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**WANG et al.**(10) **Pub. No.: US 2025/0257350 A1**(43) **Pub. Date: Aug. 14, 2025**(54) **INTEGRATIVE DNA AND RNA LIBRARY  
PREPARATIONS AND USES THEREOF**(60) Provisional application No. 62/648,174, filed on Mar.  
26, 2018.(71) Applicant: **QIAGEN Sciences, LLC**, Germantown,  
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**Daniel KIM**, Brunswick, MD (US)(51) **Int. Cl.**  
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CPC ..... **C12N 15/1065** (2013.01); **C12Q 1/6806**  
(2013.01)(21) Appl. No.: **19/006,873**(57) **ABSTRACT**(22) Filed: **Dec. 31, 2024**

The invention relates to integrated DNA and RNA library preparations and methods of making and uses thereof. The methods do not require physical separation of DNA and RNA. The methods output two separate libraries from DNA and RNA, respectively, which helps flexible manipulation on downstream sequencing platform.

**Related U.S. Application Data**(62) Division of application No. 17/041,724, filed on Sep.  
25, 2020, filed as application No. PCT/US2019/  
024107 on Mar. 26, 2019, now Pat. No. 12,215,314.**Specification includes a Sequence Listing.**

1. gDNA and RNA together

2. Enzymatic fragmentation

- DNA fragment, end polish
- RNA fragment

3. RNA Polishing

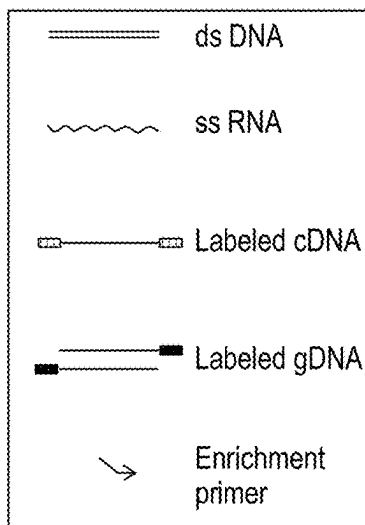
- DNA no change

4. DNA label by ligation

- RNA no change

5. RNA label by TS-RT

- DNA no change

6. Co DNA/RNA target  
enrichment

7. Library amplification

- DNA library by DNA label
- RNA library by RNA label

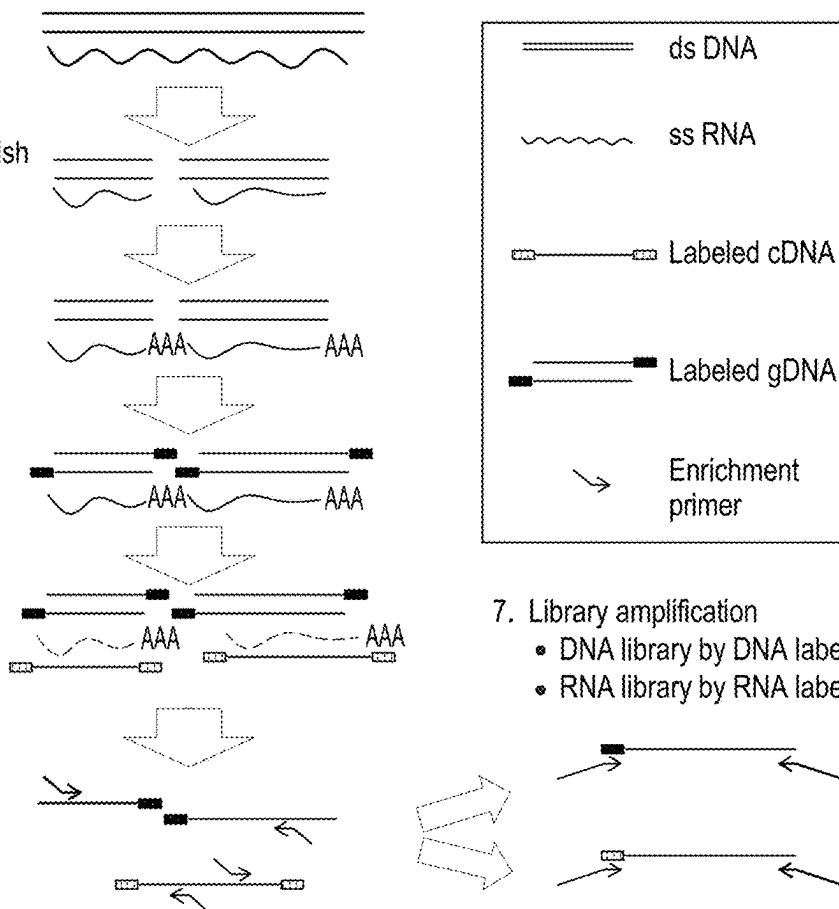
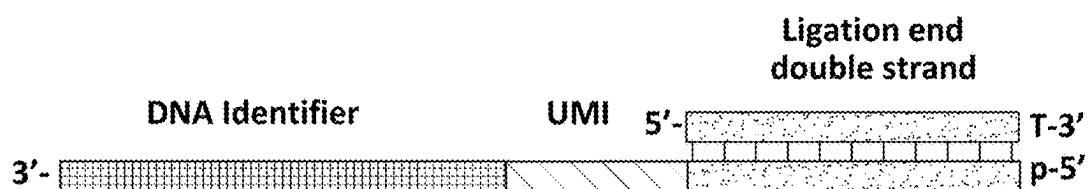
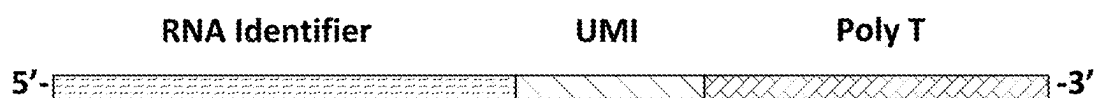


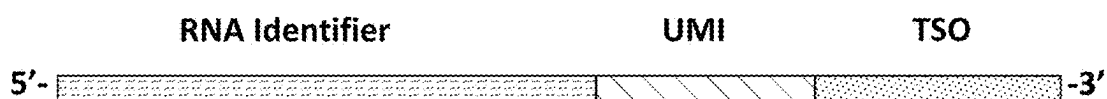
FIG. 1



DNA tag molecule that can be ligated to 3' end of double strand DNA fragments.

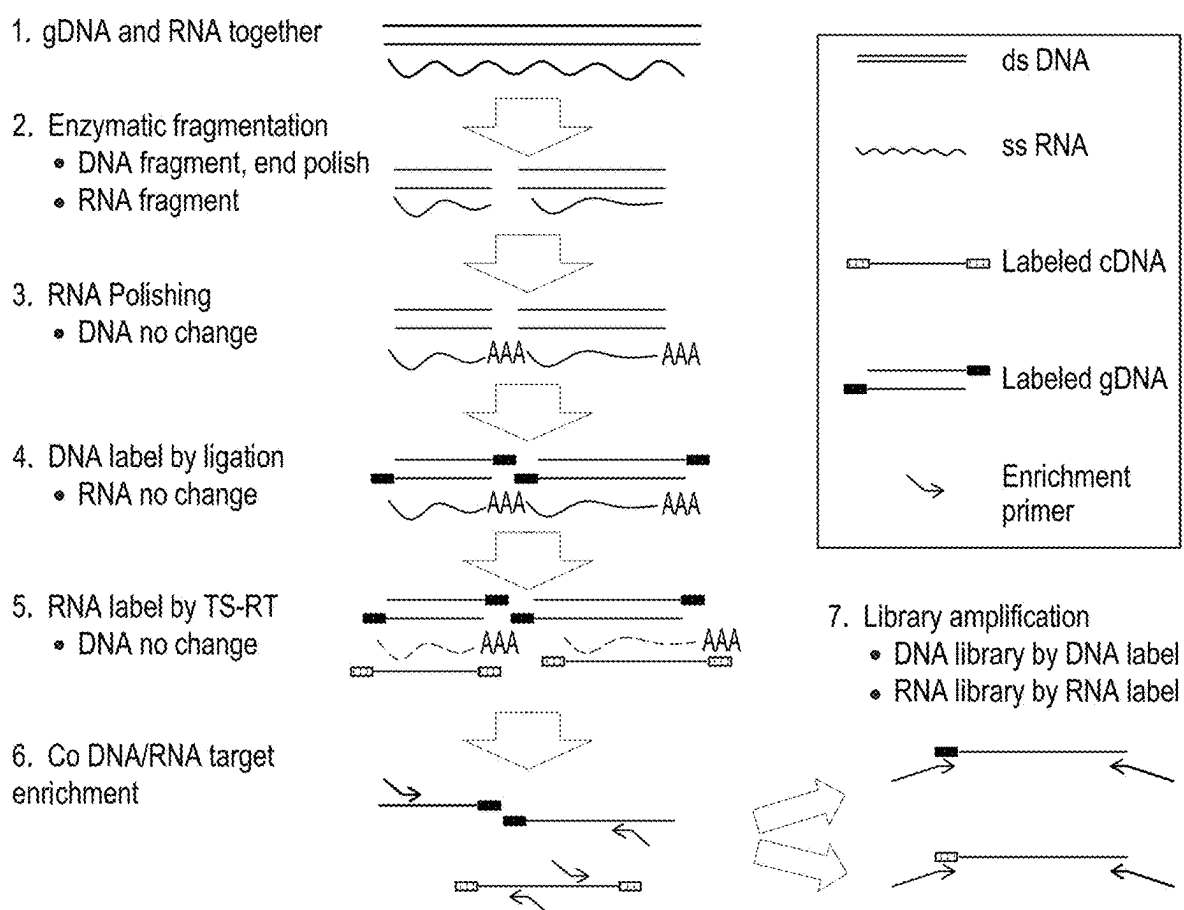


RNA tag molecule that can be used to add a 5' tag to RNA-derived cDNA fragments through reverse transcription.



RNA tag molecule that can be used to add a 3' tag to RNA-derived cDNA through template switching in RT.

FIG. 2



## INTEGRATIVE DNA AND RNA LIBRARY PREPARATIONS AND USES THEREOF

### CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a divisional of U.S. application Ser. No. 17/041,724 (now allowed), which is a 35 U.S.C. § 371 national phase of International Appl. No. PCT/US2019/024107 having an international filing date of Mar. 26, 2019, which claims benefit of U.S. Appl. No. 62/648,174, filed Mar. 26, 2018, the disclosure of each incorporated herein by reference in its entirety.

### REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

[0002] The content of the electronically submitted sequence listing in XML format (Name: 24950002US02SEQL.xml; Size: 585,728 bytes; and Date of Creation: Dec. 30, 2024) filed with this application is incorporated herein by reference in its entirety.

### BACKGROUND OF THE INVENTION

[0003] Paired DNA and RNA profiling enables researchers to gain more biological insights regarding the correlation between genotype and phenotype using samples from the same set of cell population.

[0004] To fully understand complex biological systems, researchers are getting more and more interested in multi-omic information, a full view of genomic, transcriptomic and proteomic data and their interactions. As the first step, paired DNA and RNA profiling are made possible with the advancement of sequencing technology. Traditional approaches, however, usually required preparing DNA and RNA samples in parallel, which meant the data obtained were not necessarily from the same set of cell population. Thus, these separate workflows might yield less correlative DNA and RNA data due to the heterogeneity of the sample. In addition, they added extra time and effort because of doubled workload.

[0005] In order to circumvent the disadvantage of separate workflow, researchers tried to integrate them. DR-seq (Dey S S et al, Nat. Biotechnol. 33: 285-289 (2015)) and G&T-seq (Macaulay I C et al, Nat. Methods. 72:519-22 (2015)) were among the first few attempts of integrative analysis of genomic DNA and mRNA from a single cell. However, these methods were designed specifically for single cell applications.

[0006] Another group developed an integrated DNA and RNA sequencing workflow, named Simul-seq. Reuter J A et al, Nat. Methods 75:953-958 (2016). It is a streamlined approach to profiling whole genome and transcriptome from the same set of cell population. Simul-seq is designed for whole genome and transcriptome sequencing.

[0007] There remains a need for improved, integrated DNA and RNA preparations amenable for sequencing analysis.

### BRIEF SUMMARY OF THE INVENTION

[0008] Disclosed herein are methods for preparing DNA and cDNA libraries from a sample, comprising: ligating a DNA tag to an end of a DNA molecule in a sample, wherein the DNA tag comprises a unique molecular identifier (UMI) and a DNA identifier; and performing reverse transcription

of a RNA molecule in the sample in the presence of a RNA tag, wherein the RNA tag comprises a RNA identifier, a UMI, and a poly(T).

[0009] In some embodiments, the reverse transcription is performed in the presence of a second RNA tag, wherein the second RNA tag comprises a RNA identifier, a UMI, and a template switching oligonucleotide (TSO).

[0010] In some embodiments, the methods further comprise amplifying the tagged DNA and tagged cDNA for enrichment with a set of gene specific primers. In some embodiments, the methods further comprise separating the amplified sample into first and second samples.

[0011] In some embodiments, the DNA and RNA molecules are obtained from a biological sample. In some embodiments, the DNA and RNA molecules are fragmented DNA and RNA from the biological sample.

[0012] In some embodiments, the DNA molecule contains polished ends for ligation. In some embodiments, the RNA molecule is polyadenylated.

[0013] In some embodiments, the methods do not require ribosomal depletion.

[0014] In further embodiments, the methods further comprise further amplifying the first sample with primers specific for the DNA tag. The amplification can generate a DNA library corresponding to the DNA molecules in the sample.

[0015] In further embodiments, the methods further comprise further amplifying the second sample with primers specific for the RNA tag. The amplification generates a cDNA library corresponding to the RNA molecules in a sample.

[0016] In some embodiments, the methods further comprise sequencing the DNA or cDNA library. The DNA library can be used for, but not limited to, DNA variant detection, copy number analysis, fusion gene detection, or structural variant detection. The cDNA library can be used for, but not limited to, RNA variant detection, gene expression analysis, or fusion gene detection. The libraries can be also used for paired DNA and RNA profiling.

[0017] Also disclosed herein are DNA libraries made by the methods disclosed herein. Further disclosed are cDNA libraries made by the methods disclosed herein.

[0018] Also disclosed herein are DNA tags comprising a unique molecular identifier (UMI) and a DNA identifier. In some embodiments, in the DNA tags, the UMI and the DNA identifier can be positioned in a 5' to 3' direction.

[0019] Also disclosed herein are RNA tags comprising a RNA identifier, a UMI, and a poly(T). In some embodiments, in the RNA tags, the RNA identifier, the UMI, and the poly(T) are positioned in a 5' to 3' direction. Also disclosed herein are RNA tags comprising a RNA identifier, a UMI, and a template switching oligonucleotide (TSO). In some embodiments, in the RNA tags, the RNA identifier, the UMI, and the TSO are positioned in a 5' to 3' direction.

[0020] Disclosed herein are compositions comprising at least 2 of the above described tags. Also disclosed herein are compositions comprising the DNA tag and the 2 different RNA tags as described above.

[0021] Further disclosed herein are methods for preparing targeted DNA and cDNA libraries, comprising:

[0022] (a) obtaining purified DNA and RNA from a biological sample;

[0023] (b) fragmenting the DNA and RNA;

[0024] (c) polishing the ends of the double stranded DNA fragments for ligation;

- [0025] (d) polishing the RNA fragments by polyadenylation;
- [0026] (e) ligating a DNA tag to a 3' end of the polished DNA fragments, wherein the DNA tag comprises in a 5' to 3' direction a unique molecular identifier (UMI) and a DNA identifier;
- [0027] (f) performing reverse transcription of the polished RNA fragments in the presence of a first RNA tag, wherein the first RNA tag comprises in a 5' to 3' direction a RNA identifier, a UMI, and a poly(T), and a second RNA tag, wherein the second RNA tag comprises in a 5' to 3' direction a RNA identifier, a UMI, and a template switching oligonucleotide (TSO);
- [0028] (g) amplifying the tagged DNA and tagged cDNA for enrichment with a set of gene specific primers;
- [0029] (h) separating the amplified sample into first and second samples;
- [0030] (i) amplifying the first sample with primers specific for the DNA tag; and
- [0031] (j) amplifying the second sample with primers specific for the RNA tag.

#### BRIEF DESCRIPTION OF THE DRAWINGS/FIGURES

- [0032] FIG. 1. Exemplary DNA and RNA tag molecules.
- [0033] FIG. 2. Exemplary process for generating DNA and cDNA libraries.

#### DETAILED DESCRIPTION OF THE INVENTION

[0034] Disclosed herein are innovative approaches for integrative DNA and cDNA library preparations for analysis, such as by next-generation sequencing (NGS) analysis, without physical separation of DNA and RNA. These approaches integrate UMI (unique molecular index) technology and optionally, targeted enrichment technology, seamlessly into the workflow, which improve utilization of sequencing capacity and accuracy of the results. In addition, these methods output two separate DNA and cDNA libraries from DNA and RNA, respectively, which allow flexible manipulation on downstream sequencing platform. Compared to standalone DNA library and cDNA library methods, these approaches reduce sample consumption, simplify the experimental process, and can help researchers gain biological insights in genotype and phenotype correlations and molecular mechanisms of diseases.

[0035] Methods are described herein to prepare targeted DNA and cDNA libraries without the necessity of physical separation of genomic DNA (gDNA) and mRNA. The process involves three modules: (1) assign different DNA and RNA tag molecules to each individual DNA and RNA fragment, respectively, without separating them in the system; optionally, (2) amplify and enrich a subset of the tagged DNA and RNA fragments (target enrichment); and (3) differentially PCR amplify the tagged DNA and tagged cDNA in the (enriched) product to output two libraries corresponding to the original DNA and RNA, respectively.

[0036] The DNA and RNA tag molecules used in the first module are oligonucleotides comprising at least 1) an identifying sequence to distinguish a DNA library or RNA library, and 2) a UMI sequence for identifying each individual nucleic acid molecule.

[0037] The DNA and RNA tags are essential for the final separation of DNA and cDNA libraries in module 3, where they can serve as specific amplification primer sites for DNA and RNA. The UMI sequence helps improve accuracy for both DNA and RNA NGS analysis. Exemplary tag molecules are illustrated in FIG. 1.

[0038] Two types of RNA tag molecules can be used in order to sequence the single stranded RNA from both directions, and thus, two different mechanisms can be used to attach the RNA specific sequence. Only one type of DNA tag molecule is needed because the DNA tag molecule can be ligated to both ends of the double stranded DNA.

[0039] The targeted enrichment reaction (module 2) enables focused view on relevant regions of interest and provides economic utilization of NGS sequencing capacity. It also mitigates the necessity for extra treatment of the sample associated with whole genome or transcriptome workflow, such as ribosomal RNA depletion. The enrichment is done in the same reaction for both DNA and RNA. Depending on the applications, the enrichment primer pool can be the same if the target DNA and RNA regions are the same. If different regions are of interest for the DNA and RNA, users can simply mix the corresponding enrichment primer pools, and put them into the same reaction.

[0040] Module 3 enables separated output of DNA and cDNA libraries. The sequencing depth requirements for DNA and cDNA are usually quite different, and they vary depending on the applications. The output from the methods disclosed herein gives users flexibility so that sequencing capacity can be allocated individually according to specific needs. In addition, since the samples have already been partially amplified in module 2, the separation has negligible effect on sample loss.

[0041] FIG. 2 illustrates one exemplary, optimized way to utilize the methods disclosed herein. It starts with purified (not necessarily separated) gDNA and RNA from a biological sample (step 1). The total nucleic acids are fragmented by enzymatic digestion (for DNA) and by heat hydrolysis (for RNA). The double stranded DNA fragments are end polished so that they are ready for ligation (step 2). The fragmented RNAs are end polished by polyadenylation (step 3). In the next few steps, DNA fragments are ligated to DNA tag molecules (step 4), and the RNA fragments are attached with RNA tag molecules (on both ends) by template switching reverse transcription (step 5). With both DNA and RNA tags in place, the sample is subjected to targeted enrichment reaction by a set of gene specific primers, in which the regions of interest are amplified and enriched (step 6). Finally, the sample is split into two samples, and further amplified by primers specific for the DNA tag and RNA tag, respectively, and with proper NGS adapter sequences compatible with, e.g., Illumina NGS platform (step 7). The final products are two separate DNA and cDNA libraries resulted from the original DNA and RNA material, respectively, and are ready for sequencing.

[0042] Disclosed herein are methods for preparing DNA and cDNA libraries from a sample, comprising: ligating a DNA tag to an end of a DNA molecule in a sample, wherein the DNA tag comprises a unique molecular identifier (UMI) and a DNA identifier; and performing reverse transcription of a RNA molecule in the sample in the presence of a RNA tag, wherein the RNA tag comprises a RNA identifier, a UMI, and a poly(T). The methods do not require physical separation of the DNA and RNA from the sample.

**[0043]** In some embodiments, the reverse transcription is performed in the presence of a second RNA tag, wherein the second RNA tag comprises a RNA identifier, a UMI, and a template switching oligonucleotide (TSO).

**[0044]** In some embodiments, the methods can include ribosomal depletion. Alternatively, in some embodiments, the methods do not require ribosomal depletion. Methods for ribosomal depletion are known in the art, e.g., using RiboZero gold (Illumina: MRZG126).

**[0045]** The term “sample” can include RNA, DNA, a single cell, multiple cells, fragments of cells, or an aliquot of body fluid, taken from a subject (e.g., a mammalian subject, an animal subject, a human subject, or a non-human animal subject). Samples can be selected by one of skill in the art using any known means known including but not limited to centrifugation, venipuncture, blood draw, excretion, swabbing, biopsy, needle aspirate, lavage sample, scraping, surgical incision, laser capture microdissection, gradient separation, or intervention or other means known in the art. The term “mammal” or “mammalian” as used herein includes both humans and non-humans and include but is not limited to humans, non-human primates, canines, felines, murines, bovines, equines, and porcines.

**[0046]** As used herein, the term “biological sample” is intended to include, but is not limited to, tissues, cells, biological fluids and isolates thereof, isolated from a subject, as well as tissues, cells, and fluids present within a subject.

**[0047]** As used herein, a “single cell” refers to one cell. Single cells useful in the methods described herein can be obtained from a tissue of interest, or from a biopsy, blood sample, or cell culture. Additionally, cells from specific organs, tissues, tumors, neoplasms, or the like can be obtained and used in the methods described herein. In general, cells from any population can be used in the methods, such as a population of prokaryotic or eukaryotic organisms, including bacteria or yeast.

**[0048]** A single cell suspension can be obtained using standard methods known in the art including, for example, enzymatically using trypsin or papain to digest proteins connecting cells in tissue samples or releasing adherent cells in culture, or mechanically separating cells in a sample. Samples can also be selected by one of skill in the art using one or more markers known to be associated with a sample of interest.

**[0049]** Methods for manipulating single cells are known in the art and include fluorescence activated cell sorting (FACS), micromanipulation and the use of semi-automated cell pickers (e.g., the Quixell™ cell transfer system from Stoelting Co.). Individual cells can, for example, be individually selected based on features detectable by microscopic observation, such as location, morphology, or reporter gene expression.

**[0050]** Once a desired sample has been identified, the sample is prepared and the cell(s) are lysed to release cellular contents including DNA and RNA, such as gDNA and mRNA, using methods known to those of skill in the art. Lysis can be achieved by, for example, heating the cells, or by the use of detergents or other chemical methods, or by a combination of these. Any suitable lysis method known in the art can be used.

**[0051]** Nucleic acids from a cell such as DNA or RNA are isolated using methods known to those of skill in the art.

**[0052]** The term “polynucleotide(s)” or “oligonucleotide(s)” refers to nucleic acids such as DNA molecules and RNA

molecules and analogs thereof (e.g., DNA or RNA generated using nucleotide analogs or using nucleic acid chemistry). As desired, the polynucleotides can be made synthetically, e.g., using art-recognized nucleic acid chemistry or enzymatically using, e.g., a polymerase, and, if desired, can be modified. Typical modifications include methylation, biotinylation, and other art-known modifications. In addition, a polynucleotide can be single-stranded or double-stranded and, where desired, linked to a detectable moiety. In some aspects, a polynucleotide can include hybrid molecules, e.g., comprising DNA and RNA.

**[0053]** “G,” “C,” “A,” “T” and “U” each generally stands for a nucleotide that contains guanine, cytosine, adenine, thymidine and uracil as a base, respectively. However, it will be understood that the term “ribonucleotide” or “nucleotide” can also refer to a modified nucleotide or a surrogate replacement moiety. The skilled person is well aware that guanine, cytosine, adenine, and uracil can be replaced by other moieties without substantially altering the base pairing properties of an oligonucleotide comprising a nucleotide bearing such replacement moiety. For example, without limitation, a nucleotide comprising inosine as its base can base pair with nucleotides containing adenine, cytosine, or uracil. Hence, nucleotides containing uracil, guanine, or adenine can be replaced in nucleotide sequences by a nucleotide containing, for example, inosine. In another example, adenine and cytosine anywhere in the oligonucleotide can be replaced with guanine and uracil, respectively, to form G-U Wobble base pairing with the target mRNA. Sequences containing such replacement moieties are suitable for the compositions and methods described herein.

**[0054]** The term “DNA” refers to chromosomal DNA, plasmid DNA, phage DNA, or viral DNA that is single stranded or double stranded. DNA can be obtained from prokaryotes or eukaryotes.

**[0055]** The term “genomic DNA” or gDNA” refers to chromosomal DNA.

**[0056]** The term “messenger RNA” or “mRNA” refers to an RNA that is without introns and that can be translated into a polypeptide.

**[0057]** The term “cDNA” refers to a DNA that is complementary or identical to an mRNA, in either single stranded or double stranded form.

**[0058]** As used herein, “polymerase” and its derivatives, generally refers to any enzyme that can catalyze the polymerization of nucleotides (including analogs thereof) into a nucleic acid strand. Typically, but not necessarily, such nucleotide polymerization can occur in a template-dependent fashion. Such polymerases can include without limitation naturally occurring polymerases and any subunits and truncations thereof, mutant polymerases, variant polymerases, recombinant, fusion or otherwise engineered polymerases, chemically modified polymerases, synthetic molecules or assemblies, and any analogs, derivatives or fragments thereof that retain the ability to catalyze such polymerization. Optionally, the polymerase can be a mutant polymerase comprising one or more mutations involving the replacement of one or more amino acids with other amino acids, the insertion or deletion of one or more amino acids from the polymerase, or the linkage of parts of two or more polymerases. Typically, the polymerase comprises one or more active sites at which nucleotide binding and/or catalysis of nucleotide polymerization can occur. Some exemplary polymerases include without limitation DNA polymerases

and RNA polymerases. The term “polymerase” and its variants, as used herein, also refers to fusion proteins comprising at least two portions linked to each other, where the first portion comprises a peptide that can catalyze the polymerization of nucleotides into a nucleic acid strand and is linked to a second portion that comprises a second polypeptide. In some embodiments, the second polypeptide can include a reporter enzyme or a processivity-enhancing domain. Optionally, the polymerase can possess 5' exonuclease activity or terminal transferase activity. In some embodiments, the polymerase can be optionally reactivated, for example through the use of heat, chemicals or re-addition of new amounts of polymerase into a reaction mixture. In some embodiments, the polymerase can include a hot-start polymerase or an aptamer based polymerase that optionally can be reactivated.

**[0059]** The term “extension” and its variants, as used herein, when used in reference to a given primer, comprises any in vivo or in vitro enzymatic activity characteristic of a given polymerase that relates to polymerization of one or more nucleotides onto an end of an existing nucleic acid molecule. Typically, but not necessarily such primer extension occurs in a template-dependent fashion; during template-dependent extension, the order and selection of bases is driven by established base pairing rules, which can include Watson-Crick type base pairing rules or alternatively (and especially in the case of extension reactions involving nucleotide analogs) by some other type of base pairing paradigm. In one non-limiting example, extension occurs via polymerization of nucleotides on the 3'OH end of the nucleic acid molecule by the polymerase.

**[0060]** As used herein, the terms “ligating,” “ligation,” and their derivatives refer generally to the act or process for covalently linking two or more molecules together, for example, covalently linking two or more nucleic acid molecules to each other. In some embodiments, ligation includes joining nicks between adjacent nucleotides of nucleic acids. In some embodiments, ligation includes forming a covalent bond between an end of a first and an end of a second nucleic acid molecule. In some embodiments, for example embodiments wherein the nucleic acid molecules to be ligated include conventional nucleotide residues, the ligation can include forming a covalent bond between a 5' phosphate group of one nucleic acid and a 3' hydroxyl group of a second nucleic acid thereby forming a ligated nucleic acid molecule. In some embodiments, any means for joining nicks or bonding a 5'phosphate to a 3' hydroxyl between adjacent nucleotides can be employed. In an exemplary embodiment, an enzyme such as a ligase can be used. Generally, for the purposes of this disclosure, an amplified target sequence can be ligated to an adapter to generate an adapter-ligated amplified target sequence.

**[0061]** As used herein, “ligase” and its derivatives, refers generally to any agent capable of catalyzing the ligation of two substrate molecules. In some embodiments, the ligase includes an enzyme capable of catalyzing the joining of nicks between adjacent nucleotides of a nucleic acid. In some embodiments, the ligase includes an enzyme capable of catalyzing the formation of a covalent bond between a 5' phosphate of one nucleic acid molecule to a 3' hydroxyl of another nucleic acid molecule thereby forming a ligated nucleic acid molecule. Suitable ligases can include, but not limited to, T4 DNA ligase, T4 RNA ligase, and *E. coli* DNA ligase.

**[0062]** As used herein, “ligation conditions” and its derivatives, generally refers to conditions suitable for ligating two molecules to each other. In some embodiments, the ligation conditions are suitable for sealing nicks or gaps between nucleic acids. As defined herein, a “nick” or “gap” refers to a nucleic acid molecule that lacks a directly bound 5' phosphate of a mononucleotide pentose ring to a 3' hydroxyl of a neighboring mononucleotide pentose ring within internal nucleotides of a nucleic acid sequence. As used herein, the term nick or gap is consistent with the use of the term in the art. Typically, a nick or gap can be ligated in the presence of an enzyme, such as ligase at an appropriate temperature and pH. In some embodiments, T4 DNA ligase can join a nick between nucleic acids at a temperature of about 70° C.-72° C.

**[0063]** As used herein, “blunt-end ligation” and its derivatives, refers generally to ligation of two blunt-end double-stranded nucleic acid molecules to each other. A “blunt end” refers to an end of a double-stranded nucleic acid molecule wherein substantially all of the nucleotides in the end of one strand of the nucleic acid molecule are base paired with opposing nucleotides in the other strand of the same nucleic acid molecule. A nucleic acid molecule is not blunt ended if it has an end that includes a single-stranded portion greater than two nucleotides in length, referred to herein as an “overhang.” In some embodiments, the end of nucleic acid molecule does not include any single stranded portion, such that every nucleotide in one strand of the end is based paired with opposing nucleotides in the other strand of the same nucleic acid molecule. In some embodiments, the ends of the two blunt ended nucleic acid molecules that become ligated to each other do not include any overlapping, shared or complementary sequence. Typically, blunted-end ligation excludes the use of additional oligonucleotide adapters to assist in the ligation of the double-stranded amplified target sequence to the double-stranded adapter, such as patch oligonucleotides as described in Mitra and Varley, US2010/0129874. In some embodiments, blunt-ended ligation includes a nick translation reaction to seal a nick created during the ligation process.

**[0064]** The term “amplicon” refers to the amplified product of a nucleic acid amplification reaction, e.g., RT-PCR.

**[0065]** The terms “reverse-transcriptase PCR” and “RT-PCR” refer to a type of PCR where the starting material is mRNA. The starting mRNA is enzymatically converted to complementary DNA or “cDNA” using a reverse transcriptase enzyme. The cDNA is then used as a template for a PCR reaction.

**[0066]** The terms “PCR product,” “PCR fragment,” and “amplification product” refer to the resultant mixture of compounds after two or more cycles of the PCR steps of denaturation, annealing and extension are complete. These terms encompass the case where there has been amplification of one or more segments of one or more target sequences.

**[0067]** The term “amplification reagents” refers to those reagents (deoxyribonucleotide triphosphates, buffer, etc.), needed for amplification except for primers, nucleic acid template, and the amplification enzyme. Typically, amplification reagents along with other reaction components are placed and contained in a reaction vessel (test tube, microwell, etc.). Amplification methods include PCR methods known to those of skill in the art and also include rolling circle amplification (Blanco et al., J. Biol. Chem., 264,

8935-8940, 1989), hyperbranched rolling circle amplification (Lizard et al., *Nat. Genetics*, 19, 225-232, 1998), and loop-mediated isothermal amplification (Notomi et al., *Nucl. Acids Res.*, 28, e63, 2000), each of which is hereby incorporated by reference in its entirety.

**[0068]** The term “hybridize” refers to a sequence specific non-covalent binding interaction with a complementary nucleic acid. Hybridization can occur to all or a portion of a nucleic acid sequence. Those skilled in the art will recognize that the stability of a nucleic acid duplex, or hybrids, can be determined by the  $T_m$ . Additional guidance regarding hybridization conditions can be found in: *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y., 1989, 6.3.1-6.3.6 and in: Sambrook et al., *Molecular Cloning, a Laboratory Manual*, Cold Spring Harbor Laboratory Press, Vol. 3, 1989.

**[0069]** As used herein, “incorporating” a sequence into a polynucleotide refers to covalently linking a series of nucleotides with the rest of the polynucleotide, for example at the 3' or 5' end of the polynucleotide, by phosphodiester bonds, wherein the nucleotides are linked in the order prescribed by the sequence. A sequence has been “incorporated” into a polynucleotide, or equivalently the polynucleotide “incorporates” the sequence, if the polynucleotide contains the sequence or a complement thereof. Incorporation of a sequence into a polynucleotide can occur enzymatically (e.g., by ligation or polymerization) or using chemical synthesis (e.g., by phosphoramidite chemistry).

**[0070]** As used herein, the terms “amplify” and “amplification” refer to enzymatically copying the sequence of a polynucleotide, in whole or in part, so as to generate more polynucleotides that also contain the sequence or a complement thereof. The sequence being copied is referred to as the template sequence. Examples of amplification include DNA-templated RNA synthesis by RNA polymerase, RNA-templated first-strand cDNA synthesis by reverse transcriptase, and DNA-templated PCR amplification using a thermostable DNA polymerase. Amplification includes all primer-extension reactions. Amplification includes methods such as PCR, ligation amplification (or ligase chain reaction, LCR) and amplification methods. These methods are known and widely practiced in the art. See, e.g., U.S. Pat. Nos. 4,683,195 and 4,683,202 and Innis et al., “PCR protocols: a guide to method and applications” Academic Press, Incorporated (1990) (for PCR); and Wu et al. (1989) *Genomics* 4:560-569 (for LCR). In general, the PCR procedure describes a method of gene amplification which is comprised of (i) sequence-specific hybridization of primers to specific genes within a DNA sample (or library), (ii) subsequent amplification involving multiple rounds of annealing, elongation, and denaturation using a DNA polymerase, and (iii) screening the PCR products for a band of the correct size. The primers used are oligonucleotides of sufficient length and appropriate sequence to provide initiation of polymerization, i.e. each primer is specifically designed to be complementary to each strand of the genomic locus to be amplified.

**[0071]** Reagents and hardware for conducting amplification reaction are commercially available. Primers useful to amplify sequences from a particular gene region are preferably complementary to, and hybridize specifically to sequences in the target region or in its flanking regions and can be prepared using the polynucleotide sequences pro-

vided herein. Nucleic acid sequences generated by amplification can be sequenced directly.

**[0072]** The term “associated” is used herein to refer to the relationship between a sample and the DNA molecules, RNA molecules, or other polynucleotides originating from or derived from that sample. A polynucleotide is associated with a sample if it is an endogenous polynucleotide, i.e., it occurs in the sample at the time the sample is selected or is derived from an endogenous polynucleotide. For example, the mRNAs endogenous to a cell are associated with that cell. cDNAs resulting from reverse transcription of these mRNAs, and DNA amplicons resulting from PCR amplification of the cDNAs, contain the sequences of the mRNAs and are also associated with the cell. The polynucleotides associated with a sample need not be located or synthesized in the sample and are considered associated with the sample even after the sample has been destroyed (for example, after a cell has been lysed). Molecular barcoding or other techniques can be used to determine which polynucleotides in a mixture are associated with a particular sample.

**[0073]** When hybridization occurs in an antiparallel configuration between two single-stranded polynucleotides, the reaction is called “annealing” and those polynucleotides are described as “complementary”. As used herein, and unless otherwise indicated, the term “complementary,” when used to describe a first nucleotide sequence in relation to a second nucleotide sequence, refers to the ability of a polynucleotide comprising the first nucleotide sequence to hybridize and form a duplex structure under certain conditions with a polynucleotide comprising the second nucleotide sequence, as will be understood by the skilled person. Such conditions can, for example, be stringent conditions, where stringent conditions can include: 400 mM NaCl, 40 mM PIPES pH 6.4, 1 mM EDTA, 50° C. or 70° C. for 12-16 hours followed by washing. Other conditions, such as physiologically relevant conditions as can be encountered inside an organism, can apply. The skilled person will be able to determine the set of conditions most appropriate for a test of complementarity of two sequences in accordance with the ultimate application of the hybridized nucleotides.

**[0074]** Complementary sequences include base-pairing of a region of a polynucleotide comprising a first nucleotide sequence to a region of a polynucleotide comprising a second nucleotide sequence over the length or a portion of the length of one or both nucleotide sequences. Such sequences can be referred to as “complementary” with respect to each other herein. However, where a first sequence is referred to as “substantially complementary” with respect to a second sequence herein, the two sequences can be complementary, or they can include one or more, but generally not more than about 5, 4, 3, or 2 mismatched base pairs within regions that are base-paired. For two sequences with mismatched base pairs, the sequences will be considered “substantially complementary” as long as the two nucleotide sequences bind to each other via base-pairing.

**[0075]** Conventional notation is used herein to describe nucleotide sequences: the left-hand end of a single-stranded nucleotide sequence is the 5'-end; the left-hand direction of a double-stranded nucleotide sequence is referred to as the 5'-direction. The direction of 5' to 3' addition of nucleotides to nascent RNA transcripts is referred to as the transcription direction. The DNA strand having the same sequence as an mRNA is referred to as the “coding strand”; sequences on the DNA strand having the same sequence as an mRNA



transcribed from that DNA and which are located 5' to the 5'-end of the RNA transcript are referred to as "upstream sequences"; sequences on the DNA strand having the same sequence as the RNA and which are 3' to the 3' end of the coding RNA transcript are referred to as "downstream sequences."

**[0076]** In some embodiments, the double stranded DNA fragments can be end polished so that they are amenable for ligation. For example, the ends of the DNA fragments can be polished to have blunt ends. As known in the art, this can be achieved with enzymes that can either fill in or remove the protruding strand. Another method is to perform the ligation in the presence of short synthetic oligonucleotides, called "adaptors," which have been prepared in such a way as to eventually ligate with one terminus to the fragment and make the fragment amenable for ligation with polynucleotides of interest such as DNA or RNA tags. As such, the DNA fragments can be ligated to DNA tags.

**[0077]** In some embodiments, the RNA fragments are end polished by polyadenylation. The RNA fragments can be attached to RNA tags, e.g., on both ends, by template switching reverse transcription.

**[0078]** A "DNA tag" or "DNA tag molecule" is a polynucleotide comprising a DNA identifier and a UMI. A DNA tag can be a deoxyribopolynucleotide. A "DNA identifier" is a polynucleotide sequence assigned to distinguish a gDNA molecule from a RNA molecule. A DNA tag can be ligated to the 5' or 3' end of double stranded DNA fragments.

**[0079]** A "RNA tag" or "RNA tag molecule" is a polynucleotide comprising a RNA identifier and a UMI. A RNA tag can be a deoxyribopolynucleotide. A "RNA identifier" is a polynucleotide sequence assigned to distinguish a cDNA molecule from a gDNA molecule. A RNA tag can further comprise poly(T). Alternatively, a RNA tag can further comprise a template switching oligonucleotide (TSO). A RNA tag can be used to add a 5' tag to RNA-derived cDNA fragments through reverse transcription. In some embodiments, a RNA tag can be used to add a 3' tag to RNA-derived cDNA through template switching in reverse transcription.

**[0080]** Two types of RNA tags are helpful because in order to sequence the single stranded RNA from both directions, two different mechanisms can be used to attach the RNA specific sequence. Only one type of DNA tag is needed because the DNA tag can be ligated to both ends of the double stranded DNA.

**[0081]** A composition can comprise at least 2 of the tags described above, e.g., a DNA tag and a RNA tag. A composition can also comprise the 3 tags described above, e.g., a DNA tag and the 2 types of RNA tags.

**[0082]** Unique molecular indices or identifiers (UMIs; also called Random Molecular Tags (RMTs)) are short sequences or "barcodes" of bases used to tag each DNA or RNA molecule (fragment) prior to library amplification, thereby aiding in the identification of each individual nucleic acid molecule, or PCR duplicates. Kivioja, T. et al., *Nat. Methods* 9:72-74 (2012), and Suppl. If two reads align to the same location and have the same UMI, it is highly likely that they are PCR duplicates originating from the same fragment prior to amplification. UMIs can also be used to detect and quantify unique mRNA transcripts. In some embodiments, DNA tags containing the same DNA identifier sequence contain different UMI sequences. In some embodiments, RNA tags containing the same RNA identifier sequence contain different UMI sequences.

**[0083]** The concept of UMIs is that prior to any amplification, each original target molecule is "tagged" by a unique barcode sequence. This DNA sequence must be long enough to provide sufficient permutations to assign each founder molecule a unique barcode. In some embodiments, a UMI sequence contains randomized nucleotides and is incorporated into the DNA or RNA tag. For example, a 12-base random sequence provides  $4^{12}$  or 16,777,216 UMI's for each target molecule in the sample.

**[0084]** In some embodiments, the RNA tag is a single-stranded DNA molecule and serves as a primer for reverse transcription. The RNA tag can be generated using a DNA polymerase (DNAP). Here, the binding site of the RNA tag is an RNA binding site (e.g., an mRNA binding site) and contains a sequence region complementary to a sequence region in one or more RNAs. In some embodiments, the binding site is complementary to a sequence region common to all RNAs in the sample to which the barcode adapter is added. For example, the binding site can be a poly(T) tract, which is complementary to the poly(A) tails of eukaryotic mRNAs. Alternatively, or in addition, the binding site can include a random sequence tract. Upon adding the RNA tag to the RNAs associated with a sample, reverse transcription can occur and first strands of cDNA can be synthesized, such that the RNA identifier sequence is incorporated into the first strands of cDNA. It will be recognized that reverse transcription requires appropriate conditions, for example the presence of an appropriate buffer and reverse transcriptase enzyme, and temperatures appropriate for annealing of the barcode adapter to RNAs and the activity of the enzyme. It will also be recognized that reverse transcription, involving a DNA primer and an RNA template, is most efficient when the 3' end of the primer is complementary to the template and can anneal directly to the template. Accordingly, the RNA tag can be designed so that the binding site occurs at the 3' end of the adapter molecule.

**[0085]** As described above, the present methods can employ a reverse transcriptase enzyme that adds one or more non-templated nucleotides (such as Cs) to the end of a nascent cDNA strand upon reaching the 5' end of the template RNA. These nucleotides form a 3' DNA overhang at one end of the RNA/DNA duplex. If a second RNA molecule contains a sequence region, for example, a poly-G tract at its 3' end that is complementary to the non-templated nucleotides, and binds to the non-templated nucleotides, the reverse transcriptase can switch templates and continue extending the cDNA, now using the second RNA molecule as a template. Such a second RNA molecule is referred to herein and known in the art as a template-switching oligo (TSO).

**[0086]** In embodiments of the present methods, a second RNA tag comprising a RNA identifier, UMI, and TSO can serve as a template-switching oligonucleotide for reverse transcription. Thus, the RNA identifier sequence is incorporated into the first strand of cDNA after template switching and is present in DNA molecules resulting from amplification (for example, by PCR) of the first strand of cDNA. In these embodiments, any reverse transcriptase that has template switching activity can be used. The binding site of the first RNA tag is a cDNA binding site and preferably occurs at the 3' end of the adapter molecule. The binding site can include a G-tract (comprising one or more G nucleotides), or any other sequence that is at least partially complementary to that of the 3' overhang generated by the reverse tran-

scriptase. It will be recognized that the overhang sequence, and thus an appropriate sequence for the binding site of the barcode adapter, can depend on the choice of reverse transcriptase used in the method.

**[0087]** Methods for reverse transcription and template switching are well known in the art. A procedure frequently referred to as “SMART” (switching mechanism at the 5' end of the RNA transcript) can generate full-length cDNA libraries, even from single-cell-derived RNA samples. This strategy relies on the intrinsic properties of Moloney murine leukemia virus (MMLV) reverse transcriptase and the use of a unique template switching oligonucleotide (TS oligo, or TSO). Moloney Murine Leukemia Virus Reverse Transcriptase (M-MLV RT) is an RNA-dependent DNA polymerase that can be used in cDNA synthesis with long messenger RNA templates (>5 kb). The enzyme is a product of the pol gene of M-MLV and consists of a single subunit with a molecular weight of 71 kDa. During first-strand synthesis, upon reaching the 5' end of the RNA template, the terminal transferase activity of the MMLV reverse transcriptase adds a few additional nucleotides (mostly deoxycytidine) to the 3' end of the newly synthesized cDNA strand. These bases function as a TS oligo-anchoring site. Upon base pairing between the TS oligo and the appended deoxycytidine stretch, the reverse transcriptase “switches” template strands, from cellular RNA to the TS oligo, and continues replication to the 5' end of the TS oligo. By doing so, the resulting cDNA contains the complete 5' end of the transcript, and universal sequences of choice can be added to the reverse transcription product. Along with tagging of the cDNA 3' end by oligo dT primers, this approach makes it possible to efficiently amplify the entire full-length transcript pool in a completely sequence-independent manner.

**[0088]** A TS oligo can be a DNA oligo sequence that carries 3 riboguanosines (rGrGrG) at its 3' end. The complementarity between these consecutive rG bases and the 3' dC extension of the cDNA molecule allows the subsequent template switching. The 3' most rG can also be replaced with a locked nucleic acid base (LNA) to enhance thermostability of the LNA monomer, which would be advantageous for base pairing.

**[0089]** The TSO can include a 3' portion comprising a plurality of guanosines or guanosine analogues that base pair with cytosine. Non-limiting examples of guanosines or guanosine analogues useful in the methods described herein include, but are not limited to, deoxyriboguanosine, riboguanosine, locked nucleic acid-guanosine, and peptide nucleic acid-guanosine. The guanosines can be ribonucleosides or locked nucleic acid monomers.

**[0090]** The TSO can include a 3' portion including at least 2, at least 3, at least 4, at least 5, or 2, 3, 4, or 5, or 2-5 guanosines, or guanosine analogues that base pair with cytosine. The presence of a plurality of guanosines (or guanosine analogues that base pair with cytosine) allows the TSO to anneal transiently to the exposed cytosines at the 3' end of the first strand of cDNA. This causes the reverse transcriptase to switch template and continue to synthesis a strand complementary to the TSO. In one aspect of the invention, the 3' end of the TSO can be blocked, for example by a 3' phosphate group, to prevent the TSO from functioning as a primer during cDNA synthesis.

**[0091]** Before the tagged cDNA samples are pooled, synthesis of cDNA can be stopped, for example by removing or

inactivating the reverse transcriptase. This prevents cDNA synthesis by reverse transcription from continuing in the pooled samples.

**[0092]** As used herein, “amplified target sequences” and its derivatives, refers generally to a nucleic acid sequence produced by the amplification of/amplifying the target sequences using target-specific primers and the methods provided herein. The amplified target sequences can be either of the same sense (the positive strand produced in the second round and subsequent even-numbered rounds of amplification) or antisense (i.e., the negative strand produced during the first and subsequent odd-numbered rounds of amplification) with respect to the target sequences. For the purposes of this disclosure, the amplified target sequences are typically less than 50% complementary to any portion of another amplified target sequence in the reaction.

**[0093]** The term “polymerase chain reaction” (“PCR”) of Mullis (U.S. Pat. Nos. 4,683,195, 4,683,202, and 4,965,188) refers to a method for increasing the concentration of a segment of a target sequence in a mixture of nucleic acid sequences without cloning or purification. This process for amplifying the target sequence consists of introducing a large excess of two oligonucleotide primers to the nucleic acid sequence mixture containing the desired target sequence, followed by a precise sequence of thermal cycling in the presence of a polymerase (e.g., DNA polymerase). The two primers are complementary to their respective strands of the double stranded target sequence. To effect amplification, the mixture is denatured and the primers then annealed to their complementary sequences within the target molecule. Following annealing, the primers are extended with a polymerase so as to form a new pair of complementary strands. The steps of denaturation, primer annealing, and polymerase extension can be repeated many times (i.e., denaturation, annealing and extension constitute one “cycle;” there can be numerous “cycles”) to obtain a high concentration of an amplified segment of the desired target sequence. The length of the amplified segment of the desired target sequence is determined by the relative positions of the 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.”

**[0094]** The methods disclosed herein can further comprise amplifying the tagged DNA the tagged cDNA for enrichment with a set of gene specific primers. Target enrichment can be achieved with, e.g., an SPE primer pool, DNA boosting primer, and RNA boosting primer. Amplicon-based next-generation sequencing (NGS) assays offer many advantages for targeted enrichment. For example, QIAseq NGS panels employ unique molecular indices (UMI's) to correct for PCR amplification bias and use single primer extension (SPE) technology which provides design flexibility and highly-specific target enrichment. The concept of UMIs is that prior to any amplification, each original target molecule is “tagged” by a unique barcode sequence. This DNA sequence must be long enough to provide sufficient permutations to assign each founder molecule a unique barcode. In its current form, a 12-base random sequence provides  $4^{12}$  or 16,777,216 UMI's for each target molecule in the sample.

**[0095]** As used herein, the term “primer” includes an oligonucleotide, either natural or synthetic, that is capable, upon forming a duplex with a polynucleotide template, of acting as a point of initiation of nucleic acid synthesis and being extended from its 3' end along the template so that an extended duplex is formed. The sequence of nucleotides added during the extension process is determined by the sequence of the template polynucleotide. Usually primers are extended by a DNA polymerase. Primers usually have a length in the range of between 3 to 36 nucleotides, also 5 to 24 nucleotides, also from 14 to 36 nucleotides. Primers within the scope of the invention include orthogonal primers, amplification primers, constructions primers and the like. Pairs of primers can flank a sequence of interest or a set of sequences of interest. Primers and probes can be degenerate in sequence. Primers within the scope of the present invention bind adjacent to a target sequence. A “primer” can be considered a short polynucleotide, generally with a free 3'-OH group that binds to a target or template potentially present in a sample of interest by hybridizing with the target, and thereafter promoting polymerization of a polynucleotide complementary to the target. Primers of the instant invention are comprised of nucleotides ranging from 17 to 30 nucleotides. In some embodiments, the primer is at least 17 nucleotides, or alternatively, at least 18 nucleotides, or alternatively, at least 19 nucleotides, or alternatively, at least 20 nucleotides, or alternatively, at least 21 nucleotides, or alternatively, at least 22 nucleotides, or alternatively, at least 23 nucleotides, or alternatively, at least 24 nucleotides, or alternatively, at least 25 nucleotides, or alternatively, at least 26 nucleotides, or alternatively, at least 27 nucleotides, or alternatively, at least 28 nucleotides, or alternatively, at least 29 nucleotides, or alternatively, at least 30 nucleotides, or alternatively at least 50 nucleotides, or alternatively at least 75 nucleotides or alternatively at least 100 nucleotides.

**[0096]** As used herein, “target-specific primer” and its derivatives, refers generally to a single stranded or double-stranded polynucleotide, typically an oligonucleotide, that includes at least one sequence that is at least 50% complementary, typically at least 75% complementary or at least 85% complementary, more typically at least 90% complementary, more typically at least 95% complementary, more typically at least 98% or at least 99% complementary, or 100% identical, to at least a portion of a nucleic acid molecule that includes a target sequence. In such instances, the target-specific primer and target sequence are described as “corresponding” to each other. In some embodiments, the target-specific primer is capable of hybridizing to at least a portion of its corresponding target sequence (or to a complement of the target sequence); such hybridization can optionally be performed under standard hybridization conditions or under stringent hybridization conditions. In some embodiments, the target-specific primer is not capable of hybridizing to the target sequence, or to its complement, but is capable of hybridizing to a portion of a nucleic acid strand including the target sequence, or to its complement. In some embodiments, the target-specific primer includes at least one sequence that is at least 75% complementary, typically at least 85% complementary, more typically at least 90% complementary, more typically at least 95% complementary, more typically at least 98% complementary, or more typically at least 99% complementary, to at least a portion of the target sequence itself; in other embodiments, the target-specific primer includes at least one sequence that is at least

75% complementary, typically at least 85% complementary, more typically at least 90% complementary, more typically at least 95% complementary, more typically at least 98% complementary, or more typically at least 99% complementary, to at least a portion of the nucleic acid molecule other than the target sequence. In some embodiments, the target-specific primer is substantially non-complementary to other target sequences present in the sample; optionally, the target-specific primer is substantially non-complementary to other nucleic acid molecules present in the sample. In some embodiments, nucleic acid molecules present in the sample that do not include or correspond to a target sequence (or to a complement of the target sequence) are referred to as “non-specific” sequences or “non-specific nucleic acids”. In some embodiments, the target-specific primer is designed to include a nucleotide sequence that is substantially complementary to at least a portion of its corresponding target sequence. In some embodiments, a target-specific primer is at least 95% complementary, or at least 99% complementary, or 100% identical, across its entire length to at least a portion of a nucleic acid molecule that includes its corresponding target sequence. In some embodiments, a target-specific primer can be at least 90%, at least 95% complementary, at least 98% complementary or at least 99% complementary, or 100% identical, across its entire length to at least a portion of its corresponding target sequence. In some embodiments, a forward target-specific primer and a reverse target-specific primer define a target-specific primer pair that can be used to amplify the target sequence via template-dependent primer extension. Typically, each primer of a target-specific primer pair includes at least one sequence that is substantially complementary to at least a portion of a nucleic acid molecule including a corresponding target sequence but that is less than 50% complementary to at least one other target sequence in the sample. In some embodiments, amplification can be performed using multiple target-specific primer pairs in a single amplification reaction, wherein each primer pair includes a forward target-specific primer and a reverse target-specific primer, each including at least one sequence that substantially complementary or substantially identical to a corresponding target sequence in the sample, and each primer pair having a different corresponding target sequence. In some embodiments, the target-specific primer can be substantially non-complementary at its 3' end or its 5' end to any other target-specific primer present in an amplification reaction. In some embodiments, the target-specific primer can include minimal cross hybridization to other target-specific primers in the amplification reaction. In some embodiments, target-specific primers include minimal cross-hybridization to non-specific sequences in the amplification reaction mixture. In some embodiments, the target-specific primers include minimal self-complementarity. In some embodiments, the target-specific primers can include one or more cleavable groups located at the 3' end. In some embodiments, the target-specific primers can include one or more cleavable groups located near or about a central nucleotide of the target-specific primer. In some embodiments, one of more target-specific primers includes only non-cleavable nucleotides at the 5' end of the target-specific primer. In some embodiments, a target specific primer includes minimal nucleotide sequence overlap at the 3' end or the 5' end of the primer as compared to one or more different target-specific primers, optionally in the same amplification reaction. In some

embodiments 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more, target-specific primers in a single reaction mixture include one or more of the above embodiments. In some embodiments, substantially all of the plurality of target-specific primers in a single reaction mixture includes one or more of the above embodiments.

**[0097]** Primer design is based on single primer extension, in which each genomic target is enriched by one target-specific primer and one universal primer—a strategy that removes conventional two target-specific primer design restriction and reduces the amount of required primers. All primers required for a panel are pooled into an individual primer pool to reduce panel handling and the number of pools required for enrichment and library construction.

**[0098]** The booster panel is a pool of up to 100 primers that can be used to boost the performance of certain primers in any panel (cataloged, extended, or custom), or to extend the contents of an existing custom panel. The primers are delivered as a single pool that can be spiked into the existing panel.

**[0099]** After removing unused adapters, a limited number of PCR cycles can be conducted using an adapter primer and a pool of single primers, each carrying a gene specific sequence and a 5' universal sequence. During this process, each single primer repeatedly samples the same target locus from different DNA templates. Afterwards, additional PCR cycles can be conducted using universal primers to attach complete adapter sequences and to amplify the library to the desired quantity.

**[0100]** Compared to existing targeted enrichment approaches, the SPE method relies on single end adapter ligation, which inherently has a much higher efficiency than requiring adapters to ligate to both ends of the dsDNA fragment. More DNA molecules will be available for the downstream PCR enrichment step. PCR enrichment efficiency using one primer is also better than conventional two primer approach, due to the absence of an efficiency constraint from a second primer. During the initial PCR cycles, primers have repeated opportunities to convert (i.e. capture) maximal amount of original DNA molecules into amplicons.

**[0101]** All three features help to increase the efficiency of capturing rare mutations in the sample. In addition, incorporated UMI's within the amplicon are the key to estimating the number of DNA molecules captured and to greatly reduce sequencing errors in downstream analysis. Single primer extension also permits discovery of unknown structural variants, such as gene fusions.

**[0102]** The targeted enriched sample of DNA (e.g., gDNA) and cDNA are split into 2 separate samples. A first sample can be amplified by polymerase chain reaction (PCR) using primers specific for the DNA tag to generate a DNA library corresponding to the DNA in the sample. A second sample can be amplified by PCR using primers specific for the RNA tag to generate a cDNA library corresponding to the RNA in the sample.

**[0103]** A real-time polymerase chain reaction (Real-Time PCR), also known as quantitative polymerase chain reaction (qPCR), is a laboratory technique of molecular biology based on the polymerase chain reaction (PCR). It monitors the amplification of a targeted DNA molecule during the PCR, i.e. in real-time, and not at its end, as in conventional PCR. Real-time PCR can be used quantitatively (quantitative real-time PCR), and semi-quantitatively, i.e. above/below a certain amount of DNA molecules (semi quantita-

tive real-time PCR). Other types of PCRs include but are not limited to nested PCR (used to analyze DNA sequences coming from different organisms of the same species but that can differ for a single nucleotide (SNIPS) and to ensure amplification of the sequence of interest in each of the organism analyzed) and Inverse-PCR (usually used to clone a region flanking an insert or a transposable element).

**[0104]** Two common methods for the detection of PCR products in real-time PCR are: (1) non-specific fluorescent dyes that intercalate with any double-stranded DNA, and (2) sequence-specific DNA probes consisting of oligonucleotides that are labeled with a fluorescent reporter which permits detection only after hybridization of the probe with its complementary sequence.

**[0105]** Methods and kits for performing PCR are well known in the art. PCR is a reaction in which replicate copies are made of a target polynucleotide using a pair of primers or a set of primers consisting of an upstream and a downstream primer, and a catalyst of polymerization, such as a DNA polymerase, and typically a thermally-stable polymerase enzyme. Methods for PCR are well known in the art, and taught, for example in MacPherson et al. (1991) PCR 1: A Practical Approach (IRL Press at Oxford University Press).

**[0106]** Embodiments of the invention provide 2 separate libraries for flexible manipulation downstream: a DNA library based on the original DNA and a cDNA library based on the original RNA produced by any of the methods described herein. The DNA library or cDNA library can be sequenced to provide an analysis of gene expression in single cells or in a plurality of single cells.

**[0107]** The amplified DNA or cDNA library can be sequenced and analyzed using methods known to those of skill in the art, e.g., by next-generation sequencing (NGS). In certain exemplary embodiments, RNA expression profiles are determined using any sequencing methods known in the art. Determination of the sequence of a nucleic acid sequence of interest can be performed using a variety of sequencing methods known in the art including, but not limited to, sequencing by synthesis (SBS), sequencing by hybridization (SBH), sequencing by ligation (SBL) (Shendure et al. (2005) Science 309:1728), quantitative incremental fluorescent nucleotide addition sequencing (QIFNAS), stepwise ligation and cleavage, fluorescence resonance energy transfer (FRET), molecular beacons, TaqMan reporter probe digestion, pyrosequencing, fluorescent in situ sequencing (FISSEQ), FISSEQ beads (U.S. Pat. No. 7,425, 431), wobble sequencing (PCT/US05/27695), multiplex sequencing (U.S. Ser. No. 12/027,039, filed Feb. 6, 2008; Porreca et al (2007) Nat. Methods 4:931), polymerized colony (POLONY) sequencing (U.S. Pat. Nos. 6,432,360, 6,485,944 and 6,511,803, and PCT/US05/06425); nanogrid rolling circle sequencing (ROLONY) (US2009/0018024), allele-specific oligo ligation assays (e.g., oligo ligation assay (OLA), single template molecule OLA using a ligated linear probe and a rolling circle amplification (RCA) readout, ligated padlock probes, and/or single template molecule OLA using a ligated circular padlock probe and a rolling circle amplification (RCA) readout) and the like. High-throughput sequencing methods, e.g., using platforms such as Roche 454, Illumina Solexa, AB-SOLiD, Helicos, Complete Genomics, Polonator platforms and the like, can also be utilized. A variety of light-based sequencing technologies are known in the art (Landegren et al. (1998) Genome Res.

8:769-76; Kwok (2000) *Pharmacogenomics* 1:95-100; and Shi (2001) *Clin. Chem.* 47:164-172).

**[0108]** Embodiments of the invention also provide methods for analyzing gene expression in a plurality of single cells, the method comprising the steps of preparing a cDNA library using the method described herein and sequencing the cDNA library. A “gene” refers to a polynucleotide containing at least one open reading frame (ORF) that is capable of encoding a particular polypeptide or protein after being transcribed and translated. Any of the polynucleotide sequences described herein can be used to identify larger fragments or full-length coding sequences of the gene with which they are associated. Methods of isolating larger fragment sequences are known to those of skill in the art.

**[0109]** As used herein, “expression” refers to the process by which polynucleotides are transcribed into mRNA and/or the process by which the transcribed mRNA is subsequently being translated into peptides, polypeptides, or proteins. If the polynucleotide is derived from genomic DNA, expression can include splicing of the mRNA in a eukaryotic cell.

**[0110]** The cDNA library can be sequenced by any suitable screening method. In particular, the cDNA library can be sequenced using a high-throughput screening method, such as Applied Biosystems’ SOLiD sequencing technology, or Illumina’s Genome Analyzer. In one aspect of the invention, the cDNA library can be shotgun sequenced. The number of reads can be at least 10,000, at least 1 million, at least 10 million, at least 100 million, or at least 1000 million. In another aspect, the number of reads can be from 10,000 to 100,000, or alternatively from 100,000 to 1 million, or alternatively from 1 million to 10 million, or alternatively from 10 million to 100 million, or alternatively from 100 million to 1000 million. A “read” is a length of continuous nucleic acid sequence obtained by a sequencing reaction.

**[0111]** The DNA or gDNA library generated by the methods disclosed herein can be useful for, but not limited to, DNA variant detection, copy number analysis, fusion gene detection and structural variant detection. The cDNA library generated by the methods disclosed herein can be useful for, but not limited to, RNA variant detection, gene expression analysis, and fusion gene detection. The DNA and cDNA libraries can also be used for paired DNA and RNA profiling.

**[0112]** The expression profiles described herein are useful in the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, some embodiments relate to diagnostic assays for determining the expression profile of nucleic acid sequences (e.g., RNAs), in order to determine whether an individual is at risk of developing a disorder and/or disease. Such assays can be used for prognostic or predictive purposes to thereby prophylactically treat an individual prior to the onset of the disorder and/or disease. Accordingly, in certain exemplary embodiments, methods of diagnosing and/or prognosing one or more diseases and/or disorders using one or more of expression profiling methods described herein are provided.

**[0113]** Some embodiments pertain to monitoring the influence of agents (e.g., drugs or other compounds administered either to inhibit or to treat or prevent a disorder and/or disease) on the expression profile of nucleic acid sequences (e.g., RNAs) in clinical trials. Accordingly, in certain exem-

plary embodiments, methods of monitoring one or more diseases and/or disorders before, during and/or subsequent to treatment with one or more agents using one or more of expression profiling methods described herein are provided.

**[0114]** Monitoring the influence of agents (e.g., drug compounds) on the level of expression of a marker of the invention can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent to affect an expression profile can be monitored in clinical trials of subjects receiving treatment for a disease and/or disorder associated with the expression profile. In certain exemplary embodiments, the methods for monitoring the effectiveness of treatment of a subject with an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting one or more expression profiled in the pre-administration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting one or more expression profiles in the post-administration samples; (v) comparing the one or more expression profiled in the pre-administration sample with the one or more expression profiles in the post-administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly.

**[0115]** The expression profiling methods described herein allow the quantitation of gene expression. Thus, not only tissue specificity, but also the level of expression of a variety of genes in the tissue is ascertainable. Thus, genes can be grouped on the basis of their tissue expression per se and level of expression in that tissue. This is useful, for example, in ascertaining the relationship of gene expression between or among tissues. Thus, one tissue can be perturbed and the effect on gene expression in a second tissue can be determined. In this context, the effect of one cell type on another cell type in response to a biological stimulus can be determined. Such a determination is useful, for example, to know the effect of cell-cell interaction at the level of gene expression. If an agent is administered therapeutically to treat one cell type but has an undesirable effect on another cell type, the invention provides an assay to determine the molecular basis of the undesirable effect and thus provides the opportunity to co-administer a counteracting agent or otherwise treat the undesired effect. Similarly, even within a single cell type, undesirable biological effects can be determined at the molecular level. Thus, the effects of an agent on expression of other than the target gene can be ascertained and counteracted.

**[0116]** In another embodiment, the time course of expression of one or more nucleic acid sequences (e.g., genes, mRNAs and the like) in an expression profile can be monitored. This can occur in various biological contexts, as disclosed herein, for example development of a disease and/or disorder, progression of a disease and/or disorder, and processes, such as cellular alterations associated with the disease and/or disorder.

**[0117]** The expression profiling methods described herein are also useful for ascertaining the effect of the expression of one or more nucleic acid sequences (e.g., genes, mRNAs and the like) on the expression of other nucleic acid sequences (e.g., genes, mRNAs and the like) in the same cell or in different cells. This provides, for example, for a

selection of alternate molecular targets for therapeutic intervention if the ultimate or downstream target cannot be regulated.

**[0118]** The expression profiling methods described herein are also useful for ascertaining differential expression patterns of one or more nucleic acid sequences (e.g., genes, mRNAs and the like) in normal and abnormal cells. This provides a battery of nucleic acid sequences (e.g., genes, mRNAs and the like) that could serve as a molecular target for diagnosis or therapeutic intervention.

### EXAMPLES

**[0119]** Starting Material: Purified genomic DNA and total RNA. For example, 50 ng gDNA and 50 ng total RNA was purified from THP-1 cell line. Ideally, the relative amount of gDNA and RNA should represent the content in the sample.

#### **[0120]** DNA/RNA Fragmentation:

	uL	final conc.
DNA/RNA sample	X	
H <sub>2</sub> O	11.8 - x	
10× Fragmentation Buffer	2	1×
100 mM dATP	0.6	3 mM
Exonuclease I (20 U/uL)	1.6	1.6 U/uL
5× Fragmentation Enzyme Mix	4	1×
Total volume: 20 uL		
Incubate in thermocycler with heated lid on for 4° C. 1 min → 32° C. 15 min → 75° C. 10 min → 80° C. 20 min → 4° C. hold		

#### **[0121]** RNA Polyadenylation:

	uL	final conc.
Sample from previous step	20	
H <sub>2</sub> O	0.5	
10 mM ATP	1.25	0.5 mM
10 mM 3'-dATP (blocker)	1.25	0.5 mM
T4 Polynucleotide Kinase (10 U/uL)	1	0.4 U/uL
<i>E. coli</i> Poly(A) Polymerase (5 U/uL)	1	0.2 U/uL
Total volume: 25 uL		
Incubate in thermocycler with heated lid on for 4° C. 1 min → 30° C. 10 min → 4° C. hold		

#### **[0122]** DNA Ligation:

	uL	final conc.
Sample from previous step	25	
5× Ligation Buffer	10	1×
50 uM DNA ligation Adaptor	2.8	2.8 uM
50% PEG-6000	7.2	7.2%
T4 DNA ligase (600 U/uL)	5	60 U/uL
Total volume: 50 uL		
Incubate in thermocycler with heated lid OFF for 4° C. 1 min → 20° C. 15 min → 4° C. hold		

**[0123]** Purification: Add 50 uL of ice cold water to the 50 uL sample from previous step to make 100 uL total. Do 2 rounds of 1.2× Ampure XP beads purification following manufacturer's manual with the following exceptions: 1st round elution in 52 uL water; and 2nd round elution in 13 uL water.

#### **[0124]** Reverse Transcription:

	uL	final conc.
Sample from previous step	12.87	
7.5 uM TSON10T18NV oligo	1	300 nM
25 uM TSON10forTS oligo	1	1 uM
5× SuperScript II Buffer	5	1×
25 mM each dNTP mix	1	1 mM each
0.1M DTT	1.25	5 mM
RNase Inhibitor (40 U/uL)	0.63	1 U/uL
300 mM MgCl <sub>2</sub>	0.5	6 mM
150 mM MnCl <sub>2</sub>	0.5	3 mM
MMLV Reverse Transcriptase RNase H- (200 U/uL)	1.25	10 U/uL
Total volume: 25 uL		
Incubate in thermocycler with heated lid on for 4° C. 1 min → 25° C. 10 min → 42° C. 45 min → 70° C. 15 min → 4° C. hold		

**[0125]** Purification: Add 75 uL of ice cold water to the 25 uL sample from previous step to make 100 uL total. Do 1 round of 1.2× Ampure XP beads purification following manufacturer's manual and elute in 16.8 uL water.

#### **[0126]** Target Enrichment:

	uL	final conc.
Sample from previous step	16.8	
5× V2 Buffer	8	1×
2 mM each dNTP mix	4	0.2 mM each
100 nM each SPE primer pool	8	20 nM each
10 uM DNA boosting primer	0.8	400 nM
10 uM RNA boosting primer	0.8	400 nM
Hot-Star Taq Polymerase (6 U/uL)	1.6	0.24 U/uL
Total volume: 40 uL		
Incubate in thermocycler with heated lid on for 95° C. 13 min → 98° C. 2 min → 8 cycles of (98° C. 15 sec → 68° C. 10 min) → 72° C. 5 min → 4° C. hold		

**[0127]** Purification: Add 60 uL of ice cold water to the 40 uL sample from previous step to make 100 uL total. Do double size selection 0.5×/0.5× with Ampure XP beads following manufacturer's manual and elute in 22 uL water.

**[0128]** qPCR (real-time) to determine final amplification cycles:

	For DNA library		For RNA library	
	uL	final conc.	uL	final conc.
Sample from previous step	2		2	
5× V2 Buffer	2	1×	2	1×
2 mM each dNTP mix	1	0.2 mM each	1	0.2 mM each
H <sub>2</sub> O	2.1		2.1	
20× EveGreen Dye	0.5	1×	0.5	1×
4 uM IL2N5RS2 Universal primer	1	400 nM	1	400 nM
4 uM DNA Universal Primer	1	400 nM	0	0
4 uM RNA Universal Primer	0	0	1	400 nM
Hot-Star Taq Polymerase (6 U/uL)	0.4	0.24 U/uL	0.4	0.24 U/uL
Total volume:		10 uL	Total volume:	
Run on ABI 7900 real time instrument: 95° C. 13 min → 98° C. 2 min → 30 cycles of (98° C. 15 sec → 62° C. 2 min).			Record the counts for both samples	

**[0129]** Universal PCR:

	For DNA library		For RNA library	
	uL	final conc.	uL	final conc.
Sample from Target Enrichment	9		9	
5x V2 Buffer	5	1x	5	1x
2 mM each dNTP mix	2.5	0.2 mM each	2.5	0.2 mM each
4 uM IL2N5RS2 Universal primer	2.5	400 nM	2.5	400 nM
4 uM DNA Universal Primer	2.5	400 nM	0	0
4 uM RNA Universal Primer	0	0	2.5	400 nM
H <sub>2</sub> O	2.5		2.5	
Hot-Star Taq Polymerase (6 U/uL)	1	0.24 U/uL	1	0.24 U/uL
	Total volume: 25 uL		Total volume: 25 uL	
Incubate in thermocycler with heated lid on for 95° C. 13 min → 98° C. 2 min → “X” cycles of (98° C. 15 sec → 62° C. 2 min) → 72° C. 5 min → 4° C. hold				
(X = Ct + 4) for DNA sample and RNA sample respectively.				
For example, if Ct = 19 for DNA, and 15 for RNA, then run 23 cycles for DNA, and 19 cycles for RNA				

**[0130]** Purification: Add 75 uL of ice cold water to each of the 25 uL sample from previous step to make 100 uL total. Do 1 round of 1.2x Ampure XP beads purification following manufacturer's manual and elute in 20 uL water.

**[0131]** Library Quantification using Agilent Bioanalyzer High Sensitivity DNA chip: Dilute the purified libraries to 2 ng/uL. Load 1 uL of this diluted sample on the bioanalyzer. Obtain molar concentration of the libraries based on bioanalyzer's electropherogram. The libraries are ready for sequencing.

**[0132]** Following the workflow, with 50 ng gDNA and 50 ng total RNA input, we obtained 675 ng of DNA library and 455 ng of RNA library. The same amount of 50 ng total RNA was also used with QIAseq Targeted RNAscan Panels system from QIAGEN for comparison purpose. The same amount of 50 ng gDNA was also used with QIAseq Targeted DNA Panels system from QIAGEN for comparison purpose. The samples were then put on Illumina's MiSeq machine for sequencing.

## Results

**[0133]** As shown in Table 1, compared to the standalone RNA library prep workflow (QIAseq Targeted RNAscan Panels system from QIAGEN), our method achieved around 24% of its enrichment efficiency on the 1<sup>st</sup> strand cDNA, and around 40% of its enrichment efficiency on the 2<sup>nd</sup> strand cDNA. Since RNAscan workflow had strand bias toward the 1<sup>st</sup> strand, our method had less bias and improved strand balance. The effect of enrichment efficiency on RNA analysis deserves further exploration.

TABLE 1

Workflow	RNAscan	Ours
Average UMIs/ primer 1 <sup>st</sup> strand	11061	2681

TABLE 1-continued

Workflow	RNAscan	Ours
Average UMIs/ primer 2 <sup>nd</sup> strand	5279	2077
Ratio 2 <sup>nd</sup> /1 <sup>st</sup>	0.48	0.77

**[0134]** UMI per SPE primer for RNA sample: Primers were divided into two groups based on the RNA strand they detected. As shown in Table 2, compared to the standalone DNA library prep workflow (QIAseq Targeted DNA Panels system from QIAGEN), our method achieved slightly better enrichment efficiency. Both of the methods had comparable sequencing specificity and uniformity.

TABLE 2

Workflow	Targeted DNA Panels	Ours
Average UMIs/primer	1471	1701
Average reads/UMI	3.4	3.0
Overall specificity (on-target reads/all reads)	87%	90%
Coverage uniformity (T50)	24.9	21.6

**[0135]** Sequencing specs for DNA sample in both methods: Sequence coverage uniformity was measured by T50, the percentage of total sequence throughput captured by the bottom 50% of a target region. In the perfect uniform scenario, the T50 value equals to 50.

**[0136]** Cross talk between DNA and RNA was also evaluated since they remained in the same reaction. Using the same 50 ng of DNA and RNA from THP-1 cell line, the effective leaking signal from RNA to DNA was only 0.75% of the real DNA signal, as measured by the total UMIs of the primers detecting both RNA and DNA. In this case, only the extremely highly expressed genes might have an effect on corresponding DNA copy number analysis. However, if DNA copy number analysis was limited on intron regions, this effect should disappear. The effective leaking signal from DNA to RNA was around 3% on average by the same measurement. Since there were only a few copies of genome DNA in each cell in most cases, this kind of leaking could only affect those extremely low expressing genes (less than 0.1 copy per cell), which might be lower than the background noise level. In conclusion, our method demonstrated minimal cross talk between DNA and RNA samples which might not have any significant effect in real cases.

**[0137]** The DNA library prepared by our method can be used for DNA variant detection, and copy number analysis. The RNA library prepared by our method is suitable for gene expression analysis, fusion gene detection, and RNA variant detection. Multi-modal NGS panels can be developed based on our proposed method, and be used for biomarker screening, or targeted eQTL analysis.

**[0138]** Adaptor for ligation:

Equal molar mix and annealing of the following 2 oligos to make double strand adaptor (DNA ligation Adaptor)		
SEQ ID NO:1	/5Phos/GGACTCCAATNNNNNNNNNNNACGCTAA GAAAGATCGGAAGAGCACACGTCTG/3ddC/	PAGE Purified
SEQ ID NO:2	ATT+GGAG+TCC*T/3Phos/	STD desalt
Reverse Transcription Oligos:		
SEQ ID NO:3	CGACTCACTATAGGGCTGGAATCTGACGNNNNNNNN	PAGE
TSO10T18	NNNACGTTTTTTTTTTTTTTTTTTNNV	Purified
NV oligo		
SEQ ID NO:4	/5Me-isodC//iisodG//iisodG/TAATACGACTCACTATAG	PAGE
TSO10for	GGCTGGAATCTGACGNNNNNNNNNNNATCTGCrGrGrG	Purified
TS oligo		

Target Enrichment Oligos:		
SEQ ID NO: 5	<u>AGCAGTGGTATCAACGCAGATCAAGC</u> STD	
DNA boosting	<u>AGAAGACGGCATAACGAGATTCCGAAAC</u> desalt	
primer	<u>GTGACTGGAGTTCAGACGTGTGCTCTT</u>	
	<u>CCGATCTTCTTAGCGT</u>	
SEQ ID NO: 6	<u>GTGAGTGATGGTTGAGGATGTGTGCAA</u> STD	
RNA boosting	<u>GCAGAAGACGGCATAACGAGATTACGTA</u> desalt	
primer	<u>CGGTGACTGGAGTTCAGACGTGTGCTC</u>	
	<u>TTCCGATCTCGACTCACTATAGGGCTG</u>	
	<u>GAATTCT</u>	

For each primer, the first set of underlined nucleotides is priming site for PCR amplification in Universal PCR reactions, the second set of underlined nucleotides in the middle is the sample idx (index) region, which can be replaced with respective sample index sequences, and the third set of underlined nucleotides is part of DNA or RNA identifier used for PCR amplification in target enrichment reactions.

**[0139]** uPCR Primers:

PAGE Purified

IL2N5RS2 Universal primer

SEQ ID NO: 7  
AATGATACGGCGACACCGAGATCTACACTCTTCCCTACACGACGCTC

TTCCGATCTNNNNNAATGTACAGTATTGCGTTTTG

STD desalt

DNA Universal Primer

AAGCAGTGGTATCAACGCAGAGT

STD desalt

RNA Universal Primer

GTGAGTGATGGTTGAGGATGTGTG

**[0140]** SPE Primer Pool (equal molar mix of the following oligos):

SEQ ID NO: 10  
AATGTACAGTATTGCGTTTTTGAGCCCCAAGTCTATGAGAACCTCTG

SEQ ID NO: 11  
AATGTACAGTATTGCGTTTTGTGGCACCAGCGATCAGGTCTTTAT

SEQ ID NO: 12  
AATGTACAGTATTGCGTTTTGCTGAGTGGAGTCACAGCGGAGATAGT

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SEQ ID NO: 13  
AATGTACAGTATTGCGTTTTGTGTCCACCAGTAACAACAGTTGAATGT

CC

SEQ ID NO: 14  
AATGTACAGTATTGCGTTTTGGTGTGAGGAACATACTAGTCTTTGCAA

GT

SEQ ID NO: 15  
AATGTACAGTATTGCGTTTTGTTCAAAGTTGGTCTGCTTCAGTCCAAAG

SEQ ID NO: 16  
AATGTACAGTATTGCGTTTTGCCCCAGCTTCTCTCTGCACTAAG

SEQ ID NO: 17  
AATGTACAGTATTGCGTTTTGGCCTTCCCAACATGCATTCTAACTTCTT

CC

SEQ ID NO: 18  
AATGTACAGTATTGCGTTTTGCCAGCTACTCTCAAATCAGCATCCTTT

GG

SEQ ID NO: 19  
AATGTACAGTATTGCGTTTTGCCAGTCTTCTGTGAGTCTATCCTCAGT

TC

SEQ ID NO: 20  
AATGTACAGTATTGCGTTTTGAGAGCGAACCAAGAATGCCTGTTTACAG

SEQ ID NO: 21  
AATGTACAGTATTGCGTTTTGGAGAGGCACGAGAACACATCTATTCTG

SEQ ID NO: 22  
AATGTACAGTATTGCGTTTTGTTCTCTCAGAAGTTCCTTCGTATCCTT

SEQ ID NO: 23  
AATGTACAGTATTGCGTTTTGTGATGACATGCCCCATCACTAAAACAC

SEQ ID NO: 24  
AATGTACAGTATTGCGTTTTGTGATAGAGACATGATGTAACCGTGGGAAT

TTCTTC

SEQ ID NO: 25  
AATGTACAGTATTGCGTTTTGCGTTCTAAGAGAGTGACAGAAAGGTAAAG

AGGAG



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SEQ ID NO: 26  
AATGTACAGTATTGCGTTTTGATCACAAAGTATCTTTTCTGTGGCTTAG  
AAATCTT

SEQ ID NO: 27  
AATGTACAGTATTGCGTTTTGTCAAATGTTAGCTCATTTTTGTAAATGGT  
GGCTTTT

SEQ ID NO: 28  
AATGTACAGTATTGCGTTTTGTGTACATTATAAAGATTCAGGCAATGT  
TGTTAGT

SEQ ID NO: 29  
AATGTACAGTATTGCGTTTTGAGTTTGTATGCAACATTTCTAAAGTTACC  
TACTTGT

SEQ ID NO: 30  
AATGTACAGTATTGCGTTTTGAAAATCTGTTTTCCAATAAATTTCTCAGAT  
CCAGGAA

SEQ ID NO: 31  
AATGTACAGTATTGCGTTTTGCGACCCAGTTACCATAGCAATTTAGTGAA  
ATAACTA

SEQ ID NO: 32  
AATGTACAGTATTGCGTTTTGAGAGCGCTATGTATTATTATAGCTAC  
CTGTTAA

SEQ ID NO: 33  
AATGTACAGTATTGCGTTTTGCGTTTTTGACAGTTTGACAGTTAAAGGCA  
TTTCC

SEQ ID NO: 34  
AATGTACAGTATTGCGTTTTGCTGTCTTATTTGGATATTTCTCCCAAT  
GAAAGTA

SEQ ID NO: 35  
AATGTACAGTATTGCGTTTTGGACTTTTGCAAATGTTTACATAGGTGA  
CAGATTT

SEQ ID NO: 36  
AATGTACAGTATTGCGTTTTGAAGTAGAAAATGGAAGTCTATGTGATCAA  
GAAATCG

SEQ ID NO: 37  
AATGTACAGTATTGCGTTTTGGGCCTCTTAAAGATCATGTTTGTACAGT  
GCTTA

SEQ ID NO: 38  
AATGTACAGTATTGCGTTTTGACAAGATTGGTCAGGAAAAGAGAATTGTT  
CCTATAA

SEQ ID NO: 39  
AATGTACAGTATTGCGTTTTGAGACCTGTCTCAAAAGTAAAAAGTAAGT  
TAACATG

SEQ ID NO: 40  
AATGTACAGTATTGCGTTTTGTCAAGTCTTCCAAATCCTTATGTATAGC  
AGCAAT

SEQ ID NO: 41  
AATGTACAGTATTGCGTTTTGAGGGTCGAGGAAGCCAGTTTACATCAA

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SEQ ID NO: 42  
AATGTACAGTATTGCGTTTTGAACAAAAGATATTTTCAATATTTCTGCG  
CAGGTTT

SEQ ID NO: 43  
AATGTACAGTATTGCGTTTTGGTCTCGACTTGAATTGCAAAAAGATGTTA  
GAAAAGC

SEQ ID NO: 44  
AATGTACAGTATTGCGTTTTGAAAATGTTGGCAGTCATAACATTTGAAAC  
TAATGGA

SEQ ID NO: 45  
AATGTACAGTATTGCGTTTTGAGCCTCAAACAGTTGGTTTTAAATTTGA  
AGTCT

SEQ ID NO: 46  
AATGTACAGTATTGCGTTTTGCCTCTGTGTATGTTTTAACTACAAAGC  
GAAACA

SEQ ID NO: 47  
AATGTACAGTATTGCGTTTTGGATTACCTGGTAATGAGGAAAAACAGCTT  
TAAATC

SEQ ID NO: 48  
AATGTACAGTATTGCGTTTTGAGATCTGCTGAAAAGAAATTTGTTAAAGC  
ACAATT

SEQ ID NO: 49  
AATGTACAGTATTGCGTTTTGCGGCATCCCCTACATCGAGACCTC

SEQ ID NO: 50  
AATGTACAGTATTGCGTTTTGCAGGAGCAGATCAAACGGGTGAAG

SEQ ID NO: 51  
AATGTACAGTATTGCGTTTTGCAAGTCTTTTGAGGACATCCACCAGTAC  
AG

SEQ ID NO: 52  
AATGTACAGTATTGCGTTTTGACGTGCCTGTTGGACATCCTGGATA

SEQ ID NO: 53  
AATGTACAGTATTGCGTTTTGCCTGTACTGGTGGATGTCCTCAAAGACT

SEQ ID NO: 54  
AATGTACAGTATTGCGTTTTGCCCTGAGGAGCGATGACGGAATATAAGC

SEQ ID NO: 55  
AATGTACAGTATTGCGTTTTGGTCGTATTCGTCCACAAAATGGTTCTGGA  
TC

SEQ ID NO: 56  
AATGTACAGTATTGCGTTTTGTGACTGGCAATTGTGTCAACAGGTGAAAA

SEQ ID NO: 57  
AATGTACAGTATTGCGTTTTGCGCCAGCTGGAGTTTGGTCATGTTT

SEQ ID NO: 58  
AATGTACAGTATTGCGTTTTGAATCCCTCTCATCACAATTTTATTCCACA  
ATAGTTT

SEQ ID NO: 59  
AATGTACAGTATTGCGTTTTGTCAACAACAAGAGAATCATGAAATCAAC  
CCTAGC

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SEQ ID NO: 60  
AATGTACAGTATTGCGTTTTGGATATGGAGCCAGCGTTCGATT

SEQ ID NO: 61  
AATGTACAGTATTGCGTTTTGGGCGCGGAAAGTCCTCACTCTC

SEQ ID NO: 62  
AATGTACAGTATTGCGTTTTGTATGGTGAGGTTTCGGCGTGTAAACG

SEQ ID NO: 63  
AATGTACAGTATTGCGTTTTGTGGTGACAAAGTTAGAAGGGTCCATGG

SEQ ID NO: 64  
AATGTACAGTATTGCGTTTTGCTTCTTTACCACCCAGATACGACACTA

SEQ ID NO: 65  
AATGTACAGTATTGCGTTTTGCGCTCGTGGTGGTAGTCGTCGTAT

SEQ ID NO: 66  
AATGTACAGTATTGCGTTTTGCCAGGAGGCCCTTCTGTTTACAACC

SEQ ID NO: 67  
AATGTACAGTATTGCGTTTTGCCACAAGCCCAAATATTCTACTCACTT  
TGC

SEQ ID NO: 68  
AATGTACAGTATTGCGTTTTGATCGCTGCATCAAGGAAAAGGTAATGG

SEQ ID NO: 69  
AATGTACAGTATTGCGTTTTGCGCGTAAGGATAGCAACTGAGGTTATCAC

SEQ ID NO: 70  
AATGTACAGTATTGCGTTTTGCGACCTGACGTAACCCCTTGCTTATC

SEQ ID NO: 71  
AATGTACAGTATTGCGTTTTGGGAAATGCTCTCACGTAGTCTCTCATGT  
CT

SEQ ID NO: 72  
AATGTACAGTATTGCGTTTTGGTGCATAACCCGAAGAACAATGTTGCCAC  
TA

SEQ ID NO: 73  
AATGTACAGTATTGCGTTTTGGTCAGCTCAGGATAAAGCACGGATGGATA

SEQ ID NO: 74  
AATGTACAGTATTGCGTTTTGCTCAGGATAAAAGCTTCCTTCTTAACAAG  
TTTTTCC

SEQ ID NO: 75  
AATGTACAGTATTGCGTTTTGAGAGATTGTTCCCTTGCAATGACCTCTT  
TTC

SEQ ID NO: 76  
AATGTACAGTATTGCGTTTTGCCCTCACCTTTGGAATTTACAGTCTGAA

SEQ ID NO: 77  
AATGTACAGTATTGCGTTTTGTAGGTTCTTCAGGTCTCTACACTCTCCTT  
TAAACT

SEQ ID NO: 78  
AATGTACAGTATTGCGTTTTGGAGAAGGAGTGCAATGCCAAGATTATGAT  
CC

SEQ ID NO: 79  
AATGTACAGTATTGCGTTTTGGACGTTCTCCATTGTATTGGCAGTAACCA

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SEQ ID NO: 80  
AATGTACAGTATTGCGTTTTGCACATCTCACAGGCTCTAAAGGAATTCTA  
TATCCTA

SEQ ID NO: 81  
AATGTACAGTATTGCGTTTTGGAGGCAAGAGGTGAGTAGTACCAATACTG  
TC

SEQ ID NO: 82  
AATGTACAGTATTGCGTTTTGGAGCCCCCTCCGCTTACTTGTAACTGT

SEQ ID NO: 83  
AATGTACAGTATTGCGTTTTGCCAGTAAAACGTATTGAGAAAAAGGTAA  
AGCGTTA

SEQ ID NO: 84  
AATGTACAGTATTGCGTTTTGGCTCAGAATAAATCGTAACAATCTCAAAG  
TGCATTT

SEQ ID NO: 85  
AATGTACAGTATTGCGTTTTGTGAGGTGTCCACAGGGCTCAATCTTTAC

SEQ ID NO: 86  
AATGTACAGTATTGCGTTTTGCCCTTGTATCAGTAAAGGCTATATAATA  
CCGAATT

SEQ ID NO: 87  
AATGTACAGTATTGCGTTTTGTCATGAAGAGAGTATCATCAGCTCGTTCA  
TCATC

SEQ ID NO: 88  
AATGTACAGTATTGCGTTTTGTGTCTTTCTGCCGATGTGAAATTAAGG  
TAC

SEQ ID NO: 89  
AATGTACAGTATTGCGTTTTGTCGCCCCAAATAATTTCTCGCAACA

SEQ ID NO: 90  
AATGTACAGTATTGCGTTTTGCTCATACCTCCATTCCAAGCTTTCATTGT  
CTC

SEQ ID NO: 91  
AATGTACAGTATTGCGTTTTGCCTGCCCTTATTTTAAACAGCAGGAACGA  
AT

SEQ ID NO: 92  
AATGTACAGTATTGCGTTTTGTCGATAGCGAAAGTCCTCTTTGGTCAG

SEQ ID NO: 93  
AATGTACAGTATTGCGTTTTGGTTAAAGACCAACCCTAATAAGAGACT  
TTCCAAG

SEQ ID NO: 94  
AATGTACAGTATTGCGTTTTGAAACCTTTCAGTACCTTCTTCATGGTT  
CT

SEQ ID NO: 95  
AATGTACAGTATTGCGTTTTGTTCCAGGTGATGTGCTCTATGAACTCC  
TT

SEQ ID NO: 96  
AATGTACAGTATTGCGTTTTGGGAGCGGTGCAACAGTTCAATGGT

SEQ ID NO: 97  
AATGTACAGTATTGCGTTTTGCATCCGTGGATAATGTGCACCATAACC

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SEQ ID NO: 98  
AATGTACAGTATTGCGTTTTGTGCGAGAGCCTGGACTGTTTGAAATC

SEQ ID NO: 99  
AATGTACAGTATTGCGTTTTGAAGCCAGGTCTTCCCGATGAGAGAG

SEQ ID NO: 100  
AATGTACAGTATTGCGTTTTGGGCACTCCGTGGATTTCACACAGTC

SEQ ID NO: 101  
AATGTACAGTATTGCGTTTTGCAGATATCTGCTGCCCTTTTACCTTATGG  
TTT

SEQ ID NO: 102  
AATGTACAGTATTGCGTTTTGTGTAGACTGCTTTGGGATTACGTCTATCA  
GTTG

SEQ ID NO: 103  
AATGTACAGTATTGCGTTTTGGGAAAGGAGAAAAAGGAAGTGCTACCTGA  
AC

SEQ ID NO: 104  
AATGTACAGTATTGCGTTTTGTTTTCTCCCTTCCTCCTTGAACAAAC  
AG

SEQ ID NO: 105  
AATGTACAGTATTGCGTTTTTGACAGCTTTAGGAAAATGGAATCTCTTACC  
TCCTC

SEQ ID NO: 106  
AATGTACAGTATTGCGTTTTGGGGTGTTATGGTCGCGTTGGATTTCCTG

SEQ ID NO: 107  
AATGTACAGTATTGCGTTTTGGCTACGGCGTGCAACTCACAGAAC

SEQ ID NO: 108  
AATGTACAGTATTGCGTTTTGACCGACCTCTTCCAGCGCTACTT

SEQ ID NO: 109  
AATGTACAGTATTGCGTTTTGCGGGCAGGGCTTACTTACCTTGG

SEQ ID NO: 110  
AATGTACAGTATTGCGTTTTGTAGCTACTGCCTTTCGAAGAACGAT

SEQ ID NO: 111  
AATGTACAGTATTGCGTTTTGTGTGGGTGAAAAAGATGTGGTTAAGAAA  
CAAC

SEQ ID NO: 112  
AATGTACAGTATTGCGTTTTGCCCCATATAGCTTAATCTGATGGGCATC

SEQ ID NO: 113  
AATGTACAGTATTGCGTTTTGGAAAGAGCATCAGGAACAAGCCTTGAGT  
AC

SEQ ID NO: 114  
AATGTACAGTATTGCGTTTTGTTGAGATGCCTGACAACCTTTACACCTT  
TG

SEQ ID NO: 115  
AATGTACAGTATTGCGTTTTGCTCTAGGCTGAGGGAATATGCATCTCT

SEQ ID NO: 116  
AATGTACAGTATTGCGTTTTGCGTACCCAGAAGACAATGGCCTAGCTAT

SEQ ID NO: 117  
AATGTACAGTATTGCGTTTTGGGGCAGCACAGATTCCTTAACCA

-continued

SEQ ID NO: 118  
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SEQ ID NO: 357  
AATGTACAGTATTGCGTTTTGAGGCATAGCTGACTCATCTATGTTTGT  
CT

SEQ ID NO: 358  
AATGTACAGTATTGCGTTTTGTTCTCTATTTCTTCTACTCTGACAGTATA

SEQ ID NO: 359  
AATGTACAGTATTGCGTTTTGGAACCTATTCCAACAGAACAAACCGATAAC  
ATCA

SEQ ID NO: 360  
AATGTACAGTATTGCGTTTTGTGGATAGCAAGACAATTAGAGCCCAACTT  
AGT

SEQ ID NO: 361  
AATGTACAGTATTGCGTTTTGCTACTCCTCCTGTCTCTTCCACATCATC  
AATT

SEQ ID NO: 362  
AATGTACAGTATTGCGTTTTGAGGACCTTATGTTGTATGCTGTATAAATC  
TAAAGGT

SEQ ID NO: 363  
AATGTACAGTATTGCGTTTTGGTTTGTCTCTTCTATGGTAAGTATCTTT  
CTGGATG

SEQ ID NO: 364  
AATGTACAGTATTGCGTTTTGTGGAGAGAAACAGATAAAAGTTGAGTAT  
ACGTTTA

SEQ ID NO: 365  
AATGTACAGTATTGCGTTTTGGAGGATGACGACATGTTAGTAAGCACTAC  
TACT

SEQ ID NO: 366  
AATGTACAGTATTGCGTTTTGATTCCACCATCATTTCTCTTCCAAAATT  
ATCATCC

SEQ ID NO: 367  
AATGTACAGTATTGCGTTTTGCTCAAAGCACTGCCTTCTCTCATTATCT  
CAC

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SEQ ID NO: 368  
AATGTACAGTATTGCGTTTTGAATGTATTGACCTTCTTTAAAGTGACA  
TCGATGT

SEQ ID NO: 369  
AATGTACAGTATTGCGTTTTGTGATGTTCCCAACTTCTTCTCATGGTT  
ATCTC

SEQ ID NO: 370  
AATGTACAGTATTGCGTTTTGCCCTCTGATCCCTAGATAATTTATGGGTA  
GCTAGA

SEQ ID NO: 371  
AATGTACAGTATTGCGTTTTGCACGAAATGCAGTTTTGGAATATGATTA  
ATGTT

SEQ ID NO: 372  
AATGTACAGTATTGCGTTTTGGAACAATGTTCTACGCACATTTTGTCTC  
AGTAAA

SEQ ID NO: 373  
AATGTACAGTATTGCGTTTTGTCCACGCTGCTCTCTAAATTACACTCGAA

SEQ ID NO: 374  
AATGTACAGTATTGCGTTTTGACGTAGAACACATTTTCATTTACTCCTCT  
TTGG

SEQ ID NO: 375  
AATGTACAGTATTGCGTTTTGGTACATGAATGTAAATCAAGAAAACAGA  
TGTTGTT

SEQ ID NO: 376  
AATGTACAGTATTGCGTTTTGTTCTGAACATTTATGGACACAGTCAAA  
CAACAAT

SEQ ID NO: 377  
AATGTACAGTATTGCGTTTTGTGAAGCCATTGCGAGAACTTTATCCATAA  
GTATTTC

SEQ ID NO: 378  
AATGTACAGTATTGCGTTTTGGCCAGAGCACATGAATAAATGAGCATCC  
AT

SEQ ID NO: 379  
AATGTACAGTATTGCGTTTTGGGAAGCTCTCAGGGTACAAATTTCTCAGAT  
CAT

SEQ ID NO: 380  
AATGTACAGTATTGCGTTTTGCTCAGGGTACAAATTTCTCAGATCATCAGT  
CCTC

SEQ ID NO: 381  
AATGTACAGTATTGCGTTTTGCTCTACACAAGCTTCCTTTCCGTCATGC

SEQ ID NO: 382  
AATGTACAGTATTGCGTTTTGCCCTTCAGATCTTCTCAGCATTCGAGAGA  
TC

SEQ ID NO: 383  
AATGTACAGTATTGCGTTTTGAATCGAAGCGCTACCTGATTCCAATTCC

SEQ ID NO: 384  
AATGTACAGTATTGCGTTTTGCCGACCGTAACATTTCGGTGCGTTG

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SEQ ID NO: 385  
AATGTACAGTATTGCGTTTTGACATTCTATCCAAGCTGTGTTCTATCTTG  
AGAAACT

SEQ ID NO: 386  
AATGTACAGTATTGCGTTTTGCGAGTGAGGGTTTTCTGTTTCACATC

SEQ ID NO: 387  
AATGTACAGTATTGCGTTTTGCGTGGGTCCAGTCTGCAGTTAAG

SEQ ID NO: 388  
AATGTACAGTATTGCGTTTTGGCTCAGAGCCGTTCCGAGATCTT

SEQ ID NO: 389  
AATGTACAGTATTGCGTTTTGGCGTTCCATCTCCCACCTTGTCGTAGTT

SEQ ID NO: 390  
AATGTACAGTATTGCGTTTTGCTGGCCGAGTTGGTTCATCATCATTCAA

SEQ ID NO: 391  
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SEQ ID NO: 392  
AATGTACAGTATTGCGTTTTGTGAAAAGCACTTCTGAAATAATTTCAACC  
TTCGTTT

SEQ ID NO: 393  
AATGTACAGTATTGCGTTTTGAGTACTCCATGGCTGACGAGATCTG

SEQ ID NO: 394  
AATGTACAGTATTGCGTTTTGTTGCCTTTGTTCGAAGGTCCAATGTGT

SEQ ID NO: 395  
AATGTACAGTATTGCGTTTTGCGTCCCCGCATTCCAACGCTC

SEQ ID NO: 396  
AATGTACAGTATTGCGTTTTGGGCGCGCCGTTTACTTGAAGG

SEQ ID NO: 397  
AATGTACAGTATTGCGTTTTGGCCTGGCGGTGCACACTATTCTG

SEQ ID NO: 398  
AATGTACAGTATTGCGTTTTGAGGTGCAGCCACAAAACCTTACAGATGC

SEQ ID NO: 399  
AATGTACAGTATTGCGTTTTGGTGCCGAACCAATACAACCTCTG

SEQ ID NO: 400  
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SEQ ID NO: 401  
AATGTACAGTATTGCGTTTTGCCGAGAGGGTTGATTGGTTCTG

SEQ ID NO: 402  
AATGTACAGTATTGCGTTTTGAGCCACTCGCATTTGACCATTCAACT

SEQ ID NO: 403  
AATGTACAGTATTGCGTTTTGCCACGTCTGACAGGTAGCCATGG

SEQ ID NO: 404  
AATGTACAGTATTGCGTTTTGGTGAGGCTGCTGGACGAGTACAAC

SEQ ID NO: 405  
AATGTACAGTATTGCGTTTTGCGCACCAGGTTGTACTCGTCCA

SEQ ID NO: 406  
AATGTACAGTATTGCGTTTTGCCGCTTTGTGCTTCTGTTCTTCGT

SEQ ID NO: 407  
AATGTACAGTATTGCGTTTTGCTGATTAATCGCGTAGAAAATGACCTTAT  
TTTGGAG

SEQ ID NO: 408  
AATGTACAGTATTGCGTTTTGGCTCCATCGTCTACCTGGAGATTGACAA

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SEQ ID NO: 409  
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SEQ ID NO: 410  
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SEQ ID NO: 411  
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SEQ ID NO: 412  
AATGTACAGTATTGCGTTTTGGCCAGCATGCAGTTCTAAGGCTCT

SEQ ID NO: 413  
AATGTACAGTATTGCGTTTTGGTGCCCGTCTCGACTCTTAGGC

SEQ ID NO: 414  
AATGTACAGTATTGCGTTTTGTGTAGCCGCTGATCGTGTATATGTC

SEQ ID NO: 415  
AATGTACAGTATTGCGTTTTGGACTGGTACTGGTTAGTAAAGGTTGATAA  
TATTCCA

SEQ ID NO: 416  
AATGTACAGTATTGCGTTTTGGGTGAAGTAATCAGTTTGTTCAC TAGTTA  
CGTGATT

SEQ ID NO: 417  
AATGTACAGTATTGCGTTTTGTGTGACATGCCTACTGATTATCTTCAAAC  
TCATCAC

SEQ ID NO: 418  
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CTTAACC

SEQ ID NO: 419  
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CATGATA

SEQ ID NO: 420  
AATGTACAGTATTGCGTTTTGAGTAATTTCAACTATTGGCCTAGTGAAT  
TTAAGCT

SEQ ID NO: 421  
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CTAGC

SEQ ID NO: 422  
AATGTACAGTATTGCGTTTTGCATCAACAGAAACAGAACAACTGTG  
ACAAATC

SEQ ID NO: 423  
AATGTACAGTATTGCGTTTTGCCAAAGAATATCCCTTTATATAGCAGTGG  
AACAATT

SEQ ID NO: 424  
AATGTACAGTATTGCGTTTTGCAGAATATGCAGTGATAAGTGCTGTTTCA  
TCACT

SEQ ID NO: 425  
AATGTACAGTATTGCGTTTTGTTCCCCCTGTGACGACTACTTTTCCTC

SEQ ID NO: 426  
AATGTACAGTATTGCGTTTTGCGGTCCCTATTTCTTCTCTGCTTCGT

SEQ ID NO: 427  
AATGTACAGTATTGCGTTTTGCTGAACAGTTCTGTCTCTATTACCCGACC  
TC

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SEQ ID NO: 428  
AATGTACAGTATTGCGTTTTGCGTTCATAGCCTTCTATCCGAGTATGTAG  
CA

SEQ ID NO: 429  
AATGTACAGTATTGCGTTTTGCCCTTCTGTCCTCGCAGGTTAATCC

SEQ ID NO: 430  
AATGTACAGTATTGCGTTTTGGCTTCCAGCCATTCTGAGATATCCTCAC  
AGT

SEQ ID NO: 431  
AATGTACAGTATTGCGTTTTGACCAGGAGGAACAAAGACACATGAAGATC  
AT

SEQ ID NO: 432  
AATGTACAGTATTGCGTTTTGGCGCCCCGAGTTCTTACGAATC

SEQ ID NO: 433  
AATGTACAGTATTGCGTTTTGTTTATACACAGTTTGGAGTTTGAGAATCA  
GAAGACT

SEQ ID NO: 434  
AATGTACAGTATTGCGTTTTGGGTATCTCTGGCTGATGAGATTATGAGT  
GATTCTC

SEQ ID NO: 435  
AATGTACAGTATTGCGTTTTGGCCAAGCTAGTGATTGATGTGATTGCGT  
AT

SEQ ID NO: 436  
AATGTACAGTATTGCGTTTTGCCCTCCTCTAGTACTCCCTGTTTGT

SEQ ID NO: 437  
AATGTACAGTATTGCGTTTTGTCTCCTCTGTCCTCCCAATCACTAGTCTA  
GC

SEQ ID NO: 438  
AATGTACAGTATTGCGTTTTGGCCTCGTCCCTCTTCCCTTAGGTAA

SEQ ID NO: 439  
AATGTACAGTATTGCGTTTTGTCTCTCTTCCATTAGTCTGAGTACTGAG  
TGATT

SEQ ID NO: 440  
AATGTACAGTATTGCGTTTTGAGCATTTCTTGAGACTTAAAGTGGCATTCT  
TAAAGG

SEQ ID NO: 441  
AATGTACAGTATTGCGTTTTGATTTTATTCTCAAGAGGCAGAAATACCA  
ACTTACC

SEQ ID NO: 442  
AATGTACAGTATTGCGTTTTGAATTTATAGCTCTTTTCATCTGCTTTGGT  
ATCATCA

SEQ ID NO: 443  
AATGTACAGTATTGCGTTTTGGCCTCTAATCTGATATACAGCCTTAGAAA  
GTCACA

SEQ ID NO: 444  
AATGTACAGTATTGCGTTTTGTGTGCCATTGTCTGGAGCAACAATT

AATGTACAGTATTGCGTTTTTGAGTGTACTGCTCGTTTTCTTAATTGAAA  
 AGTGAGT  
 SEQ ID NO: 446  
 AATGTACAGTATTGCGTTTTTGACCCATGAACTAATACTTATTTTGAGATT  
 GGTCCAT  
 SEQ ID NO: 447  
 AATGTACAGTATTGCGTTTTGCGTGGTGCAACAAAAGTAAGAATCCAACA  
 GTTTT  
 SEQ ID NO: 448  
 AATGTACAGTATTGCGTTTTGTGAAATGTTAAGTAAGCTTGAAATACCG  
 ATAGCAT  
 SEQ ID NO: 449  
 AATGTACAGTATTGCGTTTTTGGGGAGGAAGAAAATGAAGCACGAGGAAA  
 AC  
 SEQ ID NO: 450  
 AATGTACAGTATTGCGTTTTGATTGGGATGTACTCTAAATTTAAAGCAG  
 CAAATCA  
 SEQ ID NO: 451  
 AATGTACAGTATTGCGTTTTGTCAAGAGCAGAATTTGAGACTTTGATAT  
 TAAAACT  
 SEQ ID NO: 452  
 AATGTACAGTATTGCGTTTTGCGGTTACTAACATGTTTAGGAAATAGAC  
 AACTGTT

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AATGTACAGTATTGCGTTTTGCCTGCAACAGATCCCATATAATTAACTT  
 TCATACC  
 AATGTACAGTATTGCGTTTTGAGATGAAGAAGATGAGGAACGAGAGAGTA  
 AAAGC

**[0141]** The foregoing description of the specific embodiments will so fully reveal the general nature of the invention that others can, by applying knowledge within the skill of the art, readily modify and/or adapt for various applications, without departing from the general concept of the invention. Therefore, such adaptations and modifications are intended to be within the meaning and range of equivalents of the disclosed embodiments, based on the teaching and guidance presented herein. It is to be understood that the phraseology or terminology herein is for the purpose of description and not of limitation, such that the terminology or phraseology of the present specification is to be interpreted by the skilled artisan in light of the teachings and guidance.

[0142] The breadth and scope of the present invention should not be limited by any of the above-described exemplary embodiments but should be defined only in accordance with the following claims and their equivalents.

[0143] All of the various aspects, embodiments, and options described herein can be combined in any and all variations.

[0104d] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be herein incorporated by reference. U.S. Appl. No. 62/648,174, filed Mar. 26, 2018, is incorporated herein by reference in its entirety.

## SEQUENCE LISTING

Sequence total quantity:	454	
SEQ ID NO: 1	moltype = DNA length = 55	
FEATURE	Location/Qualifiers	
misc_feature	1..55	
	note = Adaptor	
misc_difference	11..22	
	note = n is a or c or g or t	
modified_base	55	
	mod_base = OTHER	
	note = c is dideoxycytosine	
source	1..55	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 1		
ggactccaat nnnnnnnnnn nnacgctaag aaagatcgga agagcacacg tctgc		55
SEQ ID NO: 2	moltype = DNA length = 11	
FEATURE	Location/Qualifiers	
misc_feature	1..11	
	note = adaptor	
source	1..11	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 2		
attgaggtcc t		11
SEQ ID NO: 3	moltype = DNA length = 62	
FEATURE	Location/Qualifiers	
misc_feature	1..62	
	note = Oligonucleotide	

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misc_difference      30..39
                     note = n is a or c or g or t
misc_difference      61
                     note = n is a or c or g or t
misc_difference      62
                     note = v is a or c or g
source               1..62
                     mol_type = other DNA
                     organism = synthetic construct

SEQUENCE: 3
cgactcacta tagggctgga attctgacgn nnnnnnnna cgttttttt tttttttt 60
nv                                                    62

SEQ ID NO: 4         moltype = DNA length = 56
FEATURE              Location/Qualifiers
source               1..56
                     mol_type = other DNA
                     organism = synthetic construct
misc_feature         1..56
                     note = Oligonucleotide
variation            38..47
                     note = n is a or c or g or t
modified_base        1
                     mod_base = OTHER
                     note = c is 5-methyldeoxyisocytidine
modified_base        54..56
                     mod_base = OTHER
                     note = g is riboguanosine
modified_base        2..3
                     mod_base = OTHER
                     note = g is deoxysoguanosine

SEQUENCE: 4
cggaataacg actcactata gggctggaat tctgacgnnn nnnnnnnc tgcggg 56

SEQ ID NO: 5         moltype = DNA length = 98
FEATURE              Location/Qualifiers
misc_feature         1..98
                     note = Primer
source               1..98
                     mol_type = other DNA
                     organism = synthetic construct

SEQUENCE: 5
agcagtggta tcaacgcaga gtcaacgcaga agacggcata cgagattccg aaacgtgact 60
ggagttcaga cgtgtgtctt tccgatcttt cttagcgt 98

SEQ ID NO: 6         moltype = DNA length = 115
FEATURE              Location/Qualifiers
misc_feature         1..115
                     note = Primer
source               1..115
                     mol_type = other DNA
                     organism = synthetic construct

SEQUENCE: 6
gtgagtgatg gttgaggatg tgtgcaagca gaagacggca tacgagatta cgtacggtga 60
ctggagttca gacgtgtgct cttccgatct cgactcacta tagggctgga attct 115

SEQ ID NO: 7         moltype = DNA length = 84
FEATURE              Location/Qualifiers
misc_feature         1..84
                     note = Primer
misc_difference      59..63
                     note = n is a or c or g or t
source               1..84
                     mol_type = other DNA
                     organism = synthetic construct

SEQUENCE: 7
aatgatacgg cgaccacoga gatctacact ctttccctac acgacgtctt tccgatctnn 60
nnnaatgtac agtattgcgt ttg 84

SEQ ID NO: 8         moltype = DNA length = 23
FEATURE              Location/Qualifiers
misc_feature         1..23
                     note = Primer
source               1..23
                     mol_type = other DNA
                     organism = synthetic construct

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SEQUENCE: 8  
aagcagtggg atcaacgcag agt 23

SEQ ID NO: 9                   moltype = DNA   length = 24  
FEATURE                    Location/Qualifiers  
misc\_feature               1..24  
                            note = Primer  
source                     1..24  
                            mol\_type = other DNA  
                            organism = synthetic construct

SEQUENCE: 9  
gtgagtgatg gttgaggatg tgtg 24

SEQ ID NO: 10               moltype = DNA   length = 47  
FEATURE                    Location/Qualifiers  
misc\_feature               1..47  
                            note = primer  
source                     1..47  
                            mol\_type = other DNA  
                            organism = synthetic construct

SEQUENCE: 10  
aatgtacagt attgcgtttt gagccccaag tcctatgaga acctctg 47

SEQ ID NO: 11               moltype = DNA   length = 46  
FEATURE                    Location/Qualifiers  
misc\_feature               1..46  
                            note = primer  
source                     1..46  
                            mol\_type = other DNA  
                            organism = synthetic construct

SEQUENCE: 11  
aatgtacagt attgcgtttt gtggcaccag cgatcaggtc ctttat 46

SEQ ID NO: 12               moltype = DNA   length = 47  
FEATURE                    Location/Qualifiers  
misc\_feature               1..47  
                            note = Primer  
source                     1..47  
                            mol\_type = other DNA  
                            organism = synthetic construct

SEQUENCE: 12  
aatgtacagt attgcgtttt gctgagtgga gtcacagcgg agatagt 47

SEQ ID NO: 13               moltype = DNA   length = 51  
FEATURE                    Location/Qualifiers  
misc\_feature               1..51  
                            note = Primer  
source                     1..51  
                            mol\_type = other DNA  
                            organism = synthetic construct

SEQUENCE: 13  
aatgtacagt attgcgtttt gtgttccacc agtaacaaca gttgaatgtc c 51

SEQ ID NO: 14               moltype = DNA   length = 51  
FEATURE                    Location/Qualifiers  
misc\_feature               1..51  
                            note = Primer  
source                     1..51  
                            mol\_type = other DNA  
                            organism = synthetic construct

SEQUENCE: 14  
aatgtacagt attgcgtttt ggtgtgagga acataactagt gctttgcaag t 51

SEQ ID NO: 15               moltype = DNA   length = 50  
FEATURE                    Location/Qualifiers  
misc\_feature               1..50  
                            note = Primer  
source                     1..50  
                            mol\_type = other DNA  
                            organism = synthetic construct

SEQUENCE: 15  
aatgtacagt attgcgtttt gttcaaagtt gggctctgctt cagtccaaag 50

SEQ ID NO: 16               moltype = DNA   length = 48  
FEATURE                    Location/Qualifiers  
misc\_feature               1..48

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source	note = Primer 1..48 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 16		
aatgtacagt attgcgtttt gccccagct tcttctctct gcactaag		48
SEQ ID NO: 17	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
source	note = Primer 1..51 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 17		
aatgtacagt attgcgtttt ggccttccca acatgcattc taacttcttc c		51
SEQ ID NO: 18	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
source	note = Primer 1..51 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 18		
aatgtacagt attgcgtttt gccagctact ctcaaaatca gcatacctttg g		51
SEQ ID NO: 19	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
source	note = Primer 1..51 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 19		
aatgtacagt attgcgtttt gccagctcct ctgtgagtct atcctcagtt c		51
SEQ ID NO: 20	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
source	note = Primer 1..49 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 20		
aatgtacagt attgcgtttt gagagcgaac caagaatgcc tgtttacag		49
SEQ ID NO: 21	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
source	note = Primer 1..50 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 21		
aatgtacagt attgcgtttt ggagaggcac gagaacacac atctattctg		50
SEQ ID NO: 22	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
source	note = Primer 1..50 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 22		
aatgtacagt attgcgtttt gttctcttca gaagttcctt cgtcatcctt		50
SEQ ID NO: 23	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
source	note = Primer 1..48 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 23		
aatgtacagt attgcgtttt gtgatgacat gcccatacac taaaacac		48

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SEQ ID NO: 24      moltype = DNA  length = 56
FEATURE           Location/Qualifiers
misc_feature       1..56
                   note = Primer
source             1..56
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 24
aatgtacagt attgcgtttt gtgatataga catgatgtaa ccgtgggaat ttcttc      56

SEQ ID NO: 25      moltype = DNA  length = 55
FEATURE           Location/Qualifiers
misc_feature       1..55
                   note = Primer
source             1..55
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 25
aatgtacagt attgcgtttt gcgttctaag agagtgcacag aaaggtaaag aggag      55

SEQ ID NO: 26      moltype = DNA  length = 57
FEATURE           Location/Qualifiers
misc_feature       1..57
                   note = Primer
source             1..57
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 26
aatgtacagt attgcgtttt gatcacaaag tatctttttc tgtggccttag aaatctt      57

SEQ ID NO: 27      moltype = DNA  length = 57
FEATURE           Location/Qualifiers
misc_feature       1..57
                   note = Primer
source             1..57
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 27
aatgtacagt attgcgtttt gtcaaatggt agctcatttt tgттаatggg ggctttt      57

SEQ ID NO: 28      moltype = DNA  length = 57
FEATURE           Location/Qualifiers
misc_feature       1..57
                   note = Primer
source             1..57
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 28
aatgtacagt attgcgtttt gtgtcacatt ataaagattc aggcaatggt tgttagt      57

SEQ ID NO: 29      moltype = DNA  length = 57
FEATURE           Location/Qualifiers
misc_feature       1..57
                   note = Primer
source             1..57
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 29
aatgtacagt attgcgtttt gagtttgat gcaacatttc taaagttacc tacttgt      57

SEQ ID NO: 30      moltype = DNA  length = 57
FEATURE           Location/Qualifiers
misc_feature       1..57
                   note = Primer
source             1..57
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 30
aatgtacagt attgcgtttt gaaaatctgt tttccaataa attctcagat ccaggaa      57

SEQ ID NO: 31      moltype = DNA  length = 57
FEATURE           Location/Qualifiers
misc_feature       1..57
                   note = Primer
source             1..57

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	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 31		
aatgtacagt attgcggtttt gcgacccagt taccatagca atttagtgaa ataacta		57
SEQ ID NO: 32	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 32		
aatgtacagt attgcggtttt gagaggcgct atgtgtatta ttatagctac ctgttaa		57
SEQ ID NO: 33	moltype = DNA length = 55	
FEATURE	Location/Qualifiers	
misc_feature	1..55	
	note = Primer	
source	1..55	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 33		
aatgtacagt attgcggtttt gcgtttttga cagtttgaca gttaaaggca ttccc		55
SEQ ID NO: 34	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 34		
aatgtacagt attgcggtttt gctgtcctta ttttgatat ttctccaat gaaagta		57
SEQ ID NO: 35	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 35		
aatgtacagt attgcggtttt ggactttttg caaatgttta acataggatga cagattt		57
SEQ ID NO: 36	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 36		
aatgtacagt attgcggtttt gaagtagaaa atggaagtct atgtgatcaa gaaatcg		57
SEQ ID NO: 37	moltype = DNA length = 55	
FEATURE	Location/Qualifiers	
misc_feature	1..55	
	note = Primer	
source	1..55	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 37		
aatgtacagt attgcggtttt gggcctctta aagatcatgt ttgttacagt gctta		55
SEQ ID NO: 38	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 38		
aatgtacagt attgcggtttt gacaagattg gtcaggaaaa gagaattggt cctataa		57
SEQ ID NO: 39	moltype = DNA length = 57	

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FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 39		
aatgtacagt attgcgtttt gagaccctgt ctcaaaagta aaaagtaagt taacatg		57
SEQ ID NO: 40	moltype = DNA length = 56	
FEATURE	Location/Qualifiers	
misc_feature	1..56	
	note = Primer	
source	1..56	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 40		
aatgtacagt attgcgtttt gtcagtgtct tccaaatcct tatgtatagc agcaat		56
SEQ ID NO: 41	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 41		
aatgtacagt attgcgtttt gagggctgag gaagccagtt tacatcaa		48
SEQ ID NO: 42	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 42		
aatgtacagt attgcgtttt gaacaaaaag atattttcaa tatttctgcg cagggttt		57
SEQ ID NO: 43	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 43		
aatgtacagt attgcgtttt ggtctcgact tgaattgcaa aaagatgtta gaaaagc		57
SEQ ID NO: 44	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 44		
aatgtacagt attgcgtttt gaaaatgttg gcagtcataa catttgaaac taatgga		57
SEQ ID NO: 45	moltype = DNA length = 55	
FEATURE	Location/Qualifiers	
misc_feature	1..55	
	note = Primer	
source	1..55	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 45		
aatgtacagt attgcgtttt gagcctcaaa caggttggtt ttaaatttga agtct		55
SEQ ID NO: 46	moltype = DNA length = 56	
FEATURE	Location/Qualifiers	
misc_feature	1..56	
	note = Primer	
source	1..56	
	mol_type = other DNA	
	organism = synthetic construct	

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SEQUENCE: 46  
aatgtacagt attgcgtttt gcctctgtgt gtatgtttta actacaaagc gaaaca 56

SEQ ID NO: 47           moltype = DNA   length = 57  
FEATURE                Location/Qualifiers  
misc\_feature           1..57  
                        note = Primer  
source                  1..57  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 47  
aatgtacagt attgcgtttt ggattcacct ggtaatgagg aaaacagctt taaaatc 57

SEQ ID NO: 48           moltype = DNA   length = 56  
FEATURE                Location/Qualifiers  
misc\_feature           1..56  
                        note = Primer  
source                  1..56  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 48  
aatgtacagt attgcgtttt gagatctgct gaaaagaaat ttgttaaagc acaatt 56

SEQ ID NO: 49           moltype = DNA   length = 45  
FEATURE                Location/Qualifiers  
misc\_feature           1..45  
                        note = Primer  
source                  1..45  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 49  
aatgtacagt attgcgtttt gcggcatccc ctacatcgag acctc 45

SEQ ID NO: 50           moltype = DNA   length = 46  
FEATURE                Location/Qualifiers  
misc\_feature           1..46  
                        note = Primer  
source                  1..46  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 50  
aatgtacagt attgcgtttt gcaggagca gatcaaacgg gtgaag 46

SEQ ID NO: 51           moltype = DNA   length = 51  
FEATURE                Location/Qualifiers  
misc\_feature           1..51  
                        note = Primer  
source                  1..51  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 51  
aatgtacagt attgcgtttt gcaagtcttt tgaggacatc caccagtaca g 51

SEQ ID NO: 52           moltype = DNA   length = 46  
FEATURE                Location/Qualifiers  
misc\_feature           1..46  
                        note = Primer  
source                  1..46  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 52  
aatgtacagt attgcgtttt gacgtgctg ttggacatcc tggata 46

SEQ ID NO: 53           moltype = DNA   length = 50  
FEATURE                Location/Qualifiers  
misc\_feature           1..50  
                        note = Primer  
source                  1..50  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 53  
aatgtacagt attgcgtttt gectgtactg gtggatgtcc tcaaaagact 50

SEQ ID NO: 54           moltype = DNA   length = 49  
FEATURE                Location/Qualifiers  
misc\_feature           1..49

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source	note = Primer 1..49 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 54		
aatgtacagt attgcgtttt gccctgagga gcgatgacgg aatataagc		49
SEQ ID NO: 55	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
source	note = primer 1..52 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 55		
aatgtacagt attgcgtttt ggtcgtattc gtccacaaaa tggttctgga tc		52
SEQ ID NO: 56	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
source	note = Primer 1..50 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 56		
aatgtacagt attgcgtttt gtgactggca attgtgtcaa caggtgaaaa		50
SEQ ID NO: 57	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
source	note = Primer 1..46 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 57		
aatgtacagt attgcgtttt gcgccagctg gagtttggtc atgttt		46
SEQ ID NO: 58	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
source	note = Primer 1..57 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 58		
aatgtacagt attgcgtttt gaatccctct catcacaatt tcattccaca atagttt		57
SEQ ID NO: 59	moltype = DNA length = 56	
FEATURE	Location/Qualifiers	
misc_feature	1..56	
source	note = Primer 1..56 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 59		
aatgtacagt attgcgtttt gtcaacaaca aagagaatca tgaatcaac ctagc		56
SEQ ID NO: 60	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
source	note = Primer 1..46 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 60		
aatgtacagt attgcgtttt ggatatggag ccagcgtggt ccgatt		46
SEQ ID NO: 61	moltype = DNA length = 43	
FEATURE	Location/Qualifiers	
misc_feature	1..43	
source	note = Primer 1..43 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 61		
aatgtacagt attgcgtttt gggcgcgga agtcctcact ctc		43

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SEQ ID NO: 62      moltype = DNA  length = 48
FEATURE           Location/Qualifiers
misc_feature       1..48
                   note = Primer
source            1..48
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 62
aatgtacagt attgcgtttt gtatggtagag gttcggcgtg tttaaacg          48

SEQ ID NO: 63      moltype = DNA  length = 48
FEATURE           Location/Qualifiers
misc_feature       1..48
                   note = Primer
source            1..48
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 63
aatgtacagt attgcgtttt gtggtagacaa agttagaagg gtccatgg          48

SEQ ID NO: 64      moltype = DNA  length = 50
FEATURE           Location/Qualifiers
misc_feature       1..50
                   note = Primer
source            1..50
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 64
aatgtacagt attgcgtttt gcttctttac caccacagat acgacgacta        50

SEQ ID NO: 65      moltype = DNA  length = 45
FEATURE           Location/Qualifiers
misc_feature       1..45
                   note = Primer
source            1..45
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 65
aatgtacagt attgcgtttt gcgctcgtgg tgtagtcgt cgtat              45

SEQ ID NO: 66      moltype = DNA  length = 47
FEATURE           Location/Qualifiers
misc_feature       1..47
                   note = Primer
source            1..47
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 66
aatgtacagt attgcgtttt gccaggaggc cctttctgtt tacaacc          47

SEQ ID NO: 67      moltype = DNA  length = 53
FEATURE           Location/Qualifiers
misc_feature       1..53
                   note = Primer
source            1..53
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 67
aatgtacagt attgcgtttt gccacaagc ccaaaatatt ctactcatt tgc      53

SEQ ID NO: 68      moltype = DNA  length = 49
FEATURE           Location/Qualifiers
misc_feature       1..49
                   note = Primer
source            1..49
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 68
aatgtacagt attgcgtttt gatcgctgc atcaaggaaa aggtaatgg          49

SEQ ID NO: 69      moltype = DNA  length = 50
FEATURE           Location/Qualifiers
misc_feature       1..50
                   note = Primer
source            1..50

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 69		
aatgtacagt attgcgtttt gcgcgtaagg atagcaactg aggttatcac		50
SEQ ID NO: 70	moltype = DNA length = 47	
FEATURE	Location/Qualifiers	
misc_feature	1..47	
	note = Primer	
source	1..47	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 70		
aatgtacagt attgcgtttt gcgacctgac gtaacccctt gcttatac		47
SEQ ID NO: 71	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer	
source	1..51	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 71		
aatgtacagt attgcgtttt gggaaatgct ctcacgtagt ctctcatgtc t		51
SEQ ID NO: 72	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer	
source	1..51	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 72		
aatgtacagt attgcgtttt ggtcataacc cgaagaacaa tggtgccact a		51
SEQ ID NO: 73	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
	note = Primer	
source	1..50	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 73		
aatgtacagt attgcgtttt ggtcagctca ggataaagca cggatggata		50
SEQ ID NO: 74	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 74		
aatgtacagt attgcgtttt gctcaggata aaagcttcct tcttaacaag tttttcc		57
SEQ ID NO: 75	moltype = DNA length = 53	
FEATURE	Location/Qualifiers	
misc_feature	1..53	
	note = Primer	
source	1..53	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 75		
aatgtacagt attgcgtttt gagagattgt tcccttgcac tgacctcttt ttc		53
SEQ ID NO: 76	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
	note = Primer	
source	1..50	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 76		
aatgtacagt attgcgtttt gccccctcacc tttggaattt acagtctgaa		50
SEQ ID NO: 77	moltype = DNA length = 56	

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FEATURE	Location/Qualifiers	
misc_feature	1..56	
	note = Primer	
source	1..56	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 77		
aatgtacagt attgcgtttt gtaggttctt caggtctcta cactctcctt taaact		56
SEQ ID NO: 78	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
	note = Primer	
source	1..52	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 78		
aatgtacagt attgcgtttt ggagaaggag tgcaatgcca agattatgat cc		52
SEQ ID NO: 79	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
	note = Primer	
source	1..50	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 79		
aatgtacagt attgcgtttt ggacgttctc cattgtattg gcagtaacca		50
SEQ ID NO: 80	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 80		
aatgtacagt attgcgtttt gcacatctca caggctctaa aggaattcta tatecta		57
SEQ ID NO: 81	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
	note = Primer	
source	1..52	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 81		
aatgtacagt attgcgtttt ggaggcaaga ggtgagtagt accaatactg tc		52
SEQ ID NO: 82	moltype = DNA length = 47	
FEATURE	Location/Qualifiers	
misc_feature	1..47	
	note = Primer	
source	1..47	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 82		
aatgtacagt attgcgtttt ggagccctc cgcttacttg taatctg		47
SEQ ID NO: 83	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 83		
aatgtacagt attgcgtttt gccagtaaaa cgtattgaga aaaaggtaaa agcgta		57
SEQ ID NO: 84	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	

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SEQUENCE: 84  
aatgtacagt attgcgtttt ggctcagaat aaatcgtaac aatctcaaag tgcattt 57

SEQ ID NO: 85           moltype = DNA   length = 49  
FEATURE               Location/Qualifiers  
misc\_feature           1..49  
                        note = Primer  
source                  1..49  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 85  
aatgtacagt attgcgtttt gtgagggtgc cacagggtc aatctttac 49

SEQ ID NO: 86           moltype = DNA   length = 57  
FEATURE               Location/Qualifiers  
misc\_feature           1..57  
                        note = Primer  
source                  1..57  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 86  
aatgtacagt attgcgtttt gcccttcta tcagtaaagg ctatataata ccgaatt 57

SEQ ID NO: 87           moltype = DNA   length = 55  
FEATURE               Location/Qualifiers  
misc\_feature           1..55  
                        note = Primer  
source                  1..55  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 87  
aatgtacagt attgcgtttt gtcataaga gaggatcac agctcgttca tcatac 55

SEQ ID NO: 88           moltype = DNA   length = 53  
FEATURE               Location/Qualifiers  
misc\_feature           1..53  
                        note = Primer  
source                  1..53  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 88  
aatgtacagt attgcgtttt gtgtcctttc tgccgatgtg aaattaaagg tac 53

SEQ ID NO: 89           moltype = DNA   length = 47  
FEATURE               Location/Qualifiers  
misc\_feature           1..47  
                        note = Primer  
source                  1..47  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 89  
aatgtacagt attgcgtttt gtcgccccaa ataatttcct gcgaaca 47

SEQ ID NO: 90           moltype = DNA   length = 53  
FEATURE               Location/Qualifiers  
misc\_feature           1..53  
                        note = Primer  
source                  1..53  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 90  
aatgtacagt attgcgtttt gtcataacct ccattccaag ctttcattgt ctc 53

SEQ ID NO: 91           moltype = DNA   length = 52  
FEATURE               Location/Qualifiers  
misc\_feature           1..52  
                        note = Primer  
source                  1..52  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 91  
aatgtacagt attgcgtttt gctgcccctt atttttaaca gcaggaacga at 52

SEQ ID NO: 92           moltype = DNA   length = 48  
FEATURE               Location/Qualifiers  
misc\_feature           1..48



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source	note = Primer 1..48 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 92		
aatgtacagt attgcggtttt gtcgatagcg aaagtcctct ttggtcag		48
SEQ ID NO: 93	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
source	note = Primer 1..57 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 93		
aatgtacagt attgcggtttt ggtaaagac caaccactaa ctaagagact ttccaag		57
SEQ ID NO: 94	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
source	note = Primer 1..52 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 94		
aatgtacagt attgcggtttt gaaacctctt ccagtacctt cttcatgggt ct		52
SEQ ID NO: 95	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
source	note = Primer 1..51 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 95		
aatgtacagt attgcggtttt gttccaggt gatgtgctct atgaactcct t		51
SEQ ID NO: 96	moltype = DNA length = 45	
FEATURE	Location/Qualifiers	
misc_feature	1..45	
source	note = Primer 1..45 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 96		
aatgtacagt attgcggtttt gggagcgggtg caacagttca atggt		45
SEQ ID NO: 97	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
source	note = Primer 1..48 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 97		
aatgtacagt attgcggtttt gcatccgtgg ataatgtgca ccataacc		48
SEQ ID NO: 98	moltype = DNA length = 47	
FEATURE	Location/Qualifiers	
misc_feature	1..47	
source	note = Primer 1..47 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 98		
aatgtacagt attgcggtttt gtcggagagc ctggactgtt tgaaatc		47
SEQ ID NO: 99	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
source	note = Primer 1..46 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 99		
aatgtacagt attgcggtttt gaagccaggt cttcccgatg agagag		46

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SEQ ID NO: 100           moltype = DNA   length = 46  
FEATURE                Location/Qualifiers  
misc\_feature           1..46  
                        note = Primer  
source                 1..46  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 100  
aatgtacagt attgcgtttt gggcactccg tggatttcaa acagtc           46

SEQ ID NO: 101           moltype = DNA   length = 53  
FEATURE                Location/Qualifiers  
misc\_feature           1..53  
                        note = Primer  
source                 1..53  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 101  
aatgtacagt attgcgtttt gcagatatct gctgcccttt taccttatgg ttt       53

SEQ ID NO: 102           moltype = DNA   length = 54  
FEATURE                Location/Qualifiers  
misc\_feature           1..54  
                        note = Primer  
source                 1..54  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 102  
aatgtacagt attgcgtttt gtgtagactg ctttgggatt acgtctatca gttg       54

SEQ ID NO: 103           moltype = DNA   length = 52  
FEATURE                Location/Qualifiers  
misc\_feature           1..52  
                        note = primer  
source                 1..52  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 103  
aatgtacagt attgcgtttt gggaaaggag aaaaaggaag tgctaccta ac       52

SEQ ID NO: 104           moltype = DNA   length = 51  
FEATURE                Location/Qualifiers  
misc\_feature           1..51  
                        note = Primer  
source                 1..51  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 104  
aatgtacagt attgcgtttt gttttctctc cttctctctt tgaacaaaca g       51

SEQ ID NO: 105           moltype = DNA   length = 55  
FEATURE                Location/Qualifiers  
misc\_feature           1..55  
                        note = Primer  
source                 1..55  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 105  
aatgtacagt attgcgtttt gacagcttta ggaaatgga atctcttacc tctc       55

SEQ ID NO: 106           moltype = DNA   length = 48  
FEATURE                Location/Qualifiers  
misc\_feature           1..48  
                        note = Primer  
source                 1..48  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 106  
aatgtacagt attgcgtttt ggggtgttat ggtcgcgttg gatttctg           48

SEQ ID NO: 107           moltype = DNA   length = 45  
FEATURE                Location/Qualifiers  
misc\_feature           1..45  
                        note = Primer  
source                 1..45

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 107		
aatgtacagt attgcgtttt ggctacggcg tgcaactcac agaac		45
SEQ ID NO: 108	moltype = DNA length = 44	
FEATURE	Location/Qualifiers	
misc_feature	1..44	
	note = Primer	
source	1..44	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 108		
aatgtacagt attgcgtttt gaccgacctc ttccagcgct actt		44
SEQ ID NO: 109	moltype = DNA length = 44	
FEATURE	Location/Qualifiers	
misc_feature	1..44	
	note = Primer	
source	1..44	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 109		
aatgtacagt attgcgtttt gcgggcaggg ctacttacc ttgg		44
SEQ ID NO: 110	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 110		
aatgtacagt attgcgtttt gtagctactg cctgccttcg aagaacgat		49
SEQ ID NO: 111	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer	
source	1..54	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 111		
aatgtacagt attgcgtttt gtgtgggtgg aaaaagatgt ggtaagaaa caac		54
SEQ ID NO: 112	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
	note = Primer	
source	1..50	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 112		
aatgtacagt attgcgtttt gcccccatat agcttaatct gatgggcac		50
SEQ ID NO: 113	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer	
source	1..51	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 113		
aatgtacagt attgcgtttt ggaaagagca tcaggaacaa gccttgagta c		51
SEQ ID NO: 114	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer	
source	1..51	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 114		
aatgtacagt attgcgtttt gttgagatgc ctgacaacct ttacacctt g		51
SEQ ID NO: 115	moltype = DNA length = 49	

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FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 115		
aatgtacagt attgcgtttt gctctagggc tgagggaata tgcattctct		49
SEQ ID NO: 116	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 116		
aatgtacagt attgcgtttt gcgtacccag aagacaatgg cctagctat		49
SEQ ID NO: 117	moltype = DNA length = 45	
FEATURE	Location/Qualifiers	
misc_feature	1..45	
	note = Primer	
source	1..45	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 117		
aatgtacagt attgcgtttt ggggcagcac agattccctt aacca		45
SEQ ID NO: 118	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 118		
aatgtacagt attgcgtttt gccatacctt ggctatcccc tgaaagtgtg		49
SEQ ID NO: 119	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
	note = Primer	
source	1..46	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 119		
aatgtacagt attgcgtttt ggccctgatg ctcatggagt gttcct		46
SEQ ID NO: 120	moltype = DNA length = 44	
FEATURE	Location/Qualifiers	
misc_feature	1..44	
	note = Primer	
source	1..44	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 120		
aatgtacagt attgcgtttt gcctggtggt tgggagacga ctac		44
SEQ ID NO: 121	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 121		
aatgtacagt attgcgtttt gtgctgacag gacacagaac aagatacct		49
SEQ ID NO: 122	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
	note = Primer	
source	1..52	
	mol_type = other DNA	
	organism = synthetic construct	

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SEQUENCE: 122  
aatgtacagt attgcgtttt gggtacaggt atcttggtct gtgtcctgtc ag 52

SEQ ID NO: 123           moltype = DNA   length = 43  
FEATURE                Location/Qualifiers  
misc\_feature           1..43  
                        note = Primer  
source                  1..43  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 123  
aatgtacagt attgcgtttt ggagtcctcg gctcgattca cag 43

SEQ ID NO: 124           moltype = DNA   length = 50  
FEATURE                Location/Qualifiers  
misc\_feature           1..50  
                        note = Primer  
source                  1..50  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 124  
aatgtacagt attgcgtttt gctggtcaga gaggtgtgta ctgattgtct 50

SEQ ID NO: 125           moltype = DNA   length = 57  
FEATURE                Location/Qualifiers  
misc\_feature           1..57  
                        note = Primer  
source                  1..57  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 125  
aatgtacagt attgcgtttt gaggaagat caattacatt cacaagttca cacttct 57

SEQ ID NO: 126           moltype = DNA   length = 55  
FEATURE                Location/Qualifiers  
misc\_feature           1..55  
                        note = Primer  
source                  1..55  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 126  
aatgtacagt attgcgtttt gctgcacagt tcagaggata tttaaagctca atgac 55

SEQ ID NO: 127           moltype = DNA   length = 49  
FEATURE                Location/Qualifiers  
misc\_feature           1..49  
                        note = Primer  
source                  1..49  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 127  
aatgtacagt attgcgtttt gcacagaccg tcatgcattt ctgacactc 49

SEQ ID NO: 128           moltype = DNA   length = 47  
FEATURE                Location/Qualifiers  
misc\_feature           1..47  
                        note = Primer  
source                  1..47  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 128  
aatgtacagt attgcgtttt gaggctggta cctgctcttc ttcaatc 47

SEQ ID NO: 129           moltype = DNA   length = 53  
FEATURE                Location/Qualifiers  
misc\_feature           1..53  
                        note = Primer  
source                  1..53  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 129  
aatgtacagt attgcgtttt gcgaaatcaa acagttgtct atcagagcct gtc 53

SEQ ID NO: 130           moltype = DNA   length = 55  
FEATURE                Location/Qualifiers  
misc\_feature           1..55

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source                note = Primer
                      1..55
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 130
aatgtacagt attgcgtttt gacaaaagaa aagaagtcac gtctgtatgt ggaaa      55

SEQ ID NO: 131        moltype = DNA length = 57
FEATURE              Location/Qualifiers
misc_feature          1..57
                      note = Primer
source                1..57
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 131
aatgtacagt attgcgtttt gtccaggata atacacatca cagtaaataa cactctg      57

SEQ ID NO: 132        moltype = DNA length = 55
FEATURE              Location/Qualifiers
misc_feature          1..55
                      note = Primer
source                1..55
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 132
aatgtacagt attgcgtttt gcatcctctt tgtcatcaag ctacagtctt tttga      55

SEQ ID NO: 133        moltype = DNA length = 51
FEATURE              Location/Qualifiers
misc_feature          1..51
                      note = Primer
source                1..51
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 133
aatgtacagt attgcgtttt gctcccatctt ttgtgcatct ttgttgcgtg c        51

SEQ ID NO: 134        moltype = DNA length = 55
FEATURE              Location/Qualifiers
misc_feature          1..55
                      note = Primer
source                1..55
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 134
aatgtacagt attgcgtttt gcagaactgc ctattcctaa ctgactcatc atttc      55

SEQ ID NO: 135        moltype = DNA length = 54
FEATURE              Location/Qualifiers
misc_feature          1..54
                      note = Primer
source                1..54
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 135
aatgtacagt attgcgtttt ggaattctgt ttcacgctg agtgacactc tttt      54

SEQ ID NO: 136        moltype = DNA length = 57
FEATURE              Location/Qualifiers
misc_feature          1..57
                      note = Primer
source                1..57
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 136
aatgtacagt attgcgtttt gtttttacct ttgcttttac cttttgtac ttgtgac      57

SEQ ID NO: 137        moltype = DNA length = 53
FEATURE              Location/Qualifiers
misc_feature          1..53
                      note = Primer
source                1..53
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 137
aatgtacagt attgcgtttt gagaaggagt ctggaataga aaggctaaca gaa      53

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SEQ ID NO: 138           moltype = DNA   length = 49  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..49  
                         note = Primer  
 source                 1..49  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 138  
 aatgtacagt attgcgtttt gcacaagatg tgccaaggga attgtatgc           49

SEQ ID NO: 139           moltype = DNA   length = 57  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..57  
                         note = Primer  
 source                 1..57  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 139  
 aatgtacagt attgcgtttt gaagagtcaa taggtcagag agttttatgt tcttcca       57

SEQ ID NO: 140           moltype = DNA   length = 52  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..52  
                         note = Primer  
 source                 1..52  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 140  
 aatgtacagt attgcgtttt gactgatctt ctcaaagtcg tcctccttca gt           52

SEQ ID NO: 141           moltype = DNA   length = 57  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..57  
                         note = Primer  
 source                 1..57  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 141  
 aatgtacagt attgcgtttt gaccctgaga aataatccaa ttacctgtta atcaagg       57

SEQ ID NO: 142           moltype = DNA   length = 57  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..57  
                         note = Primer  
 source                 1..57  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 142  
 aatgtacagt attgcgtttt gaaaaggat tgagtaaaat cagtcttctc tctaccc       57

SEQ ID NO: 143           moltype = DNA   length = 55  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..55  
                         note = Primer  
 source                 1..55  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 143  
 aatgtacagt attgcgtttt gccttcctcc ctctttcttt cataaaacct ctctt       55

SEQ ID NO: 144           moltype = DNA   length = 45  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..45  
                         note = Primer  
 source                 1..45  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 144  
 aatgtacagt attgcgtttt ggccagagcc acccaactct taagg                   45

SEQ ID NO: 145           moltype = DNA   length = 57  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..57  
                         note = Primer  
 source                 1..57

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	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 145		
aatgtacagt attgcgtttt gtggaagagg aatttaataa cgaacgtttt aagagga		57
SEQ ID NO: 146	moltype = DNA length = 47	
FEATURE	Location/Qualifiers	
misc_feature	1..47	
	note = Primer	
source	1..47	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 146		
aatgtacagt attgcgtttt gccatctact gccgaggatg ttccaag		47
SEQ ID NO: 147	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
	note = Primer	
source	1..46	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 147		
aatgtacagt attgcgtttt gcacagtggag ctcaagtgcg acatca		46
SEQ ID NO: 148	moltype = DNA length = 43	
FEATURE	Location/Qualifiers	
misc_feature	1..43	
	note = Primer	
source	1..43	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 148		
aatgtacagt attgcgtttt gccgactggc catctcctcg tag		43
SEQ ID NO: 149	moltype = DNA length = 45	
FEATURE	Location/Qualifiers	
misc_feature	1..45	
	note = Primer	
source	1..45	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 149		
aatgtacagt attgcgtttt ggtaccagcg cgactacgag gagat		45
SEQ ID NO: 150	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 150		
aatgtacagt attgcgtttt gtcttttctg tcaaatggag atgatctctt ctgactc		57
SEQ ID NO: 151	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 151		
aatgtacagt attgcgtttt ggggagccca tcatctgcaa aaacatcc		48
SEQ ID NO: 152	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
	note = Primer	
source	1..52	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 152		
aatgtacagt attgcgtttt gaagctgaag aagatgtgga aaagtcccaa tg		52
SEQ ID NO: 153	moltype = DNA length = 47	



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FEATURE	Location/Qualifiers	
misc_feature	1..47	
	note = Primer	
source	1..47	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 153		
aatgtacagt attgcgtttt ggcgtgggat gttttgcag atgatgg		47
SEQ ID NO: 154	moltype = DNA length = 44	
FEATURE	Location/Qualifiers	
misc_feature	1..44	
	note = Primer	
source	1..44	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 154		
aatgtacagt attgcgtttt ggcacgctga ggacgctatg gatg		44
SEQ ID NO: 155	moltype = DNA length = 43	
FEATURE	Location/Qualifiers	
misc_feature	1..43	
	note = Primer	
source	1..43	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 155		
aatgtacagt attgcgtttt ggctgaggcg cgtcttcgag aag		43
SEQ ID NO: 156	moltype = DNA length = 44	
FEATURE	Location/Qualifiers	
misc_feature	1..44	
	note = Primer	
source	1..44	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 156		
aatgtacagt attgcgtttt ggcgcttgtc gtgaaagcga acga		44
SEQ ID NO: 157	moltype = DNA length = 42	
FEATURE	Location/Qualifiers	
misc_feature	1..42	
	note = Primer	
source	1..42	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 157		
aatgtacagt attgcgtttt ggctgcccgc ccagttgtta ct		42
SEQ ID NO: 158	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer	
source	1..51	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 158		
aatgtacagt attgcgtttt gagactctgg actgatgaag caattctgag t		51
SEQ ID NO: 159	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 159		
aatgtacagt attgcgtttt gtcaccggtg acaccttaaa accaaagc		48
SEQ ID NO: 160	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
	note = Primer	
source	1..50	
	mol_type = other DNA	
	organism = synthetic construct	

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SEQUENCE: 160  
 aatgtacagt attgcgtttt gggtcccttt gtacctcctc catcttgatc 50

SEQ ID NO: 161           moltype = DNA   length = 57  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..57  
                         note = Primer  
 source                 1..57  
                         mol\_type = other DNA  
                         organism = synthetic construct

SEQUENCE: 161  
 aatgtacagt attgcgtttt ggtcagttgt ctaacaataa caaagatctg ctcttgg 57

SEQ ID NO: 162           moltype = DNA   length = 49  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..49  
                         note = Primer  
 source                 1..49  
                         mol\_type = other DNA  
                         organism = synthetic construct

SEQUENCE: 162  
 aatgtacagt attgcgtttt ggggtgggcag caagaaaaag tccagtaaa 49

SEQ ID NO: 163           moltype = DNA   length = 49  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..49  
                         note = Primer  
 source                 1..49  
                         mol\_type = other DNA  
                         organism = synthetic construct

SEQUENCE: 163  
 aatgtacagt attgcgtttt ggccaaggct ttctctggca tgatctttt 49

SEQ ID NO: 164           moltype = DNA   length = 55  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..55  
                         note = Primer  
 source                 1..55  
                         mol\_type = other DNA  
                         organism = synthetic construct

SEQUENCE: 164  
 aatgtacagt attgcgtttt gggataactt tctcagcatt tccaccagtt tcaag 55

SEQ ID NO: 165           moltype = DNA   length = 57  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..57  
                         note = Primer  
 source                 1..57  
                         mol\_type = other DNA  
                         organism = synthetic construct

SEQUENCE: 165  
 aatgtacagt attgcgtttt gtgtccctaa gttgagtaaa atgatagaga atgagtc 57

SEQ ID NO: 166           moltype = DNA   length = 50  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..50  
                         note = Primer  
 source                 1..50  
                         mol\_type = other DNA  
                         organism = synthetic construct

SEQUENCE: 166  
 aatgtacagt attgcgtttt ggctgccaga aatccagcat ccaaaatttg 50

SEQ ID NO: 167           moltype = DNA   length = 51  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..51  
                         note = Primer  
 source                 1..51  
                         mol\_type = other DNA  
                         organism = synthetic construct

SEQUENCE: 167  
 aatgtacagt attgcgtttt ggctgctttc ttttcttagt gccaggaaac t 51

SEQ ID NO: 168           moltype = DNA   length = 50  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..50

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source	note = Primer 1..50 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 168		
aatgtacagt attgcgtttt gacagtcgag acgattcatg agggaaacttc		50
SEQ ID NO: 169	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
source	note = Primer 1..48 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 169		
aatgtacagt attgcgtttt gggaaagctc ggcgtgttgg ataagaag		48
SEQ ID NO: 170	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
source	note = Primer 1..48 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 170		
aatgtacagt attgcgtttt gacgccacaa gtgactgaaa gttggaag		48
SEQ ID NO: 171	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
source	note = Primer 1..50 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 171		
aatgtacagt attgcgtttt gtgatgggct ggagatttgg catagttttc		50
SEQ ID NO: 172	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
source	note = Primer 1..50 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 172		
aatgtacagt attgcgtttt gctatgcacc cactttcaac acagttaggt		50
SEQ ID NO: 173	moltype = DNA length = 47	
FEATURE	Location/Qualifiers	
misc_feature	1..47	
source	note = Primer 1..47 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 173		
aatgtacagt attgcgtttt ggcttggtca gaagtgtgtg tgttgtc		47
SEQ ID NO: 174	moltype = DNA length = 47	
FEATURE	Location/Qualifiers	
misc_feature	1..47	
source	note = Primer 1..47 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 174		
aatgtacagt attgcgtttt gcgtagggcca gaaagttgtc cacaatg		47
SEQ ID NO: 175	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
source	note = Primer 1..52 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 175		
aatgtacagt attgcgtttt ggggatatgg attctcgtgg tagaaggtgt aa		52

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SEQ ID NO: 176                   moltype = DNA   length = 54  
 FEATURE                        Location/Qualifiers  
 misc\_feature                   1..54  
                                 note = Primer  
 source                         1..54  
                                 mol\_type = other DNA  
                                 organism = synthetic construct  
  
 SEQUENCE: 176  
 aatgtacagt attgcgtttt gctaatacacc aagttccaag tgttcagaat ctcc           54  
  
 SEQ ID NO: 177                   moltype = DNA   length = 55  
 FEATURE                        Location/Qualifiers  
 misc\_feature                   1..55  
                                 note = Primer  
 source                         1..55  
                                 mol\_type = other DNA  
                                 organism = synthetic construct  
  
 SEQUENCE: 177  
 aatgtacagt attgcgtttt gaccgtaata accaaggttc atcataggca ttgat           55  
  
 SEQ ID NO: 178                   moltype = DNA   length = 49  
 FEATURE                        Location/Qualifiers  
 misc\_feature                   1..49  
                                 note = Primer  
 source                         1..49  
                                 mol\_type = other DNA  
                                 organism = synthetic construct  
  
 SEQUENCE: 178  
 aatgtacagt attgcgtttt gtcccagtg aagttactat gcaccctat                49  
  
 SEQ ID NO: 179                   moltype = DNA   length = 54  
 FEATURE                        Location/Qualifiers  
 misc\_feature                   1..54  
                                 note = Primer  
 source                         1..54  
                                 mol\_type = other DNA  
                                 organism = synthetic construct  
  
 SEQUENCE: 179  
 aatgtacagt attgcgtttt gtgcttatgc ttgtgtttgt gtttcctctt atgg           54  
  
 SEQ ID NO: 180                   moltype = DNA   length = 54  
 FEATURE                        Location/Qualifiers  
 misc\_feature                   1..54  
                                 note = Primer  
 source                         1..54  
                                 mol\_type = other DNA  
                                 organism = synthetic construct  
  
 SEQUENCE: 180  
 aatgtacagt attgcgtttt ggettcgtgt tctccttatg cttgttcttc tcac           54  
  
 SEQ ID NO: 181                   moltype = DNA   length = 47  
 FEATURE                        Location/Qualifiers  
 misc\_feature                   1..47  
                                 note = Primer  
 source                         1..47  
                                 mol\_type = other DNA  
                                 organism = synthetic construct  
  
 SEQUENCE: 181  
 aatgtacagt attgcgtttt gctgagtggt tctttttgca ggcaaag                 47  
  
 SEQ ID NO: 182                   moltype = DNA   length = 47  
 FEATURE                        Location/Qualifiers  
 misc\_feature                   1..47  
                                 note = Primer  
 source                         1..47  
                                 mol\_type = other DNA  
                                 organism = synthetic construct  
  
 SEQUENCE: 182  
 aatgtacagt attgcgtttt gccggccaca aagcttctaa gaacaac                 47  
  
 SEQ ID NO: 183                   moltype = DNA   length = 47  
 FEATURE                        Location/Qualifiers  
 misc\_feature                   1..47  
                                 note = Primer  
 source                         1..47

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 183		
aatgtacagt attgcgtttt ggcggttcat cttgaaggct tggatgt		47
SEQ ID NO: 184	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer	
source	1..51	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 184		
aatgtacagt attgcgtttt gttcagtgaa atgaaccctt cgaatgacaa g		51
SEQ ID NO: 185	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 185		
aatgtacagt attgcgtttt gctcctcctc ctctttgcgt ttcttgtc		48
SEQ ID NO: 186	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer	
source	1..51	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 186		
aatgtacagt attgcgtttt ggcagcagag aaacaaatga aggacaaaca g		51
SEQ ID NO: 187	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
	note = Primer	
source	1..52	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 187		
aatgtacagt attgcgtttt gtaaggagga ggaagaagac aagaacgca aa		52
SEQ ID NO: 188	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
	note = Primer	
source	1..50	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 188		
aatgtacagt attgcgtttt gtaaggcagg tctgtgagca caaaatttg		50
SEQ ID NO: 189	moltype = DNA length = 45	
FEATURE	Location/Qualifiers	
misc_feature	1..45	
	note = Primer	
source	1..45	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 189		
aatgtacagt attgcgtttt gtggagctga ccagtgacaa tgacc		45
SEQ ID NO: 190	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
	note = Primer	
source	1..46	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 190		
aatgtacagt attgcgtttt gggccaagaa gtcggtggac aagaac		46
SEQ ID NO: 191	moltype = DNA length = 43	

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FEATURE	Location/Qualifiers	
misc_feature	1..43	
	note = Primer	
source	1..43	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 191		
aatgtacagt attgcgtttt ggcgcaggcg gtcattgtca ctg		43
SEQ ID NO: 192	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 192		
aatgtacagt attgcgtttt gttgctgttc ttgtccaccg acttcttg		48
SEQ ID NO: 193	moltype = DNA length = 42	
FEATURE	Location/Qualifiers	
misc_feature	1..42	
	note = Primer	
source	1..42	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 193		
aatgtacagt attgcgtttt ggcagtgcg gatctggaac tg		42
SEQ ID NO: 194	moltype = DNA length = 42	
FEATURE	Location/Qualifiers	
misc_feature	1..42	
	note = Primer	
source	1..42	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 194		
aatgtacagt attgcgtttt gcgggcgcca ctttgactac cc		42
SEQ ID NO: 195	moltype = DNA length = 45	
FEATURE	Location/Qualifiers	
misc_feature	1..45	
	note = Primer	
source	1..45	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 195		
aatgtacagt attgcgtttt ggagcacgag acgtccatcg acatc		45
SEQ ID NO: 196	moltype = DNA length = 43	
FEATURE	Location/Qualifiers	
misc_feature	1..43	
	note = Primer	
source	1..43	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 196		
aatgtacagt attgcgtttt gcggccagga actcgtcggt gaa		43
SEQ ID NO: 197	moltype = DNA length = 45	
FEATURE	Location/Qualifiers	
misc_feature	1..45	
	note = Primer	
source	1..45	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 197		
aatgtacagt attgcgtttt ggccatgccg ggagaactct aactc		45
SEQ ID NO: 198	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	

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SEQUENCE: 198  
aatgtacagt attgcgtttt gtgtaaccct cctaagtgtt catacgttgt ctgtg 54

SEQ ID NO: 199           moltype = DNA   length = 57  
FEATURE                Location/Qualifiers  
misc\_feature           1..57  
                        note = Primer  
source                  1..57  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 199  
aatgtacagt attgcgtttt ggtcttggtc tctgttatat cttgagtcta gaacagt 57

SEQ ID NO: 200           moltype = DNA   length = 49  
FEATURE                Location/Qualifiers  
misc\_feature           1..49  
                        note = Primer  
source                  1..49  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 200  
aatgtacagt attgcgtttt gcaggagaac atggaggcga gaagaaaat 49

SEQ ID NO: 201           moltype = DNA   length = 48  
FEATURE                Location/Qualifiers  
misc\_feature           1..48  
                        note = Primer  
source                  1..48  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 201  
aatgtacagt attgcgtttt ggggaaagat tggatgccgg gaatcaac 48

SEQ ID NO: 202           moltype = DNA   length = 46  
FEATURE                Location/Qualifiers  
misc\_feature           1..46  
                        note = Primer  
source                  1..46  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 202  
aatgtacagt attgcgtttt gcggaggcct gattaggtag gaggtg 46

SEQ ID NO: 203           moltype = DNA   length = 45  
FEATURE                Location/Qualifiers  
misc\_feature           1..45  
                        note = Primer  
source                  1..45  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 203  
aatgtacagt attgcgtttt ggcggcagct caacgagaat aaaca 45

SEQ ID NO: 204           moltype = DNA   length = 45  
FEATURE                Location/Qualifiers  
misc\_feature           1..45  
                        note = Primer  
source                  1..45  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 204  
aatgtacagt attgcgtttt ggcccgcatc cttactccgc ttatc 45

SEQ ID NO: 205           moltype = DNA   length = 49  
FEATURE                Location/Qualifiers  
misc\_feature           1..49  
                        note = Primer  
source                  1..49  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 205  
aatgtacagt attgcgtttt ggctggttc aaggaagtg gactcttc 49

SEQ ID NO: 206           moltype = DNA   length = 47  
FEATURE                Location/Qualifiers  
misc\_feature           1..47

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source	note = Primer 1..47 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 206		
aatgtacagt attgcgtttt ggggaatgac tgacggagaa tccaac		47
SEQ ID NO: 207	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
source	note = Primer 1..48 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 207		
aatgtacagt attgcgtttt gctaagaccg agagcctgta ggagcttt		48
SEQ ID NO: 208	moltype = DNA length = 42	
FEATURE	Location/Qualifiers	
misc_feature	1..42	
source	note = Primer 1..42 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 208		
aatgtacagt attgcgtttt ggccgggctt gtctggctcat ct		42
SEQ ID NO: 209	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
source	note = Primer 1..51 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 209		
aatgtacagt attgcgtttt gcagctcacc tccaaaaagg caaaattctt g		51
SEQ ID NO: 210	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
source	note = Primer 1..48 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 210		
aatgtacagt attgcgtttt ggcaggaggc catgatggat ttcttcaa		48
SEQ ID NO: 211	moltype = DNA length = 53	
FEATURE	Location/Qualifiers	
misc_feature	1..53	
source	note = Primer 1..53 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 211		
aatgtacagt attgcgtttt gcatgagtga aaggaaagag gaaatcccaa tcc		53
SEQ ID NO: 212	moltype = DNA length = 56	
FEATURE	Location/Qualifiers	
misc_feature	1..56	
source	note = Primer 1..56 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 212		
aatgtacagt attgcgtttt gcctatcttc cacagtactt acacaacttc ctaagc		56
SEQ ID NO: 213	moltype = DNA length = 45	
FEATURE	Location/Qualifiers	
misc_feature	1..45	
source	note = Primer 1..45 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 213		
aatgtacagt attgcgtttt gctgcgcgta gactgtccag gtttt		45



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SEQ ID NO: 214      moltype = DNA  length = 47
FEATURE            Location/Qualifiers
misc_feature        1..47
                    note = Primer
source              1..47
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 214
aatgtacagt attgcgtttt gctcacctga tccgtgacgt tgatgtc      47

SEQ ID NO: 215      moltype = DNA  length = 44
FEATURE            Location/Qualifiers
misc_feature        1..44
                    note = Primer
source              1..44
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 215
aatgtacagt attgcgtttt ggccctgatg gactctcggc tact        44

SEQ ID NO: 216      moltype = DNA  length = 53
FEATURE            Location/Qualifiers
misc_feature        1..53
                    note = Primer
source              1..53
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 216
aatgtacagt attgcgtttt ggagaaagat caggaacact tgtcccctac tag  53

SEQ ID NO: 217      moltype = DNA  length = 48
FEATURE            Location/Qualifiers
misc_feature        1..48
                    note = Primer
source              1..48
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 217
aatgtacagt attgcgtttt ggtcctccac gatctcctca tactcctc      48

SEQ ID NO: 218      moltype = DNA  length = 47
FEATURE            Location/Qualifiers
misc_feature        1..47
                    note = Primer
source              1..47
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 218
aatgtacagt attgcgtttt gtcgatggac ttgacaagcc cgtactt      47

SEQ ID NO: 219      moltype = DNA  length = 48
FEATURE            Location/Qualifiers
misc_feature        1..48
                    note = Primer
source              1..48
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 219
aatgtacagt attgcgtttt gctggacgac gaggagtatg aggagatc      48

SEQ ID NO: 220      moltype = DNA  length = 46
FEATURE            Location/Qualifiers
misc_feature        1..46
                    note = Primer
source              1..46
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 220
aatgtacagt attgcgtttt gtaccagaag tcccggcggt gataag      46

SEQ ID NO: 221      moltype = DNA  length = 49
FEATURE            Location/Qualifiers
misc_feature        1..49
                    note = Primer
source              1..49

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 221		
aatgtacagt attgcggtttt ggttcacctc tgtgtttgac tgccagaaa		49
SEQ ID NO: 222	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 222		
aatgtacagt attgcggtttt gcaatgagta ttctcttcat ttcaggtcag ttgattt		57
SEQ ID NO: 223	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 223		
aatgtacagt attgcggtttt gggctgcttt cttgaaggct attgggtat		49
SEQ ID NO: 224	moltype = DNA length = 53	
FEATURE	Location/Qualifiers	
misc_feature	1..53	
	note = Primer	
source	1..53	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 224		
aatgtacagt attgcggtttt gaggagactg gaattctcga ataaggatta aca		53
SEQ ID NO: 225	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 225		
aatgtacagt attgcggtttt ggcatagtta aaacctgtgt ttggttttgt aggtctt		57
SEQ ID NO: 226	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 226		
aatgtacagt attgcggtttt gctctgtggt ggcggatacc cttccata		48
SEQ ID NO: 227	moltype = DNA length = 53	
FEATURE	Location/Qualifiers	
misc_feature	1..53	
	note = Primer	
source	1..53	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 227		
aatgtacagt attgcggtttt gggcattcct tctttattgc cttctttaa agc		53
SEQ ID NO: 228	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
	note = Primer	
source	1..50	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 228		
aatgtacagt attgcggtttt ggctgctggt ctggctacta tgatctctac		50
SEQ ID NO: 229	moltype = DNA length = 53	

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FEATURE	Location/Qualifiers	
misc_feature	1..53	
	note = Primer	
source	1..53	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 229		
aatgtacagt attgcggtttt ggcacacagc tttaagaag ggcaataaag aag		53
SEQ ID NO: 230	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 230		
aatgtacagt attgcggtttt gtgtatgttt aattctgtac atgagcattt catcagt		57
SEQ ID NO: 231	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 231		
aatgtacagt attgcggtttt gatttcatac cttgcttaat gggtagtagat accaaaa		57
SEQ ID NO: 232	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 232		
aatgtacagt attgcggtttt gttggcgtca aatgtgccac tatcactc		48
SEQ ID NO: 233	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 233		
aatgtacagt attgcggtttt gttctctttc aagctatgat ttaggcatag agaatcg		57
SEQ ID NO: 234	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 234		
aatgtacagt attgcggtttt gctgcagttg taggtataa ctatccattt gtctgaa		57
SEQ ID NO: 235	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
	note = Primer	
source	1..52	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 235		
aatgtacagt attgcggtttt gccctaggtc agatcaccca gtcagttaaa ac		52
SEQ ID NO: 236	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
	note = Primer	
source	1..52	
	mol_type = other DNA	
	organism = synthetic construct	

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SEQUENCE: 236  
aatgtacagt attgcgtttt gtgggttaaag gtcagcccac ttaccagata tg 52

SEQ ID NO: 237           moltype = DNA   length = 49  
FEATURE                Location/Qualifiers  
misc\_feature           1..49  
                        note = Primer  
source                  1..49  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 237  
aatgtacagt attgcgtttt ggggtatgct ccccathtag aggataagg 49

SEQ ID NO: 238           moltype = DNA   length = 50  
FEATURE                Location/Qualifiers  
misc\_feature           1..50  
                        note = Primer  
source                  1..50  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 238  
aatgtacagt attgcgtttt gacgtcagat ctacagcgaa cacaactact 50

SEQ ID NO: 239           moltype = DNA   length = 50  
FEATURE                Location/Qualifiers  
misc\_feature           1..50  
                        note = Primer  
source                  1..50  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 239  
aatgtacagt attgcgtttt gagtgggtgcc agactcacat tcagttctaa 50

SEQ ID NO: 240           moltype = DNA   length = 54  
FEATURE                Location/Qualifiers  
misc\_feature           1..54  
                        note = Primer  
source                  1..54  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 240  
aatgtacagt attgcgtttt gcttgccag ttcctttctc taatgtatca tctc 54

SEQ ID NO: 241           moltype = DNA   length = 56  
FEATURE                Location/Qualifiers  
misc\_feature           1..56  
                        note = Primer  
source                  1..56  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 241  
aatgtacagt attgcgtttt gaagttttct tgtctagtat cactttccct catagg 56

SEQ ID NO: 242           moltype = DNA   length = 49  
FEATURE                Location/Qualifiers  
misc\_feature           1..49  
                        note = Primer  
source                  1..49  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 242  
aatgtacagt attgcgtttt ggggtcaac agatggtagt tggtctctg 49

SEQ ID NO: 243           moltype = DNA   length = 54  
FEATURE                Location/Qualifiers  
misc\_feature           1..54  
                        note = Primer  
source                  1..54  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 243  
aatgtacagt attgcgtttt ggctctcggt tctaacagtt cttgcattg gata 54

SEQ ID NO: 244           moltype = DNA   length = 50  
FEATURE                Location/Qualifiers  
misc\_feature           1..50

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source	note = Primer 1..50 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 244		
aatgtacagt attgcgtttt ggaggtgacc ttcaaagtca gaggtgtat		50
SEQ ID NO: 245	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
source	note = Primer 1..49 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 245		
aatgtacagt attgcgtttt ggagcaacca tcccatctgt cttgtaac		49
SEQ ID NO: 246	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
source	note = Primer 1..50 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 246		
aatgtacagt attgcgtttt gggacaagga tgagaaaccc aattggaacc		50
SEQ ID NO: 247	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
source	note = Primer 1..46 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 247		
aatgtacagt attgcgtttt gcggtccgcc aaaagatccc agattc		46
SEQ ID NO: 248	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
source	note = Primer 1..46 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 248		
aatgtacagt attgcgtttt gggaggccac taaccactt gtgatg		46
SEQ ID NO: 249	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
source	note = Primer 1..54 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 249		
aatgtacagt attgcgtttt gtccagtttc ctagaggatg taatgggatt tgtc		54
SEQ ID NO: 250	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
source	note = Primer 1..52 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 250		
aatgtacagt attgcgtttt gtcacatttg gagatgagaa acgaggtggt ct		52
SEQ ID NO: 251	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
source	note = Primer 1..48 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 251		
aatgtacagt attgcgtttt gcccttgcc tgtaacattg ctctgatc		48

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SEQ ID NO: 252      moltype = DNA  length = 52
FEATURE            Location/Qualifiers
misc_feature        1..52
                    note = Primer
source              1..52
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 252
aatgtacagt attgcgtttt gcacctcggt tctcatctcc aaatgtgac tc      52

SEQ ID NO: 253      moltype = DNA  length = 47
FEATURE            Location/Qualifiers
misc_feature        1..47
                    note = Primer
source              1..47
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 253
aatgtacagt attgcgtttt gccagtagct ttctgtttct cggcatt          47

SEQ ID NO: 254      moltype = DNA  length = 50
FEATURE            Location/Qualifiers
misc_feature        1..50
                    note = Primer
source              1..50
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 254
aatgtacagt attgcgtttt ggcagcgtca agaatgagaa gacttttgtg      50

SEQ ID NO: 255      moltype = DNA  length = 47
FEATURE            Location/Qualifiers
misc_feature        1..47
                    note = Primer
source              1..47
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 255
aatgtacagt attgcgtttt gttgcccttc tggaaattac cccgaga          47

SEQ ID NO: 256      moltype = DNA  length = 55
FEATURE            Location/Qualifiers
misc_feature        1..55
                    note = Primer
source              1..55
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 256
aatgtacagt attgcgtttt gagttccacc agctttaatt attcctctag ctctc  55

SEQ ID NO: 257      moltype = DNA  length = 56
FEATURE            Location/Qualifiers
misc_feature        1..56
                    note = Primer
source              1..56
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 257
aatgtacagt attgcgtttt ggtttcccat ggccataatt tattatctca ccacaa  56

SEQ ID NO: 258      moltype = DNA  length = 48
FEATURE            Location/Qualifiers
misc_feature        1..48
                    note = Primer
source              1..48
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 258
aatgtacagt attgcgtttt ggtcacgatg actgtattgg accctcaa          48

SEQ ID NO: 259      moltype = DNA  length = 56
FEATURE            Location/Qualifiers
misc_feature        1..56
                    note = Primer
source              1..56

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	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 259		
aatgtacagt attgcgtttt gtccagacct ttgctttaga ttggcaatta ttactg		56
SEQ ID NO: 260	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer	
source	1..51	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 260		
aatgtacagt attgcgtttt gccctaacaa cacagaagca aagcggttctt t		51
SEQ ID NO: 261	moltype = DNA length = 45	
FEATURE	Location/Qualifiers	
misc_feature	1..45	
	note = Primer	
source	1..45	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 261		
aatgtacagt attgcgtttt gcgcctcctt accacctgta ctacg		45
SEQ ID NO: 262	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
	note = Primer	
source	1..46	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 262		
aatgtacagt attgcgtttt gactatccag gcgccttcac ctactc		46
SEQ ID NO: 263	moltype = DNA length = 47	
FEATURE	Location/Qualifiers	
misc_feature	1..47	
	note = Primer	
source	1..47	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 263		
aatgtacagt attgcgtttt gctcctaggc ggtatcatcc tgggtag		47
SEQ ID NO: 264	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer	
source	1..51	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 264		
aatgtacagt attgcgtttt gcttgattct cttcagatac aaggcagatc c		51
SEQ ID NO: 265	moltype = DNA length = 55	
FEATURE	Location/Qualifiers	
misc_feature	1..55	
	note = Primer	
source	1..55	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 265		
aatgtacagt attgcgtttt ggcagatact tggacttgag taggcttatt aaacc		55
SEQ ID NO: 266	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 266		
aatgtacagt attgcgtttt ggcggctcta taaagaattg tccttatattt cgaactt		57
SEQ ID NO: 267	moltype = DNA length = 48	

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FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 267		
aatgtacagt attgcgtttt ggttcgaggc ctttctctga gcatcaag		48
SEQ ID NO: 268	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer	
source	1..51	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 268		
aatgtacagt attgcgtttt gacatcggca gaaactagat gatcagacca a		51
SEQ ID NO: 269	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 269		
aatgtacagt attgcgtttt gtttaggaaa tccacaatac tttttctgat ctcttcc		57
SEQ ID NO: 270	moltype = DNA length = 53	
FEATURE	Location/Qualifiers	
misc_feature	1..53	
	note = Primer	
source	1..53	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 270		
aatgtacagt attgcgtttt ggccaccaac ctcattctgt tttgttctct atc		53
SEQ ID NO: 271	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer	
source	1..51	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 271		
aatgtacagt attgcgtttt gctgcatttg tcctttgact ggtgtttagg t		51
SEQ ID NO: 272	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
	note = Primer	
source	1..52	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 272		
aatgtacagt attgcgtttt gcttcgaccg acaaacctga ggtcattaaa tc		52
SEQ ID NO: 273	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
	note = Primer	
source	1..46	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 273		
aatgtacagt attgcgtttt gccccacatc ccaagctagg aagacc		46
SEQ ID NO: 274	moltype = DNA length = 45	
FEATURE	Location/Qualifiers	
misc_feature	1..45	
	note = Primer	
source	1..45	
	mol_type = other DNA	
	organism = synthetic construct	



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SEQUENCE: 274  
aatgtacagt attgcgtttt gcgggccagt accttgaaag cgatg 45

SEQ ID NO: 275           moltype = DNA   length = 51  
FEATURE                Location/Qualifiers  
misc\_feature           1..51  
                        note = Primer  
source                  1..51  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 275  
aatgtacagt attgcgtttt gctaactcaa tcggcttggt gtgatgcgta t 51

SEQ ID NO: 276           moltype = DNA   length = 51  
FEATURE                Location/Qualifiers  
misc\_feature           1..51  
                        note = Primer  
source                  1..51  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 276  
aatgtacagt attgcgtttt gccctcctgg actgtagta acttagtcct c 51

SEQ ID NO: 277           moltype = DNA   length = 42  
FEATURE                Location/Qualifiers  
misc\_feature           1..42  
                        note = Primer  
source                  1..42  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 277  
aatgtacagt attgcgtttt gccctccgag ctccgcgaaa at 42

SEQ ID NO: 278           moltype = DNA   length = 57  
FEATURE                Location/Qualifiers  
misc\_feature           1..57  
                        note = Primer  
source                  1..57  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 278  
aatgtacagt attgcgtttt ggtgctaaaa agtgaagaa gaaatgagct agcaaaa 57

SEQ ID NO: 279           moltype = DNA   length = 55  
FEATURE                Location/Qualifiers  
misc\_feature           1..55  
                        note = Primer  
source                  1..55  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 279  
aatgtacagt attgcgtttt gcatatgcct cagtttgaat tcctctcaca aacaa 55

SEQ ID NO: 280           moltype = DNA   length = 51  
FEATURE                Location/Qualifiers  
misc\_feature           1..51  
                        note = Primer  
source                  1..51  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 280  
aatgtacagt attgcgtttt ggggagaaga aagagagatg tagggctaga g 51

SEQ ID NO: 281           moltype = DNA   length = 54  
FEATURE                Location/Qualifiers  
misc\_feature           1..54  
                        note = Primer  
source                  1..54  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 281  
aatgtacagt attgcgtttt ggcaagcact tctgtttttg tcttttcagt ttcg 54

SEQ ID NO: 282           moltype = DNA   length = 57  
FEATURE                Location/Qualifiers  
misc\_feature           1..57

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source	note = Primer 1..57 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 282		
aatgtacagt attgcgtttt gtctctgata tacttggatt ggtaattgag aaagtct		57
SEQ ID NO: 283	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
source	note = Primer 1..57 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 283		
aatgtacagt attgcgtttt ggtttgatat cttcccagca aaataatcag ctctcat		57
SEQ ID NO: 284	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
source	note = Primer 1..51 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 284		
aatgtacagt attgcgtttt gtagccaacc tcttttcgat gagctcacta g		51
SEQ ID NO: 285	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
source	note = Primer 1..51 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 285		
aatgtacagt attgcgtttt gtggaacaga caaactatcg actgaagttg t		51
SEQ ID NO: 286	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
source	note = Primer 1..48 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 286		
aatgtacagt attgcgtttt ggaggctgag tgcaaatttg gtctggaa		48
SEQ ID NO: 287	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
source	note = Primer 1..50 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 287		
aatgtacagt attgcgtttt ggatgggtgt ggttgtctct gatgattacc		50
SEQ ID NO: 288	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
source	note = Primer 1..46 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 288		
aatgtacagt attgcgtttt ggcaaggcga gtccagaacc aagatt		46
SEQ ID NO: 289	moltype = DNA length = 47	
FEATURE	Location/Qualifiers	
misc_feature	1..47	
source	note = Primer 1..47 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 289		
aatgtacagt attgcgtttt gtcagaagcg actgatcccc atcaagt		47

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SEQ ID NO: 290           moltype = DNA   length = 56  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..56  
                         note = Primer  
 source                 1..56  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 290  
 aatgtacagt attgcgtttt gcatatgggtc acatcacctt aactaaaccc atgttt   56  
  
 SEQ ID NO: 291           moltype = DNA   length = 57  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..57  
                         note = Primer  
 source                 1..57  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 291  
 aatgtacagt attgcgtttt gtttctcggt actgtttatt ttgaacaaaa ccaatcc   57  
  
 SEQ ID NO: 292           moltype = DNA   length = 51  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..51  
                         note = Primer  
 source                 1..51  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 292  
 aatgtacagt attgcgtttt gcctcctccc caaatccag gaacaatatg a       51  
  
 SEQ ID NO: 293           moltype = DNA   length = 57  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..57  
                         note = Primer  
 source                 1..57  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 293  
 aatgtacagt attgcgtttt gtgtgcgtca ttttatttgg gaaaatttga tactaac   57  
  
 SEQ ID NO: 294           moltype = DNA   length = 46  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..46  
                         note = Primer  
 source                 1..46  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 294  
 aatgtacagt attgcgtttt gcatgcagga gaagtcatcc cccttc           46  
  
 SEQ ID NO: 295           moltype = DNA   length = 51  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..51  
                         note = Primer  
 source                 1..51  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 295  
 aatgtacagt attgcgtttt gctgaaaac tggtggttgc ctctaggtta a       51  
  
 SEQ ID NO: 296           moltype = DNA   length = 48  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..48  
                         note = Primer  
 source                 1..48  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 296  
 aatgtacagt attgcgtttt ggcccccttc ttgctcttct tggacttg       48  
  
 SEQ ID NO: 297           moltype = DNA   length = 48  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..48  
                         note = Primer  
 source                 1..48

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 297		
aatgtacagt attgcgtttt gccaaagccaa gccaaagctgg atattgtg		48
SEQ ID NO: 298	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 298		
aatgtacagt attgcgtttt gcactcacat tgtgcagctt gtagtagag		49
SEQ ID NO: 299	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 299		
aatgtacagt attgcgtttt ggcaaagcgt ctgcatttga aggagttt		48
SEQ ID NO: 300	moltype = DNA length = 45	
FEATURE	Location/Qualifiers	
misc_feature	1..45	
	note = Primer	
source	1..45	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 300		
aatgtacagt attgcgtttt gccctcccga gaacttgccg gttaa		45
SEQ ID NO: 301	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
	note = Primer	
source	1..46	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 301		
aatgtacagt attgcgtttt ggctccccac cacaaaaacg caaatg		46
SEQ ID NO: 302	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 302		
aatgtacagt attgcgtttt ggtgtcactg acggagagca tgaagatg		48
SEQ ID NO: 303	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
	note = Primer	
source	1..46	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 303		
aatgtacagt attgcgtttt gccacccaaa gaagtgtctc ctgacc		46
SEQ ID NO: 304	moltype = DNA length = 47	
FEATURE	Location/Qualifiers	
misc_feature	1..47	
	note = Primer	
source	1..47	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 304		
aatgtacagt attgcgtttt gtccgtcagt gacacctggt acttgac		47
SEQ ID NO: 305	moltype = DNA length = 48	

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FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 305		
aatgtacagt attgcgtttt gccctagctc tgcctaccct gatctttc		48
SEQ ID NO: 306	moltype = DNA length = 47	
FEATURE	Location/Qualifiers	
misc_feature	1..47	
	note = Primer	
source	1..47	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 306		
aatgtacagt attgcgtttt gacgaggtgg acgtcttctt caatcac		47
SEQ ID NO: 307	moltype = DNA length = 43	
FEATURE	Location/Qualifiers	
misc_feature	1..43	
	note = Primer	
source	1..43	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 307		
aatgtacagt attgcgtttt ggccctgcga gtcgaggtga ttg		43
SEQ ID NO: 308	moltype = DNA length = 53	
FEATURE	Location/Qualifiers	
misc_feature	1..53	
	note = Primer	
source	1..53	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 308		
aatgtacagt attgcgtttt gccatgactc tcaggaattg gccctatact tag		53
SEQ ID NO: 309	moltype = DNA length = 56	
FEATURE	Location/Qualifiers	
misc_feature	1..56	
	note = Primer	
source	1..56	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 309		
aatgtacagt attgcgtttt gcttgggacc ttcatttcta tataaccctc atctgg		56
SEQ ID NO: 310	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 310		
aatgtacagt attgcgtttt gtgccaggaa acttttcatt gtgcctctc		49
SEQ ID NO: 311	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
	note = Primer	
source	1..50	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 311		
aatgtacagt attgcgtttt ggttacccca tggaacttac caagcactag		50
SEQ ID NO: 312	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	

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SEQUENCE: 312  
aatgtacagt attgcggtttt ggtatgaaat tcgctggagg gtcattgaat caat 54

SEQ ID NO: 313           moltype = DNA   length = 52  
FEATURE                Location/Qualifiers  
misc\_feature           1..52  
                          note = Primer  
source                  1..52  
                          mol\_type = other DNA  
                          organism = synthetic construct

SEQUENCE: 313  
aatgtacagt attgcggtttt gcaggaagga gcacttacgt tttagcatct tc 52

SEQ ID NO: 314           moltype = DNA   length = 57  
FEATURE                Location/Qualifiers  
misc\_feature           1..57  
                          note = Primer  
source                  1..57  
                          mol\_type = other DNA  
                          organism = synthetic construct

SEQUENCE: 314  
aatgtacagt attgcggtttt ggattttgag aaattccctt aatatcccca tgctcaa 57

SEQ ID NO: 315           moltype = DNA   length = 49  
FEATURE                Location/Qualifiers  
misc\_feature           1..49  
                          note = Primer  
source                  1..49  
                          mol\_type = other DNA  
                          organism = synthetic construct

SEQUENCE: 315  
aatgtacagt attgcggtttt gcacaaccac atgtgtccag tgaaaatcc 49

SEQ ID NO: 316           moltype = DNA   length = 49  
FEATURE                Location/Qualifiers  
misc\_feature           1..49  
                          note = Primer  
source                  1..49  
                          mol\_type = other DNA  
                          organism = synthetic construct

SEQUENCE: 316  
aatgtacagt attgcggtttt gtgctttcat cagcagggtt caatocaaa 49

SEQ ID NO: 317           moltype = DNA   length = 57  
FEATURE                Location/Qualifiers  
misc\_feature           1..57  
                          note = Primer  
source                  1..57  
                          mol\_type = other DNA  
                          organism = synthetic construct

SEQUENCE: 317  
aatgtacagt attgcggtttt gcatttacat catcacagag tattgcttct atggaga 57

SEQ ID NO: 318           moltype = DNA   length = 56  
FEATURE                Location/Qualifiers  
misc\_feature           1..56  
                          note = Primer  
source                  1..56  
                          mol\_type = other DNA  
                          organism = synthetic construct

SEQUENCE: 318  
aatgtacagt attgcggtttt ggtgatctct ggatgtcgga atatttagaa acctct 56

SEQ ID NO: 319           moltype = DNA   length = 57  
FEATURE                Location/Qualifiers  
misc\_feature           1..57  
                          note = Primer  
source                  1..57  
                          mol\_type = other DNA  
                          organism = synthetic construct

SEQUENCE: 319  
aatgtacagt attgcggtttt gatcttttga aaacaatggt gactacatgg acatgaa 57

SEQ ID NO: 320           moltype = DNA   length = 54  
FEATURE                Location/Qualifiers  
misc\_feature           1..54

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source	note = Primer 1..54 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 320		
aatgtacagt attgcgtttt gggctctaaaa aggtctgtgt tccttgaact taca		54
SEQ ID NO: 321		
FEATURE	moltype = DNA length = 56 Location/Qualifiers	
misc_feature	1..56	
source	note = Primer 1..56 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 321		
aatgtacagt attgcgtttt gccagcacca atacatttaa tttcttttct gcagac		56
SEQ ID NO: 322		
FEATURE	moltype = DNA length = 51 Location/Qualifiers	
misc_feature	1..51	
source	note = Primer 1..51 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 322		
aatgtacagt attgcgtttt ggctacagat ggcttgatcc tgagtcattt c		51
SEQ ID NO: 323		
FEATURE	moltype = DNA length = 48 Location/Qualifiers	
misc_feature	1..48	
source	note = Primer 1..48 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 323		
aatgtacagt attgcgtttt ggtcaggccc ataccaaggg aaaagatc		48
SEQ ID NO: 324		
FEATURE	moltype = DNA length = 51 Location/Qualifiers	
misc_feature	1..51	
source	note = Primer 1..51 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 324		
aatgtacagt attgcgtttt gacactgagt gatgtctggt cttatggcat t		51
SEQ ID NO: 325		
FEATURE	moltype = DNA length = 50 Location/Qualifiers	
misc_feature	1..50	
source	note = Primer 1..50 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 325		
aatgtacagt attgcgtttt gcactgagcg tttgttagtc ctggtgtttt		50
SEQ ID NO: 326		
FEATURE	moltype = DNA length = 53 Location/Qualifiers	
misc_feature	1..53	
source	note = Primer 1..53 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 326		
aatgtacagt attgcgtttt gcagattctc cacaatctca ctcaggtggt aaa		53
SEQ ID NO: 327		
FEATURE	moltype = DNA length = 49 Location/Qualifiers	
misc_feature	1..49	
source	note = Primer 1..49 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 327		
aatgtacagt attgcgtttt gccccacagc tacgagatca tgggtgaaat		49

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SEQ ID NO: 328           moltype = DNA   length = 57  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..57  
                         note = Primer  
 source                 1..57  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 328  
 aatgtacagt attgcgtttt gtctctattc atttttgagg ttggttggtt aacactt   57  
  
 SEQ ID NO: 329           moltype = DNA   length = 48  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..48  
                         note = Primer  
 source                 1..48  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 329  
 aatgtacagt attgcgtttt ggggagtgca ccattatcgg gaaaatgg           48  
  
 SEQ ID NO: 330           moltype = DNA   length = 56  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..56  
                         note = Primer  
 source                 1..56  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 330  
 aatgtacagt attgcgtttt ggcttattct cattcgtttc atccaggatc tcaaaa   56  
  
 SEQ ID NO: 331           moltype = DNA   length = 46  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..46  
                         note = Primer  
 source                 1..46  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 331  
 aatgtacagt attgcgtttt ggggcgacga gattaggctg ttatgc           46  
  
 SEQ ID NO: 332           moltype = DNA   length = 49  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..49  
                         note = Primer  
 source                 1..49  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 332  
 aatgtacagt attgcgtttt gccctctctgc attataagca gtgccaaaa       49  
  
 SEQ ID NO: 333           moltype = DNA   length = 50  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..50  
                         note = Primer  
 source                 1..50  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 333  
 aatgtacagt attgcgtttt ggccacatc gttgtaagcc ttacattcaa       50  
  
 SEQ ID NO: 334           moltype = DNA   length = 50  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..50  
                         note = Primer  
 source                 1..50  
                         mol\_type = other DNA  
                         organism = synthetic construct  
  
 SEQUENCE: 334  
 aatgtacagt attgcgtttt gccgtttgga aagctagtgg ttcagagttc       50  
  
 SEQ ID NO: 335           moltype = DNA   length = 50  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..50  
                         note = Primer  
 source                 1..50



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	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 335		
aatgtacagt attgcgtttt ggagatccca tcctgccaaa gtttgtgatt		50
SEQ ID NO: 336	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
	note = Primer	
source	1..50	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 336		
aatgtacagt attgcgtttt gggaaagccc ctgtttcata ctgacaaaaa		50
SEQ ID NO: 337	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer	
source	1..51	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 337		
aatgtacagt attgcgtttt gctttctccc cacagaaacc catgtatgaa g		51
SEQ ID NO: 338	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer	
source	1..51	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 338		
aatgtacagt attgcgtttt ggtttgccag ttgtgctttt tgctaaaatg c		51
SEQ ID NO: 339	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 339		
aatgtacagt attgcgtttt gccctccac cctcaggact ataccaat		48
SEQ ID NO: 340	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
	note = Primer	
source	1..46	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 340		
aatgtacagt attgcgtttt gtgctcggca gattgggata gtccg		46
SEQ ID NO: 341	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
	note = Primer	
source	1..50	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 341		
aatgtacagt attgcgtttt gggcatcctc tgtcctatct cccagataca		50
SEQ ID NO: 342	moltype = DNA length = 56	
FEATURE	Location/Qualifiers	
misc_feature	1..56	
	note = Primer	
source	1..56	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 342		
aatgtacagt attgcgtttt gaggttttat actaaactta ctttgactgg gtttgg		56
SEQ ID NO: 343	moltype = DNA length = 45	

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FEATURE	Location/Qualifiers	
misc_feature	1..45	
	note = Primer	
source	1..45	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 343		
aatgtacagt attgcgtttt gccccagag gtaagcgta tatgg		45
SEQ ID NO: 344	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 344		
aatgtacagt attgcgtttt ggcacaggga agtaggtact gggagattg		49
SEQ ID NO: 345	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 345		
aatgtacagt attgcgtttt gaggcctgca aggttttaac tggaccta		48
SEQ ID NO: 346	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 346		
aatgtacagt attgcgtttt gcgaggctg ataagtggta cctgtatgt		49
SEQ ID NO: 347	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 347		
aatgtacagt attgcgtttt ggaaaagggt cccaggtagg tccagttaa		49
SEQ ID NO: 348	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 348		
aatgtacagt attgcgtttt gctctcggtg tatttctcta cttacctgta ataatgc		57
SEQ ID NO: 349	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 349		
aatgtacagt attgcgtttt gtttattgat gtctatgaag tggtgtggtt ccttaac		57
SEQ ID NO: 350	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA	
	organism = synthetic construct	

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SEQUENCE: 350  
aatgtacagt attgcgtttt gcagaaaaca agctgccgca aagttctac 49

SEQ ID NO: 351           moltype = DNA   length = 48  
FEATURE                Location/Qualifiers  
misc\_feature           1..48  
                        note = Primer  
source                  1..48  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 351  
aatgtacagt attgcgtttt gcagggtgtg cgatgatgac actgtacg 48

SEQ ID NO: 352           moltype = DNA   length = 57  
FEATURE                Location/Qualifiers  
misc\_feature           1..57  
                        note = Primer  
source                  1..57  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 352  
aatgtacagt attgcgtttt gtcatttttc attggacttg tttgtcagc tttttgg 57

SEQ ID NO: 353           moltype = DNA   length = 55  
FEATURE                Location/Qualifiers  
misc\_feature           1..55  
                        note = Primer  
source                  1..55  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 353  
aatgtacagt attgcgtttt ggtagcccc aatatgaaaa ataaagctgg ttgga 55

SEQ ID NO: 354           moltype = DNA   length = 53  
FEATURE                Location/Qualifiers  
misc\_feature           1..53  
                        note = Primer  
source                  1..53  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 354  
aatgtacagt attgcgtttt gctgggtgga ggtttttgct aaatctggaa tga 53

SEQ ID NO: 355           moltype = DNA   length = 57  
FEATURE                Location/Qualifiers  
misc\_feature           1..57  
                        note = Primer  
source                  1..57  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 355  
aatgtacagt attgcgtttt gttctttttg actagaaac ttcagccact gtgtatt 57

SEQ ID NO: 356           moltype = DNA   length = 55  
FEATURE                Location/Qualifiers  
misc\_feature           1..55  
                        note = Primer  
source                  1..55  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 356  
aatgtacagt attgcgtttt gcatatgacc aattgcagat gagccatta ttgaa 55

SEQ ID NO: 357           moltype = DNA   length = 51  
FEATURE                Location/Qualifiers  
misc\_feature           1..51  
                        note = Primer  
source                  1..51  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 357  
aatgtacagt attgcgtttt gaggcatagc tgactcatct atgtttgttc t 51

SEQ ID NO: 358           moltype = DNA   length = 57  
FEATURE                Location/Qualifiers  
misc\_feature           1..57

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source                note = Primer
                      1..57
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 358
aatgtacagt attgcgtttt gttctctcatt tctttcactc tgacagtata aaggtaa      57

SEQ ID NO: 359        moltype = DNA length = 54
FEATURE              Location/Qualifiers
misc_feature          1..54
                      note = Primer
source               1..54
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 359
aatgtacagt attgcgtttt ggaactattc caacagaaca aaccgataac atca      54

SEQ ID NO: 360        moltype = DNA length = 53
FEATURE              Location/Qualifiers
misc_feature          1..53
                      note = Primer
source               1..53
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 360
aatgtacagt attgcgtttt gtggatagca agacaattag agcccaactt agt      53

SEQ ID NO: 361        moltype = DNA length = 54
FEATURE              Location/Qualifiers
misc_feature          1..54
                      note = Primer
source               1..54
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 361
aatgtacagt attgcgtttt gctactcttc ctgtctcttt ccacatcatc aatt      54

SEQ ID NO: 362        moltype = DNA length = 57
FEATURE              Location/Qualifiers
misc_feature          1..57
                      note = Primer
source               1..57
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 362
aatgtacagt attgcgtttt gaggacctta tgttgtatgc tgtataaatc taaaggt      57

SEQ ID NO: 363        moltype = DNA length = 57
FEATURE              Location/Qualifiers
misc_feature          1..57
                      note = Primer
source               1..57
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 363
aatgtacagt attgcgtttt ggtttgtcat cttctatggt aagtatcttt ctggatg      57

SEQ ID NO: 364        moltype = DNA length = 57
FEATURE              Location/Qualifiers
misc_feature          1..57
                      note = Primer
source               1..57
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 364
aatgtacagt attgcgtttt gtggaggaga aacagataaa agttgagtat acgttta      57

SEQ ID NO: 365        moltype = DNA length = 54
FEATURE              Location/Qualifiers
misc_feature          1..54
                      note = Primer
source               1..54
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 365
aatgtacagt attgcgtttt ggaggatgac gacatgtag taagcactac tact      54

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SEQ ID NO: 366      moltype = DNA  length = 57
FEATURE            Location/Qualifiers
misc_feature        1..57
                    note = Primer
source              1..57
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 366
aatgtacagt attgcgtttt gattccacca tcatttcctt ctccaaaatt atcatcc      57

SEQ ID NO: 367      moltype = DNA  length = 53
FEATURE            Location/Qualifiers
misc_feature        1..53
                    note = Primer
source              1..53
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 367
aatgtacagt attgcgtttt gctcaaaagc actgccttct ctcattatct cac          53

SEQ ID NO: 368      moltype = DNA  length = 57
FEATURE            Location/Qualifiers
misc_feature        1..57
                    note = Primer
source              1..57
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 368
aatgtacagt attgcgtttt gaatgtattt gaccttcttt taaagtgaca tcgatgt      57

SEQ ID NO: 369      moltype = DNA  length = 55
FEATURE            Location/Qualifiers
misc_feature        1..55
                    note = Primer
source              1..55
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 369
aatgtacagt attgcgtttt gtgatgttcc caacttcttc tctcatgggt atctc      55

SEQ ID NO: 370      moltype = DNA  length = 56
FEATURE            Location/Qualifiers
misc_feature        1..56
                    note = Primer
source              1..56
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 370
aatgtacagt attgcgtttt gccctctgat cctagataa tttatgggta gctaga      56

SEQ ID NO: 371      moltype = DNA  length = 55
FEATURE            Location/Qualifiers
misc_feature        1..55
                    note = Primer
source              1..55
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 371
aatgtacagt attgcgtttt gcacgaaatg caggttttgg aatatgatta atgtt      55

SEQ ID NO: 372      moltype = DNA  length = 56
FEATURE            Location/Qualifiers
misc_feature        1..56
                    note = Primer
source              1..56
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 372
aatgtacagt attgcgtttt ggaacaatgt tctacgcaca tttgttctc agtaaa      56

SEQ ID NO: 373      moltype = DNA  length = 50
FEATURE            Location/Qualifiers
misc_feature        1..50
                    note = Primer
source              1..50

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 373		
aatgtacagt attgcgtttt gtccacgctg ctctctaaat tacactcgaa		50
SEQ ID NO: 374	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer	
source	1..54	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 374		
aatgtacagt attgcgtttt gacgtagaac acatttcatt ttactcctct ttgg		54
SEQ ID NO: 375	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 375		
aatgtacagt attgcgtttt ggtcacatga atgtaaatca agaaaacaga tgttggt		57
SEQ ID NO: 376	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 376		
aatgtacagt attgcgtttt gttctgaact atttatggac aacagtcaaa caacaat		57
SEQ ID NO: 377	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 377		
aatgtacagt attgcgtttt gtgaagccat tgcgagaact ttatccataa gtatttc		57
SEQ ID NO: 378	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer	
source	1..51	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 378		
aatgtacagt attgcgtttt ggccagagca catgaataaa tgagcatcca t		51
SEQ ID NO: 379	moltype = DNA length = 53	
FEATURE	Location/Qualifiers	
misc_feature	1..53	
	note = Primer	
source	1..53	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 379		
aatgtacagt attgcgtttt gggaagctct cagggtacaa attctcagat cat		53
SEQ ID NO: 380	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer	
source	1..54	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 380		
aatgtacagt attgcgtttt gctcagggtgta caaattctca gatcatcagt cctc		54
SEQ ID NO: 381	moltype = DNA length = 49	

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FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 381		
aatgtacagt attgcgtttt gctctacaca agcttccttt cgcgcacgc		49
SEQ ID NO: 382	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
	note = Primer	
source	1..52	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 382		
aatgtacagt attgcgtttt gcccttcaga tcttctcagc attcgagaga tc		52
SEQ ID NO: 383	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 383		
aatgtacagt attgcgtttt gaatcgaagc gctacctgat tccaattcc		49
SEQ ID NO: 384	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
	note = Primer	
source	1..46	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 384		
aatgtacagt attgcgtttt gccgaccgta actattcggt gcgttg		46
SEQ ID NO: 385	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 385		
aatgtacagt attgcgtttt gacattctat ccaagctgtg ttctatcttg agaaact		57
SEQ ID NO: 386	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 386		
aatgtacagt attgcgtttt gcgagtgagg gttttcgttg ttcacatc		48
SEQ ID NO: 387	moltype = DNA length = 45	
FEATURE	Location/Qualifiers	
misc_feature	1..45	
	note = Primer	
source	1..45	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 387		
aatgtacagt attgcgtttt gcgtgggtcc cagctctgcag ttaag		45
SEQ ID NO: 388	moltype = DNA length = 44	
FEATURE	Location/Qualifiers	
misc_feature	1..44	
	note = Primer	
source	1..44	
	mol_type = other DNA	
	organism = synthetic construct	

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SEQUENCE: 388  
 aatgtacagt attgcgtttt ggctcagagc cgttccgaga tctt 44

SEQ ID NO: 389           moltype = DNA   length = 48  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..48  
                         note = Primer  
 source                  1..48  
                         mol\_type = other DNA  
                         organism = synthetic construct

SEQUENCE: 389  
 aatgtacagt attgcgtttt ggcgttccat ctcccacttg tcgtagtt 48

SEQ ID NO: 390           moltype = DNA   length = 49  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..49  
                         note = Primer  
 source                  1..49  
                         mol\_type = other DNA  
                         organism = synthetic construct

SEQUENCE: 390  
 aatgtacagt attgcgtttt gctggccgag ttggttcac atcattcaa 49

SEQ ID NO: 391           moltype = DNA   length = 48  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..48  
                         note = Primer  
 source                  1..48  
                         mol\_type = other DNA  
                         organism = synthetic construct

SEQUENCE: 391  
 aatgtacagt attgcgtttt gatatgtgtg tccccaaact acgacaag 48

SEQ ID NO: 392           moltype = DNA   length = 57  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..57  
                         note = Primer  
 source                  1..57  
                         mol\_type = other DNA  
                         organism = synthetic construct

SEQUENCE: 392  
 aatgtacagt attgcgtttt gtgaaaagca cttcctgaaa taatttcacc ttcgttt 57

SEQ ID NO: 393           moltype = DNA   length = 47  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..47  
                         note = Primer  
 source                  1..47  
                         mol\_type = other DNA  
                         organism = synthetic construct

SEQUENCE: 393  
 aatgtacagt attgcgtttt gaggtactcc atggctgacg agatctg 47

SEQ ID NO: 394           moltype = DNA   length = 48  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..48  
                         note = Primer  
 source                  1..48  
                         mol\_type = other DNA  
                         organism = synthetic construct

SEQUENCE: 394  
 aatgtacagt attgcgtttt gttgcctttg ttccaaggtc caatgtgt 48

SEQ ID NO: 395           moltype = DNA   length = 43  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..43  
                         note = Primer  
 source                  1..43  
                         mol\_type = other DNA  
                         organism = synthetic construct

SEQUENCE: 395  
 aatgtacagt attgcgtttt gcgtccccgc attccaacgt ctc 43

SEQ ID NO: 396           moltype = DNA   length = 42  
 FEATURE                Location/Qualifiers  
 misc\_feature           1..42



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source	note = Primer 1..42 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 396		
aatgtacagt attgcgtttt gggcgcgccg ttacttgaa gg		42
SEQ ID NO: 397	moltype = DNA length = 44	
FEATURE	Location/Qualifiers	
misc_feature	1..44	
source	note = Primer 1..44 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 397		
aatgtacagt attgcgtttt ggcctggcgg tgcacactat tctg		44
SEQ ID NO: 398	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
source	note = Primer 1..48 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 398		
aatgtacagt attgcgtttt gaggtgcagc caaaaactt acagatgc		48
SEQ ID NO: 399	moltype = DNA length = 45	
FEATURE	Location/Qualifiers	
misc_feature	1..45	
source	note = Primer 1..45 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 399		
aatgtacagt attgcgtttt ggtgccgaac caatacaacc ctctg		45
SEQ ID NO: 400	moltype = DNA length = 43	
FEATURE	Location/Qualifiers	
misc_feature	1..43	
source	note = Primer 1..43 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 400		
aatgtacagt attgcgtttt gggcggggtc caccagttag aat		43
SEQ ID NO: 401	moltype = DNA length = 44	
FEATURE	Location/Qualifiers	
misc_feature	1..44	
source	note = Primer 1..44 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 401		
aatgtacagt attgcgtttt gccgcagagg gttgtattgg ttcg		44
SEQ ID NO: 402	moltype = DNA length = 47	
FEATURE	Location/Qualifiers	
misc_feature	1..47	
source	note = Primer 1..47 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 402		
aatgtacagt attgcgtttt gagccactcg cattgacat tcaaact		47
SEQ ID NO: 403	moltype = DNA length = 44	
FEATURE	Location/Qualifiers	
misc_feature	1..44	
source	note = Primer 1..44 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 403		
aatgtacagt attgcgtttt gccacgtctg acaggtagcc atgg		44

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SEQ ID NO: 404      moltype = DNA  length = 45
FEATURE            Location/Qualifiers
misc_feature        1..45
                    note = Primer
source              1..45
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 404
aatgtacagt attgcgtttt ggtgaggctg ctggacgagt acaac          45

SEQ ID NO: 405      moltype = DNA  length = 43
FEATURE            Location/Qualifiers
misc_feature        1..43
                    note = Primer
source              1..43
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 405
aatgtacagt attgcgtttt ggcaccagg ttgtactcgt cca            43

SEQ ID NO: 406      moltype = DNA  length = 46
FEATURE            Location/Qualifiers
misc_feature        1..46
                    note = Primer
source              1..46
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 406
aatgtacagt attgcgtttt gccgcctttg tgcttctgtt cttcgt       46

SEQ ID NO: 407      moltype = DNA  length = 57
FEATURE            Location/Qualifiers
misc_feature        1..57
                    note = Primer
source              1..57
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 407
aatgtacagt attgcgtttt gctgattaat cgcgtagaaa atgaccttat ttggag  57

SEQ ID NO: 408      moltype = DNA  length = 49
FEATURE            Location/Qualifiers
misc_feature        1..49
                    note = Primer
source              1..49
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 408
aatgtacagt attgcgtttt ggtccatcg tctacctgga gattgacaa      49

SEQ ID NO: 409      moltype = DNA  length = 45
FEATURE            Location/Qualifiers
misc_feature        1..45
                    note = Primer
source              1..45
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 409
aatgtacagt attgcgtttt gtctgcacgg cctcgatctt gtagg         45

SEQ ID NO: 410      moltype = DNA  length = 48
FEATURE            Location/Qualifiers
misc_feature        1..48
                    note = Primer
source              1..48
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 410
aatgtacagt attgcgtttt ggccagcaga tgatcttccc ctactacg      48

SEQ ID NO: 411      moltype = DNA  length = 44
FEATURE            Location/Qualifiers
misc_feature        1..44
                    note = Primer
source              1..44

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 411		
aatgtacagt attgcgtttt gcgtcacgct tgaagaccac gttg		44
SEQ ID NO: 412	moltype = DNA length = 45	
FEATURE	Location/Qualifiers	
misc_feature	1..45	
	note = Primer	
source	1..45	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 412		
aatgtacagt attgcgtttt ggccagcatg cagttctaag gctct		45
SEQ ID NO: 413	moltype = DNA length = 43	
FEATURE	Location/Qualifiers	
misc_feature	1..43	
	note = Primer	
source	1..43	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 413		
aatgtacagt attgcgtttt ggtgcccgctc tcgactctta ggc		43
SEQ ID NO: 414	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer	
source	1..49	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 414		
aatgtacagt attgcgtttt gtgtagccgc tgatcgctcg gtatatgtc		49
SEQ ID NO: 415	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 415		
aatgtacagt attgcgtttt ggactgggtac tgggttagtaa aggttgataa tattcca		57
SEQ ID NO: 416	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 416		
aatgtacagt attgcgtttt ggggtgaagta atcagtttgt tcaactagtta cgtgatt		57
SEQ ID NO: 417	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 417		
aatgtacagt attgcgtttt gctgacatgc ctactgatta ttcttcaaac tcatcac		57
SEQ ID NO: 418	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 418		
aatgtacagt attgcgtttt gtgtgtgttt taattgttcc acttgagatt cttaacc		57
SEQ ID NO: 419	moltype = DNA length = 57	

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FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 419		
aatgtacagt attgcgtttt gcgtcagcat ttggaatcac ttcattctga catgata		57
SEQ ID NO: 420	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 420		
aatgtacagt attgcgtttt gagtaatttt caactattgg cctagtgaat ttaagct		57
SEQ ID NO: 421	moltype = DNA length = 55	
FEATURE	Location/Qualifiers	
misc_feature	1..55	
	note = Primer	
source	1..55	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 421		
aatgtacagt attgcgtttt gagaaagagg gaagtcacat ttatagagtg ctage		55
SEQ ID NO: 422	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 422		
aatgtacagt attgcgtttt gcatcaacag aaacagaaca acaaactgtg acaaatc		57
SEQ ID NO: 423	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 423		
aatgtacagt attgcgtttt gccaaagaat atccctttat atagcagtgg aacaatt		57
SEQ ID NO: 424	moltype = DNA length = 55	
FEATURE	Location/Qualifiers	
misc_feature	1..55	
	note = Primer	
source	1..55	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 424		
aatgtacagt attgcgtttt gcagaatatg cagtgataag tgctgtttca tcact		55
SEQ ID NO: 425	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 425		
aatgtacagt attgcgtttt gttccccctg tgacgactac ttttctc		48
SEQ ID NO: 426	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	

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SEQUENCE: 426  
aatgtacagt attgcgtttt gcgggtcccta tttcttcctc tgettcgt 48

SEQ ID NO: 427           moltype = DNA   length = 52  
FEATURE                Location/Qualifiers  
misc\_feature           1..52  
                        note = Primer  
source                  1..52  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 427  
aatgtacagt attgcgtttt gctgaacagt tctgtctcta ttaccgcacc tc 52

SEQ ID NO: 428           moltype = DNA   length = 52  
FEATURE                Location/Qualifiers  
misc\_feature           1..52  
                        note = Primer  
source                  1..52  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 428  
aatgtacagt attgcgtttt gcgttcatag ccttctatcc gagtatgtag ca 52

SEQ ID NO: 429           moltype = DNA   length = 47  
FEATURE                Location/Qualifiers  
misc\_feature           1..47  
                        note = Primer  
source                  1..47  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 429  
aatgtacagt attgcgtttt gcccttcttg tctctgcagg ttaatcc 47

SEQ ID NO: 430           moltype = DNA   length = 53  
FEATURE                Location/Qualifiers  
misc\_feature           1..53  
                        note = Primer  
source                  1..53  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 430  
aatgtacagt attgcgtttt ggcttccagc catttctgag atatoctcac agt 53

SEQ ID NO: 431           moltype = DNA   length = 52  
FEATURE                Location/Qualifiers  
misc\_feature           1..52  
                        note = Primer  
source                  1..52  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 431  
aatgtacagt attgcgtttt gaccaggagg aacaaagaca catgaagatc at 52

SEQ ID NO: 432           moltype = DNA   length = 45  
FEATURE                Location/Qualifiers  
misc\_feature           1..45  
                        note = Primer  
source                  1..45  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 432  
aatgtacagt attgcgtttt ggcgcctccg agtttcttac gaatc 45

SEQ ID NO: 433           moltype = DNA   length = 57  
FEATURE                Location/Qualifiers  
misc\_feature           1..57  
                        note = Primer  
source                  1..57  
                        mol\_type = other DNA  
                        organism = synthetic construct

SEQUENCE: 433  
aatgtacagt attgcgtttt gtttatacac agtttggagt ttgagaatca gaagact 57

SEQ ID NO: 434           moltype = DNA   length = 57  
FEATURE                Location/Qualifiers  
misc\_feature           1..57

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source	note = Primer 1..57 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 434		
aatgtacagt attgcggtttt ggggttatctc tggctgatga gattatgagt gattctc		57
SEQ ID NO: 435	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
source	note = Primer 1..51 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 435		
aatgtacagt attgcggtttt ggccaagcta gtgattgatg tgattcgcta t		51
SEQ ID NO: 436	moltype = DNA length = 47	
FEATURE	Location/Qualifiers	
misc_feature	1..47	
source	note = Primer 1..47 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 436		
aatgtacagt attgcggtttt gccctctctc tagtactccc tgtttgt		47
SEQ ID NO: 437	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
source	note = Primer 1..51 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 437		
aatgtacagt attgcggtttt gtccttcct gtcccaatca actagtctag c		51
SEQ ID NO: 438	moltype = DNA length = 46	
FEATURE	Location/Qualifiers	
misc_feature	1..46	
source	note = Primer 1..46 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 438		
aatgtacagt attgcggtttt ggcctcgctc ctcttcctt aggtaa		46
SEQ ID NO: 439	moltype = DNA length = 55	
FEATURE	Location/Qualifiers	
misc_feature	1..55	
source	note = Primer 1..55 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 439		
aatgtacagt attgcggtttt gtctctcttc ccattagtct gagtactgag tgatt		55
SEQ ID NO: 440	moltype = DNA length = 56	
FEATURE	Location/Qualifiers	
misc_feature	1..56	
source	note = Primer 1..56 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 440		
aatgtacagt attgcggtttt gagcatttct tgagacttaa agtggcattc taaagg		56
SEQ ID NO: 441	moltype = DNA length = 57	
FEATURE	Location/Qualifiers	
misc_feature	1..57	
source	note = Primer 1..57 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 441		
aatgtacagt attgcggtttt gatttttatt ctcaagaggc agaaatacca acttacc		57

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SEQ ID NO: 442      moltype = DNA  length = 57
FEATURE            Location/Qualifiers
misc_feature        1..57
                    note = Primer
source              1..57
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 442
aatgtacagt attgcgtttt gaatttatag ctcttttcat ctgctttggt atcatca    57

SEQ ID NO: 443      moltype = DNA  length = 56
FEATURE            Location/Qualifiers
misc_feature        1..56
                    note = Primer
source              1..56
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 443
aatgtacagt attgcgtttt ggcctctaatt ctgatataca gccttagaaa gtcaca    56

SEQ ID NO: 444      moltype = DNA  length = 47
FEATURE            Location/Qualifiers
misc_feature        1..47
                    note = Primer
source              1..47
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 444
aatgtacagt attgcgtttt gtgtgccatt gtcctggagc aacaatt              47

SEQ ID NO: 445      moltype = DNA  length = 57
FEATURE            Location/Qualifiers
misc_feature        1..57
                    note = Primer
source              1..57
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 445
aatgtacagt attgcgtttt gagtgtactg ctcgttttct taatttgaaa agtgagt    57

SEQ ID NO: 446      moltype = DNA  length = 57
FEATURE            Location/Qualifiers
misc_feature        1..57
                    note = Primer
source              1..57
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 446
aatgtacagt attgcgtttt gacccatgaa ctaataactta ttttgagatt ggtccat    57

SEQ ID NO: 447      moltype = DNA  length = 55
FEATURE            Location/Qualifiers
misc_feature        1..55
                    note = Primer
source              1..55
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 447
aatgtacagt attgcgtttt gcatggtgca acaaaagtaa gaatccaaca gtttt      55

SEQ ID NO: 448      moltype = DNA  length = 57
FEATURE            Location/Qualifiers
misc_feature        1..57
                    note = Primer
source              1..57
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 448
aatgtacagt attgcgtttt gttgaaatgt taagtaagct tgaaataccg atagcat    57

SEQ ID NO: 449      moltype = DNA  length = 51
FEATURE            Location/Qualifiers
misc_feature        1..51
                    note = Primer
source              1..51

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mol_type = other DNA
organism = synthetic construct
SEQUENCE: 449
aatgtacagt attgcgtttt ggggaggaag aaaatgaagc acgaggaaaa c      51

SEQ ID NO: 450      moltype = DNA length = 57
FEATURE            Location/Qualifiers
misc_feature        1..57
                    note = Primer
source              1..57
                    mol_type = other DNA
                    organism = synthetic construct
SEQUENCE: 450
aatgtacagt attgcgtttt gatttgggat gtactctaaa tttaaagcag caaatca    57

SEQ ID NO: 451      moltype = DNA length = 57
FEATURE            Location/Qualifiers
misc_feature        1..57
                    note = Primer
source              1..57
                    mol_type = other DNA
                    organism = synthetic construct
SEQUENCE: 451
aatgtacagt attgcgtttt gtcaagagca gaatttggag accttgatat taaaact    57

SEQ ID NO: 452      moltype = DNA length = 57
FEATURE            Location/Qualifiers
misc_feature        1..57
                    note = Primer
source              1..57
                    mol_type = other DNA
                    organism = synthetic construct
SEQUENCE: 452
aatgtacagt attgcgtttt gcggttacta acatgttttag ggaaatagac aactgtt    57

SEQ ID NO: 453      moltype = DNA length = 57
FEATURE            Location/Qualifiers
misc_feature        1..57
                    note = Primer
source              1..57
                    mol_type = other DNA
                    organism = synthetic construct
SEQUENCE: 453
aatgtacagt attgcgtttt gcttgacaac agatcccata taattaactt tcatacc    57

SEQ ID NO: 454      moltype = DNA length = 55
FEATURE            Location/Qualifiers
misc_feature        1..55
                    note = Primer
source              1..55
                    mol_type = other DNA
                    organism = synthetic construct
SEQUENCE: 454
aatgtacagt attgcgtttt gagatgaaga agatgaggaa cgagagagta aaagc      55

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1.-20. (canceled)

21. A DNA tag comprising a unique molecular identifier (UMI) and a DNA identifier, wherein the DNA tag further comprises a single-stranded portion at a 3' end.

22. The DNA tag of claim 21, wherein the UMI and the DNA identifier are positioned in a 5' to 3' direction.

23. A RNA tag comprising a RNA identifier, a UMI, and a poly(T) or a template switching oligonucleotide (TSO).

24. The RNA tag of claim 23, wherein the RNA identifier, the UMI, and the poly(T) are positioned in a 5' to 3' direction.

25. (canceled)

26. The RNA tag of claim 23, wherein the RNA identifier, the UMI, and the TSO are positioned in a 5' to 3' direction.

27.-29. (canceled)

30. A composition comprising a DNA tag comprising a unique molecular identifier (UMI) and a DNA identifier, and a RNA comprising a RNA identifier, a UMI, and a poly(T).

31. The composition of claim 30, wherein the DNA tag comprises the UMI and the DNA identifier positioned in a 5' to 3' direction.

32. The composition of claim 30, wherein the RNA tag comprises the RNA identifier, the UMI, and the poly(T) positioned in a 5' to 3' position.

33. The composition of claim 30, further comprising a RNA tag comprising a RNA identifier, a UMI, and a template switching oligonucleotide (TSO).

34. The composition of claim 30, further comprising a set of gene specific primers.

35. The composition of claim 30, further comprising primers specific for the DNA tag.



**36.** The composition of claim **30**, further comprising primers specific for the RNA tag.

**37.** The composition of claim **30**, wherein the DNA tag further comprises a single-stranded portion at a 3' end.

\* \* \* \* \*