACT SEQ ID NO: 2845	GCCTCCCTCGCGCCATCAGTGACGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2846
TGACGAGA SEQ ID NO: 2847	GCCTCCCTCGCGCCATCAGTGACGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2848
TGACGTCA SEQ ID NO: 2849	GCCTCCCTCGCGCCATCAGTGACGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2850
TGACGTGT SEQ ID NO: 2851	GCCTCCCTCGCGCCATCAGTGACGTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2852
TGACTCAG SEQ ID NO: 2853	GCCTCCCTCGCGCCATCAGTGACTCAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2854
TGACTCTC SEQ ID NO: 2855	GCCTCCCTCGCGCCATCAGTGACTCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2856
TGACTGAC SEQ ID NO: 2857	GCCTCCCTCGCGCCATCAGTGACTGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2858
TGACTGTG SEQ ID NO: 2859	GCCTCCCTCGCGCCATCAGTGACTGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2860
TGAGACAG SEQ ID NO: 2861	GCCTCCCTCGCGCCATCAGTGAGACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2862
TGAGACTC SEQ ID NO: 2863	GCCTCCCTCGCGCCATCAGTGAGACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2864
TGAGAGAC SEQ ID NO: 2865	GCCTCCCTCGCGCCATCAGTGAGAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2866
TGAGAGTG SEQ ID NO: 2867	GCCTCCCTCGCGCCATCAGTGAGAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2868
TGAGCACT SEQ ID NO: 2869	GCCTCCCTCGCGCCATCAGTGAGCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2870

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TGAGCAGA SEQ ID NO: 2871	GCCTCCCTCGCGCCATCAGTGAGCAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2872
TGAGCTCA SEQ ID NO: 2873	GCCTCCCTCGCGCCATCAGTGAGCTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2874
TGAGCTGT SEQ ID NO: 2875	GCCTCCCTCGCGCCATCAGTGAGCTGTCTATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2876
TGAGGACA SEQ ID NO: 2877	GCCTCCCTCGCGCCATCAGTGAGGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2878
TGAGGAGT SEQ ID NO: 2879	GCCTCCCTCGCGCCATCAGTGAGGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2880
TGAGGTCT SEQ ID NO: 2881	GCCTCCCTCGCGCCATCAGTGAGGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2882
TGAGGTGA SEQ ID NO: 2883	GCCTCCCTCGCGCCATCAGTGAGGTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2884
TGAGTCAC SEQ ID NO: 2885	GCCTCCCTCGCGCCATCAGTGAGTCACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2886
TGAGTCTG SEQ ID NO: 2887	GCCTCCCTCGCGCCATCAGTGAGTCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2888
TGAGTGAG SEQ ID NO: 2889	GCCTCCCTCGCGCCATCAGTGAGTGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2890
TGAGTGTC SEQ ID NO: 2891	GCCTCCCTCGCGCCATCAGTGAGTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2892
TGCAACCA SEQ ID NO: 2893	GCCTCCCTCGCGCCATCAGTGCAACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2894
TGCAACGT SEQ ID NO: 2895	GCCTCCCTCGCGCCATCAGTGCAACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2896
TGCAAGCT SEQ ID NO: 2897	GCCTCCCTCGCGCCATCAGTGCAAGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2898
TGCAAGGA SEQ ID NO: 2899	GCCTCCCTCGCGCCATCAGTGCAAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2900
TGCACAAC SEQ ID NO: 2901	GCCTCCCTCGCGCCATCAGTGCAACAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2902
TGCACATG SEQ ID NO: 2903	GCCTCCCTCGCGCCATCAGTGACATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2904

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TGCACTAG SEQ ID NO: 2905	GCCTCCCTCGCGCCATCAGTGCACTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2906
TGCACTTC SEQ ID NO: 2907	GCCTCCCTCGCGCCATCAGTGCACTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2908
TGCAGAAG SEQ ID NO: 2909	GCCTCCCTCGCGCCATCAGTGCAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2910
TGCAGATC SEQ ID NO: 2911	GCCTCCCTCGCGCCATCAGTGCAATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2912
TGCAGTAC SEQ ID NO: 2913	GCCTCCCTCGCGCCATCAGTGCAATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2914
TGCAGTTG SEQ ID NO: 2915	GCCTCCCTCGCGCCATCAGTGCAATTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2916
TGCATCCT SEQ ID NO: 2917	GCCTCCCTCGCGCCATCAGTGCAATCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2918
TGCATCGA SEQ ID NO: 2919	GCCTCCCTCGCGCCATCAGTGCAATCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2920
TGCATGCA SEQ ID NO: 2921	GCCTCCCTCGCGCCATCAGTGCAATGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2922
TGCATGGT SEQ ID NO: 2923	GCCTCCCTCGCGCCATCAGTGCAATGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2924
TGCTACCT SEQ ID NO: 2925	GCCTCCCTCGCGCCATCAGTGCTACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2926
TGCTACGA SEQ ID NO: 2927	GCCTCCCTCGCGCCATCAGTGCTACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2928
TGCTAGCA SEQ ID NO: 2929	GCCTCCCTCGCGCCATCAGTGCTAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2930
TGCTAGGT SEQ ID NO: 2931	GCCTCCCTCGCGCCATCAGTGCTAGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2932
TGCTCAAG SEQ ID NO: 2933	GCCTCCCTCGCGCCATCAGTGCTCAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2934
TGCTCATC SEQ ID NO: 2935	GCCTCCCTCGCGCCATCAGTGCTCATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2936
TGCTCTAC SEQ ID NO: 2937	GCCTCCCTCGCGCCATCAGTGCTCTACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2938

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TGCTCTTG SEQ ID NO: 2939	GCCTCCCTCGCGCCATCAGTGCTCTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2940
TGCTGAAC SEQ ID NO: 2941	GCCTCCCTCGCGCCATCAGTGCTGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2942
TGCTGATG SEQ ID NO: 2943	GCCTCCCTCGCGCCATCAGTGCTGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2944
TGCTGTAG SEQ ID NO: 2945	GCCTCCCTCGCGCCATCAGTGCTGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2946
TGCTGTTT SEQ ID NO: 2947	GCCTCCCTCGCGCCATCAGTGCTGTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2948
TGCTTCCA SEQ ID NO: 2949	GCCTCCCTCGCGCCATCAGTGCTTCCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2950
TGCTTCGT SEQ ID NO: 2951	GCCTCCCTCGCGCCATCAGTGCTTCGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2952
TGCTTGCT SEQ ID NO: 2953	GCCTCCCTCGCGCCATCAGTGCTTGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2954
TGCTTGGA SEQ ID NO: 2955	GCCTCCCTCGCGCCATCAGTGCTTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2956
TGGAACCT SEQ ID NO: 2957	GCCTCCCTCGCGCCATCAGTGGAACCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2958
TGGAACGA SEQ ID NO: 2959	GCCTCCCTCGCGCCATCAGTGGAACGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2960
TGGAAGCA SEQ ID NO: 2961	GCCTCCCTCGCGCCATCAGTGGAAGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2962
TGGAAGGT SEQ ID NO: 2963	GCCTCCCTCGCGCCATCAGTGGAAGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2964
TGGAACAAG SEQ ID NO: 2965	GCCTCCCTCGCGCCATCAGTGGAACAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2966
TGGAACATC SEQ ID NO: 2967	GCCTCCCTCGCGCCATCAGTGGAACATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2968
TGGAATAC SEQ ID NO: 2969	GCCTCCCTCGCGCCATCAGTGGAATACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2970
TGGAATTG SEQ ID NO: 2971	GCCTCCCTCGCGCCATCAGTGGAATTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2972

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TGGAGAAC SEQ ID NO: 2973	GCCTCCCTCGCGCCATCAGTGGAGAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2974
TGGAGATG SEQ ID NO: 2975	GCCTCCCTCGCGCCATCAGTGGAGATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2976
TGGAGTAG SEQ ID NO: 2977	GCCTCCCTCGCGCCATCAGTGGAGTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2978
TGGAGTTC SEQ ID NO: 2979	GCCTCCCTCGCGCCATCAGTGGAGTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2980
TGGATCCA SEQ ID NO: 2981	GCCTCCCTCGCGCCATCAGTGGATCCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2982
TGGATCGT SEQ ID NO: 2983	GCCTCCCTCGCGCCATCAGTGGATCGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2984
TGGATGCT SEQ ID NO: 2985	GCCTCCCTCGCGCCATCAGTGGATGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2986
TGGATGGA SEQ ID NO: 2987	GCCTCCCTCGCGCCATCAGTGGATGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2988
TGGTACCA SEQ ID NO: 2989	GCCTCCCTCGCGCCATCAGTGGTACCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2990
TGGTACGT SEQ ID NO: 2991	GCCTCCCTCGCGCCATCAGTGGTACGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2992
TGGTAGCT SEQ ID NO: 2993	GCCTCCCTCGCGCCATCAGTGGTAGCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2994
TGGTAGGA SEQ ID NO: 2995	GCCTCCCTCGCGCCATCAGTGGTAGGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2996
TGGTCAAC SEQ ID NO: 2997	GCCTCCCTCGCGCCATCAGTGGTCAACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 2998
TGGTCATG SEQ ID NO: 2999	GCCTCCCTCGCGCCATCAGTGGTCATGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3000
TGGTCTAG SEQ ID NO: 3001	GCCTCCCTCGCGCCATCAGTGGTCTAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3002
TGGTCTTC SEQ ID NO: 3003	GCCTCCCTCGCGCCATCAGTGGTCTTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3004
TGGTGAAG SEQ ID NO: 3005	GCCTCCCTCGCGCCATCAGTGGTGAAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3006

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TGGTGATC SEQ ID NO: 3007	GCCTCCCTCGCGCCATCAGTGGTGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3008
TGGTGATC SEQ ID NO: 3009	GCCTCCCTCGCGCCATCAGTGGTGATCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3010
TGGTGTTG SEQ ID NO: 3011	GCCTCCCTCGCGCCATCAGTGGTGTTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3012
TGGTTCCT SEQ ID NO: 3013	GCCTCCCTCGCGCCATCAGTGGTTCCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3014
TGGTTCGA SEQ ID NO: 3015	GCCTCCCTCGCGCCATCAGTGGTTCGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3016
TGGTTGCA SEQ ID NO: 3017	GCCTCCCTCGCGCCATCAGTGGTTGCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3018
TGGTTGGT SEQ ID NO: 3019	GCCTCCCTCGCGCCATCAGTGGTTGGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3020
TGTCACAG SEQ ID NO: 3021	GCCTCCCTCGCGCCATCAGTGTCACAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3022
TGTCACTC SEQ ID NO: 3023	GCCTCCCTCGCGCCATCAGTGTCACTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3024
TGTCAGAC SEQ ID NO: 3025	GCCTCCCTCGCGCCATCAGTGTCAGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3026
TGTCAGTG SEQ ID NO: 3027	GCCTCCCTCGCGCCATCAGTGTCAGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3028
TGTCCACT SEQ ID NO: 3029	GCCTCCCTCGCGCCATCAGTGTTCCACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3030
TGTCCAGA SEQ ID NO: 3031	GCCTCCCTCGCGCCATCAGTGTTCCAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3032
TGTCCTCA SEQ ID NO: 3033	GCCTCCCTCGCGCCATCAGTGTCCTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3034
TGTCCTGT SEQ ID NO: 3035	GCCTCCCTCGCGCCATCAGTGTCCTGTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3036
TGTCGACA SEQ ID NO: 3037	GCCTCCCTCGCGCCATCAGTGTCGACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3038
TGTCGAGT SEQ ID NO: 3039	GCCTCCCTCGCGCCATCAGTGTCGAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3040

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TGTCGTCT SEQ ID NO: 3041	GCCTCCCTCGCGCCATCAGTGTCTCATGCT SEQ ID NO: 3042
TGTCGTGA SEQ ID NO: 3043	GCCTCCCTCGCGCCATCAGTGTCTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3044
TGTCTCAC SEQ ID NO: 3045	GCCTCCCTCGCGCCATCAGTGTCTCACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3046
TGTCTCTG SEQ ID NO: 3047	GCCTCCCTCGCGCCATCAGTGTCTCTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3048
TGTCTGAG SEQ ID NO: 3049	GCCTCCCTCGCGCCATCAGTGTCTGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3050
TGTCTGTC SEQ ID NO: 3051	GCCTCCCTCGCGCCATCAGTGTCTGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3052
TGTGACAC SEQ ID NO: 3053	GCCTCCCTCGCGCCATCAGTGTGACACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3054
TGTGACTG SEQ ID NO: 3055	GCCTCCCTCGCGCCATCAGTGTGACTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3056
TGTGAGAG SEQ ID NO: 3057	GCCTCCCTCGCGCCATCAGTGTGAGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3058
TGTGAGTC SEQ ID NO: 3059	GCCTCCCTCGCGCCATCAGTGTGAGTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3060
TGTGCACA SEQ ID NO: 3061	GCCTCCCTCGCGCCATCAGTGTGCACACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3062
TGTGCAGT SEQ ID NO: 3063	GCCTCCCTCGCGCCATCAGTGTGCAGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3064
TGTGCTCT SEQ ID NO: 3065	GCCTCCCTCGCGCCATCAGTGTGCTCTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3066
TGTGCTGA SEQ ID NO: 3067	GCCTCCCTCGCGCCATCAGTGTGCTGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3068
TGTGGACT SEQ ID NO: 3069	GCCTCCCTCGCGCCATCAGTGTGGACTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3070
TGTGGAGA SEQ ID NO: 3071	GCCTCCCTCGCGCCATCAGTGTGGAGACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3072
TGTGGTCA SEQ ID NO: 3073	GCCTCCCTCGCGCCATCAGTGTGGTCACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3074

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TGTGGTGT SEQ ID NO: 3075	GCCTCCCTCGCGCCATCAGTGTGGTGTGTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3076
TGTGTGAG SEQ ID NO: 3077	GCCTCCCTCGCGCCATCAGTGTGTGAGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3078
TGTGTCTC SEQ ID NO: 3079	GCCTCCCTCGCGCCATCAGTGTGTCTCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3080
TGTGTGAC SEQ ID NO: 3081	GCCTCCCTCGCGCCATCAGTGTGTGACCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3082
TGTGTGTG SEQ ID NO: 3083	GCCTCCCTCGCGCCATCAGTGTGTGTGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3084
TTAACCGG SEQ ID NO: 3085	GCCTCCCTCGCGCCATCAGTTAACCGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3086
TTAACGCG SEQ ID NO: 3087	GCCTCCCTCGCGCCATCAGTTAACGCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3088
TTAACGGC SEQ ID NO: 3089	GCCTCCCTCGCGCCATCAGTTAACGGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3090
TTAAGCCG SEQ ID NO: 3091	GCCTCCCTCGCGCCATCAGTTAAGCCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3092
TTAAGCGC SEQ ID NO: 3093	GCCTCCCTCGCGCCATCAGTTAAGCGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3094
TTAAGGCC SEQ ID NO: 3095	GCCTCCCTCGCGCCATCAGTTAAGGCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3096
TTATCCGC SEQ ID NO: 3097	GCCTCCCTCGCGCCATCAGTTATCCGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3098
TTATCGCC SEQ ID NO: 3099	GCCTCCCTCGCGCCATCAGTTATCGCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3100
TTATGCGG SEQ ID NO: 3101	GCCTCCCTCGCGCCATCAGTTATGCGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3102
TTATGGCG SEQ ID NO: 3103	GCCTCCCTCGCGCCATCAGTTATGGCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3104
TTCCAACC SEQ ID NO: 3105	GCCTCCCTCGCGCCATCAGTTCCAACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3106
TTCCAAGG SEQ ID NO: 3107	GCCTCCCTCGCGCCATCAGTTCCAAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3108

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TTCCATCG SEQ ID NO: 3109	GCCTCCCTCGCGCCATCAGTTCCATCGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3110
TTCCATGC SEQ ID NO: 3111	GCCTCCCTCGCGCCATCAGTTCCATGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3112
TTCCGCAT SEQ ID NO: 3113	GCCTCCCTCGCGCCATCAGTTCCGCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3114
TTCCGCTA SEQ ID NO: 3115	GCCTCCCTCGCGCCATCAGTTCCGCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3116
TTCCGGAA SEQ ID NO: 3117	GCCTCCCTCGCGCCATCAGTTCCGGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3118
TTCCGGTT SEQ ID NO: 3119	GCCTCCCTCGCGCCATCAGTTCCGGTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3120
TTCTACG SEQ ID NO: 3121	GCCTCCCTCGCGCCATCAGTTCTACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3122
TTCTAGC SEQ ID NO: 3123	GCCTCCCTCGCGCCATCAGTTCTAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3124
TTCTTCC SEQ ID NO: 3125	GCCTCCCTCGCGCCATCAGTTCTTCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3126
TTCTTGG SEQ ID NO: 3127	GCCTCCCTCGCGCCATCAGTTCTTGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3128
TTGAAACG SEQ ID NO: 3129	GCCTCCCTCGCGCCATCAGTTTGAACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3130
TTGAAGC SEQ ID NO: 3131	GCCTCCCTCGCGCCATCAGTTTGAAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3132
TTGATCC SEQ ID NO: 3133	GCCTCCCTCGCGCCATCAGTTTGATCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3134
TTGATGG SEQ ID NO: 3135	GCCTCCCTCGCGCCATCAGTTTGATGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3136
TTGCCAT SEQ ID NO: 3137	GCCTCCCTCGCGCCATCAGTTTGCCATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3138
TTGCCTA SEQ ID NO: 3139	GCCTCCCTCGCGCCATCAGTTGCCTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3140
TTGCGAA SEQ ID NO: 3141	GCCTCCCTCGCGCCATCAGTTGCGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3142

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TTCGCGTT SEQ ID NO: 3143	GCCTCCCTCGCGCCATCAGTTTCGCGTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3144
TTCGGCAA SEQ ID NO: 3145	GCCTCCCTCGCGCCATCAGTTTCGGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3146
TTCGGCTT SEQ ID NO: 3147	GCCTCCCTCGCGCCATCAGTTTCGGCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3148
TTCGTACC SEQ ID NO: 3149	GCCTCCCTCGCGCCATCAGTTTCGTACCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3140
TTCGTAGG SEQ ID NO: 3141	GCCTCCCTCGCGCCATCAGTTTCGTAGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3142
TTCGTTCG SEQ ID NO: 3143	GCCTCCCTCGCGCCATCAGTTTCGTTTCGATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3144
TTCGTTGC SEQ ID NO: 3145	GCCTCCCTCGCGCCATCAGTTTCGTTGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3146
TTGCAACG SEQ ID NO: 3147	GCCTCCCTCGCGCCATCAGTTTGCAACGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3148
TTGAAGC SEQ ID NO: 3149	GCCTCCCTCGCGCCATCAGTTTGCAAGCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3150
TTGCATCC SEQ ID NO: 3151	GCCTCCCTCGCGCCATCAGTTTGATCCCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3152
TTGCATGG SEQ ID NO: 3153	GCCTCCCTCGCGCCATCAGTTTGATGGCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3154
TTGCCGAA SEQ ID NO: 3155	GCCTCCCTCGCGCCATCAGTTTGCCGAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3156
TTGCCGTT SEQ ID NO: 3157	GCCTCCCTCGCGCCATCAGTTTGCCGTTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3158
TTGCGCAA SEQ ID NO: 3159	GCCTCCCTCGCGCCATCAGTTTGCGCAACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3160
TTGCGCTT SEQ ID NO: 3161	GCCTCCCTCGCGCCATCAGTTTGCGCTTCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3162
TTGCGGAT SEQ ID NO: 3163	GCCTCCCTCGCGCCATCAGTTTGCGGATCATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3164
TTGCGGTA SEQ ID NO: 3165	GCCTCCCTCGCGCCATCAGTTTGCGGTACATGCT GCCTCCCGTAGGAGT SEQ ID NO: 3166

TABLE 1-continued

Representative 8-Nucleotide Base Error-Correcting Barcodes And Representative Primer Sequence	
Barcode	Primer
TTGCTACC SEQ ID NO: 3167	GCCTCCCTCGCGCCATCAGTTGCTACCCATGCT SEQ ID NO: 3168
TTGCTAGG SEQ ID NO: 3169	GCCTCCCTCGCGCCATCAGTTGCTAGGCATGCT SEQ ID NO: 3170
TTGCTTCG SEQ ID NO: 3171	GCCTCCCTCGCGCCATCAGTTGCTTCGCATGCT SEQ ID NO: 3172
TTGCTTGC SEQ ID NO: 3173	GCCTCCCTCGCGCCATCAGTTGCTTGCCATGCT SEQ ID NO: 3174
TTGGAACC SEQ ID NO: 3175	GCCTCCCTCGCGCCATCAGTTGGAACCCATGCT SEQ ID NO: 3176
TTGGAAGG SEQ ID NO: 3177	GCCTCCCTCGCGCCATCAGTTGGAAGGCATGCT SEQ ID NO: 3178
TTGGATCG SEQ ID NO: 3179	GCCTCCCTCGCGCCATCAGTTGGATCGCATGCT SEQ ID NO: 3180
TTGGATGC SEQ ID NO: 3181	GCCTCCCTCGCGCCATCAGTTGGATGCCATGCT SEQ ID NO: 3182
TTGGCCAA SEQ ID NO: 3183	GCCTCCCTCGCGCCATCAGTTGGCCAAATGCT SEQ ID NO: 3184
TTGGCCTT SEQ ID NO: 3185	GCCTCCCTCGCGCCATCAGTTGGCCTTCATGCT SEQ ID NO: 3186
TTGGCGAT SEQ ID NO: 3187	GCCTCCCTCGCGCCATCAGTTGGCGATCATGCT SEQ ID NO: 3188
TTGGCGTA SEQ ID NO: 3189	GCCTCCCTCGCGCCATCAGTTGGCGTACATGCT SEQ ID NO: 3190
TTGGTACG SEQ ID NO: 3191	GCCTCCCTCGCGCCATCAGTTGGTACGCATGCT SEQ ID NO: 3192
TTGGTAGC SEQ ID NO: 3193	GCCTCCCTCGCGCCATCAGTTGGTAGCCATGCT SEQ ID NO: 3194
TTGGTTCC SEQ ID NO: 3195	GCCTCCCTCGCGCCATCAGTTGGTTCCCATGCT SEQ ID NO: 3196
TTGGTTGG SEQ ID NO: 3197	GCCTCCCTCGCGCCATCAGTTGGTTGGCATGCT SEQ ID NO: 3198

In some embodiments, the present invention contemplates a method comprising filtering a set of 8 nucleotide base barcodes, and using the filtered barcodes for optimizing PCR and sequencing performance. In one embodiment, the filtering

comprises selecting a barcode comprising a GC content of between approximately 40-60%. In one embodiment, the filtering comprises selecting a barcode lacking consecutive triple repeats of the same base (i.e., for example, AAA, TTT, GGG, CCC). In one embodiment, the filtering comprises selecting a barcode lacking perfect self-complementarity or complementarity between the 8-base barcode and the primer. Decoding was performed using a Python translation of an existing C implementation of Hamming codes. R H Morelos-Zaragoza, *The Art of Error-Correcting Coding*. (John Wiley & Sons, Hoboken, N.J., 2006); and Example II.

[0111] A. Barcode Validation

[0112] Utility of some embodiments of the present invention may be illustrated by determining the bacterial composition of 286 environmental samples by PCR amplifying, sequencing, and analyzing 681,688 16S rRNA gene sequences from a single sequencing run of the Genome Sequencer FLX (454 Life Sciences, Branford, Conn.). In one particular embodiment, 286 of the 1,544 candidate codewords were used to synthesize barcoded PCR primers to use in PCR reactions amplifying a region (27F-338R) of the 16S rRNA gene that were previously determined to be a suitable region of the 16S rRNA to use for phylogenetic analysis from pyrosequencing reads. Wu et al., "Quantitative multiplexing analysis of PCR-amplified ribosomal RNA genes by hierarchical oligonucleotide primer extension reaction" *Nucleic Acids Res.* 35(11):e82 (2007).

[0113] To test these barcodes a set of 1,544 barcodes from the 2,048 possible combinations was chosen based on a nucleotide-encoding scheme that provides the largest number of valid "candidate" barcodes, and then those results were filtered based on optimal PCR and sequencing performance criteria. 286 of the 1,544 candidate barcodes were incorporated into PCR primers that were then used to amplify a region of the bacterial 16S rRNA gene in 286 separate environmental samples. Purified PCR products from each of the 286 samples were then quantified and added to a master DNA pool in equimolar ratios prior to pyrosequencing. Each of the resulting 437,544 sequences was assigned to a sample based on its barcode, aligned based on operational taxonomic units (OTUs) at 96% identity, assembled into a phylogenetic tree and clustered based on similarities in bacterial phylogenetic diversity. The results of this clustering correlated perfectly with sample type—all lung samples clustered together, as did all North American river samples, two African river samples, the microbial mat sample, air samples and hot spring samples. See, FIGS. 2 and 3. These results demonstrate that the tagged barcoding system allows phylogenetic analysis of microbial communities from hundreds of samples in a single sequencing run.

[0114] For each sample, the 16S rRNA gene was amplified using the composite forward primer

(SEQ ID NO: 3199)
5'-GCCTTGCCAGCCCGCTCAGTCAGAGTTTGATCCTGGCTCAG-3':

the underlined sequence is 454 Life Sciences® primer B, and the sequence in italics is the broadly conserved bacterial primer 27F. A two-base linker sequence ('TC') that was not observed in >250,000 aligned 16S rRNA sequences was inserted between the 454 Life Sciences® primer B and 27F to help mitigate any effect the composite primer might have on PCR efficiency. The reverse primer was 5'-GCCTC-CCTCGCGCCATCAGNNNNNNNN-CATGCTGCCTC-

CCGTAGGAGT-3' (SEQ ID NO: 3200): the underlined sequence is 454 Life Sciences® primer A, and the sequence in italics is the broad range bacterial primer 338R. NNNNNNNN designates the unique eight-base barcode used to tag each PCR product, with 'CA' inserted as a linker between the barcode and rRNA primer. Total DNA was extracted from samples of a human lung, river water, a Guerrero Negro microbial mat, particles filtered from air, and hot spring water using a modified bead-beating solvent extraction and amplified by PCR. Dojka et al., *Appl Environ Microbiol* 64 (10), 3869 (1998).

[0115] Briefly, PCR reaction conditions were as follows: 8 µl 2.5X HotMaster PCR Mix (Eppendorf), 0.3 µM each primer, and 10-100 ng template DNA in a total reaction volume of 20 µl. PCR was performed with an Eppendorf Mastercycler: 2 min at 95° C., followed by 30 cycles of 20 s at 95° C. (denaturing), 20 s at 52° C. (annealing) and 60 s at 65° C. (elongation). Four independent PCR reactions were performed for each sample, along with a no template (water) negative control. For each of 286 samples, the four replicate PCR reactions were combined, purified with Ampure magnetic purification beads (Agencourt), quantified with the Quant-iT PicoGreen dsDNA Assay Kit (Invitrogen) and a fluorospectrometer (Nanodrop ND3300), and combined in equimolar ratios to create a master DNA pool with a final concentration of 21.5 ng/µl, which was sent for pyrosequencing with primer A at 454 Life Sciences (Branford, Conn). Margulies et al., *Nature* 437(7057):376 (2005); Sogin et al., *Proc Natl Acad Sci USA* 103(32): 12115 (2006). After removal of low-quality sequences and trimming of primer sequences, 437,544 sequences remained, each representing between ~240-280 bases of 16S rRNA sequence. The quality determination of each sequencing read was based on criteria previously described. Huse et al., *Genome Biol* 8:R143 (2007). See, Example III.

[0116] Each remaining sequence was assigned to a sample based on the barcodes by:

[0117] i) picking Operational Taxonomic Units (OTUs) at 96% identity;

[0118] ii) aligning one sequence representing each of the 25,351 OTUs with NAST. DeSantis et al., *Nucleic Acids Res* 34(Web Server Issue), W394 (2006). In comparison, a recent study of 202 globally diverse environments identified only 21,752 OTUs at the 97% level. Lozupone et al., *Proc Natl Acad Sci USA* 104(27):11436 (2007).

[0119] iii) building a "relaxed neighborjoining" tree with clearcut. Sheneman et al., *Bioinformatics* 22(22):2823 (2006)., and

[0120] iv) clustering the samples based on their similarities in bacterial phylogenetic diversity with UniFrac Lozupone et al., *BMC Bioinformatics* 7:371 (2006); and Lozupone et al., *Appl Environ Microbiol* 71(12):8228 (2005).

[0121] The clustering correlated perfectly with sample types wherein: i) all lung samples clustered together; ii) all North American river samples clustered together; iii) all microbial mat samples clustered together; iv) all air samples clustered together; v) all hot spring samples clustered together; and both African river water samples clustered together. See, FIG. 2.

[0122] The clustering was further analyzed to identify distributions of different divisions of bacteria in each of in each of the major sample classes. See, FIG. 3. The samples differ from one another, for example, the cystic fibrosis lung

samples are dominated by *Firmicutes* and gamma-Proteobacteria (mostly *Pseudomonas*), whereas the Guerrero Negro microbial mat is dominated by *Bacteroidetes*, *Proteobacteria*, and *Chloroflexi*. The results indicate that the pyrosequencing reads provide data comparable to that obtained by traditional approaches.

[0123] Nineteen DNA samples were analyzed in triplicate with three independent barcode primers, and in each case the replicate samples clustered together in the UniFrac analysis. This suggests that these barcoded primers amplified equivalently in PCR. 1345 sequences (0.3%) had decoding errors, of which 1241 (92.2%) could be corrected to valid barcodes.

[0124] These results directly demonstrated that a tagged barcoding strategy can be used to obtain sequences ranging from approximately the hundreds to approximately the tens of thousands of samples in a single sequencing run. For example, nearly the total number of 16S rRNAs determined to date by Sanger sequencing can be sequenced in a single run using the compositions and methods disclosed herein. Subsequently, a phylogenetic analyses of microbial communities may be performed using the pyrosequencing data.

Experimental

[0125] The foregoing discussion of the invention has been presented for purposes of illustration and description. The foregoing is not intended to limit the invention to the form or forms disclosed herein. Although the description of the invention has included description of one or more embodiments and certain variations and modifications, other variations and modifications are within the scope of the invention, e.g., as may be within the skill and knowledge of those in the art, after understanding the present disclosure. It is intended to obtain rights which include alternative embodiments to the extent permitted, including alternate, interchangeable and/or equivalent structures, functions, ranges or steps to those claimed, whether or not such alternate, interchangeable and/or equivalent structures, functions, ranges or steps are disclosed herein, and without intending to publicly dedicate any patentable subject matter.

Example I

Generation of Error-Correcting Nucleotide Barcodes and Primers

[0126] For each sample, a 16S rRNA gene was amplified using a composite forward primer

(SEQ ID NO: 3199)
5' - GCCTTGCCAGCCCGCTCAGT**CAGAGTTGATCTGGCTCAG** - 3'

wherein the underlined sequence is 454 Life Sciences® primer B, and the bold sequence is the broadly conserved bacterial primer 27F.

[0127] Next, a two-base linker sequence ('TC') was inserted that was not observed in >250,000 aligned 16S rRNA sequences between the 454 primer B and 27F to help mitigate any effect the composite primer might have on PCR efficiency.

[0128] The reverse primer was 5'-GCCTCCCTCGCGC-CATCAGNNNNNNNNCA-**TGCTGCCT CCCGTAGGAGT** -3' (SEQ ID NO: 3200) wherein: i) the underlined sequence is 454 Life Sciences' primer A; ii) the bold sequence is the broad-range bacterial primer 338R; iii) the sequence NNNNNNNN designates the unique eight-base barcode used

to tag each PCR product; and iv) 'CA' inserted as a linker between the barcode and rRNA primer.

[0129] The first 286 barcodes identified in Table 1 were used in the collection of data presented herein.

Example II

Barcode Identification Decoding Software

[0130] This example presents exemplary software that enables Hamming coding/decoding for pyrosequencing reads and the associated unit tests. This particular program is a command-line application where command-line access depends on the operating system, for example:

[0131] Macintosh/Apple OS: Utilities/Terminal:

[0132] Microsoft Windows: Start/Run then enter "cmd.exe" in the dialog box:

[0133] Linux: Terminal or Shell.

A Python and Numpy packages, available from python.org and numpy.scipy.org, can be downloaded and installed in order to run this software using the Python and the Numpy extension module.

Example III

Representative PCR Conditions

[0134] PCR reaction conditions were as follows: 8 µl 2.5X HotMaster PCR Mix (Eppendorf), 0.3µM each primer, and 10-100 ng template DNA in a total reaction volume of 20 µl. PCR used an Eppendorf Mastercycler: 120 s at 95° C., followed by 30 cycles of 20 s at 95° C. (denaturing), 20 s at 52° C. (annealing) and 60 s at 65° C. (elongation).

Example IV

Processing 454 Reads

[0135] Sequences were processed as previously described. Huse et al., *Genome Biol* 8(7):R143 (2007). In general, the basic steps included, but were not limited to:

[0136] 1. The read length distribution was examined, and the major peak was identified. Sequences shorter than 237 nt or longer than 283 nt were dropped which were approximately ± 2 standard deviations from the mean of the major peak. This step was performed manually, by inspection of the histogram.

[0137] 2. Dropped reads with an average quality score less than 25.

[0138] 3. Dropped reads that contained any ambiguous characters.

[0139] 4. Split sequence read: first 8 nt provide the barcode ("prefix"). The remainder of the sequence ("suffix") is used for downstream analyses.

[0140] 5. Dropped sequences where the suffix does not start with the linker and primer sequence CATGCTGC-CTCCCGTAGGAGT.

[0141] 6. Checked whether the barcode is present in the list of valid barcodes:

[0142] a. If valid, remap to original sample id, assign unique sequence id to the read.

[0143] b. If not, try to correct barcode using the Hamming decoder software in accordance with Example II.

[0144] i. If corrected, remap to original sample id, assign unique sequence id to the read, and record the position and type of the error.

[0145] ii. If not corrected, drop sequence.

Example V

OTU Picking Algorithm

[0146] OTUs were chosen using the following algorithm:

[0147] 1. Identify similar sequences using megablast₂. Parameters: E-value 1e-8, minimum coverage 99%, minimum pairwise identity 96%.

[0148] 2. Find sets of sequences that are connected to one another using BLAST hits at this level.

[0149] 3. Choose OTUs as follows:

[0150] a. Connected components are candidate OTUs.

[0151] b. The candidate OTU is considered valid if the average density of connections is above 70% (i.e. if 70% of the possible pairwise connections between sequences in the set exist). If the density is lower than this, split up connected component by picking a connected subgraph where the density is above threshold, until no sequences remain in the connected component.

[0152] 4. A representative sequence was chosen from each OTU by selecting the sequence with the largest number of hits to other sequences in the OTU. Ties were broken by choosing one of the longest sequences within the OTU at random.

Example VI

NAST Alignment and Lane Mask

[0153] 1. The representative set of sequences was aligned using NAST₃ with the following parameters:

[0154] a. Minimum alignment length of 200, and 70% sequence identity.

[0155] b. The template used was the "core_set_aligned.fasta.imputed" (i.e., for example, as posted Aug. 11, 2007 on greengenes.lbl.gov/Download/Sequence_Data/Fasta_data_files/.

[0156] 2. The file PH_lanemask, as posted Jul. 18, 2007 greengenes.lbl.gov/Download/Sequence_Data/lanemask_in_1s_and_0s, was used to screen out hypervariable regions of the sequence.

Example VII

Tree Building and UniFrac Clustering

[0157] 1. A relaxed neighbor-joining tree was built using clearcut₄, using the Kimura correction but otherwise with default comparisons.

[0158] 2. Unweighted UniFrac was run using the resulting tree and the counts of each sequence in each environment. Lozupone et al., *Appl Environ Microbiol* 71(12): 8228 (2005); and Lozupone et al., *BMC Bioinformatics* 7:371 (2006).

Example VIII

Taxonomy Assignment

[0159] Taxonomy was assigned using the best BLAST hit against Greengenes₈, using an E value cutoff of 1e-10, and the Hugenholtz taxonomy. Altschul et al., *J Mol Biol* 215:403 (1990); and DeSantis et al., *Appl Environ Microbiol* 72:5069 (2006).

 SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (<http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20100323348A1>). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What is claimed is:

1. A pyrosequencing compatible primer comprising a first region containing a unique error-detecting/correcting hamming barcode.

2. The pyrosequencing compatible primer of claim 1, wherein the primer further comprises a second region complementary to a bacterial 16S rRNA gene.

3. A method of assigning sequence data to individual samples from a mixture of samples, comprising:

a) providing:

i) a pyrosequencing compatible primer comprising a first region containing a unique error-detecting/correcting barcode and a second region complementary to a target nucleic acid molecule, and

ii) a target nucleic acid molecule,

b) amplifying said target nucleic acid molecule with said primer,

c) pooling a plurality of said amplification product, and

d) pyrosequencing said pooled amplification products to determine their respective nucleotide sequences.

4. The method of claim 3, wherein said plurality of amplification products are pooled in equimolar ratios.

5. The method of claim 3, wherein said unique error-detecting/correcting barcode is a Hamming code.

6. The method of claim 3, wherein said target nucleic acid molecule comprises a portion of the 16S rRNA gene.

7. The method of claim 3, further comprising identifying amplification products with unique barcode sequence errors.

8. The method of claim 3, further comprising correcting the unique barcode sequence of amplification products containing correctable unique barcode sequence errors.

9. The method of claim 3, further comprising discarding the nucleotide sequence of amplification products containing non-correctable unique barcode sequence errors.

10. The method of claim 3, further comprising step e) aligning the nucleotide sequences of said amplification products to generate a phylogenetic tree.

11. A method comprising:

a) providing:

i) a plurality of samples comprising nucleic acid sequences;

ii) a plurality of primers error correcting or error-detecting sequence tags wherein said primers are at least partially complementary to said nucleic acid sequences;

iii) a parallel sequencing technique capable of simultaneously characterizing said nucleic acid sequences from said plurality of samples;

b) amplifying said plurality of nucleic acid samples using said plurality of primers; and

c) analyzing said sequence tags of said amplified nucleic acids.

12. The method of claim 11, wherein said sequence tag identifies a sample assignment thereby identifying one of said samples from which said nucleic acid was derived.

13. The method of claim 12, wherein said sequence tag identifies the presence of an error in said nucleic acid, thereby establishing a probability that said sample assignment is incorrect.

14. The method of claim 12, wherein said sequence tag identifies the absence of any error in said nucleic acid, thereby establishing a probability that said sample assignment is correct.

15. The method of claim 11, wherein said sequence technique comprises pyrosequencing.

* * * * *