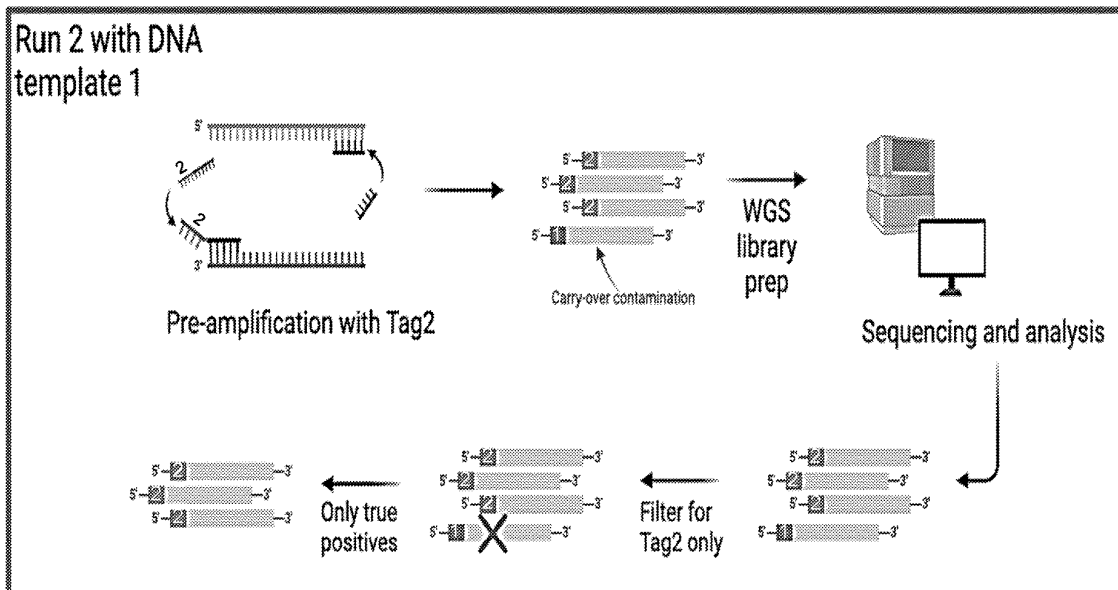
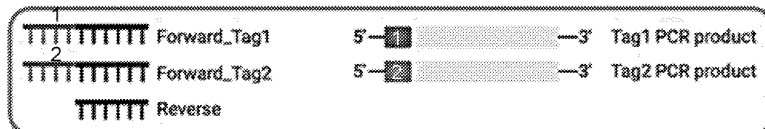




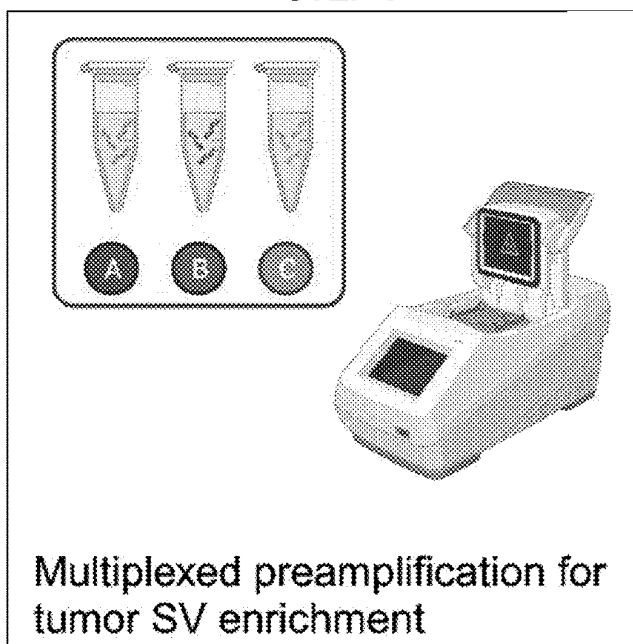
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Murtaza et al.(10) **Pub. No.: US 2026/0286436 A1**(43) **Pub. Date: Sep. 24, 2026**(54) **METHODS FOR IDENTIFYING
CROSS-CONTAMINATION AMONG
SEQUENTIAL NUCLEIC ACID
AMPLIFICATION REACTIONS**(71) Applicant: **Wisconsin Alumni Research
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WI (US)(73) Assignee: **Wisconsin Alumni Research
Foundation**, Madison, WI (US)(21) Appl. No.: **19/573,120**(22) Filed: **Mar. 20, 2026****Related U.S. Application Data**(60) Provisional application No. 63/774,954, filed on Mar.
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2600/16 (2013.01); *C40B 40/06* (2013.01);
C40B 50/06 (2013.01); *C40B 70/00* (2013.01)(57) **ABSTRACT**

The invention is directed to methods for identifying cross-contamination among sequential nucleic acid amplification reactions, such as with the use of molecularly-tagged primers in the amplification reactions.

Specification includes a Sequence Listing.

STEP 1



Amplicons that linger from Step 1 in a first experiment could end up serving as template in Step 1 and/or Step 2 subsequent experiments

FIG. 1A

STEP 2

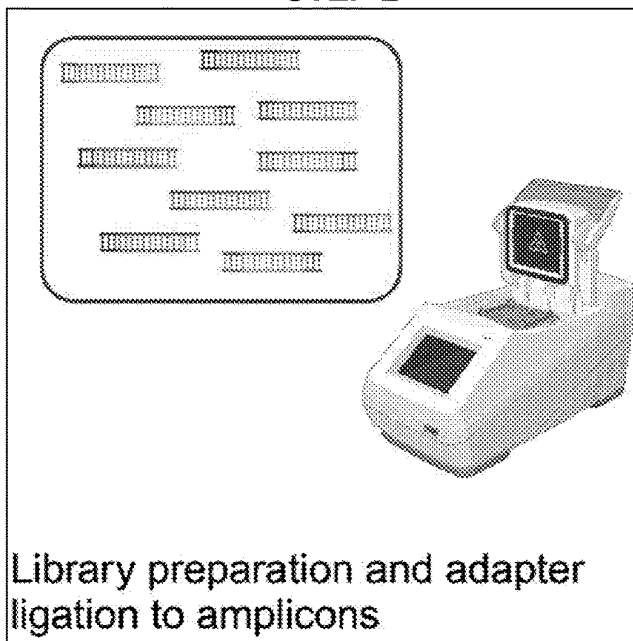


FIG. 1B

STEP 3

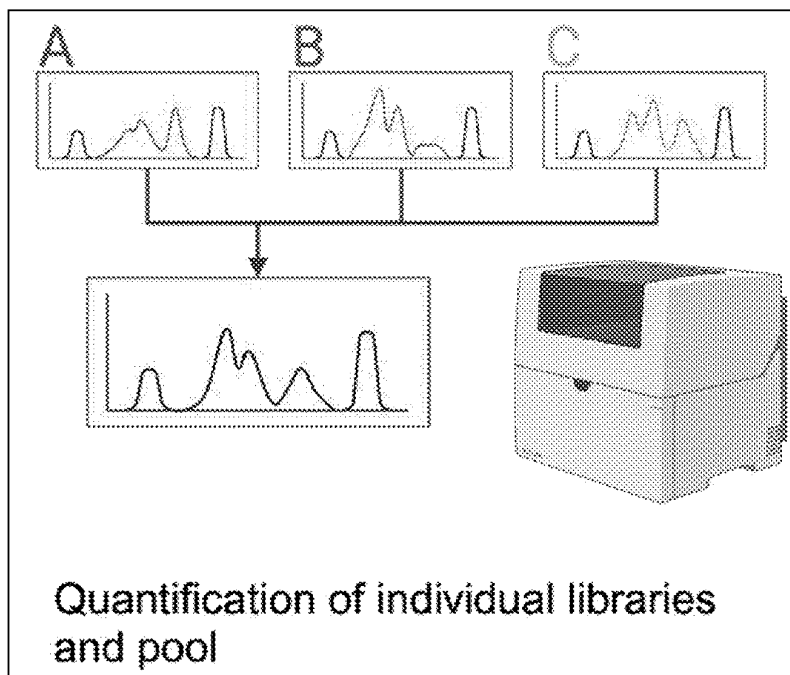


FIG. 1C

STEP 4

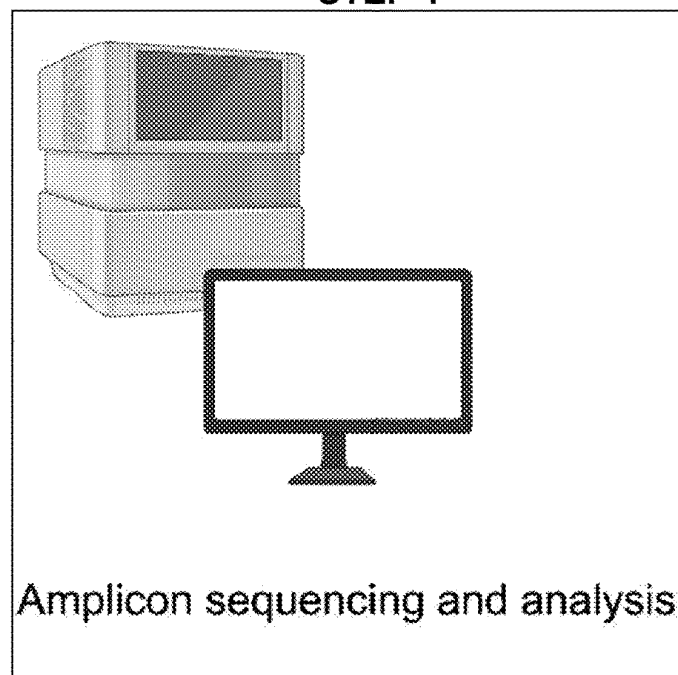


FIG. 1D

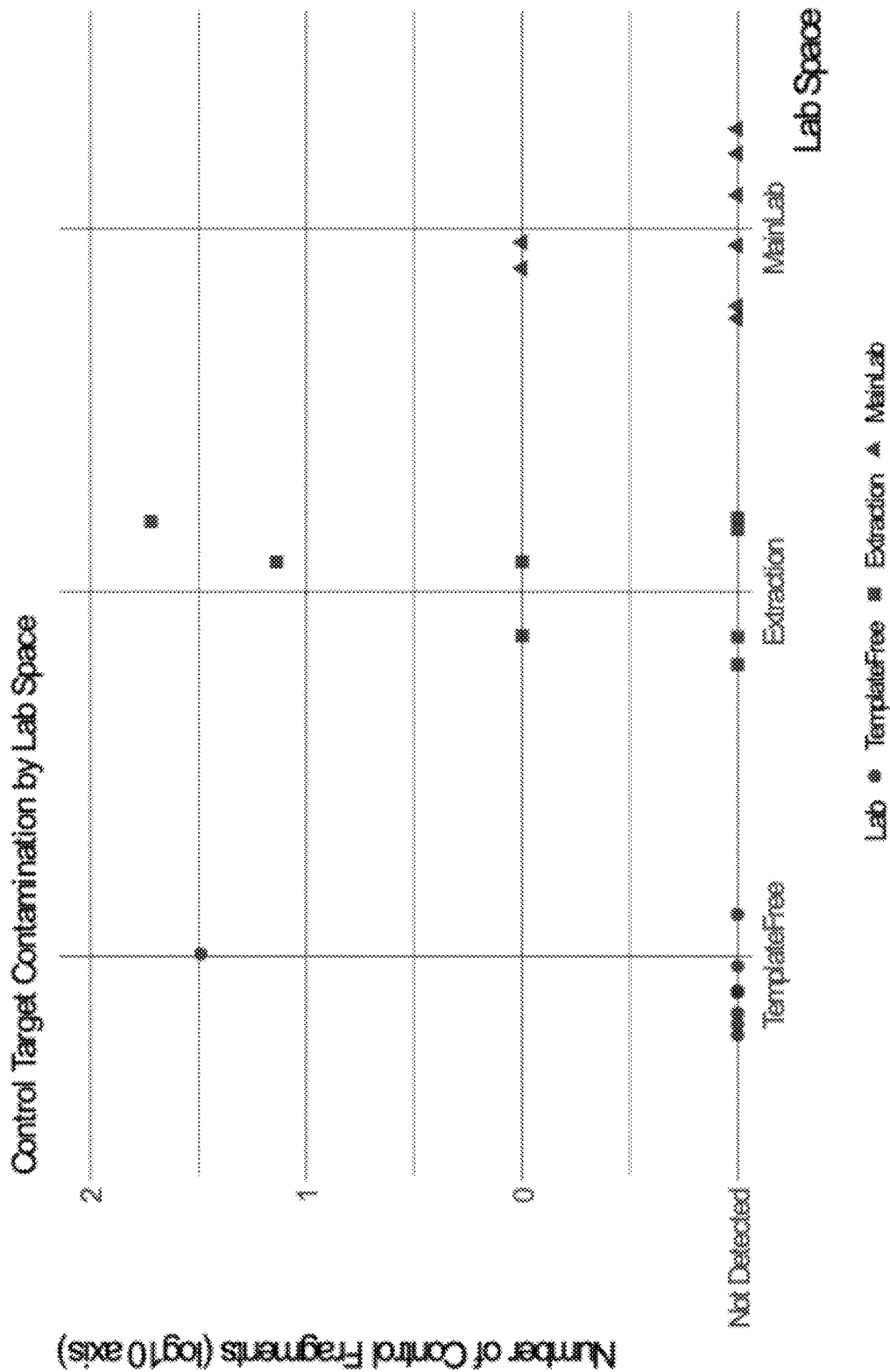


FIG. 2A

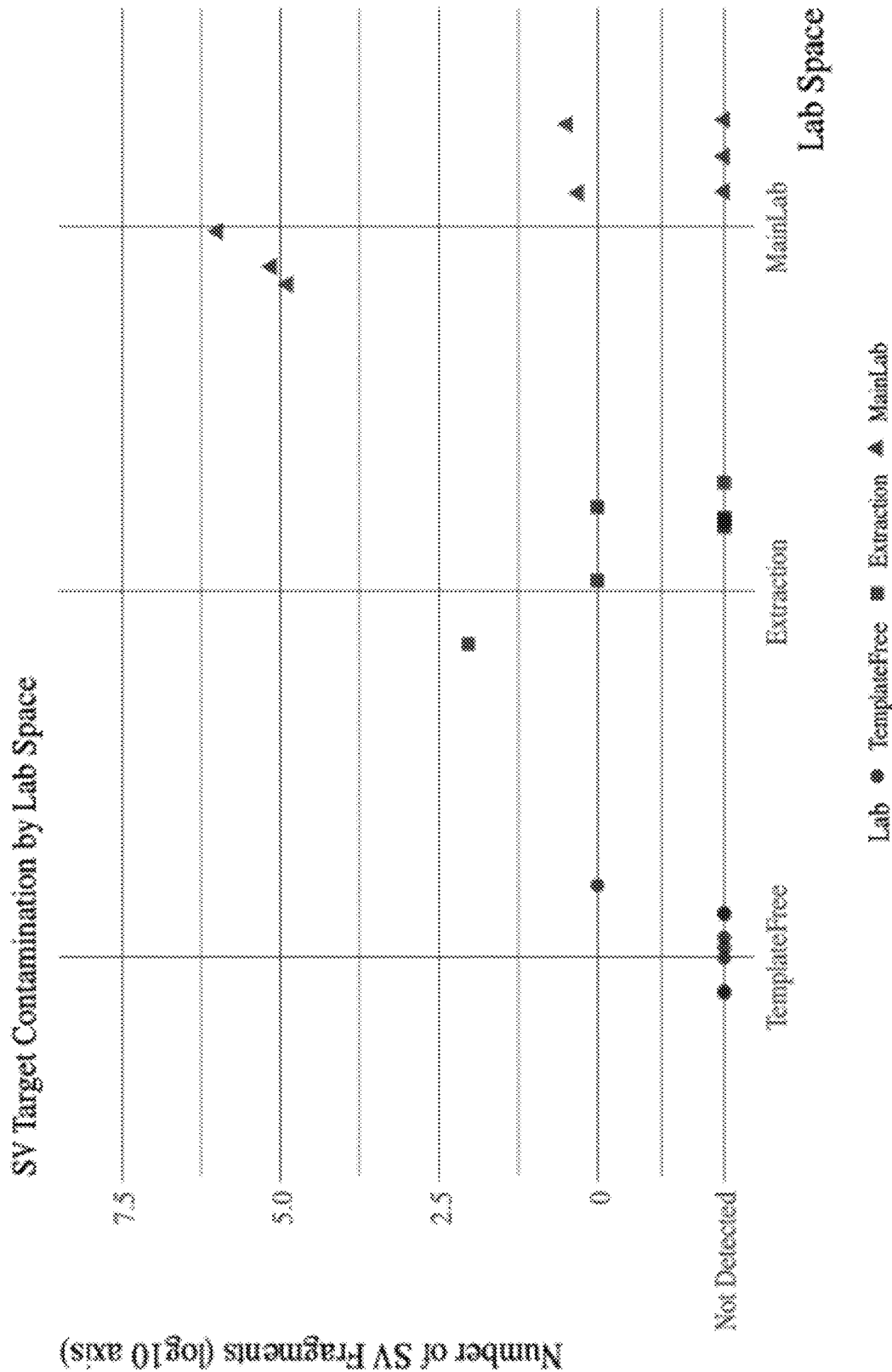


FIG. 2B

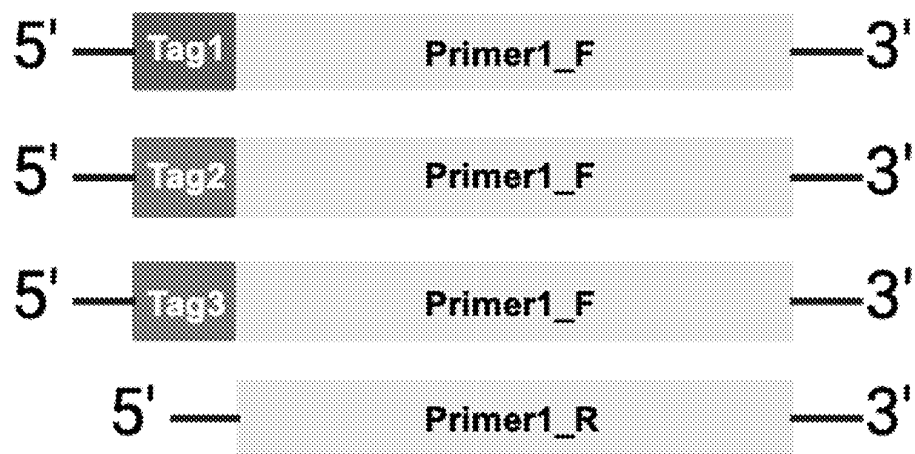
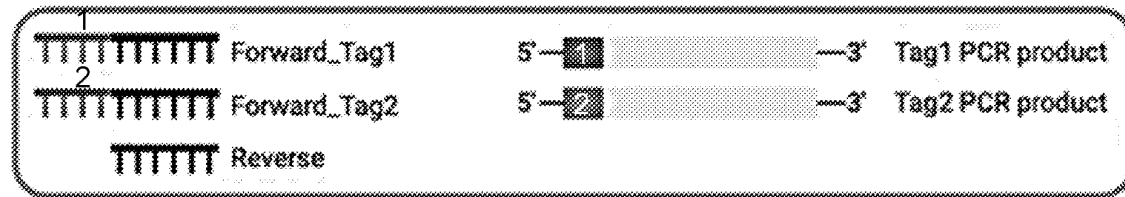


FIG. 3A



Run 1 with DNA
template 1

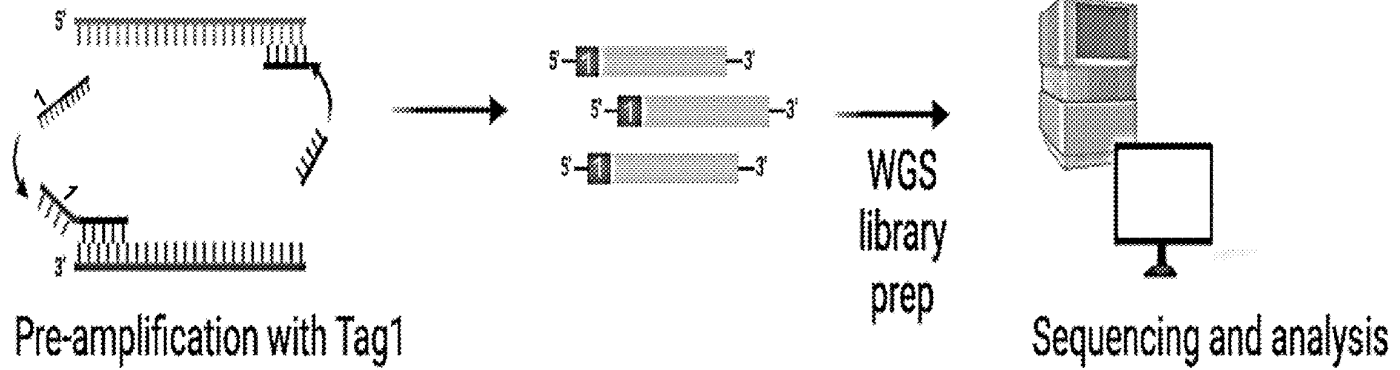


FIG. 3B

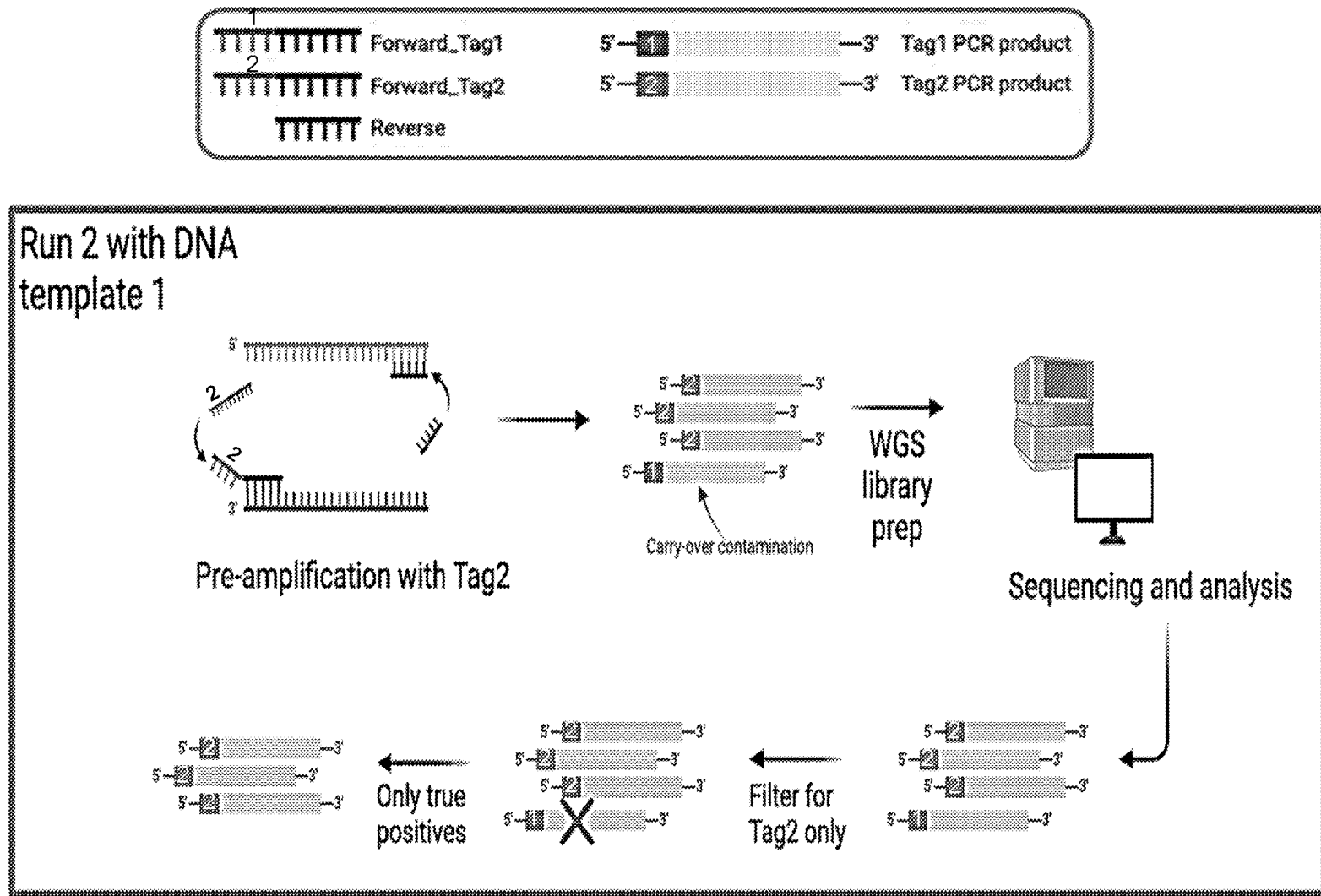


FIG. 3C

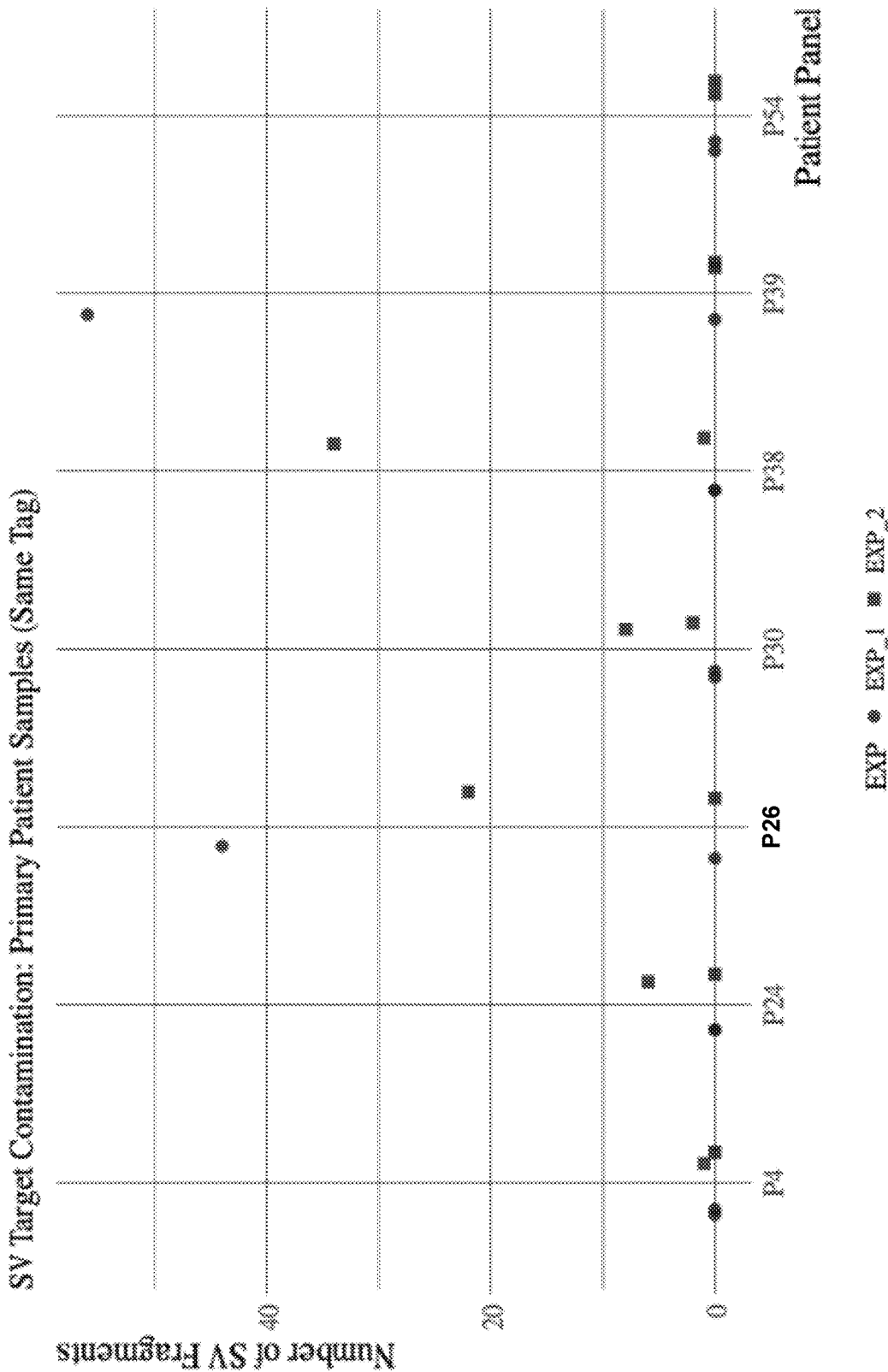


FIG. 4A

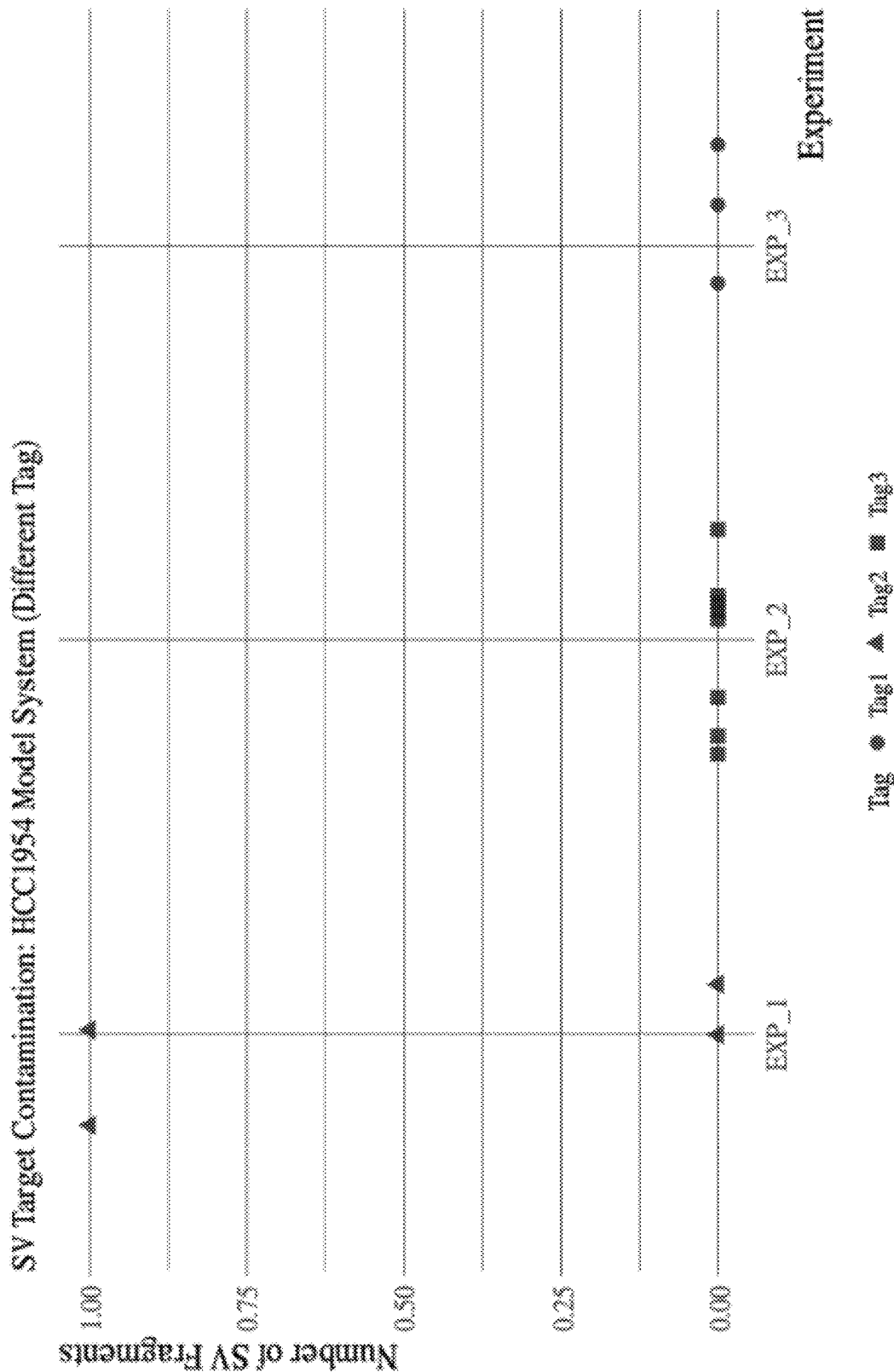


FIG. 4B

METHODS FOR IDENTIFYING CROSS-CONTAMINATION AMONG SEQUENTIAL NUCLEIC ACID AMPLIFICATION REACTIONS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] Priority is hereby claimed to U.S. Provisional Application 63/774,954, filed Mar. 20, 2025, which is incorporated herein by reference in its entirety.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

[0002] This invention was made with government support under CA243078 and CA234306 awarded by the National Institutes of Health. The government has certain rights in the invention.

SEQUENCE LISTING

[0003] The instant application contains a Sequence Listing which has been submitted in XML format and is hereby incorporated by reference in its entirety. The XML copy, created on Mar. 19, 2026, is named USPTO-260320-09824664-P240138US02-APP-SEQ LIST and is 459,815 bytes in size.

FIELD OF THE INVENTION

[0004] The invention is directed to methods for identifying cross-contamination among sequential nucleic acid amplification reactions, such as with the use of molecularly-tagged primers in the amplification reactions.

BACKGROUND

[0005] Cross-contamination between diagnostic assays based on PCR has been a long-recognized challenge in molecular diagnostics. PCR relies on exponential amplification of targeted genomic loci but the sheer molecular abundance (quantity and concentration) of the resulting amplicons can linger in laboratory surfaces and as aerosol. A key strategy to overcome such cross-contamination is a dedicated workflow that separate pre-PCR and post-PCR steps of an assay. This works remarkably well except when an assay involves multiple PCR steps, such that after some initial exponential amplification, the assay can no longer be performed in the template-free/amplicon-free labs and later PCR setups must be completed in a post-PCR environment. When the final readout is performed using next-generation sequencing, such cross-contamination before sample barcoding can make it a challenge to interpret downstream results. Tools and methods that permit distinguishing whether a detected amplicon was truly present in template DNA or if it was lingering cross-contamination from a previous experiment are needed.

SUMMARY OF THE INVENTION

[0006] One aspect of the invention is directed to methods of analyzing nucleic acids. The methods can comprise sequentially amplifying template nucleic acid with each primer set within the group. In preferred versions, the group of primer sets comprises two or more primer sets, each primer set comprises set-identity primer pairs, each set-identity primer pair consists of set-identity primers consist-

ing of a first set-identity primer and a second set-identity primer, each set-identity primer comprises a template-annealing segment on a 3' end of the set-identity primer, each set-identity primer comprises a set-identity segment on a 5' end of the set-identity primer, a combination of the set-identity segment on the first set-identity primer and the set-identity segment on the second set-identity primer in each set-identity primer pair defines a set-identity signature, and each of the set-identity signatures is defined only by set-identity primer pairs in one and only one of primer sets within the group.

[0007] The objects and advantages of the invention will appear more fully from the following detailed description of the preferred embodiment of the invention made in conjunction with the accompanying drawings.

BRIEF DESCRIPTION OF THE DRAWINGS

[0008] FIGS. 1A-1D. Possible source of contamination from experiment to experiment in an exemplary workflow (Structural Variant Enrichment and Normalization (SVEN) workflow (WO 2025/006244 A1)). FIG. 1A. Step 1, multiplexed preamplification for tumor structural variant (SV) enrichment. FIG. 1B. Step 2, library preparation and adapter ligation to amplicons. FIG. 1C. Step 3, quantification of individual libraries and pool. FIG. 1D. Step 4, amplicon sequencing and analysis. Step 1 (PCR product generation) is the likely culprit for run-to-run carryover. Contaminating carry-over DNA molecules can contaminate Step 1 (PCR product generation) or Step 2 (amplicon library construction) in subsequent runs. Amplicons that linger from Step 1 in a first run, for example, could end up serving as template in Step 1 and/or Step 2 subsequent run, thereby contaminating the subsequent experiments and leading to erroneous results.

[0009] FIGS. 2A and 2B. Target contamination in no-template controls (NTCs) by lab space with eight replicates per lab space. The template-free lab space (circle) is where reaction master mixes are created, and therefore, no contaminating molecules are anticipated, either control or structural variant (SV). The extraction lab space (square) is where DNA is extracted, prepared, or otherwise added to various molecular assays. Because this space is used for DNA extraction, some level of control target amplification and potentially SV target amplification is anticipated due to extraction/preparation of tumor templates in this space. These two spaces should have low-level contamination as these are pre-amplification spaces. Conversely, the main lab space (triangle) is a post-amplification space, and a higher degree of both control and SV contaminating amplicons is anticipated. FIG. 2A. Control target contamination. Contamination was noted in all lab spaces with the most persistent contamination noted in the extraction lab space as expected. FIG. 2B. Structural variant (SV) target contamination. NTCs demonstrated increasing SV contamination as more DNA or amplicons are expected to be present with the template-free lab having the least contamination, the extraction lab having a middle amount of contamination, and the main lab space having extremely high levels of contamination. Y-axes are log-scale; replicates without any targets identified are labelled as "Not Detected".

[0010] FIGS. 3A-3C. Tagged primer approach. FIG. 3A. 4-bp tags were added to the 5' end of only the forward primers. Reverse primer and 3' ends remained untagged to prevent color-balance concerns during paired-end sequenc-

ing. FIGS. 3B and 3C. Use of tags as a prep-to-prep contamination control, showing a first run on a template with a Tag1 forward primer (Forward_Tag1) (FIG. 3B) and a second run on the same template with a Tag2 forward primer (Forward_Tag2) (FIG. 3C), in which Tag1 amplicons from the first run are carried over as contamination into the second run and filtered out of the analysis. 5' addition does not significantly affect primer performance. Tags permit informatically filtering lingering contamination from previous runs with the same patient. The system can quantify the level of contamination, track down sources and timing of contamination, and provide longitudinal tracking for quality control at scale. The method is broadly applicable where post-amplification contamination is a concern, particularly with low-abundance targets.

[0011] FIGS. 4A and 4B. Longitudinal use of tagged system in both primary patient samples (FIG. 4A) and in model systems (FIG. 4B). FIG. 4A. SV target contamination levels when the tag remains the same between runs in patient buffy coat samples (normal, n=2). Each patient's identifier is on the x-axis. For each sample analyzed, the points on the left show results from a first run (EXP_1, circle) and the points on the right show results from a second, subsequent run (EXP_2, square). For four patient panels, there was a demonstrable increase in contamination between EXP_1 and EXP_2 using the same tag, implicating run-to-run carryover. For the remaining panels, SV detection was either decreased in the subsequent run (two panels) or both runs had no SVs detected (one panel). FIG. 4B. SV target contamination levels when the tag is switched between runs in a cell line model system that has been used extensively for development. A first run (EXP_1, n=4, circle) used Tag2 and showed a low-level of contamination. Contamination was eliminated when switching to Tag3 in a second run (EXP_2, n=8, square) and to Tag1 in a third run (EXP_3, n=3, triangle), demonstrating the utility of this tagged-primer approach.

DETAILED DESCRIPTION OF THE INVENTION

[0012] One aspect of the invention is directed to methods of analyzing nucleic acid with a group of primer sets.

[0013] The methods can comprise sequentially amplifying template nucleic acid with each primer set within the group. "Sequentially amplifying template nucleic acid with each primer set within the group" as used herein means that the primers in each individual primer set are all employed together in at least one amplification reaction that is separate from the amplification reactions employing the other primer sets and, further, that the primer sets in the group are employed in a series of amplification reactions such that no single primer set in the group is re-employed after another primer set in the group until each primer set in the group is employed in at least one amplification reaction. "Amplification reaction" as used herein refers to the replication of at least a portion of a nucleic acid template with a nucleic acid primer. "Replication" refers to the copying of a nucleic acid sequence contained in a nucleic acid template and can encompass copying the sequence from a DNA template to a DNA product, an RNA template to a DNA product, or a DNA template to an RNA product. "Primer" refers to a nucleic acid that binds to the nucleic acid template and

serves as a starting point for polymerization from same. The primers of the invention can comprise DNA, RNA, or a combination of the two.

[0014] In some versions, each sequential amplification reaction is conducted in an enclosed reaction mixture and produces an enclosed product mixture. "Enclosed mixture" and variants thereof such as "enclosed amplification mixture" and "enclosed product mixture" refer to a mixture in a given phase that is completely surrounded by an enclosure of one or more immiscible phases. In some versions, the mixture is a liquid, aqueous phase. In some versions, the enclosure is entirely a solid phase. In some versions, the enclosure is entirely a non-water-immiscible (e.g., oil) liquid phase. In some versions, the enclosure is a combination of a solid phase and a non-water-immiscible liquid phase.

[0015] In some versions, the methods comprise exposing one or more of the enclosed product mixtures. An enclosed product mixture is understood herein to be exposed when the enclosure of the product mixture is breached such that the product mixture is exposed to any substance outside the enclosure, such as surrounding gas (e.g., air), a pipet tip, a needle, a molecule introduced from outside the enclosure, etc. In some versions, each product mixture is sequentially exposed. In some versions, the product mixtures are sequentially exposed in the order in which they were generated.

[0016] Each primer set can comprise one or more primer pairs. "Primer pair" as used herein refers to a pair of primers designed to amplify a target segment of a template nucleic acid. The target segment may or may not be present in any given amplification reaction.

[0017] In the present invention, the primer pairs in each primer set comprises or consists of set-identity primer pairs. Each set-identity primer pair consists of set-identity primers consisting of a first set-identity primer and a second set-identity primer. In some versions, the first set-identity primer can be considered to be a forward primer, and the second set-identity primer can be considered to be a reverse primer. In some versions, the second set-identity primer can be considered to be a forward primer, and the first set-identity primer can be considered to be a reverse primer. "Forward primer," as understood in the art, refers to a primer that binds to an antisense strand of a nucleic acid template, and "reverse primer," as understood in the art, refers to a primer that binds to a sense strand of a nucleic acid template.

[0018] In some versions, each set-identity primer comprises a template-annealing segment on a 3' end thereof. "3' end" of a primer refers to a 3' terminal base and one or more contiguous bases upstream (e.g., 5') thereof. "Template-annealing segment" refers to a segment of the primer designed to anneal to target site on a template nucleic acid. The target site may or may not be present in any given amplification reaction. The template-annealing segment may be completely or partially complementary to the target site. However, in order to prime a polymerization reaction, at least the 3' terminal base is typically thought to be required to be complementary (form a base pair) with template nucleic acid.

[0019] In various versions of the invention, the template-annealing segment on any given set-identity primer can be at least 5 bases, at least 6 bases, at least 7 bases, at least 8 bases, at least 9 bases, at least 10 bases, at least 11 bases, at least 12 bases, at least 13 bases, at least 14 bases, at least 15 bases, at least 16 bases, at least 17 bases, at least 18 bases, at least 19 bases, at least 20 bases, at least 21 bases, at least

22 bases, at least 23 bases, at least 24 bases, at least 25 bases, at least 26 bases, at least 27 bases, at least 28 bases, at least 29 bases, or at least 30 bases.

[0020] In various versions of the invention, the template-annealing segment on each set-identity primer in each primer set can be at least 5 bases, at least 6 bases, at least 7 bases, at least 8 bases, at least 9 bases, at least 10 bases, at least 11 bases, at least 12 bases, at least 13 bases, at least 14 bases, at least 15 bases, at least 16 bases, at least 17 bases, at least 18 bases, at least 19 bases, at least 20 bases, at least 21 bases, at least 22 bases, at least 23 bases, at least 24 bases, at least 25 bases, at least 26 bases, at least 27 bases, at least 28 bases, at least 29 bases, or at least 30 bases.

[0021] In various versions of the invention, the template-annealing segment on any given set-identity primer can be up to 6 bases, up to 7 bases, up to 8 bases, up to 9 bases, up to 10 bases, up to 11 bases, up to 12 bases, up to 13 bases, up to 14 bases, up to 15 bases, up to 16 bases, up to 17 bases, up to 18 bases, up to 19 bases, up to 20 bases, up to 21 bases, up to 22 bases, up to 23 bases, up to 24 bases, up to 25 bases, up to 26 bases, up to 27 bases, up to 28 bases, up to 29 bases, up to 30 bases, up to 31 bases, up to 32 bases, up to 33 bases, up to 34 bases, up to 35 bases, up to 36 bases, up to 37 bases, up to 38 bases, up to 39 bases, up to 40 bases, up to 41 bases, up to 42 bases, up to 43 bases, up to 44 bases, up to 45 bases, up to 46 bases, up to 47 bases, up to 48 bases, up to 49 bases, up to 50 bases, up to 51 bases, up to 52 bases, up to 53 bases, up to 54 bases, up to 55 bases, up to 56 bases, up to 57 bases, up to 58 bases, up to 59 bases, or up to 60 bases or more in length.

[0022] In various versions of the invention, the template-annealing segment on each set-identity primer in each primer set can be up to 6 bases, up to 7 bases, up to 8 bases, up to 9 bases, up to 10 bases, up to 11 bases, up to 12 bases, up to 13 bases, up to 14 bases, up to 15 bases, up to 16 bases, up to 17 bases, up to 18 bases, up to 19 bases, up to 20 bases, up to 21 bases, up to 22 bases, up to 23 bases, up to 24 bases, up to 25 bases, up to 26 bases, up to 27 bases, up to 28 bases, up to 29 bases, up to 30 bases, up to 31 bases, up to 32 bases, up to 33 bases, up to 34 bases, up to 35 bases, up to 36 bases, up to 37 bases, up to 38 bases, up to 39 bases, up to 40 bases, up to 41 bases, up to 42 bases, up to 43 bases, up to 44 bases, up to 45 bases, up to 46 bases, up to 47 bases, up to 48 bases, up to 49 bases, up to 50 bases, up to 51 bases, up to 52 bases, up to 53 bases, up to 54 bases, up to 55 bases, up to 56 bases, up to 57 bases, up to 58 bases, up to 59 bases, or up to 60 bases or more in length.

[0023] As used herein, “base length” refers to the number of bases contained by a particular segment, such as a set-identity segment, and can include 0 bases (in a null limiting case) to any positive number of bases. “Base sequence” as used herein refers to a sequence of 2 or more bases as is understood in the art, except that the term as used herein, unless the context dictates otherwise, also encompasses the identity of a single base in cases where a base length of only 1 is present and a null sequence in a limiting case in which a base length of 0 is present. It is understood that two elements consisting of the same base sequence necessarily have the same base length. It is also understood that two elements consisting of different base lengths are necessarily defined by different base sequences.

[0024] In various versions of the invention, the template-annealing segment of each of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least

9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, or each of the first set-identity primers in each primer set has a base length and base sequence identical to a base length and base sequence of the template-annealing segment of at least one of the first set-identity primers in each of the other sets.

[0025] In various versions of the invention, the template-annealing segment of each of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, or each of the second set-identity primers in each primer set has a base length and base sequence identical to a base length and base sequence of the template-annealing segment of at least one of the second set-identity primers in each of the other sets.

[0026] In some versions, each set-identity primer comprises a set-identity segment on a 5' end thereof. Except in a null limiting case (discussed below) in which a particular set-identity segment has a base length of 0, the “5' end” of a primer refers to a 5' terminal base and one or more contiguous bases downstream (i.e., 3') thereof. In a null limiting case in which a particular set-identity segment has a base length of 0, “5' end” refers to the 5' terminus of the set-identity primer. “Set-identity segment” refers to a detectable characteristic on the 5' end of each set-identity primer that identifies each set-identity primer pair as a member of a given set. Exemplary detectable characteristics include labeled bases, modified bases, base lengths, or base sequences, and, in a null limiting case, a lack of any or all of any one or more of the foregoing. In preferred versions of the invention, the detectable characteristic of each set-identity segment comprises a base length, a base sequence, or a combination thereof.

[0027] The set-identity segments on each set-identity primer pair can define the primer pair as a member of a given set by defining a set-identity signature. A set-identity signature is the combination of detectable characteristics on the first and second set-identity primers of a given set-identity primer pair. The set-identity signatures can identify a set-identity primer pair as a member of a primer set by being defined by the set-identity primer pairs in only one of the sets. In other words, multiple different set-identity signatures can be defined in a given primer set, but multiple primer sets would not define the same set-identity signature.

[0028] In various versions of the invention, all the set-identity primer pairs within a given primer set together define no more than 20, no more than 15, no more than 10, no more than 5, no more than 4 no more than 3, no more than 2, or no more than 1 different set-identity signatures. In various versions of the invention, all the set-identity primer pairs within each primer set together define no more than 20, no more than 15, no more than 10, no more than 5, no more than 4 no more than 3, no more than 2, no more than 1 different set-identity signatures. In some versions, all the set-identity primer pairs within a given primer set define the same set-identity signature. In some versions, all the set-identity primer pairs within each primer set define the same set-identity signature.

[0029] It should be noted that only one detectable difference in the combination of the first and second set-identity primers in a primer pair are required to distinguish that primer pair from a primer pair of a different set. This permits

a variety of different configurations among the detectable characteristics in the set-identity segments of each set-identity primer pair. For example, a primer pair in a first set with a first set-identity primer having a set-identity segment of 0 bases and the second set-identity primer having a set-identity segment of 0 bases would distinguish from a primer pair in a second set with a first set-identity primer having a set-identity segment of 1 or more bases and the second set-identity primer having a set-identity segment of 0 bases. In another example, a primer pair in a first set with a first set-identity primer having a set-identity segment of 1 or more bases and the second set-identity primer having a set-identity segment of 0 bases would distinguish from a primer pair in a second set with a first set-identity primer having a set-identity segment of 0 bases and the second set-identity primer having a set-identity segment of 1 or more bases. In another example, a primer pair in a first set with a first set-identity primer having a set-identity segment of 1 base and the second set-identity primer having a set-identity segment of 0 bases would distinguish from a primer pair in a second set with a first set-identity primer having a set-identity segment of 2 or more bases and the second set-identity primer having a set-identity segment of 0 bases. In another example, a primer pair in a first set with a first set-identity primer having a set-identity segment of 1 or more bases defining a first sequence and the second set-identity primer having a set-identity segment of 0 bases would distinguish from a primer pair in a second set with a first set-identity primer having a set-identity segment of 1 or more bases defining a second sequence and the second set-identity primer having a set-identity segment of 0 bases. In another example, a primer pair in a first set with a first set-identity primer having a set-identity segment of 1 or more bases defining a first sequence and the second set-identity primer having a set-identity segment of 1 or more bases defining a second sequence would distinguish from a primer pair in a second set with a first set-identity primer having a set-identity segment of 1 or more bases defining a third sequence and the second set-identity primer having a set-identity segment of 1 or more bases defining the second sequence. Further examples would be evident to a practitioner in the art. As evident from above, one or more primers in different sets may comprise a null (base length of 0) set-identity segment, provided that at least one set-identity primer in each set-identity primer pair comprises a detectable characteristic that distinguishes from the set-identity primer pairs of other sets.

[0030] In various versions of the invention, the set-identity segment on any given set-identity primer can be at least 0 bases, at least 1 base, at least 2 bases, at least 3 bases, at least 4 bases, at least 5 bases, at least 6 bases, at least 7 bases, at least 8 bases, at least 9 bases, at least 10 bases, at least 11 bases, at least 12 bases, at least 13 bases, at least 14 bases, at least 15 bases, at least 16 bases, at least 17 bases, at least 18 bases, at least 19 bases, at least 20 bases, at least 21 bases, at least 22 bases, at least 23 bases, at least 24 bases, at least 25 bases, at least 26 bases, at least 27 bases, at least 28 bases, at least 29 bases, or at least 30 bases.

[0031] In various versions of the invention, the set-identity segment on each set-identity primer can be at least 0 bases, at least 1 base, at least 2 bases, at least 3 bases, at least 4 bases, at least 5 bases, at least 6 bases, at least 7 bases, at least 8 bases, at least 9 bases, at least 10 bases, at least 11 bases, at least 12 bases, at least 13 bases, at least 14 bases,

at least 15 bases, at least 16 bases, at least 17 bases, at least 18 bases, at least 19 bases, at least 20 bases, at least 21 bases, at least 22 bases, at least 23 bases, at least 24 bases, at least 25 bases, at least 26 bases, at least 27 bases, at least 28 bases, at least 29 bases, or at least 30 bases.

[0032] In various versions of the invention, the set-identity segment on any given set-identity primer can be up to 1 base, up to 2 bases, up to 3 bases, up to 4 bases, up to 5 bases, up to 6 bases, up to 7 bases, up to 8 bases, up to 9 bases, up to 10 bases, up to 11 bases, up to 12 bases, up to 13 bases, up to 14 bases, up to 15 bases, up to 16 bases, up to 17 bases, up to 18 bases, up to 19 bases, up to 20 bases, up to 21 bases, up to 22 bases, up to 23 bases, up to 24 bases, up to 25 bases, up to 26 bases, up to 27 bases, up to 28 bases, up to 29 bases, up to 30 bases, up to 31 bases, up to 32 bases, up to 33 bases, up to 34 bases, up to 35 bases, up to 36 bases, up to 37 bases, up to 38 bases, up to 39 bases, up to 40 bases, up to 41 bases, up to 42 bases, up to 43 bases, up to 44 bases, up to 45 bases, up to 46 bases, up to 47 bases, up to 48 bases, up to 49 bases, up to 50 bases, up to 51 bases, up to 52 bases, up to 53 bases, up to 54 bases, up to 55 bases, up to 56 bases, up to 57 bases, up to 58 bases, up to 59 bases, or up to 60 bases or more in length.

[0033] In various versions of the invention, the set-identity segment on each set-identity primer can be up to 1 base, up to 2 bases, up to 3 bases, up to 4 bases, up to 5 bases, up to 6 bases, up to 7 bases, up to 8 bases, up to 9 bases, up to 10 bases, up to 11 bases, up to 12 bases, up to 13 bases, up to 14 bases, up to 15 bases, up to 16 bases, up to 17 bases, up to 18 bases, up to 19 bases, up to 20 bases, up to 21 bases, up to 22 bases, up to 23 bases, up to 24 bases, up to 25 bases, up to 26 bases, up to 27 bases, up to 28 bases, up to 29 bases, up to 30 bases, up to 31 bases, up to 32 bases, up to 33 bases, up to 34 bases, up to 35 bases, up to 36 bases, up to 37 bases, up to 38 bases, up to 39 bases, up to 40 bases, up to 41 bases, up to 42 bases, up to 43 bases, up to 44 bases, up to 45 bases, up to 46 bases, up to 47 bases, up to 48 bases, up to 49 bases, up to 50 bases, up to 51 bases, up to 52 bases, up to 53 bases, up to 54 bases, up to 55 bases, up to 56 bases, up to 57 bases, up to 58 bases, up to 59 bases, or up to 60 bases or more in length.

[0034] In various versions of the invention, each set-identity segment comprises from 0 to 10 bases, such as from 0 to 9 bases, from 0 to 8 bases, from 0 to 7 bases, from 0 to 6 bases, from 0 to 5 bases, from 0 to 4 bases, from 0 to 3 bases, from 0 to 2 bases, from 0 to 1 bases, from 1 to 9 bases, from 1 to 8 bases, from 1 to 7 bases, from 1 to 6 bases, from 1 to 5 bases, from 1 to 4 bases, from 1 to 3 bases, from 1 to 2 bases, from 2 to 6 bases, from 2 to 5 bases, or from 3 to 5 bases.

[0035] In some versions, each set-identity segment on each first set-identity primer in each primer set has a different base sequence than each set-identity segment on each first set-identity primer in each other set. In some versions, the set-identity segments on all the first set-identity primers in all the sets have the same base length. In some versions, set-identity segments on all the second set-identity primers in all the sets have the same base length. In some versions, set-identity segments on all the second set-identity primers in all the sets have the same base sequence. In some versions, set-identity segments on all the second set-identity primers in all the sets have the same base length and the same base sequence.

[0036] In some versions, one or more set-identity segments comprise a non-complimentary overhang. In some versions, the set-identity segment on each first set-identity primer comprises a non-complimentary overhang. “Non-complimentary overhang” refers to a set-identity segment in which at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 99%, or 100% of the bases in the segment are non-complimentary (i.e., do not base pair) with a corresponding base on the template nucleic acid when the template-annealing segment is bound to the template nucleic acid.

[0037] In various versions of the invention, each primer set can comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, at least 30, at least 31, at least 32, at least 33, at least 34, at least 35, at least 36, at least 37, at least 38, at least 39, at least 40, at least 41, at least 42, at least 43, at least 44, at least 45, at least 46, at least 47, at least 48, at least 49, at least 50, at least 51, at least 52, at least 53, at least 54, at least 55, at least 56, at least 57, at least 58, at least 59, at least 60, at least 61, at least 62, at least 63, at least 64, at least 65, at least 66, at least 67, at least 68, at least 69, at least 70, at least 71, at least 72, at least 73, at least 74, at least 75, at least 76, at least 77, at least 78, at least 79, at least 80, at least 81, at least 82, at least 83, at least 84, at least 85, at least 86, at least 87, at least 88, at least 89, at least 90, at least 91, at least 92, at least 93, at least 94, at least 95, at least 96, at least 97, at least 98, or at least 99 set-identity primer pairs. In various versions of the invention, each primer set can comprise up to 2, up to 3, up to 4, up to 5, up to 6, up to 7, up to 8, up to 9, up to 10, up to 11, up to 12, up to 13, up to 14, up to 15, up to 16, up to 17, up to 18, up to 19, up to 20, up to 21, up to 22, up to 23, up to 24, up to 25, up to 26, up to 27, up to 28, up to 29, up to 30, up to 31, up to 32, up to 33, up to 34, up to 35, up to 36, up to 37, up to 38, up to 39, up to 40, up to 41, up to 42, up to 43, up to 44, up to 45, up to 46, up to 47, up to 48, up to 49, up to 50, up to 51, up to 52, up to 53, up to 54, up to 55, up to 56, up to 57, up to 58, up to 59, up to 60, up to 61, up to 62, up to 63, up to 64, up to 65, up to 66, up to 67, up to 68, up to 69, up to 70, up to 71, up to 72, up to 73, up to 74, up to 75, up to 76, up to 77, up to 78, up to 79, up to 80, up to 81, up to 82, up to 83, up to 84, up to 85, up to 86, up to 87, up to 88, up to 89, up to 90, up to 91, up to 92, up to 93, up to 94, up to 95, up to 96, up to 97, up to 98, up to 99, up to 100, or more set-identity primer pairs. The counted set-identity primer pairs in such cases are understood to be different from each other. Set-identity primer pairs are considered herein to be different if at least one of the respective first set-identity primers or the respective second set-identity primers have at least one difference in base length or base sequence. Set-identity primer pairs are considered herein to be the same if the respective first set-identity primers have identical base lengths and base sequences and the respective second set-identity primers have identical base lengths and base sequences. Set-identity primers are considered herein to be different if the primers have at least one difference in base length or base sequence. Set-identity primers are con-

sidered herein to be the same if the primers have identical base lengths and base sequences.

[0038] In some versions of the invention, each primer set comprises multiple copies of each first set-identity primer and each second set-identity primer. Two molecules are considered herein to be “copies” of a primer when each molecule has an identical base length and base sequence.

[0039] In various versions of the invention, the set-identity primers in each primer set can be configured to amplify at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, or at least 25 different nonoverlapping target segments. In various versions of the invention, the set-identity primers in each primer set can be configured to amplify up to 2, up to 3, up to 4, up to 5, up to 6, up to 7, up to 8, up to 9, up to 10, up to 11, up to 12, up to 13, up to 14, up to 15, up to 16, up to 17, up to 18, up to 19, up to 20, up to 21, up to 22, up to 23, up to 24, up to 25, up to 26, up to 27, up to 28, up to 29, up to 30, up to 31, up to 32, up to 33, up to 34, up to 35, up to 36, up to 37, up to 38, up to 39, up to 40, up to 41, up to 42, up to 43, up to 44, up to 45, up to 46, up to 47, up to 48, up to 49, or up to 50 or more different nonoverlapping target segments. “Different non-overlapping target segments” refers to target segments of target nucleic acid that have no overlapping bases.

[0040] In some versions, the set-identity primer pairs in each primer set are configured to amplify the same target segments.

[0041] In various versions of the invention, the group of primer sets can comprise 2 or more primer sets, 3 or more primer sets, 4 or more primer sets, 5 or more primer sets, 6 or more primer sets, 7 or more primer sets, 8 or more primer sets, 9 or more primer sets, 10 or more primer sets, 11 or more primer sets, 12 or more primer sets, 13 or more primer sets, 14 or more primer sets, 15 or more primer sets, 16 or more primer sets, 17 or more primer sets, 18 or more primer sets, 19 or more primer sets, or 20 or more primer sets. In various versions of the invention, the group of primer sets can comprise up to 2 primer sets, up to 3 primer sets, up to 4 primer sets, up to 5 primer sets, up to 6 primer sets, up to 7 primer sets, up to 8 primer sets, up to 9 primer sets, up to 10 primer sets, up to 11 primer sets, up to 12 primer sets, up to 13 primer sets, up to 14 primer sets, up to 15 primer sets, up to 16 primer sets, up to 17 primer sets, up to 18 primer sets, up to 19 primer sets, up to 20 primer sets, up to 25 primer sets, up to 30 primer set, up to 35 primer sets or more. The counted primer sets in such cases are understood to be different from each other. A first primer set is understood to be different from a second primer set if none of the set-identity signatures defined in the first primer set are defined in the second primer set.

[0042] In some versions, each sequential amplification comprises mixing the template nucleic acid and one of the primer sets, wherein the mixing for all the sequential amplifications is performed within a single enclosable mixing space. “Single enclosable mixing space” as used herein refers to a space suitable for the mixing steps that is enclosable with a barrier impassable to humans.

[0043] In some versions, the sequential amplifications can comprise generating a separate amplicon sample from each primer set. Each amplicon sample can comprise amplicons comprising one or more of the set-identity signatures. The

sequences of the amplicons in each separate amplicon sample can then be determined. From the sequences, the set-identity signatures in the sequences of the amplicons in each of the amplicon samples can be identified. Sequences of the amplicons from any given amplicon sample that comprise a set-identity signature not defined by the primer set used to generate the amplicon sample can then be informatically filtered from further analysis.

[0044] In some versions, the sequence of the amplicons in each amplicon sample are determined. The sequence determination can include any of a number of steps, such as generating one or more sequencing libraries and sequencing the sequencing libraries in a nucleic acid sequencing instrument. “Sequencing library” as used herein refers to a collection of nucleic acid fragments suitable for a sequencing instrument, such as a next-generation sequencing instrument or long-read technologies such as Oxford Nanopore and PacBio, among others. Generating a sequencing library can comprise any of a number of steps. Exemplary steps include amplicon fragmentation, nucleic acid end repair, adapter ligation, barcoding, and amplification, such as amplification with indexed or barcoded primers. For example, amplicons in an amplicon sample can then be end-repaired. The end-repaired fragmented amplicons can then be ligated to adapters. The adapters can then be used to amplify the ligated amplicons. The primers used in the amplification process can be indexed or barcoded to generate indexed or barcoded libraries.

[0045] In some versions, separate workflows are used to determine the sequences of the amplicons in the amplicon samples generated from different primer sets. “Separate workflow” in this context means that none of the amplicons or any other contents of the amplicon samples generated from different primer sets are combined or mixed in the process of determining the sequences. In some versions, a separate sequencing library is generated from each amplicon sample generated from different primer sets. In some versions, different amplicon samples generated from the same primer set can be barcoded and combined into a single sequencing library. This can occur even in cases in which amplicon samples generated from different primer sets are processed in a separate workflow.

[0046] In some versions, sequencing libraries from each separate amplicon sample are sequentially generated. In some versions, the sequencing libraries are generated from the amplicon samples in the same order in which the amplicon samples were generated. In some versions, a sequencing library from each previously generated amplicon sample is generated before each subsequent amplicon sample is generated.

[0047] In some versions, each sequencing library is separately sequenced in a sequencing instrument. In some versions, each sequencing library is sequentially sequenced in a sequencing instrument. In some versions, each sequencing library is sequentially sequenced in a sequencing instrument in the order in which the sequencing libraries were generated. In some versions, each previously generated sequencing library generated from an amplicon sample with a given primer set is sequenced in a sequencing instrument before each subsequent amplicon sample with a different primer set is generated.

[0048] In some versions, all the separate sequencing libraries are generated within a single enclosable library-generating space. “Single enclosable library-generating

space” as used herein refers to a space suitable for generating a sequencing library that is enclosable with a barrier impassable to humans.

[0049] In some versions, the template nucleic acid is the same in all the amplification reactions. In some versions, the template nucleic acid and all the amplification reactions are from a single, split sample. In some versions, the template nucleic acid in all the amplification reactions are from the same subject. In some versions, the template nucleic acid in at least one amplification reaction is different from the template nucleic acid in at least one of the other amplification reactions. In some versions, the template nucleic acid in at least one amplification reaction is from a different sample than the template nucleic acid in at least one of the other amplification reactions. In some versions, the template nucleic acid in at least one amplification reaction is from a different subject than the template nucleic acid in at least one of the other amplification reactions. In some versions, the template nucleic acid in each amplification reaction is different. In some versions, the template nucleic acid in each amplification reaction is from a different sample. In some versions, the template nucleic acid in each amplification reaction is from a different subject.

[0050] It is understood that any given amplification reaction of the invention may comprise primers other than those that are members of a set of primers of the invention.

[0051] The elements and method steps described herein can be used in any combination whether explicitly described or not.

[0052] All combinations of method steps as used herein can be performed in any order, unless otherwise specified or clearly implied to the contrary by the context in which the referenced combination is made.

[0053] As used herein, the singular forms “a,” “an,” and “the” include plural referents unless the content clearly dictates otherwise.

[0054] Numerical ranges as used herein are intended to include every number and subset of numbers contained within that range, whether specifically disclosed or not. Further, these numerical ranges should be construed as providing support for a claim directed to any number or subset of numbers in that range. For example, a disclosure of from 1 to 10 should be construed as supporting a range of from 2 to 8, from 3 to 7, from 5 to 6, from 1 to 9, from 3.6 to 4.6, from 3.5 to 9.9, and so forth.

[0055] All patents, patent publications, and peer-reviewed publications (i.e., “references”) cited herein are expressly incorporated by reference to the same extent as if each individual reference were specifically and individually indicated as being incorporated by reference. In case of conflict between the present disclosure and the incorporated references, the present disclosure controls.

[0056] It is understood that the invention is not confined to the particular construction and arrangement of parts herein illustrated and described, but embraces such modified forms thereof as come within the scope of the claims.

Examples

Tagged Primer Sets: An Approach for Overcoming Post-Amplification Contamination in Highly Sensitive Molecular Assays

Introduction

[0057] Polymerase chain reaction (PCR) has been in use in molecular biology for decades, allowing scientists to take

small amounts of DNA and generate numerous copies in an exponential manner using target-specific DNA primers (Garibyan et al. 2013). Repeated use of the same primers can lead to false positive results, as DNA from previous experiments can contaminate subsequent reactions. Sterilization between experiments and physical separation of lab spaces are used to reduce contamination risks (Mifflin 2007, Aslanzadeh 2004), but the increasing use of ultra-sensitive assays requires the development of techniques to identify, track, and exclude any contamination noise that may remain.

[0058] One ultra-sensitive assay we have recently developed is Structural Variant Enrichment and Normalization (SVEN) (WO 2025/006244 A1). This assay is designed to detect minimal residual disease in cancer patients after diagnosis using personalized structural variant (SV) target panels. Briefly, the process identifies dozens of SV breakpoints using tumor tissue from the patients. Then, PCR primer multiplexes are used to amplify these SVs from patient samples if they are present, followed by sequencing of the resulting DNA products. When tumor DNA fragments are present, even in trace amounts, we expect the SVEN to amplify these fragments so that they can be detected upon sequencing. However, we expect very few SV molecules to be present in patient blood samples. If there is carryover of residual PCR amplicons from one experiment to the next, this could lead to false positives. The current invention was designed to help identify such run-to-run contamination noise, and eventually improve our ability to detect true low-abundance tumor signal.

Identification of Contamination Source

[0059] While conducting SVEN development experiments on cell line DNA, we found increasing amounts of contamination in our no-template controls (NTCs). The impact of contaminating DNA varies significantly depending on when it is introduced (FIG. 1): If the contamination occurs before exponential amplification, it will result in a

very large number of contamination-derived amplicons in our sequencing data as these amplicons will participate in the exponential amplification reaction. If carry-over contamination occurs post-amplification at step 2 (library construction), however, few amplicons will be detected in our sequencing data. The number of amplicons in our NTCs was more consistent with post-amplification contamination during library preparation.

[0060] To further validate this finding, we prepared replicate NTCs in three physically separate lab spaces with increasing levels of potential contamination: a template-free lab (following standard procedure; circle), a DNA extraction lab (square), and the main lab space (triangle) using the HCC1954 multiplex with untagged forward primers (Table 1). Our results (FIGS. 2A and 2B and Table 2) confirmed that the number of contamination-derived amplicons was low in NTCs prepared in the template-free lab (no DNA extracted, prepared, or manipulated) and the extraction lab (where DNA is extracted, prepared, or manipulated), consistent with post-amplification contamination. In contrast, there was likely exponential amplification of contaminants in the NTCs prepared in the main lab space. The number of replicates with evidence of contamination was also higher in the main lab space and extraction lab (6/8 each) and lowest in the template-free lab (1/8). Importantly, the character of the contamination was different between the extraction and main labs despite having the same number of contaminated replicates. In the extraction lab, there was an even split between replicates that had control target contamination (4/8) and SV target contamination (3/8) including a replicate that had both control and SV contamination, which is consistent with the presence of HCC1954 tumor DNA in the extraction lab. Conversely, most of the replicates in the main lab had SV contamination (5/8) and only 2/8 replicates with control target contamination, including a replicate that had both control and SV contamination. Together, this indicates that the run-to-run carry-over contamination is significant, leading to indeterminate or even invalid results.

TABLE 1

Targets, tags, and primers employed in the experiments of FIGS. 2A and 2B.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
HCC1954v2_DNAIA_short1	—	CTTGTAACCTGGTGTTT GGTTAT (SEQ ID NO: 1)	GTAGGCTGGGTAGCCAAA TC (SEQ ID NO: 2)
HCC1954v2_DNAIA_short2	—	CCAGCCCAAGATGGA TGAAT (SEQ ID NO: 3)	CTCTTCTTTCTTTTCAGCA ACAC (SEQ ID NO: 4)
HCC1954v2_DNAIA_short3	—	GCGGTGGAAGTCATT CTGATA (SEQ ID NO: 5)	TCTCTCTCTCTCCAGTGAA CAA (SEQ ID NO: 6)
HCC1954v2_DNAIA_short4	—	GAGGGCCACAGATTG GTATT (SEQ ID NO: 7)	GATCACTTAGCTCAGGAA ACAAAC (SEQ ID NO: 8)
HCC1954v2_DNAIA_short5	—	ACTGAAAGGTCAGAT TCAGGAG (SEQ ID NO: 9)	TACCGGTTTGTGTCCAAG AG (SEQ ID NO: 10)
HCC1954v2_CWSV00079	—	TGAGGCTCGACAGGT ACCATATAGCCT (SEQ ID NO: 11)	GCCTGTGCTGCAGCCATG AGTTAG (SEQ ID NO: 12)
HCC1954v2_CWSV00085	—	GACTCCAACCATTTG TATAATCTGAAAGTT GTCT (SEQ ID NO: 13)	AAAGGAGAACTATGTGAG CTAATGCATTT (SEQ ID NO: 14)

TABLE 1-continued

Targets, tags, and primers employed in the experiments of FIGS. 2A and 2B.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
HCC1954v2_CWSV00096	—	CTGCCTGACAACGGA CTGAAA (SEQ ID NO: 15)	CTGTATATCTGGCTAGCC ATATGCAGAAA (SEQ ID NO: 16)
HCC1954v2_CWSV00142	—	TGGGCTATTTCTAACA GCTCACATGTTTACAT (SEQ ID NO: 17)	CAATCAGAAGACTGCTAG GGTGGCTGTATT (SEQ ID NO: 18)
HCC1954v2_CWSV00166	—	TTCCATAAGTGCCAG CTGGCTGAGAAATA (SEQ ID NO: 19)	GAGTGTATAGACTAGAAG TACAGCCATATAGTT (SEQ ID NO: 20)
HCC1954v2_CWSV00203	—	TCTGCTCCCAGGTTCA AGTGATTCTCAAG (SEQ ID NO: 21)	CCCTGTTGCCAGGCTAG AGTG (SEQ ID NO: 22)
HCC1954v2_CWSV00281	—	TCCGAGAGCTCACAG CTTGGCT (SEQ ID NO: 23)	GAGCGAGCTCAAGATAGA GGCAGCTAA (SEQ ID NO: 24)
HCC1954v2_CWSV00291	—	GTTTGATGGAATTCA CCAGTGTGTTT (SEQ ID NO: 25)	TCCACATCACGGGAGCAG CTG (SEQ ID NO: 26)
HCC1954v2_CWSV00362	—	ATTTAGAGAGCCTGT CACAAATGTCCATAT GAGAA (SEQ ID NO: 27)	GTCCAGCTGAGTGGAAACA TTGAAAGAAC (SEQ ID NO: 28)
HCC1954v2_CWSV00739	—	GAGAGGAGAGAGTGC AGGGTCAA (SEQ ID NO: 29)	TAGGAGGAGCCCATTGGC C (SEQ ID NO: 30)
HCC1954v2_CWSV00742	—	ACATTATTGTTAACA AGGGTTGCTTCTGGG AAGA (SEQ ID NO: 31)	GCAGGAGAATGGCATGA ACCCGG (SEQ ID NO: 32)
HCC1954v2_CWSV00743	—	CCCTGGCACCTAGTG GGTCCATAC (SEQ ID NO: 33)	AGATGTGGCTGAACTTTA AATGCATATT (SEQ ID NO: 34)
HCC1954v2_CWSV00744	—	GCACTCCAGAGACTC TGTTTCTAAA (SEQ ID NO: 35)	AAAGGGCCAGGCCTGAGT GGT (SEQ ID NO: 36)
HCC1954v2_CWSV00791	—	CAGGCATGGTAGCGC GCCT (SEQ ID NO: 37)	CTCCGGCACTGGGCAGAG GTA (SEQ ID NO: 38)
HCC1954v2_CWSV00841	—	GGAAGCCTCATAATC ATGGTGGAAGCA (SEQ ID NO: 39)	TCAGTGCTAGCTGATAAC TCTGACTTT (SEQ ID NO: 40)
HCC1954v2_CWSV00852	—	CATGTTTACCGATGA AGCTGCAA (SEQ ID NO: 41)	CACTGCATGTTCCAGTC ATAGGTGG (SEQ ID NO: 42)
HCC1954v2_CWSV00856	—	AGGAAGCTCAGCTAT ACCTGTTACTGATAAT TT (SEQ ID NO: 43)	AGACCATCTCACATGTA GACACA (SEQ ID NO: 44)
HCC1954v2_CWSV01009	—	CCCATGCAGGCCTAG GCTAGTGT (SEQ ID NO: 45)	CTTCTCCAAGTCTCTACAC TTGGCCACAA (SEQ ID NO: 46)
HCC1954v2_CWSV01021	—	ACCTAAAGGACACAT CTCAGTACATTT (SEQ ID NO: 47)	AGGATGACGCCTGGCTTG GAGAAT (SEQ ID NO: 48)
HCC1954v2_CWSV01028	—	ACTGAAGGCTCTATG TGCAGGAAGTCC (SEQ ID NO: 49)	AGCAACAAAGATTATCCT AAGACTTCTGGAGGAAG (SEQ ID NO: 50)

TABLE 1-continued

Targets, tags, and primers employed in the experiments of FIGS. 2A and 2B.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
HCC1954v2_CWSV01070	—	CCTCCCAAAGTGCTG GGATTATAGGCA (SEQ ID NO: 51)	AGGAGGGAGTGACAGGA TGTGATCTG (SEQ ID NO: 52)
HCC1954v2_CWSV01075	—	AACTGTTCTTCCAGGC CTGATTT (SEQ ID NO: 53)	AGCCTGGCCAACACAGTG AAACC (SEQ ID NO: 54)
HCC1954v2_CWSV01077	—	CCCATCCTGGCACGT ACTGCTACT (SEQ ID NO: 55)	TGACCTGTCTTGGGTAG CACTATTGGT (SEQ ID NO: 56)
HCC1954v2_CWSV01100	—	AGGCACACTCAGGCT TTACGATTCTGTGTTA (SEQ ID NO: 57)	AAAGGGATAGCAGTTTCC TGCTGTCCATAG (SEQ ID NO: 58)
HCC1954v2_CWSV01109	—	ATTCTCCCTGCAAATT GTTTGACTCTAGAAA TAGC (SEQ ID NO: 59)	CCCAGGCTGCTGGTCATG GAAA (SEQ ID NO: 60)
HCC1954v2_CWSV01130	—	GGGTAGTAGCGATCT GGTTACCCAG (SEQ ID NO: 61)	CACAGGGTTTATCTCCTC AGACAAA (SEQ ID NO: 62)
HCC1954v2_CWSV01177	—	CATTGACCCACCGGT CATTCAAGAG (SEQ ID NO: 63)	GCGGACGCCATGGAGCT (SEQ ID NO: 64)
HCC1954v2_CWSV01529	—	CTGAGGGTTATCCAA GTGACCCATTGCA (SEQ ID NO: 65)	AACACATTAGTGATGTCT CAATGCCATCC (SEQ ID NO: 66)

*SV targets and primers are indicated with "CWSV." Control targets and primers are indicated with "DNAIA."

TABLE 2

Contaminated replicates by lab space.*			
Target-type Contamination	Template-Free Lab	DNA Extraction Lab	Main Lab Space
Control only	0	3	1
SV only	0	2	4
Both	1	1	1
Total	1	6	6

*The Control only rows enumerates replicates that only had control contamination. The SV-only row enumerates replicates that had only SV target contamination. The Both row enumerates replicates that had contamination of both control and SV targets. Total is the total number of contaminated replicates with any combination between the target types.

Tagged Primer Design and Use

[0061] As all sequencing library preparation after initial amplification must occur in the main lab (post-PCR space), we expected that it would be impossible to completely eliminate DNA from previous experiments. We therefore had to develop an approach to identify and remove post-amplification contamination. We reasoned that developing multiple versions of each primer panel, differing only in the addition of a few base pairs to the 5' end of the forward primers (FIGS. 3A-3C), would allow us to identify reads that came from different experiments without significantly impacting primer performance. For each of the three versions of the primer sets, the target-specific sequence in the forward primer remains constant, while a four base pair tag

is added to the 5' end of the forward primer. All amplicons generated in a given experiment would, therefore, contain the same tag. We could then rotate through primer sets with different tags in subsequent experiments.

[0062] This approach provides a means to remove the contaminating sequences from each sample at the computational analysis stage by requiring the correct tag sequence be present on a fragment before it is included in the analysis. The source experiment of contaminating DNA from previous experiments can also be determined using their tag, enabling quantification and source tracking of between-run contamination wherein high levels of contaminating, improperly tagged reads would indicate a pre-amplification contamination event (step 1 of FIG. 1) while low levels of would indicate a post-amplification event (step 2 of FIG. 2).

[0063] The tags were limited to four base pairs in the present examples to minimize potential impacts of the tag on primer secondary structure and thermodynamics. Furthermore, the reverse primer was left untagged to maintain fluorophore diversity on the Illumina sequencer in the first cycles to prevent errors in the sequencing run. However, additional tag sets could be developed for the reverse primers to increase the possible combinations, which would be particularly powerful in environments with high-throughput, repeated sampling. The tagged system was tested using one of the multiplexes developed for our cell lines (HCC1954) to ensure that the performance of the multiplex was not significantly affected by the addition of the tags, and the results demonstrated that the primers were still working

as expected. Although there was some impact on absolute quantification between panels, relative quantification between samples using the same tagged panels remained stable between experiments. We proceeded to use them in subsequent panel designs and testing for both our cell line model system and primary patient samples.

Longitudinal Use and Results

[0064] In subsequent testing using patient-specific SV panels, we found that when the same primer tags (Tag3) are used between consecutive experiments (Table 3), residual amplicons persist (FIG. 4A), and higher levels are often found the second time a panel was used in several, but not all, the panels tested. However, implementation of rotating

tagged primer sets (Table 4), which is the intended use-case for this technology, allowed us to filter out carry-over contamination across runs using the 0% tumor fraction HCC1954 model system. We would expect no SV contamination in this model system since now tumor content is present. Our results demonstrate no carry-over contamination in the transition from EXP_1 (n=4; Tag2, circle), with two SV targets identified, to EXP_2 (n=8; Tag3, square) and EXP_3 (n=3; Tag1, triangle), which both had no SV targets identified (FIG. 4B). These results demonstrate a simple and effective method to identify, quantify, and exclude post-amplification product contamination in DNA sequencing experiments. Such a system has utility in applications where low-abundance target DNA needs to be accurately identified and quantified.

TABLE 3

Targets, tag, and, primer sequences for two consecutive experiments using the same tag (underlined) for templates P4, P24, P26, P30, P38, P39, P54 as shown in FIG. 4A.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
P4			
p04_CWSV00001	3	CATGTTTCATCACACATG CTAACACAAATCCAGTC (SEQ ID NO: 448)	CAGAATCCATGCTCTTAACC ATTATGCTCTGC (SEQ ID NO: 449)
p04_CWSV00007	3	CATGGACCGCCGGTGAGC CGG (SEQ ID NO: 450)	GAATGTACTTTGCAAGTGAG AATGACAT (SEQ ID NO: 451)
p04_CWSV00013	3	CATGTCATCCTGGACATTA GCTACCTCTGTGATTGA (SEQ ID NO: 452)	ACCCAGAGTAGGCATTAATC ATTCCAGACATTTC (SEQ ID NO: 453)
p04_CWSV00017	3	CATGGCACTTGCTCCACC TTCCAG (SEQ ID NO: 454)	GGTGAACTACTTAATGGGT GCAGGGTG (SEQ ID NO: 455)
p04_CWSV00028	3	CATGCCAGGGACCCTAGC AAACGAGCT (SEQ ID NO: 456)	TGACCCTGGTCAGTATTCCT AGGGTCC (SEQ ID NO: 457)
p04_CWSV00031	3	CATGCCATATTTATACCAG CCTGGCTCTAGGAGAGT (SEQ ID NO: 458)	TCATAGCAAGCAATGACAA TGCCAATAA (SEQ ID NO: 459)
p04_CWSV00038	3	CATGTCTCCCACTCCAG ATCCAAAGACTACTT (SEQ ID NO: 460)	TGTAGATACAGTTATTCTTT GTTACTGGTTGAAT (SEQ ID NO: 461)
p04_CWSV00040	3	CATGCGTGCACGCGCATG CAAAATAGG (SEQ ID NO: 462)	CAAATAAGCACATAAGATA AAGATCCAGCTATTT (SEQ ID NO: 463)
p04_CWSV00042	3	CATGCCCTGAACATTTTAC CATGAAATTTGTGAGCT (SEQ ID NO: 464)	GCCTAAGCCTGGAACCTAG GAGGTG (SEQ ID NO: 465)
p04_DNAIA_short1	3	CATGCTTGACCTGGTGT CGTTAT (SEQ ID NO: 113)	GTAGGCTGGGTAGCCAAAT C (SEQ ID NO: 2)
p04_DNAIA_short2	3	CATGCCAGCCCAGATGG ATGAAT (SEQ ID NO: 114)	CTCTCTTTCTTTTCAGCAAC AC (SEQ ID NO: 4)
p04_DNAIA_short3	3	CATGGCGGTGGAAGTCAT TCTGATA (SEQ ID NO: 115)	TCTCTCTCTCTCCAGTGAAC AA (SEQ ID NO: 6)
p04_DNAIA_short4	3	CATGGAGGGCCACAGATT GGTATT (SEQ ID NO: 116)	GATCACTTAGCTCAGGAAAC AAAC (SEQ ID NO: 8)
p04_DNAIA_short5	3	CATGACTGAAAGGTCAGA TTCAGGAG (SEQ ID NO: 117)	TACCGGTTTGTGTCCAAGAG (SEQ ID NO: 10)

TABLE 3-continued

Targets, tag, and, primer sequences for two consecutive experiments using the same tag (underlined> for templates P4, P24, P26, P30, P38, P39, P54 as shown in FIG. 4A.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
P24			
p24_CWSV00001	3	CATGGTTGAACCTGGGAG GCGGAGGT (SEQ ID NO: 67)	GCTCAGGCACTGAGAGTCA GCC (SEQ ID NO: 68)
p24_CWSV00005	3	CATGCAGGAGGCCAAGGG TGACGG (SEQ ID NO: 69)	GGATAGCTATTGAGAGCTTC CTTCATTG (SEQ ID NO: 70)
p24_CWSV00008	3	CATGAAGAGTACTTGACA CATGCATGAACCTCAGTAA ATT (SEQ ID NO: 71)	ATGAAGTATCATATAAGGAT ACACTCTATGCATC (SEQ ID NO: 72)
p24_CWSV00011	3	CATGGGGTCCCACATGAC AGCCATGACT (SEQ ID NO: 73)	GGTCCCAGTCCCTCAGTCTC TCCA (SEQ ID NO: 74)
p24_CWSV00012	3	CATGAAAGAAACAACTT GTCTCGGTATCCAGAAAGT GT (SEQ ID NO: 75)	ACAGTTCAAGTAGTGTTAAGA ACATTTGCA (SEQ ID NO: 76)
p24_CWSV00016	3	CATGAAGTATTCCTTCAAG CCAAGCATAGTATGTCTAG A (SEQ ID NO: 77)	GGATGGCACCTGCTGGCTAC ATTT (SEQ ID NO: 78)
p24_CWSV00022	3	CATGAGTAGTTGGGATTAC AGGCATGTGCCA (SEQ ID NO: 79)	AAGACACAAGTTTATCTATA TGACAACTTTGAC (SEQ ID NO: 80)
p24_CWSV00023	3	CATGTGTAACCTAACCTGCA CGTTGTGCACATG (SEQ ID NO: 81)	TGCCCCATTGTATTAGTCAGG CAGGGTT (SEQ ID NO: 82)
p24_CWSV00028	3	CATGCTCCTGGACTCAAGC GATCCTCCTG (SEQ ID NO: 83)	GGAGCTGGTGGAGCCTGCTC T (SEQ ID NO: 84)
p24_CWSV00040	3	CATGAATATGAAATAAAG CCACAGTAAAGATTACTC T (SEQ ID NO: 85)	GTGACCAAATAAATGTTTG TGTAATTTAAAGGA (SEQ ID NO: 86)
p24_CWSV00044	3	CATGGCCACTGCACTCCAG CCTAGGT (SEQ ID NO: 87)	GTGGCCCTAACTCGGCTCAC CATA (SEQ ID NO: 88)
p24_CWSV00046	3	CATGAAAGAATATCGATA CATGGGCAGCTGACACTT (SEQ ID NO: 89)	AAATAGCTGCTTTAGATATC TGAAGCCA (SEQ ID NO: 90)
p24_CWSV00049	3	CATGTTTGAGACACAGTTT CTCTTTGTCAACCCAG (SEQ ID NO: 91)	CCCACTGTGGAATGTCACAG CTATTT (SEQ ID NO: 92)
p24_CWSV00050	3	CATGCCCCACTGCTGGACCT TAGCACG (SEQ ID NO: 93)	TGATGCATGGCCTTAGCTGT TTACTTTGC (SEQ ID NO: 94)
p24_CWSV00053	3	CATGCTCCACATGCATAGT ATCAGCCCTCCA (SEQ ID NO: 95)	GAGGTGGAATTCAGTGA GCCGAG (SEQ ID NO: 96)
p24_CWSV00058	3	CATGAGGTGTGAGCCACC ACGCCT (SEQ ID NO: 97)	AGTGACTCACGCCTATAATC CCAGCG (SEQ ID NO: 98)
p24_CWSV00061	3	CATGTTTAAAGACAGTCTT CGCCAGGTGTGGT (SEQ ID NO: 99)	CCGAGGCAGGCCGATCACC (SEQ ID NO: 100)
p24_CWSV00068	3	CATGTTTACGAGGCCAGC ATCATCTGATACTAAA (SEQ ID NO: 101)	GTAACATAATACAAAGCTG CATCACAGCTAATCT (SEQ ID NO: 102)
p24_CWSV00078	3	CATGGGGATCCCAGACCTT GGCCAGG (SEQ ID NO: 103)	AGGTGCTTATAAATTTCTGT TACATGAAAGAATAC (SEQ ID NO: 104)

TABLE 3-continued

Targets, tag, and, primer sequences for two consecutive experiments using the same tag (underlined> for templates P4, P24, P26, P30, P38, P39, P54 as shown in FIG. 4A.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
p24_CWSV00087	3	CATGAAATTAAGAAGGTT CATCACAGTTCAAAGAAG CTC (SEQ ID NO: 105)	ATTCCTCGCTCTTATGGCTTA TACTCTAGTTGG (SEQ ID NO: 106)
p24_CWSV00088	3	CATGTGGTCTGGTCGTCCA TGCTTGCA (SEQ ID NO: 107)	CACAGTTCTCATACTCAGGA ACCCTCAT (SEQ ID NO: 108)
p24_CWSV00090	3	CATGTGGTGTGGCGCTCA GACAGTGATA (SEQ ID NO: 109)	TTTGTCAAGTTGGCCCTGATT TCAGATATCCTC (SEQ ID NO: 110)
p24_CWSV00097	3	CATGGCTTGTAATCCCAGC TACTCAGGAGGC (SEQ ID NO: 111)	TTTACCAGCACAGTGTAGA ATTGCAG (SEQ ID NO: 112)
p24_DNAIA_short1	3	CATGCTTGTTACCTGGTGTT CGGTTAT (SEQ ID NO: 113)	GTAGGCTGGGTAGCCAAAT C (SEQ ID NO: 2)
p24_DNAIA_short2	3	CATGCCAGCCCCAAGATGG ATGAAT (SEQ ID NO: 114)	CTCTTCTTTCTTTTCAGCAAC AC (SEQ ID NO: 4)
p24_DNAIA_short3	3	CATGGCGGTGGAAGTCAT TCTGATA (SEQ ID NO: 115)	TCTCTCTCTCTCCAGTGAAC AA (SEQ ID NO: 6)
p24_DNAIA_short4	3	CATGGAGGGCCACAGATT GGTATT (SEQ ID NO: 116)	GATCACTTAGCTCAGGAAAC AAAC (SEQ ID NO: 8)
p24_DNAIA_short5	3	CATGACTGAAAGGTCAGA TTCAGGAG (SEQ ID NO: 117)	TACCGGTTTGTGTCCAAGAG (SEQ ID NO: 10)
P26			
p26_CWSV00006	3	CATGACTACATTTCTGCT ATCTTGATTACAACCTTT G (SEQ ID NO: 118)	TCCGAAGGAAGTGAATTCA CCCAAGGAT (SEQ ID NO: 119)
p26_CWSV00010	3	CATGTTTGGGATGAACTG TTCCACCTCAGATTT (SEQ ID NO: 120)	TTACTGCCAGATATTCTGG TTAAGAAAC (SEQ ID NO: 121)
p26_CWSV00012	3	CATGCATAGTATTTACAT TTGTGTATTACTTCGAATT T (SEQ ID NO: 122)	AAACGTTTGGTTCATTACAA GAATAGAGGCCTTC (SEQ ID NO: 123)
p26_CWSV00014	3	CATGTCCTTGAGTCTATCT TGGAGGTGAGCAAAC (SEQ ID NO: 124)	TGCGTGGTGTGAGTAAATT ATCAATAGG (SEQ ID NO: 125)
p26_CWSV00017	3	CATGCCAAATTTAATTCAG TCTTCTTCCCATAGTGT T (SEQ ID NO: 126)	ACTCTTTATGAAGAGCAATT TGGTAGTACCTACCA (SEQ ID NO: 127)
p26_CWSV00022	3	CATGGTTCAACACCCTTTG ATGGCTCCCATG (SEQ ID NO: 128)	GGCCTCCTTGAACCTATGGTG GGCT (SEQ ID NO: 129)
p26_CWSV00030	3	CATGAAAGCAGTGTGCTG AGTGAAGAAGTCAG (SEQ ID NO: 130)	TCCTCATGTGAGTTTATGTC CTACTTGAA (SEQ ID NO: 131)
p26_CWSV00038	3	CATGTTGTGCTGCAATAAA CATAGATGCGCG (SEQ ID NO: 132)	AGTCCAAAGTTTAAGATGCC AGAGATGCA (SEQ ID NO: 133)
p26_CWSV00039	3	CATGTTTCTCCATAGACTC CTGTCTTGTGTATACAGAT G (SEQ ID NO: 134)	TTGATATAAAGCCTACTGTG ATCTTGGCACCATAC (SEQ ID NO: 135)

TABLE 3-continued

Targets, tag, and, primer sequences for two consecutive experiments using the same tag (underlined> for templates P4, P24, P26, P30, P38, P39, P54 as shown in FIG. 4A.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
p26_CWSV00041	3	CATGTTGTGGATGATTAGC ATCTTAACCATGTTGAGTC T (SEQ ID NO: 136)	TCAGGAGTTTGAGATCAGCC TGGCC (SEQ ID NO: 137)
p26_CWSV00042	3	CATGCCCAGATGTGGATGT TCATGGTCCAGA (SEQ ID NO: 138)	GGGTGGATGAGACTTCCGA AGAAC (SEQ ID NO: 139)
p26_CWSV00046	3	CATGCCCTGCGAACCGTCG ACCG (SEQ ID NO: 140)	GTGGATTACCTGAGGTCAGT AGTTCAGA (SEQ ID NO: 141)
p26_CWSV00052	3	CATGGCAGGCTGCTGGAC CCTGC (SEQ ID NO: 142)	CCTGGCTAGCTCCGAAATAT TCCAGGA (SEQ ID NO: 143)
p26_CWSV00053	3	CATGGGTTCTTCGCTACT CTGGCTCCA (SEQ ID NO: 144)	CCACCACACCCAGCTAAGTT T (SEQ ID NO: 145)
p26_CWSV00055	3	CATGGAATCTCAAACGGT ATTTAACATATAAGAAGA TTC (SEQ ID NO: 146)	CTGCATAGAATACAGCCTTA CTGAATGTTAGTCTC (SEQ ID NO: 147)
p26_CWSV00057	3	CATGAAGGCTCCTGGAGC CCTTTGAGG (SEQ ID NO: 148)	TCTGTCTGCCTGGAGCACTG ATTTCTC (SEQ ID NO: 149)
p26_CWSV00058	3	CATGTATTGGATAGTGAGC CCACCACTCAGTAACA (SEQ ID NO: 150)	CCTGAGCTAGATATAAAGA CTCTCCACGT (SEQ ID NO: 151)
p26_CWSV00062	3	CATGACCACCACGCCTGG CTAATTT (SEQ ID NO: 152)	TTTAAGCCAATAGCACCATG TTTCTTT (SEQ ID NO: 153)
p26_CWSV00064	3	CATGGGGCATTGCAGCAG GTGCAG (SEQ ID NO: 154)	GGCATTATTGCAGGGTGCC AAGC (SEQ ID NO: 155)
p26_CWSV00066	3	CATGCCTTAAACCATCACG GTGCTGCTTTGA (SEQ ID NO: 156)	AGCCTATGTGTCTCTGCA CGTGAT (SEQ ID NO: 157)
p26_CWSV00071	3	CATGATCTTACAAGAAGA CATATGCCACAGAGGAC TA (SEQ ID NO: 158)	CTGCTGAGAAATTACTGTCC CTGTGCAAA (SEQ ID NO: 159)
p26_CWSV00072	3	CATGCTGGGCATCAGAGC AAGACTCCATCT (SEQ ID NO: 160)	CCCGTGCCCACTCGCCG (SEQ ID NO: 161)
p26_CWSV00074	3	CATGCTGGGCATGCGACA TCTCTCAGG (SEQ ID NO: 162)	ATCGTCAAATGAACTCGAA ATGAATCATAATCGA (SEQ ID NO: 163)
p26_CWSV00081	3	CATGTTGCCCTGGTGCCTA GGCTGG (SEQ ID NO: 164)	GCACAACCAGAGATACATC AGCCCTAAA (SEQ ID NO: 165)
p26_CWSV00083	3	CATGGCCACCTTGGCCTC CCAAAG (SEQ ID NO: 166)	GAATGCTTGTGTTTAAATCT TCAGTGCTACTCTAG (SEQ ID NO: 167)
p26_CWSV00087	3	CATGGGGAATAGACATGC TGTGGTGGCAGA (SEQ ID NO: 168)	AGCTAATATCATGCCACTGC ACTCCAGC (SEQ ID NO: 169)
p26_CWSV00092	3	CATGATTAAGGATGAGGA CCCTGAGGTTGAGAAAC (SEQ ID NO: 170)	AGGCTTCACCAGACACCAA ATCTGC (SEQ ID NO: 171)

TABLE 3-continued

Targets, tag, and, primer sequences for two consecutive experiments using the same tag (underlined> for templates P4, P24, P26, P30, P38, P39, P54 as shown in FIG. 4A.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
p26_CWSV00106	3	CATGAGATCTGCTGTTAGT CTGATGGGCTTCC (SEQ ID NO: 172)	CCTATGCGGCCGAGCCTCC (SEQ ID NO: 173)
p26_CWSV00108	3	CATGTTTCAGCCAAGCAGT TTGAAAGGATTCT (SEQ ID NO: 174)	GGTCTCAAACCTCTGGGTTC AAGTGAAC (SEQ ID NO: 175)
p26_CWSV00110	3	CATGATTATGATAGGTATC AACACCCTTGCATTT (SEQ ID NO: 176)	ACGAATTGTGGCCAAGTCC TCAA (SEQ ID NO: 177)
p26_CWSV00115	3	CATGGGAATCTTTGTTAAT TGTTTCACGTGAAA (SEQ ID NO: 178)	GGCTGTGGAGATGCATCAGT GAATCAG (SEQ ID NO: 179)
p26_CWSV00118	3	CATGTCCATTGCCATTACT ATTTCAGAGTTACAATGTT (SEQ ID NO: 180)	TTCTCATGACAGTGCTGATC TGTGGATTT (SEQ ID NO: 181)
p26_CWSV00120	3	CATGCGAGCGGCCCAACT CCACAG (SEQ ID NO: 182)	TCTCAGCTACTCGGGAGGCT GAGAT (SEQ ID NO: 183)
p26_CWSV00134	3	CATGAAACGAGTTAATAC TTGCACCGTCTCAGACA (SEQ ID NO: 184)	TCATGGCATGGATGTACCAA AGATTT (SEQ ID NO: 185)
p26_DNAIA_short1	3	CATGCTTGTTACCTGGTGTT CGGTTAT (SEQ ID NO: 113)	GTAGGCTGGGTAGCCAAAT C (SEQ ID NO: 2)
p26_DNAIA_short2	3	CATGCCAGCCCCAAGATGG ATGAAT (SEQ ID NO: 114)	CTCTTCTTTCTTTTCAGCAAC AC (SEQ ID NO: 4)
p26_DNAIA_short3	3	CATGGCGGTGGAAGTCAT TCTGATA (SEQ ID NO: 115)	TCTCTCTCTCTCCAGTGAAC AA (SEQ ID NO: 6)
p26_DNAIA_short4	3	CATGGAGGGCCACAGATT GGTATT (SEQ ID NO: 116)	GATCACTTAGCTCAGGAAAC AAAC (SEQ ID NO: 8)
p26_DNAIA_short5	3	CATGACTGAAAGGTCAGA TTCAGGAG (SEQ ID NO: 117)	TACCGGTTTGTGTCCAAGAG (SEQ ID NO: 10)
P30			
p30_CWSV00004	3	CATGAAACACAACCACTG AGAGTGCTATTATGGTACT C (SEQ ID NO: 186)	TCCTGAGCCAGGTTTACATG GTTACCATT (SEQ ID NO: 187)
p30_CWSV00005	3	CATGGGACATTATGTTTC TCCAAAGCCCTCTG (SEQ ID NO: 188)	GTCACCATGGCCACTCTGGA GC (SEQ ID NO: 189)
p30_CWSV00016	3	CATGGAAGTTGCCAAACA GTTCTCAGAATAGTTACA C (SEQ ID NO: 190)	ATCTATCCCAAGGGCTGCT GTGAGG (SEQ ID NO: 191)
p30_CWSV00030	3	CATGTTGAATGAATGGTAC GTGCGAAGTATATGCTGA (SEQ ID NO: 192)	GTCTGGGAGGCAGAGGTTG CAGT (SEQ ID NO: 193)
p30_CWSV00031	3	CATGCCACAACCTCTTTG TTATAATTTCTCCAGTTGA G (SEQ ID NO: 194)	CTGCCTGCTGGCAGGGCTTC (SEQ ID NO: 195)
p30_CWSV00034	3	CATGGGGATAGACAGACC TGTTGAATCATAAATAGA ACA (SEQ ID NO: 196)	CAGATTCGCTAAATGATTGA CCTTGATACATTT (SEQ ID NO: 197)

TABLE 3-continued

Targets, tag, and, primer sequences for two consecutive experiments using the same tag (underlined> for templates P4, P24, P26, P30, P38, P39, P54 as shown in FIG. 4A.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
p30_CWSV00038	3	CATGACCTTCACAAAGCAT GCACTGACTGT (SEQ ID NO: 198)	TGAGCTGTGGCCACTTACTC AGGAAA (SEQ ID NO: 199)
p30_CWSV00039	3	CATGATCCCAGCACTCTGG AGGGCC (SEQ ID NO: 200)	TGGTCCCTCTGGCCAACTTG GC (SEQ ID NO: 201)
p30_CWSV00040	3	CATGTTTGCTTACCTTCCT GTACACATAAACCAAGG (SEQ ID NO: 202)	CCAACAGATGCCTCCCACTC CAAGT (SEQ ID NO: 203)
p30_CWSV00041	3	CATGTTACACATTATTTCAG CAATGGACTAGAATTGGT GC (SEQ ID NO: 204)	CACCCACCTTGGCCTCCCAA AG (SEQ ID NO: 205)
p30_CWSV00053	3	CATGCATGGCAGCATGGC AGCTTTATATCCTG (SEQ ID NO: 206)	CTCCTGCCTCAGCCTCCCGA G (SEQ ID NO: 207)
p30_CWSV00055	3	CATGGGGCTTGGCCTTAAG TGCCGT (SEQ ID NO: 208)	GACAGAGTTTCACTCTTGTT GCCCAGG (SEQ ID NO: 209)
p30_CWSV00056	3	CATGGGGTCCAGGAAAGT CGGGCAG (SEQ ID NO: 210)	GAGTTCAAGACCAGCCTCGC CAATG (SEQ ID NO: 211)
p30_CWSV00058	3	CATGTTACAGCTAATCTC TCCTGGGCACAC (SEQ ID NO: 212)	GATGGCTTGGAATCCATAA GTCCTATTT (SEQ ID NO: 213)
p30_CWSV00083	3	CATGTTTAACTGCTCAGT CTAGTTAGAATCTCTCTG T (SEQ ID NO: 214)	TGATCCCACCTGGTCTGATG GGTG (SEQ ID NO: 215)
p30_CWSV00106	3	CATGCACAGCATGAGC ATTGAAGCAGAATGAA (SEQ ID NO: 216)	GGTGCTCAGTATTCTAATTC TTTGATTCCTTGTC (SEQ ID NO: 217)
p30_CWSV00109	3	CATGCACACACACCAGCA TGCACTCA (SEQ ID NO: 218)	CCAGCATGATGTTGGTCCAA GTTGGC (SEQ ID NO: 219)
p30_CWSV00116	3	CATGGGGCCAAAGCGGAC TGAGGC (SEQ ID NO: 220)	GCCGTTGTTCTTATCATCTG TCGATACCAA (SEQ ID NO: 221)
p30_CWSV00119	3	CATGAAAGACCCAGAATA GCCAAGCTATCCTGAG (SEQ ID NO: 222)	TCCGTGTGCCCAAGTCAGTT ACCA (SEQ ID NO: 223)
p30_CWSV00126	3	CATGTGGTCCTTTCTTGCA GTAGGAGGATGTC (SEQ ID NO: 224)	TAATTGGTCAGTATCCGTAT GGGTCTTT (SEQ ID NO: 225)
p30_CWSV00128	3	CATGAAACTGCCTGATTCC ACAGCTGAGGTA (SEQ ID NO: 226)	GAGCCTTCTACCTTCAGACT CAGACTGAA (SEQ ID NO: 227)
p30_CWSV00129	3	CATGGGGATGCTTGGTGC AGGCTTCTATTT (SEQ ID NO: 228)	TGTTGGCTCCTATGTCCATT TGACATTT (SEQ ID NO: 229)
p30_CWSV00145	3	CATGGGAAATCCCTCAGTC CGGAAGTCTAGAAC (SEQ ID NO: 230)	TGCCTGTGTATATACAGCAT GTATGATGTACATTT (SEQ ID NO: 231)
p30_CWSV00148	3	CATGGCACATGCAAATAA TGCAATCATATATGGCTTA AT (SEQ ID NO: 232)	GTATCGAAGTATATAAACTG ATGGTTCACAGAGA (SEQ ID NO: 233)

TABLE 3-continued

Targets, tag, and, primer sequences for two consecutive experiments using the same tag (underlined> for templates P4, P24, P26, P30, P38, P39, P54 as shown in FIG. 4A.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
p30_CWSV00149	3	CATGTACCATAACTTAATG CCATATTTGCCATAGTTGG C (SEQ ID NO: 234)	CACGCAACCGTAGGTGTGTA TTCCAG (SEQ ID NO: 235)
p30_CWSV00155	3	CATGAAATGTAAACCTTGT CTAAATCTGGGATCTTC (SEQ ID NO: 236)	TTTGTCTCTGCTTACATTGG CTCTCTGTAATTT (SEQ ID NO: 237)
p30_CWSV00172	3	CATGAAAGCTCACAATTA CAAGTGCTAAGTCTTCAGA AA (SEQ ID NO: 238)	CCTGTATTTCTGTCTTCAC ATGGCATTCTC (SEQ ID NO: 239)
p30_CWSV00173	3	CATGCTAAATCCTTTCCCG TTAGGGACTGTTCTGATC (SEQ ID NO: 240)	GCTGCATAAATGTCTCTTT AGAGAAGTGTCTTT (SEQ ID NO: 241)
p30_CWSV00175	3	CATGAATGGTGGAGGTAG CAGCATTGCAATC (SEQ ID NO: 242)	CTTGAACCTCTGGGCTCAAG CGATC (SEQ ID NO: 243)
p30_CWSV00185	3	CATGTTACTCATTCTTAAG CACTAGGTGTGATTCTAAA T (SEQ ID NO: 244)	CATCATCCCACCAAGTTAGC TCCAA (SEQ ID NO: 245)
p30_CWSV00193	3	CATGTTAAGGCATAGCTTA GCAGTCCACCAAAGAT (SEQ ID NO: 246)	TCCCAGGTAATGCTGATGTT GCCAGT (SEQ ID NO: 247)
p30_CWSV00194	3	CATGAATGCTTAAGATATG TACCCAGCATACCTTAAAT G (SEQ ID NO: 248)	CAAGCTCAAGATTCTGTTA GTTACCAGTTTCTTT (SEQ ID NO: 249)
p30_CWSV00196	3	CATGAAAGTCACACTGTTG CTAACAAGCTGATAAA (SEQ ID NO: 250)	GGGCTCTGGTGTGACGAAGT CATTG (SEQ ID NO: 251)
p30_CWSV00197	3	CATGCTGCACTCCAGCCTG GGCG (SEQ ID NO: 252)	TAGGAGTGCTTCTCTGATGA TGTTCCACC (SEQ ID NO: 253)
p30_CWSV00198	3	CATGCATATTATATCTTTG CTTGCTAGTTTCTCATGT T (SEQ ID NO: 254)	TTATGGTTATTACTTGACAG AGGGCAGT (SEQ ID NO: 255)
p30_CWSV00215	3	CATGATGGTAGCATGACTT CCTGGCCTCTAGT (SEQ ID NO: 256)	TTGGTGCTTTATGGTTTCATT CTGAACAC (SEQ ID NO: 257)
p30_CWSV00216	3	CATGTTGGCAATGGCATT GGTTTCCTCCA (SEQ ID NO: 258)	ATGAGATAGATGACAGAAC TGACACCTAG (SEQ ID NO: 259)
p30_CWSV00218	3	CATGTAGTCTCAGCTACTT GGGAAGCTGAGG (SEQ ID NO: 260)	TCCTGGCATTGGGAAGCTT GCAC (SEQ ID NO: 261)
p30_CWSV00227	3	CATGTAAGTGGAGATAAG CTTGATGTCTTATATGG (SEQ ID NO: 262)	GGAGGAGGGCATTGAGGA GTCTCTATG (SEQ ID NO: 263)
p30_CWSV00233	3	CATGTTTATGGAGGGCCA GGTAATAGCTTTGCA (SEQ ID NO: 264)	AGTGTGATAGTGTGCGCCTG TCAACT (SEQ ID NO: 265)
p30_CWSV00250	3	CATGTGAAAGTCCACCTGT GAGTGCAGAACT (SEQ ID NO: 266)	ACCTAGCCTTTGCTCTAGCA CCGG (SEQ ID NO: 267)
p30_DNAIA_short1	3	CATGCTTGACCTGGTGTT CGGTTAT (SEQ ID NO: 113)	GTAGGCTGGGTAGCCAAAT C (SEQ ID NO: 2)

TABLE 3-continued

Targets, tag, and, primer sequences for two consecutive experiments using the same tag (underlined> for templates P4, P24, P26, P30, P38, P39, P54 as shown in FIG. 4A.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
p30_DNAIA_short2	3	CATGCCAGCCCAAGATGG ATGAAT (SEQ ID NO: 114)	CTCTTCTTTCCTTTCAGCAAC AC (SEQ ID NO: 4)
p30_DNAIA_short3	3	CATGGCGGTGGAAGTCAT TCTGATA (SEQ ID NO: 115)	TCTCTCTCTCTCCAGTGAAC AA (SEQ ID NO: 6)
p30_DNAIA_short4	3	CATGGAGGGCCACAGATT GGTATT (SEQ ID NO: 116)	GATCACTTAGCTCAGGAAAC AAAC (SEQ ID NO: 8)
p30_DNAIA_short5	3	CATGACTGAAAGGTCAGA TTCAGGAG (SEQ ID NO: 117)	TACCGGTTTGTGTCCAAGAG (SEQ ID NO: 10)
P38			
p38_CWSV00001	3	CATGGACGGAGTTTCACTC TTTCGCCAG (SEQ ID NO: 466)	AGAGGTGGCAATGGGCCGA GAT (SEQ ID NO: 467)
p38_CWSV00006	3	CATGAAAGTCTCAAGTAG TCGCATATCTGTTT (SEQ ID NO: 468)	ACTGCTGGCTGGAAACAGA GGCTAA (SEQ ID NO: 469)
p38_CWSV00011	3	CATGGTGATAATTTAAGGC AGTTTCTCATCTGCCTTC (SEQ ID NO: 470)	CATGCACTTGTAGTTCCAGG TACTAGGGAG (SEQ ID NO: 471)
p38_CWSV00014	3	CATGAAATTAGCCGGACA TGGTGGTGCATG (SEQ ID NO: 472)	GTGCGCGCCTGTAATCCCAG C (SEQ ID NO: 473)
p38_CWSV00016	3	CATGAAATCCCAAGTCAC TTTGTTTCAGAAATATTCA G (SEQ ID NO: 474)	AAAGGGACTCCAAGTATTGT ACGATGAAA (SEQ ID NO: 475)
p38_CWSV00019	3	CATGTCCTTAGACTTTCCT TGCTTTCAGTAACCTTGAG (SEQ ID NO: 476)	CACTGAGAGGCCTAGAAGC AGTGACC (SEQ ID NO: 477)
p38_CWSV00022	3	CATGTTTAGTTAGATTGTC TTCTTATTGTTGAGTTACA G (SEQ ID NO: 478)	CCACAAAGTGCAAAGTTTCA TGCAACTT (SEQ ID NO: 479)
p38_CWSV00024	3	CATGAATTACATTTAATGC CTGTTGATGAGGGCTCAA G (SEQ ID NO: 480)	GTTCTATCCATTAAGATCAT GCTCACTAATTTAGA (SEQ ID NO: 481)
p38_CWSV00029	3	CATGTTTAGTAGCATGGCC ATGTGCTTT (SEQ ID NO: 482)	GACCAGCCTAGGCAACATA GTGAGACC (SEQ ID NO: 483)
p38_CWSV00037	3	CATGGCCAAGGCCACCC TGCAG (SEQ ID NO: 484)	CAGGATTCCGTAAGCCAGGT TT (SEQ ID NO: 485)
p38_CWSV00040	3	CATGCAAATCAAATCCCA GCTGAGCCACTCTG (SEQ ID NO: 486)	TTCTCATCTTCCCAGCTGAC ATTT (SEQ ID NO: 487)
p38_CWSV00045	3	CATGAATCCACCCACCTAG AATTCTGTACTCAGC (SEQ ID NO: 488)	GACTCAATTTATGTTGTTTC CATTCAGTTT (SEQ ID NO: 489)
p38_CWSV00050	3	CATGCCACCACGCCAGCT AATTT (SEQ ID NO: 490)	AGTATGAAGCCACCTAGAT TCATTGTGAGG (SEQ ID NO: 491)
p38_DNAIA_short1	3	CATGCTTGTAACCTGGTGTT CGGTTAT (SEQ ID NO: 113)	GTAGGCTGGGTAGCCAAAT C (SEQ ID NO: 2)
p38_DNAIA_short2	3	CATGCCAGCCCAAGATGG ATGAAT (SEQ ID NO: 114)	CTCTTCTTTCCTTTCAGCAAC AC (SEQ ID NO: 4)

TABLE 3-continued

Targets, tag, and, primer sequences for two consecutive experiments using the same tag (underlined> for templates P4, P24, P26, P30, P38, P39, P54 as shown in FIG. 4A.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
p38_DNAIA_short3	3	CATGGCGGTGGAAGTCAT TCTGATA (SEQ ID NO: 115)	TCTCTCTCTCTCCAGTGAAC AA (SEQ ID NO: 6)
p38_DNAIA_short4	3	CATGGAGGGCCACAGATT GGTATT (SEQ ID NO: 116)	GATCACTTAGCTCAGGAAAC AAAC (SEQ ID NO: 8)
p38_DNAIA_short5	3	CATGACTGAAAGGTCAGA TTCAGGAG (SEQ ID NO: 117)	TACCGGTTTGTGTCCAAGAG (SEQ ID NO: 10)
P39			
p39_CWSV00002	3	CATGATTATTTTACAACCTG TGATTGGACAAGAAGAAT TC (SEQ ID NO: 492)	CGATCTCGGCTCACTGCAAC CTC (SEQ ID NO: 493)
p39_CWSV00005	3	CATGATTATTTATATGATC TTCACCTGTGCAATTCCT (SEQ ID NO: 494)	CAGGAGACCTCTCTGAGTAG TTGACAATT (SEQ ID NO: 495)
p39_CWSV00009	3	CATGATCTCTCAAGTGAGA GGATTCTTCCTTCCTGA (SEQ ID NO: 496)	GACTTCAGAAGCTAGTTACT GAAGGAATACT (SEQ ID NO: 497)
p39_CWSV00010	3	CATGAATAAGTCTCTCAGT CATTATATTAGCTTCTAAC A (SEQ ID NO: 498)	ATGTAATGACGGACTTAGTG GCAATAAA (SEQ ID NO: 499)
p39_CWSV00017	3	CATGGGGAAGAGGTCAGG ATTTCACCTATATCTG (SEQ ID NO: 500)	AATCCTCCAGCACTTTGGG AGGC (SEQ ID NO: 501)
p39_CWSV00019	3	CATGCTCAGGACTGAAGG GTTTCCAGGAC (SEQ ID NO: 502)	GCTATTCGGGAGGCTGAGG CAG (SEQ ID NO: 503)
p39_CWSV00033	3	CATGATGTTTAGTTATGCC CTATGCAGATGTCTTGGT (SEQ ID NO: 504)	TATGTCTACTCTGTAGCATT TGGTGGTTCATCC (SEQ ID NO: 505)
p39_CWSV00034	3	CATGGGACGGTACGGTG CGCG (SEQ ID NO: 506)	CAGATAATCAGCATTAAATA TATGTCCAGCATGAC (SEQ ID NO: 507)
p39_CWSV00039	3	CATGACATAAAGACTTTGC TGATGATATATTAACAAAT G (SEQ ID NO: 508)	CAATAGTGGGACAGGCATA GCATAGACATTCTC (SEQ ID NO: 509)
p39_CWSV00046	3	CATGACGGCATATCCTGCT CACCGACTT (SEQ ID NO: 510)	ATGGGCACTATTGCTTTCTA AATGCACAA (SEQ ID NO: 511)
p39_CWSV00048	3	CATGTTTCCTGTGCTGAAG TGACCCCTTGGT (SEQ ID NO: 512)	GGAAGTTCATGCCTAAGAA ACATGTAGCA (SEQ ID NO: 513)
p39_CWSV00060	3	CATGTTAGGTCTTAGATTT AAGTTCCTGATCCATTT (SEQ ID NO: 514)	TCTCGGCTCACTGCAAGCTC CG (SEQ ID NO: 515)
p39_DNAIA_short1	3	CATGCTTGTAACCTGGTGTT CGGTAT (SEQ ID NO: 113)	GTAGGCTGGGTAGCCAAAT C (SEQ ID NO: 2)
p39_DNAIA_short2	3	CATGCCAGCCCAAGATGG ATGAAT (SEQ ID NO: 114)	CTCTTCTTTCCTTTCAGCAAC AC (SEQ ID NO: 4)
p39_DNAIA_short3	3	CATGGCGGTGGAAGTCAT TCTGATA (SEQ ID NO: 115)	TCTCTCTCTCTCCAGTGAAC AA (SEQ ID NO: 6)
p39_DNAIA_short4	3	CATGGAGGGCCACAGATT GGTATT (SEQ ID NO: 116)	GATCACTTAGCTCAGGAAAC AAAC (SEQ ID NO: 8)

TABLE 3-continued

Targets, tag, and, primer sequences for two consecutive experiments using the same tag (underlined> for templates P4, P24, P26, P30, P38, P39, P54 as shown in FIG. 4A.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
p39_DNAIA_short5	3	CATGACTGAAAGGTCAGA TTCAGGAG (SEQ ID NO: 117)	TACCGGTTTGTGTCCAAGAG (SEQ ID NO: 10)
P54			
p54_CWSV00009	3	CATGGGGTGTGGTGGCTC ATGGCTG (SEQ ID NO: 268)	CATGCTTGTTACCTGGTGTTC GGTTAT (SEQ ID NO: 113)
p54_CWSV00010	3	CATGCAGAAGAGTGTGTT GCCTTCCACTGTTC (SEQ ID NO: 269)	CATGCCAGCCCAAGATGGA TGAAT (SEQ ID NO: 114)
p54_CWSV00023	3	CATGCAAACCTGCTTAGTT GTTTACCTGTGATATTGGC T (SEQ ID NO: 270)	CATGGCGGTGGAAGTCATT TGATA (SEQ ID NO: 115)
p54_CWSV00032	3	CATGACCATTTAATCCAAG CTACCCGCTATGTCG (SEQ ID NO: 271)	CATGGAGGGCCACAGATTG GTATT (SEQ ID NO: 116)
p54_CWSV00035	3	CATGGCTGAACTGGCCTA ACCTGAATGTATGTACA (SEQ ID NO: 272)	CATGACTGAAAGGTCAGATT CAGGAG (SEQ ID NO: 117)
p54_CWSV00042	3	CATGGTATTTGTATGGTCA TACACGAGGAACGCTGT A (SEQ ID NO: 273)	GGTTCAACTGAAGTGCCAGC CTGC (SEQ ID NO: 274)
p54_CWSV00048	3	CATGAAACTCCTGACCTCA AGTGATCCACCTG (SEQ ID NO: 275)	CCTCAAAGTGTCTGCAGAGC AGGAATC (SEQ ID NO: 276)
p54_CWSV00057	3	CATGTTATGGCTCAGGATA AATTCCTACATGTAGAATT C (SEQ ID NO: 277)	GAAGGATCAGAGTACCAGC ATCCGTCTTC (SEQ ID NO: 278)
p54_CWSV00095	3	CATGGGGTTTCACCATGTT GGCCAGGATG (SEQ ID NO: 279)	CAGTTTATATTCAGATAGG CAGGAGGTT (SEQ ID NO: 280)
p54_CWSV00132	3	CATGAATACCAGTAAGAG CTTGAACCTTTTAAGTTAA AC (SEQ ID NO: 281)	CTGTGCCCATTTACGCCCT GG (SEQ ID NO: 282)
p54_CWSV00144	3	CATGTGTGCAGCAGACTTC TGCTTGA (SEQ ID NO: 283)	TTTGTGAAAGGCAAATGATG CATGACAG (SEQ ID NO: 284)
p54_CWSV00162	3	CATGTACAGTATTAGGCAC CTGACTGGGTAAA (SEQ ID NO: 285)	GAAAGGTTAAGCAACTTGC CCATGGTCAA (SEQ ID NO: 286)
p54_CWSV00185	3	CATGGTGGCACATGCCTGT AATCCAGC (SEQ ID NO: 287)	AGGCCAGCCATCTCACTGC A (SEQ ID NO: 288)
p54_CWSV00191	3	CATGGATAATCTGGGTACC AGCCTTAAGGAAGGC (SEQ ID NO: 289)	GGGCCCATAGGATTTCTGGA CTGAAATCA (SEQ ID NO: 290)
p54_CWSV00206	3	CATGTTGAGCTAAGCCAGT CCATCAAGACTGG (SEQ ID NO: 291)	GAGCGATTCTCCTGCCTAGG CCT (SEQ ID NO: 292)
p54_CWSV00230	3	CATGTGCCTCGGCCTCCCA AGTAGC (SEQ ID NO: 293)	ACAGTAACCAGATCTCAGCC AATCAGAGG (SEQ ID NO: 294)

TABLE 3-continued

Targets, tag, and, primer sequences for two consecutive experiments using the same tag (underlined> for templates P4, P24, P26, P30, P38, P39, P54 as shown in FIG. 4A.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
p54_CWSV00240	3	CATGAAATTAGCTGGTGG CAGGCACCTGTA (SEQ ID NO: 295)	GGTTACAGTGAGCCATGATT GTGCCG (SEQ ID NO: 296)
p54_CWSV00260	3	CATGATTTCGAGAAATAA CTTCCGATTATTTCAGAT AG (SEQ ID NO: 297)	TAGGGCATTTCACATGGGCT CAGAAACA (SEQ ID NO: 298)
p54_CWSV00266	3	CATGAAGCCAAGGCTGAG CCAAGTCAG (SEQ ID NO: 299)	AAACTTCCAGACTGATTCCA AAGTCCAAG (SEQ ID NO: 300)
p54_CWSV00268	3	CATGTCATTGATTCCAGTG CGGTCCTAAA (SEQ ID NO: 301)	GGTGACAGAGGGAGACTCT GTCACAAA (SEQ ID NO: 302)
p54_CWSV00281	3	CATGCGCCCGACAGTGG AGACG (SEQ ID NO: 303)	TCTTCCTGTGTACCTAGGC TGGTCTCA (SEQ ID NO: 304)
p54_CWSV00305	3	CATGTGTCCCACTGGAGA ACCCTGACTAATACA (SEQ ID NO: 305)	GCTAGGATTACAGGCGTGA GCCACTAT (SEQ ID NO: 306)
p54_CWSV00320	3	CATGCTTCTACTTGTGGA CTTCTGATAGGGTCCAAAG (SEQ ID NO: 307)	AGTCATGGAGGTAGAGCCTT CTTGAAAGG (SEQ ID NO: 308)
p54_CWSV00335	3	CATGCCTCACAGGTAGGC GTGAGGATCAG (SEQ ID NO: 309)	GCCCTGAGGCTCACGTCAC TCA (SEQ ID NO: 310)
p54_CWSV00339	3	CATGCTCAACATGAAGAC AACAGGGATGAGGAGC (SEQ ID NO: 311)	ATGAAGCTAGGATTATTAAC CTAAGGGTCACCTTGT (SEQ ID NO: 312)
p54_CWSV00360	3	CATGGTCGCTCAGGCTGGT GTGCAG (SEQ ID NO: 313)	AAACACAGTCCCTGTCCTTA CAGAGCTC (SEQ ID NO: 314)
p54_CWSV00369	3	CATGGGCTTACATCTGTAA TCCCAGCACTTTGAGA (SEQ ID NO: 315)	ACTGCCTCAGTTAACCAGCA GACTTCA (SEQ ID NO: 316)
p54_CWSV00374	3	CATGCCTCCCACCTTGCC TCCCAA (SEQ ID NO: 317)	TCCTGGGCTCAAGCAATCCT CCTG (SEQ ID NO: 318)
p54_CWSV00416	3	CATGATGGATCCTGGTACC CAGAGGGAATACAA (SEQ ID NO: 319)	GGAGCTTGTACAGCAGCTA AGGTGAG (SEQ ID NO: 320)
p54_CWSV00426	3	CATGGACTCAAACCTCTGG GCTCAAGTGATCC (SEQ ID NO: 321)	TCCCTGAGATCAAGTGATTG TCCCATCTT (SEQ ID NO: 322)
p54_CWSV00428	3	CATGCCCATGGACTCGTAA TTGGTTTCCTGGA (SEQ ID NO: 323)	AATACTCTGGATGATCTTCA GGACATGTT (SEQ ID NO: 324)
p54_CWSV00432	3	CATGGTGATAGCATGCCTC TGTAGTCCCAGC (SEQ ID NO: 325)	GGAGGTGGAGGCGGGAGGA TT (SEQ ID NO: 326)
p54_CWSV00435	3	CATGAATGAGTGAGTGAC GAGGCTGCTGG (SEQ ID NO: 327)	AACCTTCATGAACGTGAGG AAGCTGA (SEQ ID NO: 328)
p54_CWSV00447	3	CATGTCTTAGCCATTGAGA TCAATCCCAGACAGACTA (SEQ ID NO: 329)	AATACTGTAGCCTTCCTAGG GCTCTCAC (SEQ ID NO: 330)

TABLE 3-continued

Targets, tag, and, primer sequences for two consecutive experiments using the same tag (underlined) for templates P4, P24, P26, P30, P38, P39, P54 as shown in FIG. 4A.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
p54_CWSV00449	3	CATGTACACCTTAACCTAG <u>CAATGCTTTCTCTCTGAG</u> (SEQ ID NO: 331)	CTGCCACAGCCTCCCATGTA GCT (SEQ ID NO: 332)
p54_CWSV00461	3	CATGTCTGCCTCAGCCTCC <u>CATGTAGC</u> (SEQ ID NO: 333)	CTAAGGAGAGACTGCTTTCT GATGCCTACC (SEQ ID NO: 334)
p54_CWSV00475	3	CATGCATGCATTGCAACGC <u>AGTGGTGC</u> (SEQ ID NO: 335)	CAGTGCTATCCAGCCCAGAT ACTATGCTTT (SEQ ID NO: 336)
p54_CWSV00512	3	CATGCTGCGAACCTTAAT <u>GCAGAGCTTGATACC</u> (SEQ ID NO: 337)	AGGATGGTATCGATCTCTTC ACCTCGTGA (SEQ ID NO: 338)
p54_CWSV00541	3	CATGCTTCCAGCTAGTTTC <u>TAGAGGTCTTGCTGGA</u> (SEQ ID NO: 339)	AAGTTGCAAACTGCATTGAG ATAGACAATAAA (SEQ ID NO: 340)
p54_CWSV00574	3	CATGCTAGGTGACAGCATT <u>GAGCAGGGCT</u> (SEQ ID NO: 341)	TGGCTAACGCCTGTGATCCC AGC (SEQ ID NO: 342)
p54_CWSV00611	3	CATGGTTCAAGAGCGATG <u>GCTCTCGAATAAA</u> (SEQ ID NO: 343)	CTCGCTGCAACTCCACCCG C (SEQ ID NO: 344)
p54_CWSV00624	3	CATGGGGCATCACACAG <u>GCTGAGGA</u> (SEQ ID NO: 345)	TTTCCTGTTATTTCTATAAG ATGCTTCCTCTGATT (SEQ ID NO: 346)
p54_CWSV00647	3	CATGGAGGTTGCATTGAG <u>CCAAGATCATGGC</u> (SEQ ID NO: 347)	GAGAATGCAGCCCAGTAGG TCTCAGC (SEQ ID NO: 348)
p54_DNAIA_short1	3	CATGCTTGTAACCTGGTGTT <u>CGGTTAT</u> (SEQ ID NO: 113)	GTAGGCTGGGTAGCCAAAT C (SEQ ID NO: 2)
p54_DNAIA_short2	3	CATGCCAGCCCAAGATGG <u>ATGAAT</u> (SEQ ID NO: 114)	CTCTTCTTTCTTTCTAGCAAC AC (SEQ ID NO: 4)
p54_DNAIA_short3	3	CATGGCGGTGGAAGTCAT <u>TCTGATA</u> (SEQ ID NO: 115)	TCTCTCTCTCTCCAGTGAAC AA (SEQ ID NO: 6)
p54_DNAIA_short4	3	CATGGAGGGCCACAGATT <u>GGTATT</u> (SEQ ID NO: 116)	GATCACTTAGCTCAGGAAAC AAAC (SEQ ID NO: 8)
p54_DNAIA_short5	3	CATGACTGAAAGGTCAGA <u>TTCAGGAG</u> (SEQ ID NO: 117)	TACCGGTTTGTGTCCAAGAG (SEQ ID NO: 10)

*Tag sequence is indicated with underline. SV targets and primers are indicated with "CWSV." Control targets and primers are indicated with "DNAIA."

TABLE 4

Targets, tag, and, primer sequences for three consecutive experiments using three different tags (underlined) on a single template (HCC1954v2) as shown in FIG. 4B.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
HCC1954v2_CWSV00079	2	<u>CGTATGAGGCTCGACA</u> GGTACCATATAGCCT (SEQ ID NO: 349)	GCCTGTCGTGCAGCCATG AGTTAG (SEQ ID NO: 12)
HCC1954v2_CWSV00085	2	<u>CGTAGACTCCAACCAT</u> TGGTATAATCTGAAAG TTGTCT (SEQ ID NO: 350)	AAAGGAGAACTATGTGA GCTAATGCATTT (SEQ ID NO: 14)

TABLE 4-continued

Targets, tag, and, primer sequences for three consecutive experiments using three different tags (underlined> on a single template (HCC1954v2) as shown in FIG. 4B.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
HCC1954v2_CWSV00096	2	<u>CGTACTGCCTGACAAC</u> GGACTGAAA (SEQ ID NO: 351)	CTGTATATCTGGCTAGCC ATATGCAGAAA (SEQ ID NO: 16)
HCC1954v2_CWSV00142	2	<u>CGTATCGGCTATTTCTA</u> ACAGCTCACATGTTTAC AT (SEQ ID NO: 352)	CAATCAGAAGACTGCTA GGGTGGCTGTATT (SEQ ID NO: 18)
HCC1954v2_CWSV00166	2	<u>CGTATTCCATAAGTGCC</u> AGCTGGCTGAGAAATA (SEQ ID NO: 353)	GAGTGTATAGACTAGAA GTACAGCCATATAGTT (SEQ ID NO: 20)
HCC1954v2_CWSV00203	2	<u>CGTATCTGCTCCCAGGT</u> TCAAGTGATTCTCAAG (SEQ ID NO: 354)	CCCTGTTGCCAGGCTAG AGTG (SEQ ID NO: 22)
HCC1954v2_CWSV00281	2	<u>CGTATCCGAGAGCTCA</u> CAGCTTGGCT (SEQ ID NO: 355)	GAGCGAGCTCAAGATAG AGGCAGCTAA (SEQ ID NO: 24)
HCC1954v2_CWSV00291	2	<u>CGTAGTTTGATGGAATT</u> CACCAGTGTGTTT (SEQ ID NO: 356)	TCCACATCAGGGGAGCA GCTG (SEQ ID NO: 26)
HCC1954v2_CWSV00362	2	<u>CGTAATTTAGAGAGCC</u> TGTCACAAATGTCCAT ATGAGAA (SEQ ID NO: 357)	GTCCAGCTGAGTGGAAC ATTGAAAGACA (SEQ ID NO: 28)
HCC1954v2_CWSV00739	2	<u>CGTAGAGAGGAGAGAG</u> TGCAGGGTCAA (SEQ ID NO: 358)	TAGGAGGAGCCATTGG CC (SEQ ID NO: 30)
HCC1954v2_CWSV00742	2	<u>CGTAACATTATTGTAA</u> CAAGGGTTGCTTCTGG GAAGA (SEQ ID NO: 359)	GCAGGAGAATGGCATGA ACCCGG (SEQ ID NO: 32)
HCC1954v2_CWSV00743	2	<u>CGTACCCCTGGCACCTA</u> GTGGGTCCATAC (SEQ ID NO: 360)	AGATGTGGCTGAACTTA AATGCATATT (SEQ ID NO: 34)
HCC1954v2_CWSV00744	2	<u>CGTAGCACTCCAGAGA</u> CTCTGTTTCTAAA (SEQ ID NO: 361)	AAAGGGCCAGGCTGAG TGGT (SEQ ID NO: 36)
HCC1954v2_CWSV00791	2	<u>CGTACAGGCATGGTAG</u> CGCGCCT (SEQ ID NO: 362)	CTCCGGCACTGGGCAGA GGTA (SEQ ID NO: 38)
HCC1954v2_CWSV00841	2	<u>CGTAGGAAGCCTCATA</u> ATCATGGTGAAGGCA (SEQ ID NO: 363)	TCACTGCTAGCTGATAAC TCTGACTTT (SEQ ID NO: 40)
HCC1954v2_CWSV00852	2	<u>CGTACATGTTTACCGAT</u> GAAGCTGCAA (SEQ ID NO: 364)	CACTGCATGTTCCAGTC ATAGGTGG (SEQ ID NO: 42)
HCC1954v2_CWSV00856	2	<u>CGTAAGGAAGCTCAGC</u> TATACCTGTTACTGATA ATTT (SEQ ID NO: 365)	AGACCCATCTCACATGTA GACACA (SEQ ID NO: 44)
HCC1954v2_CWSV01009	2	<u>CGTACCCATGCAGGCC</u> TAGGCTAGTG (SEQ ID NO: 366)	CTTCTCCAAGTCTCTACA CTTGGCCACAA (SEQ ID NO: 46)
HCC1954v2_CWSV01021	2	<u>CGTAACCTAAAGGACA</u> CATCTCAGTACATTT (SEQ ID NO: 367)	AGGATGACGCCTGGCTT GGAGAAT (SEQ ID NO: 48)
HCC1954v2_CWSV01028	2	<u>CGTAACTGAAGGCTCT</u> ATGTGCAGGAAGTCC (SEQ ID NO: 368)	AGCAACAAAGATTATCC TAAGACTTCTGGAGGAA G (SEQ ID NO: 50)

TABLE 4-continued

Targets, tag, and, primer sequences for three consecutive experiments using three different tags (underlined> on a single template (HCC1954v2) as shown in FIG. 4B.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
HCC1954v2_CWSV01070	2	<u>CGTACCTCCCAAAGTG</u> CTGGGATTATAGGCA (SEQ ID NO: 369)	AGGAGGGAGTGACAGGA TGTGATCTG (SEQ ID NO: 52)
HCC1954v2_CWSV01075	2	<u>CGTAAACTGTTCTTCCA</u> GGCCTGATTT (SEQ ID NO: 370)	AGCCTGGCCAACACAGT GAAACC (SEQ ID NO: 54)
HCC1954v2_CWSV01077	2	<u>CGTACCCATCCTGGCA</u> CGTACTGCTACT (SEQ ID NO: 371)	TGACCTGTTCTTGGGTAG CACTATTGGT (SEQ ID NO: 56)
HCC1954v2_CWSV01100	2	<u>CGTAAGGCACACTCAG</u> GCTTACGATCTTGTT TA (SEQ ID NO: 372)	AAAGGGATAGCAGTTTC CTGCTGTCCATAG (SEQ ID NO: 58)
HCC1954v2_CWSV01109	2	<u>CGTAATTCTCCCTGCAA</u> ATTGTTGACTCTAGAA ATAGC (SEQ ID NO: 373)	CCCAGGCTGCTGGTCATG GAAA (SEQ ID NO: 60)
HCC1954v2_CWSV01130	2	<u>CGTAGGGTAGTAGCGA</u> TCTGGGTTACCCAG (SEQ ID NO: 374)	CACAGGGTTTATCTCCTC AGACAAA (SEQ ID NO: 62)
HCC1954v2_CWSV01177	2	<u>CGTACATTGACCCACC</u> GGTCATTGAGGAG (SEQ ID NO: 375)	GCGGACGCCATGGAGCT (SEQ ID NO: 64)
HCC1954v2_CWSV01529	2	<u>CGTACTGAGGGTTATC</u> CAAGTGACCCATTGCA (SEQ ID NO: 376)	AACACATTAGTGATGTCT CAATGCCATCC (SEQ ID NO: 66)
HCC1954v2_DNAIA_short1	2	<u>CGTACTTGTA</u> CTCTGGTG TTCGGTTAT (SEQ ID NO: 377)	GTAGGCTGGGTAGCCAA ATC (SEQ ID NO: 2)
HCC1954v2_DNAIA_short2	2	<u>CGTACCAGCCCAAGAT</u> GGATGAAT (SEQ ID NO: 378)	CTCTTTCTTCTTTCAGC AACAC (SEQ ID NO: 4)
HCC1954v2_DNAIA_short3	2	<u>CGTAGCGGTGGAAGTC</u> ATTCTGATA (SEQ ID NO: 379)	TCTCTCTCTCTCCAGTGA ACAA (SEQ ID NO: 6)
HCC1954v2_DNAIA_short4	2	<u>CGTAGAGGGCCACAGA</u> TTGGTATT (SEQ ID NO: 380)	GATCACTTAGCTCAGGA AACAAAC (SEQ ID NO: 8)
HCC1954v2_DNAIA_short5	2	<u>CGTAACTGAAAGGTCA</u> GATTCAGGAG (SEQ ID NO: 381)	TACCGGTTTGTGTCCAAG AG (SEQ ID NO: 10)
HCC1954v2_CWSV00079	3	<u>GTACTGAGGCTCGACA</u> GGTACCATATAGCCT (SEQ ID NO: 382)	GCCTGTCGTGCAGCCATG AGTTAG (SEQ ID NO: 12)
HCC1954v2_CWSV00085	3	<u>GTACGACTCCAACCAT</u> TGGTATAATCTGAAAG TTGTCT (SEQ ID NO: 383)	AAAGGAGAACTATGTGA GCTAATGCATTT (SEQ ID NO: 14)
HCC1954v2_CWSV00096	3	<u>GTACCTGCCTGACAAC</u> GGACTGAAA (SEQ ID NO: 384)	CTGTATATCTGGCTAGCC ATATGCAGAAA (SEQ ID NO: 16)
HCC1954v2_CWSV00142	3	<u>GTACTCGGCTATTTCTA</u> ACAGCTCACATGTTTAC AT (SEQ ID NO: 385)	CAATCAGAAGACTGCTA GGGTGGCTGTATT (SEQ ID NO: 18)
HCC1954v2_CWSV00166	3	<u>GTACTTCCATAAGTGCC</u> AGCTGGCTGAGAAATA (SEQ ID NO: 386)	GAGTGTATAGACTAGAA GTACAGCCATATAGTT (SEQ ID NO: 20)

TABLE 4-continued

Targets, tag, and, primer sequences for three consecutive experiments using three different tags (underlined> on a single template (HCC1954v2) as shown in FIG. 4B.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
HCC1954v2_CWSV00203	3	GTACTCTGCTCCCAGGT <u>TCAAGTGATTCTCAAG</u> (SEQ ID NO: 387)	CCCTGTTGCCCAGGCTAG AGTG (SEQ ID NO: 22)
HCC1954v2_CWSV00281	3	GTACTCCGAGAGCTCA CAGCTTGGCT (SEQ ID NO: 388)	GAGCGAGCTCAAGATAG AGGCAGCTAA (SEQ ID NO: 24)
HCC1954v2_CWSV00291	3	GTACGTTTGATGGAATT <u>CACCAGTGTGTTT</u> (SEQ ID NO: 389)	TCCACATCACGGGAGCA GCTG (SEQ ID NO: 26)
HCC1954v2_CWSV00362	3	GTACATTTAGAGAGCC TGTCAAAATGTCCAT ATGAGAA (SEQ ID NO: 390)	GTCCAGCTGAGTGGAAC ATTGAAAGAACA (SEQ ID NO: 28)
HCC1954v2_CWSV00739	3	<u>GTACGAGAGGAGAGAG</u> TGCAGGGTCAA (SEQ ID NO: 391)	TAGGAGGAGCCCATGG CC (SEQ ID NO: 30)
HCC1954v2_CWSV00742	3	<u>GTACACATTATTGTAA</u> CAAGGGTTGCTTCTGG GAAGA (SEQ ID NO: 392)	GCAGGAGAATGGCATGA ACCCGG (SEQ ID NO: 32)
HCC1954v2_CWSV00743	3	<u>GTACCCCTGGCACCTA</u> GTGGGTCCATAC (SEQ ID NO: 393)	AGATGTGGCTGAACTTTA AATGCATATT (SEQ ID NO: 34)
HCC1954v2_CWSV00744	3	<u>GTACGCACTCCAGAGA</u> CTCTGTTTCTAAA (SEQ ID NO: 394)	AAAGGGCCAGGCCTGAG TGGT (SEQ ID NO: 36)
HCC1954v2_CWSV00791	3	<u>GTACCAGGCATGGTAG</u> CGCGCCT (SEQ ID NO: 395)	CTCCGGCACTGGGCAGA GGTA (SEQ ID NO: 38)
HCC1954v2_CWSV00841	3	<u>GTACGGAAGCCTCATA</u> ATCATGGTGAAGGCA (SEQ ID NO: 396)	TCAGTGCTAGCTGATAAC TCTGACTTT (SEQ ID NO: 40)
HCC1954v2_CWSV00852	3	<u>GTACCATGTTTACCGAT</u> GAAGCTGCAA (SEQ ID NO: 397)	CACTGCATGTTCCAGTC ATAGGTGG (SEQ ID NO: 42)
HCC1954v2_CWSV00856	3	<u>GTACAGGAAGCTCAGC</u> TATACCTGTACTGATA ATTT (SEQ ID NO: 398)	AGACCCATCTCACATGTA GACACA (SEQ ID NO: 44)
HCC1954v2_CWSV01009	3	<u>GTACCCCATGCAGGCC</u> TAGGCTAGTGT (SEQ ID NO: 399)	CTTCTCCAAGTCTCTACA CTTGGCCACAA (SEQ ID NO: 46)
HCC1954v2_CWSV01021	3	<u>GTACACCTAAAGGACA</u> CATCTCAGTACATT (SEQ ID NO: 400)	AGGATGACGCCTGGCTT GGAGAAT (SEQ ID NO: 48)
HCC1954v2_CWSV01028	3	<u>GTACACTGAAGGCTCT</u> ATGTGCAGGAAGTCC (SEQ ID NO: 401)	AGCAACAAAGATTATCC TAAGACTTCTGGAGGAA G (SEQ ID NO: 50)
HCC1954v2_CWSV01070	3	<u>GTACCTCCCAAAGTG</u> CTGGGATTATAGGCA (SEQ ID NO: 402)	AGGAGGGAGTGACAGGA TGTGATCTG (SEQ ID NO: 52)
HCC1954v2_CWSV01075	3	<u>GTACAACTGTTCTTCCA</u> GGCCTGATTT (SEQ ID NO: 403)	AGCCTGGCCAACACAGT GAAACC (SEQ ID NO: 54)

TABLE 4-continued

Targets, tag, and, primer sequences for three consecutive experiments using three different tags (underlined> on a single template (HCC1954v2) as shown in FIG. 4B.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
HCC1954v2_CWSV01077	3	GTACCCCATCCTGGCA CGTACTGCTACT (SEQ ID NO: 404)	TGACCTGTTCTTGGGTAG CACTATTGGT (SEQ ID NO: 56)
HCC1954v2_CWSV01100	3	GTACAGGCACACTCAG GCTTTACGATTCTTGT TA (SEQ ID NO: 405)	AAAGGGATAGCAGTTTC CTGCTGTCCATAG (SEQ ID NO: 58)
HCC1954v2_CWSV01109	3	GTACATTCTCCCTGCAA ATTGTTTGACTCTAGAA ATAGC (SEQ ID NO: 406)	CCCAGGCTGCTGGTCATG GAAA (SEQ ID NO: 60)
HCC1954v2_CWSV01130	3	GTACGGGTAGTAGCGA TCTGGGTACCCAG (SEQ ID NO: 407)	CACAGGGTTTATCTCCTC AGACAAA (SEQ ID NO: 62)
HCC1954v2_CWSV01177	3	GTACCATTGACCCACC GGTCATTCAGGAG (SEQ ID NO: 408)	GCGGACGCCATGGAGCT (SEQ ID NO: 64)
HCC1954v2_CWSV01529	3	GTACCTGAGGGTTATC CAAGTGACCCATTGCA (SEQ ID NO: 409)	AACACATTAGTGATGTCT CAATGCCATCC (SEQ ID NO: 66)
HCC1954v2_DNAIA_short1	3	GTACCTTGTAACCTGGTG TTCGGTTAT (SEQ ID NO: 410)	GTAGGCTGGGTAGCCAA ATC (SEQ ID NO: 2)
HCC1954v2_DNAIA_short2	3	GTACCCAGCCCAAGAT GGATGAAT (SEQ ID NO: 411)	CTCTTCTTTCCTTTCAGC AACAC (SEQ ID NO: 4)
HCC1954v2_DNAIA_short3	3	GTACGCGGTGGAAGTC ATTCTGATA (SEQ ID NO: 412)	TCTCTCTCTCCAGTGA ACAA (SEQ ID NO: 6)
HCC1954v2_DNAIA_short4	3	GTACGAGGGCCACAGA TTGGTATT (SEQ ID NO: 413)	GATCACTTAGCTCAGGA AACAAAC (SEQ ID NO: 8)
HCC1954v2_DNAIA_short5	3	GTACACTGAAAGGTCA GATTCAGGAG (SEQ ID NO: 414)	TACCGGTTTGTGTCCAAG AG (SEQ ID NO: 10)
HCC1954v2_CWSV00079	1	ACGTTGAGGCTCGACA GGTACCATATAGCCT (SEQ ID NO: 415)	GCCTGTCGTGCAGCCATG AGTTAG (SEQ ID NO: 12)
HCC1954v2_CWSV00085	1	ACGTGACTCCAACCAT TGGTATAATCTGAAAG TTGTCT (SEQ ID NO: 416)	AAAGGAGAACTATGTGA GCTAATGCATTT (SEQ ID NO: 14)
HCC1954v2_CWSV00096	1	ACGTCTGCCTGACAAC GGACTGAAA (SEQ ID NO: 417)	CTGTATATCTGGCTAGCC ATATGCAGAAA (SEQ ID NO: 16)
HCC1954v2_CWSV00142	1	ACGTTCTGGCTATTTCTA ACAGCTCACATGTTTAC AT (SEQ ID NO: 418)	CAATCAGAAGACTGCTA GGGTGGCTGTATT (SEQ ID NO: 18)
HCC1954v2_CWSV00166	1	ACGTTTCCATAAGTGCC AGCTGGCTGAGAAATA (SEQ ID NO: 419)	GAGTGATAGACTAGAA GTACAGCCATATAGTT (SEQ ID NO: 20)
HCC1954v2_CWSV00203	1	ACGTTCTGCTCCCAGGT TCAAGTGATTCTCAAG (SEQ ID NO: 420)	CCCTGTTGCCAGGCTAG AGTG (SEQ ID NO: 22)
HCC1954v2_CWSV00281	1	ACGTTCCGAGAGCTCA CAGCTTGGCT (SEQ ID NO: 421)	GAGCGAGCTCAAGATAG AGGCAGCTAA (SEQ ID NO: 24)

TABLE 4-continued

Targets, tag, and, primer sequences for three consecutive experiments using three different tags (underlined) on a single template (HCC1954v2) as shown in FIG. 4B.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
HCC1954v2_CWSV00291	1	<u>ACGTGTTTGATGGAATT</u> CACCAGTGTGTTT (SEQ ID NO: 422)	TCCACATCACGGGAGCA GCTG (SEQ ID NO: 26)
HCC1954v2_CWSV00362	1	<u>ACGTATTTAGAGAGCC</u> TGTACAAATGTCCAT ATGAGAA (SEQ ID NO: 423)	GTCCAGCTGAGTGGAAC ATTGAAAGAACA (SEQ ID NO: 28)
HCC1954v2_CWSV00739	1	<u>ACGTGAGAGGAGAGAG</u> TGCAGGGTCAA (SEQ ID NO: 424)	TAGGAGGAGCCATTGG CC (SEQ ID NO: 30)
HCC1954v2_CWSV00742	1	<u>ACGTACATTATTGTTAA</u> CAAGGGTTGCTTCTGG GAAGA (SEQ ID NO: 425)	GCAGGAGAATGGCATGA ACCCGG (SEQ ID NO: 32)
HCC1954v2_CWSV00743	1	<u>ACGTCCCTGGCACCTA</u> GTGGGTCCATAC (SEQ ID NO: 426)	AGATGTGGCTGAACTTTA AATGCATATT (SEQ ID NO: 34)
HCC1954v2_CWSV00744	1	<u>ACGTGCACTCCAGAGA</u> CTCTGTTTCTAAA (SEQ ID NO: 427)	AAAGGGCCAGGCCTGAG TGGT (SEQ ID NO: 36)
HCC1954v2_CWSV00791	1	<u>ACGTCAGGCATGGTAG</u> CGCGCCT (SEQ ID NO: 428)	CTCCGGCACTGGGCAGA GGTA (SEQ ID NO: 38)
HCC1954v2_CWSV00841	1	<u>ACGTGGAAGCCTCATA</u> ATCATGGTGAAGGCA (SEQ ID NO: 429)	TCAGTGCTAGCTGATAAC TCTGACTTT (SEQ ID NO: 40)
HCC1954v2_CWSV00852	1	<u>ACGTCATGTTTACCGAT</u> GAAGCTGCAA (SEQ ID NO: 430)	CACTGCATGTTCCAGTC ATAGGTGG (SEQ ID NO: 42)
HCC1954v2_CWSV00856	1	<u>ACGTAGGAAGCTCAGC</u> TATACCTGTACTGATA ATTT (SEQ ID NO: 431)	AGACCCATCTCACATGTA GACACA (SEQ ID NO: 44)
HCC1954v2_CWSV01009	1	<u>ACGTCCCATGCAGGCC</u> TAGGCTAGTGT (SEQ ID NO: 432)	CTTCTCCAAGTCTCTACA CTTGCCCAAA (SEQ ID NO: 46)
HCC1954v2_CWSV01021	1	<u>ACGTACCTAAAGGACA</u> CATCTCAGTACATTT (SEQ ID NO: 433)	AGGATGACGCCTGGCTT GGAGAAT (SEQ ID NO: 48)
HCC1954v2_CWSV01028	1	<u>ACGTACTGAAGGCTCT</u> ATGTGCAGGAACCTCC (SEQ ID NO: 434)	AGCAACAAAGATTATCC TAAGACTTCTGGAGGAA G (SEQ ID NO: 50)
HCC1954v2_CWSV01070	1	<u>ACGTCCTCCCAAAGTG</u> CTGGGATTATAGGCA (SEQ ID NO: 435)	AGGAGGGAGTGACAGGA TGTGATCTG (SEQ ID NO: 52)
HCC1954v2_CWSV01075	1	<u>ACGTAAGTGTCTTCCA</u> GGCCTGATTT (SEQ ID NO: 436)	AGCCTGGCCAACACAGT GAAACC (SEQ ID NO: 54)
HCC1954v2_CWSV01077	1	<u>ACGTCCCATCCTGGCA</u> CGTACTGCTACT (SEQ ID NO: 437)	TGACCTGTTCTTGGGTAG CACTATTGGT (SEQ ID NO: 56)
HCC1954v2_CWSV01100	1	<u>ACGTAGGCACACTCAG</u> GCTTTACGATTCTTGTT TA (SEQ ID NO: 438)	AAAGGGATAGCAGTTTC CTGCTGTCCATAG (SEQ ID NO: 58)

TABLE 4-continued

Targets, tag, and, primer sequences for three consecutive experiments using three different tags (underlined> on a single template (HCC1954v2) as shown in FIG. 4B.*			
Target	Tag	Forward Primer Sequence	Reverse Primer Sequence
HCC1954v2_CWSV01109	1	ACGTATTCTCCCTGCAA ATTGTTTGACTCTAGAA ATAGC (SEQ ID NO: 439)	CCCAGGCTGCTGGTCATG GAAA (SEQ ID NO: 60)
HCC1954v2_CWSV01130	1	ACGTGGGTAGTAGCGA TCTGGTTACCCAG (SEQ ID NO: 440)	CACAGGGTTTATCTCCTC AGACAAA (SEQ ID NO: 62)
HCC1954v2_CWSV01177	1	ACGTCATTGACCCACC GGTCATTCAGGAG (SEQ ID NO: 441)	GCGGACGCCATGGAGCT (SEQ ID NO: 64)
HCC1954v2_CWSV01529	1	ACGTCTGAGGGTTATC CAAGTGACCCATTGCA (SEQ ID NO: 442)	AACACATTAGTGATGTCT CAATGCCATCC (SEQ ID NO: 66)
HCC1954v2_DNAIA_short1	1	ACGTCTTGTACCTGGTG TTCGGTTAT (SEQ ID NO: 443)	GTAGGCTGGGTAGCCAA ATC (SEQ ID NO: 2)
HCC1954v2_DNAIA_short2	1	ACGTCCAGCCCAAGAT GGATGAAT (SEQ ID NO: 444)	CTCTTCTTTCCTTTCAGC AACAC (SEQ ID NO: 4)
HCC1954v2_DNAIA_short3	1	ACGTGCGGTGGAAGTC ATTCTGATA (SEQ ID NO: 445)	TCTCTCTCTCCAGTGA ACAA (SEQ ID NO: 6)
HCC1954v2_DNAIA_short4	1	ACGTGAGGGCCACAGA TTGGTATT (SEQ ID NO: 446)	GATCACTTAGCTCAGGA AACAAAC (SEQ ID NO: 8)
HCC1954v2_DNAIA_short5	1	ACGTACTGAAAGGTCA GATTCAGGAG (SEQ ID NO: 447)	TACCGGTTTGTGTCCAAG AG (SEQ ID NO: 10)

*Tag sequences are indicated with underline. SV targets and primers are indicated with "CWSV." Control targets and primers are indicated with "DNAIA."

Alternative Approaches and Applications

[0065] One simple alternative approach to the tagged-primer design is to vary the length of primers on the 5' end while keeping the 3' end constant. Since our read out is sequencing-based, this can also guide the informatic approach to distinguish different versions of the same target panel.

[0066] The application of this approach is not restricted to SVEN. Any PCR-based assay that relies on detection of amplicons (mutated or otherwise) can benefit from this approach to track, measure, and exclude run-to-run carry-over of PCR amplicons.

REFERENCES

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- [0068]** Garibyan L, Avashia N. Polymerase chain reaction. J Invest Dermatol. 2013 March; 133(3):1-4.
- [0069]** Mifflin T E. Setting up a PCR laboratory. CSH Protoc. 2007 Jul. 1; 2007:pdb.top14.

SEQUENCE LISTING

Sequence total quantity: 515
 SEQ ID NO: 1 moltype = DNA length = 22
 FEATURE Location/Qualifiers
 source 1..22
 mol_type = other DNA
 organism = synthetic construct
 SEQUENCE: 1
 cttgtacctg gtgttcggtt at
 SEQ ID NO: 2 moltype = DNA length = 20
 FEATURE Location/Qualifiers

22

-continued

source	1..20 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 2		
gtaggctggg tagccaaatc		20
SEQ ID NO: 3	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 3		
ccagcccaag atggatgaat		20
SEQ ID NO: 4	moltype = RNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23 mol_type = other RNA organism = synthetic construct	
SEQUENCE: 4		
ctctctcttc ctttcagcaa cac		23
SEQ ID NO: 5	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
source	1..21 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 5		
gcggtggaag tcattctgat a		21
SEQ ID NO: 6	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 6		
tctctctctc tccagtgaac aa		22
SEQ ID NO: 7	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 7		
gagggccaca gattggtatt		20
SEQ ID NO: 8	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 8		
gatcacttag ctcaggaaac aaac		24
SEQ ID NO: 9	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 9		
actgaaaggt cagattcagg ag		22
SEQ ID NO: 10	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
source	1..20 mol_type = other DNA organism = synthetic construct	
SEQUENCE: 10		
taccggtttg tgtccaagag		20
SEQ ID NO: 11	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27 mol_type = other DNA organism = synthetic construct	

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SEQUENCE: 11
 tgaggctcga caggtacat atagcct 27

SEQ ID NO: 12 moltype = DNA length = 24
 FEATURE Location/Qualifiers
 source 1..24
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 12
 gctgtcgtg cagccatgag ttag 24

SEQ ID NO: 13 moltype = DNA length = 34
 FEATURE Location/Qualifiers
 source 1..34
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 13
 gactccaacc attggtataa tctgaaagtt gtct 34

SEQ ID NO: 14 moltype = DNA length = 29
 FEATURE Location/Qualifiers
 source 1..29
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 14
 aaaggagaac tatgtgagct aatgcattt 29

SEQ ID NO: 15 moltype = DNA length = 21
 FEATURE Location/Qualifiers
 source 1..21
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 15
 ctgcctgaca acggactgaa a 21

SEQ ID NO: 16 moltype = DNA length = 29
 FEATURE Location/Qualifiers
 source 1..29
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 16
 ctgtatatct ggctagccat atgcagaaa 29

SEQ ID NO: 17 moltype = DNA length = 32
 FEATURE Location/Qualifiers
 source 1..32
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 17
 tcggctatctt ctaacagctc acatgtttac at 32

SEQ ID NO: 18 moltype = DNA length = 30
 FEATURE Location/Qualifiers
 source 1..30
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 18
 caatcagaag actgctaggg tggtgtatt 30

SEQ ID NO: 19 moltype = DNA length = 29
 FEATURE Location/Qualifiers
 source 1..29
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 19
 ttccataagt gccagctggc tgagaaata 29

SEQ ID NO: 20 moltype = DNA length = 33
 FEATURE Location/Qualifiers
 source 1..33
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 20
 gagtgtatag actagaagta cagccatata gtt 33

SEQ ID NO: 21	moltype = DNA length = 29
FEATURE	Location/Qualifiers
source	1..29
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 21	
tctgctccca ggttcaagtg attctcaag	29
SEQ ID NO: 22	moltype = DNA length = 22
FEATURE	Location/Qualifiers
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 22	
ccctgttgcc caggctagag tg	22
SEQ ID NO: 23	moltype = DNA length = 22
FEATURE	Location/Qualifiers
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 23	
tccgagagct cacagcttgg ct	22
SEQ ID NO: 24	moltype = DNA length = 27
FEATURE	Location/Qualifiers
source	1..27
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 24	
gagcgagctc aagatagagg cagctaa	27
SEQ ID NO: 25	moltype = DNA length = 26
FEATURE	Location/Qualifiers
source	1..26
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 25	
gtttgatgga attcaccagt gtgttt	26
SEQ ID NO: 26	moltype = DNA length = 21
FEATURE	Location/Qualifiers
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 26	
tccacatcac gggagcagct g	21
SEQ ID NO: 27	moltype = DNA length = 35
FEATURE	Location/Qualifiers
source	1..35
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 27	
atttagagag cctgtcaca atgtccatat gagaa	35
SEQ ID NO: 28	moltype = DNA length = 29
FEATURE	Location/Qualifiers
source	1..29
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 28	
gtccagctga gtggaacatt gaaagaaca	29
SEQ ID NO: 29	moltype = DNA length = 23
FEATURE	Location/Qualifiers
source	1..23
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 29	
gagaggagag agtgcagggt caa	23
SEQ ID NO: 30	moltype = DNA length = 19
FEATURE	Location/Qualifiers
source	1..19

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SEQUENCE: 30	mol_type = other DNA organism = synthetic construct	
taggaggagc ccattggcc		19
SEQ ID NO: 31	moltype = DNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 31		
acattattgt taacaagggt tgcttctggg aaga		34
SEQ ID NO: 32	moltype = DNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 32		
gcaggagaat ggcattgaacc cgg		23
SEQ ID NO: 33	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 33		
ccctggcacc tagtgggtcc atac		24
SEQ ID NO: 34	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 34		
agatgtggct gaactttaaa tgcatatt		28
SEQ ID NO: 35	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 35		
gcactccaga gactctgttt ctaaa		25
SEQ ID NO: 36	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
source	1..21	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 36		
aaagggccag gcctgagtgg t		21
SEQ ID NO: 37	moltype = DNA length = 19	
FEATURE	Location/Qualifiers	
source	1..19	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 37		
caggcatggt agcgcgcct		19
SEQ ID NO: 38	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
source	1..21	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 38		
ctccggcact gggcagaggt a		21
SEQ ID NO: 39	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 39		
ggaagcctca taatcatggt ggaaggca		28

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SEQ ID NO: 40      moltype = DNA  length = 27
FEATURE           Location/Qualifiers
source            1..27
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 40
tcagtgcctag ctgataactc tgacttt                27

SEQ ID NO: 41      moltype = DNA  length = 24
FEATURE           Location/Qualifiers
source            1..24
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 41
catgtttacc gatgaagctg caaaa                    24

SEQ ID NO: 42      moltype = DNA  length = 26
FEATURE           Location/Qualifiers
source            1..26
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 42
cactgcatgt tcccagtcac aggtgg                    26

SEQ ID NO: 43      moltype = DNA  length = 33
FEATURE           Location/Qualifiers
source            1..33
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 43
aggaagctca gctatacctg ttactgataa ttt          33

SEQ ID NO: 44      moltype = DNA  length = 24
FEATURE           Location/Qualifiers
source            1..24
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 44
agacccatct cacatgtaga caca                      24

SEQ ID NO: 45      moltype = DNA  length = 23
FEATURE           Location/Qualifiers
source            1..23
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 45
cccatgcagg cctaggctag tgt                        23

SEQ ID NO: 46      moltype = DNA  length = 29
FEATURE           Location/Qualifiers
source            1..29
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 46
cttctccaag tctctacact tggccacaa                29

SEQ ID NO: 47      moltype = DNA  length = 27
FEATURE           Location/Qualifiers
source            1..27
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 47
acctaaagga cacatctcag tacattt                    27

SEQ ID NO: 48      moltype = DNA  length = 24
FEATURE           Location/Qualifiers
source            1..24
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 48
aggatgacgc ctggcttgga gaat                      24

SEQ ID NO: 49      moltype = DNA  length = 27
FEATURE           Location/Qualifiers
source            1..27

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 49		
actgaaggct ctatgtgcag gaactcc		27
SEQ ID NO: 50	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 50		
agcaacaaag attatcctaa gacttctgga ggaag		35
SEQ ID NO: 51	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 51		
cctcccaaag tgctgggatt ataggca		27
SEQ ID NO: 52	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 52		
aggagggagt gacaggatgt gatctg		26
SEQ ID NO: 53	moltype = DNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 53		
aactgttctt ccaggcctga ttt		23
SEQ ID NO: 54	moltype = DNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 54		
agcctggcca acacagtga acc		23
SEQ ID NO: 55	moltype = RNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other RNA organism = synthetic construct	
SEQUENCE: 55		
cccatcctgg cacgtactgc tact		24
SEQ ID NO: 56	moltype = RNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other RNA organism = synthetic construct	
SEQUENCE: 56		
tgacctgttc ttgggtagca ctattggt		28
SEQ ID NO: 57	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 57		
aggcacactc aggccttacg attcttggtt a		31
SEQ ID NO: 58	moltype = DNA length = 30	
FEATURE	Location/Qualifiers	
source	1..30	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 58		
aaagggatag cagtttctcg ctgtccatag		30

SEQ ID NO: 59	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 59		
attctccctg caaattgttt gactctagaa atagc	35	
SEQ ID NO: 60	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 60		
cccaggctgc tggtcatgga aa	22	
SEQ ID NO: 61	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 61		
gggtagtagc gatctggggtt acccag	26	
SEQ ID NO: 62	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 62		
cacagggttt atctcctcag acaaa	25	
SEQ ID NO: 63	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 63		
cattgaccca ccggtcattc aggag	25	
SEQ ID NO: 64	moltype = DNA length = 17	
FEATURE	Location/Qualifiers	
source	1..17	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 64		
gcggacgcc a tggagct	17	
SEQ ID NO: 65	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 65		
ctgagggtta tccaagtgac ccattgca	28	
SEQ ID NO: 66	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 66		
aacacattag tgatgtctca atgccatcc	29	
SEQ ID NO: 67	moltype = RNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 67		
catggttgaa cctggggaggc ggaggt	26	
SEQ ID NO: 68	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 68		
gctcaggcac tgagagtcag cc		22
SEQ ID NO: 69	moltype = RNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other RNA organism = synthetic construct	
SEQUENCE: 69		
catgcaggag gccaaaggtg acgg		24
SEQ ID NO: 70	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 70		
ggatagctat tgagagcttc cttcatttg		29
SEQ ID NO: 71	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 71		
catgaagagt acttgacaca tgcataaact cagtaaatt		39
SEQ ID NO: 72	moltype = DNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 72		
atgaagtatc atataagat acactctatg catc		34
SEQ ID NO: 73	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 73		
catggggtcc cacatgacag ccatgact		28
SEQ ID NO: 74	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 74		
ggtcccagtc cctcagtc tc		24
SEQ ID NO: 75	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 75		
catgaaagaa acaaacttgt ctcggtatcc agaaagtgt		39
SEQ ID NO: 76	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 76		
acagttcagt agtgtaaga acatttgca		29
SEQ ID NO: 77	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 77		
catgaactat tccttaagc caagcatagt atgtctaga		39

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SEQ ID NO: 78	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 78		
ggatggcacc tgctggctac attt	24	
SEQ ID NO: 79	moltype = RNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 79		
catgagtagt tgggattaca ggcatgtgcc a	31	
SEQ ID NO: 80	moltype = RNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 80		
aagacacaag tttatctata tgacaaactt tgac	34	
SEQ ID NO: 81	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 81		
catgtgtaac taacctgcac gttgtgcaca tg	32	
SEQ ID NO: 82	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 82		
tgcccattgt attagtcagg caggggt	27	
SEQ ID NO: 83	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 83		
catgtcctg gactcaagcg atcctcctg	29	
SEQ ID NO: 84	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
source	1..21	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 84		
ggagctggtg gagcctgctc t	21	
SEQ ID NO: 85	moltype = DNA length = 38	
FEATURE	Location/Qualifiers	
source	1..38	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 85		
catgaatatg aaataaagcc cacagtaaag attactct	38	
SEQ ID NO: 86	moltype = DNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 86		
gtgaccaaac taaatgtttg tgtactttaa agga	34	
SEQ ID NO: 87	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 87		
catggccact gcactccagc ctaggt		26
SEQ ID NO: 88	moltype = RNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other RNA organism = synthetic construct	
SEQUENCE: 88		
gtggccctaa ctgggtcac cata		24
SEQ ID NO: 89	moltype = DNA length = 36	
FEATURE	Location/Qualifiers	
source	1..36	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 89		
catgaaagaa tatcgataca tgggcagctg acactt		36
SEQ ID NO: 90	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 90		
aaatagctgc tttagatata tgaagcca		28
SEQ ID NO: 91	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 91		
catgtttgag acacagtttc tctctgtca cccag		35
SEQ ID NO: 92	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 92		
cccactgtgg aatgtcacag ctattt		26
SEQ ID NO: 93	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 93		
catgccact gctggacctt agcacg		26
SEQ ID NO: 94	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 94		
tgatgcatgg ccttagctgt ttactttgc		29
SEQ ID NO: 95	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 95		
catgctccac atgcatagta tcagccctcc a		31
SEQ ID NO: 96	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 96		
gaggtggaaa ttgcagttag ccgag		25

SEQ ID NO: 97	moltype = DNA length = 24
FEATURE	Location/Qualifiers
source	1..24
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 97	
catgaggtgt gagccaccac gcct	24
SEQ ID NO: 98	moltype = DNA length = 26
FEATURE	Location/Qualifiers
source	1..26
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 98	
agtgactcac gcctataatc ccacgg	26
SEQ ID NO: 99	moltype = DNA length = 32
FEATURE	Location/Qualifiers
source	1..32
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 99	
catgtttaaa gacagttcttc gccaggtgtg gt	32
SEQ ID NO: 100	moltype = DNA length = 19
FEATURE	Location/Qualifiers
source	1..19
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 100	
ccgaggcagg ccgatcacc	19
SEQ ID NO: 101	moltype = DNA length = 35
FEATURE	Location/Qualifiers
source	1..35
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 101	
catgtttacg aggccagcat catcctgata ctaaa	35
SEQ ID NO: 102	moltype = DNA length = 34
FEATURE	Location/Qualifiers
source	1..34
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 102	
gtaacataat acaaagctgc atcacagcta atct	34
SEQ ID NO: 103	moltype = DNA length = 26
FEATURE	Location/Qualifiers
source	1..26
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 103	
catgggggatc ccagaccttg gccagg	26
SEQ ID NO: 104	moltype = DNA length = 35
FEATURE	Location/Qualifiers
source	1..35
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 104	
aggtgcttat aaatttctgt tacatgaag aatac	35
SEQ ID NO: 105	moltype = DNA length = 39
FEATURE	Location/Qualifiers
source	1..39
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 105	
catgaaatta agaaggttca tcacagtcca aagaagctc	39
SEQ ID NO: 106	moltype = DNA length = 32
FEATURE	Location/Qualifiers
source	1..32

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 106		
attccccgctc ttatgggetta tactctagtt gg		32
SEQ ID NO: 107	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 107		
catgtgggtct ggctgtccat gcttgca		27
SEQ ID NO: 108	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 108		
cacagttctc atactcagga accctcat		28
SEQ ID NO: 109	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 109		
catgtgggtgt tggcgctcag acagtgata		29
SEQ ID NO: 110	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 110		
tttgtcagtt ggccctgatt tcagatatcc tc		32
SEQ ID NO: 111	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 111		
catggcttgt aatcccagct actcaggagg c		31
SEQ ID NO: 112	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 112		
tttcaccagc acagtgtaga attgcag		27
SEQ ID NO: 113	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 113		
catgcttgta cctggtgttc ggttat		26
SEQ ID NO: 114	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 114		
catgccagcc caagatggat gaat		24
SEQ ID NO: 115	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 115		
catggcggtg gaagtcattc tgata		25

SEQ ID NO: 116	moltype = DNA length = 24
FEATURE	Location/Qualifiers
source	1..24
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 116	
catggagggc cacagattgg tatt	24
SEQ ID NO: 117	moltype = DNA length = 26
FEATURE	Location/Qualifiers
source	1..26
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 117	
catgactgaa aggtcagatt caggag	26
SEQ ID NO: 118	moltype = DNA length = 39
FEATURE	Location/Qualifiers
source	1..39
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 118	
catgactaca ttctctgcta tcttgattta caactcttg	39
SEQ ID NO: 119	moltype = DNA length = 28
FEATURE	Location/Qualifiers
source	1..28
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 119	
tccgaaggaa gtgaattcac ccaaggat	28
SEQ ID NO: 120	moltype = DNA length = 34
FEATURE	Location/Qualifiers
source	1..34
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 120	
catgtttggg atgaaactgt tccacctcag attt	34
SEQ ID NO: 121	moltype = DNA length = 29
FEATURE	Location/Qualifiers
source	1..29
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 121	
ttactgccag agtattctgg ttaagaaac	29
SEQ ID NO: 122	moltype = DNA length = 39
FEATURE	Location/Qualifiers
source	1..39
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 122	
catgcatagt atttcacatt tgtgtattac ttcgaattt	39
SEQ ID NO: 123	moltype = DNA length = 34
FEATURE	Location/Qualifiers
source	1..34
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 123	
aaacgtttgg ttcattacaa gaatagaggc cttc	34
SEQ ID NO: 124	moltype = DNA length = 34
FEATURE	Location/Qualifiers
source	1..34
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 124	
catgtccttg agtctatctt ggaggtgagc aaac	34
SEQ ID NO: 125	moltype = DNA length = 29
FEATURE	Location/Qualifiers
source	1..29

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 125		
tgcggtggtg gcagtaaatt atcaatagg		29
SEQ ID NO: 126	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 126		
catgccaaat ttaattcagt cttctctccc atagtgtct		39
SEQ ID NO: 127	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 127		
actctttatg aagagcaatt tggtagtacc tacca		35
SEQ ID NO: 128	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 128		
catggttcaa caccctttga tggctcccat g		31
SEQ ID NO: 129	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 129		
ggcctccttg aactatggtg ggct		24
SEQ ID NO: 130	moltype = DNA length = 33	
FEATURE	Location/Qualifiers	
source	1..33	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 130		
catgaaagca gtgtgctgag tgaagaagt cag		33
SEQ ID NO: 131	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 131		
tctcatgtg agtttatgtc ctacttgaa		29
SEQ ID NO: 132	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 132		
catgttgtgc tgcaataaac atagatgcgc g		31
SEQ ID NO: 133	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 133		
agtccaaagt ttaagatgcc agagatgca		29
SEQ ID NO: 134	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 134		
catgtttctc catagactcc tgttcttggt atacagatg		39

SEQ ID NO: 135	moltype = DNA length = 35
FEATURE	Location/Qualifiers
source	1..35
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 135	
ttgatataaa gcctactgtg atcttggcac catac	35
SEQ ID NO: 136	moltype = DNA length = 39
FEATURE	Location/Qualifiers
source	1..39
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 136	
catgttggtg atgattagca tcttaacat gttgagtct	39
SEQ ID NO: 137	moltype = DNA length = 25
FEATURE	Location/Qualifiers
source	1..25
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 137	
tcaggagttt gagatcagcc tggcc	25
SEQ ID NO: 138	moltype = DNA length = 31
FEATURE	Location/Qualifiers
source	1..31
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 138	
catgccaga tgtggatgtt catggtccag a	31
SEQ ID NO: 139	moltype = DNA length = 25
FEATURE	Location/Qualifiers
source	1..25
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 139	
gggtggatga gactttccga agaac	25
SEQ ID NO: 140	moltype = DNA length = 23
FEATURE	Location/Qualifiers
source	1..23
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 140	
catgccctgc gaaccgtcga ccg	23
SEQ ID NO: 141	moltype = DNA length = 29
FEATURE	Location/Qualifiers
source	1..29
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 141	
gtggattacc tgaggtcagt agttcaaga	29
SEQ ID NO: 142	moltype = DNA length = 23
FEATURE	Location/Qualifiers
source	1..23
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 142	
catggcaggc tgctggacc tgc	23
SEQ ID NO: 143	moltype = DNA length = 27
FEATURE	Location/Qualifiers
source	1..27
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 143	
cctggctagc tccgaaatat tccagga	27
SEQ ID NO: 144	moltype = DNA length = 28
FEATURE	Location/Qualifiers
source	1..28

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SEQUENCE: 144	mol_type = other DNA organism = synthetic construct	
catgggttcc ttcgctactc tggctcca		28
SEQ ID NO: 145	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
source	1..21	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 145		
ccaccacacc cagctaagtt t		21
SEQ ID NO: 146	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 146		
catggaatct caaacggtat ttaacatata agaagattc		39
SEQ ID NO: 147	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 147		
ctgcatagaa tacagcctta ctgaatgtta gtctc		35
SEQ ID NO: 148	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 148		
catgaaggct cctggagccc ttgagg		27
SEQ ID NO: 149	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 149		
tctgtctgcc tggagcactg atttctc		27
SEQ ID NO: 150	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 150		
catgtattgg atagtggacc caccactcag taaca		35
SEQ ID NO: 151	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 151		
cctgagctag atataaagac tctccacgt		29
SEQ ID NO: 152	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 152		
catgaccacc acgcctggct aattt		25
SEQ ID NO: 153	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 153		
tttaagccaa tagcaccatg tttcttt		27

SEQ ID NO: 154	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 154		
catgggggcat tgcagcaggt gcag		24
SEQ ID NO: 155	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 155		
ggcatttatt gcagggtgcc aagc		24
SEQ ID NO: 156	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 156		
catgccttaa accatcacgg tgctgctttg a		31
SEQ ID NO: 157	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 157		
agcctatgtg tgtctctgca cgtgat		26
SEQ ID NO: 158	moltype = DNA length = 38	
FEATURE	Location/Qualifiers	
source	1..38	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 158		
catgatctta caagaagaca tatgcccaca gaggacta		38
SEQ ID NO: 159	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 159		
ctgctgagaa attactgtcc ctgtgcaaa		29
SEQ ID NO: 160	moltype = DNA length = 30	
FEATURE	Location/Qualifiers	
source	1..30	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 160		
catgctgggc atcagagcaa gactccatct		30
SEQ ID NO: 161	moltype = DNA length = 18	
FEATURE	Location/Qualifiers	
source	1..18	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 161		
cccgtgccac actcgccg		18
SEQ ID NO: 162	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 162		
catgctgggc atgcgacatc tctcag		27
SEQ ID NO: 163	moltype = DNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 163		
atcgtcaaat gaactcgaaa tgaatcataa tcga		34
SEQ ID NO: 164	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 164		
catgttgccc tggcgcttag gctgg		25
SEQ ID NO: 165	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 165		
gcacaaccag agatacatca gccctaaa		28
SEQ ID NO: 166	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 166		
catggccac cttggcctcc caaag		25
SEQ ID NO: 167	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 167		
gaatgcttgt gtttaaatct tcagtgtcac tctag		35
SEQ ID NO: 168	moltype = DNA length = 30	
FEATURE	Location/Qualifiers	
source	1..30	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 168		
catggggaat agacatgctg tggtggcaga		30
SEQ ID NO: 169	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 169		
agctaataatc atgccactgc actccagc		28
SEQ ID NO: 170	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 170		
catgattaag gatgaggacc ctgaggttca gaaac		35
SEQ ID NO: 171	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 171		
aggcttcacc agacacaaa tctgc		25
SEQ ID NO: 172	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 172		
catgagatct gctgttagtc tgatgggctt cc		32

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SEQ ID NO: 173	moltype = DNA length = 19	
FEATURE	Location/Qualifiers	
source	1..19	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 173		
cctatgcggc cgagcctcc		19
SEQ ID NO: 174	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 174		
catgtttcag ccaagcagtt tgaaggatt ct		32
SEQ ID NO: 175	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 175		
ggtctcaaac tcctgggttc aagtgaac		28
SEQ ID NO: 176	moltype = DNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 176		
catgattatg ataggtatca acacccttgc attt		34
SEQ ID NO: 177	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 177		
acgaatttgt ggccaagtcc tcaaa		25
SEQ ID NO: 178	moltype = DNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 178		
catgggaatc tttgttaatt gtttcacgtg gaaa		34
SEQ ID NO: 179	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 179		
ggctgtggag atgcatcagt gaatcag		27
SEQ ID NO: 180	moltype = DNA length = 38	
FEATURE	Location/Qualifiers	
source	1..38	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 180		
catgtccatt gccattacta ttccagagtt acaatgtt		38
SEQ ID NO: 181	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 181		
ttctcatgac agtgctgac tgtggattt		29
SEQ ID NO: 182	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 182		
catgcgagcg gcccaactcc acag		24
SEQ ID NO: 183	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 183		
tctcagctac tcgggaggct gagat		25
SEQ ID NO: 184	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 184		
catgaaacga gttaatactt gcaccgtctc agaca		35
SEQ ID NO: 185	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 185		
tcatggcatg gatgtaccaa agatatt		26
SEQ ID NO: 186	moltype = DNA length = 38	
FEATURE	Location/Qualifiers	
source	1..38	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 186		
catgaaacac aaccactgag agtgctatta tggctactc		38
SEQ ID NO: 187	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 187		
tcctgagcca ggtttacatg gttaccatt		29
SEQ ID NO: 188	moltype = DNA length = 33	
FEATURE	Location/Qualifiers	
source	1..33	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 188		
catgggacat tcatgtttct ccaaagccct ctg		33
SEQ ID NO: 189	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 189		
gtcaccatgg ccactctgga gc		22
SEQ ID NO: 190	moltype = DNA length = 38	
FEATURE	Location/Qualifiers	
source	1..38	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 190		
catggaagtt gccaaacagt tcttcagaat agttacac		38
SEQ ID NO: 191	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 191		
atctatccca aagggtgct gtgagg		26

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SEQ ID NO: 192 moltype = DNA length = 37
 FEATURE Location/Qualifiers
 source 1..37
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 192
 catgttgaat gaatggtacg tgcgaagtat atgctga 37

SEQ ID NO: 193 moltype = DNA length = 23
 FEATURE Location/Qualifiers
 source 1..23
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 193
 gtctgggagg cagaggttgc agt 23

SEQ ID NO: 194 moltype = DNA length = 39
 FEATURE Location/Qualifiers
 source 1..39
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 194
 catgccacaa acctctttgt tataatttct ccagttgag 39

SEQ ID NO: 195 moltype = DNA length = 20
 FEATURE Location/Qualifiers
 source 1..20
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 195
 ctgcctgctg gcagggttc 20

SEQ ID NO: 196 moltype = DNA length = 39
 FEATURE Location/Qualifiers
 source 1..39
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 196
 catggggata gacagacctg ttgaatcata aatagaaca 39

SEQ ID NO: 197 moltype = DNA length = 32
 FEATURE Location/Qualifiers
 source 1..32
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 197
 cagattcgct aaatgattga ccttgtacat tt 32

SEQ ID NO: 198 moltype = DNA length = 30
 FEATURE Location/Qualifiers
 source 1..30
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 198
 catgaccttc acaaagcatg cactgactgt 30

SEQ ID NO: 199 moltype = DNA length = 26
 FEATURE Location/Qualifiers
 source 1..26
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 199
 tgagctgtgg ccacttactc aggaaa 26

SEQ ID NO: 200 moltype = DNA length = 25
 FEATURE Location/Qualifiers
 source 1..25
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 200
 catgatccca gcactctgga gggcc 25

SEQ ID NO: 201 moltype = DNA length = 22
 FEATURE Location/Qualifiers
 source 1..22

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 201		
tggtccctct ggccaacttg gc		22
SEQ ID NO: 202	moltype = RNA length = 36	
FEATURE	Location/Qualifiers	
source	1..36	
	mol_type = other RNA organism = synthetic construct	
SEQUENCE: 202		
catgtttgcc taccttcctg tacacataaa ccaagg		36
SEQ ID NO: 203	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 203		
ccaacagatg cctcccactc caagt		25
SEQ ID NO: 204	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 204		
catgttacac attattcagc aatggactag aattggtgc		39
SEQ ID NO: 205	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 205		
caccacacctt ggccctccaa ag		22
SEQ ID NO: 206	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 206		
catgcatggc agcatggcag ctttatatcc tg		32
SEQ ID NO: 207	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
source	1..21	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 207		
ctcctgcctc agcctccga g		21
SEQ ID NO: 208	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 208		
catggggctt ggccctaagt gccgt		25
SEQ ID NO: 209	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 209		
gacagagttt cactcttggt gccag		27
SEQ ID NO: 210	moltype = RNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other RNA organism = synthetic construct	
SEQUENCE: 210		
catgggggtcc aggaaagtgc ggcag		25

SEQ ID NO: 211	motype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 211		
gagttcaaga ccagcctcgc caatg		25
SEQ ID NO: 212	motype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 212		
catgttcaca gctaatactct cctgggcaca c		31
SEQ ID NO: 213	motype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 213		
gatggcttgg aaatccataa gtcctattt		29
SEQ ID NO: 214	motype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 214		
catgtttaac ctgctcagtc tagttagaac atctctcgt		39
SEQ ID NO: 215	motype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 215		
tgatccacc tggtctgatg ggtg		24
SEQ ID NO: 216	motype = DNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 216		
catgcacaga gcatgagcat tgaagcagaa tgaa		34
SEQ ID NO: 217	motype = DNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 217		
ggtgctcagt attctaattc ttgtattcct tgtc		34
SEQ ID NO: 218	motype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 218		
catgcacaca caccagcatg cacactca		28
SEQ ID NO: 219	motype = RNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 219		
ccagcatgat gttggtccaa gttggc		26
SEQ ID NO: 220	motype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 220		
catggggcca aagcggactg aggc		24
SEQ ID NO: 221	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 221		
gccgttggtc ttatcatctg tcgataccaa a		31
SEQ ID NO: 222	moltype = RNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other RNA organism = synthetic construct	
SEQUENCE: 222		
catgaaagac ccagaatagc caaagctatc ctgag		35
SEQ ID NO: 223	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 223		
tccgtgtgcc caagtcagtt acca		24
SEQ ID NO: 224	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 224		
catgtggtcc tttcttcgag taggaggatg tc		32
SEQ ID NO: 225	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 225		
taattggtca gtatccgat gggtcttt		28
SEQ ID NO: 226	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 226		
catgaaactg cctgattcca cagctgaggt a		31
SEQ ID NO: 227	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 227		
gagccttcta ccttcagact cagactgaa		29
SEQ ID NO: 228	moltype = RNA length = 30	
FEATURE	Location/Qualifiers	
source	1..30	
	mol_type = other RNA organism = synthetic construct	
SEQUENCE: 228		
catggggatg cttggtgcag gcttctat		30
SEQ ID NO: 229	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 229		
tgttggctcc tatgtccatt tgacattt		28

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SEQ ID NO: 230 moltype = DNA length = 33
 FEATURE Location/Qualifiers
 source 1..33
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 230
 catgggaaat ccctcagtc ggaagtctag aac 33

SEQ ID NO: 231 moltype = DNA length = 35
 FEATURE Location/Qualifiers
 source 1..35
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 231
 tgctgtgta tatacagcat gtatgatgta cattt 35

SEQ ID NO: 232 moltype = DNA length = 39
 FEATURE Location/Qualifiers
 source 1..39
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 232
 catggcacat gcaaataatg caatcatata tggcttaat 39

SEQ ID NO: 233 moltype = DNA length = 34
 FEATURE Location/Qualifiers
 source 1..34
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 233
 gtatcgaagt atataaactg atggttcaca gaga 34

SEQ ID NO: 234 moltype = DNA length = 39
 FEATURE Location/Qualifiers
 source 1..39
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 234
 catgtacat aacttaatgc catatttgcc atagtggc 39

SEQ ID NO: 235 moltype = DNA length = 26
 FEATURE Location/Qualifiers
 source 1..26
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 235
 cacgcaaccg taggtgtgta ttccag 26

SEQ ID NO: 236 moltype = DNA length = 36
 FEATURE Location/Qualifiers
 source 1..36
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 236
 catgaaatgt aaaccttgtc taaatctggg atcttc 36

SEQ ID NO: 237 moltype = DNA length = 34
 FEATURE Location/Qualifiers
 source 1..34
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 237
 tttgtctctg cttacatttg gctctctgta attt 34

SEQ ID NO: 238 moltype = DNA length = 39
 FEATURE Location/Qualifiers
 source 1..39
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 238
 catgaaagct cacaattaca agtgctaagt cttcagaaa 39

SEQ ID NO: 239 moltype = DNA length = 32
 FEATURE Location/Qualifiers
 source 1..32

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 239		
cctgtatttc tgtgtcttca catggcattc tc		32
SEQ ID NO: 240	moltype = DNA length = 37	
FEATURE	Location/Qualifiers	
source	1..37	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 240		
catgctaaat cctttcccg tagggactgt tctgac		37
SEQ ID NO: 241	moltype = DNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 241		
gctgcataaa tgtcttcttt agagaagtgt cttt		34
SEQ ID NO: 242	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 242		
catgaatggt ggaggtagca gcattgcaat c		31
SEQ ID NO: 243	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 243		
cttgaactcc tgggctcaag cgatc		25
SEQ ID NO: 244	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 244		
catgttactc attcttaagc actaggtgtg attctaaat		39
SEQ ID NO: 245	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 245		
catcatccca ccaaggttagc tccaa		25
SEQ ID NO: 246	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 246		
catgttaagg catagcttag cagtccacca aagat		35
SEQ ID NO: 247	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 247		
tcccaggtaa tgctgatgtt gccagt		26
SEQ ID NO: 248	moltype = RNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other RNA organism = synthetic construct	
SEQUENCE: 248		
catgaatgct taagatatgt acccagcata ccttaaatg		39

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SEQ ID NO: 249      moltype = DNA  length = 35
FEATURE            Location/Qualifiers
source             1..35
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 249
caagctcaag atttctgtta gttaccagtt tcttt                35

SEQ ID NO: 250      moltype = DNA  length = 35
FEATURE            Location/Qualifiers
source             1..35
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 250
catgaaagtc acactgttgc taacaagctg ataaa                35

SEQ ID NO: 251      moltype = RNA  length = 25
FEATURE            Location/Qualifiers
source             1..25
                   mol_type = other RNA
                   organism = synthetic construct

SEQUENCE: 251
gggctctggt gtgacgaagt cattg                            25

SEQ ID NO: 252      moltype = DNA  length = 23
FEATURE            Location/Qualifiers
source             1..23
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 252
catgctgcac tccagcctgg gcg                              23

SEQ ID NO: 253      moltype = DNA  length = 29
FEATURE            Location/Qualifiers
source             1..29
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 253
taggagtgct tctctgatga tgttccacc                        29

SEQ ID NO: 254      moltype = DNA  length = 39
FEATURE            Location/Qualifiers
source             1..39
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 254
catgcatatt atatctttgc ttgcctagtt tctcatggt            39

SEQ ID NO: 255      moltype = DNA  length = 28
FEATURE            Location/Qualifiers
source             1..28
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 255
ttatggttat tacttgacag agggcagt                         28

SEQ ID NO: 256      moltype = RNA  length = 32
FEATURE            Location/Qualifiers
source             1..32
                   mol_type = other RNA
                   organism = synthetic construct

SEQUENCE: 256
catgatggta gcatgacttc ctggcctcta gt                   32

SEQ ID NO: 257      moltype = DNA  length = 29
FEATURE            Location/Qualifiers
source             1..29
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 257
ttgtgtcttt atggtttcat tctgaacac                       29

SEQ ID NO: 258      moltype = DNA  length = 30
FEATURE            Location/Qualifiers
source             1..30

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 258		
catgttggca atggcatttg gtttctctcca		30
SEQ ID NO: 259	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 259		
atgagataga tgacagaact gacacctag		29
SEQ ID NO: 260	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 260		
catgtagtct cagctacttg ggaagctgag g		31
SEQ ID NO: 261	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 261		
tcctggcatt tgggaagctt gcac		24
SEQ ID NO: 262	moltype = DNA length = 36	
FEATURE	Location/Qualifiers	
source	1..36	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 262		
catgtaagtg gagataagct tgtatgtctt atatgg		36
SEQ ID NO: 263	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 263		
ggaggagggc atttgaggag tctctatg		28
SEQ ID NO: 264	moltype = DNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 264		
catgtttatt ggagggccag gtaatagctt tgca		34
SEQ ID NO: 265	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 265		
agtgtgatag tgtgcgctg tcaact		26
SEQ ID NO: 266	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 266		
catgtgaaag tccacctgtg agttgcagaa ct		32
SEQ ID NO: 267	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 267		
acctagcctt tgctctagca ccgg		24

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SEQ ID NO: 268	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 268		
catgggggtgt ggtggctcat ggctg		25
SEQ ID NO: 269	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 269		
catgcagaag agtgtgttgc cttccactgt tc		32
SEQ ID NO: 270	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 270		
catgcaaaact tgcttagttg tttacctgtg atattggct		39
SEQ ID NO: 271	moltype = DNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 271		
catgaccatt taatccaagc taccgctat gtcg		34
SEQ ID NO: 272	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 272		
catgggctgaa ctggcctaac ctgaatgtat gtaca		35
SEQ ID NO: 273	moltype = DNA length = 38	
FEATURE	Location/Qualifiers	
source	1..38	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 273		
catgggtattt gtaggtcat acacgaggaa ctgctgta		38
SEQ ID NO: 274	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 274		
ggttcaactg aagtgccagc ctgc		24
SEQ ID NO: 275	moltype = RNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other RNA	
	organism = synthetic construct	
SEQUENCE: 275		
catgaaactc ctgacctcaa gtgatccacc tg		32
SEQ ID NO: 276	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 276		
cctcaaagtg tctgcagagc aggaatc		27
SEQ ID NO: 277	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 277		
catgttatgg ctcaggataa attcctacat gtagaattc		39
SEQ ID NO: 278	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 278		
gaaggatcag agtaccagca tccgtcttc		29
SEQ ID NO: 279	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 279		
catggggttt caccatgttg gccaggatg		29
SEQ ID NO: 280	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 280		
cagtttatat tccagatagg caggagggt		29
SEQ ID NO: 281	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 281		
catgaatacc agtaagagct tgaactttgt aagttaaac		39
SEQ ID NO: 282	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 282		
ctgtgcccatttcacgcctt gg		22
SEQ ID NO: 283	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 283		
catgtgtgca gcagacttct gcctgga		27
SEQ ID NO: 284	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 284		
tttgtgaaag gcaaatgatg catgacag		28
SEQ ID NO: 285	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 285		
catgtacagt attaggcacc tgactgggta aa		32
SEQ ID NO: 286	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 286		
gaaaggttaa gcaacttgcc catgggtcaa		29

SEQ ID NO: 287	moltype = DNA length = 28
FEATURE	Location/Qualifiers
source	1..28
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 287	
catggtgcca catgcctgta atcccagc	28
SEQ ID NO: 288	moltype = DNA length = 21
FEATURE	Location/Qualifiers
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 288	
aggcccagcc atctcactgc a	21
SEQ ID NO: 289	moltype = DNA length = 34
FEATURE	Location/Qualifiers
source	1..34
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 289	
catggataat ctgggtacca gccttaagga aggc	34
SEQ ID NO: 290	moltype = DNA length = 29
FEATURE	Location/Qualifiers
source	1..29
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 290	
gggcccatag gatttctgga ctgaaatca	29
SEQ ID NO: 291	moltype = DNA length = 32
FEATURE	Location/Qualifiers
source	1..32
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 291	
catgttgagc taagccagtc catcaagact gg	32
SEQ ID NO: 292	moltype = DNA length = 23
FEATURE	Location/Qualifiers
source	1..23
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 292	
gagcgattct cctgcctagg cct	23
SEQ ID NO: 293	moltype = DNA length = 25
FEATURE	Location/Qualifiers
source	1..25
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 293	
catgtgcctc ggccctccaa gtagc	25
SEQ ID NO: 294	moltype = DNA length = 29
FEATURE	Location/Qualifiers
source	1..29
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 294	
acagtaacca gatctcagcc aatcagagg	29
SEQ ID NO: 295	moltype = DNA length = 30
FEATURE	Location/Qualifiers
source	1..30
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 295	
catgaaatta gctggtggca ggcacctgta	30
SEQ ID NO: 296	moltype = DNA length = 26
FEATURE	Location/Qualifiers
source	1..26

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 296		
ggttacagtg agccatgatt gtgccg		26
SEQ ID NO: 297	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 297		
catgatttcg agaaataact tccgatttat ttcagatag		39
SEQ ID NO: 298	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 298		
tagggcattt cacatgggct cagaaaca		28
SEQ ID NO: 299	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 299		
catgaagcca aggctgagcc aagtcag		27
SEQ ID NO: 300	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 300		
aaacttccag actgattcca aagtccaag		29
SEQ ID NO: 301	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 301		
catgtcattg attccagtgc ggctctaaa		29
SEQ ID NO: 302	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 302		
ggtgacagag ggagactctg tcacaaa		27
SEQ ID NO: 303	moltype = DNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 303		
catgcgccg gacagtggag acg		23
SEQ ID NO: 304	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 304		
tcttctgtg ttacctaggc tggctca		28
SEQ ID NO: 305	moltype = DNA length = 33	
FEATURE	Location/Qualifiers	
source	1..33	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 305		
catgtgtccc actggagaac cctgactaat aca		33

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SEQ ID NO: 306      moltype = DNA  length = 27
FEATURE            Location/Qualifiers
source              1..27
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 306
gctaggatta caggcgtgag ccactat                               27

SEQ ID NO: 307      moltype = DNA  length = 38
FEATURE            Location/Qualifiers
source              1..38
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 307
catgcttcta cttgttgagc ttctgatagg gtccaaag                   38

SEQ ID NO: 308      moltype = DNA  length = 29
FEATURE            Location/Qualifiers
source              1..29
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 308
agtcacggag gtagagcctt cttgaaagg                               29

SEQ ID NO: 309      moltype = DNA  length = 29
FEATURE            Location/Qualifiers
source              1..29
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 309
catgcctcac aggtaggcgt gaggatcag                               29

SEQ ID NO: 310      moltype = DNA  length = 22
FEATURE            Location/Qualifiers
source              1..22
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 310
gccctgaggc tcacgtcact ca                                     22

SEQ ID NO: 311      moltype = DNA  length = 34
FEATURE            Location/Qualifiers
source              1..34
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 311
catgctcaac atgaagacaa cagggatgag gagc                        34

SEQ ID NO: 312      moltype = DNA  length = 35
FEATURE            Location/Qualifiers
source              1..35
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 312
atgaagctag gattattaac ctaagggtca cttgt                       35

SEQ ID NO: 313      moltype = DNA  length = 25
FEATURE            Location/Qualifiers
source              1..25
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 313
catggtcgct caggctggtg tgcag                                   25

SEQ ID NO: 314      moltype = DNA  length = 28
FEATURE            Location/Qualifiers
source              1..28
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 314
aacacagtc cctgtcctta cagagctc                               28

SEQ ID NO: 315      moltype = DNA  length = 35
FEATURE            Location/Qualifiers
source              1..35

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 315		
catgggctta catctgtaat cccagcactt tgaga		35
SEQ ID NO: 316	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 316		
actgctcag ttaaccagca gacttca		27
SEQ ID NO: 317	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 317		
catgctccc accttggcct cccaa		25
SEQ ID NO: 318	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 318		
tctgggctc aagcaatcct cctg		24
SEQ ID NO: 319	moltype = DNA length = 33	
FEATURE	Location/Qualifiers	
source	1..33	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 319		
catgatggat cctggtaccc agaggaata caa		33
SEQ ID NO: 320	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 320		
ggagcttgta cagcagctaa ggtgag		26
SEQ ID NO: 321	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 321		
catggactca aactcctggg ctcaagtgat cc		32
SEQ ID NO: 322	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 322		
tccctgagat caagtgattg tcccatctt		29
SEQ ID NO: 323	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 323		
catgcccatg gactcgtaat tggtttctg ga		32
SEQ ID NO: 324	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 324		
aatactctgg atgatcttca ggacatggt		29

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SEQ ID NO: 325	moltype = DNA length = 31
FEATURE	Location/Qualifiers
source	1..31
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 325	
catggtgata gcatgcctct gtagtcccag c	31
SEQ ID NO: 326	moltype = DNA length = 21
FEATURE	Location/Qualifiers
source	1..21
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 326	
ggagggtggag gcgggaggat t	21
SEQ ID NO: 327	moltype = RNA length = 29
FEATURE	Location/Qualifiers
source	1..29
	mol_type = other RNA
	organism = synthetic construct
SEQUENCE: 327	
catgaatgag tgagtgcaga ggctgctgg	29
SEQ ID NO: 328	moltype = DNA length = 27
FEATURE	Location/Qualifiers
source	1..27
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 328	
aacccttcat gaacgtgagg aagctga	27
SEQ ID NO: 329	moltype = DNA length = 37
FEATURE	Location/Qualifiers
source	1..37
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 329	
catgtcttag ccattcagat caatcccaga cagacta	37
SEQ ID NO: 330	moltype = DNA length = 29
FEATURE	Location/Qualifiers
source	1..29
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 330	
aatactgtag ccttcctagg gctctcaca	29
SEQ ID NO: 331	moltype = RNA length = 38
FEATURE	Location/Qualifiers
source	1..38
	mol_type = other RNA
	organism = synthetic construct
SEQUENCE: 331	
catgtacacc ttaacctagc aatgctttct cttctgag	38
SEQ ID NO: 332	moltype = DNA length = 23
FEATURE	Location/Qualifiers
source	1..23
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 332	
ctgccacagc ctcccatgta gct	23
SEQ ID NO: 333	moltype = DNA length = 27
FEATURE	Location/Qualifiers
source	1..27
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 333	
catgtctgcc tcagcctccc atgtagc	27
SEQ ID NO: 334	moltype = DNA length = 30
FEATURE	Location/Qualifiers
source	1..30

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 334		
ctaaggagag actgctttct gatgcctacc		30
SEQ ID NO: 335	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 335		
catgcatgca ttgcaacgca gtgggtgc		27
SEQ ID NO: 336	moltype = DNA length = 30	
FEATURE	Location/Qualifiers	
source	1..30	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 336		
cagtgtatc cagccagat actatgcttt		30
SEQ ID NO: 337	moltype = DNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 337		
catgctgcga acacttaatg cagagcttga tacc		34
SEQ ID NO: 338	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 338		
aggatgggtat cgatctcttc acctcgtga		29
SEQ ID NO: 339	moltype = DNA length = 36	
FEATURE	Location/Qualifiers	
source	1..36	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 339		
catgcttcca gctagtttct agaggtcttg tctgga		36
SEQ ID NO: 340	moltype = DNA length = 33	
FEATURE	Location/Qualifiers	
source	1..33	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 340		
aagttgcaaa ctgcattgag atagacaatt aaa		33
SEQ ID NO: 341	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 341		
catgctaggt gacagcattg agcagggt		29
SEQ ID NO: 342	moltype = DNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 342		
tggttaacgc ctgtgatccc agc		23
SEQ ID NO: 343	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 343		
catggttcaa gagcgatggc tctcgaataa a		31

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SEQ ID NO: 344	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
source	1..21	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 344		
ctcgctgcaa cttccaccgc c		21
SEQ ID NO: 345	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 345		
catggggcat caccacaggc tgagga		26
SEQ ID NO: 346	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 346		
tttctgtta tttctataag atgcttctc tgatt		35
SEQ ID NO: 347	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 347		
catggagggt gcattgagcc aagatcatgg c		31
SEQ ID NO: 348	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 348		
gagaatgcag cccagtaggt ctcagc		26
SEQ ID NO: 349	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 349		
cgtatgaggc tcgacaggta ccatatagcc t		31
SEQ ID NO: 350	moltype = DNA length = 38	
FEATURE	Location/Qualifiers	
source	1..38	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 350		
cgtagactcc aaccattggt ataactgaa agttgtct		38
SEQ ID NO: 351	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 351		
cgtactgctt gacaacggac tgaaa		25
SEQ ID NO: 352	moltype = DNA length = 36	
FEATURE	Location/Qualifiers	
source	1..36	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 352		
cgtatcggct atttctaaca gctcacatgt ttacat		36
SEQ ID NO: 353	moltype = DNA length = 33	
FEATURE	Location/Qualifiers	
source	1..33	

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 353		
cgtattccat aagtgccagc tggctgagaa ata		33
SEQ ID NO: 354	moltype = DNA length = 33	
FEATURE	Location/Qualifiers	
source	1..33	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 354		
cgtatctgct cccaggttca agtgattctc aag		33
SEQ ID NO: 355	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 355		
cgtatccgag agctcacagc ttggct		26
SEQ ID NO: 356	moltype = DNA length = 30	
FEATURE	Location/Qualifiers	
source	1..30	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 356		
cgtagtgtga tggaattcac cagtgtgttt		30
SEQ ID NO: 357	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 357		
cgtaatttag agagcctgtc acaaagtcc atatgagaa		39
SEQ ID NO: 358	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 358		
cgtagagagg agagagtgc ggggtcaa		27
SEQ ID NO: 359	moltype = DNA length = 38	
FEATURE	Location/Qualifiers	
source	1..38	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 359		
cgtaacatta ttgttaacaa ggggtgcttc tgggaaga		38
SEQ ID NO: 360	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 360		
cgtaccctgg cacctagtgg gtccatac		28
SEQ ID NO: 361	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 361		
cgtagcactc cagagactct gtttctaaa		29
SEQ ID NO: 362	moltype = DNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 362		
cgtacaggca tggtagcgcg cct		23

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SEQ ID NO: 363 moltype = DNA length = 32
 FEATURE Location/Qualifiers
 source 1..32
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 363
 cgtaggaagc ctcataatca tggtaggaagg ca 32

SEQ ID NO: 364 moltype = DNA length = 28
 FEATURE Location/Qualifiers
 source 1..28
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 364
 cgtacatggt taccgatgaa gctgcaaa 28

SEQ ID NO: 365 moltype = DNA length = 37
 FEATURE Location/Qualifiers
 source 1..37
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 365
 cgtaaggaag ctcagctata cctgttactg ataattt 37

SEQ ID NO: 366 moltype = DNA length = 27
 FEATURE Location/Qualifiers
 source 1..27
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 366
 cgtacccatg caggcctagg ctagtgt 27

SEQ ID NO: 367 moltype = DNA length = 31
 FEATURE Location/Qualifiers
 source 1..31
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 367
 cgtaacctaa aggacacatc tcagtacatt t 31

SEQ ID NO: 368 moltype = DNA length = 31
 FEATURE Location/Qualifiers
 source 1..31
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 368
 cgtaactgaa ggctctatgt gcaggaaactc c 31

SEQ ID NO: 369 moltype = DNA length = 31
 FEATURE Location/Qualifiers
 source 1..31
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 369
 cgtacctccc aaagtgtctgg gattataggc a 31

SEQ ID NO: 370 moltype = DNA length = 27
 FEATURE Location/Qualifiers
 source 1..27
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 370
 cgtaaaactgt tcttccaggc ctgattt 27

SEQ ID NO: 371 moltype = DNA length = 28
 FEATURE Location/Qualifiers
 source 1..28
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 371
 cgtacccatc ctggcacgta ctgctact 28

SEQ ID NO: 372 moltype = DNA length = 35
 FEATURE Location/Qualifiers
 source 1..35

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 372		
cgtaaggcac actcaggctt tacgattctt gttta		35
SEQ ID NO: 373	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 373		
cgtaattctc cctgcaaatt gtttgactct agaaatagc		39
SEQ ID NO: 374	moltype = DNA length = 30	
FEATURE	Location/Qualifiers	
source	1..30	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 374		
cgtagggtag tagcgatctg ggttaccag		30
SEQ ID NO: 375	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 375		
cgtacattga cccaccggtc attcaggag		29
SEQ ID NO: 376	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 376		
cgtactgagg gttatccaag tgacccattg ca		32
SEQ ID NO: 377	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 377		
cgtacttgta cctgggtgtc ggttat		26
SEQ ID NO: 378	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 378		
cgtaccagcc caagatggat gaat		24
SEQ ID NO: 379	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 379		
cgtagcggtg gaagtcattc tgata		25
SEQ ID NO: 380	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 380		
cgtagagggc cacagattgg tatt		24
SEQ ID NO: 381	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 381		
cgtaactgaa aggtcagatt caggag		26

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SEQ ID NO: 382      moltype = DNA  length = 31
FEATURE            Location/Qualifiers
source             1..31
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 382
gtactgaggc tcgacaggta ccatatagcc t                               31

SEQ ID NO: 383      moltype = DNA  length = 38
FEATURE            Location/Qualifiers
source             1..38
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 383
gtacgactcc aaccattggt ataatctgaa agttgtct                               38

SEQ ID NO: 384      moltype = DNA  length = 25
FEATURE            Location/Qualifiers
source             1..25
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 384
gtacctgctt gacaacggac tgaaa                                         25

SEQ ID NO: 385      moltype = DNA  length = 36
FEATURE            Location/Qualifiers
source             1..36
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 385
gtactcggct atttctaaca gctcacatgt ttacat                             36

SEQ ID NO: 386      moltype = DNA  length = 33
FEATURE            Location/Qualifiers
source             1..33
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 386
gtacttccat aagtgccagc ttgctgagaa ata                               33

SEQ ID NO: 387      moltype = DNA  length = 33
FEATURE            Location/Qualifiers
source             1..33
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 387
gtactctgct cccagggtca agtgattctc aag                               33

SEQ ID NO: 388      moltype = DNA  length = 26
FEATURE            Location/Qualifiers
source             1..26
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 388
gtactccgag agctcacagc ttggct                                         26

SEQ ID NO: 389      moltype = DNA  length = 30
FEATURE            Location/Qualifiers
source             1..30
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 389
gtacgtttga tggaattcac cagtgtgttt                                   30

SEQ ID NO: 390      moltype = DNA  length = 39
FEATURE            Location/Qualifiers
source             1..39
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 390
gtacatttag agagcctgtc acaaatgtcc atatgagaa                         39

SEQ ID NO: 391      moltype = DNA  length = 27
FEATURE            Location/Qualifiers
source             1..27

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 391		
gtacgagagg agagagtgca ggggtcaa		27
SEQ ID NO: 392	moltype = DNA length = 38	
FEATURE	Location/Qualifiers	
source	1..38	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 392		
gtacacatta ttgttaacaa ggggtgcttc tgggaaga		38
SEQ ID NO: 393	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 393		
gtaccctgg cacctagtg gtccatac		28
SEQ ID NO: 394	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 394		
gtacgcactc cagagactct gtttctaaa		29
SEQ ID NO: 395	moltype = DNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 395		
gtaccaggca tggtagcgcg cct		23
SEQ ID NO: 396	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 396		
gtacggaagc ctacataatca tgggtgaagg ca		32
SEQ ID NO: 397	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 397		
gtaccatggt taccgatgaa gctgcaaa		28
SEQ ID NO: 398	moltype = DNA length = 37	
FEATURE	Location/Qualifiers	
source	1..37	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 398		
gtacaggaag ctacagctata cctgttactg ataattt		37
SEQ ID NO: 399	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 399		
gtaccccatg caggcctagg ctagtgt		27
SEQ ID NO: 400	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 400		
gtacacctaa aggacacatc tcagtacatt t		31

SEQ ID NO: 401	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 401		
gtacactgaa ggctctatgt gcaggaactc c		31
SEQ ID NO: 402	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 402		
gtaccctccc aaagtgtctgg gattataggc a		31
SEQ ID NO: 403	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 403		
gtacaactgt tcttcaggc ctgattt		27
SEQ ID NO: 404	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 404		
gtaccctcac ctggcacgta ctgctact		28
SEQ ID NO: 405	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 405		
gtacaggcac actcaggctt tacgattctt gttta		35
SEQ ID NO: 406	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 406		
gtacattctc cctgc aaatt gtttgactct agaaatagc		39
SEQ ID NO: 407	moltype = DNA length = 30	
FEATURE	Location/Qualifiers	
source	1..30	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 407		
gtacgggtag tagcgatctg ggttaccag		30
SEQ ID NO: 408	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 408		
gtaccattga cccaccggtc attcaggag		29
SEQ ID NO: 409	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 409		
gtacctgagg gttatccaag tgaccattg ca		32
SEQ ID NO: 410	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 410		
gtaccttgta cctgggtgttc ggttat		26
SEQ ID NO: 411	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 411		
gtaccagcc caagatggat gaat		24
SEQ ID NO: 412	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 412		
gtacgcggtg gaagtcattc tgata		25
SEQ ID NO: 413	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 413		
gtacgagggc cacagattgg tatt		24
SEQ ID NO: 414	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 414		
gtacactgaa aggtcagatt caggag		26
SEQ ID NO: 415	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 415		
acgttgaggc tcgacaggta ccatatagcc t		31
SEQ ID NO: 416	moltype = DNA length = 38	
FEATURE	Location/Qualifiers	
source	1..38	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 416		
acgtgactcc aaccattggt ataactgaa agttgtct		38
SEQ ID NO: 417	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 417		
acgtctgect gacaacggac tgaaa		25
SEQ ID NO: 418	moltype = DNA length = 36	
FEATURE	Location/Qualifiers	
source	1..36	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 418		
acgttcggct atttctaaca gctcacatgt ttacat		36
SEQ ID NO: 419	moltype = DNA length = 33	
FEATURE	Location/Qualifiers	
source	1..33	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 419		
acgtttccat aagtgcagc tggctgagaa ata		33

SEQ ID NO: 420	moltype = DNA length = 33
FEATURE	Location/Qualifiers
source	1..33
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 420	
acgttctgct cccaggttca agtgattctc aag	33
SEQ ID NO: 421	moltype = RNA length = 26
FEATURE	Location/Qualifiers
source	1..26
	mol_type = other RNA
	organism = synthetic construct
SEQUENCE: 421	
acgttccgag agctcacagc ttggct	26
SEQ ID NO: 422	moltype = DNA length = 30
FEATURE	Location/Qualifiers
source	1..30
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 422	
acgtgtttga tggaattcac cagtgtgttt	30
SEQ ID NO: 423	moltype = DNA length = 39
FEATURE	Location/Qualifiers
source	1..39
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 423	
acgtatttag agagcctgtc acaaatgtcc atatgagaa	39
SEQ ID NO: 424	moltype = DNA length = 27
FEATURE	Location/Qualifiers
source	1..27
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 424	
acgtgagagg agagagtgca ggggtcaa	27
SEQ ID NO: 425	moltype = DNA length = 38
FEATURE	Location/Qualifiers
source	1..38
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 425	
acgtacatta ttgttaacaa ggggtgtctc tggaaga	38
SEQ ID NO: 426	moltype = DNA length = 28
FEATURE	Location/Qualifiers
source	1..28
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 426	
acgtccctgg cacctagtgg gtccatac	28
SEQ ID NO: 427	moltype = DNA length = 29
FEATURE	Location/Qualifiers
source	1..29
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 427	
acgtgcactc cagagactct gtttctaaa	29
SEQ ID NO: 428	moltype = DNA length = 23
FEATURE	Location/Qualifiers
source	1..23
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 428	
acgtcaggca tggtagcgcg cct	23
SEQ ID NO: 429	moltype = DNA length = 32
FEATURE	Location/Qualifiers
source	1..32

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 429		
acgtggaagc ctcataatca tgggtggaagg ca		32
SEQ ID NO: 430	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 430		
acgtcatgtt taccgatgaa gctgcaaa		28
SEQ ID NO: 431	moltype = DNA length = 37	
FEATURE	Location/Qualifiers	
source	1..37	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 431		
acgtaggaag ctcagctata cctgttactg ataattt		37
SEQ ID NO: 432	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 432		
acgtcccatg caggcctagg ctagtgt		27
SEQ ID NO: 433	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 433		
acgtacctaa aggacacatc tcagtacatt t		31
SEQ ID NO: 434	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 434		
acgtactgaa ggctctatgt gcaggaaetc c		31
SEQ ID NO: 435	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 435		
acgtcctccc aaagtgctgg gattataggc a		31
SEQ ID NO: 436	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 436		
acgtaactgt tcttccaggc ctgattt		27
SEQ ID NO: 437	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 437		
acgtcccatc ctggcacgta ctgctact		28
SEQ ID NO: 438	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 438		
acgtaggcac actcaggctt tacgattctt gtta		35

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SEQ ID NO: 439      moltype = DNA  length = 39
FEATURE            Location/Qualifiers
source              1..39
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 439
acgtattctc cctgcaaatt gtttgactct agaaatagc          39

SEQ ID NO: 440      moltype = DNA  length = 30
FEATURE            Location/Qualifiers
source              1..30
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 440
acgtgggtag tagcgatctg ggttaccag          30

SEQ ID NO: 441      moltype = DNA  length = 29
FEATURE            Location/Qualifiers
source              1..29
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 441
acgtcattga cccaccggtc attcaggag          29

SEQ ID NO: 442      moltype = DNA  length = 32
FEATURE            Location/Qualifiers
source              1..32
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 442
acgtctgagg gttatccaag tgaccattg ca          32

SEQ ID NO: 443      moltype = DNA  length = 26
FEATURE            Location/Qualifiers
source              1..26
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 443
acgtcttgta cctggtgttc ggttat          26

SEQ ID NO: 444      moltype = DNA  length = 24
FEATURE            Location/Qualifiers
source              1..24
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 444
acgtccagcc caagatggat gaat          24

SEQ ID NO: 445      moltype = DNA  length = 25
FEATURE            Location/Qualifiers
source              1..25
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 445
acgtgcggtg gaagtcattc tgata          25

SEQ ID NO: 446      moltype = DNA  length = 24
FEATURE            Location/Qualifiers
source              1..24
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 446
acgtgagggc cacagattgg tatt          24

SEQ ID NO: 447      moltype = DNA  length = 26
FEATURE            Location/Qualifiers
source              1..26
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 447
acgtactgaa aggtcagatt caggag          26

SEQ ID NO: 448      moltype = DNA  length = 36
FEATURE            Location/Qualifiers
source              1..36

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 448		
catgttcac acacacatgc taacacaaat ccagtc		36
SEQ ID NO: 449	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 449		
cagaatccat gctcttaacc attatgctct gc		32
SEQ ID NO: 450	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
source	1..21	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 450		
catggaccgc cggtagccg g		21
SEQ ID NO: 451	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 451		
gaatgtactt tgcaagttag aatgacat		28
SEQ ID NO: 452	moltype = DNA length = 36	
FEATURE	Location/Qualifiers	
source	1..36	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 452		
catgtcatcc tggacattag ctacctctgt gattga		36
SEQ ID NO: 453	moltype = DNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 453		
accagagta ggcattaatc attccagaca tttc		34
SEQ ID NO: 454	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 454		
catggcactt gcctccacct tcccag		26
SEQ ID NO: 455	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 455		
ggtgaaacta cttaatgggt gcagggtg		28
SEQ ID NO: 456	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 456		
catgccaggg accctagcaa acgagct		27
SEQ ID NO: 457	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 457		
tgaccctggt cagtattcct agggctcc		27

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SEQ ID NO: 458 moltype = DNA length = 36
 FEATURE Location/Qualifiers
 source 1..36
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 458
 catgccatat ttataccagc ctggctctag gagagt 36

SEQ ID NO: 459 moltype = DNA length = 29
 FEATURE Location/Qualifiers
 source 1..29
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 459
 tcatagcaag caatgacaat gccaatataa 29

SEQ ID NO: 460 moltype = DNA length = 34
 FEATURE Location/Qualifiers
 source 1..34
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 460
 catgtctccc acactccaga tccaaagact actt 34

SEQ ID NO: 461 moltype = DNA length = 34
 FEATURE Location/Qualifiers
 source 1..34
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 461
 tgtagataca gttattcttt gttactgggt gaat 34

SEQ ID NO: 462 moltype = DNA length = 26
 FEATURE Location/Qualifiers
 source 1..26
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 462
 catgctgtgca cgcgcatgca aatagg 26

SEQ ID NO: 463 moltype = DNA length = 34
 FEATURE Location/Qualifiers
 source 1..34
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 463
 caaataagca cataagataa agatccagct attt 34

SEQ ID NO: 464 moltype = DNA length = 36
 FEATURE Location/Qualifiers
 source 1..36
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 464
 catgccctga acatttcacc atgaaatttg tgagct 36

SEQ ID NO: 465 moltype = DNA length = 25
 FEATURE Location/Qualifiers
 source 1..25
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 465
 gcctaagcct ggaacctagg aggtg 25

SEQ ID NO: 466 moltype = DNA length = 29
 FEATURE Location/Qualifiers
 source 1..29
 mol_type = other DNA
 organism = synthetic construct

 SEQUENCE: 466
 catggacgga gtttcactct ttcgccag 29

SEQ ID NO: 467 moltype = DNA length = 22
 FEATURE Location/Qualifiers
 source 1..22

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 467		
agaggtggca atgggccgag at		22
SEQ ID NO: 468	moltype = DNA length = 33	
FEATURE	Location/Qualifiers	
source	1..33	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 468		
catgaaagtc tcaagtagtc ggcatactg ttt		33
SEQ ID NO: 469	moltype = DNA length = 25	
FEATURE	Location/Qualifiers	
source	1..25	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 469		
actgctggct ggaaacagag gctaa		25
SEQ ID NO: 470	moltype = DNA length = 37	
FEATURE	Location/Qualifiers	
source	1..37	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 470		
catggtgata atttaagga gtttctcatc tgccttc		37
SEQ ID NO: 471	moltype = DNA length = 30	
FEATURE	Location/Qualifiers	
source	1..30	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 471		
catgcacttg tagttccagg tactaggag		30
SEQ ID NO: 472	moltype = DNA length = 30	
FEATURE	Location/Qualifiers	
source	1..30	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 472		
catgaaatta gccggacatg gtgggtcatg		30
SEQ ID NO: 473	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
source	1..21	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 473		
gtgcgcgcct gtaatccag c		21
SEQ ID NO: 474	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 474		
catgaaattc ccaagtcact ttgttcagaa atatttcag		39
SEQ ID NO: 475	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 475		
aaagggactc caagtattgt acgatgaaa		29
SEQ ID NO: 476	moltype = DNA length = 38	
FEATURE	Location/Qualifiers	
source	1..38	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 476		
catgtcctta gactttcctt gctttcagta accttgag		38

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SEQ ID NO: 477	moltype = DNA length = 26	
FEATURE	Location/Qualifiers	
source	1..26	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 477		
cactgagagg cctagaagca gtgacc	26	
SEQ ID NO: 478	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 478		
catgtttagt tagattgtct tcttattgtt gagttacag	39	
SEQ ID NO: 479	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 479		
ccacaaagtg caaagtttca tgcaactt	28	
SEQ ID NO: 480	moltype = DNA length = 38	
FEATURE	Location/Qualifiers	
source	1..38	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 480		
catgaattac atttaatgcc tgttgatgag ggctcaag	38	
SEQ ID NO: 481	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 481		
gttctatcca ttaagatcat gctcactaat ttaga	35	
SEQ ID NO: 482	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 482		
catgtttagt agcatggcca tgtgcttt	28	
SEQ ID NO: 483	moltype = DNA length = 27	
FEATURE	Location/Qualifiers	
source	1..27	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 483		
gaccagccta ggcaacatag tgagacc	27	
SEQ ID NO: 484	moltype = DNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 484		
catggccaag gccacccctg cag	23	
SEQ ID NO: 485	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 485		
caggattccg taagccaggt tt	22	
SEQ ID NO: 486	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
source	1..32	

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 486		
catgcaaate aaatcccage	tgagccactc tg	32
SEQ ID NO: 487	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 487		
ttctcatctt cccagctgac	attt	24
SEQ ID NO: 488	moltype = DNA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 488		
catgaatcca cccacctaga	attctgtact cagc	34
SEQ ID NO: 489	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 489		
gactcaattt atgttggttc	cattccagtt t	31
SEQ ID NO: 490	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
source	1..24	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 490		
catgccacca cgcccagcta	attt	24
SEQ ID NO: 491	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 491		
agtatgaagc ccacctagat	tcattgtgag g	31
SEQ ID NO: 492	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 492		
catgatttat ttacaactgt	gattggacaa gaagaattc	39
SEQ ID NO: 493	moltype = DNA length = 23	
FEATURE	Location/Qualifiers	
source	1..23	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 493		
cgatctggc tcactgcaac	ctc	23
SEQ ID NO: 494	moltype = DNA length = 37	
FEATURE	Location/Qualifiers	
source	1..37	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 494		
catgattatt tatatgatct	tcacctgtgc aattcct	37
SEQ ID NO: 495	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 495		
caggagacct ctctgagtag	ttgacaatt	29

SEQ ID NO: 496	moltype = DNA	length = 36	
FEATURE	Location/Qualifiers		
source	1..36		
	mol_type = other DNA		
	organism = synthetic construct		
SEQUENCE: 496			
catgatctct	caagtgagag	gattcttctt	tcttga
SEQ ID NO: 497	moltype = DNA	length = 31	
FEATURE	Location/Qualifiers		
source	1..31		
	mol_type = other DNA		
	organism = synthetic construct		
SEQUENCE: 497			
gacttcagaa	gctagttact	gaaggaatac	t
SEQ ID NO: 498	moltype = DNA	length = 39	
FEATURE	Location/Qualifiers		
source	1..39		
	mol_type = other DNA		
	organism = synthetic construct		
SEQUENCE: 498			
catgaataag	tctctcagtc	attatatattag	cttctaaca
SEQ ID NO: 499	moltype = DNA	length = 28	
FEATURE	Location/Qualifiers		
source	1..28		
	mol_type = other DNA		
	organism = synthetic construct		
SEQUENCE: 499			
atgtaatgac	ggacttagtg	gcaataaa	
SEQ ID NO: 500	moltype = DNA	length = 35	
FEATURE	Location/Qualifiers		
source	1..35		
	mol_type = other DNA		
	organism = synthetic construct		
SEQUENCE: 500			
catggggaag	aggtcaggat	ttgcacctat	atctg
SEQ ID NO: 501	moltype = DNA	length = 24	
FEATURE	Location/Qualifiers		
source	1..24		
	mol_type = other DNA		
	organism = synthetic construct		
SEQUENCE: 501			
aatctctcca	gcactttggg	aggc	
SEQ ID NO: 502	moltype = DNA	length = 30	
FEATURE	Location/Qualifiers		
source	1..30		
	mol_type = other DNA		
	organism = synthetic construct		
SEQUENCE: 502			
catgctcagg	actgaagggt	ttcccaggac	
SEQ ID NO: 503	moltype = DNA	length = 22	
FEATURE	Location/Qualifiers		
source	1..22		
	mol_type = other DNA		
	organism = synthetic construct		
SEQUENCE: 503			
gctattcggg	aggctgaggc	ag	
SEQ ID NO: 504	moltype = DNA	length = 37	
FEATURE	Location/Qualifiers		
source	1..37		
	mol_type = other DNA		
	organism = synthetic construct		
SEQUENCE: 504			
catgatgttt	agttatgccc	tatgcagatg	tcttggt
SEQ ID NO: 505	moltype = DNA	length = 33	
FEATURE	Location/Qualifiers		
source	1..33		

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	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 505		
tatgtctact ctgtagcatt tgggtggttca tcc		33
SEQ ID NO: 506	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
source	1..22	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 506		
catggggacg gtacgggtgcg cg		22
SEQ ID NO: 507	moltype = DNA length = 35	
FEATURE	Location/Qualifiers	
source	1..35	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 507		
cagataatca gcattaataa tatgtccagc atgac		35
SEQ ID NO: 508	moltype = DNA length = 39	
FEATURE	Location/Qualifiers	
source	1..39	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 508		
catgacataa agacttttgcg gatgatatat taacaaatg		39
SEQ ID NO: 509	moltype = DNA length = 33	
FEATURE	Location/Qualifiers	
source	1..33	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 509		
caatagtggg acaggcatag catagacatt ctc		33
SEQ ID NO: 510	moltype = DNA length = 28	
FEATURE	Location/Qualifiers	
source	1..28	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 510		
catgacggca tatcctgctc accgactt		28
SEQ ID NO: 511	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 511		
atgggcacta ttgctttcta aatgcacaa		29
SEQ ID NO: 512	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
source	1..31	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 512		
catgtttcct gtgctgaagt gaccctttgg t		31
SEQ ID NO: 513	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
source	1..29	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 513		
ggaagtccat gcctaagaaa catgtagca		29
SEQ ID NO: 514	moltype = DNA length = 36	
FEATURE	Location/Qualifiers	
source	1..36	
	mol_type = other DNA organism = synthetic construct	
SEQUENCE: 514		
catgttaggt cttagattta agttcctgat ccattt		36

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SEQ ID NO: 515      moltype = DNA   length = 22
FEATURE             Location/Qualifiers
source              1..22
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 515
tctcggtca ctgcaagctc cg

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22

1. A method of analyzing nucleic acid with a group of primer sets, the method comprising sequentially amplifying template nucleic acid with each primer set within the group, wherein:

- the group of primer sets comprises two or more primer sets;
- each primer set comprises set-identity primer pairs;
- each set-identity primer pair consists of set-identity primers consisting of a first set-identity primer and a second set-identity primer;
- each set-identity primer comprises a template-annealing segment on a 3' end of the set-identity primer;
- each set-identity primer comprises a set-identity segment on a 5' end of the set-identity primer;
- a combination of the set-identity segment on the first set-identity primer and the set-identity segment on the second set-identity primer in each set-identity primer pair defines a set-identity signature; and
- each of the set-identity signatures is defined only by set-identity primer pairs in one and only one of the primer sets within the group.

2. The method of claim 1, wherein each set-identity signature is defined by base length and base sequence of the set-identity segments on the first and second set-identity primers.

3. The method of claim 1, wherein each set-identity segment comprises from 0 to 10 bases.

4. The method of claim 1, wherein all the set-identity segments on all the second set-identity primers have a same base length and base sequence.

5. The method of claim 1, wherein each set-identity segment on each second set-identity primer has a base length of 0 bases.

6. The method of claim 1, wherein each set-identity segment on each first set-identity primer has a base length from 0 to 6 bases.

7. The method of claim 1, wherein all the set-identity segments on all the first set-identity primers have a same base length.

8. The method of claim 1, wherein each set-identity segment on each first set-identity primer within each primer set has a different base sequence than each set-identity segment on each first set-identity primer in each of the other primer sets.

9. The method of claim 1, wherein the set-identity segment on each first set-identity primer comprises a non-complimentary 5' overhang.

10. The method of claim 1, wherein each primer set comprises at least 1 set-identity primer pair and up to 100 set-identity primer pairs, or at least 2 set-identity primer pairs and up to 100 set-identity primer pairs.

11. (canceled)

12. The method of claim 1, wherein:

the template-annealing segment of each of the first set-identity primers in each primer set has a base length and base sequence identical to a base length and base sequence of the template-annealing segment of at least one of the first set-identity primers in each of the other sets; and/or

the template-annealing segment of each of the second set-identity primers in each primer set has a base length and base sequence identical to a base length and base sequence of the template-annealing segment of at least one of the second set-identity primers in each of the other sets.

13. The method of claim 1, wherein each primer set comprises multiple copies of each first set-identity primer and each second set-identity primer.

14. The method of claim 1, wherein all the set-identity primer pairs within each primer set together define no more than 10 different set-identity signatures.

15. The method of claim 1, wherein all the set-identity primer pairs within each primer set define the same set-identity signature.

16. The method of claim 1, wherein the group of primer sets comprises three or more primer sets.

17. The method of claim 1, wherein each sequential amplification comprises mixing the template nucleic acid and one of the primer sets, wherein the mixing for all the sequential amplifications is performed within a single enclosable mixing space.

18. The method of claim 1, further comprising:

generating a separate amplicon sample from each sequential amplification with each of the primer sets, wherein each amplicon sample comprises amplicons comprising one or more of the set-identity signatures; and

determining sequences of the amplicons in each separate amplicon sample, wherein the determining the sequences of the amplicons in each separate amplicon sample comprises determining the sequences of the amplicons in each separate amplicon sample in a separate workflow.

19. The method of claim 18, further comprising identifying the set-identity signatures in the sequences of the amplicons in each of the amplicon samples and informatively filtering the sequences of the amplicons in any given amplicon sample that comprise one of the set-identity signatures not defined by any of the set-identity primer pairs in the primer set employed in generating the given amplicon sample.

20. (canceled)

21. The method of claim 18, wherein the determining the sequences of the amplicons in each separate amplicon sample comprises generating a separate sequencing library

from each separate amplicon sample, wherein the generating the separate sequencing libraries:

comprises sequentially generating each of the separate sequencing libraries;

is performed within a single enclosable library-generating space; and

comprises one or more steps selected from the group consisting of amplicon fragmentation, nucleic acid end repair, adapter ligation, and amplification with indexed or barcoded primers.

22-24. (canceled)

25. The method of claim **21**, further comprising separately sequencing with a sequencing instrument each of the separate sequencing libraries, wherein the separately sequencing comprises sequentially sequencing with a sequencing instrument each of the sequencing libraries.

26. (canceled)

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