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(54) **DIGITAL COUNTING OF INDIVIDUAL MOLECULES BY STOCHASTIC ATTACHMENT OF DIVERSE LABELS**

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C40B 30/04 (2006.01)
C12Q 1/68 (2006.01)

(52) **U.S. Cl.**
USPC **506/9**; 435/6.1

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CPC .. C12Q 1/6858; C12Q 1/6816; C12Q 1/6809; C12Q 2525/191; C12Q 1/6837; C12Q 2537/157; C12Q 2537/16
See application file for complete search history.

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(57) **ABSTRACT**

Compositions, methods and kits are disclosed for high-sensitivity single molecule digital counting by the stochastic labeling of a collection of identical molecules by attachment of a diverse set of labels. Each copy of a molecule randomly chooses from a non-depleting reservoir of diverse labels. Detection may be by a variety of methods including hybridization based or sequencing. Molecules that would otherwise be identical in information content can be labeled to create a separately detectable product that is unique or approximately unique in a collection. This stochastic transformation relaxes the problem of counting molecules from one of locating and identifying identical molecules to a series of binary digital questions detecting whether preprogrammed labels are present. The methods may be used, for example, to estimate the number of separate molecules of a given type or types within a sample.

95 Claims, 30 Drawing Sheets

10x Genomics EX1033

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FIG. 1

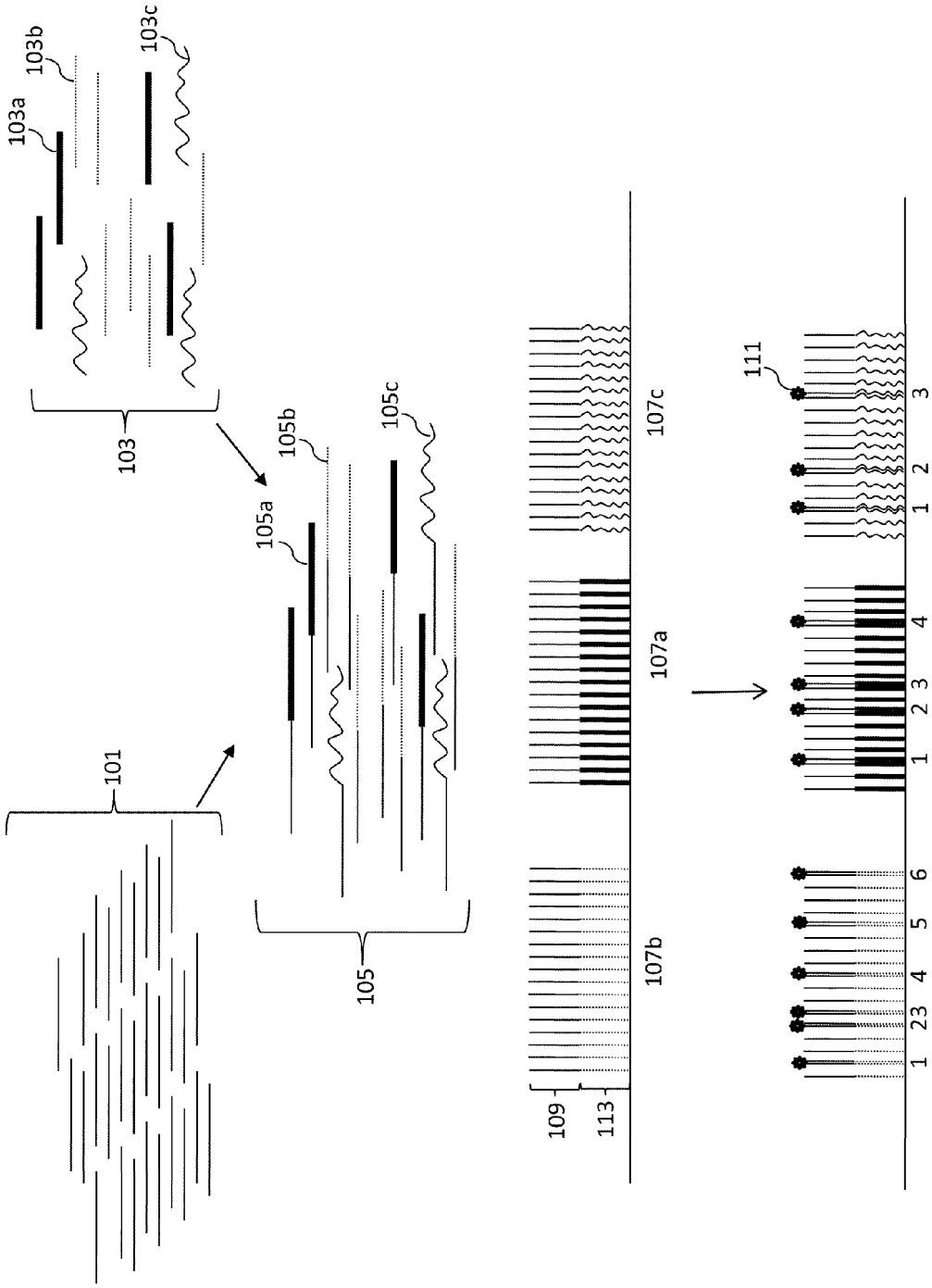

101
103
103a
103b
103c
105
105a
105b
105c
107a
107b
107c
109
111
113
1
2
3
4
5
6

FIG. 2A

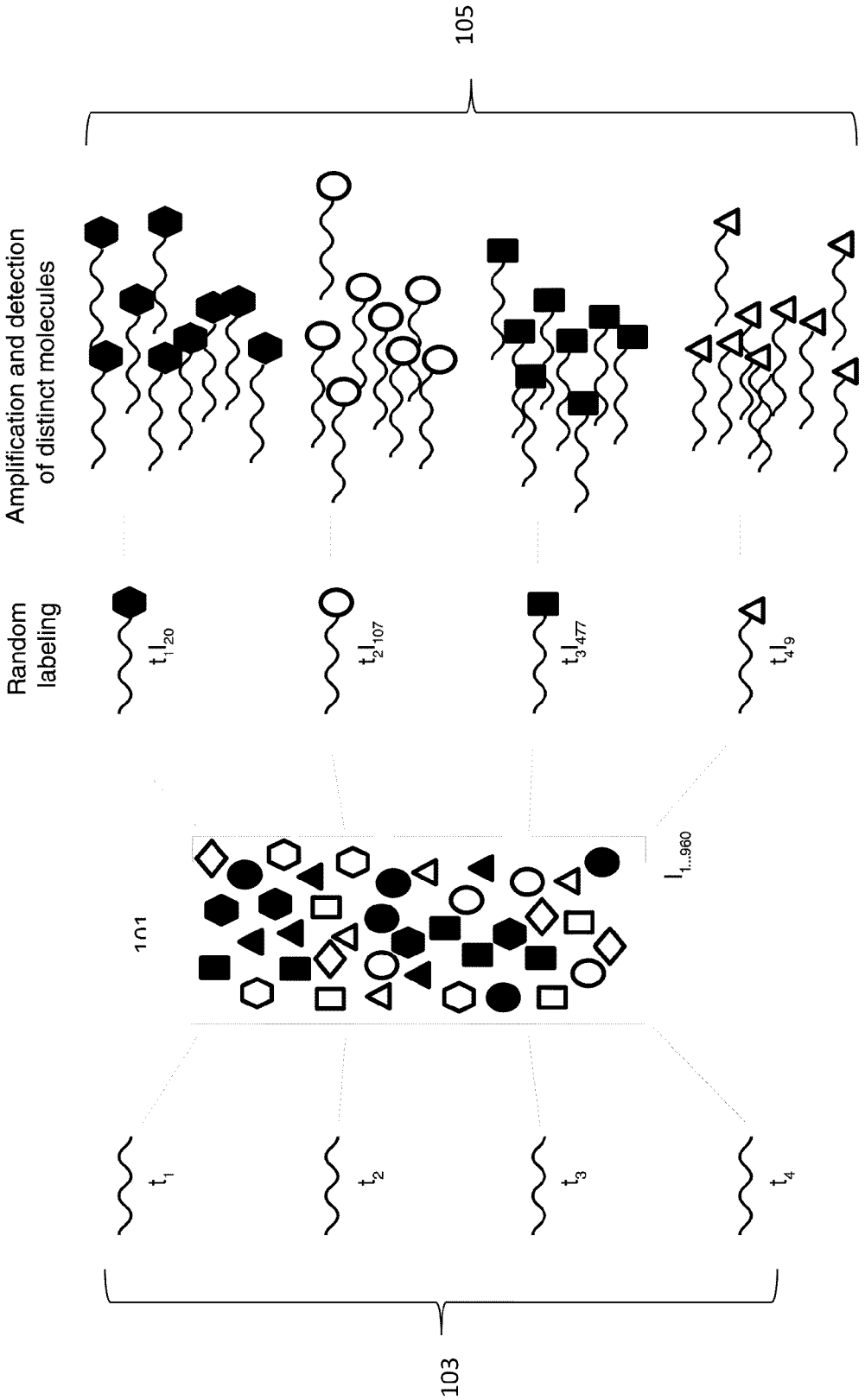

105
Amplification and detection of distinct molecules
Random labeling
t_1l_{20}
t_2l_{107}
t_3l_{477}
t_4l_9
$l_{1...960}$
101
t_1
t_2
t_3
t_4
103

FIG. 2B

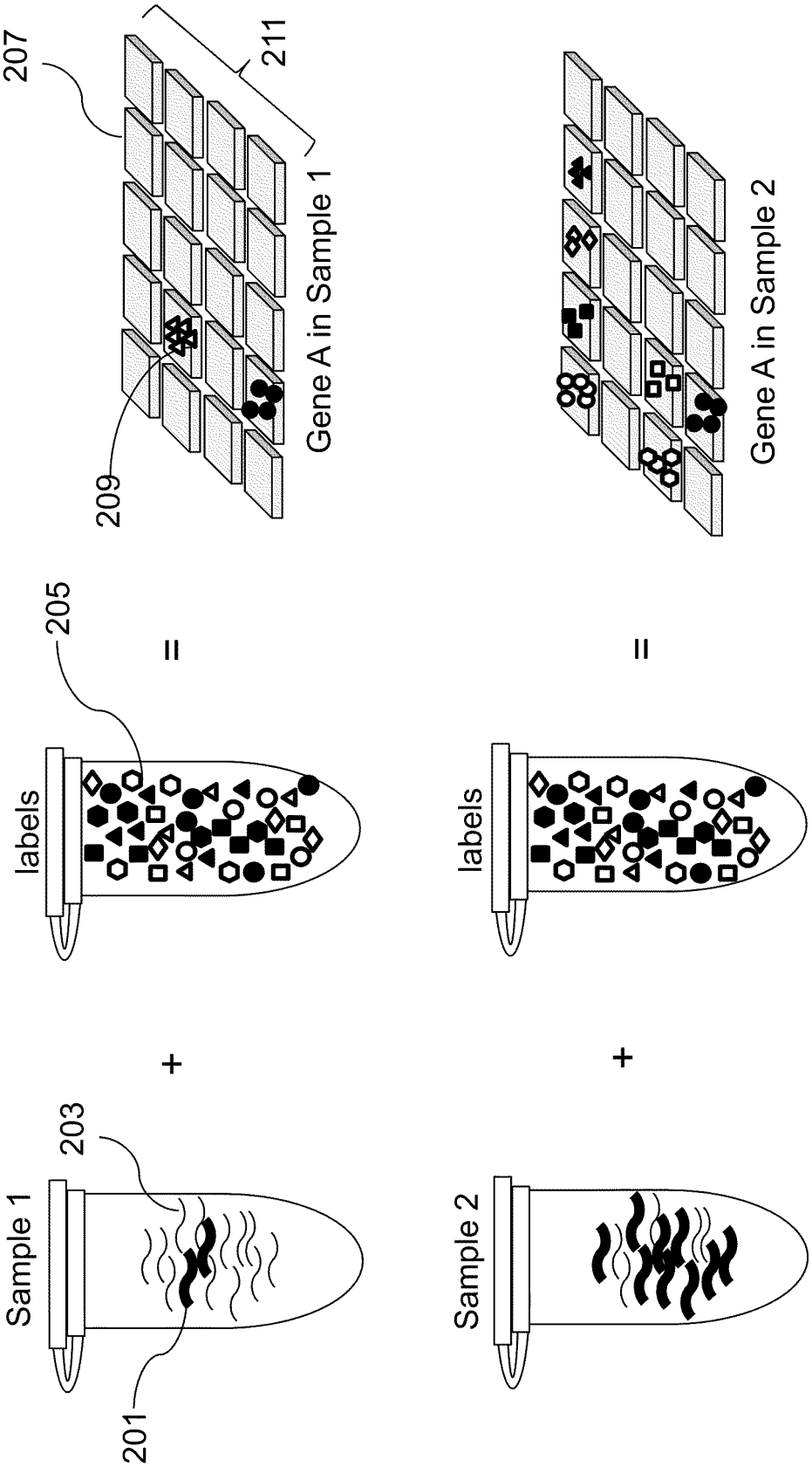
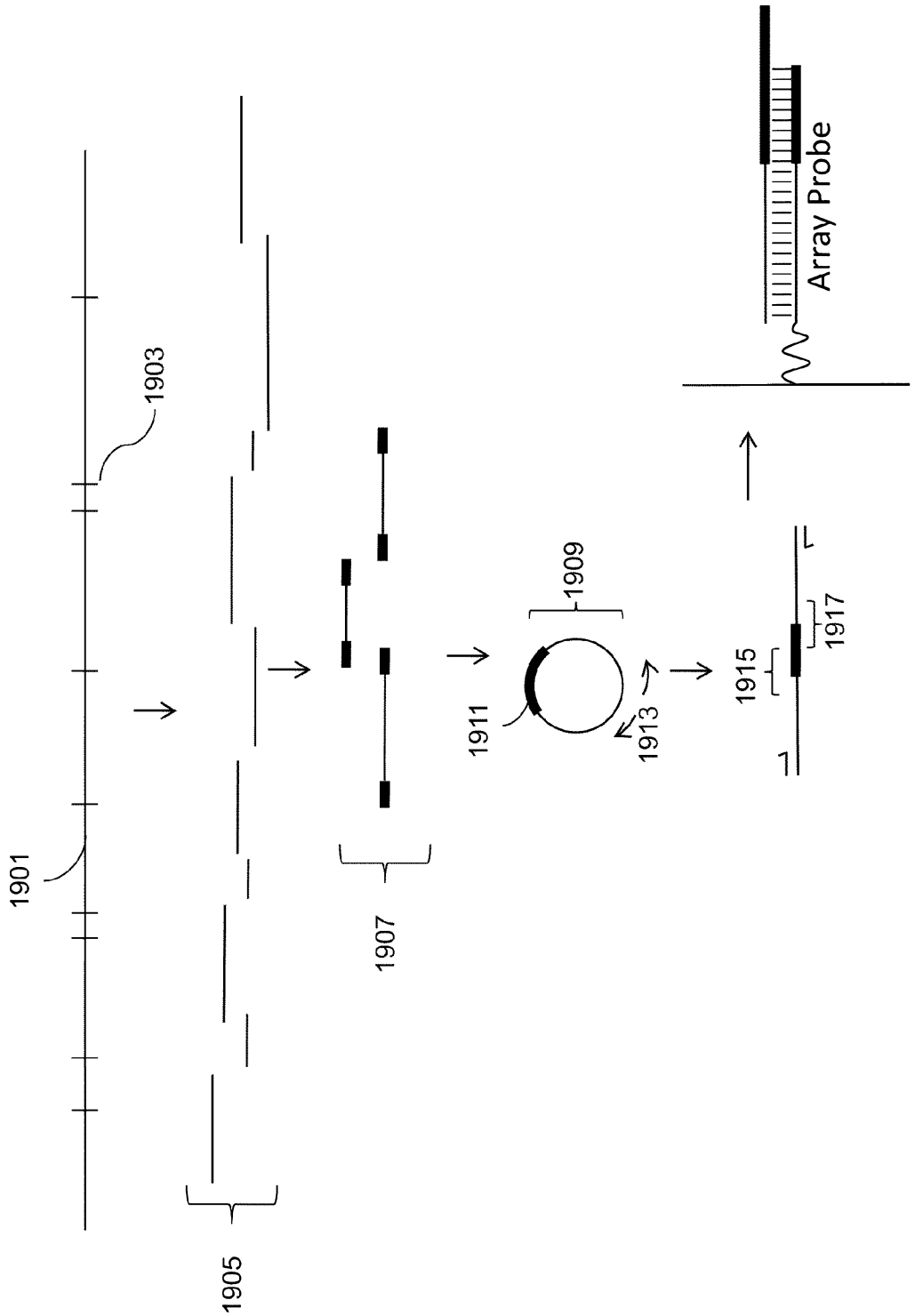

Sample 1
203
201
+
labels
205
=
207
209
211
Gene A in Sample 1
Sample 2
+
labels
=
Gene A in Sample 2

FIG.3



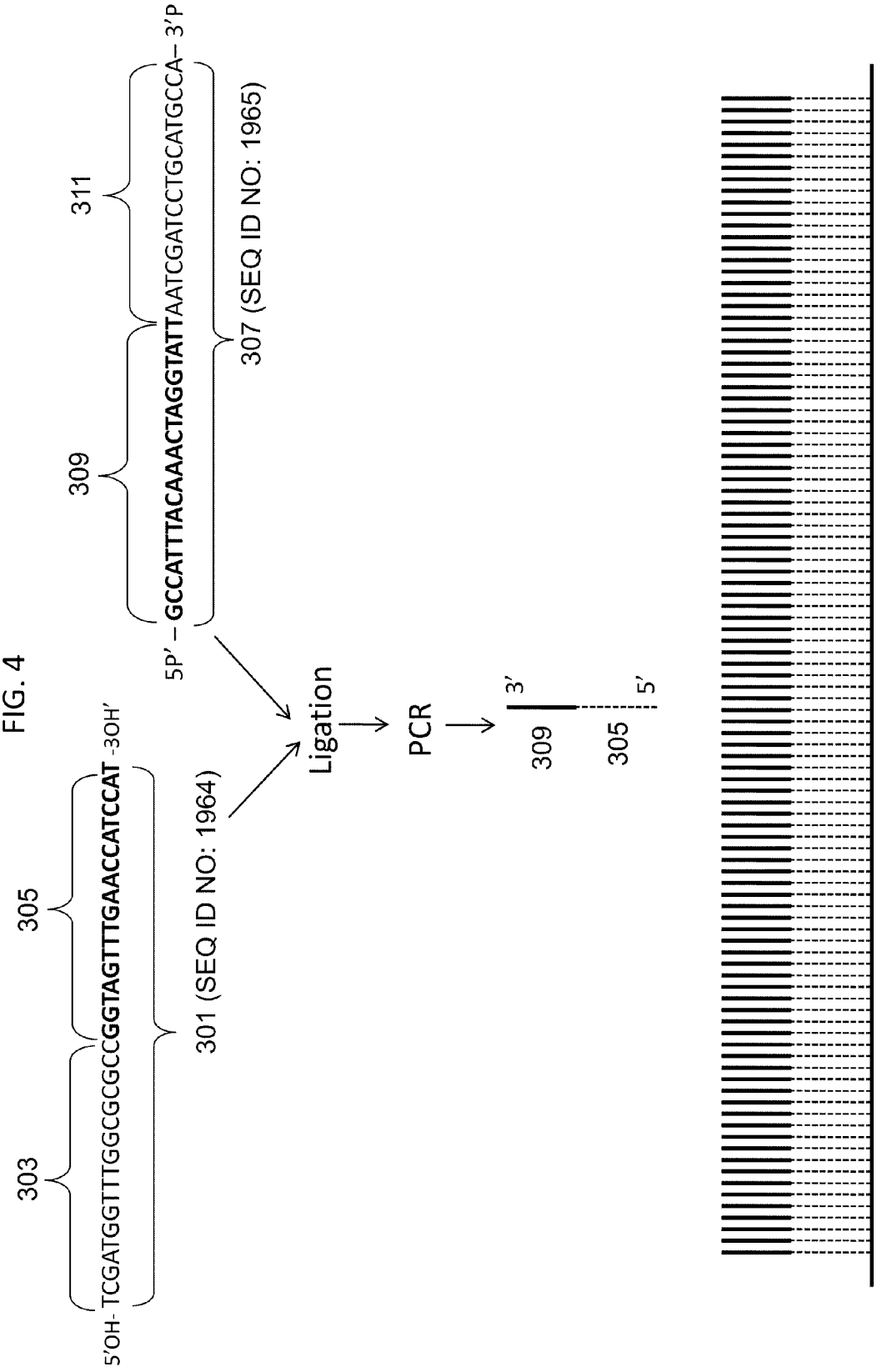

303
305
309
311
5'OH- TCGATGGTTTGGCGCGCCGGTAGTTTGAACCATCCAT -3OH'
5P' – GCCATTTACAAACTAGGTATTAATCGATCCTGCATGCCA– 3'P
301 (SEQ ID NO: 1964)
307 (SEQ ID NO: 1965)
Ligation
PCR
3'
5'
309
305

FIG. 4

FIG. 5

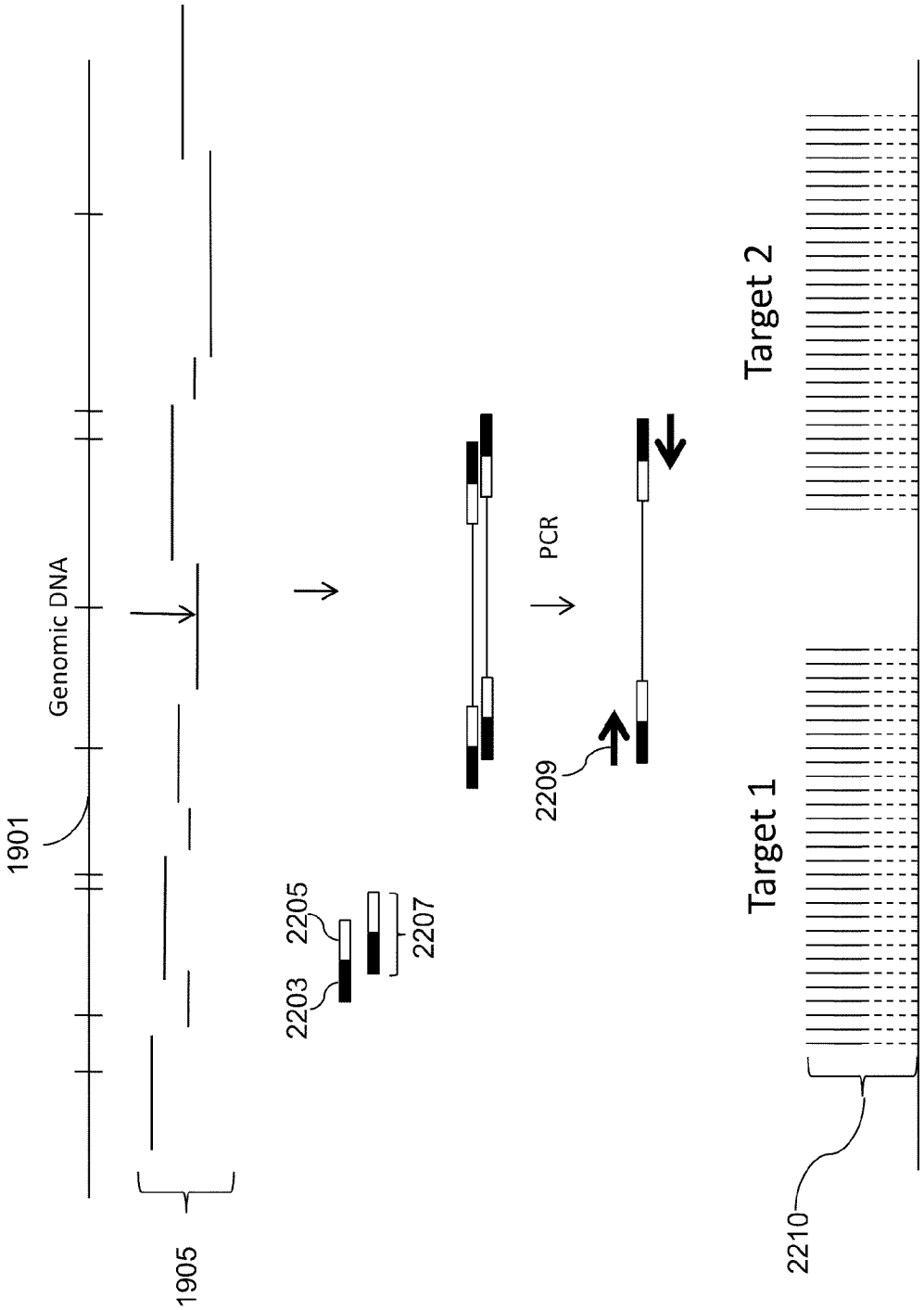

Genomic DNA
1901
1905
2205
2203
2207
PCR
2209
Target 2
Target 1
2210

FIG. 6

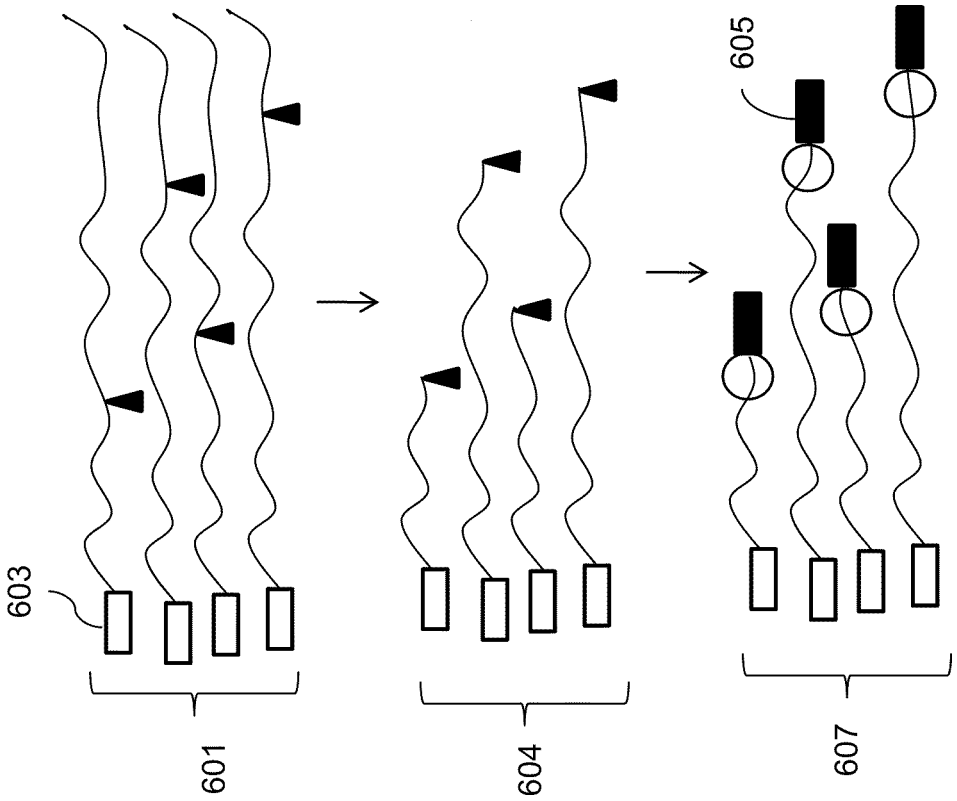


FIG. 7

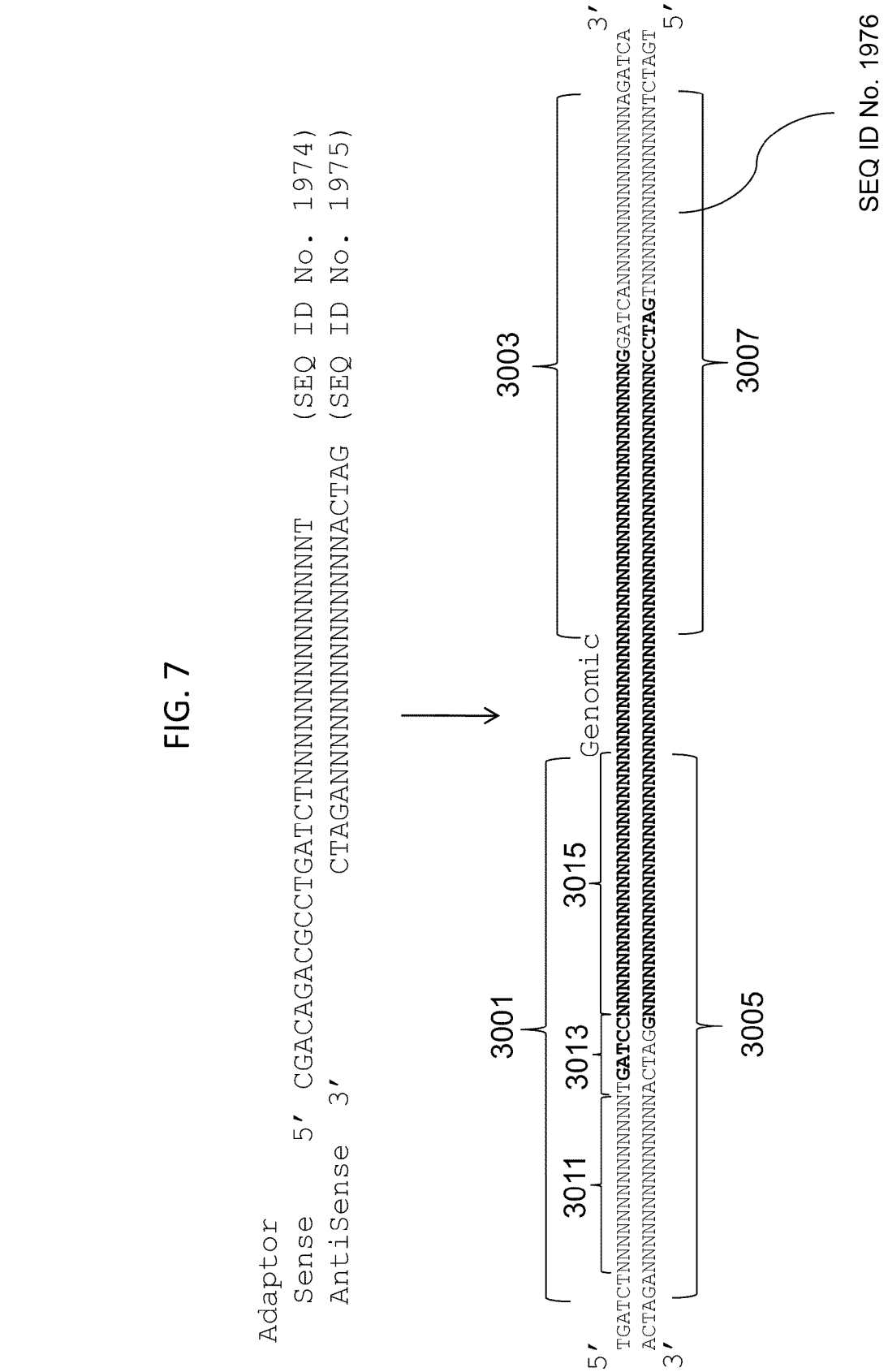
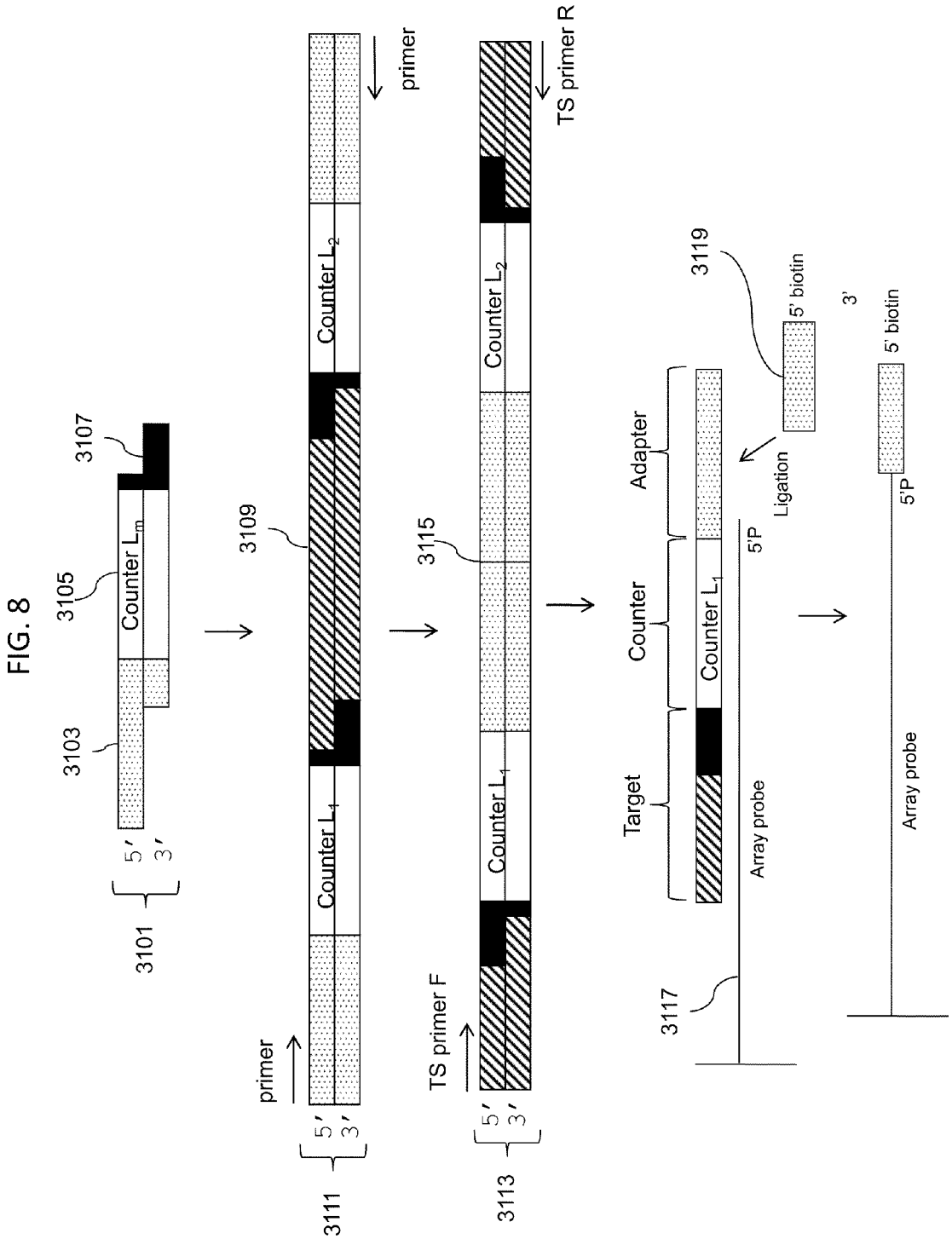

Adaptor
Sense 5′ CGACAGACGCCTGATCTNNNNNNNNNNNNNNNNNNNT (SEQ ID No. 1974)
AntiSense 3′ CTAGANNNNNNNNNNNNNNNNNNACTAG (SEQ ID No. 1975)
3001
3003
3005
3007
3011
3013
3015
Genomic
5′
3′
5′
3′
SEQ ID No. 1976

FIG. 8


3101
3103
3105
3107
Counter L_m
5′
3′
3109
Counter L_1
Counter L_2
primer
3111
primer
3113
3115
Counter L_1
Counter L_2
TS primer F
TS primer R
3117
Target
Counter
Adapter
Counter L_1
Array probe
5'P
3119
Ligation
5' biotin
3'
5' biotin
5'P
Array probe

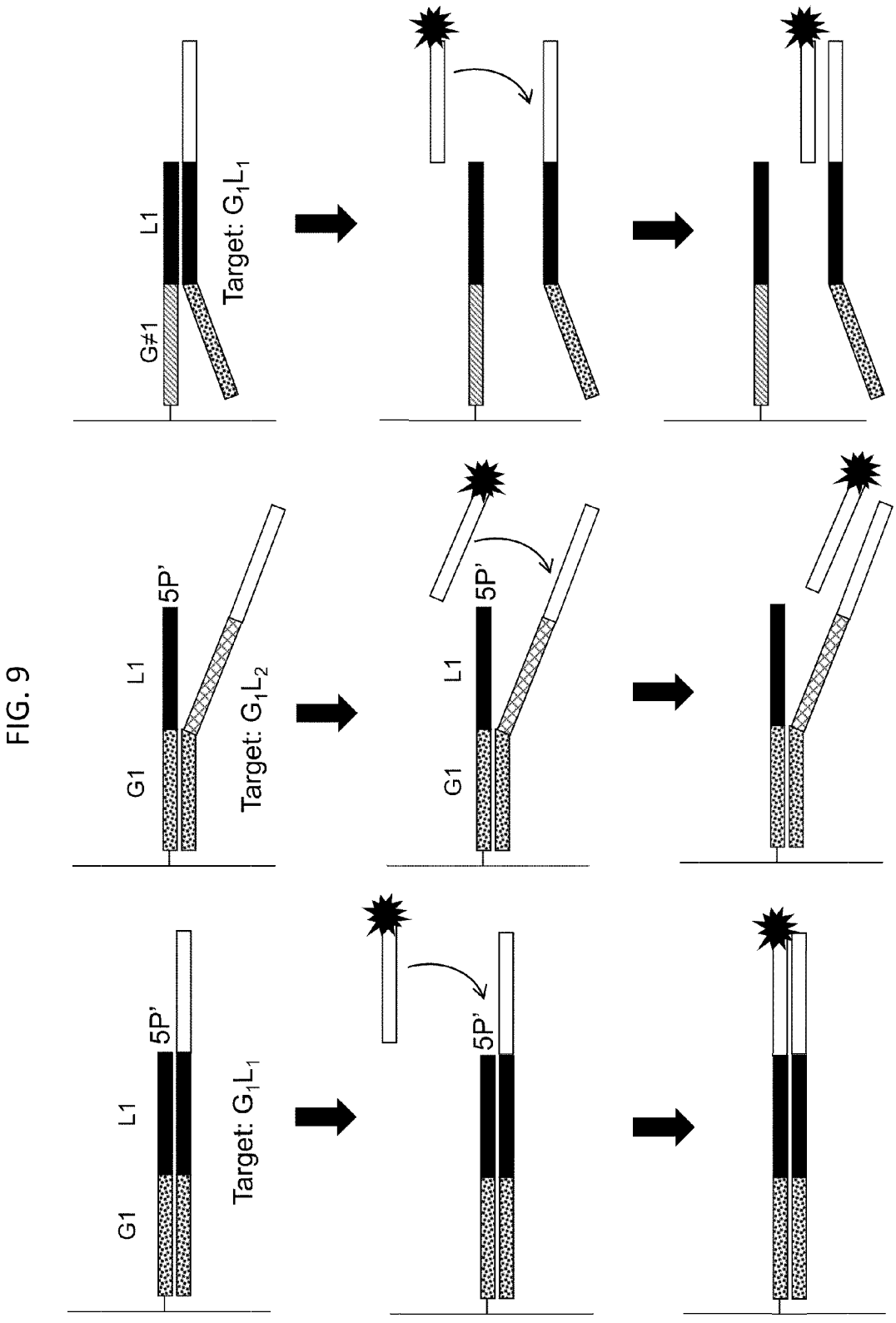
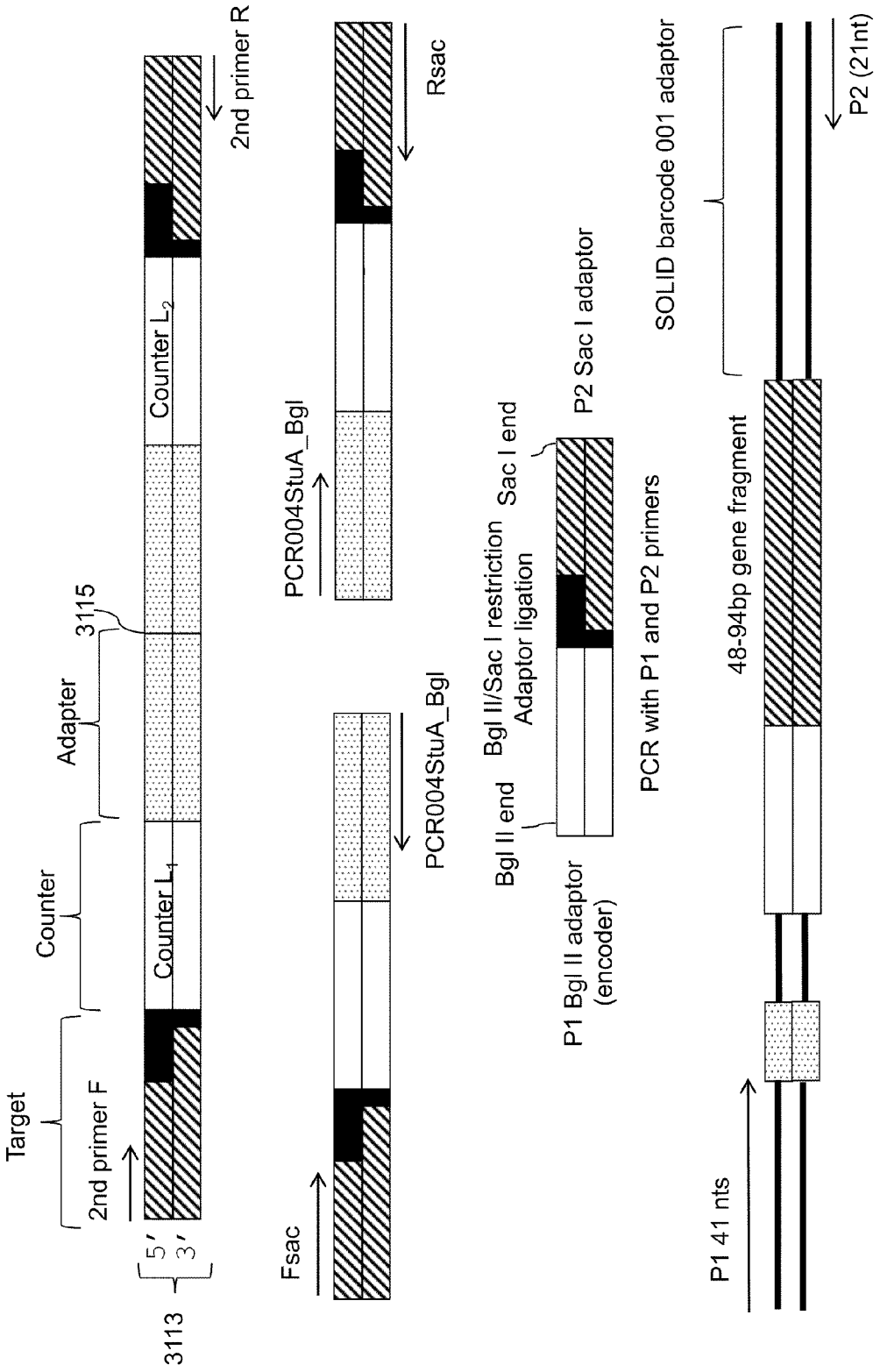


FIG. 9

FIG. 10


Target
2nd primer F
Counter
Adapter
3115
Counter L1
Counter L2
2nd primer R
5′
3′
3113
Fsac
PCR004StuA_Bgl
PCR004StuA_Bgl
Rsac
Bgl II end
Bgl II/Sac I restriction
Adaptor ligation
Sac I end
P2 Sac I adaptor
P1 Bgl II adaptor
(encoder)
PCR with P1 and P2 primers
SOLID barcode 001 adaptor
48-94bp gene fragment
P1 41 nts
P2 (21nt)

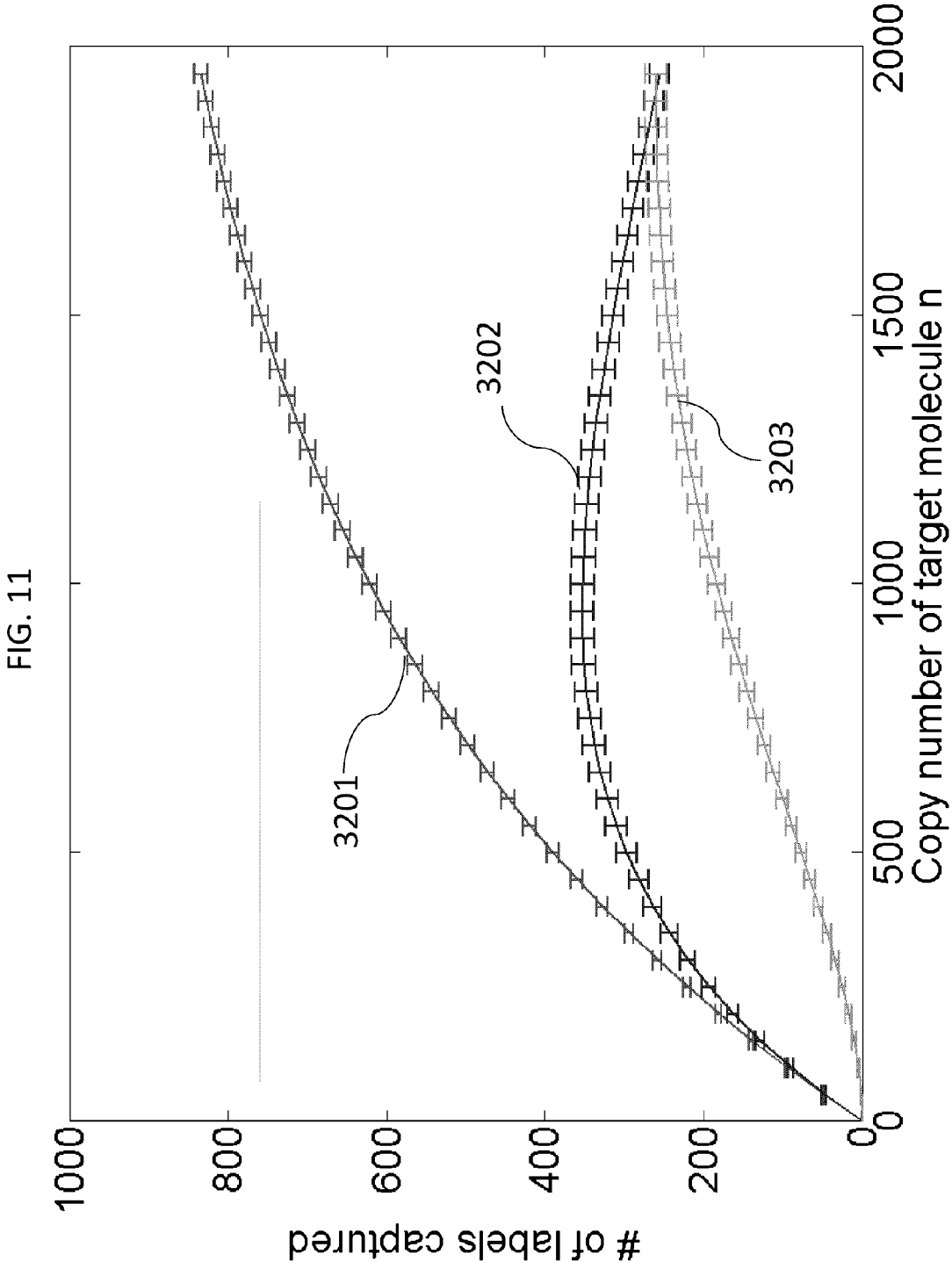

1000
800
600
400
200
0
of labels captured
0
500
1000
1500
2000
Copy number of target molecule n
3201
3202
3203

FIG. 11

FIG. 12

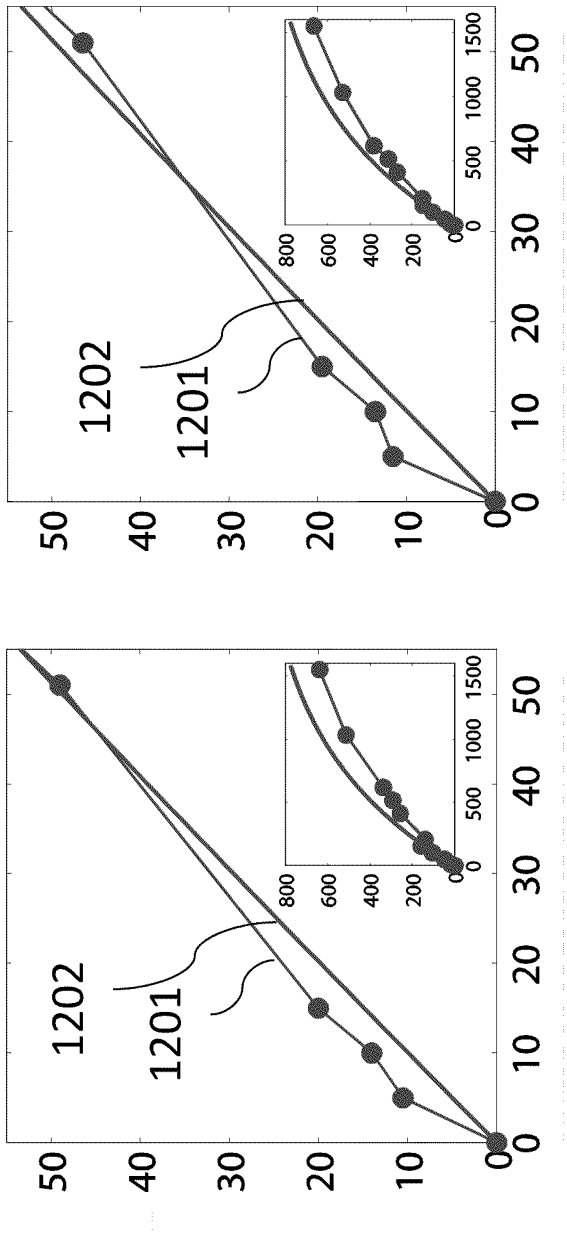


FIG. 13

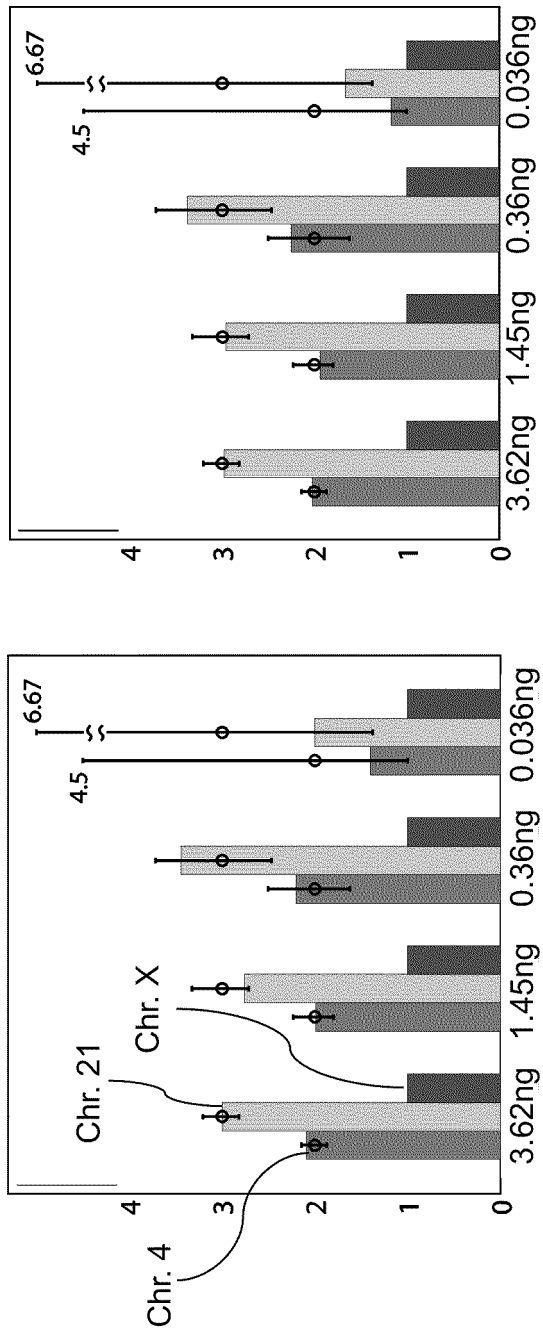


FIG. 14

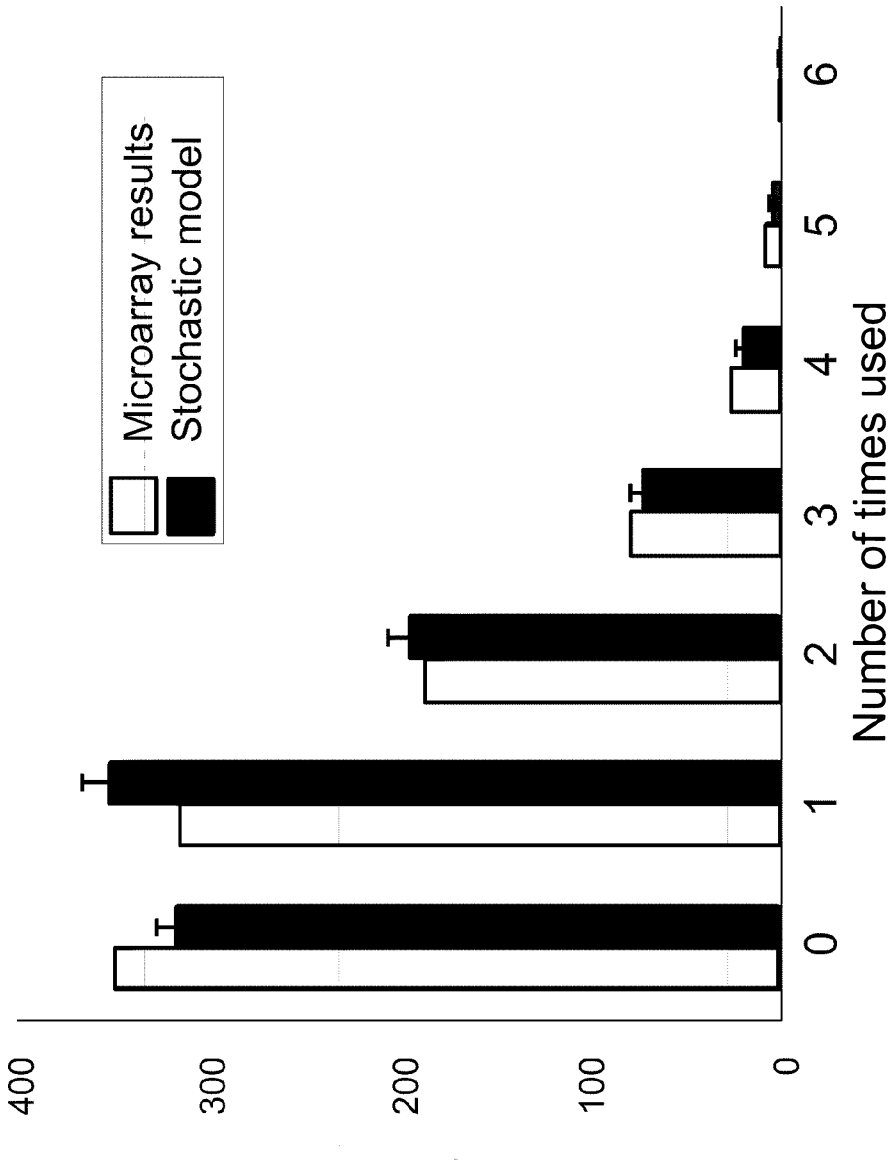

Microarray results
Stochastic model
400
300
200
100
0
0
1
2
3
4
5
6
Number of times used

FIG. 15

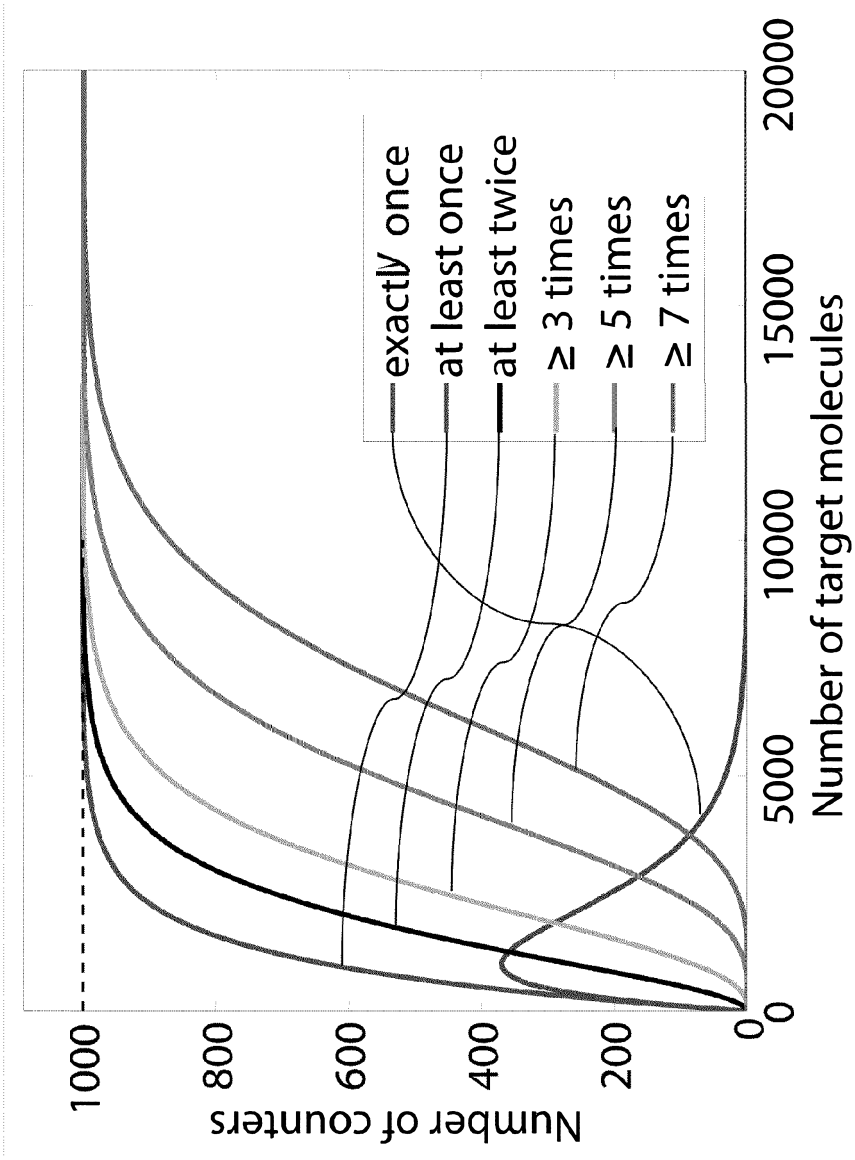

Number of counters
1000
800
600
400
200
0
0
5000
10000
15000
20000
Number of target molecules
exactly once
at least once
at least twice
≥ 3 times
≥ 5 times
≥ 7 times

FIG. 16

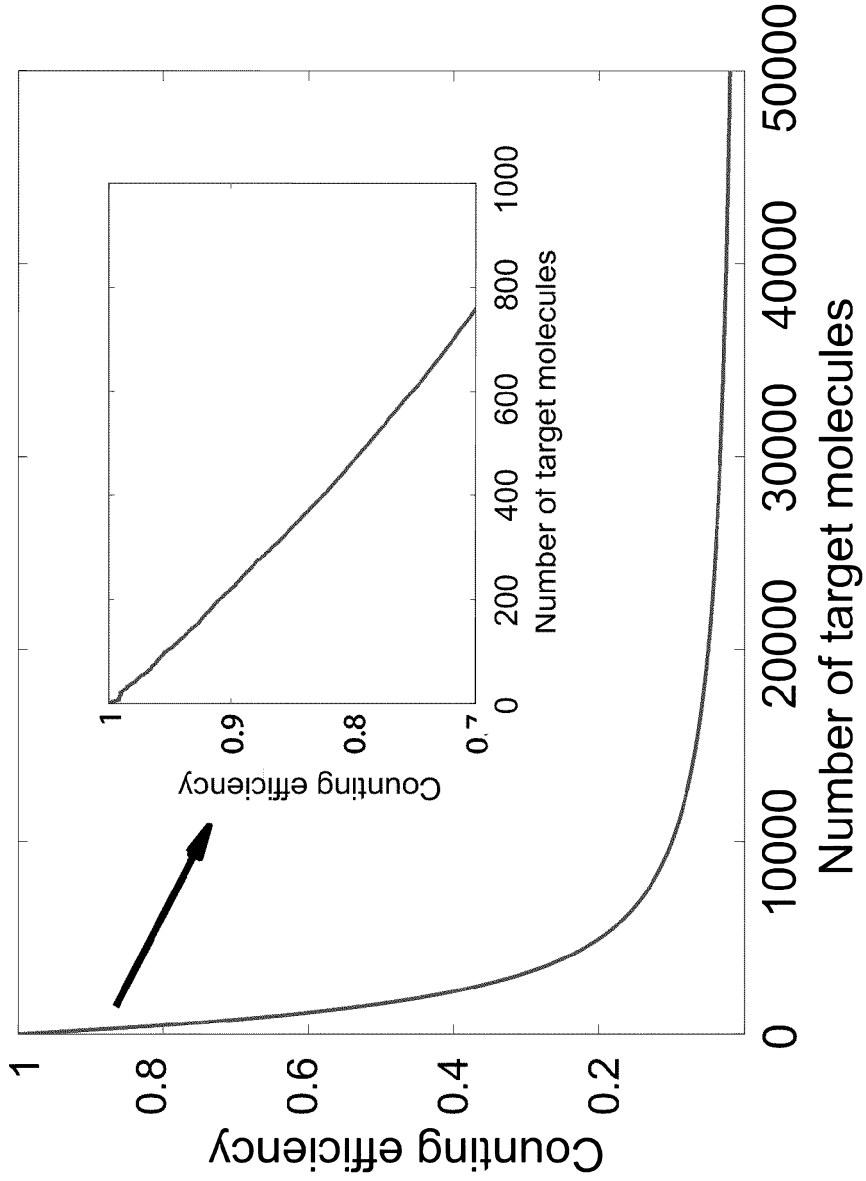

Counting efficiency
1
0.8
0.6
0.4
0.2
0
10000
20000
30000
40000
50000
Number of target molecules
Counting efficiency
1
0.9
0.8
0.7
0
200
400
600
800
1000
Number of target molecules

FIG. 17.

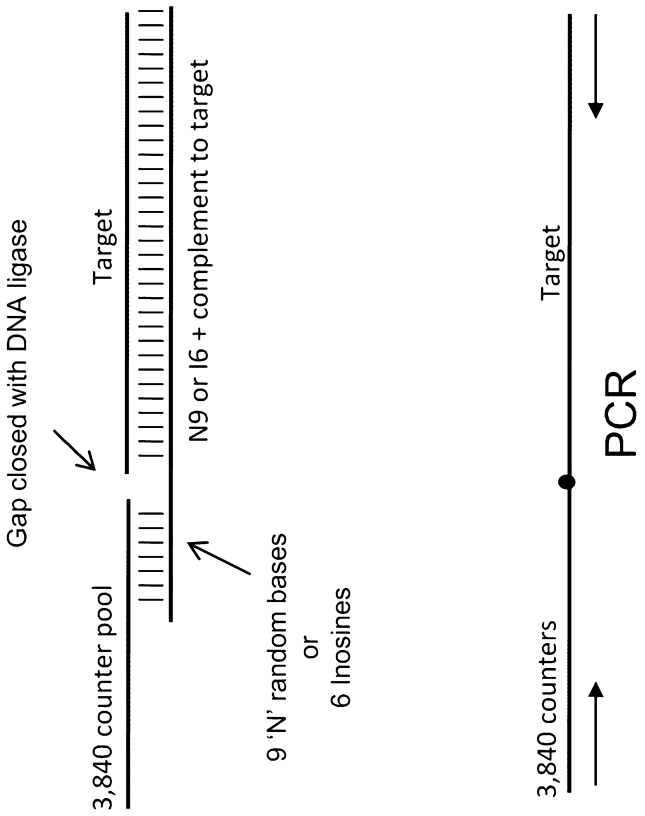

Gap closed with DNA ligase
Target
3,840 counter pool
N9 or I6 + complement to target
9 'N' random bases
or
6 Inosines
Target
3,840 counters
PCR

FIG. 18

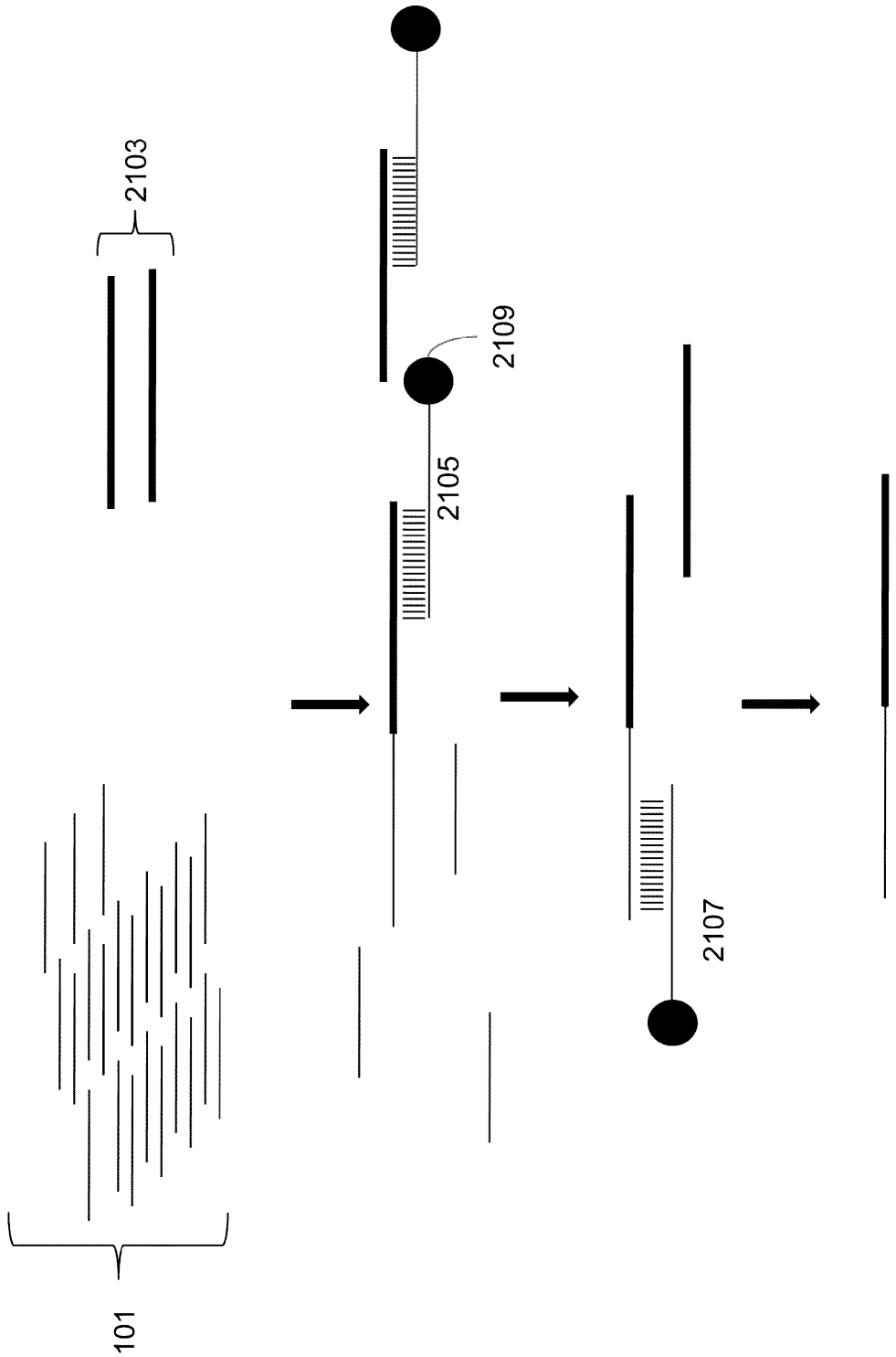


FIG. 19

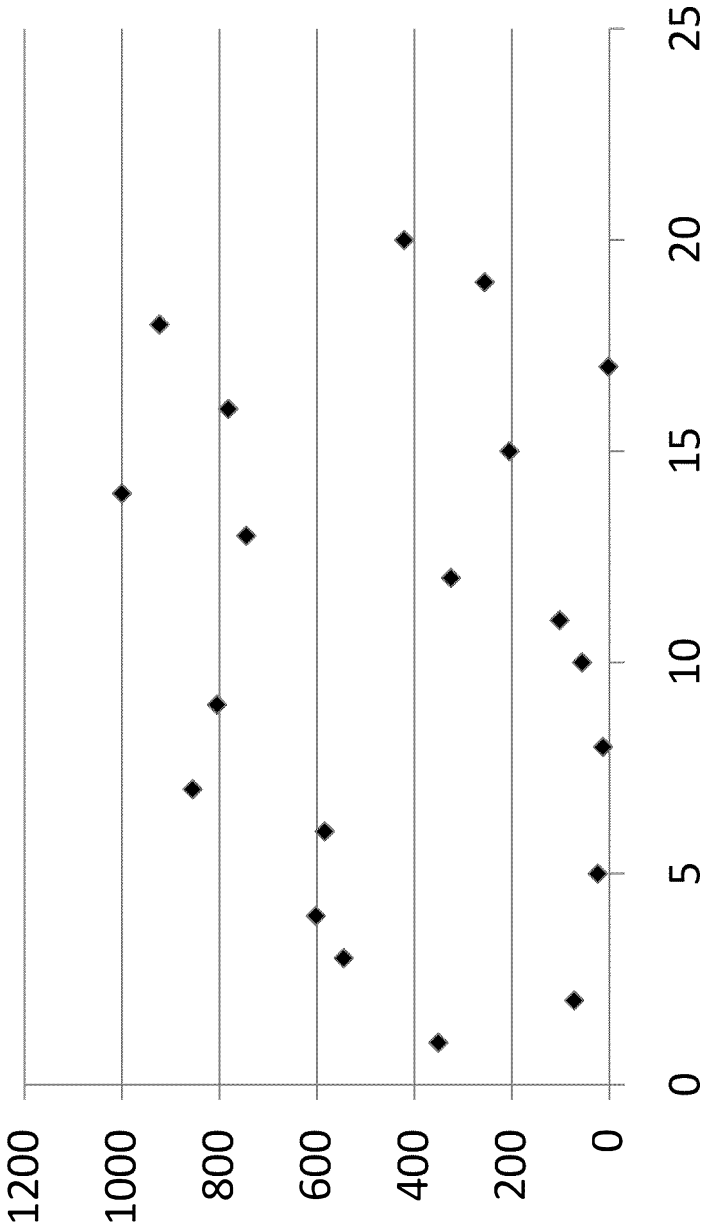
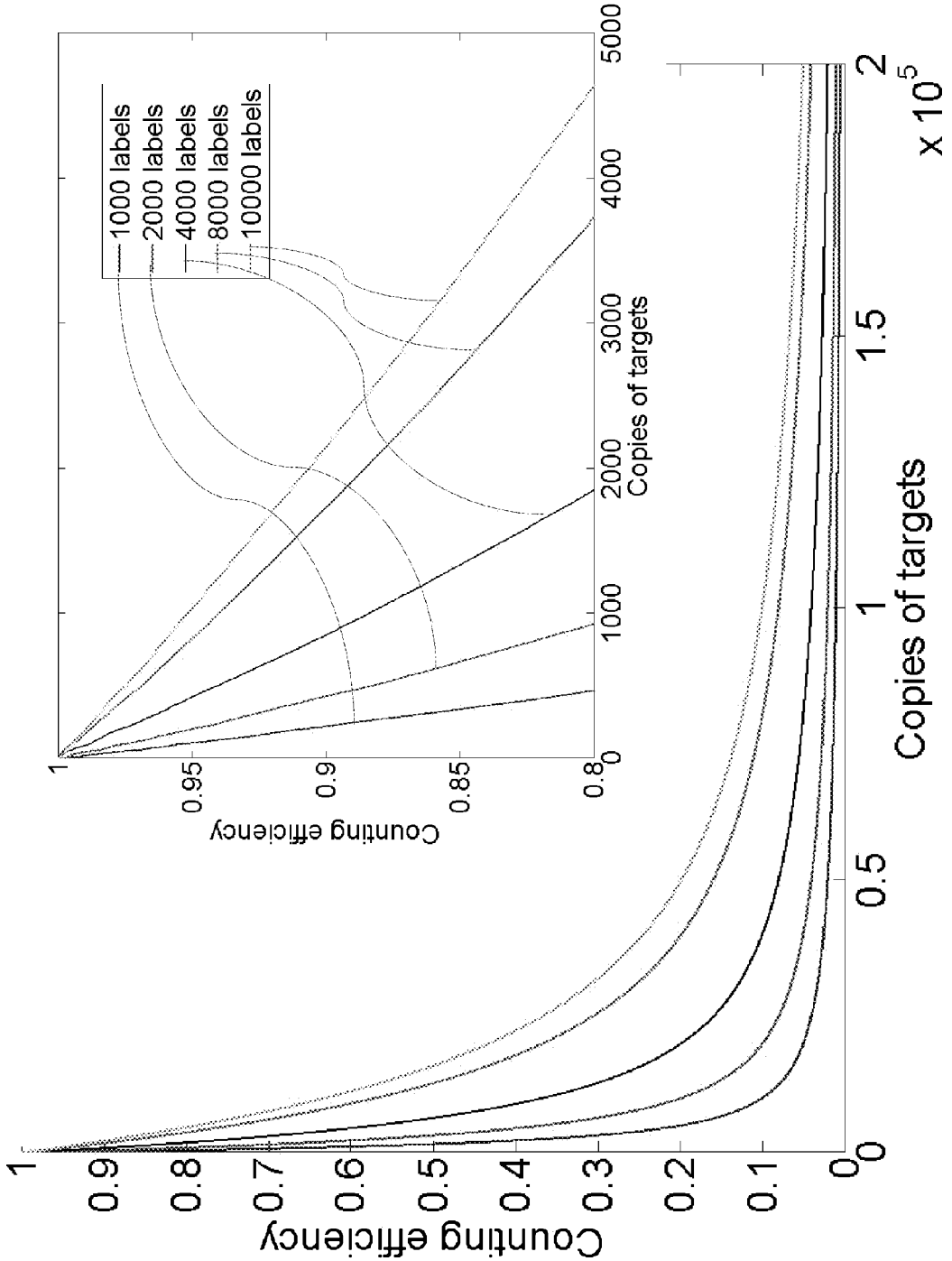


FIG. 20


Counting efficiency
Copies of targets
x 10^5
1000 labels
2000 labels
4000 labels
8000 labels
10000 labels
Counting efficiency
Copies of targets

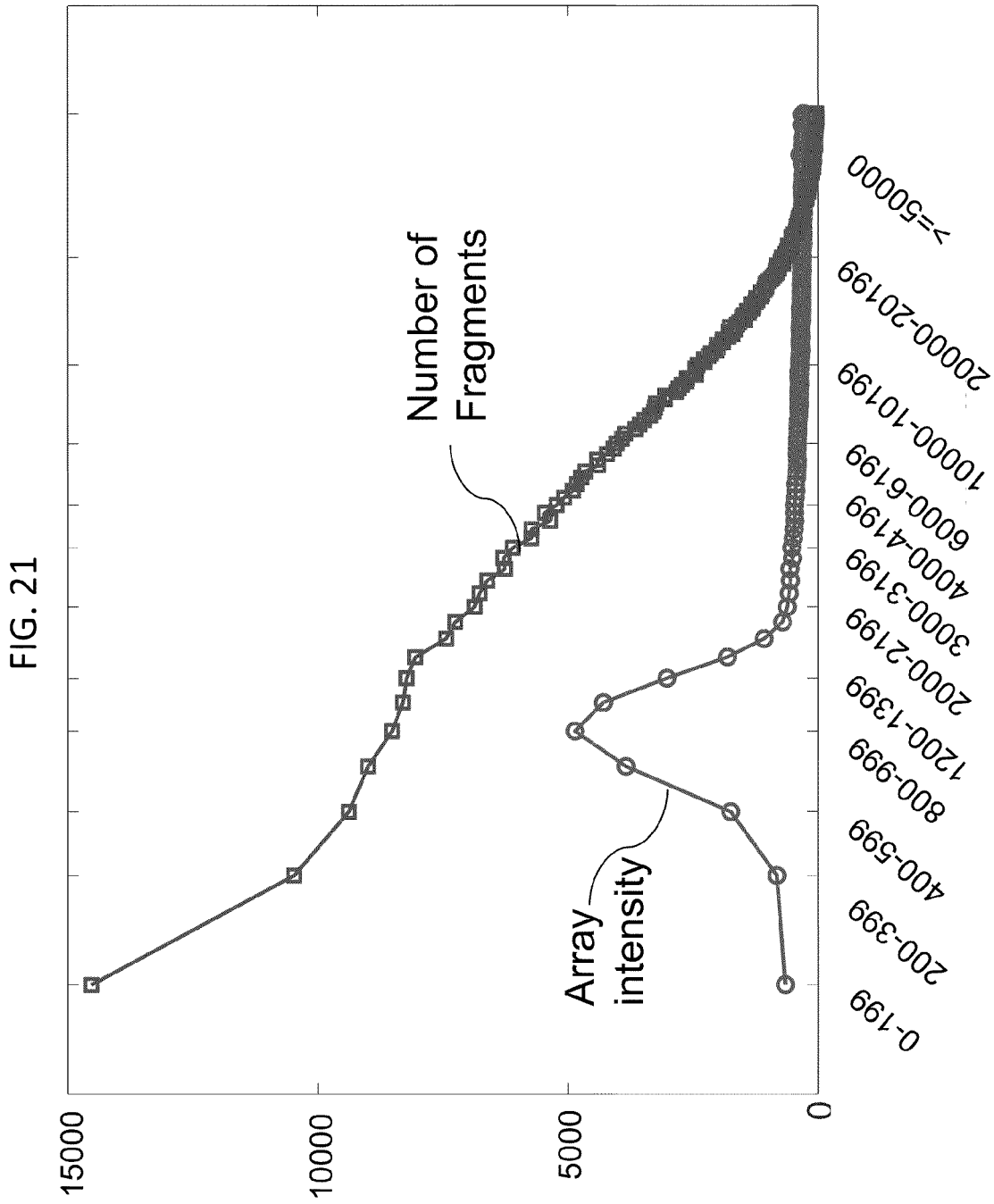

Number of Fragments
Array intensity
15000
10000
5000
0
0-199
200-399
400-599
800-999
1200-1399
2000-2199
3000-3199
4000-4199
6000-6199
10000-10199
20000-20199
>=50000

FIG. 21

FIG. 22

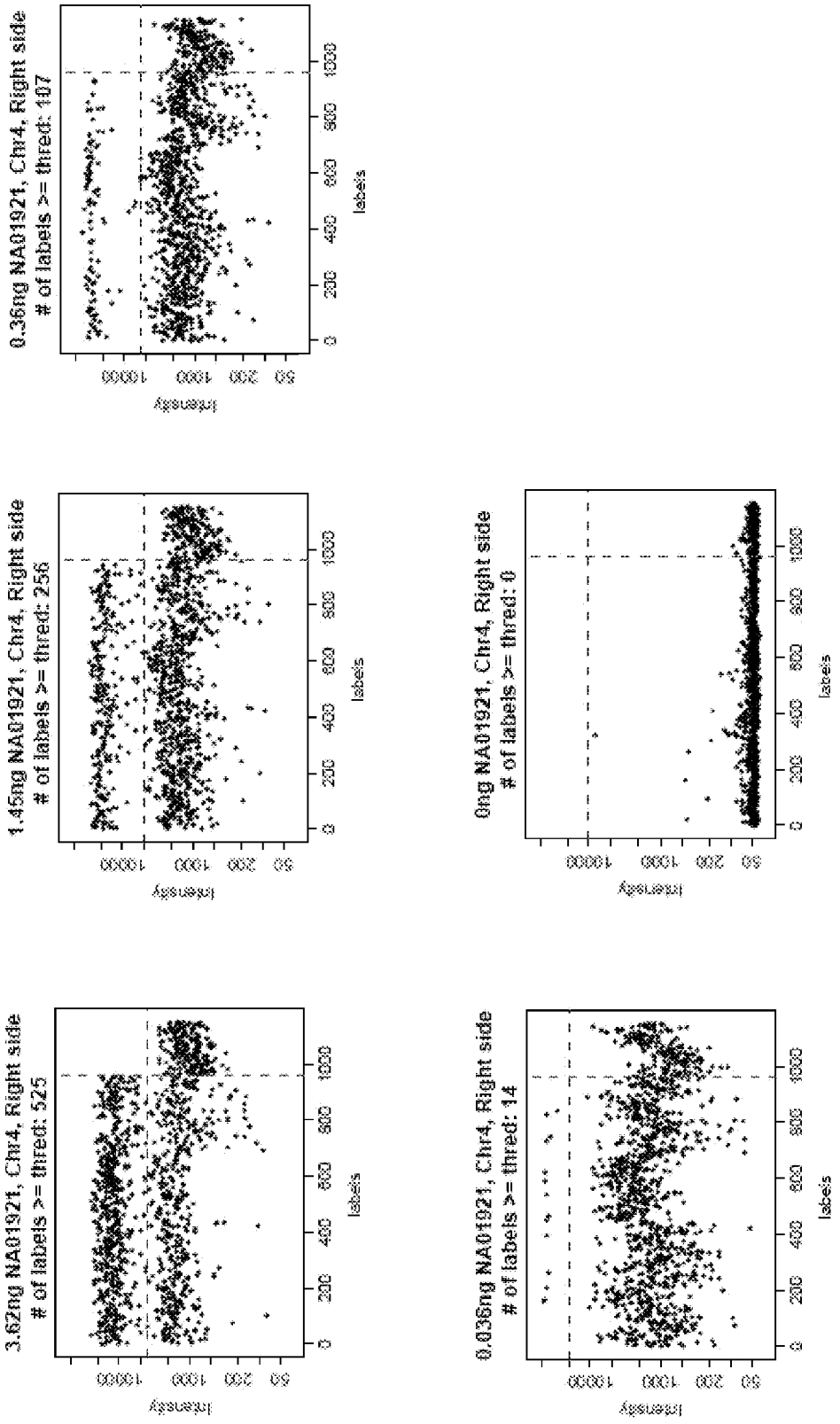

0.36ng NA01921, Chr4, Right side
of labels >= thred: 107
1.45ng NA01921, Chr4, Right side
of labels >= thred: 256
0ng NA01921, Chr4, Right side
of labels >= thred: 0
3.62ng NA01921, Chr4, Right side
of labels >= thred: 525
0.036ng NA01921, Chr4, Right side
of labels >= thred: 14
Intensity
labels

FIG. 23

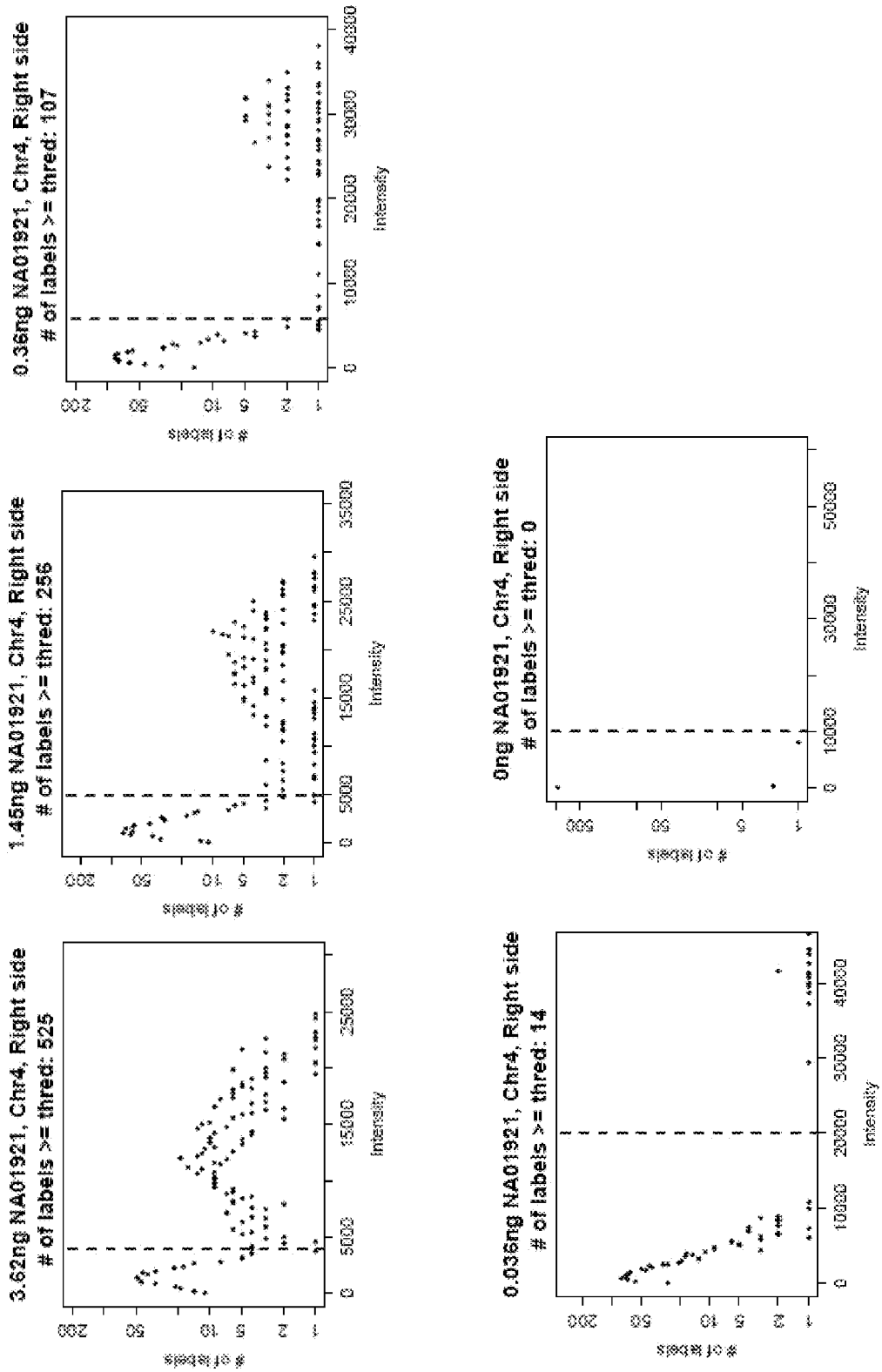

3.62ng NA01921, Chr4, Right side
of labels >= thred: 525
1.45ng NA01921, Chr4, Right side
of labels >= thred: 256
0.36ng NA01921, Chr4, Right side
of labels >= thred: 107
0ng NA01921, Chr4, Right side
of labels >= thred: 0
0.036ng NA01921, Chr4, Right side
of labels >= thred: 14
of labels
Intensity

FIG. 24

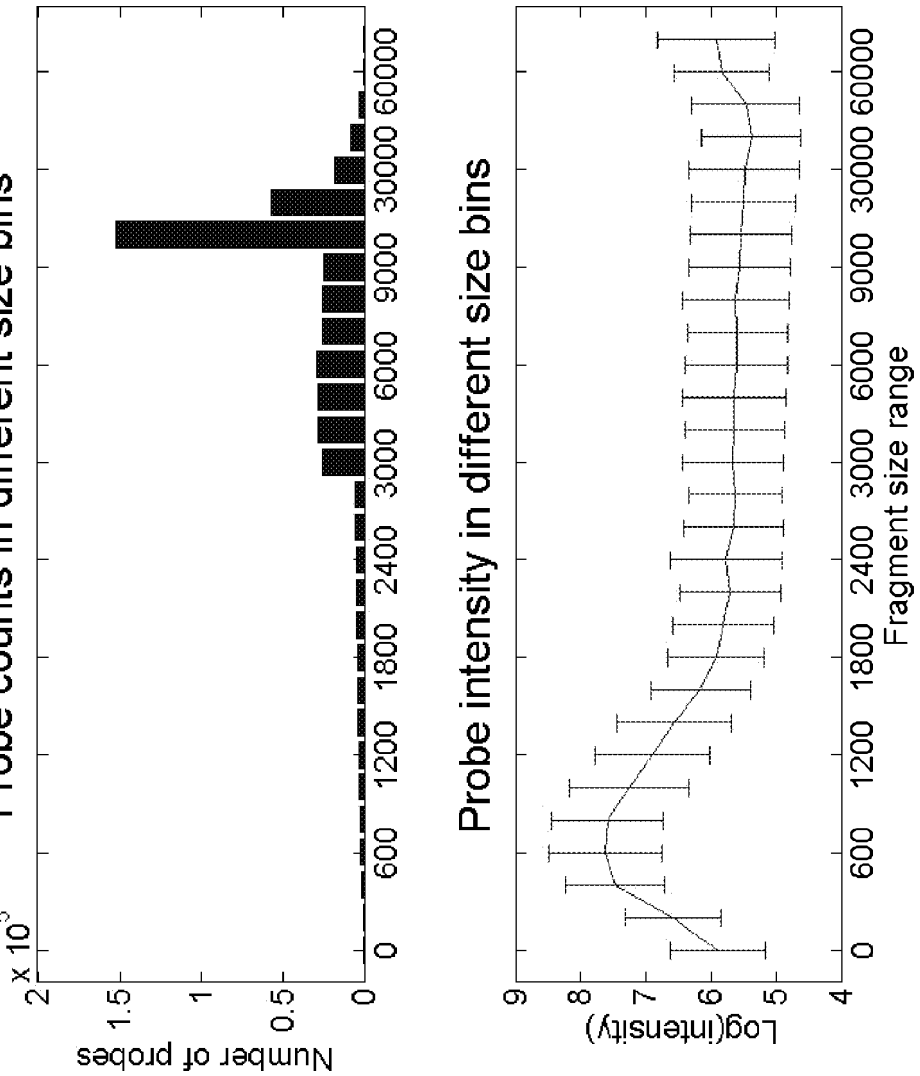
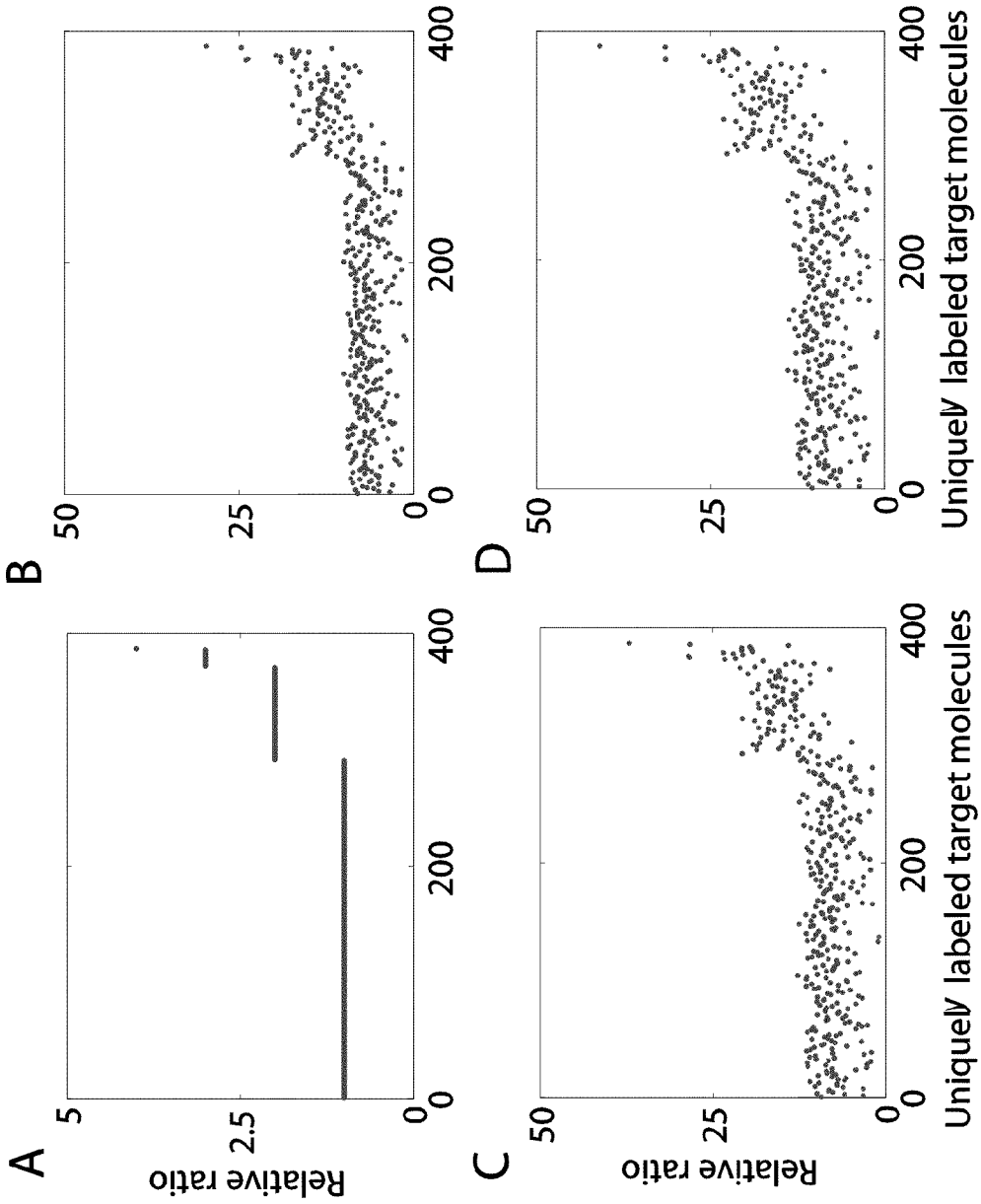

Probe counts in different size bins
Number of probes
x 10^5
2
1.5
1
0.5
0
0 600 1200 1800 2400 3000 6000 9000 30000 60000
Probe intensity in different size bins
Log(intensity)
9
8
7
6
5
4
0 600 1200 1800 2400 3000 6000 9000 30000 60000
Fragment size range

FIG. 25


A
B
C
D
Relative ratio
Uniquely labeled target molecules
0
200
400
0
25
50
2.5
5

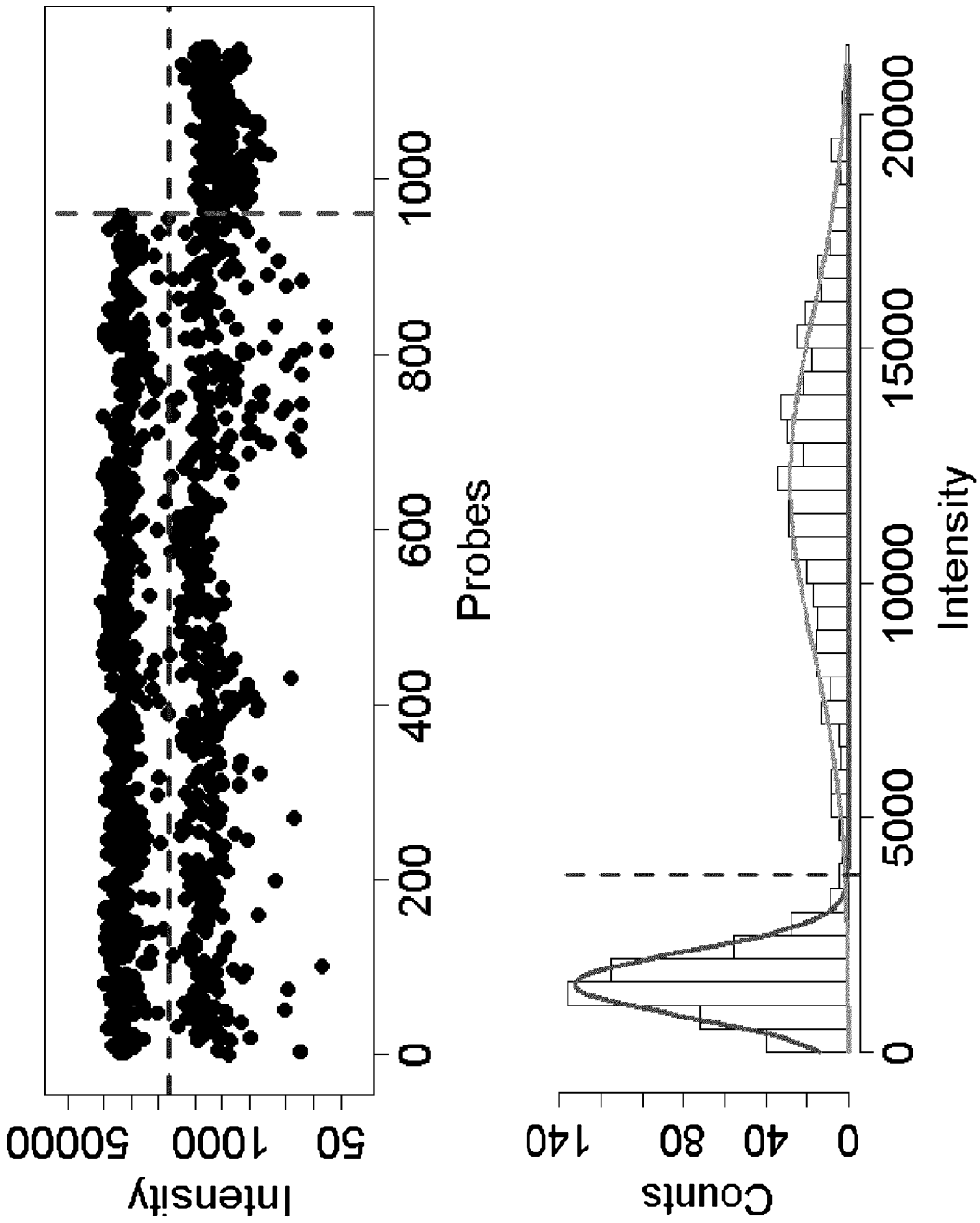

Intensity
50
1000
50000
Probes
0
200
400
600
800
1000
Counts
0
40
80
140
Intensity
0
5000
10000
15000
20000

FIG. 26

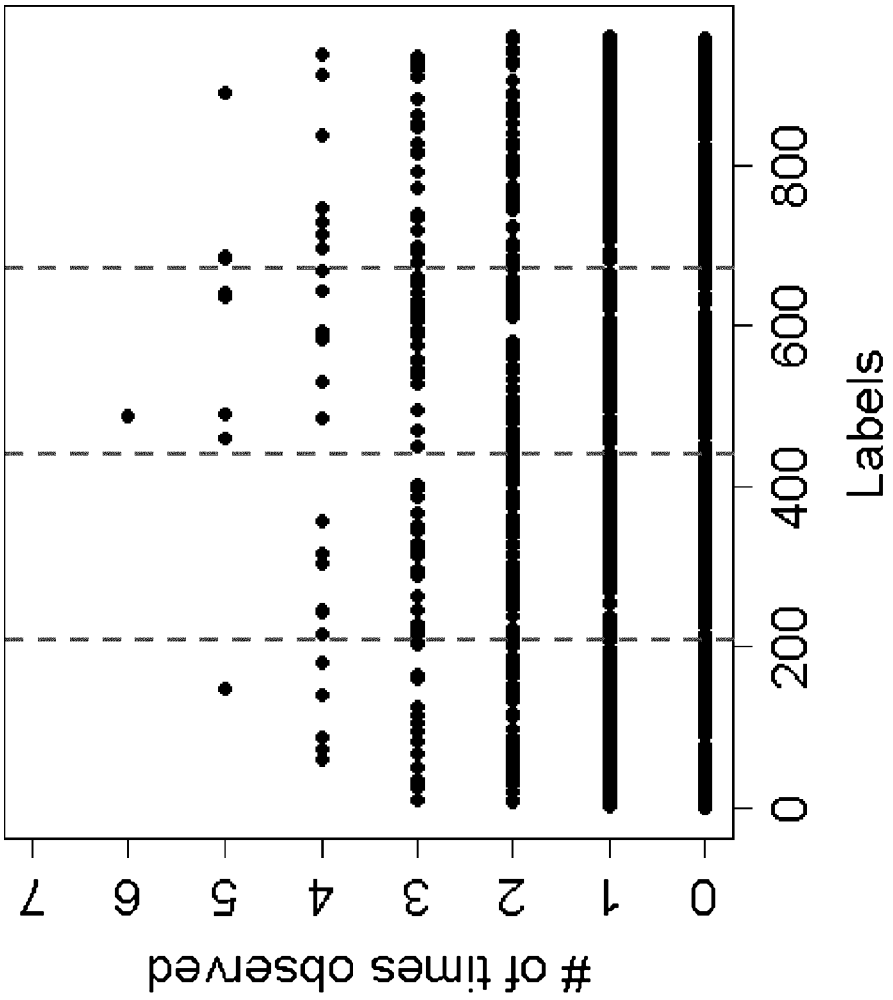


FIG. 27

FIG. 28

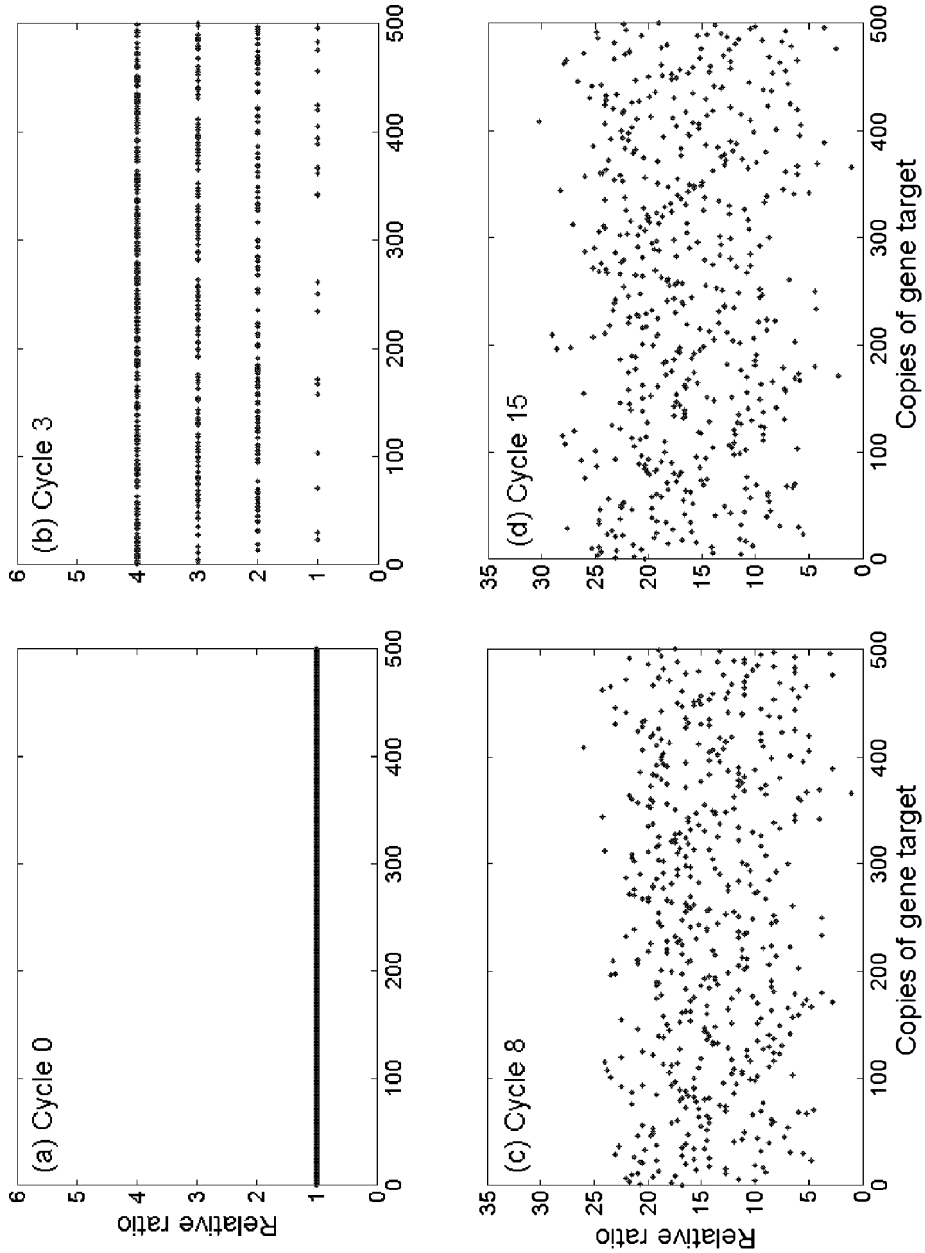
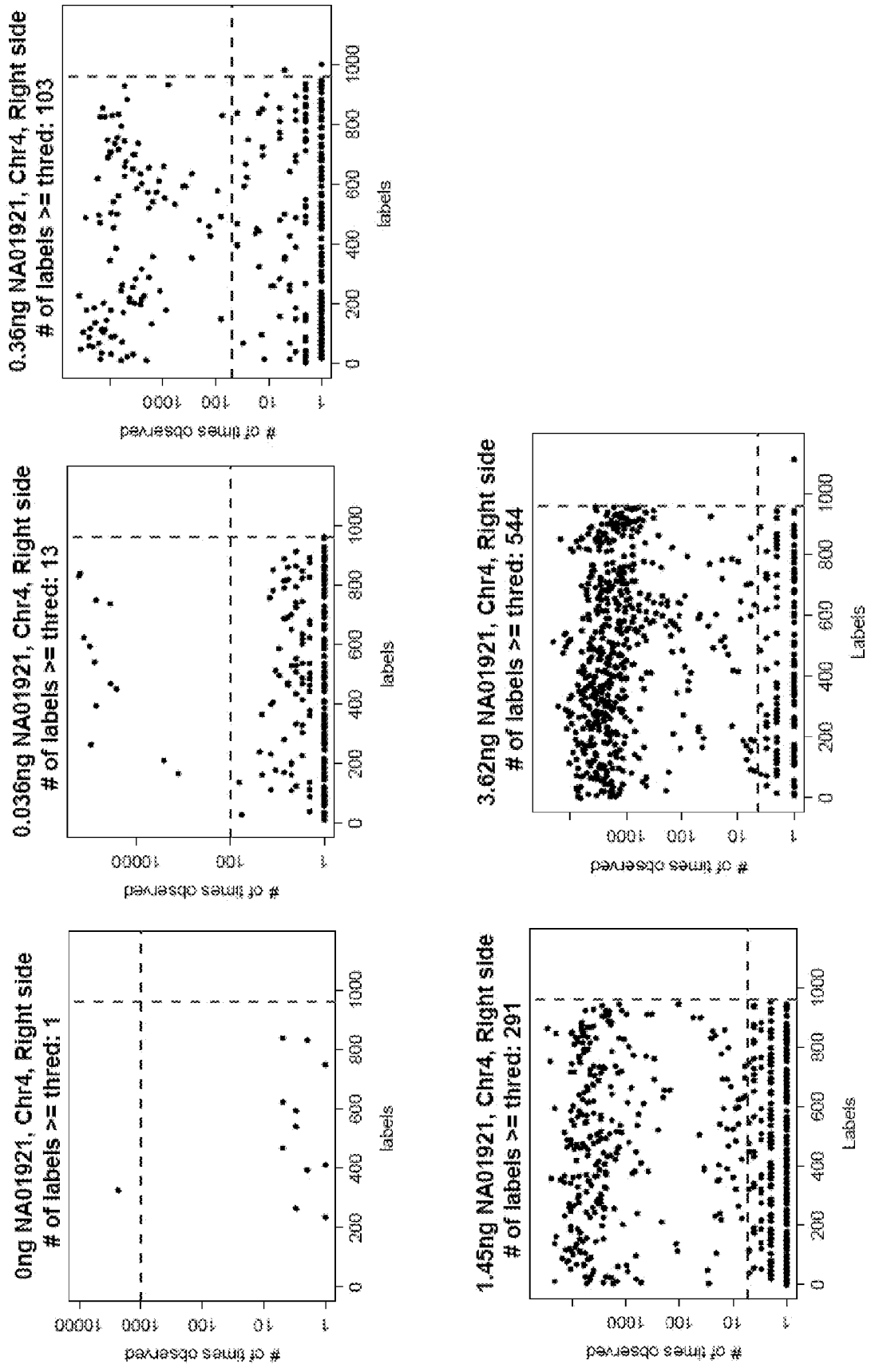

(a) Cycle 0
(b) Cycle 3
(c) Cycle 8
(d) Cycle 15
Relative ratio
Copies of gene target

Fig. 29


0ng NA01921, Chr4, Right side
of labels >= thred: 1
0.036ng NA01921, Chr4, Right side
of labels >= thred: 13
0.36ng NA01921, Chr4, Right side
of labels >= thred: 103
1.45ng NA01921, Chr4, Right side
of labels >= thred: 291
3.62ng NA01921, Chr4, Right side
of labels >= thred: 544
of times observed
labels
Labels

DIGITAL COUNTING OF INDIVIDUAL MOLECULES BY STOCHASTIC ATTACHMENT OF DIVERSE LABELS

RELATED APPLICATIONS

This application claims priority to U.S. Provisional application No. 61/286,768 filed Dec. 15, 2009, the entire disclosure of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

Methods, compositions and products for counting individual molecules by stochastic attachment of diverse labels from a set of labels, followed by amplification and detection are disclosed.

BACKGROUND OF THE INVENTION

Many processes are characterized or regulated by the absolute or relative amounts of a plurality of items. For example, in biology, the level of expression of particular genes or groups of genes or the number of copies of chromosomal regions can be used to characterize the status of a cell or tissue. Analog methods such as microarray hybridization methods and real-time PCR are alternatives, but digital readout methods such as those disclosed herein have advantages over analog methods. Methods for estimating the abundance or relative abundance of genetic material having increased accuracy of counting would be beneficial.

The availability of convenient and efficient methods for the accurate identification of genetic variation and expression patterns among large sets of genes may be applied to understanding the relationship between an organism's genetic make-up and the state of its health or disease, Collins et al, Science, 282: 682-689 (1998). In this regard, techniques have been developed for the analysis of large populations of polynucleotides based either on specific hybridization of probes to microarrays, e.g. Lockhart et al. Hacia et al, *Nature Genetics,* 21: 4247 (1999), or on the counting of tags or signatures of DNA fragments, e.g. Velculescu et al, *Science,* 270: 484487 (1995); Brenner et al, *Nature Biotechnology,* 18: 630-634 (2000). These techniques have been used in discovery research to identify subsets of genes that have coordinated patterns of expression under a variety of circumstances or that are correlated with, and predictive of events, of interest, such as toxicity, drug responsiveness, risk of relapse, and the like, e.g. Golub et al, *Science,* 286: 531-537 (1999); Alizadeh et al, *Nature,* 403: 503-511 (2000); Perou et al, *Nature,* 406: 747-752 (2000); Shipp et al, *Nature Medicine,* 8: 68-74 (2002); Hakak et al, *Proc. Natl. Acad. Sci.,* 98: 47454751 (2001); Thomas et al, *Mol. Pharmacol.,* 60: 1189-1194 (2001); De Primo et al, BMC Cancer 2003, 3:3; and the like. Not infrequently the subset of genes found to be relevant has a size in the range of from ten or under to a few hundred.

In addition to gene expression, techniques have also been developed to measure genome-wide variation in gene copy number. For example, in the field of oncology, there is interest in measuring genome-wide copy number variation of local regions that characterize many cancers and that may have diagnostic or prognostic implications. For a review see Zhang et al. *Annu. Rev. Genomics Hum. Genet.* 2009. 10:451-81.

While such hybridization-based techniques offer the advantages of scale and the capability of detecting a wide range of gene expression or copy number levels, such measurements may be subject to variability relating to probe

hybridization differences and cross-reactivity, element-to-element differences within microarrays, and microarray-to-microarray differences, Audic and Claverie, *Genomic Res.,* 7: 986-995 (1997); Wittes and Friedman, *J. Natl. Cancer Inst.* 91: 400-401 (1999).

On the other hand, techniques that provide digital representations of abundance, such as SAGE (Velculescu et al, cited above) or MPSS (Brenner et al, cited above), are statistically more robust; they do not require repetition or standardization of counting experiments as counting statistics are well-modeled by the Poisson distribution, and the precision and accuracy of relative abundance measurements may be increased by increasing the size of the sample of tags or signatures counted, e.g. Audic and Claverie (cited above).

Both digital and non-digital hybridization-based assays have been implemented using oligonucleotide tags that are hybridized to their complements, typically as part of a detection or signal generation schemes that may include solid phase supports, such as microarrays, microbeads, or the like, e.g. Brenner et al, Proc. Natl. Acad. Sci., 97: 1665-1670 (2000); Church et al, Science, 240: 185-188 (1988); Chee, *Nucleic Acids Research,* 19: 3301-3305 (1991); Shoemaker et al., *Nature Genetics,* 14: 450456 (1996); Wallace, U.S. Pat. No. 5,981,179; Gerry et al, *J. Mol. Biol.,* 292: 251-262 (1999); Fan et al., *Genome Research,* 10: 853-860 (2000); Ye et al., *Human Mutation,* 17: 305-316 (2001); and the like. Bacterial transcript imaging by hybridization of total RNA to nucleic acid arrays may be conducted as described in Saizieu et al., *Nature Biotechnology,* 16:45-48 (1998). Accessing genetic information using high density DNA arrays is further described in Chee et al., *Science* 274:610-614 (1996). Tagging approaches have also been used in combination with next-generation sequencing methods, see for example, Smith et al. NAR (May 11, 2010), 1-7.

A common feature among all of these approaches is a one-to-one correspondence between probe sequences and oligonucleotide tag sequences. That is, the oligonucleotide tags have been employed as probe surrogates for their favorable hybridizations properties, particularly under multiplex assay conditions.

Determining small numbers of biological molecules and their changes is essential when unraveling mechanisms of cellular response, differentiation or signal transduction, and in performing a wide variety of clinical measurements. Although many analytical methods have been developed to measure the relative abundance of different molecules through sampling (e.g., microarrays and sequencing), few techniques are available to determine the absolute number of molecules in a sample. This can be an important goal, for example in single cell measurements of copy number or stochastic gene expression, and is especially challenging when the number of molecules of interest is low in a background of many other species. As an example, measuring the relative copy number or expression level of a gene across a wide number of genes can currently be performed using PCR, hybridization to a microarray or by direct sequence counting. PCR and microarray analysis rely on the specificity of hybridization to identify the target of interest for amplification or capture respectively, then yield an analog signal proportional to the original number of molecules. A major advantage of these approaches is in the use of hybridization to isolate the specific molecules of interest within the background of many other molecules, generating specificity for the readout or detection step. The disadvantage is that the readout signal to noise is proportional to all molecules (specific and non-specific) specified by selective amplification or hybridization. The situation is reversed for sequence counting. No intended

sequence specificity is imposed in the sequence capture step, and all molecules are sequenced. The major advantage is that the detection step simply yields a digital list of those sequences found, and since there is no specificity in the isolation step, all sequences must be analyzed at a sufficient statistical depth in order to learn about a specific sequence. Although very major technical advances in sequencing speed and throughput have occurred, the statistical requirements imposed to accurately measure small changes in concentration of a specific gene within the background of many other sequences requires measuring many sequences that don't matter to find the ones that do matter. Each of these techniques, PCR, array hybridization and sequence counting is a comparative technique in that they primarily measure relative abundance, and do not typically yield an absolute number of molecules in a solution. A method of absolute counting of nucleic acids is digital PCR (B. Vogelstein, K. W. Kinzler, *Proc Natl Acad Sci USA* 96, 9236 (Aug. 3, 1999)), where solutions are progressively diluted into individual compartments until there is an average probability of one molecule per two wells, then detected by PCR. Although digital PCR can be used as a measure of absolute abundance, the dilutions must be customized for each type of molecule, and thus in practice is generally limited to the analysis of a small number of different molecules.

SUMMARY OF THE INVENTION

High-sensitivity single molecule digital counting by the stochastic labeling of a collection of identical molecules is disclosed. Each copy of a molecule randomly chooses from a non-depleting reservoir of diverse labels. The uniqueness of each labeled molecule is determined by the statistics of random choice, and depends on the number of copies of identical molecules in the collection compared to the diversity of labels. The size of the resulting set of labeled molecules is determined by the stochastic nature of the labeling process, and analysis reveals the original number of molecules. When the number of copies of a molecule to the diversity of labels is low, the labeled molecules are highly unique, and the digital counting efficiency is high. This stochastic transformation relaxes the problem of counting molecules from one of locating and identifying identical molecules to a series of yes/no digital questions detecting whether preprogrammed labels are present. The conceptual framework for stochastic mapping of a variety of molecule types is developed and the utility of the methods are demonstrated by stochastically labeling 360,000 different fragments of the human genome. The labeled fragments for a target molecule of choice are detected with high specificity using a microarray readout system, and with DNA sequencing. The results are consistent with a stochastic process, and yield highly precise relative and absolute counting statistics of selected molecules within a vast background of other molecules.

Methods are disclosed herein for digital counting of individual molecules of one or more targets. In preferred embodiments the targets are nucleic acids, but may be a variety of biological or non-biological elements. Targets are labeled so that individual occurrences of the same target are marked by attachment of a different label to difference occurrences. The attachment of the label confers a separate, determinable identity to each occurrence of targets that may otherwise be indistinguishable. Preferably the labels are different sequences that tag or mark each target occurrence uniquely. The resulting modified target comprises the target sequence and the unique identifier (which may be referred to herein as tag, counter, label, or marker). The junction of the target and identifier forms a uniquely detectable mechanism for counting the occurrence of that copy of the target. The attachment of the identifier to each occurrence of the target is a random sampling event. Each occurrence of target could choose any of the labels. Each identifier is present in multiple copies so selection of one copy does not remove that identifier sequence from the pool of identifiers so it is possible that the same identifier will be selected twice. The probability of that depends on the number of target occurrences relative to the number of different identifier sequences.

Each stochastic attachment event, where a target occurrence is attached to a unique identifier, results in the creation of a novel sequence formed at the junction of the identifier and the target. For a given target, all resulting products will contain the same target portion, but each will contain a different identifier sequence (T1L1, T1L2, . . . T1LN where N is the number of different occurrences of target1, "T1" and L is the identifier, L1, L2 . . . LN). In preferred aspects the occurrences are detected by hybridization. In some aspects the methods and systems include a probe array comprising features, wherein each feature has a different combination of target sequence with identifiers, 1 to N wherein N is the number of unique identifiers in the pool of identifiers. The array has N features for each target, so if there are 8 targets to be analyzed there are 8 times N features on the array to interrogate the 8 targets.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** is a schematic of a method of stochastic labeling and counting by hybridization to an array of support bound probes.

FIG. **2**A shows a schematic of labeling target molecules with a pool of labels.

FIG. **2**B shows a schematic of detection of labeled targets on an array having features that are label specific and target specific.

FIG. **3** shows a schematic of a method for circularizing targets and amplifying with gene specific primers.

FIG. **4** shows a schematic of a method for detection of ligation products by hybridization to array probes that are complementary to the sequence resulting from the ligation.

FIG. **5** shows a schematic of a method for target preparation.

FIG. **6** shows a method for stochastic counting by fragmentation where the unique end of the fragment is the label used for counting.

FIG. **7** provides an example of a genomic target ligated at either end to a label adaptor.

FIG. **8** shows a schematic of the arrangement and position of the adaptors, PCR primers, and the biotinylated array-ligation probe in one exemplary sample prep method.

FIG. **9** is a schematic of a method for using ligation based read out on arrays to detect labeled targets and minimize partial target hybridization.

FIG. **10** shows the arrangement of the adaptors, labels and primers used to convert the labeled sample into sequencing template.

FIG. **11** is a plot of the number of labels from a non-depleting reservoir of 960 labels that are predicted to be captured at least once, exactly once or exactly twice.

FIG. **12** is a plot of counting results for 4 different DNA copy number titrations using microarray hybridization (on left) or DNA sequencing (on right).

FIG. **13** shows relative copy ratios of three tested gene targets representing copy number 1, 2 or 3 at different dilutions as analyzed using the disclosed methods.

FIG. **14** shows a comparison between experimentally observed label usage with those predicted from stochastic modeling.

FIG. **15** shows a plot of the expected label usage (y-axis) when ligating to a given number of target molecules (x-axis).

FIG. **16** shows a plot of number of target molecules (x-axis) compared to counting efficiency (y-axis).

FIG. **17** shows a schematic of a method for attaching labels to targets using a splint having a variable region.

FIG. **18** shows a schematic of a method for enriching for molecules that contain labels, target or both.

FIG. **19** shows a scatter plot of a series of different target plus label combinations.

FIG. **20** shows a plot of counting efficiency versus copies of target as the number of labels varies. The inset is a magnification of the upper left portion of the graph.

FIG. **21** is a plot of the array intensity observed for fragments in a given size range compared to the number of fragments in a given size range when fragments are binned according to size.

FIG. **22** shows labels observed by microarray hybridization plotted against intensity (y-axis) for each of 960 labels for the chromosome 4 gene target.

FIG. **23** shows frequency plots (y-axis, log-scale) of intensity distributions of the 960 labels in the microarray experiments with the counting threshold applied indicated by the dashed line.

FIG. **24** shows plots showing fragment size distribution and mean raw intensity on chromosome 22 tiling probes on the "CNVtype" array.

FIG. **25** shows a simulated PCR run showing the replication outcome for 500 molecules of a target fragment ligated to a library of 960 label counters.

FIG. **26** shows intensities of 1,152 array probes associated with a single gene target on chromosome 4 in the upper panel and a histogram of the intensity data corresponding to 960 labels in the lower panel.

FIG. **27** shows a plot of the number of times each of the 960 labels was observed in ligations with low DNA target amounts.

FIG. **28** shows an example of a replication process on a collection of 390 uniquely labeled target molecules resulting from 960 diverse labels independently marked with 500 copies of a target molecule.

FIG. **29** shows plots of labels observed in the mapped reads from the first sequencing run for chromosome 4 with the horizontal dashed line indicating the counting threshold applied and the vertical dashed line indicating the break separating the 192 negative controls from the expected labels (controls to the right of the line).

DETAILED DESCRIPTION OF THE INVENTION

Reference will now be made in detail to exemplary embodiments of the invention. While the invention will be described in conjunction with the exemplary embodiments, it will be understood that they are not intended to limit the invention to these embodiments. On the contrary, the invention is intended to cover alternatives, modifications and equivalents, which may be included within the spirit and scope of the invention.

The invention has many preferred embodiments and relies on many patents, applications and other references for details known to those of the art. Therefore, when a patent, application, or other reference, such as a printed publication, is cited or repeated below, it should be understood that it is incorporated by reference in its entirety for all purposes and particularly for the proposition that is recited.

As used in this application, the singular form "a," "an," and "the" include plural references unless the context clearly dictates otherwise. For example, the term "an agent" includes a plurality of agents, including mixtures thereof.

An individual is not limited to a human being, but may also be other organisms including, but not limited to, mammals, plants, bacteria, or cells derived from any of the above.

Throughout this disclosure, various aspects of this invention can be presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the invention. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 3, 4, 5, and 6. This applies regardless of the breadth of the range.

The practice of the present invention may employ, unless otherwise indicated, conventional techniques and descriptions of organic chemistry, polymer technology, molecular biology (including recombinant techniques), cell biology, biochemistry, and immunology, which are within the skill of the art. Such conventional techniques include polymer array synthesis, hybridization, ligation, and detection of hybridization using a label. Specific illustrations of suitable techniques can be had by reference to the example herein below. However, other equivalent conventional procedures can, of course, also be used. Such conventional techniques and descriptions can be found in standard laboratory manuals such as *Genome Analysis: A Laboratory Manual Series* (*Vols. I-IV*), *Using Antibodies: A Laboratory Manual, Cells: A Laboratory Manual, PCR Primer: A Laboratory Manual*, and Molecular *Cloning: A Laboratory Manual* (all from Cold Spring Harbor Laboratory Press), *Gait, "Oligonucleotide Synthesis: A Practical Approach"* 1984, *IRL Press, London*, Nelson and Cox (2000), Lehninger et al., (2008) *Principles of Biochemistry* 5th Ed., W.H. Freeman Pub., New York, N.Y. and Berg et al. (2006) *Biochemistry,* 6th Ed., W.H. Freeman Pub., New York, N.Y., all of which are herein incorporated in their entirety by reference for all purposes.

The present invention can employ solid substrates, including arrays in some preferred embodiments. Methods and techniques applicable to polymer (including protein) array synthesis have been described in U.S. Patent Pub. No. 20050074787, WO 00/58516, U.S. Pat. Nos. 5,143,854, 5,242,974, 5,252,743, 5,324,633, 5,384,261, 5,405,783, 5,424,186, 5,451,683, 5,482,867, 5,491,074, 5,527,681, 5,550,215, 5,571,639, 5,578,832, 5,593,839, 5,599,695, 5,624,711, 5,631,734, 5,795,716, 5,831,070, 5,837,832, 5,856,101, 5,858,659, 5,936,324, 5,968,740, 5,974,164, 5,981,185, 5,981,956, 6,025,601, 6,033,860, 6,040,193, 6,090,555, 6,136,269, 6,269,846 and 6,428,752, in PCT Publication No. WO 99/36760 and WO 01/58593, which are all incorporated herein by reference in their entirety for all purposes.

Patents that describe synthesis techniques in specific embodiments include U.S. Pat. Nos. 5,412,087, 6,147,205, 6,262,216, 6,310,189, 5,889,165, and 5,959,098. Nucleic acid arrays are described in many of the above patents, but the same techniques may be applied to polypeptide arrays.

The present invention also contemplates many uses for polymers attached to solid substrates. These uses include gene expression monitoring, profiling, library screening, genotyping and diagnostics. Gene expression monitoring and profiling methods can be shown in U.S. Pat. Nos. 5,800,992, 6,013,449, 6,020,135, 6,033,860, 6,040,138, 6,177,248 and 6,309,822. Genotyping and uses therefore are shown in U.S. Patent Publication Nos. 20030036069 and 20070065816 and U.S. Pat. Nos. 5,856,092, 6,300,063, 5,858,659, 6,284,460, 6,361,947, 6,368,799 and 6,333,179. Other uses are embodied in U.S. Pat. Nos. 5,871,928, 5,902,723, 6,045,996, 5,541,061, and 6,197,506.

The present invention also contemplates sample preparation methods in certain embodiments. Prior to or concurrent with analysis, the sample may be amplified by a variety of mechanisms. In some aspects nucleic acid amplification methods such as PCR may be combined with the disclosed methods and systems. See, for example, *PCR Technology: Principles and Applications for DNA Amplification* (Ed. H. A. Erlich, Freeman Press, NY, N.Y., 1992); *PCR Protocols: A Guide to Methods and Applications* (Eds. Innis, et al., Academic Press, San Diego, Calif., 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (Eds. McPherson et al., IRL Press, Oxford); and U.S. Pat. Nos. 4,683,202, 4,683,195, 4,800,159, 4,965,188, and 5,333,675, each of which is incorporated herein by reference in their entireties for all purposes. Enzymes and related methods of use in molecular biology that may be used in combination with the disclosed methods and systems are reviewed, for example, in Rittie and Perbal, *J. Cell Commun. Signal.* (2008) 2:25-45. The sample may be amplified on the array. See, for example, U.S. Pat. No. 6,300,070 and which is incorporated herein by reference in its entirety for all purposes.

Many of the methods and systems disclosed herein utilize enzyme activities. A variety of enzymes are well known, have been characterized and many are commercially available from one or more supplier. For a review of enzyme activities commonly used in molecular biology see, for example, Rittie and Perbal, *J. Cell Commun. Signal.* (2008) 2:25-45, incorporated herein by reference in its entirety. Exemplary enzymes include DNA dependent DNA polymerases (such as those shown in Table 1 of Rittie and Perbal), RNA dependent DNA polymerase (see Table 2 of Rittie and Perbal), RNA polymerases, ligases (see Table 3 of Rittie and Perbal), enzymes for phosphate transfer and removal (see Table 4 of Rittie and Perbal), nucleases (see Table 5 of Rittie and Perbal), and methylases.

Other methods of genome analysis and complexity reduction include, for example, AFLP, see U.S. Pat. No. 6,045,994, which is incorporated herein by reference, and arbitrarily primed-PCR (AP-PCR) see McClelland and Welsh, in *PCR Primer: A laboratory Manual*, (1995) eds. C. Dieffenbach and G. Dveksler, Cold Spring Harbor Lab Press, for example, at p 203, which is incorporated herein by reference in its entirety. Additional methods of sample preparation and techniques for reducing the complexity of a nucleic sample are described in Dong et al., *Genome Research* 11, 1418 (2001), in U.S. Pat. Nos. 6,361,947, 6,391,592, 6,458,530 and U.S. Patent Publication Nos. 20030039069, 20050079536, 20030096235, 20030082543, 20040072217, 20050142577, 20050233354, 20050227244, 20050208555, 20050074799, 20050042654 and 20040067493, which are each incorporated herein by reference in their entireties.

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, and WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals.

Sample preparation methods are also contemplated in many embodiments. Prior to or concurrent with analysis, the genomic sample may be amplified by a variety of mechanisms, some of which may employ PCR. See, e.g., *PCR Technology: Principles and Applications for DNA Amplification* (Ed. H. A. Erlich, Freeman Press, NY, N.Y., 1992); *PCR Protocols: A Guide to Methods and Applications* (Eds. Innis, et al., Academic Press, San Diego, Calif., 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (Eds. McPherson et al., IRL Press, Oxford); and U.S. Pat. Nos. 4,683,202, 4,683,195, 4,800,159 4,965,188, and 5,333,675, and each of which is incorporated herein by reference in their entireties for all purposes. See also U.S. Pat. No. 6,300,070 which is incorporated herein by reference. Additional methods of sample preparation and techniques for reducing the complexity of a nucleic sample are described in Dong et al., *Genome Research* 11, 1418 (2001), in U.S. Pat. Nos. 6,361,947, 6,391,592 and U.S. Patent Pub. Nos. 20030096235, 20030082543 and 20030036069.

Other suitable amplification methods include the ligase chain reaction (LCR) (for example, Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988) and Barringer et al. *Gene* 89:117 (1990)), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989) and W088/10315), self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA,* 87, 1874 (1990) and WO90/06995), selective amplification of target polynucleotide sequences (U.S. Pat. No. 6,410,276), consensus sequence primed polymerase chain reaction (CP-PCR) (U.S. Pat. No. 4,437,975), arbitrarily primed polymerase chain reaction (AP-PCR) (U.S. Pat. Nos. 5,413,909, 5,861,245), rolling circle amplification (RCA) (for example, Fire and Xu, PNAS 92:4641 (1995) and Liu et al., J. Am. Chem. Soc. 118:1587 (1996)) and nucleic acid based sequence amplification (NABSA). (See, U.S. Pat. Nos. 5,409,818, 5,554,517, and 6,063,603, each of which is incorporated herein by reference). Other amplification methods that may be used are described in, U.S. Pat. Nos. 6,582,938, 5,242,794, 5,494,810, 4,988,617, and US Pub. No. 20030143599 each of which is incorporated herein by reference.

Molecular inversion probes may also be used for amplification of selected targets. MIPs may be generated so that the ends of the pre-circle probe are complementary to regions that flank the region to be amplified. The gap can be closed by extension of the end of the probe so that the complement of the target is incorporated into the MIP prior to ligation of the ends to form a closed circle. The closed circle can be amplified as previously disclosed in Hardenbol et al., *Genome Res.* 15:269-275 (2005) and in U.S. Pat. No. 6,858,412.

In some embodiments, amplification may include the use of a strand displacing polymerase that may be primed by selected primers or by a mixture of primers, for example, random hexamers. See for example Lasken and Egholm, *Trends Biotechnol.* 2003 21(12):531-5; Barker et al. *Genome Res.* 2004 May; 14(5):901-7; Dean et al. *Proc Natl Acad Sci USA.* 2002; 99(8):5261-6; and Paez, J. G., et al. *Nucleic Acids Res.* 2004; 32(9):e71. Other amplification methods that may be used include: Qbeta Replicase, described in PCT Patent Application No. PCT/US87/00880, isothermal amplification methods such as SDA, described in Walker et al. 1992, Nucleic Acids Res. 20(7):1691-6, 1992, and rolling circle

amplification, described in U.S. Pat. No. 5,648,245. DNA may also be amplified by multiplex locus-specific PCR or using adaptor-ligation and single primer PCR. Other available methods of amplification, such as balanced PCR (Makrigiorgos, et al. (2002), *Nat Biotechnol, Vol.* 20, pp. 936-9), may also be used.

Methods of ligation will be known to those of skill in the art and are described, for example in Sambrook et at. (2001) and the New England BioLabs catalog both of which are incorporated herein by reference for all purposes. Methods include using T4 DNA Ligase which catalyzes the formation of a phosphodiester bond between juxtaposed 5' phosphate and 3' hydroxyl termini in duplex DNA or RNA with blunt and sticky ends; Taq DNA Ligase which catalyzes the formation of a phosphodiester bond between juxtaposed 5' phosphate and 3' hydroxyl termini of two adjacent oligonucleotides which are hybridized to a complementary target DNA; *E. coli* DNA ligase which catalyzes the formation of a phosphodiester bond between juxtaposed 5'-phosphate and 3'-hydroxyl termini in duplex DNA containing cohesive ends; and T4 RNA ligase which catalyzes ligation of a 5' phosphoryl-terminated nucleic acid donor to a 3' hydroxyl-terminated nucleic acid acceptor through the formation of a 3'->5' phosphodiester bond, substrates include single-stranded RNA and DNA as well as dinucleoside pyrophosphates; or any other methods described in the art. Fragmented DNA may be treated with one or more enzymes, for example, an endonuclease, prior to ligation of adaptors to one or both ends to facilitate ligation by generating ends that are compatible with ligation.

Fixed content mapping arrays are available from Affymetrix, for example, the SNP 6.0 array. Methods for using mapping arrays see, for example, Kennedy et al., *Nat. Biotech.* 21:1233-1237 (2003), Matsuzaki et al., *Genome Res.* 14:414-425 (2004), Matsuzaki et al., *Nat. Meth.* 1:109-111 (2004) and U.S. Patent Pub. Nos. 20040146890 and 20050042654, each incorporated herein by reference. Applications of microarrays for SNP genotyping have been described in e.g., U.S. Pat. Nos. 6,300,063, 6,361,947, 6,368,799 and US Patent Publication Nos. 20040067493, 20030232353, 20030186279, 20050260628, 20070065816 and 20030186280, all incorporated herein by reference in their entireties for all purposes.

Selected panels of SNPs can also be interrogated using a panel of locus specific probes in combination with a universal array as described in Hardenbol et al., *Genome Res.* 15:269-275 (2005) and in U.S. Pat. No. 6,858,412. Universal tag arrays and reagent kits for performing such locus specific genotyping using panels of custom molecular inversion probes (MIPs) are available from Affymetrix.

Computer implemented methods for determining genotype using data from mapping arrays are disclosed, for example, in Liu, et al., *Bioinformatics* 19:2397-2403 (2003), Rabbee and Speed, *Bioinformatics,* 22:7-12 (2006), and Di et al., *Bioinformatics* 21:1958-63 (2005). Computer implemented methods for linkage analysis using mapping array data are disclosed, for example, in Ruschendorf and Nurnberg, *Bioinformatics* 21:2123-5 (2005) and Leykin et al., *BMC Genet.* 6:7, (2005). Computer methods for analysis of genotyping data are also disclosed in U.S. Patent Pub. Nos. 20060229823, 20050009069, 20040138821, 20060024715, 20050250151 and 20030009292.

Methods for analyzing chromosomal copy number using mapping arrays are disclosed, for example, in Bignell et al., *Genome Res.* 14:287-95 (2004), Lieberfarb, et al., *Cancer Res.* 63:4781-4785 (2003), Zhao et al., *Cancer Res.* 64:3060-71 (2004), Huang et al., *Hum Genomics* 1:287-299 (2004), Nannya et al., *Cancer Res.* 65:6071-6079 (2005), Slater et al., *Am. J. Hum. Genet.* 77:709-726 (2005) and Ishikawa et al., *Biochem. and Biophys. Res. Comm.,* 333:1309-1314 (2005). Computer implemented methods for estimation of copy number based on hybridization intensity are disclosed in U.S. Patent Pub. Nos. 20040157243, 20050064476, 20050130217, 20060035258, 20060134674 and 20060194243.

Additional methods of sample preparation and techniques for reducing the complexity of a nucleic sample are described in Dong et al., *Genome Research* 11, 1418 (2001), in U.S. Pat. Nos. 6,361,947, 6,391,592 and 6,872,529 and U.S. Patent Publication Nos. 20030036069, 20030096235 and 20030082543. Additional methods of using a genotyping array are disclosed, for example, in U.S. Patent Publication Nos. 20040146883, 20030186280, 20030186279, 20040067493, 20030232353, 20060292597, 20050233354, 20050074799, 20070065816 and 20040185475.

Methods for conducting polynucleotide hybridization assays have been well developed in the art. Hybridization assay procedures and conditions will vary depending on the application and are selected in accordance with known general binding methods, including those referred to in: Maniatis et al. *Molecular Cloning: A Laboratory Manual* (2nd Ed. Cold Spring Harbor, N.Y., 1989); Berger and Kimmel *Methods in Enzymology, Vol.* 152, *Guide to Molecular Cloning Techniques* (Academic Press, Inc., San Diego, Calif., 1987); Young and Davis, *P.N.A.S,* 80: 1194 (1983). Methods and apparatus for carrying out repeated and controlled hybridization reactions have been described in U.S. Pat. Nos. 5,871,928, 5,874,219, 6,045,996 and 6,386,749, 6,391,623 each of which are incorporated herein by reference.

The present invention also contemplates signal detection of hybridization between ligands in certain preferred embodiments. See U.S. Pat. Nos. 5,143,854, 5,578,832, 5,631,734, 5,834,758, 5,936,324, 5,981,956, 6,025,601, 6,141,096, 6,185,030, 6,201,639, 6,218,803, and 6,225,625 in U.S. Patent Pub. No. 20040012676 and in PCT Application PCT/US99/06097 (published as WO99/47964), each of which also is hereby incorporated by reference in its entirety for all purposes.

Methods and apparatus for signal detection and processing of intensity data are disclosed in, for example, U.S. Pat. Nos. 5,143,854, 5,547,839, 5,578,832, 5,631,734, 5,800,992, 5,834,758, 5,856,092, 5,902,723, 5,936,324, 5,981,956, 6,025,601, 6,090,555, 6,141,096, 6,185,030, 6,201,639; 6,218,803; and 6,225,625, in U.S. Patent Pub. Nos. 20040012676 and 20050059062 and in PCT Application PCT/US99/06097 (published as WO99/47964), each of which also is hereby incorporated by reference in its entirety for all purposes.

The practice of the present invention may also employ conventional biology methods, software and systems. Computer software products of the invention typically include computer readable medium having computer-executable instructions for performing the logic steps of the method of the invention. Suitable computer readable medium include floppy disk, CD-ROM/DVD/DVD-ROM, hard-disk drive, flash memory, ROM/RAM, magnetic tapes, etc. The computer-executable instructions may be written in a suitable computer language or combination of several languages. Basic computational biology methods are described in, for example, Setubal and Meidanis et al., *Introduction to Computational Biology Methods* (PWS Publishing Company, Boston, 1997); Salzberg, Searles, Kasif, (Ed.), *Computational Methods in Molecular Biology*, (Elsevier, Amsterdam, 1998); Rashidi and Buehler, *Bioinformatics Basics: Applica-*

tion in Biological Science and Medicine (CRC Press, London, 2000) and Ouelette and Bzevanis *Bioinformatics: A Practical Guide for Analysis of Gene and Proteins* (Wiley & Sons, Inc., 2nd ed., 2001). See U.S. Pat. No. 6,420,108.

The present invention may also make use of various computer program products and software for a variety of purposes, such as probe design, management of data, analysis, and instrument operation. See, U.S. Pat. Nos. 5,593,839, 5,795,716, 5,733,729, 5,974,164, 6,066,454, 6,090,555, 6,185,561, 6,188,783, 6,223,127, 6,229,911 and 6,308,170. Computer methods related to genotyping using high density microarray analysis may also be used in the present methods, see, for example, US Patent Pub. Nos. 20050250151, 20050244883, 20050108197, 20050079536 and 20050042654.

Additionally, the present disclosure may have preferred embodiments that include methods for providing genetic information over networks such as the Internet as shown in U.S. Patent Pub. Nos. 20030097222, 20020183936, 20030100995, 20030120432, 20040002818, 20040126840, and 20040049354.

An allele refers to one specific form of a genetic sequence (such as a gene) within a cell, an individual or within a population, the specific form differing from other forms of the same gene in the sequence of at least one, and frequently more than one, variant sites within the sequence of the gene. The sequences at these variant sites that differ between different alleles are termed "variances", "polymorphisms", or "mutations". At each autosomal specific chromosomal location or "locus" an individual possesses two alleles, one inherited from one parent and one from the other parent, for example one from the mother and one from the father. An individual is "heterozygous" at a locus if it has two different alleles at that locus. An individual is "homozygous" at a locus if it has two identical alleles at that locus.

Single nucleotide polymorphisms (SNPs) are positions at which two alternative bases occur at appreciable frequency (>1%) in a given population. SNPs are a common type of human genetic variation and are useful in the performance of genome wide association studies (GWAS). GWAS may be used, for example for the analysis of biological pathways, see Wang and Hakonarson, Nat. Rev. Genet. 2010, 11:843-854. Other common variation includes single base deletions or insertions of a nucleotide relative to a reference allele. Copy number variants (CNVs), transversions and other rearrangements are also forms of genetic variation.

The term genotyping refers to the determination of the genetic information an individual carries at one or more positions in the genome. For example, genotyping may comprise the determination of which allele or alleles an individual carries for a single SNP or the determination of which allele or alleles an individual carries for a plurality of SNPs or CNVs. A diploid individual may be homozygous for each of the two possible alleles (for example, AA or BB) or heterozygous (for example, AB). For additional information regarding genotyping and genome structure see, *Color Atlas of Genetics*, Ed. Passarge, Thieme, New York, N.Y. (2001), which is incorporated by reference.

Normal cells that are heterozygous at one or more loci may give rise to tumor cells that are homozygous at those loci. This loss of heterozygosity (LOH) may result from structural deletion of normal genes or loss of the chromosome carrying the normal gene, mitotic recombination between normal and mutant genes, followed by formation of daughter cells homozygous for deleted or inactivated (mutant) genes; or loss of the chromosome with the normal gene and duplication of the chromosome with the deleted or inactivated (mutant) gene.

The term "array" as used herein refers to an intentionally created collection of molecules which can be prepared either synthetically or biosynthetically. The molecules in the array can be identical or different from each other. The array can assume a variety of formats, for example, libraries of soluble molecules; libraries of compounds tethered to resin beads, silica chips, microparticles, nanoparticles or other solid supports.

The term "complementary" as used herein refers to the hybridization or base pairing between nucleotides or nucleic acids, such as, for instance, between the two strands of a double stranded DNA molecule or between an oligonucleotide primer and a primer binding site on a single stranded nucleic acid to be sequenced or amplified. See, M. Kanehisa Nucleic Acids Res. 12:203 (1984), incorporated herein by reference.

The term "copy number variation" or "CNV" refers to differences in the copy number of genetic information. In many aspects it refers to differences in the per genome copy number of a genomic region. For example, in a diploid organism the expected copy number for autosomal genomic regions is 2 copies per genome. Such genomic regions should be present at 2 copies per cell. For a recent review see Zhang et al. *Annu. Rev. Genomics Hum. Genet.* 2009. 10:451-81. CNV is a source of genetic diversity in humans and can be associated with complex disorders and disease, for example, by altering gene dosage, gene disruption, or gene fusion. They can also represent benign polymorphic variants. CNVs can be large, for example, larger than 1 Mb, but many are smaller, for example between 100 bp and 1 Mb. More than 38,000 CNVs greater than 100 bp (and less than 3 Mb) have been reported in humans. Along with SNPs these CNVs account for a significant amount of phenotypic variation between individuals. In adition addition to having deleterious impacts, e.g. causing disease, they may also result in advantageous variation.

Digital PCR is a technique where a limiting dilution of the sample is made across a large number of separate PCR reactions so that most of the reactions have no template molecules and give a negative amplification result. Those reactions that are positive at the reaction endpoint are counted as individual template molecules present in the original sample in a 1 to 1 relationship. See Kalina et al. NAR 25:1999-2004 (1997) and Vogelstein and Kinzler, PNAS 96:9236-9241 (1999). This method is an absolute counting method where solutions are partitioned into containers until there is an average probability of one molecule per two containers or when, $P_0=(1-e^{-n/c})=½$; where n is the number of molecules and c is the number of containers, or n/c is 0.693. Quantitative partitioning is assumed, and the dynamic range is governed by the number of containers available for stochastic separation. The molecules are then detected by PCR and the number of positive containers is counted. Each successful amplification is counted as one molecule, independent of the actual amount of product. PCR-based techniques have the additional advantage of only counting molecules that can be amplified, e.g. that are relevant to the massively parallel PCR step in the sequencing workflow. Because digital PCR has single molecule sensitivity, only a few hundred library molecules are required for accurate quantification. Elimination of the quantification bottleneck reduces the sample input requirement from micrograms to nanograms or less, opening the way for minute and/or precious samples onto the next-generation sequencing platforms without the distorting effects of pre-

amplification. Digital PCR has been used to quantify sequencing libraries to eliminate uncertainty associated with the construction and application of standard curves to PCR-based quantification and enable direct sequencing without titration runs. See White et al. *BMC Genomics* 10: 116 (2009).

To vary dynamic range, micro-fabrication can be used to substantially increase the number of containers. See, Fan et al. *Am J Obstet Gynecol* 200, 543 el (May, 2009).

Similarly, in stochastic labeling as disclosed herein, the same statistical conditions are met when $P_0=(1-e^{-n/m})=½$; where m is the number of labels, and one half of the labels will be used at least once when n/m=0.693. The dynamic range is governed by the number of labels used, and the number of labels can be easily increased to extend the dynamic range. The number of containers in digital PCR plays the same role as the number of labels in stochastic labeling and by substituting containers for labels identical statistical equations may be applied. Using the principles of physical separation, digital PCR stochastically expands identical molecules into physical space, whereas the principle governing stochastic labeling is identity based and expands identical molecules into identity space.

The term "hybridization" as used herein refers to the process in which two single-stranded polynucleotides bind non-covalently to form a stable double-stranded polynucleotide; triple-stranded hybridization is also theoretically possible. The resulting (usually) double-stranded polynucleotide is a "hybrid." The proportion of the population of polynucleotides that forms stable hybrids is referred to herein as the "degree of hybridization." Hybridizations may be performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25° C. For example, conditions of 5× SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30° C. are suitable for allele-specific probe hybridizations. For stringent conditions, see, for example, Sambrook, Fritsche and Maniatis. "Molecular Cloning A laboratory Manual" 2nd Ed. Cold Spring Harbor Press (1989) which is hereby incorporated by reference in its entirety for all purposes above. In some aspects salt concentrations for hybridization are preferably between about 200 mM and about 1M or between about 200 mM and about 500 mM. Hybridization temperatures can be as low as 5° C., but are typically greater than 22° C., more typically greater than about 30° C., and preferably in excess of about 37° C. Longer fragments may require higher hybridization temperatures for specific hybridization. As other factors may affect the stringency of hybridization, including base composition and length of the complementary strands, presence of organic solvents and extent of base mismatching, the combination of parameters is more important than the absolute measure of any one alone.

The term "mRNA" or sometimes refer by "mRNA transcripts" as used herein, include, but not limited to pre-mRNA transcript(s), transcript processing intermediates, mature mRNA(s) ready for translation and transcripts of the gene or genes, or nucleic acids derived from the mRNA transcript(s). Transcript processing may include splicing, editing and degradation. As used herein, a nucleic acid derived from an mRNA transcript refers to a nucleic acid for whose synthesis the mRNA transcript or a subsequence thereof has ultimately served as a template. Thus, a cDNA reverse transcribed from an mRNA, an RNA transcribed from that cDNA, a DNA amplified from the cDNA, an RNA transcribed from the amplified DNA, etc., are all derived from the mRNA transcript and detection of such derived products is indicative of the presence and/or abundance of the original transcript in a sample. Thus, mRNA derived samples include, but are not limited to, mRNA transcripts of the gene or genes, cDNA reverse transcribed from the mRNA, cRNA transcribed from the cDNA, DNA amplified from the genes, RNA transcribed from amplified DNA, and the like.

The term "nucleic acid" as used herein refers to a polymeric form of nucleotides of any length, either ribonucleotides, deoxyribonucleotides or peptide nucleic acids (PNAs), that comprise purine and pyrimidine bases, or other natural, chemically or biochemically modified, non-natural, or derivatized nucleotide bases. The backbone of the polynucleotide can comprise sugars and phosphate groups, as may typically be found in RNA or DNA, or modified or substituted sugar or phosphate groups. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. The sequence of nucleotides may be interrupted by non-nucleotide components. Thus the terms nucleoside, nucleotide, deoxynucleoside and deoxynucleotide generally include analogs such as those described herein. These analogs are those molecules having some structural features in common with a naturally occurring nucleoside or nucleotide such that when incorporated into a nucleic acid or oligonucleoside sequence, they allow hybridization with a naturally occurring nucleic acid sequence in solution. Typically, these analogs are derived from naturally occurring nucleosides and nucleotides by replacing and/or modifying the base, the ribose or the phosphodiester moiety. The changes can be tailor made to stabilize or destabilize hybrid formation or enhance the specificity of hybridization with a complementary nucleic acid sequence as desired.

The term "oligonucleotide" or sometimes refer by "polynucleotide" as used herein refers to a nucleic acid ranging from at least 2, preferable at least 8, and more preferably at least 20 nucleotides in length or a compound that specifically hybridizes to a polynucleotide. Polynucleotides of the present invention include sequences of deoxyribonucleic acid (DNA) or ribonucleic acid (RNA) which may be isolated from natural sources, recombinantly produced or artificially synthesized and mimetics thereof. A further example of a polynucleotide of the present invention may be peptide nucleic acid (PNA). The invention also encompasses situations in which there is a nontraditional base pairing such as Hoogsteen base pairing which has been identified in certain tRNA molecules and postulated to exist in a triple helix. "Polynucleotide" and "oligonucleotide" are used interchangeably in this application.

The term "polymorphism" as used herein refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphism may comprise one or more base changes, an insertion, a repeat, or a deletion. A polymorphic locus may be as small as one base pair. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has

two forms. A triallelic polymorphism has three forms. Single nucleotide polymorphisms (SNPs) are included in polymorphisms.

The term "primer" as used herein refers to a single-stranded oligonucleotide capable of acting as a point of initiation for template-directed DNA synthesis under suitable conditions for example, buffer and temperature, in the presence of four different nucleoside triphosphates and an agent for polymerization, such as, for example, DNA or RNA polymerase or reverse transcriptase. The length of the primer, in any given case, depends on, for example, the intended use of the primer, and generally ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template but must be sufficiently complementary to hybridize with such template. The primer site is the area of the template to which a primer hybridizes. The primer pair is a set of primers including a 5' upstream primer that hybridizes with the 5' end of the sequence to be amplified and a 3' downstream primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

The term "probe" as used herein refers to a surface-immobilized molecule that can be recognized by a particular target. See U.S. Pat. No. 6,582,908 for an example of arrays having all possible combinations of probes with 10, 12, and more bases. Examples of probes that can be investigated by this invention include, but are not restricted to, agonists and antagonists for cell membrane receptors, toxins and venoms, viral epitopes, hormones (for example, opioid peptides, steroids, etc.), hormone receptors, peptides, enzymes, enzyme substrates, cofactors, drugs, lectins, sugars, oligonucleotides, nucleic acids, oligosaccharides, proteins, and monoclonal antibodies.

The term "solid support", "support", and "substrate" as used herein are used interchangeably and refer to a material or group of materials having a rigid or semi-rigid surface or surfaces. In many embodiments, at least one surface of the solid support will be substantially flat, although in some embodiments it may be desirable to physically separate synthesis regions for different compounds with, for example, wells, raised regions, pins, etched trenches, or the like. According to other embodiments, the solid support(s) will take the form of beads, resins, gels, microspheres, or other geometric configurations. See U.S. Pat. No. 5,744,305 and US Patent Pub. Nos. 20090149340 and 20080038559 for exemplary substrates.

A stochastic process is the counterpart to a deterministic process. Instead of dealing with only one possible "reality" of how the process might evolve under time, in a stochastic or random process there is some indeterminacy in its future evolution described by probability distributions. This means that even if the initial condition (or starting point) is known, there are many possibilities the process might go to, but some paths are more probable and others less.

In the simplest possible case, a stochastic process amounts to a sequence of random variables known as a time series (for example, see Markov chain). Another basic type of a stochastic process is a random field, whose domain is a region of space, in other words, a random function whose arguments are drawn from a range of continuously changing values. One approach to stochastic processes treats them as functions of one or several deterministic arguments ("inputs", in most cases regarded as "time") whose values ("outputs") are random variables: non-deterministic (single) quantities which have certain probability distributions. Random variables corresponding to various times (or points, in the case of random fields) may be completely different. The main requirement is that these different random quantities all have the same "type". Although the random values of a stochastic process at different times may be independent random variables, in most commonly considered situations they exhibit complicated statistical correlations.

Familiar examples of processes modeled as stochastic time series include stock market and exchange rate fluctuations, signals such as speech, audio and video, medical data such as a patient's EKG, EEG, blood pressure or temperature, and random movement such as Brownian motion or random walks. Examples of random fields include static images, random terrain (landscapes), or composition variations of an heterogeneous material.

The stochastic labeling process can be generalized as follows. Consider n copies of a given target molecule T, where $T=\{t_i, i=1, 2, \ldots, n\}$, and a non-depleting reservoir of m diverse labels L, where $L=\{l_j, j=1, 2, \ldots, m\}$. T reacts with L stochastically, such that each t_i will choose exactly one $l_{j(i)}$, $1\leq j(i)\leq m$ to take on a new identity $t_i l_{j(i)}$, and may be identified by its label subscript. Therefore, the new collection of molecules T* may be denoted as $T^*=\{tl_{j(i)}, i=1, 2, \ldots, n, 1\leq j(i)\leq m\}$.

When different copies of the target molecules react with the same label, j(i) for those molecules will assume the same value, therefore, the number of uniquely labeled target molecules k cannot be greater than m. The stochastic mapping of the set of labels on a target may be described by a stochastic operator S with m members, acting upon a target population of n, such that $S(m)T(n)=T^*(m, n)$ generating the set $T^*=\{tl_{j(i),\, i=}1, 2, \ldots, n, 1\leq j(i)\leq m\}$. For simplicity, we may write $T^*=\{tl_k\}$. Furthermore, since S operates on all molecules randomly, it will independently act on many different target sequences and the method can be expanded to count copies of multiple target sequences, w, simultaneously: $ST^w=ST_1+ST_2+\ldots+ST_w=T_1^*+T_2^*+\ldots T_w^*=\{tl_k\}_1+\{tl_k\}_2+\ldots+\{tl_k\}_w$, where each T_i^*, i=1, 2, . . . , w consists of a set $\{tl_k\}_i$. The net result of S operating on a specific target population is to map the number of molecules, n, of that target, to the number of labels captured, k, which is a random variable.

Since target molecules randomly react with a label with probability 1/m, the probability of a label being captured by exactly x out of n copies of a target molecule can be modeled as a Binomial distribution,

$$P(x)=\frac{n!}{x!(n-x)!}\left(\frac{1}{m}\right)^x\left(1-\frac{1}{m}\right)^{n-x},$$

where x! denotes the factorial of x. The probability that a label will not be captured by any copy of the target molecule is $P(0)=(1-1/m)^n$, and the probability that a label will be captured at least once is 1−P(0). When $n\to\infty$ and $1/m\to 0$ in the way that $n/m\to\lambda$, P(x) converges to the Poisson distribution with mean λ, i.e.,

$$P(x)=\frac{\lambda^x}{x!}e^{-\lambda}.$$

To compute the number of unique labels captured by n copies of a target molecule, we introduce an index random variable, X_i, which is 1 if a label has been captured at least

once, and 0 otherwise. The number of unique labels captured is thus

$$k = \sum_{i=1}^{m} X_i.$$

The mean and variance of k can be derived,

$$E[k] = m\left[1 - \left(1 - \frac{1}{m}\right)^n\right] \quad (1)$$

$$\mathrm{Var}[k] = m\left[1 - \left(1 - \frac{1}{m}\right)^n\right]\left(1 - \frac{1}{m}\right)^n + m(m-1)\left[\left(1 - \frac{2}{m}\right)^n - \left(1 - \frac{1}{m}\right)^{2n}\right] \quad (2)$$

Similarly, to compute the number of labels captured by exactly x copies of a target molecule, we introduce another index random variable, Y_i, which is 1 if a label has been captured exactly x times, and 0 otherwise. The number of labels captured x times is thus

$$t = \sum_{i=1}^{m} Y_i.$$

The mean and variance of t are,

$$E[t] = \frac{m \cdot n!}{x!(n-x)!}\left(\frac{1}{m}\right)^x\left(1 - \frac{1}{m}\right)^{n-x} \quad (3)$$

$$\mathrm{Var}[t] = A(1-A) + (m-1)m \cdot \binom{n}{2x} \cdot \left(\frac{2}{m}\right)^{2x}\left(1 - \frac{2}{m}\right)^{n-2x}\binom{2x}{x}\left(\frac{1}{2}\right)^{2x} \quad (4)$$

where

$$A = m \cdot \binom{n}{x}\left(\frac{1}{m}\right)^x\left(1 - \frac{1}{m}\right)^{n-x},$$

and the combination

$$\binom{n}{x} = \frac{n!}{x!(n-x)!}.$$

The equations were experimentally validated by performing numerical simulations with 5000 independent runs for each simulated case. Complete agreement with the analytical solutions was observed.

Stochastic Labeling of Individual Molecules

Methods are disclosed herein that may be applied to determining small numbers of biological molecules and their changes in response to, for example, cellular response, differentiation or signal transduction. The methods may also be used in performing a wide variety of clinical measurements. Although many analytical methods have been developed to measure the relative abundance of different molecules through sampling (e.g., microarrays and sequencing), the methods disclosed herein are able to determine the absolute number of molecules in a sample.

Methods for performing single molecule digital counting by the stochastic labeling of a collection of identical molecules are disclosed. As illustrated in FIGS. **1**, **2**A and **2**B, each copy of a molecule (from a collection of identical target molecules **103**) randomly captures a label by choosing from a large, non-depleting reservoir of diverse labels **101**. The uniqueness of each labeled molecule is governed by the statistics of random choice, and depends on the number of copies of identical molecules in the collection compared to the diversity of labels. Once the molecules are labeled each has been given a unique identity and can now be separately detected. In some aspects, it is preferable to first amplify the labeled targets prior to detection so that simple present/absent threshold detection methods can be used. Counting the number of labels is used to determine the original number of molecules in solution. In some aspects, the molecules to be counted are each members of a class that shares some common feature, for example, they may each be a single copy of a particular gene sequence or nucleic acid sequence. Counting may be applied, for example, to mRNA targets, splice products, alternatively spliced products, structural RNAs, tRNA, miRNA, siRNA, microRNA and the like. Similarly, counting may be applied to DNA, for example, gene copy number, chromosome number, mitochondrial DNA, bacterial genomes, pathogen nucleic acid, viral nucleic acids and the like. Counting may be applied in research of disease in humans or other mammals or agricultural organisms, e.g. cattle, chicken, wheat, rice, fish, etc. Counting may also be applied to counting aspects of microbes, such as environmental measurements, e.g. water quality testing. The methods may be particularly useful where small numbers of items are to be counted and an accurate count is desirable rather than a relative estimate.

One embodiment is illustrated schematically in FIG. **1**. The library of different label-tag sequences **101** is combined with a sample that includes an unknown number of targets of interest **103**. Three different species of target are shown, **103***a*, **103***b* and **103***c*, present at 4, 6 and **3** copies respectively. The individual label-tag oligonucleotides from library **101** are covalently attached to the different targets to form target-label-tag molecules **105**. Each target has a collection of different label-tag molecules **105***a*, **105***b* and **105***c* and within each target-specific collection the members differ in the label-tag oligo that is attached. On the array **107**, each target is tiled in combination with all possible label-tag combinations represented with each different combination being present at a different known or determinable location on the array. In the figure each different possible combination of target and label-tag is represented by a single probe for illustration purposes, but on the array each different probe is preferably present in a feature having multiple copies of the same probe sequence. The array is divided into subarrays **107***a*, **107***b* and **107***c* for illustrative purposes. The upper portion **109** of the probes varies at each feature according to the different label-tag. The lower portion **113** is the same for all features of each subarray and is complementary to the target. After hybridization individual features of the array are labeled through hybridization of the complementary target-label-tag molecule to the feature. The figure shows a detectable label **111** may be used to detect features where a target-label-tag is hybridized.

FIG. **2**A illustrates the attachment of different labels from the pool **101** to each of 4 different copies of the same target "t". Label 20 is attached to t1, label 107 to t2, label 477 to t**3** and label 9 to t4. The labeled targets are then amplified to generate four unique populations, each population representing a single occurrence of the target in the starting sample.

FIG. **2**B illustrates the method for a comparison of two samples, sample 1 and 2. The target **201** Gene A is present in 2 copies in sample 1 and 9 copies in sample 2. Both samples

have non-target molecules **203**. The labels **205** are combined with the samples and target molecules are attached to individual label-tag molecules in a stochastic manner. The targets with attached label-tags are hybridized to an array **211** having many features, there is a feature for each possible target-label-tag combination. Some of the features are labeled, for example, **209** and others are not, for example, **207**. The labeled features indicate the presence of a specific target-label-tag combination and each corresponds to a count. As shown for gene A in sample 1 there are two labeled features so the count is 2. For Gene A in sample 2 there are 9 labeled features so the count is 9.

The stochastic labeling process can be generalized as follows for illustrative purposes. Consider a given target sequence defined as $T=\{t_1, t_2 \ldots t_n\}$; where n is the number of copies of T. A set of labels is defined as $L=\{l_1, l_2 \ldots l_m\}$; where m is the number of different labels. T reacts stochastically with L, such that each t becomes attached to one l. If the l's are in non-depleting excess, each t will choose one l randomly, and will take on a new identity $l_i t_j$; where l_i is chosen from L and j is the jth copy from the set of n molecules. We identify each new molecule $l_i t_j$ by its label subscript and drop the subscript for the copies of T, because they are identical. The new collection of molecules becomes $T^*=l_1 t+l_2 t+ \ldots l_i t$; where l_i is the ith choice from the set of m labels. It is important to emphasize that the subscripts of l at this point refer only to the ith choice and provide no information about the identity of each l. In fact, l_1 and l_2 will have some probability of being identical, depending upon the diversity m of the set of labels. Overall, T* will contain a set of k unique labels resulting from n targets choosing from the non-depleting reservoir of m labels. Or, $T^*(m,n)=\{tl_k\}$; where k represents the number of unique labels that have been captured. In all cases, k will be smaller than m, approaching m only when n becomes very large. We can define the stochastic attachment of the set of labels on a target using a stochastic operator S with m members, acting upon a target population of n, such that S(m)T(n)=T*(m,n) generating the set $\{tl_k\}$. Furthermore, since S operates on all molecules randomly, it can independently act on many different target sequences. Hence, the method can simultaneously count copies of multiple target sequences. The distribution of outcomes generated by the number of trials n, from a diversity of m, can be approximated by the Poisson equation, $P_x=\lambda^x/x!e^{-(n/m)}$. P_0 is the probability that a label will not be chosen in n trials, and therefore, $1-P_0$ is the probability that a label will occur at least once. It follows that the number of unique labels captured is given by: $k=m(1-P_0)=m(1-e^{-(n/m)})$.

Given k, we can calculate n. In addition to using the Poisson approximation, the relationship for k, n and m can be described analytically using the binomial distribution, or simulated using a random number generator, each yielding similar results.

The outcome of stochastic labeling is illustrated by examining the graph of k verses n (curve **3201** in FIG. **11**) calculated using a label diversity (m) of 960. As expected, the number of unique labels captured depends on the ratio of molecules to labels, n/m. When n is much smaller than m, each molecule almost always captures a unique label, and counting k is equivalent to counting n. As n increases, k increases more slowly as given by eq. 1, and yet remains a very precise estimate of n. For example, when n/m is ~0.01, the ratio of unique labels to molecules k/n ~0.99, and we expect an increase of 10 molecules will generate 10+/−X new labels. As n/m approaches 0.5 (i.e., ~480 molecules reacted with 960 labels), k/n ~0.79 and ~6+/−X new labels are expected with an increase of 10 molecules. At high n/m, k increases more slowly as labels in the library are more likely to be captured more than once. Curve **3202** in FIG. **11** shows the number of labels chosen exactly once, and curve **3203** shows the number of labels chosen exactly twice as n increases. Curve **3201** shows the number of labels captured at least once. A more complete description of the number of times a label is chosen as a function of n is shown in FIG. **15**.

The methods and examples below demonstrate that a population of indistinguishable molecules can be stochastically expanded to a population of uniquely identifiable and countable molecules. High-sensitivity threshold detection of single molecules is demonstrated, and the process can be used to count both the absolute and relative number of molecules in a sample. The method should be well suited for determining the absolute number of multiple target molecules in a specified container, for example in high-sensitivity clinical assays, or for determining the number of transcripts in single cells. The approach should also be compatible with other molecular assay systems. For example, antibodies could be stochastically labeled with DNA fragments and those that bind antigen harvested. After amplification, the number of labels detected will reflect the original number of antigens in solutions. In the examples shown here, DNA is used because of the great diversity of sequences available, and because it is easily detectable. In principle, any molecular label could be used, for example fluorescent groups or mass spectroscopy tags, as long as they are easily detected and they have sufficient diversity for the desired application. Although many of the examples refer to populations

It is instructive to contrast the attributes of stochastic labeling with other quantitative methods. Microarray and sequencing technologies are commonly used to obtain relative abundance of multiple targets in a sample. In the case of microarray analysis, intensity values reflect the relative amount of hybridization bound target and can be used to compare to the intensity of other targets in the sample. In the case of sequencing, the relative number of times a sequence is found is compared to the number of times other sequences are found. Although the techniques differ by using intensity in one case and a digital count in the other, they both provide relative comparisons of the number of molecules in solution. In order to obtain absolute numbers, quantitative capture of all sequences would need to be assured; however in practice the efficiency of capture with microarray and sequencing technologies is unknown.

Digital PCR is an absolute counting method where solutions are stochastically partitioned into multi-well containers until there is an average probability of one molecule per two containers, then detected by PCR. This condition is satisfied when, $P_0=(1-e^{-n/c})=½$; where n is the number of molecules and c is the number of containers, or n/c is 0.693. Quantitative partitioning is assumed, and the dynamic range is governed by the number of containers available for stochastic separation. Once the molecules are partitioned, high efficiency PCR detection gives the yes/no answer and absolute counting enabled. To vary dynamic range, micro-fabrication can be used to substantially increase the number of containers. Similarly, in stochastic labeling, the same statistical conditions are met when $P_0=(1-e^{-n/m})=½$; where m is the number of labels, and one half of the labels will be used at least once when n/m=0.693. The dynamic range is governed by the number of labels used, and the number of labels can be easily increased to extend the dynamic range. The number of containers in digital PCR plays the same role as the number of labels in stochastic labeling and by substituting containers for labels we can write identical statistical equations. Using the principles of physical separation, digital PCR stochastically

expands identical molecules into physical space, whereas the principle governing stochastic labeling is identity based and expands identical molecules into identity space.

New methods and compositions for single molecule counting employing the use of stochastic labeling are disclosed herein. In preferred aspects, a diverse set of labels is randomly attached to a population of identical molecules is converted into a population of distinct molecules suitable for threshold detection. Random attachment as used herein refers to a process whereby any label can be attached to a given molecule with the same probability. To demonstrate stochastic labeling methods experimentally the absolute and relative number of selected genes were determined after stochastically labeling 360,000 different fragments of the human genome. The approach does not require the physical separation of molecules and may take advantage of highly parallel methods such as microarray and sequencing technologies to simultaneously count absolute numbers of multiple targets. In some embodiments, stochastic labeling may be used for determining the absolute number of RNA or DNA molecules within single cells.

The methods disclosed herein may be used to take quantitative measurements of copies of identical molecules in a solution by transformation of the information to a digital process for detecting the presence of different labels. The stochastic properties of the method have been measured, and the relative and absolute digital counting of nucleic acid molecules is demonstrated. The method is extremely sensitive, quantitative, and can be multiplexed to high levels. In some aspects a microarray-based detection method is used, but the method is extendable to many other detection formats.

In some aspects, the methods are based on probability theory, where the outcome of chemical reactions occurring between a set of labeling molecules and a set of target molecules is modeled and tested. When all of the molecules in a uniform mixture of fixed volume collide and react randomly, the chemical events follow a stochastic process governed in part by the molecule concentration of each species (D. T. Gillespie, *The Journal of Physical Chemistry* 81, 2340 (1977)).

Methods for analyzing genomic information often utilize a correlation between a measurement of the amount of material associated with a location. The location can be, for example, a feature of an array that contains a specific sequence that is known or can be determined or any type of solid support such as a bead, particle, membrane, etc. A common aspect to these methods is often hybridization of a target to be measured to a complementary probe attached to the solid support. The probe may be, for example, an oligonucleotide of known or determinable sequence, but may also be BACs, PACs, or PCR amplicons.

Because of the density of different features that can be obtained using synthesis methods such as photolithography, microarrays can be applied to high density applications. For example, at feature sizes of 1 micron square an array can have about 10^8 features per cm^2. Within a feature, depending on the chemistry used for synthesis, the probes are spaced typically at about 10 nm spacing resulting in about 10^4 molecules in a $micron^2$. At approximately full saturation about 10% of those probes are hybridized with target. There are then about 640 functional molecules in an array having 1 $micron^2$ spacing between features (~800 nm^2 functional area). This relatively small number of functional molecules in a feature limits the dynamic range for estimating relative concentration from hybridization signal intensity.

Methods are disclosed herein to overcome the dynamic range limitations observed with small feature sizes and small numbers of molecules on the array surface, by using a counting or digital readout as a substitute for the typical analog signal resulting from array hybridization.

Methods that use signal intensity to estimate relative concentrations of targets typically label the targets with a detectable label, often after an amplification step, and through hybridization of the labeled target to the probe, the probe and thus the feature is also labeled. The amount of label is detected and correlated with a measurement of the amount of target in the sample. The estimate of amount of a given target in a sample is typically relative to other targets in the sample or to previously obtained measurements and may be based on comparison to targets present in the sample at known or expected levels or to controls within the sample. This type of analysis can and has been used successfully, for example, to estimate genomic copy number to detect copy number variation in individuals or in cell populations (see, for example, Pinkel & Albertson, *Annu. Rev. Genomics Hum. Genet.* 6, 331-354 (2005), Lucito et al. *Genome Res.* 13, 229102305 (2004), Sebat et al. *Science* 305, 525-528 (2004), Zhou et al., *Nat. Biotechnol.* 19, 78-81 (2001) and Zhao et al. *Cancer Res.* 65, 5561-5570 (2005) and US Patent Pub. Nos. 20040157243 and 20060035258) or to estimate gene expression levels (see, for example, Lockhart et al., *Nat. Biotechnol.* 14:1675-1680 (1996), and Wodicka et al., *Nat. Biotechnol.* 15:1359-1367 (1997)).

Correlating intensity of hybridization signal or signal intensity with concentration of target molecules has limitations and can typically provide only an estimate of the absolute amount of a target, and may not be an accurate count of the actual amount of target present. The estimate may be an under or over estimate, particularly when comparing different targets or different samples. This is the result of many different factors, including but not limited to, differences between probes, feature specific effects, sample specific effects, feature size (as it decreases the ability to correlate accurately decreases) and experimental variation. Much of this variation can be addressed by data analysis methods, but the methods do not provide counting of individual molecules or events and are therefore subject to estimation errors.

In preferred aspects methods are disclosed for attaching a different label-tag sequence to each molecule of a particular target sequence or more preferably a collection of target sequences of interest. For example, a sample having 100 molecules of target type 1 is mixed with an excess, for example, 1000 different label-tag sequences, forming a library of label-tag sequences under ligation conditions. Multiple copies of the library of label-tag sequences are added so there are preferably many copies of each label-tag. Different label-tag sequences from the library are appended to each of the 100 target molecules so that each of the 100 molecules of the first target sequence has a unique label-tag sequence appended thereto. This results in 100 different target-label-tag combinations. The target-label-tag molecules may then be amplified to enrich the target-label-tag products relative to other non-targets. Amplification after labeling alters the absolute amount of the target, but because each occurrence in the original sample has been uniquely labeled this will not alter the count. The amplified target-label-tag products, whether amplified or not, can then be labeled with a detectable label, and hybridized to an array of probes. The features of the array that have target-label-tag hybridized thereto can be detected, for example, by labeling the hybridization complex with a fluorescent label and detecting the presence of signal at the features. In this example, because there are 1000 different labels possible and a single target being analyzed, there are 1000 different possible label-target sequences that might be

generated so an array having a different feature for each of the 1000 different possibilities can be used. Assuming each target is labeled and no label is used twice, 100 of the 1000 different features should be detectable, indicating the corresponding label has been used.

Consider 1 copy of a target molecule in solution identified as t_1. React this target against a set of 10 labels, $L_m=\{l_1, l_2, \ldots l_{10}\}$. Each label has a 0.1 probability chosen. Next consider multiple copies of the target, t_n, reacted against the set of L_m (assume non-depleting reservoir of labels). For simplicity, consider 3 copies oft: t_1, t_2 and t_3. Target t_1 will choose a label, t_2 has a 0.9 probability of choosing a different label, t_3 has a predictable probability of choosing the same label as t_1 or t_2. For n copies choosing from m labels, outcomes can be modeled by the binomial distribution as discussed above. For 3 targets and 10 labels, the probability of a label not being chosen, P_0 is $(1-(1/10))^3=0.729$. The probability P_1 of being chosen exactly once is $(3/10)(1-(1/10))^2=0.243$. The probability of being chosen twice, P_2 is 0.027 and the probability P_3 of being chosen 3 times is 0.001. Since P_0 is the probability of not being chosen, $1-P_0$ is the probability of being chosen at least once. We define $k=m(1-P_0)$ as the number of labels we expect to see in an experiment. Conversely, if we know m, and observe k we can solve for the number of molecules. In the previous example where n=3 and m=10 we expect to see $10(1-P_0)$ or 2.71 labels as our most probable outcome. Increasing m dramatically increases our counting efficiency, accuracy and dynamic range, e.g. for m=1,000, k(number of labels expected for n=10, k=9.96, for n=20, k=19.8.

Once the target molecules are labeled with the counter they can be amplified freely without impacting the counting since the readout is either yes, indicating detection or no indication not detected. In one aspect, a simple detector having m elements for each target sequence can be constructed. The detector may be an array. An array having 10^8 features or elements could assay 10^5 different targets using 10^3 different labels, for example. Other detection methods do not require individual elements for each counter, for example, sequencing.

In preferred aspects the "counter library" or "label-tag library" has approximately the same number of copies of each label-tag in the library. The label-tag sequences are not target specific, but are like the tags that have been used for other tagging applications, for example, the Affymetrix GENFLEX tag array. Preferably all label-tags in a set of label-tags will have similar hybridization characteristics so that the label-tags of the set can be detected under similar conditions.

For each target there are a series of features on the array, preferably one feature for each label-tag. In each of these features the portion of the probe that hybridizes to the target (or target complement) is the same but the label-tag complement is different in each feature. For example, to detect a first target RNA, "RNA1", there would be a series of features each having a different probe (RNA1-tag1, RNA1-tag2, ... RNA1-tagN). For each target to be detected there is a similar set of features, e.g. RNA2-tag1, RNA2-tag2, ... RNA2-tagN. The set of label-tags is N tags and it is the unique combination of the label-tag with the target sequence that creates a novel sequence to be detected, for example, by hybridization.

Label-tag attachment to individual targets is a stochastic process whereby the probability of any given label-tag being attached to any target is stochastic. There is a random selection of label-tags by attaching the label-tags to the end of a known target sequence in a sequence independent manner. The label-tag is attached without requirement for it to hybridize to any portion of the target so there is no or minimal bias as to which label-tag sequence is attached. Individual molecules all look the same for the purpose of attachment of the label-tag.

The label-tag may be attached to the target by any method available. In one embodiment, the label-tag is attached by ligation of the label-tag to one of the ends of the target. In preferred aspects the probes of the array are complementary to a predicted junction between target and label so it is preferable that the labels are attached to all occurrences of a target at the same position. This is facilitated if the termini of each occurrence of a selected target are the same and are known. In one aspect, target occurrences are fragmented with a restriction enzyme so that defined ends of known sequence are formed.

After label-tag attachment in some embodiments the target-label-tag segment is amplified. Attachment of universal primers to either end followed by PCR amplification is one method for amplifying. The universal primers may be added along with the label or at a subsequent ligation step.

For RNA targets an RNA ligase, such as T4 RNA ligase may be used. T4 RNA ligase 1 catalyses the ligation of a 5' phosphryl-terminated nucleic acid donor to a 3' hydroxyl-terminated nucleic acid acceptor. Substrates include single-stranded RNA and DNA. See, for example, Romaniuk, P. and Uhlenbeck, O. (1983) R. Wu, L. Grossman and K. Moldave (Eds.), *Methods Enzymol.,* 100, pp. 52-56. New York: Academic Press and Moore, M. J. and Sharp, P. A. (1992) *Science,* 256, 992-997. RNA targets may also be circularized and used as template for rolling circle amplification using an enzyme having reverse transcriptase activity. T4 RNA ligase 1 may be used for circularization of RNA by ligating the ends of the molecule together. T4 RNA ligase 1 can also be used to ligate RNA to DNA.

Full-length mRNA can be selected by treating total or poly(A) RNA with calf intestinal phosphatase (CIP) to remove the 5' phosphate from all molecules which contain free 5' phosphates (e.g. ribosomal RNA, fragmented mRNA, tRNA and genomic DNA). Full-length mRNAs are not affected. The RNA can them be treated with tobacco acid pyrophosphatase (TAP) to remove the cap structure from the full-length mRNA leaving a 5'-monophosphate. A synthetic RNA adapter can be ligated to the RNA population. Only molecules containing a 5'-phosphate, (i.e. the uncapped, full-length mRNAs) will ligate to the adapters. Preferably the adapter has a variable label sequence, and may also have a constant sequence for priming. Preferably, the constant sequence is 5' of the variable sequence. In some aspects, the adapter ligated mRNA may then be copied to form a first strand cDNA by, for example, random priming or priming using oligo dT. The cDNA may subsequently be amplified by, for example, PCR.

T4 RNA ligase may also be used for ligation of a DNA oligo to single stranded DNA. See, for example, Troutt et al., (1992) *Proc. Natl, Acad. Sci. USA,* 89, 9823-9825.

In other aspects, the ligated target-label-tag molecule may be enriched in the sample relative to other nucleic acids or other molecules. This enrichment may be, for example, by preferentially amplifying the target-label-tag methods, using for example, a DNA or RNA polymerase, or by degrading non target-label-tag molecules preferentially.

In one aspect, the target-label-tag molecule may be nuclease resistant while the unligated target and unligated label molecules may be nuclease sensitive. A nuclease can be added to the sample after ligation so that ligated target-label-tag molecules are not digested but non-ligated molecules are digested. For example, the targets may be resistant to a 5' exonuclease (but not a 3' exonuclease) while the labels are

resistant to a 3' exonuclease but not a 5' exonuclease. Ligating target to label generates a molecule that is resistant to 5' and 3' exonuclease activity. After ligation the sample may be treated with a 5' exonuclease activity, a 3' exonuclease activity or both 5' and 3' exonuclease activities. For examples of nucleases see Rittie and Perbal, *J. Cell Commun. Signal.* (2008) 2:25-45, which is incorporated by reference (in particular see Table 5). Exo VII, for example degrades single stranded DNA from both the 5' and 3' ends so the sample could be treated with Exo VII after ligation to degrade molecules that are not ligation products.

In another aspect amplification may include a rolling circle amplification (RCA) step. See for example, Baner et al. (1998) NAR 26:5073, Lizardi et al. (1998) Nat. Genet. 19:225, Fire and Xu, (1995) PNAS 92:4641-5, Zhao et al. Angew Chem Int Ed Engl. 2008; 47:6330-6337 and Nilsson et al. (2008), Trends in Biotechnology, 24:83-88. The targets may be ligated so that they have a label and a universal priming (UP) sequence attached to the 5' end of the targets. The UP-label-target is then ligated to form a circle. A primer complementary to the UP is then hybridized to the circles and extended using a strand displacing polymerase. The resulting amplification product contains multiple copies of the complement of the circle, UP-target-L.

In another aspect, targets may be labeled in a copying step. For example, a primer having a 3' target specific region and a 5' variable label region may be hybridized to the targets, either RNA or DNA, and extended to create a single complimentary copy of the target. Each extension product will have a different label and the junction between the label and the target specific region is known. The extension may be performed in the presence of nuclease resistant nucleotides so that the extension product is resistant to nuclease but the unextended primers are not. After extension the reaction is treated with a 3'-5' exonuclease activity to digest unextended primer. Exonuclease I, for example, removes nucleotides from single stranded DNA in the 3' to 5' direction and Exo III removes nucleotides from the 3' termini of duplex DNA. Exonuclease T (or RNase T) is a single-stranded RNA or DNA specific nuclease that requires a free 3' terminus and removes nucleotides in the 3' to 5' direction. The extension products are then detected by hybridization to probes that are complementary to the primers and include the unique label portion and the constant target specific portion. If the target is RNA it can be digested with RNase H after extension. The extension product may also be amplified before hybridization.

In some aspects the probability that any two targets are labeled with the same label may be decreased by using two or more labeling steps. For example, a first labeling step where each target has a label selected from a set of labels followed by a second labeling set using the same set of labels. The first labeling event will be independent of the second so the probability that the first and second labeling events will both be the same in two independent targets is the product of the probability of two targets having the same label in either step. If there are N possible labels, and the first target is labeled first with label N1 and then with label N4, the probability that a second target will be labeled also with N1 and then N4 is $1/N^2$. So if there are 100 different labels, the probability that two targets will be labeled with the same label in the first round and the same label in the second round is $1/10{,}000$.

In another aspect a first round of labeling may be done with 16 probes (for example, all possible 2 base combinations) and then a second round of labeling is done using the same 16 probes. The chance of any one probe attaching to a given target occurrence in the first round is 1 out of 16, the chance that the same probe will attach to the second target is $1/16$ and the chance that the same two probes will attach is $1/16 \times 1/16$ or $1/256$.

In another aspect reversible terminators are used to add a sequence to the end of each target being counted. For example, a 6 base sequence may be added and the chance of two being the same is 1 in 4^6 or 1 in 4096. See, for example, WO 93/06121 and U.S. Pat. No. 6,140,493 which disclose stochastic methods for synthesizing random oligomers.

There is a finite set of labels, L_{1-x} and each target to be detected is present in the sample at a certain integer occurrence ($T1_{1-t}^{1}$, $T2_{1-t}^{2}$, . . . TN_{1-t}^{n}). In a preferred aspect, the method is used to count the number of each of the different targets, (e.g. how many occurrences of T1, how many of T2, . . . how many of TN) in the sample. The targets are independently labeled with the label molecules. Labeling is stochastic, so that any given target occurrence can be labeled with any one of the labels. For example, T1-1/L689, T1-2/L3, T1-3/L4,567 and so on. For Target 2, any given occurrence can also be labeled with any of the label molecules. This might generate, for example, (T2-1, L5), (T2-2, L198), (T2-3, L34) and so on. There are multiple copies of each label so T2-1 might be labeled with L5 and T1-500 may also be labeled with L5.

The methods disclosed herein may be used to measure random cell-to-cell variations in gene expression within an isogenic population of cells. Such variation can lead to transitions between alternative states for individual cells. For example, cell-to-cell variation in the expression of comK in *B. subtilis* has been shown to select cells for transition to the competent state in which genes encoding for DNA uptake proteins are expressed. See, Maamar et al. *Science* 317:526-529 (2007) which is incorporated herein by reference.

In some aspects the labels are generated within the target to be counted. For example, the label may be a unique cleavage site in a target fragment as shown in FIG. **6**. Each of the copies of the target to be counted **601** have a common sequence at one end identified in the figure as **603**. This may be a common sequence that has been added to the targets through ligation or primer extension or it may be a naturally occurring sequence in the target. The targets are fragmented randomly, for example by shearing or sonnication resulting in cleavage at the points indicated by the arrows to generate cleavage products **604**. Cleavage is at a different and unique site in each of the fragments and results in a unique sequence in the target immediately to the left of the point of cleavage in the illustration (indicated by circles in fragments **607**). This unique sequence can function as a label for the disclosed methods. A second common sequence **605** may be attached to each of the targets immediately downstream of the cleavage point, through for example ligation of an adaptor sequence. The resulting targets **607** can be analyzed directly to determine how many unique sequences are present and using this number as an indication of the number of targets in the starting sample. This is illustrated for nucleic acids, but could similarly be applied to proteins or other contiguous strings of monomers or units that are assembled in a non repeating pattern.

FIG. **7** shows a strategy for selecting probes for target fragments. For a double stranded fragment there are 4 possible junctions that can be targeted with array probes **3001**, **3003**, **3005** and **3007**. Each of these junction regions as shown has a counter region **3011** denoted by N's, a fixed sequence **3013** that is defined by the restriction enzyme used for fragmentation and a target specific region **3015**. The region **3015** is shown as N's but in preferred aspects it is a known and predictable sequence of the target that is adjacent to the

selected restriction site. In a preferred aspect, the array probes are complementary to at least a portion of **3011**, a portion of **3015** and all of **3013**. For each target sequence-counter combination there are 4 different probes that could be included on the array. For example, if the targets are 10 loci from each of 4 chromosomes and 4 probes per fragment are included for 1200 different labels (1000 specific plus 200 non-specific) the array would have 192,000 total probes (4×10×4×1200).

In some aspects methods for selecting a collection of labels optimized for use in the disclosed methods is contemplated. For example, a list of all possible 14 mers may be used as a starting pool (4^{14} is ~268 million different sequences). Different label lengths can be used resulting in different numbers of starting sequences. Eliminate all labels that are not at least 50% GC content. Eliminate all labels that do not use each of the 4 possible nucleotides at least twice. Eliminate all labels that have more than two Gs or Cs in tandem, e.g. a probe with GGG or CCC would be eliminated, or with more than three As or Ts in tandem, e.g. AAAA or TTTT would be removed. Remove labels that contain a selected restriction site. Remove labels having a Tm that is outside of the range (38.5 to 39.5° C.). In other embodiments the range may be about 38 to 40, 38-39, or 39-40. Remove probes that have self complementarity beyond a selected threshold. Perform a hierarchical clustering to maximize sequence differences between labels to minimize cross hybridization, same label to same probe. Minimize self-complementarity within the collection to reduce tendency of two labels binding to each other.

FIG. **8** shows a counter adaptor **3101** that includes a counter region **3103**, a constant region for priming **3105** and a sticky end **3107** for ligation to an overhang created by restriction digestion, for example with BamHI. After ligation of the adaptors **3101** to the target fragment **3109** there are two adaptors ligated to the target fragment, one at either end. It is probable that the counters on the two ends will be different although there is a predictable probability of having the same counter ligated to both ends of the same fragment. After adaptor ligation the fragment **3111** can be amplified by PCR using a common primer to the **3103** region of the adaptor. The adaptor may first be filled in to make it double stranded. The PCR amplification may be used to preferentially amplify fragments of a selected size range, for example, 300 to 2 kb. Smaller fragments are not amplified as efficiently because of self complementarity between the ends of the individual strands (capable of forming a panhandle structure that inhibits amplification) and longer fragments (longer than about 3 kb) also don't amplify well.

After circularization, the uncircularized fragments can be digested using an exonuclease, for example. The circularized fragments can be amplified using target specific primers to generate amplification product **3113**. In the figure the target specific primers are identified as TS primer F and TS primer R. Whereas the primers used to amplify **3111** are common to all adaptor ligated fragments and will amplify all fragments that are in the size range to be amplified using PCR, the TS primers are specific for selected targets to be analyzed. The amplification product **3113** has in the 5' to 3' direction, target specific sequence, overhang sequence, a first counter, first adaptor sequence, circularization junction **3115**, second adaptor sequence, second counter, second overhang sequence and a second target specific sequence. The first and second counter are different (although they may be the same at a low probability) and the first and second target sequence are different. The product **3113** or preferably fragments thereof can be detected by a variety of methods, for example, an array of probes as exemplified by probe **3117** can be used. The array probe **3117** is complementary to a region of the target, the overhang region and the counter. When hybridized the target will have an overhanging single stranded region that corresponds to the adaptor sequence. A labeled probe **3119** that is complementary to one strand of the adaptor can be hybridized and the ligated to the array probe as shown, and as described below.

FIG. **9** shows a method for reading out the labeled targets on arrays. On the left, the target with G_1 ligated to L_1, "G_1L_1", is shown hybridizing to the complementary array probe over the entire length of the probe. On the right target G_1 ligated to label L_2 is shown partially hybridized to the G_1L_1 probe on the array. On the left the biotin labeled constant segment can hybridize to the G_1L_1 target and ligate to the 5' end of the G_1L_1 array probe. The constant segment can hybridize to the L_2 segment but will not ligate to L_1. This allows for labeling of properly hybridized target-label pairs with both hybridization and ligation discrimination. The lower panel shows an example where the target or G portion is not matching with the probe on the array. This will not ligate efficiently because it hybridizes less stably.

The left panel shows the results when target G_1 ligated to label L_1 to form G_1L^1 hybridizes to the complementary G_1L_1 probe on the array. The constant region (in white) can hybridize to its labeled complement so that the **3'** end of the labeled complement is juxtaposed with the 5' end of the L_1 region of the probe on the array and the ends can be ligated. In the center panel the target hybridizing to the G_1L_1 probe is non-cognate, the label region is L_2 and not L_1 so it does not hybridize to the L_1 region of the probe. The labeled oligo can hybridize to the partially hybridized target but it is not juxtaposed with the 5' end of the L_1 region of the probe so it should not ligate to the probe. In the right panel the target shown hybridized has the L_1 region and is complementary to the array probe at that region, but the array probe has a G region that is not G_1 so the G_1L_1 target does not hybridize. The labeled oligo can hybridize to the target but because the L1:L1 region is short the duplex is not stable and the labeled oligo does not ligate to the end of the array probe.

If you have N targets T ($T_1, T_2, \ldots T_N$) and each is present at a number of copies C ($C_1, C_2, \ldots C_x$) where X varies from target to target ($X_{T1}, X_{T2}, \ldots X_{TN}$) and you ligate to a set of Y different labels ($L_1, L_2, \ldots L_Y$) then you generate, for example, $T_1C_1L_1$, $T_1C_2L_2$, $\ldots T_NC_XL_{XT1}$, where X<<<Y). So, for example, if T1 is gene A and T2 is gene B and gene A is present in the sample at 500 copies and gene B is present at 100 copies, each copy of gene A, 1 to 500, will be attached to a different label (so there will be ~500 different labels attached to the gene A copies), and each copy of gene B, 1 to 100, will be attached to a different label.

A method for counting the number of occurrences of each of a plurality of same targets in a mixture of targets comprising multiple occurrences of each type of a plurality of different targets. In preferred aspects, the mixture of targets is a nucleic acid sample that contains different amounts of multiple target sequences. For example, there may be target sequences 1, 2, **3**, 4 and 5 that are expression products from 5 different genes, occur in the sample as follows: 1000 copies of target 1, 100 copies of target 2, 500 copies of target **3**, 10 copies of target 4 and 50 copies of target 5. The targets are preferably of known sequence and are treated so that they may be ligated to a label-tag sequence.

FIG. **1** shows one embodiment of the method. Labels or counters **101** are combined with assay targets **103** so that each target is combined with one label to form label-targets **105**. The process of combining an individual target with individual label molecules is a stochastic process. The number of labels each target type combines with is directly proportional to the

number of individual targets of that target type or the copy number of the target. The number of labels is counted by hybridization to arrays where individual label-targets are detected at different features.

The targets are mixed with a collection of label-tag sequences, each label-tag being a different sequence and the collection having a number that is preferably 10 times the number of copies of the most abundant target to be counted. In a preferred aspect, the label-tags are a collection of known sequences such as a collection of all possible timers (N_6). Each of the label-tag sequences is present in multiple copies in the mixture, but all are present at approximately equal amounts. The label-tag sequences are ligated to the targets. Ligation is random so that any given label-tag has about the same probability of ligating to any one target occurrence. So if there are 1000 different targets each could be ligated to a different label-tag sequence and the probability that any two target occurrences will have the same label-tag ligated is low. Because the ligation is a random stochastic process there is a known probability that if there are C copies of a given target and N different label-tags that any two copies of a target T will have the same label.

T1, T2, . . . TN. C1, C2, . . . CX, L1, L2, . . . LY where T are the different targets and there are N different targets, C are the different copies of a target and there are X copies of that target and L are the different label label-tags and there are Y label tags. X varies for each target and determining X is one of the objects of the present invention. The relationship between X and Y determines the probability that two C's will have the same L. In preferred aspects Y is greater than X for each target to be counted. This reduces the probability of undercounting due to double labeling. If C1 and C2 of T1 are both labeled with L3 both copies will be counted as a single occurrence, resulting in under counting. Undercounting can also be adjusted for by estimating the number of copies that are likely to be multiply labeled and adjusting the final count upwards to take those into account. For example, if there is a likelihood that 5 of 1000 copies will be labeled with the same label tag then the final number should be adjusted up by 0.5%.

In preferred aspects, the detection is by hybridization to an array of probes. The array has a collection of features for each target that includes a different feature for each label tag. For example, if there are X label tags there are X features for each target, T1L1, T1L2, . . . T1LX and the same for target 2, T2L1, T2L2, . . . T2LX, out to TNL1, TNL2, . . . TNLX. The number of features of the array is on the order of X times N. Each probe has a target complementary sequence and a label tag complementary sequence. Within a set of probes for a given target the target segment of the probe would remain constant and the label tag portion varies from feature to feature so that each label tag sequence is represented by at least one feature for each target.

In one aspect, the methods may be used to count the number of copies of each of a plurality of targets in a sample. The amount of target containing sample mixed with the label tags may be diluted so that the number of copies of each target to be counted is less than the number of label tags. For example, if the targets to be counted are present at about 1,000 copies per cell and there are 10,000 label tags you want to have the amount of sample in the mixture to be about the equivalent of one cell's worth of RNA. You can mix that with multiple copies of each label-tag, but you want to keep the absolute number of copies of target below the number of types of label tag sequences. Dilution of the sample and use of an appropriately small amount of starting material may be used. If a target sequence is present at low copy number per cell it is possible to use the nucleic acid from a larger number of cells. For example, to measure the DNA copy number of a chromosomal region relative to other chromosomal regions the expected copy number is low (e.g. 2 for normal) so if there are 10,000 different label tags, the number of genomes that can be added to the sample for attachment of label tags can be high, e.g. 500 to 1000.

In one aspect, the methods are used to identify regions of genomic amplification and chromosomal abnormalities. For example, the methods may be used to detect trisomy. Most of the chromosomal regions will be present in 2 copies per cell and the region of trisomy will be present in 3 copies per cell. You would expect to observe a 3:2 ratio in your count. For example, if you have 500 genomes you would have 1000 copies of most regions and 1500 copies of the trisomy regions. Small errors in the counting, resulting from undercounting, would have little or no effect on the counting.

In some aspects, controls of known copy number may be spiked in to a sample to determine accuracy.

Stochastic labeling of $t_{1,N}$ (collection of essential identical molecules of copy 1, 2 . . . N of target 1) by $L_{1,m}$ (effectively an infinite reservoir of diversity m when m is much greater than N). This allows for complete or near complete resolution of members of $t_{1,N}$, by imparting separate identities to the members of the collection of $t_{1,N}$ (provided that M is sufficiently smaller than N in the labeling). This provides for a stochastic or random projection of $t_{1,N}$ onto $L_{1,m}$. In some aspects $L_{1,m}$ is a library and the members of the library that are associated with $t_{1,N}$ can be counted to determine the number of copies of the target. In some aspects the methods can be described as indexing the members of the target. This provides a method to follow individual molecules that are members of a type of molecule that would not otherwise be distinguishable one from another.

Because stochastic labeling can impart identifiability to otherwise non-identifiable molecules it can impart identifiability to any two targets that may be very similar, but different. Examples of targets that may be highly similar but could be separately counted using the disclosed methods, include, for example, alternative splice forms of a gene, and sequences that have one or more variations, including a variation in a single base (e.g. SNP or indels (insertion or deletions of short regions, e.g. 1-5 bases). In some aspects the methods impart a clonal labeling, that allows a single copy to be separately detected and separately isolated from the solution.

Some nucleic acid sequencing reactions use methods that stochastically attach targets to a solid support followed by amplification of the attached target and analysis. The target attaches in an unknown location and the location can be determined by sequencing the amplified target at specific locations. In contrast, the disclosed methods provide for clonal amplification of known targets in a known location. The stochastic nature of the formation of the target-label-tag molecule provides a mechanism for isolating single occurrences of selected targets that can be subsequently amplified and analyzed. In some aspects the label can be used as a handle for isolating clonal populations of targets. The labeling step generates an indexed library that has a variety of applications. For example, the indexed library could be used for sequencing applications. The method adds distinguishability to any set of molecules, even molecules that are not distinguishable by other mechanisms because they may share common regions or even been identical. The indexed library can be stored and used multiple times to generate samples for analysis. Some applications include, for example, genotyping polymorphisms, studying RNA processing, and selecting clonal representatives to do sequencing.

In some aspects the methods are used to stochastically label a polyclonal antibody population. This may be used to identify different polyclonal populations.

The methods may be used to convert an analog readout of hybridization signal intensities on arrays into a measurable process that can be scored digitally on the arrays. The method leverages a random process where the tagging of assayed molecules is governed by stochastic behavior. In a random process, the more copies of a given target, the greater the probability of being tagged with multiple labels. A count of the number of incorporated labels for each target can approximate the abundance level of a given target of interest. The ability to count labels on microarrays would be a clear cost-advantage over the other existing techniques.

Serial analysis of gene expression (SAGE) is another method for analysis of gene expression patterns. SAGE relies on short sequence tags (10-14 bp) within transcripts as an indicator of the presence of a given transcript. The tags are separated from the rest of the RNA and collected. The tags can be linked together to form long serial molecules that can be cloned and sequenced. Quantitation of the number of times a particular tag is observed provides an estimate of the relative expression level of the corresponding transcript, relative to other tagged transcripts. See, for example, Velculescu et al. Science 270, 484-487 (1995) and Velculescu et al. Cell 88 (1997). Again this method provides a relative estimate of the abundance of a transcript and not an actual count of the number of times that transcript appears. Other methods based on counting and estimating relative abundance have also been described. See, for example, Wang et al. *Nat. Rev. Genet.* 10, 57-63 (2009). Additional methods for digital profiling are disclosed, for example, in U.S. Patent Pub. 20050250147 and U.S. Pat. No. 7,537,897.

A stochastic counting assay system as described herein can also be a sub-system within a much larger bio-analysis system. The bio-analysis system could include all the aspects of sample preparation prior to, for example, optical detection, the post processing of data collected in the optical detection phase and finally decision making based on these results. Sample preparation may include steps such as: extraction of the sample from the tested subject (human, animal, plant environment etc.); separation of different parts of the sample to achieve higher concentration and purity of the molecules under investigation; sample amplification (e.g. through PCR); attachment of fluorescence tags or markers to different parts of the sample; and transfer of the sample or a portion of the sample into a reaction vessel or site on a substrate. The post processing of the collected data may include: normalization; background and noise reduction; and statistical analysis such as averaging over repeated tests or correlation between different tests. The decision making may include: testing against a predefined set of rules and comparison to information stored in external data-bases.

The applications and uses of the stochastic labeling and counting methods and systems described herein can produce one or more result useful to diagnose a disease state of an individual, for example, a patient. In one embodiment, a method of diagnosing a disease comprises reviewing or analyzing data relating to the presence and/or the concentration level of a target in a sample. A conclusion based review or analysis of the data can be provided to a patient, a health care provider or a health care manager. In one embodiment the conclusion is based on the review or analysis of data regarding a disease diagnosis. It is envisioned that in another embodiment that providing a conclusion to a patient, a health care provider or a health care manager includes transmission of the data over a network.

Accordingly, business methods relating to the stochastic labeling and counting methods and methods related to use thereof as described herein are provided. One aspect of the invention is a business method comprising screening patient test samples for the amount of a biologically active analyte present in the sample to produce data regarding the analyte, collecting the analyte data, providing the analyte data to a patient, a health care provider or a health care manager for making a conclusion based on review or analysis of the data regarding a disease diagnosis or prognosis or to determine a treatment regimen. In one embodiment the conclusion is provided to a patient, a health care provider or a health care manager includes transmission of the data over a network.

Applications for the disclosed methods include diagnosing a cancerous condition or diagnosing viral, bacterial, and other pathological or nonpathological infections, as described in U.S. Pat. No. 5,800,992. Additional applications of the disclosed methods and systems include, pathogens detection and classification; chemical/biological warfare real-time detection; chemical concentration control; dangerous substance (e.g., gas, liquid) detection and alarm; sugar and insulin levels detection in diabetic patients; pregnancy testing; detection of viral and bacterial infectious diseases (e.g. AIDS, Bird Flu, SARS, West Nile virus); environmental pollution monitoring (e.g., water, air); and quality control in food processing.

Any available mechanism for detection of the labels may be used. While many of the embodiments discussed above use an array readout form, it will be obvious to one of skill in the art that other methods for readout may be used. For example, sequencing may be preferred in some embodiments.

In some aspects the readout is on an array. The array may be a solid support having immobilized nucleic acid probes attached to the surface in an ordered arrangement. The probes may be, for example, synthesized in situ on the support in known locations using photolithography or the probes may be spotted onto the support in an array format. As discussed above, in some embodiments the array includes a probe feature for each possible label-target combination. A feature preferably includes many copies of a single probe sequence. The feature may also have some probes that are not full length, resulting from truncation of synthesis. The photo activation process may not be 100% efficient so some probes are terminated at each step without having subsequent bases added. These truncated probes have the sequence of a portion of the full length probe.

Sequencing readout. After attachment of the labels to the targets in a stochastic manner, the targets may be amplified according to any of the methods disclosed herein and the amplification product may be subjected to any available sequencing method.

A number of alternative sequencing techniques have been developed and many are available commercially. For a review see, for example, Ansorge New Biotechnology 25(4):195-203 (2009), which is incorporated herein by reference. These include the use of microarrays of genetic material that can be manipulated so as to permit parallel detection of the ordering of nucleotides in a multitude of fragments of genetic material. The arrays typically include many sites formed or disposed on a substrate. Additional materials, typically single nucleotides or strands of nucleotides (oligonucleotides) are introduced and permitted or encouraged to bind to the template of genetic material to be sequenced, thereby selectively marking the template in a sequence dependent manner. Sequence information may then be gathered by imaging the sites. In certain current techniques, for example, each nucleotide type is

tagged with a fluorescent tag or dye that permits analysis of the nucleotide attached at a particular site to be determined by analysis of image data.

In another aspect, mass spec analysis may be used to detect the labels and count the targets. The labels can be distinguishable based on size or other property that can be detected. Many of the examples provided herein identify the label based on unique nucleic acid sequence but any distinguishable label may be used, for example, the pool of labels may be labels that are differentially detectable based on fluorescence emission at a unique wavelength.

FIG. **9** shows a method for reading out the labeled targets on arrays. On the left, the target with G_1 ligated to L_1, "G_1L_1", is shown hybridizing to the complementary array probe over the entire length of the probe. On the right target G_1 ligated to label L_2 is shown partially hybridized to the G_1L_1 probe on the array. On the left the biotin labeled constant segment can hybridize to the G_1L_1 target and ligate to the 5' end of the G_1L_1 array probe. The constant segment can hybridize to the L_2 segment but will not ligate to L_1. This allows for labeling of properly hybridized target-label pairs with both hybridization and ligation discrimination. The lower panel shows an example where the target or G portion is not matching with the probe on the array. This will not ligate efficiently because it hybridizes less stably.

The left panel shows the results when target G_1 ligated to label L_1 to form G_1L_1 hybridizes to the complementary G_1L_1 probe on the array. The constant region (in white) can hybridize to its labeled complement so that the 3' end of the labeled complement is juxtaposed with the 5' end of the L_1 region of the probe on the array and the ends can be ligated. In the center panel the target hybridizing to the G_1L_1 probe is non-cognate, the label region is L_2 and not L_1 so it does not hybridize to the L_1 region of the probe. The labeled oligo can hybridize to the partially hybridized target but it is not juxtaposed with the 5' end of the L_1 region of the probe so it should not ligate to the probe. In the right panel the target shown hybridized has the L_1 region and is complementary to the array probe at that region, but the array probe has a G region that is not G_1 so the G_1L_1 target does not hybridize. The labeled oligo can hybridize to the target but because the L1:L1 region is short the duplex is not stable and the labeled oligo does not ligate to the end of the array probe.

The methods are broadly applicable to counting a population of molecules by performing a stochastic operation on the population to generate a stochastic population of identifiable molecules. The targets need not be identical. For example, the methods may be used to count the absolute number of members of a group. In one aspect, a sample having an unknown number of copies of a selected nucleic acid target is fragmented randomly so that on average each copy of the target has a different end resulting from a distinct fragmentation event. A common adaptor sequence can be ligated to the end of each fragment and used for amplification of the fragments. Each ligation event generates a new molecule having a junction formed by the end of the random fragment and the adaptor sequence. The new junction can be detected by, for example, sequencing using a primer complementary to the adaptor or a region of the adaptor. Because the fragmentation was a stochastic process the number of different ends detected is a count of the number of different starting target molecules, assuming one fragment per starting target molecule.

The examples provided herein demonstrate the concept of using a stochastic labeling strategy in the high sensitivity detection and counting of individual DNA molecules. The difficult task of quantifying single nucleic acid molecules is converted into a simple qualitative assay that leverages the statistics of random probability; and at the same time, the requirement of single molecule detection sensitivity is achieved with PCR for the robust amplification of single DNA molecules. In some aspects improved methods for amplification will be used. For example, linear amplification methods may be used to mitigate the representation distortions created by exponential cycling in PCR. Given the lack of available techniques for single molecule counting, and the increasing need for its use, the new concept of stochastic labeling is likely to find numerous applications in the near future.

EXAMPLES

To demonstrate stochastic labeling, we performed an experiment to count small numbers of nucleic acid molecules in solution. Genomic DNA from a male individual with Trisomy 21 was used to determine the absolute and relative number of DNA copies of chromosomes X, 4 and 21, representing 1, 2 and 3 target copies of each chromosome, respectively. Genomic DNA isolated from cultured B-Lymphocytes of a male Caucasian with Trisomy 21 was purchased from The Coriell Institute for Medical Research (Catalog #GM01921). The DNA quantity was determined by PICOGREEN dye (Invitrogen) measurements using the lambda phage DNA provided in the kit as reference standard. DNA quality was assessed by agarose gel electrophoresis.

The DNA concentration in the stock solution was measured by quantitative staining with picogreen fluorescent dye, and dilutions containing 3.62 ng, 1.45 ng, 0.36 ng and 0.036 ng were prepared. In each dilution, the number of copies of target molecules in the sample was calculated from a total DNA mass of 3.5 pg per haploid nucleus (see, T. R. Gregory et al., *Nucleic Acids Res* 35, D332 (2007), and represent approximately 500, 200, 50 and 5 haploid genomes. The absolute quantity of DNA in the sample was determined by optical density measurements and quantitative staining with PICOGREEN fluorescent dye (Invitrogen) prior to making dilutions.

As outlined in FIG. 3, the genomic DNA sample **1901** was first digested to completion with the BamHI restriction endonuclease to produce 360,679 DNA fragments **1905**. A diverse set of labels consisting of 960 14-nucleotide sequences was synthesized as adaptors harboring BamHI overhangs (SEQ ID Nos. 44-1963). Genomic DNA was digested to completion with BamHI (New England BioLabs, NEB) and ligated to a pool of adaptors consisting of an equal concentration of 960 distinct labels. Each adaptor consists of a universal PCR priming site, a 14 nucleotide long counter sequence and a BamHI overhang (similar to the form of the adaptor shown in FIG. **7**). The sequence of the label adaptors SEQ ID Nos. 44-1963 were selected from an all-possible 4^{14} nucleotide combination to be of similar melting temperature, minimal self-complementation, and maximal differences between one-another. Homopolymer runs and the sequence of the BamHI restriction site were avoided. Each pair, for example, SEQ ID Nos. 44 and 45, form an adaptor pair that has a region of complementarity starting at base 12 in SEQ ID No. 44 and base 5 in SEQ ID No. 45:

```
5' CGACAGACGCCTGATCTTTTGTTAGCCGGAGT 3'   SEQ ID 44

3' ACTAGAAAACAATCGGCCTCACTAG 5'          SEQ ID 45
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The adaptors have a 5' overhang of 11 bases in the even numbered SEQ IDs and 4 bases (GATC) in the odd numbered SEQ IDs. Oligonucleotides were synthesized (Integrated

DNA Technologies) and annealed to form double-stranded adaptors prior to pooling. For ligation, the digested DNA was diluted to the desired quantity and added to 100 pmoles (equivalent to 6×10^{13} molecules) of pooled label-adaptors, and 2×10^{6} units (equivalent to 1×10^{13} molecules) of T4 DNA ligase (NEB) in a 30 μl reaction. The reaction was incubated at 20° C. for 3 hours until inactivation at 65° C. for 20 minutes.

For the stochastic labeling reaction, each DNA fragment-end randomly attaches to a single label by means of enzymatic ligation of compatible cohesive DNA ends to generate labeled fragments **1907**. High coupling efficiency is achieved through incubation with a large molar excess of labels and DNA ligase enzyme (~10^{13} molecules each). At this stage, the labeling process is complete, and the samples can be amplified as desired for detection. A universal primer may be added, and the entire population of labeled DNA fragments may be PCR amplified. The PCR reaction preferentially amplifies approximately 80,000 fragments in the 150 bp-2 kb size range (FIG. **21**). Adaptor-ligated fragments were amplified in a 50 μl reaction containing 1× TITANIUM Taq PCR buffer (Clontech), 1M betaine (Sigma-Aldrich), 0.3 mM dNTPs, 4 μM PCR004StuA primer (SEQ ID No. 1974), 2.5 U Taq DNA Polymerase (USB), and 1× TITANIUM Taq DNA polymerase (Clontech). An initial PCR extension was performed with 5 minutes at 72° C.; 3 minutes at 94° C.; followed by 5 cycles of 94° C. for 30 seconds, 45° C. for 45 seconds and 68° C. for 15 seconds. This was followed by 25 cycles of 94° C. for 30 seconds, 60° C. for 45 seconds and 68° C. for 15 seconds and a final extension step of 7 minutes at 68° C. PCR products were assessed with agarose gel electrophoresis and purified using the QIAQUICK PCR purification kit (Qiagen).

The purified PCR product was denatured at 95° C. for 3 minutes prior to phosphorylation with T4 polynucleotide kinase (NEB). The phosphorylated DNA was ethanol precipitated and circularized using the CIRCLIGASE II ssDNA Ligase Kit (Epicentre). Circularization was performed at 60° C. for 2 hours followed by 80° C. inactivation for 10 minutes in a 40 μl reaction consisting of 1× CIRCLIGASE II reaction buffer, 2.5 mM $MnCl_2$, 1M betaine, and 200 U CIRCLIGASE II ssDNA ligase. Uncirculated DNAs were removed by treatment with 20 U Exonuclease I (Epicentre) at 37° C. for 30 minutes. Remaining DNA was purified with ethanol precipitation and quantified with OD_{260} measurement.

Amplification of gene targets. Three assay regions were tested: One on each of chromosomes 4, 21 and X. The genomic location (fragment starting and ending positions are provided), of the selected fragments are as follows: Chr4 106415806_106416680 (SEQ ID No. 1), Chr21 38298439_38299372 (SEQ ID No. 2), and ChrX 133694723_133695365 (SEQ ID No. 3). The lengths are 875, 934 and 643 bases respectively. The circularized DNA was amplified with gene specific primers (SEQ ID Nos. 4-9) in a multiplex inverse PCR reaction. PCR primers were picked using Primer3 (available from the FRODO web site hosted by MIT) to yield amplicons ranging between 121 and 168 bp. PCR was carried out with 1× TITANIUM Taq PCR buffer (Clontech), 0.3 mM dNTPs, 0.4 μM each primer, 1× TITANIUM Taq DNA Polymerase (Clontech), and ~200 ng of the circularized DNA. After denaturation at 94° C. for 2 minutes, reactions were cycled 30 times as follows: 94° C. for 20 seconds, 60° C. for 20 seconds, and 68° C. for 20 seconds, with a 68° C. final hold for 4 minutes. PCR products were assessed on a 4-20% gradient polyacrylamide gel (Invitrogen) and precipitated with ethanol.

The amplified DNA was fragmented with DNase I, end-labeled with Biotin, and hybridized to a whole-genome tiling array which spans the entire non-repetitive portion of the genome with uniform coverage at an average probe spacing of ~200 nt (see Matsuzaki et al., *Genome Biol* 10, R125 (2009) and Wagner et al. *Systematic Biology* 43, 250(1994)). In FIG. **21**, probe intensity ("Array Intensity") from the whole-genome tiling array (y-axis) is grouped into 200 nt bins by the length of the BamHI fragment on which it resides. High probe intensity demonstrates the amplification of fragments in the 600 bp~1.2 kb size range (x-axis, log-scale). The computed size distribution of BamHI restricted fragments in the reference genome sequence (NCBI Build 36) is shown by the curve labeled "Number of Fragments". After circularization of the amplified products to obtain circles **1909**, three test target fragments were isolated using gene-specific PCR; one on each of chromosomes X, 4, and 21, and prepared for detection.

The three labeled targets were counted using two sampling techniques: DNA microarrays and next-generation sequencing. For the array counting, a custom DNA array detector capable of distinguishing the set of labels bound to the targets was constructed by dedicating one array element for each of the 960 target-label combinations. Each array element consists of a complementary target sequence adjacent to one of the complements of the 960 label sequences (as shown in FIG. **1**).

Array Design: For each gene target assayed, the array probes tiled consist of all possible combinations of the 960 counter sequences connected to the two BamHI genomic fragment ends (FIG. **8**). An additional 192 counter sequences that were not included in the adaptor pool were also tiled to serve as non-specific controls. This tiling strategy enables counter detection separately at each paired end, since each target fragment is ligated to two independent counters (one on either end).

Arrays were synthesized following standard Affymetrix GENECHIP manufacturing methods utilizing lithography and phosphoramidite nucleoside monomers bearing photolabile 5'-protecting groups. Array probes were synthesized with 5' phosphate ends to allow for ligation. Fused-silica wafer substrates were prepared by standard methods with trialkoxy aminosilane as previously described in Fodor et al., Science 251:767 (1991). After the final lithographic exposure step, the wafer was de-protected in an ethanolic amine solution for a total of 8 hrs prior to dicing and packaging.

Hybridization to Arrays: PCR products were digested with Stu I (NEB), and treated with Lambda exonuclease (USB). 5 μg of the digested DNA was hybridized to a GeneChip array in 112.5 μl of hybridization solution containing 80 μg denatured Herring sperm DNA (Promega), 25% formamide, 2.5 pM biotin-labeled gridding oligo, and 70 μl hybridization buffer (4.8M TMACl, 15 mM Tris pH 8, and 0.015% Triton X-100). Hybridizations were carried out in ovens for 16 hours at 50° C. with rotation at 30 rpm. Following hybridization, arrays were washed in 0.2×SSPE containing 0.005% Trition X-100 for 30 minutes at 37° C., and with TE (10 mM Tris, 1 mM EDTA, pH 8) for 15 minutes at 37° C. A short biotin-labeled oligonucleotide (see **3119** in FIG. **8**) was annealed to the hybridized DNAs, and ligated to the array probes with *E. coli* DNA ligase (USB). Excess unligated oligonucleotides were removed with TE wash for 10 minutes at 50° C. The arrays were stained with Streptavidin, R-phycoerythrin conjugate (Invitrogen) and scanned on the GCS3000 instrument (Affymetrix).

In order to maximize the specificity of target-label hybridization and scoring, we employed a ligation labeling procedure on the captured sequences (FIG. **8**). We set thresholds to best separate the intensity data from the array into two clusters, one of low intensity and one of high intensity to classify

labels as either being used or not (FIGS. **22**, **23** and **29**). We score a label as "present" and counted if its signal intensity exceeded the threshold. To count labels we set thresholds for the array intensity, or the number of sequencing reads. Appropriate thresholds were straightforward to determine when used and un-used labels fall into two distinct clusters separated by a significant gap. In situations where a gap was not obvious, the function normalmixEM in the R package mixtools was used to classify labels. This function uses the Expectation Maximization (EM) algorithm to fit the data by mixtures of two normal distributions iteratively. The two normal distributions correspond to the two clusters to be identified. The cluster of labels with a high value is counted as "used", and the other as "not used". The average of the minimum and maximum of the two clusters, $(I_{min}+I_{max})/2$, was applied as the threshold for separating the two clusters.

Sampling error calculation. A sampling error can be introduced when preparing dilutions of the stock DNA solution. This error is a direct consequence of random fluctuations in the number of molecules in the volume of solution sampled. For example, when exactly 10 μl of a 100 μl solution containing 100 molecules is measured, the actual number of molecules in the sampled aliquot may not be exactly 10. The lower the concentration of the molecules in the entire solution, the higher the sampling error, and the more likely the actual abundance in the sampled aliquot will deviate from the expected abundance (n=10). To calculate sampling errors, we determined the number of molecules for each chromosome target in our stock DNA solution and performed numerical simulations to follow our dilution steps in preparing the test samples (3.62 ng, 1.45 ng, 0.36 ng and 0.036 ng). To illustrate, if the dilution step is sampling 1 μl of a 25 μl solution containing 250 molecules, we create 25 bins and randomly assign each of the 250 molecules into one of the bins. We randomly choose one bin and count the number of molecules assigned to that bin to simulate the process of sampling $1/25^{th}$ of the entire solution. If a serial dilution was performed, we would repeat the simulation process accordingly. For each dilution, the observed copy number ratios of Chr 4:X or 21:X for 10,000 independent trials are summarized as observed medians, along with the 10th and 90th percentiles and shown in FIGS. **12** and **13**.

As an alternate form of detection, the samples were submitted to two independent DNA sequencing runs (FIG. **10**). The arrangement and position of the adaptors and PCR primers used to convert the DNA sample hybridized to microarrays into sequencing templates are shown in the figure. The circularized junction **3115** is located between the two counter labels. PCR primers that have restriction sites are used to amplify two fragments. The fragments are digested with the restriction enzymes to generate ends compatible with ligation to sequencing adaptors. The sequencing adaptors are ligated to the ends to generate a fragment that has the label sequence and a portion of the target that is 48 to 94 base pairs in length are flanked by sequences for use with SOLID sequencing.

Validation by DNA sequencing (First SOLID run). DNA targets that were used for hybridization to arrays were converted to libraries for sequencing on the SOLID instrument (ABI). P1 and P2 SOLID amplification primers were added to the DNA ends through adaptor ligation and strand extension from gene-specific primers flanked by P1 or P2 sequences (FIG. **10**). Each sample received a unique ligation adaptor harboring a 4-base encoder (SEQ ID Nos. 34-43) that unambiguously identifies the originating sample of any resulting read. Each adaptor includes two strands, SEQ ID Nos. 34 and 35, 36 and 37, 38 and 39, 40 and 41 or 42 and 43, that hybridize to form a double stranded region of 29 base pairs and a single stranded 4 base overhang (GATC). Individual libraries were prepared for each sample, and quantified with picogreen before equal amounts of each sample was combined into a single pooled library. DNA sequencing was performed on SOLID v3 by Cofactor Genomics. A total of ~46 million 50 base reads were generated. Each read is composed of three segments, corresponding to the sample encoder, label sequence and gene fragment (FIG. **10**). We removed reads if: uncalled color bases were present, the average Quality Value (aQV) of the whole read <10, the aQV of the sample encoder <20, or the aQV of the label sequence <18. 40% of the raw reads were removed. Filtered reads were mapped to reference sequences using the program Short Oligonucleotide Color Space (SOCS), available from ABI with a maximum tolerance of 4 color mismatches between the first 45 color bases in each read and reference sequences (the last 5 color bases on 3'end of each read were trimmed in alignment). About 64.3% reads were uniquely mapped to reference sequences, of which 89.5% (16 million) have high mapping quality, i.e., with no mismatch in the sample encoder and at most 1 mismatch in the label sequence. These high-quality reads, accounting for ~35% of the total reads generated, were used in subsequent counting analysis.

Sequencing replication (Second SOLID run). An aliquot of the exact same DNA library originally sequenced by Cofactor Genomics was subsequently re-sequenced by Beckman Coulter Genomics. Approximately 50 million 35 base reads were generated, and processed following the same rules. Approximately 61% of the raw reads passed quality filters, of which 81% uniquely mapped to a reference sequence with a maximum tolerance of 3 color mismatches (An adjusted mismatch tolerance was applied in the alignment step to account for the shorter length of these reads). Of the mapped reads, 91% (22.5 million) are of high mapping quality, i.e., with perfect match in the sample encoder and at most 1 mismatch in the label sequence. These high-quality reads (45% of the total raw reads generated) were used for counting analysis.

Between several hundred thousand to several million reads were used to score the captured labels. Table 1 shows the number of mapped reads from SOLID DNA sequencing.

TABLE 1

DNA sample			5 ng	2 ng	0.5 ng	0.05 ng	0 ng
Chr4	Left side	1st SOLiD run	709,076	252,211	237,380	316,629	1,204
		2nd SOLiD run	621,372	73,962	189,937	237,520	411
	Right side	1st SOLiD run	1,724,955	1,662,958	1,114,246	2,201,078	3,353
		2nd SOLiD run	1,422,673	1,359,512	839,775	980,616	2,386
Chr21	Left side	1st SOLiD run	1,615,416	1,474,208	832,234	1,428,540	1,851
		2nd SOLiD run	1,296,685	1,038,456	622,429	930,461	840
	Right side	1st SOLiD run	1,124,772	886,421	551,192	849,204	821
		2nd SOLiD run	910,298	522,358	367,207	479,621	224

TABLE 1-continued

DNA sample			5 ng	2 ng	0.5 ng	0.05 ng	0 ng
ChrX	Left side	1st SOLiD run	444,960	316,975	254,386	515,213	744
		2nd SOLiD run	266,606	157,860	137,706	220,121	5
	Right side	1st SOLiD run	1,227,047	921,214	777,033	1,064,531	64
		2nd SOLiD run	1,043,475	768,296	559,038	695,873	43

We set thresholds for the number of sequencing reads observed for each label, and score a label as "present" and counted if the number of sequencing reads exceeded the threshold. Label usage summaries from experimental observations or from the stochastic modeling are shown in Table 2. The number of attached labels, k, detected for each target in each dilution either by microarray counting or sequence counting is presented in Table 2, and plotted in FIGS. **4** and **5**.

Several dilutions (3.62 ng, 1.45 ng, 0.36 ng and 0.036 ng) of DNA isolated from cultured of a Trisomy 21 male individual were processed for microarray hybridization (FIG. **12** left) and DNA sequencing (FIG. **12** right). Three gene targets were tested from chromosome X, 4 and 21, and observed numbers of detected labels are shown (lines **1201**). The number of target molecules for each sample was determined from the amount of DNA used, assuming a single haploid nucleus corresponds to 3.5 pg. For comparison, the calculated number of labels expected to appear using a stochastic model are also plotted (lines **1202**). Numerical values are provided in Table 4. Relative copy ratios of the three gene targets (FIG. **13**): ChrX (right bar), Chr4 (left bar) and Chr2l (center bar) representing one, two and three copies per cell, respectively. Different dilutions (3.62 ng, 1.45 ng, 0.36 ng and 0.036 ng) of the DNA isolated from cultured lymphoblasts of a Trisomy 21 male individual were processed for microarray hybridization and DNA sequencing. The calculated number of target molecules was determined from the number of labels detected on microarrays (Table 4, column 9) or from the SOLiD sequencing data. For each sample dilution, the copy number ratio of each gene target relative to ChrX is shown for Microarray (FIG. **13** left) and SOLiD sequencing (FIG. **13** right). For comparison, relative copy ratios obtained from in silico sampling simulations are also shown in (FIG. **13** left) and (FIG. **13** right), where circles indicate the median values from 10,000 independent trials and error bars indicate the 10th and 90th percentiles. The 90th percentile values of the relative copy ratios at the lowest concentration (0.036 ng) are explicitly labeled in the plots.

TABLE 2

DNA sample			3.62 ng	1.45 ng	0.36 ng	0.036 ng	0 ng
Chr4		Stochastic Model	633	336	98	10	0
	Left side	Microarray	501	260	102	14	0
		1st SOLiD run	513	251	101	14	0
		2nd SOLiD run	516	273	102	14	0
	Right side	Array	525	256	107	14	0
		1st SOLiD run	544	291	103	13	1
		2nd SOLiD run	557	307	103	13	1
Chr21		Stochastic Model	769	457	143	15	0
	Left side	Microarray	651	335	160	20	0
		1st SOLiD run	678	381	152	20	0
		2nd SOLiD run	665	358	161	18	0
	Right side	Microarray	627	341	157	20	0
		1st SOLiD run	650	381	146	19	0
		2nd SOLiD run	653	379	146	19	0
ChrX		Stochastic Model	400	186	50	5	0
	Left side	Microarray	281	148	50	11	0
		1st SOLiD run	290	149	43	11	0
		2nd SOLiD run	300	150	45	11	0

TABLE 2-continued

DNA sample			3.62 ng	1.45 ng	0.36 ng	0.036 ng	0 ng
	Right side	Microarray	306	133	48	10	1
		1st SOLiD run	336	153	50	12	0
		2nd SOLiD run	344	167	43	11	0

The counting results span a range of approximately 1,500 to 5 molecules, and it is useful to consider the results in two counting regimes, below and above 200 molecules. There is a striking agreement between the experimentally observed number of molecules and that expected from dilution in the first regime where the ratio of molecules to labels (n/m) <0.2 (Table 2). Below 200 molecules the data are in tight agreement, including the data from the lowest number of molecules, 5, 10 and 15 where the counting results are all within the expected sampling error for the experiment (The sampling error for 10 molecules is estimated to be 10±6.4, where 10 and 6.4 are the mean and two standard deviations from 10,000 independent simulation trials).

In the second regime above 200 molecules, there is an approximate 10-25% undercounting of molecules, increasing as the number of molecules increases. We attribute this deviation to be due to a distortion in the amplification reaction. PCR-introduced distortion occurs from small amounts of any complex template due to the differences in amplification efficiency between individual templates (2, 3). In the present case, stochastic labeling will produce only one (at low n/m ratios), and increasingly several copies (at higher n/m ratios) of each template. Modeling suggests that simple random dropout of sequences (PCR efficiencies under 100%) generate significant distortion in the final numbers of each molecule after amplification. At any labeling ratio, random dropout of sequences due to PCR efficiency will result in an undercount of the original number of molecules. At high n/m ratios, the number of labels residing on multiple targets will increase and have a statistical survival advantage through the PCR reaction causing greater distortion. In support of this argument, we observe a wide range of intensities on the microarray and a wide range in the number of occurrences of specific sequences in the sequencing experiments (FIGS. **22**, **29**). This effect can be reduced by carrying out the reaction at n/m ratios near or less than 0.2, increasing the number of labels m, further optimization of the amplification reaction, or by employing a linear amplification method. Other factors, such as errors from inaccurate pipetting, could also contribute.

The lymphoblast cell line used in this study provides an internal control for the relative measurement of copy number for genes residing on chromosomes X, 4 and 21. FIG. **13** presents the relative number of molecules from all three chromosomes normalized to copy number 1 for the X chromosome. As shown, the measurements above 50 molecules all yield highly precise relative copy number values. At low numbers of molecules (0.036 ng), uncertainty results because the stochastic variation of molecules captured by sampling an

aliquot for dilution are significant. Numerical simulations were performed to estimate the sampling variation, and summarized medians, along with the 10th and 90th percentiles of the copy number ratios and are shown in FIG. **13** as circles and range bars, respectively. At the most extreme dilutions, where ~5, 10, and 15 molecules are expected for the chromosome X, 4 and 21 genes, the copy number ratios fall within the expected sampling error.

Overall, the identity of labels detected on the microarrays and in sequencing are in good agreement, with only a small subset of labels unique to each process (Table 7). Despite a high sequencing sampling depth (Table 1), a small number of labels with high microarray intensity appear to be missing or under-represented in the sequencing results. In contrast, labels that appear in high numbers in the sequencing reaction always correlate with high microarray intensities. No trivial explanation could be found for the labels that are missing from any given sequencing experiment. While under-represented in some experiments, the same labels appear as present with high sequence counts in other experiments, suggesting that the sequences are compatible with the sequencing reactions.

PCR validation. We used PCR as an independent method to investigate isolated cases of disagreement, and demonstrated that the labels were present in the samples used for the sequencing runs.

PCR was used to detect the presence of 16 label sequences (Table 3) which were either observed as high or low hybridization intensity on microarrays, and observed with either high or low numbers of mapped reads in SOLID sequencing. The Chr4 gene target was PCR amplified with 3 dilutions (0.1 pg, 1 pg, and 10 pg) of the 3.62 ng NA01921 sample, using the DNA target that was hybridized to microarrays, or the prepared SOLID library template. PCR products were resolved on 4% agarose gels and fluorescent DNA bands were detected after ethidium bromide staining.

TABLE 3

PCR detection for the presence of label sequences in the processed DNA sample that was hybridized to microarray, or in the DNA sequencing library.

Label ID	Label Sequence	1st SOLiD reads	2nd SOLiD reads	Microarray intensity	Microarray target template	SOLiD library template
112	AGATCTTGTGTCCG	0	2	15,907	1	2
182	ATCTTCGACACTGG	0	1	10,304	3	4
779	TCGAGATGGTGTTC	0	4	9,411	5	6
782	TCGGATAGAGAGCA	0	0	6,716	7	8
783	TCGGTACCAACAAC	1	4	13,132	9	10
290	CCAAGGTTTGGTGA	1	17	10,777	11	12
780	TCGCAAGAGGTAAG	1	1	8,915	13	14
570	GGAGTTACGGCTTT	1	2	8,252	15	16
741	TCAACCAGTAAGCC	794	400	466	17*	18*
424	CTGTAAACAACGCC	1,191	1,292	527	19*	20*
242	CACGATAGTTTGCC	905	781	1,103	21*	22
859	TGTACTAACACGCC	920	892	1,107	23*	24*
83	ACGCTAACTCCTTG	8,629	7,704	19,500	25	26
383	CGTTTACGATGTGG	7,278	6,402	19,022	27	28
804	TCTTAGGAAACGCC	0	0	70	29*	30*
834	TGCAATAGACGACC	0	1	72	31*	32*

Each PCR contained 0.1 pg of template, which represents approximately 1 x 10^6 DNA molecules.
The number of mapped sequencing reads and the microarray intensity of each of the 16 labels for this selected gene target (Chr4, 3.62 ng) are listed.
The last 2 columns show the gel lane number containing the indicated sample.
Those numbers indicated by an * correspond to reactions where PCR failed to detect the label sequence in the sample.

Although we can clearly confirm their presence in the sequencing libraries, it is unclear as to why these labels are missing or under-represented in the final sequencing data.

To test the stochastic behavior of label selection, we pooled the results of multiple reactions at low target concentrations (0.36 and 0.036 ng), where the probability that a label will be chosen more than once is small.

FIG. **14** shows that the number of times each label is used closely follows modeling for 1,064 data points obtained from microarray counting. The graph is a comparison between experimentally observed label usage rates (microarray results) with those predicted from stochastic model (stochastic model). At low target molecule numbers, the chance of multiple target ligations to the same label sequence is low. It is therefore reasonable to consider data from experiments

with low target numbers (0.036 ng and 0.36 ng of DNA), from those experiments, a total of 1,064 labels were observed, with the total frequency of label usage ranging from 0 to 6. The theoretically expected label usage frequency for 1,064 target molecules was obtained by performing 5000 simulation runs, with multiple independent reactions simulated in each run. The error bars indicate one standard deviation from the corresponding means.

Furthermore, since each end of a target sequence chooses a label independently, we can compare the likely hood of the same label occurring on both ends of a target at high copy numbers. Table 4 columns 10-11 present the experimentally observed frequency of labels occurring in common across both ends of a target and their expected frequency from numerical simulations. No evidence of non-stochastic behavior was observed in this data.

given the estimated number of target molecules in 2nd column; column 4: number of labels expected to be observed in common across the paired-ends (predicted by theoretical models), given the estimated number of target molecules in 2nd column; column 5: empirically observed number of labels used at the left end of gene target; column 6: empirically observed number of labels used at the right end of gene target; column 7: empirically observed number of labels used in common across the paired-ends; column 8: number of target molecules predicted by theoretical models, based on the empirically observed number of labels used (i.e., number in 7th column); column 9: number of labels expected to be observed in common across the paired-ends, given the number of target molecules in 8th column; column 10: empirically observed number of labels that were used in common across the paired-ends of the gene target.

TABLE 4

Gene target	Genomic DNA amount (ng)	Estimated # of molecules at either end	Expected # of labels at either end	Expected # of labels in common across paired-ends	Microarray observed # of labels L	R	Avg	# of molecules inferred from microarray observed # of labels	Expected # of labels in common across paired-ends	Microarray observed # of labels in common across paired-ends
Chr4	3.62	1034	633	417.68 ± 11.35	501	525	513	733	273.96 ± 10.24	303
	1.45	414	336	117.92 ± 7.83	260	256	258	300	69.22 ± 6.43	63
	0.36	103	98	9.93 ± 2.81	102	107	104	110	11.26 ± 2.99	20
	0.036	10	10	0.11 ± 0.32	14	14	14	14	0.20 ± 0.44	0
	0	0	0	0	0	0	0	0	0	0
Chr21	3.62	1551	769	616.74 ± 11.94	651	627	639	1051	425.28 ± 11.37	453
	1.45	620	457	217.36 ± 9.51	335	341	338	416	118.79 ± 7.83	130
	0.36	155	143	21.37 ± 3.98	160	157	158	172	25.86 ± 4.38	32
	0.036	15	15	0.24 ± 0.48	20	20	20	20	0.40 ± 0.62	0
	0	0	0	0	0	0	0	0	0	0
ChrX	3.62	517	400	166.63 ± 8.81	281	306	294	351	90.14 ± 7.08	103
	1.45	207	186	36.26 ± 4.98	148	133	140	151	20.34 ± 3.94	23
	0.36	51	50	2.58 ± 1.52	50	48	49	50	2.45 ± 1.51	4
	0.036	5	5	0.03 ±0.16	11	10	10	10	0.10 ± 0.31	2
	0	0	0	0	0	1	0	0	0	0
1	2	3	4	5	6	7	8	9	10	11

Labels detected on microarray experiments are quantified in Table 4. Indicated quantities (col. 2) of genomic DNA derived from a Trisomy 21 male sample were tested on 3 chromosome targets (col. 1). The estimated number of copies of target molecules (or haploid genome equivalents, col. 3), the number of labels expected by the stochastic model (col. 4), and the actual number of labels detected on microarrays (col. 6-8) are summarized. Because each gene target fragment paired-end consists of random, independent label ligation events at the left (L) and the right (R) termini, the number of identical labels expected (col. 5) can be predicted from computer simulations, and compared to the number actually detected (col. 11). Given the number of labels detected (col. 8), we obtain the corresponding number of copies of target molecules (col. 9) in our stochastic model, and the predicted occurrences of identical labels across paired-ends (col. 10). The numbers in col. 5 and 10 are the means from 5,000 independent simulation runs along with one standard deviation of the corresponding means, given the number of labels at either end (col. 4 and col. 9).

The detailed column information for Table 4 is as follows: column 1: name of tested gene targets; column 2: estimated number of target molecules at either left or right end, this number is determined by PICOGREEN dye measurement (Molecular Probes, Inc.), the DNA concentration is also listed in this column; column 3: number of labels expected to be observed/used at either end (predicted by theoretical models),

In another example, an array was designed having 48 target sequences. Each target was paired with one of 3840 labels or "counters" for a total of 48×3840 or 184,320 probes. The probes were 30 mers (30 nucleotides in length) and the assay was designed to test whether or not the 30 mer imparts sufficient discrimination. Of the 30 bases, 15 bases are from the labels and the other 15 bases are derived from the targets. The probes were assayed to determine if each label-target combination hybridizes specifically. A phage RNA ligase was used to join labels with targets. Universal priming sites of 18 bases were included on the 5' end of the labels and the 3' end of the targets, facilitating PCR amplification of the joined label-targets. The method is diagramed in FIG. **4**.

The 3840 distinct label oligos (counters) were single stranded oligos pooled from the DdeI TACL primer panel (40 primer plates by 96 wells per plate for 3840 different oligos). An example label oligo **301** is shown

(SEQ ID NO: 1964)

5' TCGATGGTTTGGCGCGCCGGTAGTTTGAACCATCCAT-3'.

The 48 different primers used as "targets" were synthesized using as target 48 different 21 nucleotide sequences from the

Affymetrix TrueTag 5K_A array. An example target oligo **307** is shown

(SEQ ID NO: 1965)
5' GCCATTTACAAACTAGGTATTAATCGATCCTGCATGCC-3'.

The "label" or "counter" oligo has an 18 nt common sequence at the 5' end and a 15-28 nt "label" (or "counter") sequence at the 3' end. An example "label" **305** is shown. The universal primer **303** common to all or a group of the label oligos has sequence 5' TCGATGGTTTGGCGCGCC-3' (SEQ ID NO: 1966) at the 5' end and each target oligonucleotide has common sequence **311** 5' AATCGATCCTGCATGCCA-3' (SEQ ID NO: 1967) at the 3' end as universal priming sequence. The target oligos vary in sequence at the 5' ends **309**.

A 1:1 dilution of each of the 3840 counters was mixed with various dilutions of each of the 48 target oligos to simulate different expression levels under ligation conditions so that the 5' end of the target oligos can be ligated to the 3' end of the label oligos. In preferred aspects T4 RNA ligase may be used to join the ends of the single stranded oligos. The 5' and 3' ends of the target oligos are phosphorylated and the 5' and 3' ends of the label oligos are hydroxylated. After the ligation the products are amplified by PCR using primers to the universal priming sequences. Only those fragments that have both universal priming sequences **303** and **311** will amplify efficiently.

Each of the 48 target sequences may be tiled with each of the 3,840 counters, resulting in a total number of features on array=48×3,840=184,320. This is the number of different possible combinations of target with label. The product of the ligation and amplification reactions is hybridized to the array. For each target, the number of features that light up is determined and can be compared to the known copy number of each target in the input sample.

To test the digital counting methods, also referred to as stochastic labeling a collection of label-tag sequences was provided. Each has a common 5' universal priming sequence, preferably 15-20 bases in length to facilitate amplification, and a 3' label sequence, preferably 17-21 bases in length. Each type of primer in the collection has the same universal priming sequence but each type has a label sequence that is different from all of the other types in the collection. In one aspect there are about 4,000 to 5,000 different types of label sequences in the collection to be used. For testing the method, a set of 50 target sequences was synthesized. The target sequences each have a universal priming sequence at the 3' end (5'GCTAGGGCTAATATC-3'SEQ ID NO: 1968, was used in this experiment). Each of the 50 oligo target sequences that were generated has a different 21 base sequence from the GENFLEX array collection of sequences, for example, 5' GCCATTTACAAACTAGGTATT'3' SEQ ID NO: 1970. The collection of label-tag oligos and the collection of target oligos was mixed. Various dilutions of the different targets were used in the mixture of targets to simulate a mixed population present at different levels, for example, different expression or copy number levels. T4 RNA ligase was added to ligate the label-tag oligos to the target oligos. There are 5000 different types of label oligos and 50 different types of target oligos so the majority of the target oligos of the same type will be labeled with a type of label oligo that is different from all of the other target oligos of that type. So target oligo type 1, occurrence 1 will be labeled with a label oligo type A (11A) and target oligo type 1, occurrence 2, will be labeled with a different label oligo, label oligo type B (12B). There is a finite and calculable probability that two or more occurrences of the same target type will be labeled with the same label oligo (11A and 12A), but that probability decreases as the number of different types of label oligos increases relative to the number of occurrences of any given type of target.

The ligated target/label oligos are then amplified using primers to the universal priming sites. Labels can be incorporated during amplification. The labeled amplification product is then hybridized to an array. For each different possible combination of target (50) and label (5000) there is a different probe on the array that targets that junction of the target ligated to the label. There will therefore be 50×5000 different probes on the array or 250,000 different probes.

Scanned images of the 48×3840 array were analyzed and compared to expected results. A total of 8 of the 48 targets were ligated to a pool of 3840 labels (counters). The assay was as shown in FIG. 3. The conditions were single strand deoxyoligonucleotide ligation using a phage RNA ligase to join the labels with targets. Universal priming sites on the targets and labels were included to enable PCR amplification of the joined label-targets. The ligation conditions were essentially as described in (Tessier, D. C. et al. (1986) *Anal Biochem.* 158, 171-178, 50 mM Tris-HCl, pH 8, 10 mM MgCl2; 10 ug/mL BSA, 25% PEG, 1 mM HCC, 20 uM ATP; 5:1 acceptor (labels) to donor (the 8 targets) ratio at 25 C overnight. The products were amplified using PCR, purified, biotin labeled with TdT, hybridized to the array, washed, stained, and scanned. The expected 8 blocks show hybridization to the array in the expected patterns.

Different ligation conditions were also tested by ligating either a single target or a pool of 48 targets to the 3,840 counters. The concentrations of the targets used in the experiment were high as in the previous experiment so most counters will be ligated to targets. In ligation 1 a single target was ligated to 3,840 labels. In ligation 2, 48 targets at 1:1 copy number were ligated to 3,840 labels. Ligation 3 is a negative control for PCR so no DNA was added. PCR with the pair of universal primers was performed using the ligation products as template and the products separated on a gel. As expected a band was observed from ligations 1 and 2, but not 3. The PCR products were labeled and hybridized to the array and the scan images after array hybridization were analyzed. As expected no signal was observed for ligation 3, all of the targets were observed for ligation 2 and the single expected target was observed for ligation 1. The single target lights up in the correct region of the chip, but background signal was also observed in unexpected locations. Increased stringency of hybridization conditions can be used to minimize hybridization to unexpected probes of the array.

In another example, conditions for optimization of hybridization to decrease cross hybridization were tested. The products used were as described above and hybridization was performed with formamide and with or without non-specific competitor (herring sperm DNA). The non-specific signal is significantly decreased in the presence of formamide, with and without non specific competitor. This demonstrates that even though the targets and counters alone have 15 bases of complementarity to probes on the array, the combination of target plus counter and the resulting increase to 30 bases of complementarity to the probes, results in specific hybridization. Within the block of 3,480 probes, there is heterogeneity in the hybridization intensity. Preliminary sequence analysis shows a strong correlation of GC content with high signals. To minimize this array probes may be selected to have similar melting temps for the counters or the target-counter combination may be optimized to obtain similar hybridization sta-

bilities. For example, if two targets are to be analyzed the portions of each target that are to be part of the probe may be selected to have similar TMs.

To test the efficiency of T4 RNA ligase in the ligation of labels to targets, DNA ligase from *E. coli* was tested. This required a slight modification of the sample prep (as depicted in FIG. **7**) by creating an overhang site for duplex ligation. The target in this example has a double stranded target specific portion and a single stranded overhang. The overhang may be, for example, a run of inosine bases, for example 6 to 9, or a string of random bases, for example, N6-16. DNA ligase is used to close the gap and generate a ligated product that includes the target strand and a label/counter from the pool of 3,840 counters. The PCR is carried out in the same manner as above using common primers.

The expected targets were observed, but some non-specific bands were also detected in the amplified DNA, even in the absence of the target. This suggests that the some of the 3,840 labels are combining with each other when this method is used. Selection of an optimized pool of labels may be used to mitigate such interference.

In another example random primed PCR was tested. Instead of a ligation step, the targets have a **3'** random region, that can be, for example, a degenerate region or an inosine region. The labels hybridize to the random region and the random region is used as a primer for extension through the label during the PCR step to append a copy of the label and the universal priming site at the 5' end of the label oligo to the **3'** end of the target. The extended target has a copy of the label sequence and the universal priming sequence and can be amplified by PCR.

In another example, a purification method for removing excess un-ligated counters was tested. The method is shown schematically in FIG. **18**. The counters **101** and the targets **2103** are ligated to form counter-target molecules as shown previously. A support bound probe that is complementary to the universal primer at the end of the target oligonucleotides **2105**, is used to separate counter-targets and targets from un-ligated counters. The support **2109** may be, for example, a magnetic bead. A second separation can be used to separate counter-targets from un-ligated targets. The second separation uses a support bound probe complementary to the universal priming sequence at the end of the counters **2107**. The single capture reduces background amplification. A double round of capture may also be used.

In FIG. **19** a scatter plot is shown to illustrate one way of representing the combinations of different target occurrences ligated randomly to different labels in the set. The plot shows combinations for 20 different target occurrences (labeled 1 to 20) representing 20 copies of the same target. The Y-axis represents different labels identified by a number from 1 to 1000. Each of the targets can be labeled with any of the 1000 labels, for example target 1 is labeled with label 351 and has coordinates (1, 351). The labels are distinct and distinguishable while the targets are the same in this example.

FIG. **3** shows a schematic where genomic DNA **1901** is fragmented, for example at restriction sites **1903** to produce fragments **1905**. The fragments are ligated with labels to form fragments labeled at both ends **1907**. All fragments can be ligated to the labels. The label-ligated fragments are circularized, for example, by ligation of the label ends to form closed circles **1909** with first and second labels forming a single label **1911**. The circularized fragments can be treated with exonuclease to remove unligated fragments. The circle and label can be amplified using gene-specific PCR primers **1913**. The PCR product has the label region **1911** flanked by target specific regions. The array probe is preferably complementary to the junction between the target specific region and the label. There are two such junctions **1915** and **1917** in the PCR product and each could be targeted on either strand (since the product is double stranded). The products may be fragmented, labeled and hybridized to an array of probes to the junctions. The label-target combination can be hybridized to an array for counting.

FIG. **20** shows a graph of counting efficiency on Y axis and copies of target on X axis. The different lines represent different numbers of labels being used, from 1000 to 10,000. The inset graph is a blow up of the upper left hand region of the larger graph and shows how counting efficiency changes with the number of labels. Fewer labels results in a more rapid decrease in counting efficiency as the number of targets increases.

In another embodiment, illustrated schematically in FIG. **5**, genomic DNA **1901** is fragmented with a restriction enzyme, for example, BamHI, which generates a single stranded overhang for sticky ended ligation. The fragments **1905** are ligated to adaptors **2207** that include a label **2205** and a universal priming site **2203**. Different adaptors vary in the label portion **2205** but have a common priming site **2203**. The label is **3'** of the universal priming site so that it is between the fragment and the universal priming site. The adaptor ligated fragments are amplified by PCR using primer **2209**. The PCR product can be fragmented, labeled with a detectable label and hybridized to an array. The resulting strands are detected by hybridization to an array having target-label probes **2210** and having different features for each target-label combination. Features are shown for each of Target 1 and Target 2. The array has a different feature for each target-label-tag combination. The PCR amplicons may be fragmented prior to array hybridization. Preferably the fragments are labeled, for example, by TdT incorporation of a nucleotide that can be detected, such as a biotin containing nucleotide.

The probes of the array are complementary to the junction between the label and the restriction fragment. The sequences at the ends of the individual strands of the restriction fragments are predicted based on in silico digestion of the human genome. Also, fragments are targeted that are within the size range that is known to amplify efficiently by adaptor ligation PCR, for example, 200 bases to 2 kb. The adaptor has two segments, a constant priming region **2203** and a variable label region **2205**. Together **2203** and **2205** form the label adaptor **2207**. The primer **2209** has the same sequence 5' to **3'** as the **2203**. The schematic is drawn showing only one strand, but one of skill in the art would understand that in a preferred embodiment the genomic DNA is double stranded and the restriction fragments have two strands, which may be referred to as a top strand and a bottom strand. The convention is that the top strand is drawn 5' to **3'** left to right and the bottom strand is the complement of the top strand and is drawn **3'** to 5' left to right. Adaptors are preferably double stranded for at least a portion of the adaptor, they may have single stranded overhangs, for example to have "sticky ends" that facilitate hybridization and ligation to the overhang resulting from restriction digestion. In a preferred aspect, the same adaptor can be ligated to the two ends of a strand of a restriction fragment and may be ligated to one or both strands. The adaptor may be ligated to the ends of the top strand in opposite orientations as shown in FIG. **5**, so that the label is internal to the priming site at both ends. The adaptor may have a top and a bottom strand and the top strand may be ligated to the top strand of the fragment and the bottom strand ligated to the bottom strand of the fragment. The top and bottom strands of the adaptor may be complementary over the entire length, but

often have single stranded regions at one end to facilitate sticky ended ligation to an overhang created by a restriction enzyme.

To test this method several adaptors were generated. The test adaptor has PCR002 (SEQ ID No. 1969) as top or sense strand and BamAdaAS (SEQ ID No. 1970) as bottom or antisense strand.

```
PCR002
5' ATTATGAGCACGACAGACGCCTGATCT (1969)

BamAdaAS
3' AATACTCGTGCTGTCTGCGGACTAGACTAG 5'P(1970)
```

The single stranded region on the right is the BamHI single stranded overhang. The adaptor also has a half Bgl II site. The "full length-label" adaptor has SEQ ID No. 1972 as top or sense strand and SEQ ID No. 1973 as bottom or antisense strand.

```
Sense
5' ATTATGAGCACGACAGACGCCTGATCTNNNNNNNNNNNNNNT

AntiSense
3' AATACTCGTGCTGTCTGCGGACTAGANNNNNNNNNNNNNNNACTAG
```

A 5' phosphate may be added to one or both strands of the adaptor using, for example, T4 polynucleotide kinase. In some aspects a truncated adaptor may be used. An example of such an adaptor is shown in FIG. **7**, the top or sense strand is SEQ ID No. 1974 and the bottom or antisense strand is SEQ ID No. 1975. SEQ ID NOs. 1974 and 1975 are sub-sequences of SEQ ID NOs. 1972 and 1973 respectively. The N's in SEQ ID Nos. 1972-1975 indicate a variable sequence in the adaptor that is different for each different label. For example, if there are 1,920 different labels to be used then the N_{14} represents the 1,920 different labels.

In some aspects it is preferable to use shorter oligos. The full length adaptor includes 87 bases. The truncated adaptor has 57 bases. Since 2 different oligos must be synthesized for each different label adaptor (e.g. 1,920 labels requires 3,840 different oligos) shorter adaptors are more economical. The separate oligos are preferably annealed together prior to being combined into a pool for ligation to fragments. The primer may be, for example, SEQ ID NO. 1969 or the 5' 17 bases of SEQ ID No. 1974.

FIG. **24** shows the results of a control experiment where the test adaptor was ligated to fragmented genomic DNA and analyzed on an array having genomic probes. The DNA was subjected to fragmentation with a BamHI, the test adaptor was ligated to the ends and SEQ ID No. 1969 was used as a primer for PCR amplification. The PCR products were fragmented and end labeled using TdT and hybridized to a CNV-type and HG49 arrays. The upper plot is the number of probes (number of different features where each feature corresponds to a different probe sequence) complementary to restriction fragments in the different size bins shown on the X-axis. The sizes and sequences of restriction fragments from a selected genome can be predicted and binned according to size. The probes of the tiling array (probes essentially all non-redundant sequences in the genome) can be assigned to the restriction fragment to which the probe is complementary. Longer fragments will have larger numbers of probes that are complementary to that fragment, simply because the fragment is longer. Restriction fragment size is distributed based on the frequency of the occurrence of the recognition site. Note that the X axis does not increase linearly. While there are more probes that are complementary to fragments in the bins of size greater than 3000, particularly in the bins between 9000 and 30,000, the intensity in those size bins is less than the intensity of the bins that are about 400 to about 1800. The larger fragments, greater than 9000 bases, for example, do not amplify efficiently with PCR, resulting in lower representation of those large fragments in the hybridization.

In another example, a truncated label adaptor was used (SEQ ID Nos. 1974 and 1975). The adaptor ligated fragments were extended to fill in the ends with polymerase prior to PCR. Hybridization was done in duplicate to either the CNV-type array or HG49 design C. Fragmented DNA and non-fragmented DNA were plotted. The intensity of the DNA that was not fragmented prior to hybridization is less than the intensity of the fragmented DNA. The peak of the intensity for both plots is at a fragment size of about 900 base pairs.

FIG. **11** shows a theoretical modeling of the number of counters predicted to be observed at least once **3201**, exactly once **3202** or exactly twice **3203**. A non-depleting reservoir of 960 diverse labels was considered. Equation (1) was used to calculate the at least once curve, equation (2) the exactly once curve and equation (3) the exactly twice curve. The error bars indicate one standard deviation from the corresponding mean value.

$$E[k] = m\left[1 - \left(1 - \frac{1}{m}\right)^n\right] \quad (1)$$

$$\mathrm{Var}[k] = m\left[1 - \left(1 - \frac{1}{m}\right)^n\right]\left(1 - \frac{1}{m}\right)^n + m(m-1)\left[\left(1 - \frac{2}{m}\right)^n - \left(1 - \frac{1}{m}\right)^{2n}\right] \quad (2)$$

FIG. **12** shows counting results for DNA copy number titrations using microarray hybridization on the left or DNA sequencing on the right. Dilutions (3.62 ng, 1.45 ng, 0.36 ng and 0.036 ng) of a DNA sample isolated from cultured lymphoblasts of a Trisomy 21 male individual were processed for microarray hybridization (left) and DNA sequencing (right). Three chromosome targets were tested and observed numbers of counters (Y-axis) are shown (curve **1201**). The number of target molecules for each sample (X-axis) was determined from the amount of DNA used, assuming a single cell corresponds to 10 pg. For comparison, the theoretical counter usage rates from the stochastic model equation are also plotted **1202**. Numerical values are provided in Table 4.

BamHI cuts the human genome into an estimated 360,679 fragments with a size distribution of 6 bp to 30,020,000 bp. The median size is 5142 bp and the mean is 8320 bp. There are 79,517 fragments in the size range of 150 bp to 2 kb. For testing it may be desirable to choose fragments that meet selected criteria, for example, within a selected size range, select fragments that have more than 1 probe on the HG49m array, exclude fragments that are in known CNV regions, or exclude fragments having a SNP in the first or last 20-30 bases.

The upper panel of FIG. **26** shows the intensities of 1,152 array probes associated with one gene target on chromosome 4, chr4_01s. The data are from the array with 5 ng DNA, i.e., 1000 copies of the tested gene target. The 1,152 probes shown share the same genomic sequence portion, but have different label sequences. Each black dot represents one label sequence. The left 960 dots (on the left side of the dashed vertical line) correspond to specific labels (i.e., labels used in ligation reaction), and the 192 dots to the right of the dashed vertical line correspond to non-specific labels (i.e., labels not used in ligation reaction). The probe intensities were plotted

in natural log scale on the y-axis. The horizontal dashed line is the threshold determined by analysis algorithm, which has a value of 3,800.

The array design for the experiment represented in FIG. **26** is as follows. For each gene target assayed, the array probe consists of all possible combinations of the 960 label sequence and either of the two BamHI genomic fragment ends. An additional 192 label sequences that were not included in the adaptor pool were also tiled to serve as non-specific controls. This tiling strategy enables consistency check on the number of labels used at the paired ends, since each target fragment is ligated to two independent labels (one on either end), and for the same target fragment, the counts on the left and right side should be very similar.

The lower panel of FIG. **26** shows the histogram of the intensity data corresponding to 960 specific labels. Also shown in the figure are the 2 fitted normal distributions. The fitted distributions have the mean and standard deviation of 1447±680 and 12186±3580, respectively. The vertical dashed line in the lower panel is the threshold, which has the same value as the horizontal dashed line shown in the upper panel. Based on such threshold, 501 probes (i.e., labels) were counted as "used".

FIG. **27** shows the number of times observed for each of the 960 specific labels. Empirically, we did not observe 349 labels in any of the 20 cases. By model, we would expect to observe 643.05±9.96 labels at least once, which means we expect not to observe 307~327 labels. This result shown was obtained by grouping labels used in independent ligation reactions together. To more accurately estimate the frequency of usage of labels, only data from experiments with low concentrations (0.05 ng and 0.5 ng of DNA ligation amount) were considered. Under each concentration, 5 different gene targets independently ligated to labels at both ends. Therefore, a total of 20 independent reactions (2 concentrations×5 gene targets×2 ends) were grouped together. Of these reactions, 1,064 labels were observed; some were observed more often than the others, the frequency of usage of labels ranges from 0 to 6.

FIG. **28** shows one example of the replication process of 500 copies of a gene target. In each subplot, copies of target molecules were plotted in the same order. The y-axis is the relative ratio of the number of amplified molecules over the minimal number of amplified molecules in each PCR cycle. Before PCR, all copies are of equal amount, i.e., each copy has one molecule at cycle 0 (subplot (a)). As the PCR process goes on, we start to see differences in the number of amplified molecules corresponding to different copies of target molecules. For example, in cycle 3 (subplot (b)), the ratio between most and least abundant of amplified molecules is 4. Such ratio becomes larger as the number of PCR cycle increases. In cycle 8 and 15, the ratio becomes 26 and 30, in cycles 8 and 15 respectively (see subplots (c) and (d)). This suggests that the differential usage of labels may be observed before PCR is started. Such difference in the amount of molecules associated with different labels will carry on as PCR process goes on.

PCR simulation. We defined n copies of a gene fragment T, each ligated to a single counter randomly selected from an infinite pool of m unique counters to generate a collection of k resulting counter-ligated gene target molecules $T^*=\{tl_i, i=1,2,\ldots,k\}$. We assumed that each counter-ligated gene target molecule tl_i replicates randomly and independently of other target molecules; and that the replication probability p (i.e., amplification efficiency) of different molecules, tl_i, remains constant throughout the PCR process. For each tl_i, we denote the number of molecules at PCR cycle c as N_i^c. When c=0, N_i^0 is the initial number of tl_i. The PCR process at cycle c+1 can be modeled as a series of N_i^c independent trials that determine the replicability of each of the N_i^c molecules with replication probability p. Let ΔN_i^c represent the number of molecules replicated at cycle c+1, then the number of molecule tl_i after cycle c+1 is $N_i^{c+1}=N_i^c+\Delta N_i^c$, where the probability of ΔN_i^c is

$$p(\Delta N_i^c \mid N_i^c) = \binom{N_i^c}{\Delta N_i^c} p^{\Delta N_i^c} (1-p)^{N_i^c - \Delta N_i^c}. \quad (2)$$

We determined the relative abundance of different counter-ligated gene target molecules tl_i upon completion of the simulated PCR run for n=500, 50, or 5, and p=0.8, 0.7 or 0.6 (Table 5). In each case, we performed 1,000 independent runs to simulate 30 cycles of adaptor PCR, followed by 30 cycles of gene-specific PCR.

Table 5. Shows summary statistics drawn from 100 independent simulation runs modeling PCR, ligation at each end of targets is considered.

	Initial copy number					
	N = 5		N = 50		N = 500	
	Side					
	Left	Right	Left	Right	Left	Right
# of labels observed	5	5	48.61 0.99	48.64 1.09	388.91 6.85	389.27 7.18
Max	(1.43 0.19) * 10^11	(1.43 0.19) * 10^11	(2.18 0.49) * 10^10	(2.13 0.47) * 10^10	(4.52 0.59) * 10^9	(4.44 0.55) * 10^9
Min	(5.73 2.27) * 10^10	(5.73 2.27) * 10^10	(2.35 1.06) * 10^9	(2.35 1.06) * 10^9	(1.15 0.49) * 10^8	(1.23 0.49) * 10^8
Ratio btw max & min	3.13 2.44	3.13 2.44	14.10 11.41	13.87 13.42	43.42 25.66	44.92 30.04
Mean	(1.00 0.16) * 10^11	(1.00 0.16) * 10^11	(1.03 0.06) * 10^10	(1.03 0.06) * 10^10	(1.27 0.03) * 10^9	(1.27 0.03) * 10^9
Standard deviation	(3.44 1.02) * 10^10	(3.44 1.02) * 10^10	(3.98 0.52) * 10^9	(3.94 0.54) * 10^9	(6.75 0.41) * 10^8	(6.69 0.40) * 10^8
Coef. of variation	0.36 0.13	0.36 0.13	0.39 0.05	0.38 0.05	0.53 0.03	0.53 0.03

Focusing on the experiments with concentrations of 0.5 and 0.05 ng, (3rd and 4th in each group of 5), which provide the most accurate count of labels, there are 20 different opportunities for a given label to be observed (2 concentrations×5 amplicons×2 sides (left or right)). We observed 1,064 labels over the 20 opportunities.

To observe the distortion of the relative abundance of DNA molecules in the reaction resulting from the PCR process, dispersion in the quantitative distribution of PCR amplified DNA molecules was analyzed. A model of the PCR process was generated to understand the dispersion in the distribution of amplified molecules (FIG. **25**, Table 6). A series of 1,000 independent simulation runs were performed to simulate the replication of uniquely labeled target molecules through PCR processes. For each run, we measured the distribution of the final amount of PCR products and quantified the dispersion of distribution using two measures: ratio of the maximal to the minimal amount, and coefficient of variation of final PCR products. This demonstrates that the degree of dispersion increases with the incidence of replicate use of identical counters, which may be in-part responsible for the deviation observed when assaying high target copy numbers. Table 6 lists the ratio and CV for distributions corresponding to different concentrations and replication probabilities (one sided ligation considered).

TABLE 6

	replication probability	n = 5	n = 50	n = 500
Ratio of max to min	p = 0.6	5.69 ± 4.95	26.16 ± 23.78	124.18 ± 88.04
amount of PCR	p = 0.7	4.59 ± 8.03	16.22 ± 15.53	71.55 ± 55.13
amplified product	p = 0.8	2.82 ± 1.51	11.54 ± 9.53	42.24 ± 27.49
Coefficient of	p = 0.6	0.48 ± 0.16	0.51 ± 0.06	0.62 ± 0.03
Variation (CV)	p = 0.7	0.41 ± 0.14	0.44 ± 0.05	0.57 ± 0.02
	p = 0.8	0.34 ± 0.12	0.36 ± 0.05	0.52 ± 0.02

Example 1 of a method for selecting a collection of labels starting with all possible 14 mers (4^{14} or ~268 million possible labels). Step 1: clustering based on the last 7 bases: all sequences with the same last 7 bases are grouped together; within each cluster, randomly pick one sequence, this gives us 11,025 sequences, denoted by set A. Step 2: clustering based on the first 7 bases: all sequences with the same first 7 bases are grouped together; within each cluster, randomly pick one sequence, this gives us 13,377 sequences, denoted by set B. Step 3: get the union set of set A and B, the combined set has 24,073 sequences. Then do clustering based on the middle 6 bases, randomly pick one sequence out of every cluster, this gives us 3,084 sequences, denoted by set C. Step 4: calculate the all-against-all alignment score of set C, which gives us a 3,084×3,084 self-similarity score matrix, denoted by S. Step 5: filter based on the score matrix. If an element of the score matrix S(i,j) has a high value, that means, the corresponding sequences i and j are very similar to each other. Starting from the elements with top self-similarity score, randomly pick one and discard the other; repeat this process until the number of retained sequences <2000. Until this step, 1,927 sequences were retained.

For the retained 1,927 sequences, an all-against-all complement score was calculated for each. This gave a 1,927×1,927 cross complement score matrix. A step similar to step 5 was performed, to avoid labels with maximal cross-complement with other labels. Starting from the pairs with top cross-complement score, one was randomly picked and the other discarded. This process was repeated until the number of retained sequences was 1920. Next the 1920 labels were split into 2 sets, with one set (denoted by set A) consisting of sequences that are maximum different from one-another; and the other set (denoted by set B) consisting of the remaining sequences. The procedure used to split sequences was as follows. Starting from the original 1920 by 1920 similarity score matrix, for each sequence, (1) sum up all its similarity scores with the rest of the sequences in the pool, that is, for each sequence, calculate a total similarity score. (2) Sort the total similarity scores of all sequences and select the sequence with the lowest total score, and move it to set A. (3) Remove the row and column corresponding to the selected sequence, i.e., both the number of rows and columns in the similarity score matrix are reduced by 1. Repeat steps 1-3, until the number of rows and columns in the similarity score matrix reaches 960 or half of the original. The selected sequences belong to set A and the remaining sequences belong to set B.

In another embodiment a collection of labels is selected using the following steps. Starting with all possible 14 mers (4^{14} or ~268 million possible labels) eliminate all that do not have 50% GC content. Eliminate those were each nucleotide does not occur at least twice. Eliminate those that have more than two G/C in tandem or more than three A/T in tandem. Eliminate those that contain a selected restriction site. That reduces the original set to ~33 million or 12.43% of the original set. From that set select those that have a Tm within the range of 38.5° C. to 39.5° C. This step results in a set of ~7 million or 2.73% of the original set. Remove those that have regions of self-complementarity. The resulting set in this example was now 521,291. A hierarchical clustering was performed to identify a set that has maximum sequence difference between one-another. The resulting set contained 1,927 labels. Labels were removed if the sequence had a tendency to bind to other labels in the set. This reduced the set to 1,920 labels. A final set of 960 labels was selected from the 1,920 as being maximally different for the "specific" labels and 192 additional counters to tile on the array as "non-specific" controls.

Selection of Targets and design of test array. Regions selected to assay as targets included Chr X, Chr Y, Chr 4 as a reference and Chr 21 for Trisomy. Locations on the chromosomes for assaying were selected to avoid centromeres and telomeres. Fragments were selected based on Bam HI fragments of between about 400 and 600 base pairs. Fragment intensity was checked using HG49 array hybridization. The first and the last 26 nucleotides of the fragments (from and including the Bam HI site) were tiled. Repeats were avoided and GC % was optimized.

The array format was 100/25. Feature size is Sum. There are 436×436 features or 190,096 features. Synthesis was NNPOC, 43 mer probes, 5' up, no phosphate. The chip name is STCL-test2. The gridding probe used was the same as the HG49. No QC probes were included.

Aside from reducing whole chromosomes into 360,679 smaller molecular weight DNA pieces more suitable for liga-

tion reactions, restriction digestion also serves to reduce the overall sequence complexity of the sample, as only an estimated 79,517 fragments reside in the 150 bp-2 kb size range that is effectively amplified by PCR. To detect and quantify counters that have been selected by the target molecules, the labeled genomic target fragments may be circularized and PCR amplified to prepare for analysis, for example, using microarray hybridization or DNA sequencing. A representative BamHI target fragment was sampled for each of the three test chromosomes. Simultaneous measurements of all three chromosomes serve as an internal control independent of dilution or other systematic errors. A suitable DNA array detector capable of distinguishing the set of counters bound to copies of the target molecules was constructed using photolithography (S. P. Fodor et al., *Science* 251, 767 (Feb. 15, 1991).). Each array element for a target to be evaluated consists of a target complementary sequence adjacent to one of the complements to the 960 counter sequences (FIGS. **1** and **2**A). For increased specificity, a ligation-readout was performed on the microarray after hybridization to avoid false positive detection of the cross-hybridization of identical targets with different counters. As a means of validation through a secondary measure, samples hybridized to microarrays were subsequently sampled by DNA sequencing (FIGS. **10** and **29**).

An equation to model the stochastic labeling of target molecules with a small library of 960 counters, and validate our equation model with numerical simulations is disclosed. In the model, the diversity of counters selected by, and ligated to target molecules in the reaction solution (simplified as 'used') is dictated by the number of copies of molecules present for each target fragment in the reaction (FIG. **12**). Under conditions where the size of the counter library is much greater than the number of copies of a given target molecule, the counting efficiency is high, and counting the number of counters used is equivalent to counting the number of copies of the original target molecules (FIG. **16**). When the number of target copies approaches and exceeds the number of different counters in the reaction, any counter in the library is more likely to be used multiple times (FIG. **15**). The number of counters used at least once is an important measure because it serves as the basis for drawing yes/no conclusions in our digital readout on microarrays. Under stochastic labeling conditions, we expect that the absolute quantity of single DNA molecules can be accurately determined by proxy counts of labeling events. Indeed, microarray experiments demonstrate a high degree of correlation between the number of copies of target molecules added to the reaction and the number of counters used, as detected on microarrays (FIG. **12**). In particular, counter usage precisely profiles the number of target molecules under conditions of high counting efficiency. Subtle deviations from the model may represent minor dilution errors in the preparation of the sample. However, within that sample dilution, the relative counter ratios of the three internally built-in markers are highly accurate (FIG. **13**). FIG. **13** shows comparison of relative copy ratios of the three gene targets tested: ChrX, Chr4 and Chr21 representing genetic material of one, two and three copies per cell. Different dilutions (5 ng, 2 ng, 0.5 ng and 0.05 ng) of a DNA sample isolated from cultured lymphoblasts of a Trisomy 21 male individual were processed for microarray hybridization and DNA sequencing. The calculated number of target molecules (see, Table 4, column 9) was inferred from the number of counters detected on microarrays (A), and was also calculated for the SOLID sequencing data (B). For each sample dilution, the target copy number ratio of each gene target relative to ChrX is shown.

On the other hand, when target copies exceed ~100, detected labeling events appear to indicate fewer than actual molecules in solution (FIG. **12** inset in graph on left). This deviation was reproducible and consistently observed across multiple microarray experiments, and was also observed in the DNA sequencing experiments (FIG. **12** inset in graph on right). Under-counts of expected labeling events may originate from inadequate detection sensitivity of the microarray platform or from other systematic or indeterminate deficiencies in the sample preparation procedure. PCR, for example, is prone to amplification bias (T. Kanagawa, *J Biosci Bioeng* 96, 317 (2003) and M. F. Polz, C. M. Cavanaugh, *Appl Environ Microbiol* 64, 3724 (1998)), which could hinder the comprehensive detection of labeling events that may be genuinely stochastic.

To confirm the microarray results, a digital sequence counting of individual molecules in the DNA samples hybridized to microarrays was used as a means of validation, and to detect the presence of any false negatives that may have escaped microarray detection. Analysis of mapped sequence reads resulted in counts in agreement to the microarray observations. Furthermore, a second, independent sequencing run was repeated with similar findings (Table **3**).

An additional feature of digital sequence counting is that unlike the microarray intensity data (FIGS. **22** and **23**), which offers lower resolution into the measurement of the concentration dispersion of PCR amplified molecules, sequence counting clearly demonstrates significant variation in the representation of amplified targets (FIG. **29**), This is consistent with the computed PCR model. Overall, detected counters on the microarray and sequencing experiments correlate well, but a small subset of counters appear to be unique to each process (Table 7). The observed number of labels in common between the microarray and the two sets of sequencing experiments are summarized in the table. The number of labels in each category is included. The categories are as follows: A+1+2 for labels detected in each of the 3 experiments, 1+2 for labels detected only in sequencing runs 1 and 2, 1+A for labels detected in sequencing run 1 and by array, and so on for the amounts of DNA shown in column 3.

TABLE 7

DNA sample			A + 1 + 2	1 + 2	1 + A	2 + A	1	2	A
Chr4	Left side	0.036 ng	13	0	0	0	0	0	1
		0.36 ng	96	3	0	1	2	2	5
		1.45 ng	228	13	4	22	6	10	6
		3.62 ng	484	23	2	3	4	6	12
	Right side	0.036 ng	14	0	0	0	0	0	0
		0.36 ng	100	1	0	0	2	2	7
		1.45 ng	249	25	2	0	15	33	5
		3.62 ng	511	22	2	1	9	23	11
Chr21	Left side	0.036 ng	18	0	2	0	0	0	0
		0.36 ng	150	0	2	4	0	7	4
		1.45 ng	324	17	8	1	32	16	2
		3.62 ng	637	14	10	0	17	14	4
	Right side	0.05 ng	18	0	1	1	0	0	0
		0.36 ng	144	0	2	2	0	0	9
		1.45 ng	330	34	2	3	15	12	6
		3.62 ng	615	29	1	7	5	2	4
ChrX	Left side	0.036 ng	11	0	0	0	0	0	0
		0.36 ng	42	0	0	0	1	3	8
		1.45 ng	137	3	1	5	8	5	5
		3.62 ng	274	12	0	2	4	12	5
	Right side	0.036 ng	10	1	0	0	1	0	0
		0.36 ng	43	0	3	0	4	0	2
		1.45 ng	127	15	0	0	11	25	6
		3.62 ng	298	12	3	3	24	31	2

For the reverse scenario, high numbers of mapped sequence reads were always observed to correlate with high microarray intensities in these examples. No systematic or sequence correlations, or explanations were identified for the counters that are absent from any given sequencing experiment for which the microarray readout demonstrates a strong signal. While obviously underrepresented in some experiments, the same counters are sometimes present in high sequence counts in other experiments, suggesting that they are available for sequencing. PCR was used to resolve these isolated cases of disagreement and demonstrate these were false negatives in the sequencing experiments (Table 3). Despite their presence in the sequencing library, it is unclear why the counters were not observed or were underrepresented in the original sequencing run, and also in the subsequent replicate sequencing run.

Aside from the comparative analysis of absolute and relative counts of the numbers of target molecules and counter labels, additional ways to assess the stochasticity of the labeling process were evaluated. First, if the labeling process is random, the frequency of incorporation of identical counters in independent events across the paired left and right termini of target fragments should closely resemble outcomes from numerical simulation. Observed counts on microarrays do in fact match closely with numbers obtained from computer simulations (Table 4, columns 10-11). Second, if the target molecules are labeled randomly with an equal likelihood of incorporation for any member of the 960 counters in the library, we would expect the number of repeated observations of counters to follow a stochastic nature. For this analysis, we accumulated a total of 1,064 counter observations over several microarray experiments restricted to low target copy numbers. Exclusion of data from high copy targets was necessary to avoid undercounting labeling events from multiple incidences of identical counters attaching individually to numerous target copies. As a further and final demonstration of stochastic labeling, results show that the frequency of label usage follows a pattern consistent with outcomes from numerical simulation.

CONCLUSION

While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby. All cited references, including patent and non-patent literature, are incorporated herein by reference in their entireties for all purposes and particularly to disclose and describe the methods or materials in connection with which the publications are cited.

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<220> FEATURE:
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ctgcaggttc atatttgaat tcttctaatc ccatgaaccc ttaccctggg cttttgaatc 180

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aagaccctct gtctaagctc agtctaccac ccatccatac actttaccag ccaaggtttg 360

gaaatagcca gagttttaca tctaaatact taggttatgg aaaccaaaat atgcagggag 420

atggtttcag cagttgtacc attagaccaa atgtacatca tgtagggaaa ttgcctcctt 480

atcccactca tgagatggat ggccacttca tgggagccac ctctagatta ccacccaatc 540

tgagcaatcc aaacatggac tataaaaatg gtgaacatca ttcaccttct cacataatcc 600

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acaaggagaa tgacatgctt tcccacacag ctaatgggtt atcaaagatg cttccagctc 720

ttaaccatga tagaactgct tgtgtccaag gaggcttaca caaattaagt gatgctaatg 780

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tctcagttcc tgtcttctcc cagagggtgg caggtagctg gggaagagat gactgggagt 180

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ggggcttaga agttttgtct gttgggggaa atctctgcag gctcaaaaag taacccaggg 300

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<400> SEQUENCE: 7

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<400> SEQUENCE: 8

ggcctcagga atagctaggg 20

<210> SEQ ID NO 9
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 9

tgtgtatgag ggggtgtgtg 20

<210> SEQ ID NO 10
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 10

tgatctagat cttgtgtccg 20

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<210> SEQ ID NO 11
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 11

tgatctatct tcgacactgg 20

<210> SEQ ID NO 12
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 12

tgatcttcga gatggtgttc 20

<210> SEQ ID NO 13
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 13

tgatcttcgg atagagagca 20

<210> SEQ ID NO 14
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 14

tgatcttcgg taccaacaac 20

<210> SEQ ID NO 15
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 15

tgatctccaa ggtttggtga 20

<210> SEQ ID NO 16
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 16

tgatcttcgc aagaggtaag 20

<210> SEQ ID NO 17
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 17

tgatctggag ttacggcttt 20

<210> SEQ ID NO 18
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 18

tgatcttcaa ccagtaagcc 20

<210> SEQ ID NO 19
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<212> TYPE: DNA
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<400> SEQUENCE: 19

tgatctctgt aaacaacgcc 20

<210> SEQ ID NO 20
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 20

tgatctcacg atagtttgcc 20

<210> SEQ ID NO 21
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<212> TYPE: DNA
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<400> SEQUENCE: 21

tgatcttgta ctaacacgcc 20

<210> SEQ ID NO 22
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 22

tgatctacgc taactccttg 20

<210> SEQ ID NO 23
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<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 23

tgatctcgtt tacgatgtgg 20

<210> SEQ ID NO 24

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<211> LENGTH: 20
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<400> SEQUENCE: 24

tgatcttctt aggaaacgcc 20

<210> SEQ ID NO 25
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<212> TYPE: DNA
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<400> SEQUENCE: 25

tgatcttgca atagacgacc 20

<210> SEQ ID NO 26
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<212> TYPE: DNA
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<400> SEQUENCE: 26

ccactacgcc tccgctttcc tctctatggg cagtcggtga t 41

<210> SEQ ID NO 27
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<212> TYPE: DNA
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<400> SEQUENCE: 27

ctgccccggg ttcctcattc 20

<210> SEQ ID NO 28
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 28

ggagctcgga caacgatgag gtctggt 27

<210> SEQ ID NO 29
<211> LENGTH: 27
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 29

ggagctctag ggctggtgct tccatag 27

<210> SEQ ID NO 30
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 30

ggagctcgcc cctccacagt caactaa 27

<210> SEQ ID NO 31
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 31

ggagctccgc ttgtcctgaa ggtcagt 27

<210> SEQ ID NO 32
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 32

ggagctcggc ctcaggaata gctaggg 27

<210> SEQ ID NO 33
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 33

ggagctctgt gtatgagggg gtgtgtg 27

<210> SEQ ID NO 34
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 34

ttcctctcta tgggcagtcg gtgatcgaa 29

<210> SEQ ID NO 35
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 35

gatcttcgat caccgactgc ccatagagag gaa 33

<210> SEQ ID NO 36
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 36

ttcctctcta tgggcagtcg gtgatgttg 29

<210> SEQ ID NO 37
<211> LENGTH: 33
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 37

gatccaacat caccgactgc ccatagagag gaa 33

<210> SEQ ID NO 38
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 38

ttcctctcta tgggcagtcg gtgataaga 29

<210> SEQ ID NO 39
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 39

gatctcttat caccgactgc ccatagagag gaa 33

<210> SEQ ID NO 40
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 40

ttcctctcta tgggcagtcg gtgattttc 29

<210> SEQ ID NO 41
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 41

gatcgaaaat caccgactgc ccatagagag gaa 33

<210> SEQ ID NO 42
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 42

ttcctctcta tgggcagtcg gtgattacc 29

<210> SEQ ID NO 43
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 43

gatcggtaat caccgactgc ccatagagag gaa 33

<210> SEQ ID NO 44
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 44

cgacagacgc ctgatctttt gttagccgga gt 32

<210> SEQ ID NO 45
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 45

gatcactccg gctaacaaaa gatca 25

<210> SEQ ID NO 46
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 46

cgacagacgc ctgatctttt ctcgaccact gt 32

<210> SEQ ID NO 47
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 47

gatcacagtg gtcgagaaaa gatca 25

<210> SEQ ID NO 48
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 48

cgacagacgc ctgatctttt ctagctaccg ct 32

<210> SEQ ID NO 49
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 49

gatcagcggt agctagaaaa gatca 25

<210> SEQ ID NO 50
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 50

cgacagacgc ctgatctttt cgttaggagg ct 32

<210> SEQ ID NO 51
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 51

gatcagcctc ctaacgaaaa gatca 25

<210> SEQ ID NO 52
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 52

cgacagacgc ctgatctttt cctgaacgac ct 32

<210> SEQ ID NO 53
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 53

gatcaggtcg ttcaggaaaa gatca 25

<210> SEQ ID NO 54
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 54

cgacagacgc ctgatctttt ccatagcgtc ct 32

<210> SEQ ID NO 55
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 55

gatcaggacg ctatggaaaa gatca 25

<210> SEQ ID NO 56
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 56

cgacagacgc ctgatctttt cactacggct ct 32

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<210> SEQ ID NO 57
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 57

gatcagagcc gtagtgaaaa gatca 25

<210> SEQ ID NO 58
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 58

cgacagacgc ctgatctttt caccagtcca gt 32

<210> SEQ ID NO 59
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 59

gatcactgga ctggtgaaaa gatca 25

<210> SEQ ID NO 60
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 60

cgacagacgc ctgatctttt actgcgacct ct 32

<210> SEQ ID NO 61
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 61

gatcagaggt cgcagtaaaa gatca 25

<210> SEQ ID NO 62
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 62

cgacagacgc ctgatctttt acgcctctga ct 32

<210> SEQ ID NO 63
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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<400> SEQUENCE: 63

gatcagtcag aggcgtaaaa gatca 25

<210> SEQ ID NO 64
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 64

cgacagacgc ctgatctttt acctggactg ct 32

<210> SEQ ID NO 65
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 65

gatcagcagt ccaggtaaaa gatca 25

<210> SEQ ID NO 66
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 66

cgacagacgc ctgatctttt acaggagagc gt 32

<210> SEQ ID NO 67
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 67

gatcacgctc tcctgtaaaa gatca 25

<210> SEQ ID NO 68
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 68

cgacagacgc ctgatctttt aactgaggcg gt 32

<210> SEQ ID NO 69
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 69

gatcaccgcc tcagttaaaa gatca 25

<210> SEQ ID NO 70
<211> LENGTH: 32

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 70

cgacagacgc ctgatctttt aaccaggagc gt 32

<210> SEQ ID NO 71
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 71

gatcacgctc ctggttaaaa gatca 25

<210> SEQ ID NO 72
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 72

cgacagacgc ctgatctttg ttccacctca gt 32

<210> SEQ ID NO 73
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 73

gatcactgag gtggaacaaa gatca 25

<210> SEQ ID NO 74
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 74

cgacagacgc ctgatctttg ttaggcaggt ct 32

<210> SEQ ID NO 75
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 75

gatcagacct gcctaacaaa gatca 25

<210> SEQ ID NO 76
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 76

cgacagacgc ctgatctttg tgtagaccgt gt 32

<210> SEQ ID NO 77
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 77

gatcacacgg tctacacaaa gatca 25

<210> SEQ ID NO 78
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 78

cgacagacgc ctgatctttg tatcctcacg ct 32

<210> SEQ ID NO 79
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 79

gatcagcgtg aggatacaaa gatca 25

<210> SEQ ID NO 80
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 80

cgacagacgc ctgatctttg tagacagagc gt 32

<210> SEQ ID NO 81
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 81

gatcacgctc tgtctacaaa gatca 25

<210> SEQ ID NO 82
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 82

cgacagacgc ctgatctttg tacgtgtagg ct 32

<210> SEQ ID NO 83
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 83

gatcagccta cacgtacaaa gatca 25

<210> SEQ ID NO 84
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 84

cgacagacgc ctgatctttg gttaaggctc gt 32

<210> SEQ ID NO 85
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 85

gatcacgagc cttaaccaaa gatca 25

<210> SEQ ID NO 86
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 86

cgacagacgc ctgatctttg gtctcaaggt gt 32

<210> SEQ ID NO 87
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 87

gatcacacct tgagaccaaa gatca 25

<210> SEQ ID NO 88
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 88

cgacagacgc ctgatctttg gagagaacag ct 32

<210> SEQ ID NO 89
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 89

gatcagctgt tctctccaaa gatca 25

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<210> SEQ ID NO 90
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 90

cgacagacgc ctgatctttg gaatctgctg gt 32

<210> SEQ ID NO 91
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 91

gatcaccagc agattccaaa gatca 25

<210> SEQ ID NO 92
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 92

cgacagacgc ctgatctttg gaatcaggac gt 32

<210> SEQ ID NO 93
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 93

gatcacgtcc tgattccaaa gatca 25

<210> SEQ ID NO 94
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 94

cgacagacgc ctgatctttg gaagacgaga ct 32

<210> SEQ ID NO 95
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 95

gatcagtctc gtcttccaaa gatca 25

<210> SEQ ID NO 96
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 96

cgacagacgc ctgatctttg ctctactcac gt 32

<210> SEQ ID NO 97
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 97

gatcacgtga gtagagcaaa gatca 25

<210> SEQ ID NO 98
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 98

cgacagacgc ctgatctttg ctaaccagga ct 32

<210> SEQ ID NO 99
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 99

gatcagtcct ggttagcaaa gatca 25

<210> SEQ ID NO 100
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 100

cgacagacgc ctgatctttg cgtgagagat ct 32

<210> SEQ ID NO 101
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 101

gatcagatct ctcacgcaaa gatca 25

<210> SEQ ID NO 102
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<400> SEQUENCE: 102

cgacagacgc ctgatctttg catctcacca gt 32

<210> SEQ ID NO 103

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<211> LENGTH: 25
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 103

gatcactggt gagatgcaaa gatca 25

<210> SEQ ID NO 104
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 104

cgacagacgc ctgatctttg cagatgagga ct 32

<210> SEQ ID NO 105
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 105

gatcagtcct catctgcaaa gatca 25

<210> SEQ ID NO 106
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 106

cgacagacgc ctgatctttg atgtgagcct gt 32

<210> SEQ ID NO 107
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<400> SEQUENCE: 107

gatcacaggc tcacatcaaa gatca 25

<210> SEQ ID NO 108
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<212> TYPE: DNA
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<400> SEQUENCE: 108

cgacagacgc ctgatctttg atggaacgga ct 32

<210> SEQ ID NO 109
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gatcagtccg ttccatcaaa gatca 25

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<211> LENGTH: 32
<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 110

cgacagacgc ctgatctttg agcacaagga gt 32

<210> SEQ ID NO 111
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 111

gatcactcct tgtgctcaaa gatca 25

<210> SEQ ID NO 112
<211> LENGTH: 32
<212> TYPE: DNA
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<400> SEQUENCE: 112

cgacagacgc ctgatctttg acgtatggag ct 32

<210> SEQ ID NO 113
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<212> TYPE: DNA
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<400> SEQUENCE: 113

gatcagctcc atacgtcaaa gatca 25

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<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 114

cgacagacgc ctgatctttg acggagatga ct 32

<210> SEQ ID NO 115
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<212> TYPE: DNA
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gatcagtcat ctccgtcaaa gatca 25

<210> SEQ ID NO 116
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 116

cgacagacgc ctgatctttg acacgaagag gt 32

<210> SEQ ID NO 117
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<212> TYPE: DNA
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<400> SEQUENCE: 117

gatcacctct tcgtgtcaaa gatca 25

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<400> SEQUENCE: 118

cgacagacgc ctgatctttc ttggagtagc gt 32

<210> SEQ ID NO 119
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<212> TYPE: DNA
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<400> SEQUENCE: 119

gatcacgcta ctccaagaaa gatca 25

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<211> LENGTH: 32
<212> TYPE: DNA
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<400> SEQUENCE: 120

cgacagacgc ctgatctttc tgagtgtgac gt 32

<210> SEQ ID NO 121
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 121

gatcacgtca cactcagaaa gatca 25

<210> SEQ ID NO 122
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 122

cgacagacgc ctgatctttc tccgacactt gt 32

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<210> SEQ ID NO 123
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 123

gatcacaagt gtcggagaaa gatca 25

<210> SEQ ID NO 124
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<400> SEQUENCE: 124

cgacagacgc ctgatctttc gaggttgaca gt 32

<210> SEQ ID NO 125
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<400> SEQUENCE: 125

gatcactgtc aacctcgaaa gatca 25

<210> SEQ ID NO 126
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<212> TYPE: DNA
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<400> SEQUENCE: 126

cgacagacgc ctgatctttc gaagagaacg gt 32

<210> SEQ ID NO 127
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<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 127

gatcaccgtt ctcttcgaaa gatca 25

<210> SEQ ID NO 128
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 128

cgacagacgc ctgatctttc cttcaactcg gt 32

<210> SEQ ID NO 129
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 129

gatcaccgag ttgaaggaaa gatca 25

<210> SEQ ID NO 130
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 130

cgacagacgc ctgatctttc ctggagacac tt 32

<210> SEQ ID NO 131
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 131

gatcaagtgt ctccaggaaa gatca 25

<210> SEQ ID NO 132
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 132

cgacagacgc ctgatctttc ctctgaaacc gt 32

<210> SEQ ID NO 133
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 133

gatcacggtt tcagaggaaa gatca 25

<210> SEQ ID NO 134
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 134

cgacagacgc ctgatctttc ctattgaccg ct 32

<210> SEQ ID NO 135
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 135

gatcagcggt caataggaaa gatca 25

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<210> SEQ ID NO 136
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 136

cgacagacgc ctgatctttc cggtgatgat gt 32

<210> SEQ ID NO 137
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 137

gatcacatca tcaccggaaa gatca 25

<210> SEQ ID NO 138
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 138

cgacagacgc ctgatctttc cgacaagact ct 32

<210> SEQ ID NO 139
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 139

gatcagagtc ttgtcggaaa gatca 25

<210> SEQ ID NO 140
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 140

cgacagacgc ctgatctttc catgtcgagt ct 32

<210> SEQ ID NO 141
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 141

gatcagactc gacatggaaa gatca 25

<210> SEQ ID NO 142
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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<400> SEQUENCE: 142

cgacagacgc ctgatctttc cacgttagtc ct 32

<210> SEQ ID NO 143
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 143

gatcaggact aacgtggaaa gatca 25

<210> SEQ ID NO 144
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 144

cgacagacgc ctgatctttc caagaagcca gt 32

<210> SEQ ID NO 145
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 145

gatcactggc ttcttggaaa gatca 25

<210> SEQ ID NO 146
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 146

cgacagacgc ctgatctttc atgaaggacg gt 32

<210> SEQ ID NO 147
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 147

gatcaccgtc cttcatgaaa gatca 25

<210> SEQ ID NO 148
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 148

cgacagacgc ctgatctttc ataaccgagc ct 32

<210> SEQ ID NO 149
<211> LENGTH: 25

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 149

gatcaggctc ggttatgaaa gatca 25

<210> SEQ ID NO 150
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 150

cgacagacgc ctgatctttc aggttggtag ct 32

<210> SEQ ID NO 151
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 151

gatcagctac caacctgaaa gatca 25

<210> SEQ ID NO 152
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 152

cgacagacgc ctgatctttc aggagccaat ct 32

<210> SEQ ID NO 153
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 153

gatcagattg gctcctgaaa gatca 25

<210> SEQ ID NO 154
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 154

cgacagacgc ctgatctttc accggatctt ct 32

<210> SEQ ID NO 155
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 155

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gatcagaaga tccggtgaaa gatca 25

<210> SEQ ID NO 156
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 156

cgacagacgc ctgatctttc aagtggagac gt 32

<210> SEQ ID NO 157
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 157

gatcacgtct ccacttgaaa gatca 25

<210> SEQ ID NO 158
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 158

cgacagacgc ctgatctttc aaacggagag gt 32

<210> SEQ ID NO 159
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 159

gatcacctct ccgtttgaaa gatca 25

<210> SEQ ID NO 160
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 160

cgacagacgc ctgatcttta tgtcagaggc gt 32

<210> SEQ ID NO 161
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 161

gatcacgcct ctgacataaa gatca 25

<210> SEQ ID NO 162
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 162

cgacagacgc ctgatcttta tgtacgctcg gt 32

<210> SEQ ID NO 163
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 163

gatcaccgag cgtacataaa gatca 25

<210> SEQ ID NO 164
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 164

cgacagacgc ctgatcttta tggcgtggat ct 32

<210> SEQ ID NO 165
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 165

gatcagatcc acgccataaa gatca 25

<210> SEQ ID NO 166
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 166

cgacagacgc ctgatcttta tgagcgacga gt 32

<210> SEQ ID NO 167
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 167

gatcactcgt cgctcataaa gatca 25

<210> SEQ ID NO 168
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 168

cgacagacgc ctgatcttta tccacgacag ct 32

<210> SEQ ID NO 169
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 169

gatcagctgt cgtggataaa gatca 25

<210> SEQ ID NO 170
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 170

cgacagacgc ctgatcttta tagtcgcgtg gt 32

<210> SEQ ID NO 171
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 171

gatcaccacg cgactataaa gatca 25

<210> SEQ ID NO 172
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 172

cgacagacgc ctgatcttta taaggccacc gt 32

<210> SEQ ID NO 173
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 173

gatcacggtg gccttataaa gatca 25

<210> SEQ ID NO 174
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 174

cgacagacgc ctgatcttta gtttcggcag gt 32

<210> SEQ ID NO 175
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 175

gatcacctgc cgaaactaaa gatca 25

<210> SEQ ID NO 176
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 176

cgacagacgc ctgatcttta gtgtactggc gt 32

<210> SEQ ID NO 177
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 177

gatcacgcca gtacactaaa gatca 25

<210> SEQ ID NO 178
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 178

cgacagacgc ctgatcttta gtctccaccg at 32

<210> SEQ ID NO 179
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 179

gatcatcggt ggagactaaa gatca 25

<210> SEQ ID NO 180
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 180

cgacagacgc ctgatcttta gtatgctcgc ct 32

<210> SEQ ID NO 181
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 181

gatcaggcga gcatactaaa gatca 25

<210> SEQ ID NO 182

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<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 182

cgacagacgc ctgatcttta gcctccaatc gt 32

<210> SEQ ID NO 183
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 183

gatcacgatt ggaggctaaa gatca 25

<210> SEQ ID NO 184
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 184

cgacagacgc ctgatcttta gaactctggc gt 32

<210> SEQ ID NO 185
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 185

gatcacgcca gagttctaaa gatca 25

<210> SEQ ID NO 186
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 186

cgacagacgc ctgatcttta gaacgcgaga gt 32

<210> SEQ ID NO 187
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 187

gatcactctc gcgttctaaa gatca 25

<210> SEQ ID NO 188
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 188

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cgacagacgc ctgatcttta gaaccgacac ct 32

<210> SEQ ID NO 189
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 189

gatcaggtgt cggttctaaa gatca 25

<210> SEQ ID NO 190
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 190

cgacagacgc ctgatcttta ctcagaaccg ct 32

<210> SEQ ID NO 191
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 191

gatcagcggt tctgagtaaa gatca 25

<210> SEQ ID NO 192
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 192

cgacagacgc ctgatcttta cgagaggcaa ct 32

<210> SEQ ID NO 193
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 193

gatcagttgc ctctcgtaaa gatca 25

<210> SEQ ID NO 194
<211> LENGTH: 32
<212> TYPE: DNA
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<400> SEQUENCE: 194

cgacagacgc ctgatcttta ccttggagcc tt 32

<210> SEQ ID NO 195
<211> LENGTH: 25
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 195

gatcaaggct ccaaggtaaa gatca 25

<210> SEQ ID NO 196
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 196

cgacagacgc ctgatcttta ccagacaagc ct 32

<210> SEQ ID NO 197
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<212> TYPE: DNA
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<400> SEQUENCE: 197

gatcaggctt gtctggtaaa gatca 25

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<220> FEATURE:
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<400> SEQUENCE: 198

cgacagacgc ctgatcttta aggcgagaca gt 32

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gatcactgtc tcgccttaaa gatca 25

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cgacagacgc ctgatcttta aggacgcaag gt 32

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gatcaccttg cgtccttaaa gatca 25

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cgacagacgc ctgatcttta agcggaactg gt 32

<210> SEQ ID NO 203
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gatcaccagt tccgcttaaa gatca 25

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<400> SEQUENCE: 204

cgacagacgc ctgatcttta agccatctcc gt 32

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gatcacggag atggcttaaa gatca 25

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<400> SEQUENCE: 206

cgacagacgc ctgatcttta acgatcctgc ct 32

<210> SEQ ID NO 207
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 207

gatcaggcag gatcgttaaa gatca 25

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<223> OTHER INFORMATION: synthetic oligonucleotide

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cgacagacgc ctgatcttta accggacact ct 32

<210> SEQ ID NO 209
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gatcagagtg tccggttaaa gatca 25

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<220> FEATURE:
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<400> SEQUENCE: 210

cgacagacgc ctgatcttta acatcggcct ct 32

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gatcagaggc cgatgttaaa gatca 25

<210> SEQ ID NO 212
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cgacagacgc ctgatcttta acaagcggag gt 32

<210> SEQ ID NO 213
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gatcacctcc gcttgttaaa gatca 25

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<400> SEQUENCE: 214

cgacagacgc ctgatcttta aagcacggag gt 32

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<210> SEQ ID NO 215
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<400> SEQUENCE: 215

gatcacctcc gtgctttaaa gatca 25

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<400> SEQUENCE: 216

cgacagacgc ctgatcttgt ttagcacctc ct 32

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<400> SEQUENCE: 217

gatcaggagg tgctaaacaa gatca 25

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<400> SEQUENCE: 218

cgacagacgc ctgatcttgt tctgaaggct gt 32

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<400> SEQUENCE: 219

gatcacagcc ttcagaacaa gatca 25

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 220

cgacagacgc ctgatcttgt tatgaggacg ct 32

<210> SEQ ID NO 221
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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<400> SEQUENCE: 221

gatcagcgtc ctcataacaa gatca 25

<210> SEQ ID NO 222
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 222

cgacagacgc ctgatcttgt gtacaagcag gt 32

<210> SEQ ID NO 223
<211> LENGTH: 25
<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 223

gatcacctgc ttgtacacaa gatca 25

<210> SEQ ID NO 224
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 224

cgacagacgc ctgatcttgt ggttcatacg gt 32

<210> SEQ ID NO 225
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 225

gatcaccgta tgaaccacaa gatca 25

<210> SEQ ID NO 226
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 226

cgacagacgc ctgatcttgt ggattactgg ct 32

<210> SEQ ID NO 227
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 227

gatcagccag taatccacaa gatca 25

<210> SEQ ID NO 228
<211> LENGTH: 32

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 228

cgacagacgc ctgatcttgt gaagatgcct gt 32

<210> SEQ ID NO 229
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 229

gatcacaggc atcttcacaa gatca 25

<210> SEQ ID NO 230
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 230

cgacagacgc ctgatcttgt ctgacctcca tt 32

<210> SEQ ID NO 231
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 231

gatcaatgga ggtcagacaa gatca 25

<210> SEQ ID NO 232
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 232

cgacagacgc ctgatcttgt ctacactccg at 32

<210> SEQ ID NO 233
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 233

gatcatcgga gtgtagacaa gatca 25

<210> SEQ ID NO 234
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 234

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cgacagacgc ctgatcttgt cggagaacaa gt 32

<210> SEQ ID NO 235
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 235

gatcacttgt tctccgacaa gatca 25

<210> SEQ ID NO 236
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 236

cgacagacgc ctgatcttgt cataggcgtt ct 32

<210> SEQ ID NO 237
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 237

gatcagaacg cctatgacaa gatca 25

<210> SEQ ID NO 238
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 238

cgacagacgc ctgatcttgt cactcttcac gt 32

<210> SEQ ID NO 239
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 239

gatcacgtga agagtgacaa gatca 25

<210> SEQ ID NO 240
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 240

cgacagacgc ctgatcttgt atttccgagg ct 32

<210> SEQ ID NO 241
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 241

gatcagcctc ggaaatacaa gatca 25

<210> SEQ ID NO 242
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 242

cgacagacgc ctgatcttgt atgactgtgg ct 32

<210> SEQ ID NO 243
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 243

gatcagccac agtcatacaa gatca 25

<210> SEQ ID NO 244
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 244

cgacagacgc ctgatcttgt actgcaactg gt 32

<210> SEQ ID NO 245
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 245

gatcaccagt tgcagtacaa gatca 25

<210> SEQ ID NO 246
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 246

cgacagacgc ctgatcttgt actaacacgc ct 32

<210> SEQ ID NO 247
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 247

gatcaggcgt gttagtacaa gatca 25

<210> SEQ ID NO 248
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 248

cgacagacgc ctgatcttgt acctcctgca tt 32

<210> SEQ ID NO 249
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 249

gatcaatgca ggaggtacaa gatca 25

<210> SEQ ID NO 250
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 250

cgacagacgc ctgatcttgg tgtacttagc gt 32

<210> SEQ ID NO 251
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 251

gatcacgcta agtacaccaa gatca 25

<210> SEQ ID NO 252
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 252

cgacagacgc ctgatcttgg tggtcaaagt ct 32

<210> SEQ ID NO 253
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 253

gatcagactt tgaccaccaa gatca 25

<210> SEQ ID NO 254
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 254

cgacagacgc ctgatcttgg tcgaacaaga gt 32

<210> SEQ ID NO 255
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 255

gatcactctt gttcgaccaa gatca 25

<210> SEQ ID NO 256
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 256

cgacagacgc ctgatcttgg tacaatagcg gt 32

<210> SEQ ID NO 257
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 257

gatcaccgct attgtaccaa gatca 25

<210> SEQ ID NO 258
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 258

cgacagacgc ctgatcttgg cttctaatcg gt 32

<210> SEQ ID NO 259
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 259

gatcaccgat tagaagccaa gatca 25

<210> SEQ ID NO 260
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 260

cgacagacgc ctgatcttgg cttaccaact gt 32

<210> SEQ ID NO 261

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 261

gatcacagtt ggtaagccaa gatca 25

<210> SEQ ID NO 262
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 262

cgacagacgc ctgatcttgg ctattacgtg gt 32

<210> SEQ ID NO 263
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 263

gatcaccacg taatagccaa gatca 25

<210> SEQ ID NO 264
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 264

cgacagacgc ctgatcttgg caaaccacta gt 32

<210> SEQ ID NO 265
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 265

gatcactagt ggtttgccaa gatca 25

<210> SEQ ID NO 266
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 266

cgacagacgc ctgatcttgg atagccgaag at 32

<210> SEQ ID NO 267
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 267

gatcatcttc ggctatccaa gatca 25

<210> SEQ ID NO 268
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 268

cgacagacgc ctgatcttgg agatcaaacg gt 32

<210> SEQ ID NO 269
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 269

gatcaccgtt tgatctccaa gatca 25

<210> SEQ ID NO 270
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 270

cgacagacgc ctgatcttgg agagcacaat gt 32

<210> SEQ ID NO 271
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 271

gatcacattg tgctctccaa gatca 25

<210> SEQ ID NO 272
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 272

cgacagacgc ctgatcttgg agagaaccga tt 32

<210> SEQ ID NO 273
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 273

gatcaatcgg ttctctccaa gatca 25

<210> SEQ ID NO 274
<211> LENGTH: 32
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 274

cgacagacgc ctgatcttgc ttaggaatcg gt 32

<210> SEQ ID NO 275
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 275

gatcaccgat tcctaagcaa gatca 25

<210> SEQ ID NO 276
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 276

cgacagacgc ctgatcttgc ttaccactga ct 32

<210> SEQ ID NO 277
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 277

gatcagtcag tggtaagcaa gatca 25

<210> SEQ ID NO 278
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 278

cgacagacgc ctgatcttgc tcaaagctac ct 32

<210> SEQ ID NO 279
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 279

gatcaggtag ctttgagcaa gatca 25

<210> SEQ ID NO 280
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 280

cgacagacgc ctgatcttgc gatagtggtt ct 32

<210> SEQ ID NO 281
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 281

gatcagaacc actatcgcaa gatca 25

<210> SEQ ID NO 282
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 282

cgacagacgc ctgatcttgc gaagtagaga ct 32

<210> SEQ ID NO 283
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 283

gatcagtctc tacttcgcaa gatca 25

<210> SEQ ID NO 284
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 284

cgacagacgc ctgatcttgc ctaaacgatc ct 32

<210> SEQ ID NO 285
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 285

gatcaggatc gtttaggcaa gatca 25

<210> SEQ ID NO 286
<211> LENGTH: 32
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 286

cgacagacgc ctgatcttgc caacttctct gt 32

<210> SEQ ID NO 287
<211> LENGTH: 25
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 287

gatcacagag aagttggcaa gatca 25

<210> SEQ ID NO 288
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 288

cgacagacgc ctgatcttgc caactatacc gt 32

<210> SEQ ID NO 289
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gatcacggta tagttggcaa gatca 25

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 290

cgacagacgc ctgatcttgc atcttcactg gt 32

<210> SEQ ID NO 291
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gatcaccagt gaagatgcaa gatca 25

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<400> SEQUENCE: 292

cgacagacgc ctgatcttgc atatccttcc gt 32

<210> SEQ ID NO 293
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<400> SEQUENCE: 293

gatcacggaa ggatatgcaa gatca 25

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<210> SEQ ID NO 294
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<400> SEQUENCE: 294

cgacagacgc ctgatcttgc aatcctacgt ct 32

<210> SEQ ID NO 295
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<400> SEQUENCE: 295

gatcagacgt aggattgcaa gatca 25

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<400> SEQUENCE: 296

cgacagacgc ctgatcttgc aatagacgac ct 32

<210> SEQ ID NO 297
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<400> SEQUENCE: 297

gatcaggtcg tctattgcaa gatca 25

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<400> SEQUENCE: 298

cgacagacgc ctgatcttga tttacctcgc ct 32

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<400> SEQUENCE: 299

gatcaggcga ggtaaatcaa gatca 25

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<400> SEQUENCE: 300

cgacagacgc ctgatcttga ttagttccgc ct 32

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<400> SEQUENCE: 301

gatcaggcgg aactaatcaa gatca 25

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<400> SEQUENCE: 302

cgacagacgc ctgatcttga ttactccgtg ct 32

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<400> SEQUENCE: 303

gatcagcacg gagtaatcaa gatca 25

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<400> SEQUENCE: 304

cgacagacgc ctgatcttga tggttcactg gt 32

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 305

gatcaccagt gaaccatcaa gatca 25

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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 306

cgacagacgc ctgatcttga tgagaagacg ct 32

<210> SEQ ID NO 307
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 307

gatcagcgtc ttctcatcaa gatca 25

<210> SEQ ID NO 308
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 308

cgacagacgc ctgatcttga tccgtccaaa gt 32

<210> SEQ ID NO 309
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<212> TYPE: DNA
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<400> SEQUENCE: 309

gatcactttg gacggatcaa gatca 25

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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 310

cgacagacgc ctgatcttga tccacaacga gt 32

<210> SEQ ID NO 311
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 311

gatcactcgt tgtggatcaa gatca 25

<210> SEQ ID NO 312
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 312

cgacagacgc ctgatcttga tcaacacctc gt 32

<210> SEQ ID NO 313
<211> LENGTH: 25
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 313

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gatcacgagg tgttgatcaa gatca 25

<210> SEQ ID NO 314
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 314

cgacagacgc ctgatcttga tatcctgtgc gt 32

<210> SEQ ID NO 315
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 315

gatcacgcac aggatatcaa gatca 25

<210> SEQ ID NO 316
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 316

cgacagacgc ctgatcttga tactcaacgg ct 32

<210> SEQ ID NO 317
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 317

gatcagccgt tgagtatcaa gatca 25

<210> SEQ ID NO 318
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 318

cgacagacgc ctgatcttga gtccagaagg tt 32

<210> SEQ ID NO 319
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 319

gatcaacctt ctggactcaa gatca 25

<210> SEQ ID NO 320
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 320

cgacagacgc ctgatcttga ggttacaagg ct 32

<210> SEQ ID NO 321
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 321

gatcagcctt gtaacctcaa gatca 25

<210> SEQ ID NO 322
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 322

cgacagacgc ctgatcttga ggtcttcgga tt 32

<210> SEQ ID NO 323
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 323

gatcaatccg aagacctcaa gatca 25

<210> SEQ ID NO 324
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 324

cgacagacgc ctgatcttga gcaactgaag gt 32

<210> SEQ ID NO 325
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 325

gatcaccttc agttgctcaa gatca 25

<210> SEQ ID NO 326
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 326

cgacagacgc ctgatcttga gagttgccat gt 32

<210> SEQ ID NO 327
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 327

gatcacatgg caactctcaa gatca 25

<210> SEQ ID NO 328
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 328

cgacagacgc ctgatcttga gacaaccact gt 32

<210> SEQ ID NO 329
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 329

gatcacagtg gttgtctcaa gatca 25

<210> SEQ ID NO 330
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 330

cgacagacgc ctgatcttga ctctctacgc tt 32

<210> SEQ ID NO 331
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 331

gatcaagcgt agagagtcaa gatca 25

<210> SEQ ID NO 332
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 332

cgacagacgc ctgatcttga ctactcaccg tt 32

<210> SEQ ID NO 333
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 333

gatcaacggt gagtagtcaa gatca 25

<210> SEQ ID NO 334
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 334

cgacagacgc ctgatcttga cgaaactgga gt 32

<210> SEQ ID NO 335
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 335

gatcactcca gtttcgtcaa gatca 25

<210> SEQ ID NO 336
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 336

cgacagacgc ctgatcttga ccttcaacct gt 32

<210> SEQ ID NO 337
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 337

gatcacaggt tgaaggtcaa gatca 25

<210> SEQ ID NO 338
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 338

cgacagacgc ctgatcttga caagtcacac ct 32

<210> SEQ ID NO 339
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 339

gatcaggtgt gacttgtcaa gatca 25

<210> SEQ ID NO 340

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<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 340

cgacagacgc ctgatcttga atctctgcca ct 32

<210> SEQ ID NO 341
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 341

gatcagtggc agagattcaa gatca 25

<210> SEQ ID NO 342
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 342

cgacagacgc ctgatcttga aggactacgg tt 32

<210> SEQ ID NO 343
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 343

gatcaaccgt agtccttcaa gatca 25

<210> SEQ ID NO 344
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 344

cgacagacgc ctgatcttga agcaacctga gt 32

<210> SEQ ID NO 345
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 345

gatcactcag gttgcttcaa gatca 25

<210> SEQ ID NO 346
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 346

cgacagacgc ctgatcttga acaccttctg gt 32

<210> SEQ ID NO 347
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 347

gatcaccaga aggtgttcaa gatca 25

<210> SEQ ID NO 348
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 348

cgacagacgc ctgatcttga aatactccgc ct 32

<210> SEQ ID NO 349
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 349

gatcaggcgg agtatttcaa gatca 25

<210> SEQ ID NO 350
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 350

cgacagacgc ctgatcttct ttgataccgc ct 32

<210> SEQ ID NO 351
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 351

gatcaggcgg tatcaaagaa gatca 25

<210> SEQ ID NO 352
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 352

cgacagacgc ctgatcttct ttccagcagt ct 32

<210> SEQ ID NO 353
<211> LENGTH: 25
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 353

gatcagactg ctggaaagaa gatca 25

<210> SEQ ID NO 354
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 354

cgacagacgc ctgatcttct ttaggatgcg gt 32

<210> SEQ ID NO 355
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 355

gatcaccgca tcctaaagaa gatca 25

<210> SEQ ID NO 356
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 356

cgacagacgc ctgatcttct taggaaacgc ct 32

<210> SEQ ID NO 357
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 357

gatcaggcgt ttcctaagaa gatca 25

<210> SEQ ID NO 358
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 358

cgacagacgc ctgatcttct taactcgtgc ct 32

<210> SEQ ID NO 359
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 359

gatcaggcac gagttaagaa gatca 25

<210> SEQ ID NO 360
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 360

cgacagacgc ctgatcttct gtcctccgaa tt 32

<210> SEQ ID NO 361
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 361

gatcaattcg gaggacagaa gatca 25

<210> SEQ ID NO 362
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 362

cgacagacgc ctgatcttct ggaatgaggc tt 32

<210> SEQ ID NO 363
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 363

gatcaagcct cattccagaa gatca 25

<210> SEQ ID NO 364
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 364

cgacagacgc ctgatcttct gccaaagact ct 32

<210> SEQ ID NO 365
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 365

gatcagagtc tttggcagaa gatca 25

<210> SEQ ID NO 366
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 366

cgacagacgc ctgatcttct ctgaaactgc ct 32

<210> SEQ ID NO 367
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 367

gatcaggcag tttcagagaa gatca 25

<210> SEQ ID NO 368
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 368

cgacagacgc ctgatcttct cgttggaagt ct 32

<210> SEQ ID NO 369
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 369

gatcagactt ccaacgagaa gatca 25

<210> SEQ ID NO 370
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 370

cgacagacgc ctgatcttct ccaggttcac at 32

<210> SEQ ID NO 371
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 371

gatcatgtga acctggagaa gatca 25

<210> SEQ ID NO 372
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 372

cgacagacgc ctgatcttct ccaaggtgtc tt 32

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<210> SEQ ID NO 373
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 373

gatcaagaca ccttggagaa gatca 25

<210> SEQ ID NO 374
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 374

cgacagacgc ctgatcttct caaggacaac gt 32

<210> SEQ ID NO 375
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 375

gatcacgttg tccttgagaa gatca 25

<210> SEQ ID NO 376
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 376

cgacagacgc ctgatcttct caacatggct ct 32

<210> SEQ ID NO 377
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 377

gatcagagcc atgttgagaa gatca 25

<210> SEQ ID NO 378
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 378

cgacagacgc ctgatcttct atcacaaggc gt 32

<210> SEQ ID NO 379
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<400> SEQUENCE: 379

gatcacgcct tgtgatagaa gatca 25

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 380

cgacagacgc ctgatcttct aggtatgcgg tt 32

<210> SEQ ID NO 381
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 381

gatcaaccgc atacctagaa gatca 25

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 382

cgacagacgc ctgatcttct agcaacggaa ct 32

<210> SEQ ID NO 383
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 383

gatcagttcc gttgctagaa gatca 25

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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 384

cgacagacgc ctgatcttct aacggtggtc tt 32

<210> SEQ ID NO 385
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 385

gatcaagacc accgttagaa gatca 25

<210> SEQ ID NO 386
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 386

cgacagacgc ctgatcttct aaagcgtcca ct 32

<210> SEQ ID NO 387
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<223> OTHER INFORMATION: synthetic oligonucleotide

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gatcagtgga cgctttagaa gatca 25

<210> SEQ ID NO 388
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<220> FEATURE:
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<400> SEQUENCE: 388

cgacagacgc ctgatcttct aaagaccgca ct 32

<210> SEQ ID NO 389
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<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

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gatcagtgcg gtctttagaa gatca 25

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 390

cgacagacgc ctgatcttcg taggagaagc tt 32

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 391

gatcaagctt ctcctacgaa gatca 25

<210> SEQ ID NO 392
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 392

cgacagacgc ctgatcttcg tacctccaag at 32

<210> SEQ ID NO 393
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 393

gatcatcttg gaggtacgaa gatca 25

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<400> SEQUENCE: 394

cgacagacgc ctgatcttcg taatacgctc ct 32

<210> SEQ ID NO 395
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<220> FEATURE:
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<400> SEQUENCE: 395

gatcaggagc gtattacgaa gatca 25

<210> SEQ ID NO 396
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<400> SEQUENCE: 396

cgacagacgc ctgatcttcg gttagattgg ct 32

<210> SEQ ID NO 397
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 397

gatcagccaa tctaaccgaa gatca 25

<210> SEQ ID NO 398
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<400> SEQUENCE: 398

cgacagacgc ctgatcttcg gtaccaacaa ct 32

<210> SEQ ID NO 399
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
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<400> SEQUENCE: 399

gatcagttgt tggtaccgaa gatca 25

<210> SEQ ID NO 400
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 400

cgacagacgc ctgatcttcg gatagagagc at 32

<210> SEQ ID NO 401
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 401

gatcatgctc tctatccgaa gatca 25

<210> SEQ ID NO 402
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 402

cgacagacgc ctgatcttcg gaaagacgta gt 32

<210> SEQ ID NO 403
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 403

gatcactacg tctttccgaa gatca 25

<210> SEQ ID NO 404
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 404

cgacagacgc ctgatcttcg caagaggtaa gt 32

<210> SEQ ID NO 405
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 405

gatcacttac ctcttgcgaa gatca 25

<210> SEQ ID NO 406
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 406

cgacagacgc ctgatcttcg agatggtgtt ct 32

<210> SEQ ID NO 407
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 407

gatcagaaca ccatctcgaa gatca 25

<210> SEQ ID NO 408
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 408

cgacagacgc ctgatcttcg aagaagatgc ct 32

<210> SEQ ID NO 409
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 409

gatcaggcat cttcttcgaa gatca 25

<210> SEQ ID NO 410
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 410

cgacagacgc ctgatcttcg aactacacag ct 32

<210> SEQ ID NO 411
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 411

gatcagctgt gtagttcgaa gatca 25

<210> SEQ ID NO 412
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 412

cgacagacgc ctgatcttcc ttacggactc at 32

<210> SEQ ID NO 413
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 413

gatcatgagt ccgtaaggaa gatca 25

<210> SEQ ID NO 414
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 414

cgacagacgc ctgatcttcc tgttggtgaa gt 32

<210> SEQ ID NO 415
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 415

gatcacttca ccaacaggaa gatca 25

<210> SEQ ID NO 416
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 416

cgacagacgc ctgatcttcc tggatggaag tt 32

<210> SEQ ID NO 417
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 417

gatcaacttc catccaggaa gatca 25

<210> SEQ ID NO 418
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 418

cgacagacgc ctgatcttcc tcaagttcgt ct 32

<210> SEQ ID NO 419

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 419

gatcagacga acttgaggaa gatca 25

<210> SEQ ID NO 420
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 420

cgacagacgc ctgatcttcc taccggactt tt 32

<210> SEQ ID NO 421
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 421

gatcaaaagt ccggtaggaa gatca 25

<210> SEQ ID NO 422
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 422

cgacagacgc ctgatcttcc gtgaaaggaa gt 32

<210> SEQ ID NO 423
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 423

gatcacttcc tttcacggaa gatca 25

<210> SEQ ID NO 424
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 424

cgacagacgc ctgatcttcc ggatatgttg ct 32

<210> SEQ ID NO 425
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 425

gatcagcaac atatccggaa gatca 25

<210> SEQ ID NO 426
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 426

cgacagacgc ctgatcttcc gctaaatgtc ct 32

<210> SEQ ID NO 427
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 427

gatcaggaca tttagcggaa gatca 25

<210> SEQ ID NO 428
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 428

cgacagacgc ctgatcttcc gaaactatgc ct 32

<210> SEQ ID NO 429
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 429

gatcaggcat agtttcggaa gatca 25

<210> SEQ ID NO 430
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 430

cgacagacgc ctgatcttcc actaggcaaa ct 32

<210> SEQ ID NO 431
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 431

gatcagtttg cctagtggaa gatca 25

<210> SEQ ID NO 432
<211> LENGTH: 32
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 432

cgacagacgc ctgatcttcc acgaatagca ct 32

<210> SEQ ID NO 433
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 433

gatcagtgct attcgtggaa gatca 25

<210> SEQ ID NO 434
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 434

cgacagacgc ctgatcttcc acgaaggaat ct 32

<210> SEQ ID NO 435
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 435

gatcagattc cttcgtggaa gatca 25

<210> SEQ ID NO 436
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 436

cgacagacgc ctgatcttcc accagagaac tt 32

<210> SEQ ID NO 437
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 437

gatcaagttc tctggtggaa gatca 25

<210> SEQ ID NO 438
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 438

cgacagacgc ctgatcttcc acatacaggc tt 32

<210> SEQ ID NO 439
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 439

gatcaagcct gtatgtggaa gatca 25

<210> SEQ ID NO 440
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 440

cgacagacgc ctgatcttcc aagtccgttt ct 32

<210> SEQ ID NO 441
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 441

gatcagaaac ggacttggaa gatca 25

<210> SEQ ID NO 442
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 442

cgacagacgc ctgatcttca ttctggcact ct 32

<210> SEQ ID NO 443
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 443

gatcagagtg ccagaatgaa gatca 25

<210> SEQ ID NO 444
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 444

cgacagacgc ctgatcttca tgtagtgtgg ct 32

<210> SEQ ID NO 445
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 445

gatcagccac actacatgaa gatca 25

<210> SEQ ID NO 446
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 446

cgacagacgc ctgatcttca tggttgtgga ct 32

<210> SEQ ID NO 447
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 447

gatcagtcca caaccatgaa gatca 25

<210> SEQ ID NO 448
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 448

cgacagacgc ctgatcttca tcttacacgg ct 32

<210> SEQ ID NO 449
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 449

gatcagccgt gtaagatgaa gatca 25

<210> SEQ ID NO 450
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 450

cgacagacgc ctgatcttca tacggaacac ct 32

<210> SEQ ID NO 451
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 451

gatcaggtgt tccgtatgaa gatca 25

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<210> SEQ ID NO 452
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 452

cgacagacgc ctgatcttca taacactcgg ct 32

<210> SEQ ID NO 453
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 453

gatcagccga gtgttatgaa gatca 25

<210> SEQ ID NO 454
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 454

cgacagacgc ctgatcttca gtgaccaaac ct 32

<210> SEQ ID NO 455
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 455

gatcaggttt ggtcactgaa gatca 25

<210> SEQ ID NO 456
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 456

cgacagacgc ctgatcttca gtcattccgt ct 32

<210> SEQ ID NO 457
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 457

gatcagacgg aatgactgaa gatca 25

<210> SEQ ID NO 458
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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<400> SEQUENCE: 458

cgacagacgc ctgatcttca gcatggaaag gt 32

<210> SEQ ID NO 459
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 459

gatcaccttt ccatgctgaa gatca 25

<210> SEQ ID NO 460
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 460

cgacagacgc ctgatcttca gcaaagagtc ct 32

<210> SEQ ID NO 461
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 461

gatcaggact ctttgctgaa gatca 25

<210> SEQ ID NO 462
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 462

cgacagacgc ctgatcttca gagtagagcg tt 32

<210> SEQ ID NO 463
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 463

gatcaacgct ctactctgaa gatca 25

<210> SEQ ID NO 464
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 464

cgacagacgc ctgatcttca gaaggagttg ct 32

<210> SEQ ID NO 465
<211> LENGTH: 25

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 465

gatcagcaac tccttctgaa gatca 25

<210> SEQ ID NO 466
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 466

cgacagacgc ctgatcttca cttagcggaa ct 32

<210> SEQ ID NO 467
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 467

gatcagttcc gctaagtgaa gatca 25

<210> SEQ ID NO 468
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 468

cgacagacgc ctgatcttca cggaggaaat gt 32

<210> SEQ ID NO 469
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 469

gatcacattt cctccgtgaa gatca 25

<210> SEQ ID NO 470
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 470

cgacagacgc ctgatcttca cacctggaaa ct 32

<210> SEQ ID NO 471
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<212> TYPE: DNA
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<400> SEQUENCE: 471

gatcagtttc caggtgtgaa gatca 25

<210> SEQ ID NO 472
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 472

cgacagacgc ctgatcttca caatctcagg ct 32

<210> SEQ ID NO 473
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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gatcagcctg agattgtgaa gatca 25

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cgacagacgc ctgatcttca atgagtgtcc gt 32

<210> SEQ ID NO 475
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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gatcacggac actcattgaa gatca 25

<210> SEQ ID NO 476
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cgacagacgc ctgatcttca atcacagagc ct 32

<210> SEQ ID NO 477
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<212> TYPE: DNA
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gatcaggctc tgtgattgaa gatca 25

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<220> FEATURE:
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<400> SEQUENCE: 478

cgacagacgc ctgatcttca aggctgaaag gt 32

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<400> SEQUENCE: 479

gatcaccttt cagccttgaa gatca 25

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<400> SEQUENCE: 480

cgacagacgc ctgatcttca agactaaccg ct 32

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<220> FEATURE:
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<400> SEQUENCE: 481

gatcagcggt tagtcttgaa gatca 25

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<400> SEQUENCE: 482

cgacagacgc ctgatcttca accagtaagc ct 32

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gatcaggctt actggttgaa gatca 25

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<400> SEQUENCE: 484

cgacagacgc ctgatcttca aagtatccgc ct 32

<210> SEQ ID NO 485
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gatcaggcgg atactttgaa gatca 25

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cgacagacgc ctgatcttat tgccgagttc ct 32

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gatcaggaac tcggcaataa gatca 25

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cgacagacgc ctgatcttat tgccaccaca gt 32

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<400> SEQUENCE: 489

gatcactgtg gtggcaataa gatca 25

<210> SEQ ID NO 490
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<400> SEQUENCE: 490

cgacagacgc ctgatcttat tccgaacctg ct 32

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<400> SEQUENCE: 491

gatcagcagg ttcggaataa gatca 25

<210> SEQ ID NO 492
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<400> SEQUENCE: 492

cgacagacgc ctgatcttat tcagccgttc ct 32

<210> SEQ ID NO 493
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 493

gatcaggaac ggctgaataa gatca 25

<210> SEQ ID NO 494
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<212> TYPE: DNA
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<400> SEQUENCE: 494

cgacagacgc ctgatcttat gttgccaggt gt 32

<210> SEQ ID NO 495
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 495

gatcacacct ggcaacataa gatca 25

<210> SEQ ID NO 496
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 496

cgacagacgc ctgatcttat gcacacagac ct 32

<210> SEQ ID NO 497
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 497

gatcaggtct gtgtgcataa gatca 25

<210> SEQ ID NO 498

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<211> LENGTH: 32
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 498

cgacagacgc ctgatcttat gcaaggagtc gt 32

<210> SEQ ID NO 499
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 499

gatcacgact ccttgcataa gatca 25

<210> SEQ ID NO 500
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 500

cgacagacgc ctgatcttat ctcgactgcc tt 32

<210> SEQ ID NO 501
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 501

gatcaaggca gtcgagataa gatca 25

<210> SEQ ID NO 502
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 502

cgacagacgc ctgatcttat cgccaagaag gt 32

<210> SEQ ID NO 503
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 503

gatcaccttc ttggcgataa gatca 25

<210> SEQ ID NO 504
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 504

cgacagacgc ctgatcttat cgcacctcaa gt 32

<210> SEQ ID NO 505
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 505

gatcacttga ggtgcgataa gatca 25

<210> SEQ ID NO 506
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 506

cgacagacgc ctgatcttat cgattggctg gt 32

<210> SEQ ID NO 507
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 507

gatcaccagc caatcgataa gatca 25

<210> SEQ ID NO 508
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 508

cgacagacgc ctgatcttat cattgccgac ct 32

<210> SEQ ID NO 509
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 509

gatcaggtcg gcaatgataa gatca 25

<210> SEQ ID NO 510
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 510

cgacagacgc ctgatcttat caggtgttcg ct 32

<210> SEQ ID NO 511
<211> LENGTH: 25
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 511

gatcagcgaa cacctgataa gatca 25

<210> SEQ ID NO 512
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 512

cgacagacgc ctgatcttat aggcggaaac gt 32

<210> SEQ ID NO 513
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 513

gatcacgttt ccgcctataa gatca 25

<210> SEQ ID NO 514
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 514

cgacagacgc ctgatcttat aggagcgagc at 32

<210> SEQ ID NO 515
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 515

gatcatgctc gctcctataa gatca 25

<210> SEQ ID NO 516
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 516

cgacagacgc ctgatcttat agaacgcacg gt 32

<210> SEQ ID NO 517
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 517

gatcaccgtg cgttctataa gatca 25

<210> SEQ ID NO 518
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 518

cgacagacgc ctgatcttat acggcacaag gt 32

<210> SEQ ID NO 519
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 519

gatcaccttg tgccgtataa gatca 25

<210> SEQ ID NO 520
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 520

cgacagacgc ctgatcttat accttgtgcc gt 32

<210> SEQ ID NO 521
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 521

gatcacggca caaggtataa gatca 25

<210> SEQ ID NO 522
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 522

cgacagacgc ctgatcttat aagccttgcc gt 32

<210> SEQ ID NO 523
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 523

gatcacggca aggcttataa gatca 25

<210> SEQ ID NO 524
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 524

cgacagacgc ctgatcttag ttaacaccgc ct 32

<210> SEQ ID NO 525
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 525

gatcaggcgg tgttaactaa gatca 25

<210> SEQ ID NO 526
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 526

cgacagacgc ctgatcttag tctatggcgg tt 32

<210> SEQ ID NO 527
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 527

gatcaaccgc catagactaa gatca 25

<210> SEQ ID NO 528
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 528

cgacagacgc ctgatcttag taccgctttg gt 32

<210> SEQ ID NO 529
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 529

gatcaccaaa gcggtactaa gatca 25

<210> SEQ ID NO 530
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 530

cgacagacgc ctgatcttag gtggctttac gt 32

<210> SEQ ID NO 531
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 531

gatcacgtaa agccacctaa gatca 25

<210> SEQ ID NO 532
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 532

cgacagacgc ctgatcttag gtacggcttt gt 32

<210> SEQ ID NO 533
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 533

gatcacaaag ccgtacctaa gatca 25

<210> SEQ ID NO 534
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 534

cgacagacgc ctgatcttag gcttcactgg tt 32

<210> SEQ ID NO 535
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 535

gatcaaccag tgaagcctaa gatca 25

<210> SEQ ID NO 536
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 536

cgacagacgc ctgatcttag gccatcaaca ct 32

<210> SEQ ID NO 537
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 537

gatcagtgtt gatggcctaa gatca 25

<210> SEQ ID NO 538
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 538

cgacagacgc ctgatcttag gattgaacgg ct 32

<210> SEQ ID NO 539
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 539

gatcagccgt tcaatcctaa gatca 25

<210> SEQ ID NO 540
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 540

cgacagacgc ctgatcttag ctcaaacgtc ct 32

<210> SEQ ID NO 541
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 541

gatcaggacg tttgagctaa gatca 25

<210> SEQ ID NO 542
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 542

cgacagacgc ctgatcttag cggattggtt ct 32

<210> SEQ ID NO 543
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 543

gatcagaacc aatccgctaa gatca 25

<210> SEQ ID NO 544
<211> LENGTH: 32

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 544

cgacagacgc ctgatcttag atttccacgg ct 32

<210> SEQ ID NO 545
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 545

gatcagccgt ggaaatctaa gatca 25

<210> SEQ ID NO 546
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 546

cgacagacgc ctgatcttag attgccgagt gt 32

<210> SEQ ID NO 547
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 547

gatcacactc ggcaatctaa gatca 25

<210> SEQ ID NO 548
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 548

cgacagacgc ctgatcttag aacgtggaag ct 32

<210> SEQ ID NO 549
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 549

gatcagcttc cacgttctaa gatca 25

<210> SEQ ID NO 550
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 550

cgacagacgc ctgatcttag aaactccgca ct 32

<210> SEQ ID NO 551
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 551

gatcagtgcg gagtttctaa gatca 25

<210> SEQ ID NO 552
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 552

cgacagacgc ctgatcttac ttcggacaac ct 32

<210> SEQ ID NO 553
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 553

gatcaggttg tccgaagtaa gatca 25

<210> SEQ ID NO 554
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 554

cgacagacgc ctgatcttac tgtatccgcc tt 32

<210> SEQ ID NO 555
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 555

gatcaaggcg gatacagtaa gatca 25

<210> SEQ ID NO 556
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 556

cgacagacgc ctgatcttac tgctgactcc tt 32

<210> SEQ ID NO 557
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 557

gatcaaggag tcagcagtaa gatca 25

<210> SEQ ID NO 558
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 558

cgacagacgc ctgatcttac tcgtgaaagc ct 32

<210> SEQ ID NO 559
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 559

gatcaggctt tcacgagtaa gatca 25

<210> SEQ ID NO 560
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 560

cgacagacgc ctgatcttac tcgaagccaa ct 32

<210> SEQ ID NO 561
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 561

gatcagttgg cttcgagtaa gatca 25

<210> SEQ ID NO 562
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 562

cgacagacgc ctgatcttac tccagtttgc ct 32

<210> SEQ ID NO 563
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 563

gatcaggcaa actggagtaa gatca 25

<210> SEQ ID NO 564
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 564

cgacagacgc ctgatcttac tattgtggcg gt 32

<210> SEQ ID NO 565
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 565

gatcaccgcc acaatagtaa gatca 25

<210> SEQ ID NO 566
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 566

cgacagacgc ctgatcttac tagacacacg ct 32

<210> SEQ ID NO 567
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 567

gatcagcgtg tgtctagtaa gatca 25

<210> SEQ ID NO 568
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 568

cgacagacgc ctgatcttac ggtctttcca ct 32

<210> SEQ ID NO 569
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<212> TYPE: DNA
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gatcagtgga aagaccgtaa gatca 25

<210> SEQ ID NO 570
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 570

cgacagacgc ctgatcttac ctaacagccg at 32

<210> SEQ ID NO 571
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 571

gatcatcggc tgttaggtaa gatca 25

<210> SEQ ID NO 572
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 572

cgacagacgc ctgatcttac cggtggttag tt 32

<210> SEQ ID NO 573
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 573

gatcaactaa ccaccggtaa gatca 25

<210> SEQ ID NO 574
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 574

cgacagacgc ctgatcttac cataagtgcc gt 32

<210> SEQ ID NO 575
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gatcacggca cttatggtaa gatca 25

<210> SEQ ID NO 576
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 576

cgacagacgc ctgatcttac caatgtccag ct 32

<210> SEQ ID NO 577

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<211> LENGTH: 25
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<400> SEQUENCE: 577

gatcagctgg acattggtaa gatca 25

<210> SEQ ID NO 578
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 578

cgacagacgc ctgatcttac atgttcgctc ct 32

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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 579

gatcaggagc gaacatgtaa gatca 25

<210> SEQ ID NO 580
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 580

cgacagacgc ctgatcttac atcatccagc gt 32

<210> SEQ ID NO 581
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 581

gatcacgctg gatgatgtaa gatca 25

<210> SEQ ID NO 582
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 582

cgacagacgc ctgatcttac acaagatcgc ct 32

<210> SEQ ID NO 583
<211> LENGTH: 25
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 583

gatcaggcga tcttgtgtaa gatca 25

<210> SEQ ID NO 584
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<220> FEATURE:
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<400> SEQUENCE: 584

cgacagacgc ctgatcttac aaagtccgtc ct 32

<210> SEQ ID NO 585
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<400> SEQUENCE: 585

gatcaggacg gactttgtaa gatca 25

<210> SEQ ID NO 586
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 586

cgacagacgc ctgatcttaa ttcgtccgtc ct 32

<210> SEQ ID NO 587
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 587

gatcaggacg gacgaattaa gatca 25

<210> SEQ ID NO 588
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 588

cgacagacgc ctgatcttaa tgaggagcac gt 32

<210> SEQ ID NO 589
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 589

gatcacgtgc tcctcattaa gatca 25

<210> SEQ ID NO 590
<211> LENGTH: 32
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 590

cgacagacgc ctgatcttaa gtgaagaccg ct 32

<210> SEQ ID NO 591
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 591

gatcagcggt cttcacttaa gatca 25

<210> SEQ ID NO 592
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 592

cgacagacgc ctgatcttaa gtcgtggttc gt 32

<210> SEQ ID NO 593
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 593

gatcacgaac cacgacttaa gatca 25

<210> SEQ ID NO 594
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 594

cgacagacgc ctgatcttaa gctctccgtt gt 32

<210> SEQ ID NO 595
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 595

gatcacaacg gagagcttaa gatca 25

<210> SEQ ID NO 596
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 596

cgacagacgc ctgatcttaa gccactccag at 32

<210> SEQ ID NO 597
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 597

gatcatctgg agtggcttaa gatca 25

<210> SEQ ID NO 598
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 598

cgacagacgc ctgatcttaa gagaggtgcc at 32

<210> SEQ ID NO 599
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 599

gatcatggca cctctcttaa gatca 25

<210> SEQ ID NO 600
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 600

cgacagacgc ctgatcttaa gacctcaccg at 32

<210> SEQ ID NO 601
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 601

gatcatcggt gaggtcttaa gatca 25

<210> SEQ ID NO 602
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 602

cgacagacgc ctgatcttaa ctcaaccgga ct 32

<210> SEQ ID NO 603
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 603

gatcagtccg gttgagttaa gatca 25

<210> SEQ ID NO 604
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 604

cgacagacgc ctgatcttaa cctctcgctt gt 32

<210> SEQ ID NO 605
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 605

gatcacaagc gagaggttaa gatca 25

<210> SEQ ID NO 606
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 606

cgacagacgc ctgatcttaa ccgctttcct gt 32

<210> SEQ ID NO 607
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 607

gatcacagga aagcggttaa gatca 25

<210> SEQ ID NO 608
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 608

cgacagacgc ctgatcttaa cactctggca ct 32

<210> SEQ ID NO 609
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 609

gatcagtgcc agagtgttaa gatca 25

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<210> SEQ ID NO 610
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 610

cgacagacgc ctgatcttaa atgcggagga ct 32

<210> SEQ ID NO 611
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 611

gatcagtcct ccgcatttaa gatca 25

<210> SEQ ID NO 612
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 612

cgacagacgc ctgatcttaa ataggctggc gt 32

<210> SEQ ID NO 613
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 613

gatcacgcca gcctatttaa gatca 25

<210> SEQ ID NO 614
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 614

cgacagacgc ctgatcttaa acctcggaca ct 32

<210> SEQ ID NO 615
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 615

gatcagtgtc cgaggtttaa gatca 25

<210> SEQ ID NO 616
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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<400> SEQUENCE: 616

cgacagacgc ctgatctgtt tgaaccgagg at 32

<210> SEQ ID NO 617
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 617

gatcatcctc ggttcaaaca gatca 25

<210> SEQ ID NO 618
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 618

cgacagacgc ctgatctgtt tcgacttcac gt 32

<210> SEQ ID NO 619
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 619

gatcacgtga agtcgaaaca gatca 25

<210> SEQ ID NO 620
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 620

cgacagacgc ctgatctgtt tcacgaccaa gt 32

<210> SEQ ID NO 621
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 621

gatcacttgg tcgtgaaaca gatca 25

<210> SEQ ID NO 622
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 622

cgacagacgc ctgatctgtt tatgccactc gt 32

<210> SEQ ID NO 623
<211> LENGTH: 25

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 623

gatcacgagt ggcataaaca gatca 25

<210> SEQ ID NO 624
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 624

cgacagacgc ctgatctgtt taatcgaccg ct 32

<210> SEQ ID NO 625
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 625

gatcagcggt cgattaaaca gatca 25

<210> SEQ ID NO 626
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 626

cgacagacgc ctgatctgtt gtaatggctc gt 32

<210> SEQ ID NO 627
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 627

gatcacgagc cattacaaca gatca 25

<210> SEQ ID NO 628
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 628

cgacagacgc ctgatctgtt ggttcaagtc gt 32

<210> SEQ ID NO 629
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 629

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gatcacgact tgaaccaaca gatca 25

<210> SEQ ID NO 630
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 630

cgacagacgc ctgatctgtt ggtaactggc tt 32

<210> SEQ ID NO 631
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 631

gatcaagcca gttaccaaca gatca 25

<210> SEQ ID NO 632
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 632

cgacagacgc ctgatctgtt ggcataacga gt 32

<210> SEQ ID NO 633
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 633

gatcactcgt tatgccaaca gatca 25

<210> SEQ ID NO 634
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 634

cgacagacgc ctgatctgtt ggaacagcaa gt 32

<210> SEQ ID NO 635
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 635

gatcacttgc tgttccaaca gatca 25

<210> SEQ ID NO 636
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 636

cgacagacgc ctgatctgtt gctctcaacc tt 32

<210> SEQ ID NO 637
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 637

gatcaaggtt gagagcaaca gatca 25

<210> SEQ ID NO 638
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 638

cgacagacgc ctgatctgtt gctcaatctc gt 32

<210> SEQ ID NO 639
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 639

gatcacgaga ttgagcaaca gatca 25

<210> SEQ ID NO 640
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 640

cgacagacgc ctgatctgtt gcaggaaagt ct 32

<210> SEQ ID NO 641
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 641

gatcagactt tcctgcaaca gatca 25

<210> SEQ ID NO 642
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 642

cgacagacgc ctgatctgtt gcaaacctct ct 32

<210> SEQ ID NO 643
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 643

gatcagagag gtttgcaaca gatca 25

<210> SEQ ID NO 644
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 644

cgacagacgc ctgatctgtt gaatgccgta gt 32

<210> SEQ ID NO 645
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 645

gatcactacg gcattcaaca gatca 25

<210> SEQ ID NO 646
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 646

cgacagacgc ctgatctgtt ctggaggcat tt 32

<210> SEQ ID NO 647
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 647

gatcaaatgc ctccagaaca gatca 25

<210> SEQ ID NO 648
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 648

cgacagacgc ctgatctgtt ctgcaacctc tt 32

<210> SEQ ID NO 649
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 649

gatcaagagg ttgcagaaca gatca 25

<210> SEQ ID NO 650
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 650

cgacagacgc ctgatctgtt cgaggaagac at 32

<210> SEQ ID NO 651
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 651

gatcatgtct tcctcgaaca gatca 25

<210> SEQ ID NO 652
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 652

cgacagacgc ctgatctgtt cctatcacgc tt 32

<210> SEQ ID NO 653
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 653

gatcaagcgt gataggaaca gatca 25

<210> SEQ ID NO 654
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 654

cgacagacgc ctgatctgtt ccgaaagcaa gt 32

<210> SEQ ID NO 655
<211> LENGTH: 25
<212> TYPE: DNA
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<400> SEQUENCE: 655

gatcacttgc tttcggaaca gatca 25

<210> SEQ ID NO 656

<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 656

cgacagacgc ctgatctgtt cagttccacc at 32

<210> SEQ ID NO 657
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 657

gatcatggtg gaactgaaca gatca 25

<210> SEQ ID NO 658
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 658

cgacagacgc ctgatctgtt cagagatggc at 32

<210> SEQ ID NO 659
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 659

gatcatgcca tctctgaaca gatca 25

<210> SEQ ID NO 660
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 660

cgacagacgc ctgatctgtt cacagccaaa gt 32

<210> SEQ ID NO 661
<211> LENGTH: 25
<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 661

gatcactttg gctgtgaaca gatca 25

<210> SEQ ID NO 662
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 662

cgacagacgc ctgatctgtt caaatgcgga gt 32

<210> SEQ ID NO 663
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 663

gatcactccg catttgaaca gatca 25

<210> SEQ ID NO 664
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 664

cgacagacgc ctgatctgtt atgaagcacc gt 32

<210> SEQ ID NO 665
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 665

gatcacggtg cttcataaca gatca 25

<210> SEQ ID NO 666
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 666

cgacagacgc ctgatctgtt agttgatgcc gt 32

<210> SEQ ID NO 667
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<212> TYPE: DNA
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<400> SEQUENCE: 667

gatcacggca tcaactaaca gatca 25

<210> SEQ ID NO 668
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 668

cgacagacgc ctgatctgtt agaaagcgca gt 32

<210> SEQ ID NO 669
<211> LENGTH: 25
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 669

gatcactgcg ctttctaaca gatca 25

<210> SEQ ID NO 670
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 670

cgacagacgc ctgatctgtt acacagctcc at 32

<210> SEQ ID NO 671
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 671

gatcatggag ctgtgtaaca gatca 25

<210> SEQ ID NO 672
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 672

cgacagacgc ctgatctgtg tcattagcgg at 32

<210> SEQ ID NO 673
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 673

gatcatccgc taatgacaca gatca 25

<210> SEQ ID NO 674
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 674

cgacagacgc ctgatctgtg tatgttcgca gt 32

<210> SEQ ID NO 675
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 675

gatcactgcg aacatacaca gatca 25

<210> SEQ ID NO 676
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 676

cgacagacgc ctgatctgtg tataccgcct tt 32

<210> SEQ ID NO 677
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 677

gatcaaaggc ggtatacaca gatca 25

<210> SEQ ID NO 678
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 678

cgacagacgc ctgatctgtg taaaccgcat gt 32

<210> SEQ ID NO 679
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 679

gatcacatgc ggtttacaca gatca 25

<210> SEQ ID NO 680
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 680

cgacagacgc ctgatctgtg gtcaattcgt gt 32

<210> SEQ ID NO 681
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 681

gatcacacga attgaccaca gatca 25

<210> SEQ ID NO 682
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 682

cgacagacgc ctgatctgtg cttcaaaggt gt 32

<210> SEQ ID NO 683
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 683

gatcacacct ttgaagcaca gatca 25

<210> SEQ ID NO 684
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 684

cgacagacgc ctgatctgtg cagaggaaac tt 32

<210> SEQ ID NO 685
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 685

gatcaagttt cctctgcaca gatca 25

<210> SEQ ID NO 686
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 686

cgacagacgc ctgatctgtg caatatcggt gt 32

<210> SEQ ID NO 687
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 687

gatcacaccg atattgcaca gatca 25

<210> SEQ ID NO 688
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 688

cgacagacgc ctgatctgtg aggttccagt tt 32

<210> SEQ ID NO 689
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 689

gatcaaactg gaacctcaca gatca 25

<210> SEQ ID NO 690
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 690

cgacagacgc ctgatctgtg aattccttgc gt 32

<210> SEQ ID NO 691
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 691

gatcacgcaa ggaattcaca gatca 25

<210> SEQ ID NO 692
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 692

cgacagacgc ctgatctgtg aagtaagccg at 32

<210> SEQ ID NO 693
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 693

gatcatcggc ttacttcaca gatca 25

<210> SEQ ID NO 694
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 694

cgacagacgc ctgatctgtc tttgaacgtg gt 32

<210> SEQ ID NO 695
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 695

gatcaccacg ttcaaagaca gatca 25

<210> SEQ ID NO 696
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 696

cgacagacgc ctgatctgtc tgaaaccacc at 32

<210> SEQ ID NO 697
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 697

gatcatggtg gtttcagaca gatca 25

<210> SEQ ID NO 698
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 698

cgacagacgc ctgatctgtc tcgaaacctg tt 32

<210> SEQ ID NO 699
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 699

gatcaacagg tttcgagaca gatca 25

<210> SEQ ID NO 700
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 700

cgacagacgc ctgatctgtc gtaagaggca at 32

<210> SEQ ID NO 701
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 701

gatcattgcc tcttacgaca gatca 25

<210> SEQ ID NO 702
<211> LENGTH: 32

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 702

cgacagacgc ctgatctgtc gaaacttggt gt 32

<210> SEQ ID NO 703
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 703

gatcacacca agtttcgaca gatca 25

<210> SEQ ID NO 704
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 704

cgacagacgc ctgatctgtc ctatgttgcc at 32

<210> SEQ ID NO 705
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 705

gatcatggca acataggaca gatca 25

<210> SEQ ID NO 706
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 706

cgacagacgc ctgatctgtc cacctaaacg at 32

<210> SEQ ID NO 707
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 707

gatcatcgtt taggtggaca gatca 25

<210> SEQ ID NO 708
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 708

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cgacagacgc ctgatctgtc caaatcacag ct 32

<210> SEQ ID NO 709
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 709

gatcagctgt gatttggaca gatca 25

<210> SEQ ID NO 710
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 710

cgacagacgc ctgatctgtc caaagctacc at 32

<210> SEQ ID NO 711
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 711

gatcatggta gctttggaca gatca 25

<210> SEQ ID NO 712
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 712

cgacagacgc ctgatctgtc actttgcatc ct 32

<210> SEQ ID NO 713
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 713

gatcaggatg caaagtgaca gatca 25

<210> SEQ ID NO 714
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 714

cgacagacgc ctgatctgtc aaacagccat ct 32

<210> SEQ ID NO 715
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 715

gatcagatgg ctgtttgaca gatca 25

<210> SEQ ID NO 716
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 716

cgacagacgc ctgatctgta tttggacacg ct 32

<210> SEQ ID NO 717
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 717

gatcagcgtg tccaaataca gatca 25

<210> SEQ ID NO 718
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 718

cgacagacgc ctgatctgta tttccgaccg tt 32

<210> SEQ ID NO 719
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 719

gatcaacggt cggaaataca gatca 25

<210> SEQ ID NO 720
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 720

cgacagacgc ctgatctgta ttgacgcttg gt 32

<210> SEQ ID NO 721
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 721

gatcaccaag cgtcaataca gatca 25

<210> SEQ ID NO 722
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 722

cgacagacgc ctgatctgta tacgcaaacc gt 32

<210> SEQ ID NO 723
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 723

gatcacggtt tgcgtataca gatca 25

<210> SEQ ID NO 724
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 724

cgacagacgc ctgatctgta taacgccacc at 32

<210> SEQ ID NO 725
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 725

gatcatggtg gcgttataca gatca 25

<210> SEQ ID NO 726
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 726

cgacagacgc ctgatctgta gtgtcaaagc gt 32

<210> SEQ ID NO 727
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 727

gatcacgctt tgacactaca gatca 25

<210> SEQ ID NO 728
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 728

cgacagacgc ctgatctgta ggcggatttc tt 32

<210> SEQ ID NO 729
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 729

gatcaagaaa tccgcctaca gatca 25

<210> SEQ ID NO 730
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 730

cgacagacgc ctgatctgta ggcaaacggt at 32

<210> SEQ ID NO 731
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 731

gatcataccg tttgcctaca gatca 25

<210> SEQ ID NO 732
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 732

cgacagacgc ctgatctgta cgtcctttcc at 32

<210> SEQ ID NO 733
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 733

gatcatggaa aggacgtaca gatca 25

<210> SEQ ID NO 734
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 734

cgacagacgc ctgatctgta ccacacgctt at 32

<210> SEQ ID NO 735

<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 735

gatcataagc gtgtggtaca gatca 25

<210> SEQ ID NO 736
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 736

cgacagacgc ctgatctgta atgttgtccg ct 32

<210> SEQ ID NO 737
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 737

gatcagcgga caacattaca gatca 25

<210> SEQ ID NO 738
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 738

cgacagacgc ctgatctgta atccgagcca tt 32

<210> SEQ ID NO 739
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 739

gatcaatggc tcggattaca gatca 25

<210> SEQ ID NO 740
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 740

cgacagacgc ctgatctgta agttccgcat gt 32

<210> SEQ ID NO 741
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 741

gatcacatgc ggaacttaca gatca 25

<210> SEQ ID NO 742
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 742

cgacagacgc ctgatctgta agtccgttgg tt 32

<210> SEQ ID NO 743
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 743

gatcaaccaa cggacttaca gatca 25

<210> SEQ ID NO 744
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 744

cgacagacgc ctgatctgta acgtttgctg gt 32

<210> SEQ ID NO 745
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 745

gatcaccagc aaacgttaca gatca 25

<210> SEQ ID NO 746
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 746

cgacagacgc ctgatctgta aattggcacg gt 32

<210> SEQ ID NO 747
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 747

gatcaccgtg ccaatttaca gatca 25

<210> SEQ ID NO 748
<211> LENGTH: 32
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 748

cgacagacgc ctgatctgta aacgatggca gt 32

<210> SEQ ID NO 749
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 749

gatcactgcc atcgtttaca gatca 25

<210> SEQ ID NO 750
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 750

cgacagacgc ctgatctggt ttcaatgtcg gt 32

<210> SEQ ID NO 751
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 751

gatcaccgac attgaaacca gatca 25

<210> SEQ ID NO 752
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 752

cgacagacgc ctgatctggt tgatgacctg tt 32

<210> SEQ ID NO 753
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 753

gatcaacagg tcatcaacca gatca 25

<210> SEQ ID NO 754
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 754

cgacagacgc ctgatctggt tgaccgaaag at 32

<210> SEQ ID NO 755
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 755

gatcatcttt cggtcaacca gatca 25

<210> SEQ ID NO 756
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 756

cgacagacgc ctgatctggt tcttccacca at 32

<210> SEQ ID NO 757
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 757

gatcattggt ggaagaacca gatca 25

<210> SEQ ID NO 758
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 758

cgacagacgc ctgatctggt tcttaccacg tt 32

<210> SEQ ID NO 759
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 759

gatcaacgtg gtaagaacca gatca 25

<210> SEQ ID NO 760
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 760

cgacagacgc ctgatctggt tctattgccg at 32

<210> SEQ ID NO 761
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 761

gatcatcggc aatagaacca gatca 25

<210> SEQ ID NO 762
<211> LENGTH: 32
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 762

cgacagacgc ctgatctggt tccaatcacg at 32

<210> SEQ ID NO 763
<211> LENGTH: 25
<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 763

gatcatcgtg attggaacca gatca 25

<210> SEQ ID NO 764
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 764

cgacagacgc ctgatctggt tcaacattcg gt 32

<210> SEQ ID NO 765
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 765

gatcaccgaa tgttgaacca gatca 25

<210> SEQ ID NO 766
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 766

cgacagacgc ctgatctggt taaagccgag at 32

<210> SEQ ID NO 767
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 767

gatcatctcg gctttaacca gatca 25

<210> SEQ ID NO 768
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 768

cgacagacgc ctgatctggt gttaccgatg tt 32

<210> SEQ ID NO 769
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 769

gatcaacatc ggtaacacca gatca 25

<210> SEQ ID NO 770
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 770

cgacagacgc ctgatctggt gaaccaaatg ct 32

<210> SEQ ID NO 771
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 771

gatcagcatt tggttcacca gatca 25

<210> SEQ ID NO 772
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 772

cgacagacgc ctgatctggt gaaatcgcaa gt 32

<210> SEQ ID NO 773
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 773

gatcacttgc gatttcacca gatca 25

<210> SEQ ID NO 774
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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<400> SEQUENCE: 774

cgacagacgc ctgatctggt ccaattctcg tt 32

<210> SEQ ID NO 775
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 775

gatcaacgag aattggacca gatca 25

<210> SEQ ID NO 776
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 776

cgacagacgc ctgatctggt cacaaacacc tt 32

<210> SEQ ID NO 777
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 777

gatcaaggtg tttgtgacca gatca 25

<210> SEQ ID NO 778
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 778

cgacagacgc ctgatctggt ataacgagcg at 32

<210> SEQ ID NO 779
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 779

gatcatcgct cgttatacca gatca 25

<210> SEQ ID NO 780
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 780

cgacagacgc ctgatctggt aggtttcagc at 32

<210> SEQ ID NO 781
<211> LENGTH: 25

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 781

gatcatgctg aaacctacca gatca 25

<210> SEQ ID NO 782
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 782

cgacagacgc ctgatctggt actccaaacg at 32

<210> SEQ ID NO 783
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 783

gatcatcgtt tggagtacca gatca 25

<210> SEQ ID NO 784
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 784

cgacagacgc ctgatctggt acacaaatcg ct 32

<210> SEQ ID NO 785
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 785

gatcagcgat ttgtgtacca gatca 25

<210> SEQ ID NO 786
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 786

cgacagacgc ctgatctggt acaaacactg ct 32

<210> SEQ ID NO 787
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 787

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gatcagcagt gtttgtacca gatca 25

<210> SEQ ID NO 788
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 788

cgacagacgc ctgatctggt aagacgcaat gt 32

<210> SEQ ID NO 789
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 789

gatcacattg cgtcttacca gatca 25

<210> SEQ ID NO 790
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 790

cgacagacgc ctgatctggt aaatgcaacg gt 32

<210> SEQ ID NO 791
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 791

gatcaccgtt gcatttacca gatca 25

<210> SEQ ID NO 792
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 792

cgacagacgc ctgatctggt aaagcacatc gt 32

<210> SEQ ID NO 793
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 793

gatcacgatg tgctttacca gatca 25

<210> SEQ ID NO 794
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 794

cgacagacgc ctgatctggc ttcctaaacg tt 32

<210> SEQ ID NO 795
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 795

gatcaacgtt taggaagcca gatca 25

<210> SEQ ID NO 796
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 796

cgacagacgc ctgatctggc taaatgacgt gt 32

<210> SEQ ID NO 797
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 797

gatcacacgt catttagcca gatca 25

<210> SEQ ID NO 798
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 798

cgacagacgc ctgatctggc taaacacctc at 32

<210> SEQ ID NO 799
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 799

gatcatgagg tgtttagcca gatca 25

<210> SEQ ID NO 800
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 800

cgacagacgc ctgatctggc ctcaaatacc at 32

<210> SEQ ID NO 801
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 801

gatcatggta tttgaggcca gatca 25

<210> SEQ ID NO 802
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 802

cgacagacgc ctgatctggc atttcaacca gt 32

<210> SEQ ID NO 803
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 803

gatcactggt tgaaatgcca gatca 25

<210> SEQ ID NO 804
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 804

cgacagacgc ctgatctggc acaagaggat tt 32

<210> SEQ ID NO 805
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 805

gatcaaatcc tcttgtgcca gatca 25

<210> SEQ ID NO 806
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 806

cgacagacgc ctgatctggc aatttgacag gt 32

<210> SEQ ID NO 807
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 807

gatcacctgt caaattgcca gatca 25

<210> SEQ ID NO 808
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 808

cgacagacgc ctgatctggc aacttcatcc tt 32

<210> SEQ ID NO 809
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 809

gatcaaggat gaagttgcca gatca 25

<210> SEQ ID NO 810
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 810

cgacagacgc ctgatctggc aacaatccat ct 32

<210> SEQ ID NO 811
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 811

gatcagatgg attgttgcca gatca 25

<210> SEQ ID NO 812
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 812

cgacagacgc ctgatctgga tttcatgtgc gt 32

<210> SEQ ID NO 813
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 813

gatcacgcac atgaaatcca gatca 25

<210> SEQ ID NO 814

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<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 814

cgacagacgc ctgatctgga ttgtttcacg gt 32

<210> SEQ ID NO 815
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 815

gatcaccgtg aaacaatcca gatca 25

<210> SEQ ID NO 816
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 816

cgacagacgc ctgatctgga ttgtcactgg tt 32

<210> SEQ ID NO 817
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 817

gatcaaccag tgacaatcca gatca 25

<210> SEQ ID NO 818
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 818

cgacagacgc ctgatctgga ttagctccgt tt 32

<210> SEQ ID NO 819
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 819

gatcaaacgg agctaatcca gatca 25

<210> SEQ ID NO 820
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 820

cgacagacgc ctgatctgga tgtttacgct gt 32

<210> SEQ ID NO 821
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 821

gatcacagcg taaacatcca gatca 25

<210> SEQ ID NO 822
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 822

cgacagacgc ctgatctgga tcacaacatg ct 32

<210> SEQ ID NO 823
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 823

gatcagcatg ttgtgatcca gatca 25

<210> SEQ ID NO 824
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 824

cgacagacgc ctgatctgga gttacggctt tt 32

<210> SEQ ID NO 825
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 825

gatcaaaagc cgtaactcca gatca 25

<210> SEQ ID NO 826
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 826

cgacagacgc ctgatctgga ggacttcgtt tt 32

<210> SEQ ID NO 827
<211> LENGTH: 25
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 827

gatcaaaacg aagtcctcca gatca 25

<210> SEQ ID NO 828
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 828

cgacagacgc ctgatctgga ctccacacaa tt 32

<210> SEQ ID NO 829
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 829

gatcaattgt gtggagtcca gatca 25

<210> SEQ ID NO 830
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 830

cgacagacgc ctgatctgga ctattctgcg tt 32

<210> SEQ ID NO 831
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 831

gatcaacgca gaatagtcca gatca 25

<210> SEQ ID NO 832
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 832

cgacagacgc ctgatctgga caccatttcg at 32

<210> SEQ ID NO 833
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 833

gatcatcgaa atggtgtcca gatca 25

<210> SEQ ID NO 834
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 834

cgacagacgc ctgatctgga caatcaccag tt 32

<210> SEQ ID NO 835
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 835

gatcaactgg tgattgtcca gatca 25

<210> SEQ ID NO 836
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 836

cgacagacgc ctgatctgga attgtgcctt gt 32

<210> SEQ ID NO 837
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 837

gatcacaagg cacaattcca gatca 25

<210> SEQ ID NO 838
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 838

cgacagacgc ctgatctgga attgtacgca gt 32

<210> SEQ ID NO 839
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 839

gatcactgcg tacaattcca gatca 25

<210> SEQ ID NO 840
<211> LENGTH: 32
<212> TYPE: DNA
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<220> FEATURE:

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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 840

cgacagacgc ctgatctgga atgcaaactg gt 32

<210> SEQ ID NO 841
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 841

gatcaccagt ttgcattcca gatca 25

<210> SEQ ID NO 842
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 842

cgacagacgc ctgatctgga agatgccgtt at 32

<210> SEQ ID NO 843
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 843

gatcataacg gcatcttcca gatca 25

<210> SEQ ID NO 844
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<212> TYPE: DNA
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<400> SEQUENCE: 844

cgacagacgc ctgatctgga acatcagcct tt 32

<210> SEQ ID NO 845
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 845

gatcaaaggc tgatgttcca gatca 25

<210> SEQ ID NO 846
<211> LENGTH: 32
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 846

cgacagacgc ctgatctgga acatagagcg tt 32

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<210> SEQ ID NO 847
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 847

gatcaacgct ctatgttcca gatca 25

<210> SEQ ID NO 848
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 848

cgacagacgc ctgatctgga aactaaggcg tt 32

<210> SEQ ID NO 849
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 849

gatcaacgcc ttagtttcca gatca 25

<210> SEQ ID NO 850
<211> LENGTH: 32
<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 850

cgacagacgc ctgatctgga aacaccttgg at 32

<210> SEQ ID NO 851
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<400> SEQUENCE: 851

gatcatccaa ggtgtttcca gatca 25

<210> SEQ ID NO 852
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 852

cgacagacgc ctgatctgct ttcacacttc gt 32

<210> SEQ ID NO 853
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<400> SEQUENCE: 853

gatcacgaag tgtgaaagca gatca 25

<210> SEQ ID NO 854
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 854

cgacagacgc ctgatctgct ttaatgcgag gt 32

<210> SEQ ID NO 855
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<400> SEQUENCE: 855

gatcacctcg cattaaagca gatca 25

<210> SEQ ID NO 856
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 856

cgacagacgc ctgatctgct tgaaccatcc tt 32

<210> SEQ ID NO 857
<211> LENGTH: 25
<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 857

gatcaaggat ggttcaagca gatca 25

<210> SEQ ID NO 858
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 858

cgacagacgc ctgatctgct ggaaagtgaa ct 32

<210> SEQ ID NO 859
<211> LENGTH: 25
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 859

gatcagttca ctttccagca gatca 25

<210> SEQ ID NO 860
<211> LENGTH: 32

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 860

cgacagacgc ctgatctgct gaagacaacc tt 32

<210> SEQ ID NO 861
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 861

gatcaaggtt gtcttcagca gatca 25

<210> SEQ ID NO 862
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 862

cgacagacgc ctgatctgct ccataaagcc tt 32

<210> SEQ ID NO 863
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 863

gatcaaggct ttatggagca gatca 25

<210> SEQ ID NO 864
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 864

cgacagacgc ctgatctgct catttcctcg at 32

<210> SEQ ID NO 865
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 865

gatcatcgag gaaatgagca gatca 25

<210> SEQ ID NO 866
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 866

cgacagacgc ctgatctgct caccaacaga tt 32

<210> SEQ ID NO 867
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 867

gatcaatctg ttggtgagca gatca 25

<210> SEQ ID NO 868
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 868

cgacagacgc ctgatctgct cacaaatacc gt 32

<210> SEQ ID NO 869
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 869

gatcacggta tttgtgagca gatca 25

<210> SEQ ID NO 870
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 870

cgacagacgc ctgatctgct atttggcgat ct 32

<210> SEQ ID NO 871
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 871

gatcagatcg ccaaatagca gatca 25

<210> SEQ ID NO 872
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 872

cgacagacgc ctgatctgct atttacgcca ct 32

<210> SEQ ID NO 873
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 873

gatcagtggc gtaaatagca gatca 25

<210> SEQ ID NO 874
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 874

cgacagacgc ctgatctgct attgctcctg at 32

<210> SEQ ID NO 875
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 875

gatcatcagg agcaatagca gatca 25

<210> SEQ ID NO 876
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 876

cgacagacgc ctgatctgct accaaaccag tt 32

<210> SEQ ID NO 877
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 877

gatcaactgg tttggtagca gatca 25

<210> SEQ ID NO 878
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 878

cgacagacgc ctgatctgct aaggcaaact gt 32

<210> SEQ ID NO 879
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 879

gatcacagtt tgccttagca gatca 25

<210> SEQ ID NO 880
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 880

cgacagacgc ctgatctgct aaagagtggc at 32

<210> SEQ ID NO 881
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 881

gatcatgcca ctctttagca gatca 25

<210> SEQ ID NO 882
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 882

cgacagacgc ctgatctgcg tttactcctc at 32

<210> SEQ ID NO 883
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 883

gatcatgagg agtaaacgca gatca 25

<210> SEQ ID NO 884
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 884

cgacagacgc ctgatctgcg ttaatcctcc tt 32

<210> SEQ ID NO 885
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 885

gatcaaggag gattaacgca gatca 25

<210> SEQ ID NO 886
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 886

cgacagacgc ctgatctgcg aatctcttgt gt 32

<210> SEQ ID NO 887
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 887

gatcacacaa gagattcgca gatca 25

<210> SEQ ID NO 888
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 888

cgacagacgc ctgatctgcg aaatacaggt gt 32

<210> SEQ ID NO 889
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 889

gatcacacct gtatttcgca gatca 25

<210> SEQ ID NO 890
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 890

cgacagacgc ctgatctgcg aaacattgag gt 32

<210> SEQ ID NO 891
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 891

gatcacctca atgtttcgca gatca 25

<210> SEQ ID NO 892
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 892

cgacagacgc ctgatctgcc ttaaactccg at 32

<210> SEQ ID NO 893

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 893

gatcatcgga gtttaaggca gatca 25

<210> SEQ ID NO 894
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 894

cgacagacgc ctgatctgcc tggaaattgt gt 32

<210> SEQ ID NO 895
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 895

gatcacacaa tttccaggca gatca 25

<210> SEQ ID NO 896
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 896

cgacagacgc ctgatctgcc tccttaatcg tt 32

<210> SEQ ID NO 897
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 897

gatcaacgat taaggaggca gatca 25

<210> SEQ ID NO 898
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 898

cgacagacgc ctgatctgcc ggataaaggt tt 32

<210> SEQ ID NO 899
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 899

gatcaaacct ttatccggca gatca 25

<210> SEQ ID NO 900
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 900

cgacagacgc ctgatctgcc gcaaataatc ct 32

<210> SEQ ID NO 901
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 901

gatcaggatt atttgcggca gatca 25

<210> SEQ ID NO 902
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 902

cgacagacgc ctgatctgcc attgaaacac ct 32

<210> SEQ ID NO 903
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 903

gatcaggtgt ttcaatggca gatca 25

<210> SEQ ID NO 904
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 904

cgacagacgc ctgatctgcc ataatgacac gt 32

<210> SEQ ID NO 905
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 905

gatcacgtgt cattatggca gatca 25

<210> SEQ ID NO 906
<211> LENGTH: 32
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 906

cgacagacgc ctgatctgcc aattgacctc tt 32

<210> SEQ ID NO 907
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 907

gatcaagagg tcaattggca gatca 25

<210> SEQ ID NO 908
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 908

cgacagacgc ctgatctgcc aatatcctcg tt 32

<210> SEQ ID NO 909
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 909

gatcaacgag gatattggca gatca 25

<210> SEQ ID NO 910
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 910

cgacagacgc ctgatctgca ttccaactac gt 32

<210> SEQ ID NO 911
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 911

gatcacgtag ttggaatgca gatca 25

<210> SEQ ID NO 912
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 912

cgacagacgc ctgatctgca ttaccagacg at 32

<210> SEQ ID NO 913
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 913

gatcatcgtc tggtaatgca gatca 25

<210> SEQ ID NO 914
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 914

cgacagacgc ctgatctgca tgatttggct ct 32

<210> SEQ ID NO 915
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 915

gatcagagcc aaatcatgca gatca 25

<210> SEQ ID NO 916
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 916

cgacagacgc ctgatctgca tatacgccac tt 32

<210> SEQ ID NO 917
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 917

gatcaagtgg cgtatatgca gatca 25

<210> SEQ ID NO 918
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 918

cgacagacgc ctgatctgca tataccaccg tt 32

<210> SEQ ID NO 919
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 919

gatcaacggt ggtatatgca gatca 25

<210> SEQ ID NO 920
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 920

cgacagacgc ctgatctgca tacaaggctc at 32

<210> SEQ ID NO 921
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 921

gatcatgagc cttgtatgca gatca 25

<210> SEQ ID NO 922
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 922

cgacagacgc ctgatctgca taaagatgcc gt 32

<210> SEQ ID NO 923
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 923

gatcacggca tctttatgca gatca 25

<210> SEQ ID NO 924
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 924

cgacagacgc ctgatctgca catatcaacc gt 32

<210> SEQ ID NO 925
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 925

gatcacggtt gatatgtgca gatca 25

<210> SEQ ID NO 926
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 926

cgacagacgc ctgatctgca cactttatcc gt 32

<210> SEQ ID NO 927
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 927

gatcacggat aaagtgtgca gatca 25

<210> SEQ ID NO 928
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 928

cgacagacgc ctgatctgca atttggtcga gt 32

<210> SEQ ID NO 929
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 929

gatcactcga ccaaattgca gatca 25

<210> SEQ ID NO 930
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 930

cgacagacgc ctgatctgca atacacgtca ct 32

<210> SEQ ID NO 931
<211> LENGTH: 25
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 931

gatcagtgac gtgtattgca gatca 25

<210> SEQ ID NO 932
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 932

cgacagacgc ctgatctgca agttagtcgg at 32

<210> SEQ ID NO 933
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 933

gatcatccga ctaacttgca gatca 25

<210> SEQ ID NO 934
<211> LENGTH: 32
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 934

cgacagacgc ctgatctgca actcctcatg tt 32

<210> SEQ ID NO 935
<211> LENGTH: 25
<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 935

gatcaacatg aggagttgca gatca 25

<210> SEQ ID NO 936
<211> LENGTH: 32
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 936

cgacagacgc ctgatctgca acattcagac ct 32

<210> SEQ ID NO 937
<211> LENGTH: 25
<212> TYPE: DNA
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<400> SEQUENCE: 937

gatcaggtct gaatgttgca gatca 25

<210> SEQ ID NO 938
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 938

cgacagacgc ctgatctgca aatgatccac ct 32

<210> SEQ ID NO 939
<211> LENGTH: 25

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 939

gatcaggtgg atcatttgca gatca 25

<210> SEQ ID NO 940
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 940

cgacagacgc ctgatctgca aagcctcact at 32

<210> SEQ ID NO 941
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 941

gatcatagtg aggctttgca gatca 25

<210> SEQ ID NO 942
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<400> SEQUENCE: 942

cgacagacgc ctgatctgca aactctcaac gt 32

<210> SEQ ID NO 943
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gatcacgttg agagtttgca gatca 25

<210> SEQ ID NO 944
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<220> FEATURE:
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<400> SEQUENCE: 944

cgacagacgc ctgatctgca aacctgtcct at 32

<210> SEQ ID NO 945
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<400> SEQUENCE: 945

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gatcatagga caggtttgca gatca 25

<210> SEQ ID NO 946
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 946

cgacagacgc ctgatctgat tggtgcttac gt 32

<210> SEQ ID NO 947
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<400> SEQUENCE: 947

gatcacgtaa gcaccaatca gatca 25

<210> SEQ ID NO 948
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 948

cgacagacgc ctgatctgat tctgattggc gt 32

<210> SEQ ID NO 949
<211> LENGTH: 25
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 949

gatcacgcca atcagaatca gatca 25

<210> SEQ ID NO 950
<211> LENGTH: 32
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 950

cgacagacgc ctgatctgat tcgcatctcc tt 32

<210> SEQ ID NO 951
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 951

gatcaaggag atgcgaatca gatca 25

<210> SEQ ID NO 952
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 952

cgacagacgc ctgatctgat tatcgttgcc gt 32

<210> SEQ ID NO 953
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 953

gatcacggca acgataatca gatca 25

<210> SEQ ID NO 954
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 954

cgacagacgc ctgatctgat gctaaaccgt gt 32

<210> SEQ ID NO 955
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 955

gatcacacgg tttagcatca gatca 25

<210> SEQ ID NO 956
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 956

cgacagacgc ctgatctgat ctccatcgct tt 32

<210> SEQ ID NO 957
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 957

gatcaaagcg atggagatca gatca 25

<210> SEQ ID NO 958
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 958

cgacagacgc ctgatctgat ctacgccaca at 32

<210> SEQ ID NO 959
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 959

gatcattgtg gcgtagatca gatca 25

<210> SEQ ID NO 960
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 960

cgacagacgc ctgatctgat ccttgcacct tt 32

<210> SEQ ID NO 961
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 961

gatcaaaggt gcaaggatca gatca 25

<210> SEQ ID NO 962
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 962

cgacagacgc ctgatctgat atttgctcgc ct 32

<210> SEQ ID NO 963
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 963

gatcaggcga gcaaatatca gatca 25

<210> SEQ ID NO 964
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 964

cgacagacgc ctgatctgat atttgcgcct gt 32

<210> SEQ ID NO 965
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 965

gatcacaggc gcaaatatca gatca 25

<210> SEQ ID NO 966
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 966

cgacagacgc ctgatctgat agtgctttgc gt 32

<210> SEQ ID NO 967
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 967

gatcacgcaa agcactatca gatca 25

<210> SEQ ID NO 968
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 968

cgacagacgc ctgatctgat aatgccgtgt gt 32

<210> SEQ ID NO 969
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 969

gatcacacac ggcattatca gatca 25

<210> SEQ ID NO 970
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 970

cgacagacgc ctgatctgat aatcaccgcc at 32

<210> SEQ ID NO 971
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 971

gatcatggcg gtgattatca gatca 25

<210> SEQ ID NO 972

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<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 972

cgacagacgc ctgatctgat aagtcgtggc at 32

<210> SEQ ID NO 973
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 973

gatcatgcca cgacttatca gatca 25

<210> SEQ ID NO 974
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 974

cgacagacgc ctgatctgat aactgtggcg at 32

<210> SEQ ID NO 975
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 975

gatcatcgcc acagttatca gatca 25

<210> SEQ ID NO 976
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 976

cgacagacgc ctgatctgag ttgaaatgcc gt 32

<210> SEQ ID NO 977
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 977

gatcacggca tttcaactca gatca 25

<210> SEQ ID NO 978
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 978

cgacagacgc ctgatctgag tcaaactccg tt 32

<210> SEQ ID NO 979
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 979

gatcaacgga gtttgactca gatca 25

<210> SEQ ID NO 980
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 980

cgacagacgc ctgatctgag taatccgcac at 32

<210> SEQ ID NO 981
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 981

gatcatgtgc ggattactca gatca 25

<210> SEQ ID NO 982
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 982

cgacagacgc ctgatctgag gtttgttcac gt 32

<210> SEQ ID NO 983
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 983

gatcacgtga acaaacctca gatca 25

<210> SEQ ID NO 984
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 984

cgacagacgc ctgatctgag gccattgttt gt 32

<210> SEQ ID NO 985
<211> LENGTH: 25
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 985

gatcacaaac aatggcctca gatca 25

<210> SEQ ID NO 986
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 986

cgacagacgc ctgatctgag gataaacggc tt 32

<210> SEQ ID NO 987
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 987

gatcaagccg tttatcctca gatca 25

<210> SEQ ID NO 988
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 988

cgacagacgc ctgatctgag cgaaatcatg gt 32

<210> SEQ ID NO 989
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 989

gatcaccatg atttcgctca gatca 25

<210> SEQ ID NO 990
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 990

cgacagacgc ctgatctgag cctccacaat tt 32

<210> SEQ ID NO 991
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 991

gatcaaattg tggaggctca gatca 25

<210> SEQ ID NO 992
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 992

cgacagacgc ctgatctgag atacaaccgc tt 32

<210> SEQ ID NO 993
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 993

gatcaagcgg ttgtatctca gatca 25

<210> SEQ ID NO 994
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 994

cgacagacgc ctgatctgag ataacgctcg at 32

<210> SEQ ID NO 995
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 995

gatcatcgag cgttatctca gatca 25

<210> SEQ ID NO 996
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 996

cgacagacgc ctgatctgag acttatgcgg tt 32

<210> SEQ ID NO 997
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 997

gatcaaccgc ataagtctca gatca 25

<210> SEQ ID NO 998
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 998

cgacagacgc ctgatctgag accacacact tt 32

<210> SEQ ID NO 999
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 999

gatcaaagtg tgtggtctca gatca 25

<210> SEQ ID NO 1000
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1000

cgacagacgc ctgatctgag aatgctacgg tt 32

<210> SEQ ID NO 1001
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1001

gatcaaccgt agcattctca gatca 25

<210> SEQ ID NO 1002
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1002

cgacagacgc ctgatctgag aaccttgagc at 32

<210> SEQ ID NO 1003
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1003

gatcatgctc aaggttctca gatca 25

<210> SEQ ID NO 1004
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1004

cgacagacgc ctgatctgac tttgacggtt gt 32

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<210> SEQ ID NO 1005
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1005

gatcacaacc gtcaaagtca gatca 25

<210> SEQ ID NO 1006
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1006

cgacagacgc ctgatctgac ttggatggct tt 32

<210> SEQ ID NO 1007
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1007

gatcaaagcc atccaagtca gatca 25

<210> SEQ ID NO 1008
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1008

cgacagacgc ctgatctgac ttccaaaccg at 32

<210> SEQ ID NO 1009
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1009

gatcatcggt ttggaagtca gatca 25

<210> SEQ ID NO 1010
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1010

cgacagacgc ctgatctgac taactgcacc at 32

<210> SEQ ID NO 1011
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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<400> SEQUENCE: 1011

gatcatggtg cagttagtca gatca 25

<210> SEQ ID NO 1012
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1012

cgacagacgc ctgatctgac gtttcctcca tt 32

<210> SEQ ID NO 1013
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1013

gatcaatgga ggaaacgtca gatca 25

<210> SEQ ID NO 1014
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1014

cgacagacgc ctgatctgac cattcttccg at 32

<210> SEQ ID NO 1015
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1015

gatcatcgga agaatggtca gatca 25

<210> SEQ ID NO 1016
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1016

cgacagacgc ctgatctgac caactaaccg tt 32

<210> SEQ ID NO 1017
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1017

gatcaacggt tagttggtca gatca 25

<210> SEQ ID NO 1018
<211> LENGTH: 32

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1018

cgacagacgc ctgatctgac atgctttacg gt 32

<210> SEQ ID NO 1019
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1019

gatcaccgta aagcatgtca gatca 25

<210> SEQ ID NO 1020
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1020

cgacagacgc ctgatctgac aatggagacg tt 32

<210> SEQ ID NO 1021
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1021

gatcaacgtc tccattgtca gatca 25

<210> SEQ ID NO 1022
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1022

cgacagacgc ctgatctgaa tttgtccagc gt 32

<210> SEQ ID NO 1023
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1023

gatcacgctg gacaaattca gatca 25

<210> SEQ ID NO 1024
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1024

cgacagacgc ctgatctgaa tttgagcgga ct 32

<210> SEQ ID NO 1025
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<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1025

gatcagtccg ctcaaattca gatca 25

<210> SEQ ID NO 1026
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1026

cgacagacgc ctgatctgaa tttcagagcg gt 32

<210> SEQ ID NO 1027
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1027

gatcaccgct ctgaaattca gatca 25

<210> SEQ ID NO 1028
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1028

cgacagacgc ctgatctgaa tgtctctcgc tt 32

<210> SEQ ID NO 1029
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1029

gatcaagcga gagacattca gatca 25

<210> SEQ ID NO 1030
<211> LENGTH: 32
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<400> SEQUENCE: 1030

cgacagacgc ctgatctgaa tggtcttggc tt 32

<210> SEQ ID NO 1031
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1031

gatcaagcca agaccattca gatca 25

<210> SEQ ID NO 1032
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1032

cgacagacgc ctgatctgaa tgcctcttcc at 32

<210> SEQ ID NO 1033
<211> LENGTH: 25
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<400> SEQUENCE: 1033

gatcatggaa gaggcattca gatca 25

<210> SEQ ID NO 1034
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1034

cgacagacgc ctgatctgaa tgattgccga gt 32

<210> SEQ ID NO 1035
<211> LENGTH: 25
<212> TYPE: DNA
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<400> SEQUENCE: 1035

gatcactcgg caatcattca gatca 25

<210> SEQ ID NO 1036
<211> LENGTH: 32
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<400> SEQUENCE: 1036

cgacagacgc ctgatctgaa tgaactgagc gt 32

<210> SEQ ID NO 1037
<211> LENGTH: 25
<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 1037

gatcacgctc agttcattca gatca 25

<210> SEQ ID NO 1038
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1038

cgacagacgc ctgatctgaa tcgagaagcc tt 32

<210> SEQ ID NO 1039
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1039

gatcaaggct tctcgattca gatca 25

<210> SEQ ID NO 1040
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1040

cgacagacgc ctgatctgaa tcctcaccga at 32

<210> SEQ ID NO 1041
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1041

gatcattcgg tgaggattca gatca 25

<210> SEQ ID NO 1042
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1042

cgacagacgc ctgatctgaa tcatttggcg gt 32

<210> SEQ ID NO 1043
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1043

gatcaccgcc aaatgattca gatca 25

<210> SEQ ID NO 1044
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1044

cgacagacgc ctgatctgaa tatgcctcgg tt 32

<210> SEQ ID NO 1045
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1045

gatcaaccga ggcatattca gatca 25

<210> SEQ ID NO 1046
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1046

cgacagacgc ctgatctgaa gttgttgacc gt 32

<210> SEQ ID NO 1047
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1047

gatcacggtc aacaacttca gatca 25

<210> SEQ ID NO 1048
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1048

cgacagacgc ctgatctgaa gttcgcaaga gt 32

<210> SEQ ID NO 1049
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1049

gatcactctt gcgaacttca gatca 25

<210> SEQ ID NO 1050
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1050

cgacagacgc ctgatctgaa gttatggcac gt 32

<210> SEQ ID NO 1051

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1051

gatcacgtgc cataacttca gatca 25

<210> SEQ ID NO 1052
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1052

cgacagacgc ctgatctgaa ggcaattcga gt 32

<210> SEQ ID NO 1053
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1053

gatcactcga attgccttca gatca 25

<210> SEQ ID NO 1054
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1054

cgacagacgc ctgatctgaa gactcgttgg at 32

<210> SEQ ID NO 1055
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1055

gatcatccaa cgagtcttca gatca 25

<210> SEQ ID NO 1056
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1056

cgacagacgc ctgatctgaa gacacttccg at 32

<210> SEQ ID NO 1057
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1057

gatcatcgga agtgtcttca gatca 25

<210> SEQ ID NO 1058
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1058

cgacagacgc ctgatctgaa ctctttcacg ct 32

<210> SEQ ID NO 1059
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1059

gatcagcgtg aaagagttca gatca 25

<210> SEQ ID NO 1060
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1060

cgacagacgc ctgatctgaa cgtactcacc at 32

<210> SEQ ID NO 1061
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1061

gatcatggtg agtacgttca gatca 25

<210> SEQ ID NO 1062
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1062

cgacagacgc ctgatctgaa ccttgcttcc tt 32

<210> SEQ ID NO 1063
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1063

gatcaaggaa gcaaggttca gatca 25

<210> SEQ ID NO 1064
<211> LENGTH: 32
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1064

cgacagacgc ctgatctgaa attcgtgctg gt 32

<210> SEQ ID NO 1065
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1065

gatcaccagc acgaatttca gatca 25

<210> SEQ ID NO 1066
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1066

cgacagacgc ctgatctgaa attcctcgcc tt 32

<210> SEQ ID NO 1067
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1067

gatcaaggcg aggaatttca gatca 25

<210> SEQ ID NO 1068
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1068

cgacagacgc ctgatctgaa atgcttggac gt 32

<210> SEQ ID NO 1069
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1069

gatcacgtcc aagcatttca gatca 25

<210> SEQ ID NO 1070
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1070

cgacagacgc ctgatctgaa agtccaccga tt 32

<210> SEQ ID NO 1071
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1071

gatcaatcgg tggactttca gatca 25

<210> SEQ ID NO 1072
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1072

cgacagacgc ctgatctgaa actctgcaac ct 32

<210> SEQ ID NO 1073
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1073

gatcaggttg cagagtttca gatca 25

<210> SEQ ID NO 1074
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1074

cgacagacgc ctgatctgaa acggatggct at 32

<210> SEQ ID NO 1075
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1075

gatcatagcc atccgtttca gatca 25

<210> SEQ ID NO 1076
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1076

cgacagacgc ctgatctgaa accattccac gt 32

<210> SEQ ID NO 1077
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1077

gatcacgtgg aatggtttca gatca 25

<210> SEQ ID NO 1078
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1078

cgacagacgc ctgatctctt tgacggagtg tt 32

<210> SEQ ID NO 1079
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1079

gatcaacact ccgtcaaaga gatca 25

<210> SEQ ID NO 1080
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1080

cgacagacgc ctgatctctt tgaaggcagg at 32

<210> SEQ ID NO 1081
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1081

gatcatcctg ccttcaaaga gatca 25

<210> SEQ ID NO 1082
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1082

cgacagacgc ctgatctctt tcctaagccg tt 32

<210> SEQ ID NO 1083
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1083

gatcaacggc ttaggaaaga gatca 25

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<210> SEQ ID NO 1084
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1084

cgacagacgc ctgatctctt gtgaggcgta tt 32

<210> SEQ ID NO 1085
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1085

gatcaatacg cctcacaaga gatca 25

<210> SEQ ID NO 1086
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1086

cgacagacgc ctgatctctt gccaacagaa ct 32

<210> SEQ ID NO 1087
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1087

gatcagttct gttggcaaga gatca 25

<210> SEQ ID NO 1088
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1088

cgacagacgc ctgatctctt gatatggcgg tt 32

<210> SEQ ID NO 1089
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1089

gatcaaccgc catatcaaga gatca 25

<210> SEQ ID NO 1090
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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<400> SEQUENCE: 1090

cgacagacgc ctgatctctt gaggttagcg at 32

<210> SEQ ID NO 1091
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1091

gatcatcgct aacctcaaga gatca 25

<210> SEQ ID NO 1092
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1092

cgacagacgc ctgatctctt gaacacagca ct 32

<210> SEQ ID NO 1093
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1093

gatcagtgct gtgttcaaga gatca 25

<210> SEQ ID NO 1094
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1094

cgacagacgc ctgatctctt cttgaatcgc ct 32

<210> SEQ ID NO 1095
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1095

gatcaggcga ttcaagaaga gatca 25

<210> SEQ ID NO 1096
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1096

cgacagacgc ctgatctctt cgcaatgaac ct 32

<210> SEQ ID NO 1097
<211> LENGTH: 25

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1097

gatcaggttc attgcgaaga gatca 25

<210> SEQ ID NO 1098
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1098

cgacagacgc ctgatctctt ccaagaatcg ct 32

<210> SEQ ID NO 1099
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1099

gatcagcgat tcttggaaga gatca 25

<210> SEQ ID NO 1100
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1100

cgacagacgc ctgatctctt caacaagacg ct 32

<210> SEQ ID NO 1101
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1101

gatcagcgtc ttgttgaaga gatca 25

<210> SEQ ID NO 1102
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1102

cgacagacgc ctgatctctt agaggcgaac at 32

<210> SEQ ID NO 1103
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1103

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gatcatgttc gcctctaaga gatca 25

<210> SEQ ID NO 1104
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1104

cgacagacgc ctgatctctt acatgaggcg tt 32

<210> SEQ ID NO 1105
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1105

gatcaacgcc tcatgtaaga gatca 25

<210> SEQ ID NO 1106
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1106

cgacagacgc ctgatctctt acagcaaagg ct 32

<210> SEQ ID NO 1107
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1107

gatcagcctt tgctgtaaga gatca 25

<210> SEQ ID NO 1108
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1108

cgacagacgc ctgatctctt aaggtggctg tt 32

<210> SEQ ID NO 1109
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1109

gatcaacagc caccttaaga gatca 25

<210> SEQ ID NO 1110
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
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<400> SEQUENCE: 1110

cgacagacgc ctgatctctt aaagcggatg ct 32

<210> SEQ ID NO 1111
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1111

gatcagcatc cgctttaaga gatca 25

<210> SEQ ID NO 1112
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 1112

cgacagacgc ctgatctctg tttaagtggc gt 32

<210> SEQ ID NO 1113
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1113

gatcacgcca cttaaacaga gatca 25

<210> SEQ ID NO 1114
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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cgacagacgc ctgatctctg ttgtgaagtg ct 32

<210> SEQ ID NO 1115
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gatcagcact tcacaacaga gatca 25

<210> SEQ ID NO 1116
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cgacagacgc ctgatctctg taaacaacgc ct 32

<210> SEQ ID NO 1117
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<400> SEQUENCE: 1117

gatcaggcgt tgtttacaga gatca 25

<210> SEQ ID NO 1118
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1118

cgacagacgc ctgatctctg gtaaagtggc tt 32

<210> SEQ ID NO 1119
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1119

gatcaagcca ctttaccaga gatca 25

<210> SEQ ID NO 1120
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1120

cgacagacgc ctgatctctg gatcaaacgg tt 32

<210> SEQ ID NO 1121
<211> LENGTH: 25
<212> TYPE: DNA
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<400> SEQUENCE: 1121

gatcaaccgt ttgatccaga gatca 25

<210> SEQ ID NO 1122
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1122

cgacagacgc ctgatctctg ctaagaaccg tt 32

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<211> LENGTH: 25
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1123

gatcaacggt tcttagcaga gatca 25

<210> SEQ ID NO 1124
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<400> SEQUENCE: 1124

cgacagacgc ctgatctctg cataacgagg tt 32

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<400> SEQUENCE: 1125

gatcaacctc gttatgcaga gatca 25

<210> SEQ ID NO 1126
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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cgacagacgc ctgatctctg cagaaaggag tt 32

<210> SEQ ID NO 1127
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<400> SEQUENCE: 1127

gatcaactcc tttctgcaga gatca 25

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<211> LENGTH: 32
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<400> SEQUENCE: 1128

cgacagacgc ctgatctctg acaggtggaa at 32

<210> SEQ ID NO 1129
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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gatcatttcc acctgtcaga gatca 25

<210> SEQ ID NO 1130

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<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1130

cgacagacgc ctgatctctg aataaggcgg at 32

<210> SEQ ID NO 1131
<211> LENGTH: 25
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1131

gatcatccgc cttattcaga gatca 25

<210> SEQ ID NO 1132
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1132

cgacagacgc ctgatctctg aacttggtgg tt 32

<210> SEQ ID NO 1133
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1133

gatcaaccac caagttcaga gatca 25

<210> SEQ ID NO 1134
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1134

cgacagacgc ctgatctctg aaccgcctaa at 32

<210> SEQ ID NO 1135
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1135

gatcatttag gcggttcaga gatca 25

<210> SEQ ID NO 1136
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1136

cgacagacgc ctgatctctg aaataccgcc tt 32

<210> SEQ ID NO 1137
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1137

gatcaaggcg gtatttcaga gatca 25

<210> SEQ ID NO 1138
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1138

cgacagacgc ctgatctctc tccgaaactg tt 32

<210> SEQ ID NO 1139
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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gatcaacagt ttcggagaga gatca 25

<210> SEQ ID NO 1140
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1140

cgacagacgc ctgatctctc gttgtaatgc ct 32

<210> SEQ ID NO 1141
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1141

gatcaggcat tacaacgaga gatca 25

<210> SEQ ID NO 1142
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1142

cgacagacgc ctgatctctc gacaaagagg tt 32

<210> SEQ ID NO 1143
<211> LENGTH: 25
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1143

gatcaacctc tttgtcgaga gatca 25

<210> SEQ ID NO 1144
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1144

cgacagacgc ctgatctctc gaatcaagcc tt 32

<210> SEQ ID NO 1145
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1145

gatcaaggct tgattcgaga gatca 25

<210> SEQ ID NO 1146
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1146

cgacagacgc ctgatctctc cggaaacact tt 32

<210> SEQ ID NO 1147
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1147

gatcaaagtg tttccggaga gatca 25

<210> SEQ ID NO 1148
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1148

cgacagacgc ctgatctctc caaacgagct at 32

<210> SEQ ID NO 1149
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1149

gatcatagct cgtttggaga gatca 25

<210> SEQ ID NO 1150
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1150

cgacagacgc ctgatctctc atttgtacgg ct 32

<210> SEQ ID NO 1151
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1151

gatcagccgt acaaatgaga gatca 25

<210> SEQ ID NO 1152
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1152

cgacagacgc ctgatctctc atcatttcgg ct 32

<210> SEQ ID NO 1153
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1153

gatcagccga aatgatgaga gatca 25

<210> SEQ ID NO 1154
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1154

cgacagacgc ctgatctctc agaatgccac at 32

<210> SEQ ID NO 1155
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1155

gatcatgtgg cattctgaga gatca 25

<210> SEQ ID NO 1156
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1156

cgacagacgc ctgatctctc aatcaggcac at 32

<210> SEQ ID NO 1157
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1157

gatcatgtgc ctgattgaga gatca 25

<210> SEQ ID NO 1158
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1158

cgacagacgc ctgatctctc aacggtcttc tt 32

<210> SEQ ID NO 1159
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1159

gatcaagaag accgttgaga gatca 25

<210> SEQ ID NO 1160
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1160

cgacagacgc ctgatctcta ttgccacgac tt 32

<210> SEQ ID NO 1161
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1161

gatcaagtcg tggcaataga gatca 25

<210> SEQ ID NO 1162
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1162

cgacagacgc ctgatctcta tgtttcacgg ct 32

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<210> SEQ ID NO 1163
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1163

gatcagccgt gaaacataga gatca 25

<210> SEQ ID NO 1164
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1164

cgacagacgc ctgatctcta tcttggtgcg at 32

<210> SEQ ID NO 1165
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1165

gatcatcgca ccaagataga gatca 25

<210> SEQ ID NO 1166
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1166

cgacagacgc ctgatctcta gttggtgcag tt 32

<210> SEQ ID NO 1167
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1167

gatcaactgc accaactaga gatca 25

<210> SEQ ID NO 1168
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1168

cgacagacgc ctgatctcta gtggcaaggt tt 32

<210> SEQ ID NO 1169
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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<400> SEQUENCE: 1169

gatcaaacct tgccactaga gatca 25

<210> SEQ ID NO 1170
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1170

cgacagacgc ctgatctcta ggtaaacggc at 32

<210> SEQ ID NO 1171
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1171

gatcatgccg tttacctaga gatca 25

<210> SEQ ID NO 1172
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1172

cgacagacgc ctgatctcta gagtgtgcgt tt 32

<210> SEQ ID NO 1173
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1173

gatcaaacgc acactctaga gatca 25

<210> SEQ ID NO 1174
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1174

cgacagacgc ctgatctcta ctgcgaaaca ct 32

<210> SEQ ID NO 1175
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1175

gatcagtgtt tcgcagtaga gatca 25

<210> SEQ ID NO 1176
<211> LENGTH: 32

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1176

cgacagacgc ctgatctcta atcacggcaa ct 32

<210> SEQ ID NO 1177
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1177

gatcagttgc cgtgattaga gatca 25

<210> SEQ ID NO 1178
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1178

cgacagacgc ctgatctcta agttgcgagg at 32

<210> SEQ ID NO 1179
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1179

gatcatcctc gcaacttaga gatca 25

<210> SEQ ID NO 1180
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1180

cgacagacgc ctgatctcta agtgctggtg tt 32

<210> SEQ ID NO 1181
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1181

gatcaacacc agcacttaga gatca 25

<210> SEQ ID NO 1182
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1182

cgacagacgc ctgatctcta aggaactgcg at 32

<210> SEQ ID NO 1183
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1183

gatcatcgca gttccttaga gatca 25

<210> SEQ ID NO 1184
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1184

cgacagacgc ctgatctcta aatgtccacg ct 32

<210> SEQ ID NO 1185
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1185

gatcagcgtg gacatttaga gatca 25

<210> SEQ ID NO 1186
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1186

cgacagacgc ctgatctcta aatcgccaac gt 32

<210> SEQ ID NO 1187
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1187

gatcacgttg gcgatttaga gatca 25

<210> SEQ ID NO 1188
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1188

cgacagacgc ctgatctcta aatacgtgcg gt 32

<210> SEQ ID NO 1189
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1189

gatcaccgca cgtatttaga gatca 25

<210> SEQ ID NO 1190
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1190

cgacagacgc ctgatctcta aaggcgatgg tt 32

<210> SEQ ID NO 1191
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1191

gatcaaccat cgcctttaga gatca 25

<210> SEQ ID NO 1192
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1192

cgacagacgc ctgatctcgt ttggaatggt ct 32

<210> SEQ ID NO 1193
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1193

gatcagacca ttccaaacga gatca 25

<210> SEQ ID NO 1194
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1194

cgacagacgc ctgatctcgt ttctcacagg tt 32

<210> SEQ ID NO 1195
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1195

gatcaacctg tgagaaacga gatca 25

<210> SEQ ID NO 1196
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1196

cgacagacgc ctgatctcgt ttcgaggtag tt 32

<210> SEQ ID NO 1197
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1197

gatcaactac ctcgaaacga gatca 25

<210> SEQ ID NO 1198
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1198

cgacagacgc ctgatctcgt ttacgatgtg gt 32

<210> SEQ ID NO 1199
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1199

gatcaccaca tcgtaaacga gatca 25

<210> SEQ ID NO 1200
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1200

cgacagacgc ctgatctcgt tgtgtgaagt ct 32

<210> SEQ ID NO 1201
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1201

gatcagactt cacacaacga gatca 25

<210> SEQ ID NO 1202
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1202

cgacagacgc ctgatctcgt tggtaattcg gt 32

<210> SEQ ID NO 1203
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1203

gatcaccgaa ttaccaacga gatca 25

<210> SEQ ID NO 1204
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1204

cgacagacgc ctgatctcgt tggaatctgg tt 32

<210> SEQ ID NO 1205
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1205

gatcaaccag attccaacga gatca 25

<210> SEQ ID NO 1206
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1206

cgacagacgc ctgatctcgt tggaagacag at 32

<210> SEQ ID NO 1207
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1207

gatcatctgt cttccaacga gatca 25

<210> SEQ ID NO 1208
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1208

cgacagacgc ctgatctcgt tcgttaggtg at 32

<210> SEQ ID NO 1209

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1209

gatcatcacc taacgaacga gatca 25

<210> SEQ ID NO 1210
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1210

cgacagacgc ctgatctcgt tcctcaacag at 32

<210> SEQ ID NO 1211
<211> LENGTH: 25
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<400> SEQUENCE: 1211

gatcatctgt tgaggaacga gatca 25

<210> SEQ ID NO 1212
<211> LENGTH: 32
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<400> SEQUENCE: 1212

cgacagacgc ctgatctcgt tcatttccga gt 32

<210> SEQ ID NO 1213
<211> LENGTH: 25
<212> TYPE: DNA
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<400> SEQUENCE: 1213

gatcactcgg aaatgaacga gatca 25

<210> SEQ ID NO 1214
<211> LENGTH: 32
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cgacagacgc ctgatctcgt tcaactactg ct 32

<210> SEQ ID NO 1215
<211> LENGTH: 25
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<400> SEQUENCE: 1215

gatcagcagt agttgaacga gatca 25

<210> SEQ ID NO 1216
<211> LENGTH: 32
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<400> SEQUENCE: 1216

cgacagacgc ctgatctcgt tatggatgtg ct 32

<210> SEQ ID NO 1217
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<212> TYPE: DNA
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<400> SEQUENCE: 1217

gatcagcaca tccataacga gatca 25

<210> SEQ ID NO 1218
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1218

cgacagacgc ctgatctcgt taagtctcgg tt 32

<210> SEQ ID NO 1219
<211> LENGTH: 25
<212> TYPE: DNA
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<400> SEQUENCE: 1219

gatcaaccga gacttaacga gatca 25

<210> SEQ ID NO 1220
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1220

cgacagacgc ctgatctcgt gtttaggtcg at 32

<210> SEQ ID NO 1221
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1221

gatcatcgac ctaaacacga gatca 25

<210> SEQ ID NO 1222
<211> LENGTH: 32
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1222

cgacagacgc ctgatctcgt ggcaataaag gt 32

<210> SEQ ID NO 1223
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1223

gatcaccttt attgccacga gatca 25

<210> SEQ ID NO 1224
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1224

cgacagacgc ctgatctcgt ggaaacagga tt 32

<210> SEQ ID NO 1225
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1225

gatcaatcct gtttccacga gatca 25

<210> SEQ ID NO 1226
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1226

cgacagacgc ctgatctcgt gacatttggt gt 32

<210> SEQ ID NO 1227
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1227

gatcacacca aatgtcacga gatca 25

<210> SEQ ID NO 1228
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1228

cgacagacgc ctgatctcgt atatcgcacc tt 32

<210> SEQ ID NO 1229
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1229

gatcaaggtg cgatatacga gatca 25

<210> SEQ ID NO 1230
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1230

cgacagacgc ctgatctcgt ataaggtcgc at 32

<210> SEQ ID NO 1231
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1231

gatcatgcga ccttatacga gatca 25

<210> SEQ ID NO 1232
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1232

cgacagacgc ctgatctcgt agtaaagcgg at 32

<210> SEQ ID NO 1233
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1233

gatcatccgc tttactacga gatca 25

<210> SEQ ID NO 1234
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1234

cgacagacgc ctgatctcgt aatgacgaag ct 32

<210> SEQ ID NO 1235
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1235

gatcagcttc gtcattacga gatca 25

<210> SEQ ID NO 1236
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1236

cgacagacgc ctgatctcgt aacataacgg ct 32

<210> SEQ ID NO 1237
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1237

gatcagccgt tatgttacga gatca 25

<210> SEQ ID NO 1238
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1238

cgacagacgc ctgatctcgt aacaagcact ct 32

<210> SEQ ID NO 1239
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1239

gatcagagtg cttgttacga gatca 25

<210> SEQ ID NO 1240
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1240

cgacagacgc ctgatctcgt aaatgcggaa gt 32

<210> SEQ ID NO 1241
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1241

gatcacttcc gcatttacga gatca 25

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<210> SEQ ID NO 1242
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1242

cgacagacgc ctgatctcgt aaagtcggag at 32

<210> SEQ ID NO 1243
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1243

gatcatctcc gactttacga gatca 25

<210> SEQ ID NO 1244
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1244

cgacagacgc ctgatctcgt aaacaggagc tt 32

<210> SEQ ID NO 1245
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1245

gatcaagctc ctgtttacga gatca 25

<210> SEQ ID NO 1246
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1246

cgacagacgc ctgatctcgg ttgtattcgg at 32

<210> SEQ ID NO 1247
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1247

gatcatccga atacaaccga gatca 25

<210> SEQ ID NO 1248
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1248

cgacagacgc ctgatctcgg ttatttcgag ct 32

<210> SEQ ID NO 1249
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1249

gatcagctcg aaataaccga gatca 25

<210> SEQ ID NO 1250
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1250

cgacagacgc ctgatctcgg tgttaatgtg ct 32

<210> SEQ ID NO 1251
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1251

gatcagcaca ttaacaccga gatca 25

<210> SEQ ID NO 1252
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1252

cgacagacgc ctgatctcgg tatacaaggc at 32

<210> SEQ ID NO 1253
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1253

gatcatgcct tgtataccga gatca 25

<210> SEQ ID NO 1254
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1254

cgacagacgc ctgatctcgg taagtttgtg ct 32

<210> SEQ ID NO 1255
<211> LENGTH: 25

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1255

gatcagcaca aacttaccga gatca 25

<210> SEQ ID NO 1256
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1256

cgacagacgc ctgatctcgg taacaacctg at 32

<210> SEQ ID NO 1257
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1257

gatcatcagg ttgttaccga gatca 25

<210> SEQ ID NO 1258
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1258

cgacagacgc ctgatctcgg cgaatttatg gt 32

<210> SEQ ID NO 1259
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1259

gatcaccata aattcgccga gatca 25

<210> SEQ ID NO 1260
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1260

cgacagacgc ctgatctcgg atcacctttg tt 32

<210> SEQ ID NO 1261
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1261

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gatcaacaaa ggtgatccga gatca 25

<210> SEQ ID NO 1262
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1262

cgacagacgc ctgatctcgg aacacaccta tt 32

<210> SEQ ID NO 1263
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1263

gatcaatagg tgtgttccga gatca 25

<210> SEQ ID NO 1264
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1264

cgacagacgc ctgatctcgc ttatctgtgg at 32

<210> SEQ ID NO 1265
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1265

gatcatccac agataagcga gatca 25

<210> SEQ ID NO 1266
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1266

cgacagacgc ctgatctcgc gatgtttaag gt 32

<210> SEQ ID NO 1267
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1267

gatcaccttа aacatcgcga gatca 25

<210> SEQ ID NO 1268
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1268

cgacagacgc ctgatctcgc ctttaacctt gt 32

<210> SEQ ID NO 1269
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1269

gatcacaagg ttaaaggcga gatca 25

<210> SEQ ID NO 1270
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1270

cgacagacgc ctgatctcgc caaagaggta tt 32

<210> SEQ ID NO 1271
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1271

gatcaatacc tctttggcga gatca 25

<210> SEQ ID NO 1272
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1272

cgacagacgc ctgatctcga tttggttacg gt 32

<210> SEQ ID NO 1273
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1273

gatcaccgta accaaatcga gatca 25

<210> SEQ ID NO 1274
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1274

cgacagacgc ctgatctcga tctggtttgg at 32

<210> SEQ ID NO 1275
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1275

gatcatccaa accagatcga gatca 25

<210> SEQ ID NO 1276
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1276

cgacagacgc ctgatctcga ggcaaatagg tt 32

<210> SEQ ID NO 1277
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1277

gatcaaccta tttgcctcga gatca 25

<210> SEQ ID NO 1278
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1278

cgacagacgc ctgatctcga atgtgtgact gt 32

<210> SEQ ID NO 1279
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1279

gatcacagtc acacattcga gatca 25

<210> SEQ ID NO 1280
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1280

cgacagacgc ctgatctcga acttctggtg at 32

<210> SEQ ID NO 1281
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1281

gatcatcacc agaagttcga gatca 25

<210> SEQ ID NO 1282
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1282

cgacagacgc ctgatctcga aatctaggcg at 32

<210> SEQ ID NO 1283
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1283

gatcatcgcc tagatttcga gatca 25

<210> SEQ ID NO 1284
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1284

cgacagacgc ctgatctcga aacagtggag tt 32

<210> SEQ ID NO 1285
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1285

gatcaactcc actgtttcga gatca 25

<210> SEQ ID NO 1286
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1286

cgacagacgc ctgatctcct ttcagtgtcc at 32

<210> SEQ ID NO 1287
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1287

gatcatggac actgaaagga gatca 25

<210> SEQ ID NO 1288

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<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1288

cgacagacgc ctgatctcct ttaaggagcg at 32

<210> SEQ ID NO 1289
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1289

gatcatcgct ccttaaagga gatca 25

<210> SEQ ID NO 1290
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1290

cgacagacgc ctgatctcct tctattcggc at 32

<210> SEQ ID NO 1291
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1291

gatcatgccg aatagaagga gatca 25

<210> SEQ ID NO 1292
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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cgacagacgc ctgatctcct tattccagcg tt 32

<210> SEQ ID NO 1293
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<400> SEQUENCE: 1293

gatcaacgct ggaataagga gatca 25

<210> SEQ ID NO 1294
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1294

cgacagacgc ctgatctcct taactttgcc gt 32

<210> SEQ ID NO 1295
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1295

gatcacggca aagttaagga gatca 25

<210> SEQ ID NO 1296
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1296

cgacagacgc ctgatctcct taaagcggac at 32

<210> SEQ ID NO 1297
<211> LENGTH: 25
<212> TYPE: DNA
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gatcatgtcc gctttaagga gatca 25

<210> SEQ ID NO 1298
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1298

cgacagacgc ctgatctcct gatttggacg at 32

<210> SEQ ID NO 1299
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gatcatcgtc caaatcagga gatca 25

<210> SEQ ID NO 1300
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1300

cgacagacgc ctgatctcct gaattgctcc tt 32

<210> SEQ ID NO 1301
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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1301

gatcaaggag caattcagga gatca 25

<210> SEQ ID NO 1302
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1302

cgacagacgc ctgatctcct gaagaatggc at 32

<210> SEQ ID NO 1303
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1303

gatcatgcca ttcttcagga gatca 25

<210> SEQ ID NO 1304
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1304

cgacagacgc ctgatctcct ctttgaagcc tt 32

<210> SEQ ID NO 1305
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<400> SEQUENCE: 1305

gatcaaggct tcaaagagga gatca 25

<210> SEQ ID NO 1306
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1306

cgacagacgc ctgatctcct cgcaaaggtt at 32

<210> SEQ ID NO 1307
<211> LENGTH: 25
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1307

gatcataacc tttgcgagga gatca 25

<210> SEQ ID NO 1308
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<212> TYPE: DNA
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<400> SEQUENCE: 1308

cgacagacgc ctgatctcct atggaagcga at 32

<210> SEQ ID NO 1309
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1309

gatcattcgc ttccatagga gatca 25

<210> SEQ ID NO 1310
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1310

cgacagacgc ctgatctcct atcaaagcgg tt 32

<210> SEQ ID NO 1311
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1311

gatcaaccgc tttgatagga gatca 25

<210> SEQ ID NO 1312
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1312

cgacagacgc ctgatctcct aattgtcgtg ct 32

<210> SEQ ID NO 1313
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1313

gatcagcacg acaattagga gatca 25

<210> SEQ ID NO 1314
<211> LENGTH: 32
<212> TYPE: DNA
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<220> FEATURE:

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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1314

cgacagacgc ctgatctcct aattcgtgcc tt 32

<210> SEQ ID NO 1315
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1315

gatcaaggca cgaattagga gatca 25

<210> SEQ ID NO 1316
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1316

cgacagacgc ctgatctcct aagattcgcc at 32

<210> SEQ ID NO 1317
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1317

gatcatggcg aatcttagga gatca 25

<210> SEQ ID NO 1318
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1318

cgacagacgc ctgatctcct aacgaaagcc tt 32

<210> SEQ ID NO 1319
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1319

gatcaaggct ttcgttagga gatca 25

<210> SEQ ID NO 1320
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1320

cgacagacgc ctgatctccg tgtggaattt gt 32

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<210> SEQ ID NO 1321
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1321

gatcacaaat tccacacgga gatca 25

<210> SEQ ID NO 1322
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1322

cgacagacgc ctgatctccg tatttcagcc tt 32

<210> SEQ ID NO 1323
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1323

gatcaaggct gaaatacgga gatca 25

<210> SEQ ID NO 1324
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1324

cgacagacgc ctgatctccg gtaatgtgtg tt 32

<210> SEQ ID NO 1325
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1325

gatcaacaca cattaccgga gatca 25

<210> SEQ ID NO 1326
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1326

cgacagacgc ctgatctccg gcttaaacaa ct 32

<210> SEQ ID NO 1327
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1327

gatcagttgt ttaagccgga gatca 25

<210> SEQ ID NO 1328
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1328

cgacagacgc ctgatctccg gaggaattga at 32

<210> SEQ ID NO 1329
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1329

gatcattcaa ttcctccgga gatca 25

<210> SEQ ID NO 1330
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1330

cgacagacgc ctgatctccg gaatttggaa ct 32

<210> SEQ ID NO 1331
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1331

gatcagttcc aaattccgga gatca 25

<210> SEQ ID NO 1332
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1332

cgacagacgc ctgatctccg gaaattgatg ct 32

<210> SEQ ID NO 1333
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1333

gatcagcatc aatttccgga gatca 25

<210> SEQ ID NO 1334
<211> LENGTH: 32

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1334

cgacagacgc ctgatctccg cggaattaaa gt 32

<210> SEQ ID NO 1335
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1335

gatcacttta attccgcgga gatca 25

<210> SEQ ID NO 1336
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1336

cgacagacgc ctgatctccg atttgtgatg ct 32

<210> SEQ ID NO 1337
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1337

gatcagcatc acaaatcgga gatca 25

<210> SEQ ID NO 1338
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1338

cgacagacgc ctgatctccg atttaccgtc tt 32

<210> SEQ ID NO 1339
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1339

gatcaagacg gtaaatcgga gatca 25

<210> SEQ ID NO 1340
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1340

cgacagacgc ctgatctccg attgtgtagg tt 32

<210> SEQ ID NO 1341
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1341

gatcaaccta cacaatcgga gatca 25

<210> SEQ ID NO 1342
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1342

cgacagacgc ctgatctcca tttcacggtc tt 32

<210> SEQ ID NO 1343
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1343

gatcaagacc gtgaaatgga gatca 25

<210> SEQ ID NO 1344
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1344

cgacagacgc ctgatctcca tttaggcagg tt 32

<210> SEQ ID NO 1345
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1345

gatcaacctg cctaaatgga gatca 25

<210> SEQ ID NO 1346
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1346

cgacagacgc ctgatctcca ttgttagcgt ct 32

<210> SEQ ID NO 1347
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1347

gatcagacgc taacaatgga gatca 25

<210> SEQ ID NO 1348
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1348

cgacagacgc ctgatctcca ttgaacgaac ct 32

<210> SEQ ID NO 1349
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1349

gatcaggttc gttcaatgga gatca 25

<210> SEQ ID NO 1350
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1350

cgacagacgc ctgatctcca ttaggcgaga at 32

<210> SEQ ID NO 1351
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1351

gatcattctc gcctaatgga gatca 25

<210> SEQ ID NO 1352
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1352

cgacagacgc ctgatctcca tgatgtgaac gt 32

<210> SEQ ID NO 1353
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1353

gatcacgttc acatcatgga gatca 25

<210> SEQ ID NO 1354
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1354

cgacagacgc ctgatctcca tagaatccgc at 32

<210> SEQ ID NO 1355
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1355

gatcatgcgg attctatgga gatca 25

<210> SEQ ID NO 1356
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1356

cgacagacgc ctgatctcca tacttgtcgc tt 32

<210> SEQ ID NO 1357
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1357

gatcaagcga caagtatgga gatca 25

<210> SEQ ID NO 1358
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1358

cgacagacgc ctgatctcca taacgtgtcc at 32

<210> SEQ ID NO 1359
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1359

gatcatggac acgttatgga gatca 25

<210> SEQ ID NO 1360
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1360

cgacagacgc ctgatctcca gttgttcctc at 32

<210> SEQ ID NO 1361
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1361

gatcatgagg aacaactgga gatca 25

<210> SEQ ID NO 1362
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1362

cgacagacgc ctgatctcca gttatgttcg ct 32

<210> SEQ ID NO 1363
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1363

gatcagcgaa cataactgga gatca 25

<210> SEQ ID NO 1364
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1364

cgacagacgc ctgatctcca gtgttgagtg tt 32

<210> SEQ ID NO 1365
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1365

gatcaacact caacactgga gatca 25

<210> SEQ ID NO 1366
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1366

cgacagacgc ctgatctcca ggtgaaagtg at 32

<210> SEQ ID NO 1367

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1367

gatcatcact ttcacctgga gatca 25

<210> SEQ ID NO 1368
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1368

cgacagacgc ctgatctcca gaaggttgtc at 32

<210> SEQ ID NO 1369
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1369

gatcatgaca accttctgga gatca 25

<210> SEQ ID NO 1370
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1370

cgacagacgc ctgatctcca ctggtggaaa tt 32

<210> SEQ ID NO 1371
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1371

gatcaatttc caccagtgga gatca 25

<210> SEQ ID NO 1372
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1372

cgacagacgc ctgatctcca cgttgagaag at 32

<210> SEQ ID NO 1373
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1373

gatcatcttc tcaacgtgga gatca 25

<210> SEQ ID NO 1374
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1374

cgacagacgc ctgatctcca cattagcgtt ct 32

<210> SEQ ID NO 1375
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1375

gatcagaacg ctaatgtgga gatca 25

<210> SEQ ID NO 1376
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1376

cgacagacgc ctgatctcca caagttccga tt 32

<210> SEQ ID NO 1377
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1377

gatcaatcgg aacttgtgga gatca 25

<210> SEQ ID NO 1378
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1378

cgacagacgc ctgatctcca atttagccac gt 32

<210> SEQ ID NO 1379
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1379

gatcacgtgg ctaaattgga gatca 25

<210> SEQ ID NO 1380
<211> LENGTH: 32
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1380

cgacagacgc ctgatctcca attgcgtctt ct 32

<210> SEQ ID NO 1381
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1381

gatcagaaga cgcaattgga gatca 25

<210> SEQ ID NO 1382
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1382

cgacagacgc ctgatctcca attacagacg ct 32

<210> SEQ ID NO 1383
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1383

gatcagcgtc tgtaattgga gatca 25

<210> SEQ ID NO 1384
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1384

cgacagacgc ctgatctcca aggtttggtg at 32

<210> SEQ ID NO 1385
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1385

gatcatcacc aaaccttgga gatca 25

<210> SEQ ID NO 1386
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1386

cgacagacgc ctgatctcca agagtggtca at 32

<210> SEQ ID NO 1387
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1387

gatcattgac cactcttgga gatca 25

<210> SEQ ID NO 1388
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1388

cgacagacgc ctgatctcca agaatacggc tt 32

<210> SEQ ID NO 1389
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1389

gatcaagccg tattcttgga gatca 25

<210> SEQ ID NO 1390
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1390

cgacagacgc ctgatctcca acactggaac tt 32

<210> SEQ ID NO 1391
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1391

gatcaagttc cagtgttgga gatca 25

<210> SEQ ID NO 1392
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1392

cgacagacgc ctgatctcca aactgctgaa ct 32

<210> SEQ ID NO 1393
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1393

gatcagttca gcagtttgga gatca 25

<210> SEQ ID NO 1394
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1394

cgacagacgc ctgatctcca aacattagcc gt 32

<210> SEQ ID NO 1395
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<212> TYPE: DNA
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gatcacggct aatgtttgga gatca 25

<210> SEQ ID NO 1396
<211> LENGTH: 32
<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 1396

cgacagacgc ctgatctcat ttgtgcggta gt 32

<210> SEQ ID NO 1397
<211> LENGTH: 25
<212> TYPE: DNA
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<400> SEQUENCE: 1397

gatcactacc gcacaaatga gatca 25

<210> SEQ ID NO 1398
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<212> TYPE: DNA
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<400> SEQUENCE: 1398

cgacagacgc ctgatctcat ttgcgacctt ct 32

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<400> SEQUENCE: 1399

gatcagaagg tcgcaaatga gatca 25

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<210> SEQ ID NO 1400
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<400> SEQUENCE: 1400

cgacagacgc ctgatctcat ttgatcgtgg ct 32

<210> SEQ ID NO 1401
<211> LENGTH: 25
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<400> SEQUENCE: 1401

gatcagccac gatcaaatga gatca 25

<210> SEQ ID NO 1402
<211> LENGTH: 32
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1402

cgacagacgc ctgatctcat ttcatgcggt ct 32

<210> SEQ ID NO 1403
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1403

gatcagaccg catgaaatga gatca 25

<210> SEQ ID NO 1404
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1404

cgacagacgc ctgatctcat ttactggtgc gt 32

<210> SEQ ID NO 1405
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1405

gatcacgcac cagtaaatga gatca 25

<210> SEQ ID NO 1406
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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<400> SEQUENCE: 1406

cgacagacgc ctgatctcat tgttctaccg ct 32

<210> SEQ ID NO 1407
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1407

gatcagcggt agaacaatga gatca 25

<210> SEQ ID NO 1408
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1408

cgacagacgc ctgatctcat tgtggatgct gt 32

<210> SEQ ID NO 1409
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1409

gatcacagca tccacaatga gatca 25

<210> SEQ ID NO 1410
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1410

cgacagacgc ctgatctcat tggaacggac tt 32

<210> SEQ ID NO 1411
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1411

gatcaagtcc gttccaatga gatca 25

<210> SEQ ID NO 1412
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1412

cgacagacgc ctgatctcat tgaactctcg ct 32

<210> SEQ ID NO 1413
<211> LENGTH: 25

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1413

gatcagcgag agttcaatga gatca 25

<210> SEQ ID NO 1414
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1414

cgacagacgc ctgatctcat tctaaggcgg tt 32

<210> SEQ ID NO 1415
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1415

gatcaaccgc cttagaatga gatca 25

<210> SEQ ID NO 1416
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1416

cgacagacgc ctgatctcat tcgtagttgg ct 32

<210> SEQ ID NO 1417
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1417

gatcagccaa ctacgaatga gatca 25

<210> SEQ ID NO 1418
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1418

cgacagacgc ctgatctcat tccaatgtcg ct 32

<210> SEQ ID NO 1419
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1419

gatcagcgac attggaatga gatca 25

<210> SEQ ID NO 1420
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1420

cgacagacgc ctgatctcat tatgtcacgc ct 32

<210> SEQ ID NO 1421
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1421

gatcaggcgt gacataatga gatca 25

<210> SEQ ID NO 1422
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1422

cgacagacgc ctgatctcat tatggtgcgt ct 32

<210> SEQ ID NO 1423
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1423

gatcagacgc accataatga gatca 25

<210> SEQ ID NO 1424
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1424

cgacagacgc ctgatctcat taaccgtccg at 32

<210> SEQ ID NO 1425
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1425

gatcatcgga cggttaatga gatca 25

<210> SEQ ID NO 1426
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1426

cgacagacgc ctgatctcat ggtgattgtc gt 32

<210> SEQ ID NO 1427
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1427

gatcacgaca atcaccatga gatca 25

<210> SEQ ID NO 1428
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1428

cgacagacgc ctgatctcat ggccaaactt ct 32

<210> SEQ ID NO 1429
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1429

gatcagaagt ttggccatga gatca 25

<210> SEQ ID NO 1430
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1430

cgacagacgc ctgatctcat gacaggtggt tt 32

<210> SEQ ID NO 1431
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1431

gatcaaacca cctgtcatga gatca 25

<210> SEQ ID NO 1432
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1432

cgacagacgc ctgatctcat ctcaagtccg tt 32

<210> SEQ ID NO 1433
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1433

gatcaacgga cttgagatga gatca 25

<210> SEQ ID NO 1434
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1434

cgacagacgc ctgatctcat cgagaaatgg ct 32

<210> SEQ ID NO 1435
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1435

gatcagccat ttctcgatga gatca 25

<210> SEQ ID NO 1436
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1436

cgacagacgc ctgatctcat cgaagacacc tt 32

<210> SEQ ID NO 1437
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1437

gatcaaggtg tcttcgatga gatca 25

<210> SEQ ID NO 1438
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1438

cgacagacgc ctgatctcat agttaccgcc at 32

<210> SEQ ID NO 1439
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1439

gatcatggcg gtaactatga gatca 25

<210> SEQ ID NO 1440
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1440

cgacagacgc ctgatctcat agtcgtttgg ct 32

<210> SEQ ID NO 1441
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1441

gatcagccaa acgactatga gatca 25

<210> SEQ ID NO 1442
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1442

cgacagacgc ctgatctcat acttgagcgg at 32

<210> SEQ ID NO 1443
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1443

gatcatccgc tcaagtatga gatca 25

<210> SEQ ID NO 1444
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1444

cgacagacgc ctgatctcat aattcgcgtg gt 32

<210> SEQ ID NO 1445
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1445

gatcaccacg cgaattatga gatca 25

<210> SEQ ID NO 1446

<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1446

cgacagacgc ctgatctcag ttgtagttgc gt 32

<210> SEQ ID NO 1447
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1447

gatcacgcaa ctacaactga gatca 25

<210> SEQ ID NO 1448
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1448

cgacagacgc ctgatctcag gttcacttcc at 32

<210> SEQ ID NO 1449
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1449

gatcatggaa gtgaacctga gatca 25

<210> SEQ ID NO 1450
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1450

cgacagacgc ctgatctcag gcgaggttta tt 32

<210> SEQ ID NO 1451
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1451

gatcaataaa cctcgcctga gatca 25

<210> SEQ ID NO 1452
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1452

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cgacagacgc ctgatctcag gaataagcgg tt 32

<210> SEQ ID NO 1453
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1453

gatcaaccgc ttattcctga gatca 25

<210> SEQ ID NO 1454
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1454

cgacagacgc ctgatctcag attctttccg ct 32

<210> SEQ ID NO 1455
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1455

gatcagcgga aagaatctga gatca 25

<210> SEQ ID NO 1456
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1456

cgacagacgc ctgatctcag atcctttgcc at 32

<210> SEQ ID NO 1457
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1457

gatcatggca aaggatctga gatca 25

<210> SEQ ID NO 1458
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1458

cgacagacgc ctgatctcac tttccgttga ct 32

<210> SEQ ID NO 1459
<211> LENGTH: 25
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1459

gatcagtcaa cggaaagtga gatca 25

<210> SEQ ID NO 1460
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1460

cgacagacgc ctgatctcac tttaagcacc gt 32

<210> SEQ ID NO 1461
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1461

gatcacggtg cttaaagtga gatca 25

<210> SEQ ID NO 1462
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1462

cgacagacgc ctgatctcac tgttattcgc ct 32

<210> SEQ ID NO 1463
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1463

gatcaggcga ataacagtga gatca 25

<210> SEQ ID NO 1464
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1464

cgacagacgc ctgatctcac tcttgtaacg ct 32

<210> SEQ ID NO 1465
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1465

gatcagcgtt acaagagtga gatca 25

<210> SEQ ID NO 1466
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1466

cgacagacgc ctgatctcac tccaaggtca at 32

<210> SEQ ID NO 1467
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1467

gatcattgac cttggagtga gatca 25

<210> SEQ ID NO 1468
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1468

cgacagacgc ctgatctcac tagtttgcgt ct 32

<210> SEQ ID NO 1469
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1469

gatcagacgc aaactagtga gatca 25

<210> SEQ ID NO 1470
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1470

cgacagacgc ctgatctcac taatgaacgg ct 32

<210> SEQ ID NO 1471
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1471

gatcagccgt tcattagtga gatca 25

<210> SEQ ID NO 1472
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1472

cgacagacgc ctgatctcac gttatcttgg ct 32

<210> SEQ ID NO 1473
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1473

gatcagccaa gataacgtga gatca 25

<210> SEQ ID NO 1474
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1474

cgacagacgc ctgatctcac ggagatggtt tt 32

<210> SEQ ID NO 1475
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1475

gatcaaaacc atctccgtga gatca 25

<210> SEQ ID NO 1476
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1476

cgacagacgc ctgatctcac ggaagagatg tt 32

<210> SEQ ID NO 1477
<211> LENGTH: 25
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<400> SEQUENCE: 1477

gatcaacatc tcttccgtga gatca 25

<210> SEQ ID NO 1478
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1478

cgacagacgc ctgatctcac gatttagcac ct 32

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<210> SEQ ID NO 1479
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1479

gatcaggtgc taaatcgtga gatca 25

<210> SEQ ID NO 1480
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<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1480

cgacagacgc ctgatctcac gatagtttgc ct 32

<210> SEQ ID NO 1481
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1481

gatcaggcaa actatcgtga gatca 25

<210> SEQ ID NO 1482
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<212> TYPE: DNA
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<400> SEQUENCE: 1482

cgacagacgc ctgatctcac cttattgcac gt 32

<210> SEQ ID NO 1483
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<400> SEQUENCE: 1483

gatcacgtgc aataaggtga gatca 25

<210> SEQ ID NO 1484
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1484

cgacagacgc ctgatctcac ctccggttaa at 32

<210> SEQ ID NO 1485
<211> LENGTH: 25
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<223> OTHER INFORMATION: synthetic oligonucleotide

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<400> SEQUENCE: 1485

gatcatttaa ccggaggtga gatca 25

<210> SEQ ID NO 1486
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1486

cgacagacgc ctgatctcac ctatgcgaaa ct 32

<210> SEQ ID NO 1487
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<400> SEQUENCE: 1487

gatcagtttc gcataggtga gatca 25

<210> SEQ ID NO 1488
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1488

cgacagacgc ctgatctcac attggcagaa ct 32

<210> SEQ ID NO 1489
<211> LENGTH: 25
<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1489

gatcagttct gccaatgtga gatca 25

<210> SEQ ID NO 1490
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1490

cgacagacgc ctgatctcac ataggagcgt tt 32

<210> SEQ ID NO 1491
<211> LENGTH: 25
<212> TYPE: DNA
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<400> SEQUENCE: 1491

gatcaaacgc tcctatgtga gatca 25

<210> SEQ ID NO 1492
<211> LENGTH: 32

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1492

cgacagacgc ctgatctcac aatgttgcct ct 32

<210> SEQ ID NO 1493
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<400> SEQUENCE: 1493

gatcagaggc aacattgtga gatca 25

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<400> SEQUENCE: 1494

cgacagacgc ctgatctcac aatatgtccg ct 32

<210> SEQ ID NO 1495
<211> LENGTH: 25
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<400> SEQUENCE: 1495

gatcagcgga catattgtga gatca 25

<210> SEQ ID NO 1496
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1496

cgacagacgc ctgatctcaa ttcgagcaac ct 32

<210> SEQ ID NO 1497
<211> LENGTH: 25
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1497

gatcaggttg ctcgaattga gatca 25

<210> SEQ ID NO 1498
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1498

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cgacagacgc ctgatctcaa tgttgctgag gt 32

<210> SEQ ID NO 1499
<211> LENGTH: 25
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1499

gatcacctca gcaacattga gatca 25

<210> SEQ ID NO 1500
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1500

cgacagacgc ctgatctcaa tggatgacgg at 32

<210> SEQ ID NO 1501
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1501

gatcatccgt catccattga gatca 25

<210> SEQ ID NO 1502
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1502

cgacagacgc ctgatctcaa tcttcgttgg ct 32

<210> SEQ ID NO 1503
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1503

gatcagccaa cgaagattga gatca 25

<210> SEQ ID NO 1504
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1504

cgacagacgc ctgatctcaa tcctttctgc gt 32

<210> SEQ ID NO 1505
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1505

gatcacgcag aaaggattga gatca 25

<210> SEQ ID NO 1506
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1506

cgacagacgc ctgatctcaa gtttgagtgg ct 32

<210> SEQ ID NO 1507
<211> LENGTH: 25
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1507

gatcagccac tcaaacttga gatca 25

<210> SEQ ID NO 1508
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1508

cgacagacgc ctgatctcaa gtagtcggtg tt 32

<210> SEQ ID NO 1509
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1509

gatcaacacc gactacttga gatca 25

<210> SEQ ID NO 1510
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1510

cgacagacgc ctgatctcaa gccttggaaa ct 32

<210> SEQ ID NO 1511
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1511

gatcagtttc caaggcttga gatca 25

<210> SEQ ID NO 1512
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1512

cgacagacgc ctgatctcaa gcatgtgagg at 32

<210> SEQ ID NO 1513
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1513

gatcatcctc acatgcttga gatca 25

<210> SEQ ID NO 1514
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1514

cgacagacgc ctgatctcaa gattccgtcc at 32

<210> SEQ ID NO 1515
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1515

gatcatggac ggaatcttga gatca 25

<210> SEQ ID NO 1516
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1516

cgacagacgc ctgatctcaa gaattggagc gt 32

<210> SEQ ID NO 1517
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1517

gatcacgctc caattcttga gatca 25

<210> SEQ ID NO 1518
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1518

cgacagacgc ctgatctcaa gaagtgtgtg ct 32

<210> SEQ ID NO 1519
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1519

gatcagcaca cacttcttga gatca 25

<210> SEQ ID NO 1520
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1520

cgacagacgc ctgatctcaa gaactggtgg at 32

<210> SEQ ID NO 1521
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1521

gatcatccac cagttcttga gatca 25

<210> SEQ ID NO 1522
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1522

cgacagacgc ctgatctcaa ctttgatccg ct 32

<210> SEQ ID NO 1523
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1523

gatcagcgga tcaaagttga gatca 25

<210> SEQ ID NO 1524
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1524

cgacagacgc ctgatctcaa cgtggtttct gt 32

<210> SEQ ID NO 1525

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1525

gatcacagaa accacgttga gatca 25

<210> SEQ ID NO 1526
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1526

cgacagacgc ctgatctcaa cacctcttgg at 32

<210> SEQ ID NO 1527
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1527

gatcatccaa gaggtgttga gatca 25

<210> SEQ ID NO 1528
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1528

cgacagacgc ctgatctcaa attgcctcgt ct 32

<210> SEQ ID NO 1529
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1529

gatcagacga ggcaatttga gatca 25

<210> SEQ ID NO 1530
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1530

cgacagacgc ctgatctcaa atgatgcgga gt 32

<210> SEQ ID NO 1531
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1531

gatcactccg catcatttga gatca 25

<210> SEQ ID NO 1532
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1532

cgacagacgc ctgatctcaa atccttcgct gt 32

<210> SEQ ID NO 1533
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1533

gatcacagcg aaggatttga gatca 25

<210> SEQ ID NO 1534
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1534

cgacagacgc ctgatctcaa atcatcggct ct 32

<210> SEQ ID NO 1535
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1535

gatcagagcc gatgatttga gatca 25

<210> SEQ ID NO 1536
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1536

cgacagacgc ctgatctcaa atacaggtcg ct 32

<210> SEQ ID NO 1537
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1537

gatcagcgac ctgtatttga gatca 25

<210> SEQ ID NO 1538
<211> LENGTH: 32
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1538

cgacagacgc ctgatctcaa ataagcggtg gt 32

<210> SEQ ID NO 1539
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1539

gatcaccacc gcttatttga gatca 25

<210> SEQ ID NO 1540
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1540

cgacagacgc ctgatctcaa agaggtttgg ct 32

<210> SEQ ID NO 1541
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1541

gatcagccaa acctctttga gatca 25

<210> SEQ ID NO 1542
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1542

cgacagacgc ctgatctcaa acgtgttcct ct 32

<210> SEQ ID NO 1543
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1543

gatcagagga acacgtttga gatca 25

<210> SEQ ID NO 1544
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1544

cgacagacgc ctgatctatt tggcagaggt ct 32

<210> SEQ ID NO 1545
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1545

gatcagacct ctgccaaata gatca 25

<210> SEQ ID NO 1546
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1546

cgacagacgc ctgatctatt tgaggacacg gt 32

<210> SEQ ID NO 1547
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1547

gatcaccgtg tcctcaaata gatca 25

<210> SEQ ID NO 1548
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1548

cgacagacgc ctgatctatt tccggttgag gt 32

<210> SEQ ID NO 1549
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1549

gatcacctca accggaaata gatca 25

<210> SEQ ID NO 1550
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1550

cgacagacgc ctgatctatt tatcggagcg gt 32

<210> SEQ ID NO 1551
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1551

gatcaccgct ccgataaata gatca 25

<210> SEQ ID NO 1552
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1552

cgacagacgc ctgatctatt ggcaaggaga ct 32

<210> SEQ ID NO 1553
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1553

gatcagtctc cttgccaata gatca 25

<210> SEQ ID NO 1554
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1554

cgacagacgc ctgatctatt gccaagtcct ct 32

<210> SEQ ID NO 1555
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1555

gatcagagga cttggcaata gatca 25

<210> SEQ ID NO 1556
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1556

cgacagacgc ctgatctatt ctatggtccg ct 32

<210> SEQ ID NO 1557
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1557

gatcagcgga ccatagaata gatca 25

<210> SEQ ID NO 1558
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1558

cgacagacgc ctgatctatt ccaacgacca gt 32

<210> SEQ ID NO 1559
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1559

gatcactggt cgttggaata gatca 25

<210> SEQ ID NO 1560
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1560

cgacagacgc ctgatctatt atgcgagagg ct 32

<210> SEQ ID NO 1561
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1561

gatcagcctc tcgcataata gatca 25

<210> SEQ ID NO 1562
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1562

cgacagacgc ctgatctatt aggacacacg gt 32

<210> SEQ ID NO 1563
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1563

gatcaccgtg tgtcctaata gatca 25

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<400> SEQUENCE: 1564

cgacagacgc ctgatctatt acgtaccagc ct 32

<210> SEQ ID NO 1565
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gatcaggctg gtacgtaata gatca 25

<210> SEQ ID NO 1566
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<400> SEQUENCE: 1566

cgacagacgc ctgatctatt acctcagtcg ct 32

<210> SEQ ID NO 1567
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gatcagcgac tgaggtaata gatca 25

<210> SEQ ID NO 1568
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<220> FEATURE:
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<400> SEQUENCE: 1568

cgacagacgc ctgatctatt acaaggcgag gt 32

<210> SEQ ID NO 1569
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<400> SEQUENCE: 1569

gatcacctcg ccttgtaata gatca 25

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cgacagacgc ctgatctatt aaggcaccac ct 32

<210> SEQ ID NO 1571
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<212> TYPE: DNA
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gatcaggtgg tgccttaata gatca 25

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<400> SEQUENCE: 1572

cgacagacgc ctgatctatt aactgcctcc gt 32

<210> SEQ ID NO 1573
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<223> OTHER INFORMATION: synthetic oligonucleotide

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gatcacggag gcagttaata gatca 25

<210> SEQ ID NO 1574
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<212> TYPE: DNA
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<400> SEQUENCE: 1574

cgacagacgc ctgatctatg tttcaggtcg gt 32

<210> SEQ ID NO 1575
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<400> SEQUENCE: 1575

gatcaccgac ctgaaacata gatca 25

<210> SEQ ID NO 1576
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<212> TYPE: DNA
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<400> SEQUENCE: 1576

cgacagacgc ctgatctatg ttagacgcag gt 32

<210> SEQ ID NO 1577
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<400> SEQUENCE: 1577

gatcacctgc gtctaacata gatca 25

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<400> SEQUENCE: 1578

cgacagacgc ctgatctatg tgtatcaggc gt 32

<210> SEQ ID NO 1579
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<400> SEQUENCE: 1579

gatcacgcct gatacacata gatca 25

<210> SEQ ID NO 1580
<211> LENGTH: 32
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<400> SEQUENCE: 1580

cgacagacgc ctgatctatg gttactgctc gt 32

<210> SEQ ID NO 1581
<211> LENGTH: 25
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<400> SEQUENCE: 1581

gatcacgagc agtaaccata gatca 25

<210> SEQ ID NO 1582
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<400> SEQUENCE: 1582

cgacagacgc ctgatctatg gaggctttgt ct 32

<210> SEQ ID NO 1583
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<212> TYPE: DNA
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gatcagacaa agcctccata gatca 25

<210> SEQ ID NO 1584
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<400> SEQUENCE: 1584

cgacagacgc ctgatctatg cttgtggact ct 32

<210> SEQ ID NO 1585
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<212> TYPE: DNA
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<400> SEQUENCE: 1585

gatcagagtc cacaagcata gatca 25

<210> SEQ ID NO 1586
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<400> SEQUENCE: 1586

cgacagacgc ctgatctatg ctaaaggtcg gt 32

<210> SEQ ID NO 1587
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<400> SEQUENCE: 1587

gatcaccgac ctttagcata gatca 25

<210> SEQ ID NO 1588
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1588

cgacagacgc ctgatctatg cctttacctc gt 32

<210> SEQ ID NO 1589
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1589

gatcacgagg taaaggcata gatca 25

<210> SEQ ID NO 1590
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1590

cgacagacgc ctgatctatg atgtctgtgc ct 32

<210> SEQ ID NO 1591
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1591

gatcaggcac agacatcata gatca 25

<210> SEQ ID NO 1592
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1592

cgacagacgc ctgatctatg agaagccagt gt 32

<210> SEQ ID NO 1593
<211> LENGTH: 25
<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1593

gatcacactg gcttctcata gatca 25

<210> SEQ ID NO 1594
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1594

cgacagacgc ctgatctatg acctgttgtg gt 32

<210> SEQ ID NO 1595
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1595

gatcaccaca acaggtcata gatca 25

<210> SEQ ID NO 1596
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1596

cgacagacgc ctgatctatg aagtcacgag gt 32

<210> SEQ ID NO 1597
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1597

gatcacctcg tgacttcata gatca 25

<210> SEQ ID NO 1598
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1598

cgacagacgc ctgatctatc ttgaggtgtg ct 32

<210> SEQ ID NO 1599
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1599

gatcagcaca cctcaagata gatca 25

<210> SEQ ID NO 1600
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1600

cgacagacgc ctgatctatc ttcgacactg gt 32

<210> SEQ ID NO 1601
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1601

gatcaccagt gtcgaagata gatca 25

<210> SEQ ID NO 1602
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1602

cgacagacgc ctgatctatc tccaagcaca gt 32

<210> SEQ ID NO 1603
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1603

gatcactgtg cttggagata gatca 25

<210> SEQ ID NO 1604

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<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1604

cgacagacgc ctgatctatc taccgaacac gt 32

<210> SEQ ID NO 1605
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1605

gatcacgtgt tcggtagata gatca 25

<210> SEQ ID NO 1606
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1606

cgacagacgc ctgatctatc gaatgagcag gt 32

<210> SEQ ID NO 1607
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1607

gatcacctgc tcattcgata gatca 25

<210> SEQ ID NO 1608
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1608

cgacagacgc ctgatctatc cgtattgagc ct 32

<210> SEQ ID NO 1609
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1609

gatcaggctc aatacggata gatca 25

<210> SEQ ID NO 1610
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1610

cgacagacgc ctgatctatc catgagcaac ct 32

<210> SEQ ID NO 1611
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1611

gatcaggttg ctcatggata gatca 25

<210> SEQ ID NO 1612
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1612

cgacagacgc ctgatctatc atgcctaacc gt 32

<210> SEQ ID NO 1613
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1613

gatcacggtt aggcatgata gatca 25

<210> SEQ ID NO 1614
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1614

cgacagacgc ctgatctatc aggtgaatgg ct 32

<210> SEQ ID NO 1615
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1615

gatcagccat tcacctgata gatca 25

<210> SEQ ID NO 1616
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1616

cgacagacgc ctgatctatc accatgttcc gt 32

<210> SEQ ID NO 1617
<211> LENGTH: 25
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1617

gatcacggaa catggtgata gatca 25

<210> SEQ ID NO 1618
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1618

cgacagacgc ctgatctatc aacagtccag ct 32

<210> SEQ ID NO 1619
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1619

gatcagctgg actgttgata gatca 25

<210> SEQ ID NO 1620
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1620

cgacagacgc ctgatctata ttaccgcgac ct 32

<210> SEQ ID NO 1621
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1621

gatcaggtcg cggtaatata gatca 25

<210> SEQ ID NO 1622
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1622

cgacagacgc ctgatctata tggacgaacg gt 32

<210> SEQ ID NO 1623
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1623

gatcaccgtt cgtccatata gatca 25

<210> SEQ ID NO 1624
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1624

cgacagacgc ctgatctata tgcggtgtct gt 32

<210> SEQ ID NO 1625
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1625

gatcacagac accgcatata gatca 25

<210> SEQ ID NO 1626
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1626

cgacagacgc ctgatctata tctcgtgtgc ct 32

<210> SEQ ID NO 1627
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1627

gatcaggcac acgagatata gatca 25

<210> SEQ ID NO 1628
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1628

cgacagacgc ctgatctata tccaaccagc gt 32

<210> SEQ ID NO 1629
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1629

gatcacgctg gttggatata gatca 25

<210> SEQ ID NO 1630
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1630

cgacagacgc ctgatctata taaggcaggc gt 32

<210> SEQ ID NO 1631
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1631

gatcacgcct gccttatata gatca 25

<210> SEQ ID NO 1632
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1632

cgacagacgc ctgatctata gtgcaagtcg gt 32

<210> SEQ ID NO 1633
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1633

gatcaccgac ttgcactata gatca 25

<210> SEQ ID NO 1634
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1634

cgacagacgc ctgatctata gtgagaacgg ct 32

<210> SEQ ID NO 1635
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1635

gatcagccgt tctcactata gatca 25

<210> SEQ ID NO 1636
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1636

cgacagacgc ctgatctata ggcaggtttc gt 32

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<210> SEQ ID NO 1637
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1637

gatcacgaaa cctgcctata gatca 25

<210> SEQ ID NO 1638
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1638

cgacagacgc ctgatctata gatcgatggc gt 32

<210> SEQ ID NO 1639
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1639

gatcacgcca tcgatctata gatca 25

<210> SEQ ID NO 1640
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1640

cgacagacgc ctgatctata ctctgttccg ct 32

<210> SEQ ID NO 1641
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1641

gatcagcgga acagagtata gatca 25

<210> SEQ ID NO 1642
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1642

cgacagacgc ctgatctata ctaacggacg ct 32

<210> SEQ ID NO 1643
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1643

gatcagcgtc cgttagtata gatca 25

<210> SEQ ID NO 1644
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1644

cgacagacgc ctgatctata cgttctgctc ct 32

<210> SEQ ID NO 1645
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1645

gatcaggagc agaacgtata gatca 25

<210> SEQ ID NO 1646
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1646

cgacagacgc ctgatctata atctcgaccg ct 32

<210> SEQ ID NO 1647
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1647

gatcagcggt cgagattata gatca 25

<210> SEQ ID NO 1648
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1648

cgacagacgc ctgatctata agcggagtgt ct 32

<210> SEQ ID NO 1649
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1649

gatcagacac tccgcttata gatca 25

<210> SEQ ID NO 1650
<211> LENGTH: 32

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1650

cgacagacgc ctgatctata agcctggaac gt 32

<210> SEQ ID NO 1651
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1651

gatcacgttc caggcttata gatca 25

<210> SEQ ID NO 1652
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1652

cgacagacgc ctgatctata agacggtgag ct 32

<210> SEQ ID NO 1653
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1653

gatcagctca ccgtcttata gatca 25

<210> SEQ ID NO 1654
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cgacagacgc ctgatctata agaacctccg ct 32

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gatcagcgga ggttcttata gatca 25

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cgacagacgc ctgatctata aatggccgga gt 32

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gatcactccg gccatttata gatca 25

<210> SEQ ID NO 1658
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cgacagacgc ctgatctagt tggcctgaaa gt 32

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gatcactttc aggccaacta gatca 25

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cgacagacgc ctgatctagt tgcatctctg gt 32

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gatcaccaga gatgcaacta gatca 25

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cgacagacgc ctgatctagt tctccgactt gt 32

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gatcacaagt cggagaacta gatca 25

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cgacagacgc ctgatctagt tctcaaccag ct 32

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gatcagctgg ttgagaacta gatca 25

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cgacagacgc ctgatctagt tatggaagcc gt 32

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gatcacggct tccataacta gatca 25

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cgacagacgc ctgatctagt gtctaatgcg gt 32

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gatcaccgca ttagacacta gatca 25

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cgacagacgc ctgatctagt ggtttcgtca gt 32

<210> SEQ ID NO 1671
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gatcactgac gaaaccacta gatca 25

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cgacagacgc ctgatctagt cggaaccttt gt 32

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gatcacaaag gttccgacta gatca 25

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<400> SEQUENCE: 1674

cgacagacgc ctgatctagt caacgacatc ct 32

<210> SEQ ID NO 1675
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gatcaggatg tcgttgacta gatca 25

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cgacagacgc ctgatctagt caacaccagt ct 32

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gatcagactg gtgttgacta gatca 25

<210> SEQ ID NO 1678
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<400> SEQUENCE: 1678

cgacagacgc ctgatctagt atagccaccg at 32

<210> SEQ ID NO 1679
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gatcatcggt ggctatacta gatca 25

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<400> SEQUENCE: 1680

cgacagacgc ctgatctagt agtacgaggc at 32

<210> SEQ ID NO 1681
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<400> SEQUENCE: 1681

gatcatgcct cgtactacta gatca 25

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<211> LENGTH: 32
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<400> SEQUENCE: 1682

cgacagacgc ctgatctagt agaacatgcg gt 32

<210> SEQ ID NO 1683

<211> LENGTH: 25
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<400> SEQUENCE: 1683

gatcaccgca tgttctacta gatca 25

<210> SEQ ID NO 1684
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<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1684

cgacagacgc ctgatctagt actgtgcttg gt 32

<210> SEQ ID NO 1685
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<400> SEQUENCE: 1685

gatcaccaag cacagtacta gatca 25

<210> SEQ ID NO 1686
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<212> TYPE: DNA
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<400> SEQUENCE: 1686

cgacagacgc ctgatctagt acacatcacc gt 32

<210> SEQ ID NO 1687
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<400> SEQUENCE: 1687

gatcacggtg atgtgtacta gatca 25

<210> SEQ ID NO 1688
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<400> SEQUENCE: 1688

cgacagacgc ctgatctagg tttacgcctt ct 32

<210> SEQ ID NO 1689
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<400> SEQUENCE: 1689

gatcagaagg cgtaaaccta gatca 25

<210> SEQ ID NO 1690
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<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1690

cgacagacgc ctgatctagg ttcttagcgt gt 32

<210> SEQ ID NO 1691
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<212> TYPE: DNA
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<400> SEQUENCE: 1691

gatcacacgc taagaaccta gatca 25

<210> SEQ ID NO 1692
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<400> SEQUENCE: 1692

cgacagacgc ctgatctagg ctttatccgt gt 32

<210> SEQ ID NO 1693
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gatcacacgg ataaagccta gatca 25

<210> SEQ ID NO 1694
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cgacagacgc ctgatctagg cttcttcaca ct 32

<210> SEQ ID NO 1695
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<400> SEQUENCE: 1695

gatcagtgtg aagaagccta gatca 25

<210> SEQ ID NO 1696
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<212> TYPE: DNA

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<400> SEQUENCE: 1696

cgacagacgc ctgatctagg caaagttcag gt 32

<210> SEQ ID NO 1697
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<400> SEQUENCE: 1697

gatcacctga actttgccta gatca 25

<210> SEQ ID NO 1698
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<400> SEQUENCE: 1698

cgacagacgc ctgatctagg accttaccac at 32

<210> SEQ ID NO 1699
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<400> SEQUENCE: 1699

gatcatgtgg taaggtccta gatca 25

<210> SEQ ID NO 1700
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<212> TYPE: DNA
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<400> SEQUENCE: 1700

cgacagacgc ctgatctagg aatgtatcgg ct 32

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<400> SEQUENCE: 1701

gatcagccga tacattccta gatca 25

<210> SEQ ID NO 1702
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<400> SEQUENCE: 1702

cgacagacgc ctgatctagg aatcatcagc gt 32

<210> SEQ ID NO 1703
<211> LENGTH: 25
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<400> SEQUENCE: 1703

gatcacgctg atgattccta gatca 25

<210> SEQ ID NO 1704
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 1704

cgacagacgc ctgatctagc tccatttacc gt 32

<210> SEQ ID NO 1705
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1705

gatcacggta aatggagcta gatca 25

<210> SEQ ID NO 1706
<211> LENGTH: 32
<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1706

cgacagacgc ctgatctagc taaagcaggt ct 32

<210> SEQ ID NO 1707
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gatcagacct gctttagcta gatca 25

<210> SEQ ID NO 1708
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<400> SEQUENCE: 1708

cgacagacgc ctgatctagc gtttactgag gt 32

<210> SEQ ID NO 1709
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<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1709

gatcacctca gtaaacgcta gatca 25

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cgacagacgc ctgatctagc ctttgtcact ct 32

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gatcagagtg acaaaggcta gatca 25

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<212> TYPE: DNA
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<400> SEQUENCE: 1712

cgacagacgc ctgatctagc cttcattcct gt 32

<210> SEQ ID NO 1713
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<400> SEQUENCE: 1713

gatcacagga atgaaggcta gatca 25

<210> SEQ ID NO 1714
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1714

cgacagacgc ctgatctagc ctattgttcc gt 32

<210> SEQ ID NO 1715
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<212> TYPE: DNA
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<400> SEQUENCE: 1715

gatcacggaa caataggcta gatca 25

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<210> SEQ ID NO 1716
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1716

cgacagacgc ctgatctagc ctatacaccg at 32

<210> SEQ ID NO 1717
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1717

gatcatcggt gtataggcta gatca 25

<210> SEQ ID NO 1718
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1718

cgacagacgc ctgatctagc ctaaaccact gt 32

<210> SEQ ID NO 1719
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1719

gatcacagtg gtttaggcta gatca 25

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<400> SEQUENCE: 1720

cgacagacgc ctgatctagc caaagtatcc gt 32

<210> SEQ ID NO 1721
<211> LENGTH: 25
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1721

gatcacggat actttggcta gatca 25

<210> SEQ ID NO 1722
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1722

cgacagacgc ctgatctagc attgtctcac ct 32

<210> SEQ ID NO 1723
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 1723

gatcaggtga gacaatgcta gatca 25

<210> SEQ ID NO 1724
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<212> TYPE: DNA
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<400> SEQUENCE: 1724

cgacagacgc ctgatctagc atagtgaacc gt 32

<210> SEQ ID NO 1725
<211> LENGTH: 25
<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 1725

gatcacggtt cactatgcta gatca 25

<210> SEQ ID NO 1726
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1726

cgacagacgc ctgatctagc aactaccatc gt 32

<210> SEQ ID NO 1727
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1727

gatcacgatg gtagttgcta gatca 25

<210> SEQ ID NO 1728
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1728

cgacagacgc ctgatctagc aacatctacg gt 32

<210> SEQ ID NO 1729
<211> LENGTH: 25

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1729

gatcaccgta gatgttgcta gatca 25

<210> SEQ ID NO 1730
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1730

cgacagacgc ctgatctagc aaagtggagt ct 32

<210> SEQ ID NO 1731
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1731

gatcagactc cactttgcta gatca 25

<210> SEQ ID NO 1732
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1732

cgacagacgc ctgatctaga tgtggtgttc ct 32

<210> SEQ ID NO 1733
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1733

gatcaggaac accacatcta gatca 25

<210> SEQ ID NO 1734
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1734

cgacagacgc ctgatctaga tgtaagtgcc gt 32

<210> SEQ ID NO 1735
<211> LENGTH: 25
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1735

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gatcacggca cttacatcta gatca 25

<210> SEQ ID NO 1736
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<400> SEQUENCE: 1736

cgacagacgc ctgatctaga tgccttcctt gt 32

<210> SEQ ID NO 1737
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<400> SEQUENCE: 1737

gatcacaagg aaggcatcta gatca 25

<210> SEQ ID NO 1738
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<400> SEQUENCE: 1738

cgacagacgc ctgatctaga tgattccggt gt 32

<210> SEQ ID NO 1739
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<400> SEQUENCE: 1739

gatcacaccg gaatcatcta gatca 25

<210> SEQ ID NO 1740
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1740

cgacagacgc ctgatctaga tcttgtgtcc gt 32

<210> SEQ ID NO 1741
<211> LENGTH: 25
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1741

gatcacggac acaagatcta gatca 25

<210> SEQ ID NO 1742
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1742

cgacagacgc ctgatctaga tcctcattcg ct 32

<210> SEQ ID NO 1743
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1743

gatcagcgaa tgaggatcta gatca 25

<210> SEQ ID NO 1744
<211> LENGTH: 32
<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1744

cgacagacgc ctgatctaga tagtgttcgg ct 32

<210> SEQ ID NO 1745
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<400> SEQUENCE: 1745

gatcagccga acactatcta gatca 25

<210> SEQ ID NO 1746
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1746

cgacagacgc ctgatctaga ggttgttgtc ct 32

<210> SEQ ID NO 1747
<211> LENGTH: 25
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1747

gatcaggaca acaacctcta gatca 25

<210> SEQ ID NO 1748
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1748

cgacagacgc ctgatctaga ggaacttgac gt 32

<210> SEQ ID NO 1749
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<212> TYPE: DNA
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<400> SEQUENCE: 1749

gatcacgtca agttcctcta gatca 25

<210> SEQ ID NO 1750
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<212> TYPE: DNA
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<400> SEQUENCE: 1750

cgacagacgc ctgatctaga ctacaatccg ct 32

<210> SEQ ID NO 1751
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<400> SEQUENCE: 1751

gatcagcgga ttgtagtcta gatca 25

<210> SEQ ID NO 1752
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<220> FEATURE:
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<400> SEQUENCE: 1752

cgacagacgc ctgatctaga ccacttacac gt 32

<210> SEQ ID NO 1753
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<400> SEQUENCE: 1753

gatcacgtgt aagtggtcta gatca 25

<210> SEQ ID NO 1754
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1754

cgacagacgc ctgatctaga cagccacctt at 32

<210> SEQ ID NO 1755
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gatcataagg tggctgtcta gatca 25

<210> SEQ ID NO 1756
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<400> SEQUENCE: 1756

cgacagacgc ctgatctaga caacctctgg at 32

<210> SEQ ID NO 1757
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gatcatccag aggttgtcta gatca 25

<210> SEQ ID NO 1758
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<400> SEQUENCE: 1758

cgacagacgc ctgatctaga caaaccttcc gt 32

<210> SEQ ID NO 1759
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gatcacggaa ggtttgtcta gatca 25

<210> SEQ ID NO 1760
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<400> SEQUENCE: 1760

cgacagacgc ctgatctaga atcactacgc ct 32

<210> SEQ ID NO 1761
<211> LENGTH: 25
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gatcaggcgt agtgattcta gatca 25

<210> SEQ ID NO 1762

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<211> LENGTH: 32
<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 1762

cgacagacgc ctgatctact ttgtggagag ct 32

<210> SEQ ID NO 1763
<211> LENGTH: 25
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<400> SEQUENCE: 1763

gatcagctct ccacaaagta gatca 25

<210> SEQ ID NO 1764
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1764

cgacagacgc ctgatctact tggtaagagc gt 32

<210> SEQ ID NO 1765
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1765

gatcacgctc ttaccaagta gatca 25

<210> SEQ ID NO 1766
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1766

cgacagacgc ctgatctact tgagcagaac ct 32

<210> SEQ ID NO 1767
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1767

gatcaggttc tgctcaagta gatca 25

<210> SEQ ID NO 1768
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1768

cgacagacgc ctgatctact tcgttgagtc ct 32

<210> SEQ ID NO 1769
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1769

gatcaggact caacgaagta gatca 25

<210> SEQ ID NO 1770
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1770

cgacagacgc ctgatctact tcgagttgtc ct 32

<210> SEQ ID NO 1771
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1771

gatcaggaca actcgaagta gatca 25

<210> SEQ ID NO 1772
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1772

cgacagacgc ctgatctact tagaagcgac ct 32

<210> SEQ ID NO 1773
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1773

gatcaggtcg cttctaagta gatca 25

<210> SEQ ID NO 1774
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1774

cgacagacgc ctgatctact tagaacaggc gt 32

<210> SEQ ID NO 1775
<211> LENGTH: 25
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1775

gatcacgcct gttctaagta gatca 25

<210> SEQ ID NO 1776
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1776

cgacagacgc ctgatctact taagcgagga ct 32

<210> SEQ ID NO 1777
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1777

gatcagtcct cgcttaagta gatca 25

<210> SEQ ID NO 1778
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1778

cgacagacgc ctgatctact ggtgtttgga ct 32

<210> SEQ ID NO 1779
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1779

gatcagtcca aacaccagta gatca 25

<210> SEQ ID NO 1780
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1780

cgacagacgc ctgatctact gatgagttgg ct 32

<210> SEQ ID NO 1781
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1781

gatcagccaa ctcatcagta gatca 25

<210> SEQ ID NO 1782
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1782

cgacagacgc ctgatctact cggaacattg gt 32

<210> SEQ ID NO 1783
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1783

gatcaccaat gttccgagta gatca 25

<210> SEQ ID NO 1784
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1784

cgacagacgc ctgatctact caatagaccg ct 32

<210> SEQ ID NO 1785
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1785

gatcagcggt ctattgagta gatca 25

<210> SEQ ID NO 1786
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1786

cgacagacgc ctgatctact acactgaacc gt 32

<210> SEQ ID NO 1787
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1787

gatcacggtt cagtgtag 18

<210> SEQ ID NO 1788
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1788

cgacagacgc ctgatctact acaagtccac gt 32

<210> SEQ ID NO 1789
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1789

gatcacgtgg acttgtag 18

<210> SEQ ID NO 1790
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1790

cgacagacgc ctgatctact aagagttgcc gt 32

<210> SEQ ID NO 1791
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1791

gatcacggca actcttagta gatca 25

<210> SEQ ID NO 1792
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1792

cgacagacgc ctgatctacg ttctccttag ct 32

<210> SEQ ID NO 1793
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1793

gatcagctaa ggagaacgta gatca 25

<210> SEQ ID NO 1794
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1794

cgacagacgc ctgatctacg tgtaggtgtt ct 32

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<210> SEQ ID NO 1795
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1795

gatcagaaca cctacacgta gatca 25

<210> SEQ ID NO 1796
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1796

cgacagacgc ctgatctacg tagttggtct gt 32

<210> SEQ ID NO 1797
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1797

gatcacagac caactacgta gatca 25

<210> SEQ ID NO 1798
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1798

cgacagacgc ctgatctacg ctaactcctt gt 32

<210> SEQ ID NO 1799
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1799

gatcacaagg agttagcgta gatca 25

<210> SEQ ID NO 1800
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1800

cgacagacgc ctgatctacg ccaaatccta gt 32

<210> SEQ ID NO 1801
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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<400> SEQUENCE: 1801

gatcactagg atttggcgta gatca 25

<210> SEQ ID NO 1802
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1802

cgacagacgc ctgatctacg attctgtgag gt 32

<210> SEQ ID NO 1803
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1803

gatcacctca cagaatcgta gatca 25

<210> SEQ ID NO 1804
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1804

cgacagacgc ctgatctacg attccaccaa gt 32

<210> SEQ ID NO 1805
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1805

gatcacttgg tggaatcgta gatca 25

<210> SEQ ID NO 1806
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1806

cgacagacgc ctgatctacg atattgcctc ct 32

<210> SEQ ID NO 1807
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1807

gatcaggagg caatatcgta gatca 25

<210> SEQ ID NO 1808
<211> LENGTH: 32

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1808

cgacagacgc ctgatctacg atagaggttg ct 32

<210> SEQ ID NO 1809
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1809

gatcagcaac ctctatcgta gatca 25

<210> SEQ ID NO 1810
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1810

cgacagacgc ctgatctacg aatgactgga gt 32

<210> SEQ ID NO 1811
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1811

gatcactcca gtcattcgta gatca 25

<210> SEQ ID NO 1812
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1812

cgacagacgc ctgatctacg aaatcctagc ct 32

<210> SEQ ID NO 1813
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1813

gatcaggcta ggatttcgta gatca 25

<210> SEQ ID NO 1814
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1814

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cgacagacgc ctgatctacc ttagtagccg at 32

<210> SEQ ID NO 1815
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1815

gatcatcggc tactaaggta gatca 25

<210> SEQ ID NO 1816
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1816

cgacagacgc ctgatctacc tggtgtttac gt 32

<210> SEQ ID NO 1817
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1817

gatcacgtaa acaccaggta gatca 25

<210> SEQ ID NO 1818
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1818

cgacagacgc ctgatctacc tggcctcttt at 32

<210> SEQ ID NO 1819
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1819

gatcataaag aggccaggta gatca 25

<210> SEQ ID NO 1820
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1820

cgacagacgc ctgatctacc tggaaaggac tt 32

<210> SEQ ID NO 1821
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1821

gatcaagtcc tttccaggta gatca 25

<210> SEQ ID NO 1822
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1822

cgacagacgc ctgatctacc tgaggtgttt gt 32

<210> SEQ ID NO 1823
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1823

gatcacaaac acctcaggta gatca 25

<210> SEQ ID NO 1824
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1824

cgacagacgc ctgatctacc tattctgtgc gt 32

<210> SEQ ID NO 1825
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1825

gatcacgcac agaataggta gatca 25

<210> SEQ ID NO 1826
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1826

cgacagacgc ctgatctacc gttgttagtc ct 32

<210> SEQ ID NO 1827
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1827

gatcaggact aacaacggta gatca 25

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<210> SEQ ID NO 1828
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1828

cgacagacgc ctgatctacc gtgtatggtt gt 32

<210> SEQ ID NO 1829
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1829

gatcacaacc atacacggta gatca 25

<210> SEQ ID NO 1830
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1830

cgacagacgc ctgatctacc ggtgtaagag at 32

<210> SEQ ID NO 1831
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1831

gatcatctct tacaccggta gatca 25

<210> SEQ ID NO 1832
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1832

cgacagacgc ctgatctacc ggaaatggat gt 32

<210> SEQ ID NO 1833
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1833

gatcacatcc atttccggta gatca 25

<210> SEQ ID NO 1834
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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<400> SEQUENCE: 1834

cgacagacgc ctgatctacc gattgaggag at 32

<210> SEQ ID NO 1835
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1835

gatcatctcc tcaatcggta gatca 25

<210> SEQ ID NO 1836
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1836

cgacagacgc ctgatctacc atctgtcttc gt 32

<210> SEQ ID NO 1837
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1837

gatcacgaag acagatggta gatca 25

<210> SEQ ID NO 1838
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1838

cgacagacgc ctgatctacc agttgacttc ct 32

<210> SEQ ID NO 1839
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1839

gatcaggaag tcaactggta gatca 25

<210> SEQ ID NO 1840
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1840

cgacagacgc ctgatctacc actttcggat ct 32

<210> SEQ ID NO 1841

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1841

gatcagatcc gaaagtggta gatca 25

<210> SEQ ID NO 1842
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1842

cgacagacgc ctgatctacc aatagcggat ct 32

<210> SEQ ID NO 1843
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1843

gatcagatcc gctattggta gatca 25

<210> SEQ ID NO 1844
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1844

cgacagacgc ctgatctacc aaggtatgca gt 32

<210> SEQ ID NO 1845
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1845

gatcactgca taccttggta gatca 25

<210> SEQ ID NO 1846
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1846

cgacagacgc ctgatctacc aaatagctcc gt 32

<210> SEQ ID NO 1847
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1847

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gatcacggag ctatttggta gatca 25

<210> SEQ ID NO 1848
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1848

cgacagacgc ctgatctaca tttgacctcc gt 32

<210> SEQ ID NO 1849
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1849

gatcacggag gtcaaatgta gatca 25

<210> SEQ ID NO 1850
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1850

cgacagacgc ctgatctaca tgttcctctc gt 32

<210> SEQ ID NO 1851
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1851

gatcacgaga ggaacatgta gatca 25

<210> SEQ ID NO 1852
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1852

cgacagacgc ctgatctaca tgtgtggagt ct 32

<210> SEQ ID NO 1853
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1853

gatcagactc cacacatgta gatca 25

<210> SEQ ID NO 1854
<211> LENGTH: 32
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1854

cgacagacgc ctgatctaca tacctagccg at 32

<210> SEQ ID NO 1855
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1855

gatcatcggc taggtatgta gatca 25

<210> SEQ ID NO 1856
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1856

cgacagacgc ctgatctaca gttcgttgag gt 32

<210> SEQ ID NO 1857
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1857

gatcacctca acgaactgta gatca 25

<210> SEQ ID NO 1858
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1858

cgacagacgc ctgatctaca ggaattgagg ct 32

<210> SEQ ID NO 1859
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1859

gatcagcctc aattcctgta gatca 25

<210> SEQ ID NO 1860
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1860

cgacagacgc ctgatctaca gaagttgagc ct 32

<210> SEQ ID NO 1861
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1861

gatcaggctc aacttctgta gatca 25

<210> SEQ ID NO 1862
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1862

cgacagacgc ctgatctaca cctaatgacc gt 32

<210> SEQ ID NO 1863
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1863

gatcacggtc attaggtgta gatca 25

<210> SEQ ID NO 1864
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1864

cgacagacgc ctgatctaca ataggtgctc gt 32

<210> SEQ ID NO 1865
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1865

gatcacgagc acctattgta gatca 25

<210> SEQ ID NO 1866
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1866

cgacagacgc ctgatctaca acgataggct ct 32

<210> SEQ ID NO 1867
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1867

gatcagagcc tatcgttgta gatca 25

<210> SEQ ID NO 1868
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1868

cgacagacgc ctgatctaca acaggtcttc ct 32

<210> SEQ ID NO 1869
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1869

gatcaggaag acctgttgta gatca 25

<210> SEQ ID NO 1870
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1870

cgacagacgc ctgatctaat tggtctcgtg gt 32

<210> SEQ ID NO 1871
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1871

gatcaccacg agaccaatta gatca 25

<210> SEQ ID NO 1872
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1872

cgacagacgc ctgatctaat tctgctctcg gt 32

<210> SEQ ID NO 1873
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1873

gatcaccgag agcagaatta gatca 25

<210> SEQ ID NO 1874
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1874

cgacagacgc ctgatctaat tcgaccacca gt 32

<210> SEQ ID NO 1875
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1875

gatcactggt ggtcgaatta gatca 25

<210> SEQ ID NO 1876
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1876

cgacagacgc ctgatctaat tcacctctgg ct 32

<210> SEQ ID NO 1877
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1877

gatcagccag aggtgaatta gatca 25

<210> SEQ ID NO 1878
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1878

cgacagacgc ctgatctaat tagctggacg gt 32

<210> SEQ ID NO 1879
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1879

gatcaccgtc cagctaatta gatca 25

<210> SEQ ID NO 1880
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1880

cgacagacgc ctgatctaat gtcctggttg gt 32

<210> SEQ ID NO 1881
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1881

gatcaccaac caggacatta gatca 25

<210> SEQ ID NO 1882
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1882

cgacagacgc ctgatctaat ggagtcaagg ct 32

<210> SEQ ID NO 1883
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1883

gatcagcctt gactccatta gatca 25

<210> SEQ ID NO 1884
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1884

cgacagacgc ctgatctaat gatacggcag gt 32

<210> SEQ ID NO 1885
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1885

gatcacctgc cgtatcatta gatca 25

<210> SEQ ID NO 1886
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1886

cgacagacgc ctgatctaat ctatccacgg ct 32

<210> SEQ ID NO 1887
<211> LENGTH: 25

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1887

gatcagccgt ggatagatta gatca 25

<210> SEQ ID NO 1888
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1888

cgacagacgc ctgatctaat ctaccttgcc gt 32

<210> SEQ ID NO 1889
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1889

gatcacggca aggtagatta gatca 25

<210> SEQ ID NO 1890
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1890

cgacagacgc ctgatctaat cgaaggtagg ct 32

<210> SEQ ID NO 1891
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1891

gatcagccta ccttcgatta gatca 25

<210> SEQ ID NO 1892
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1892

cgacagacgc ctgatctaat ccttgcctct gt 32

<210> SEQ ID NO 1893
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1893

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gatcacagag gcaaggatta gatca 25

<210> SEQ ID NO 1894
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1894

cgacagacgc ctgatctaat ccgtcttgtc ct 32

<210> SEQ ID NO 1895
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1895

gatcaggaca agacggatta gatca 25

<210> SEQ ID NO 1896
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1896

cgacagacgc ctgatctaat cactgtctcc gt 32

<210> SEQ ID NO 1897
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1897

gatcacggag acagtgatta gatca 25

<210> SEQ ID NO 1898
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1898

cgacagacgc ctgatctaat attcggaggc gt 32

<210> SEQ ID NO 1899
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1899

gatcacgcct ccgaatatta gatca 25

<210> SEQ ID NO 1900
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1900

cgacagacgc ctgatctaat attcgcctcc gt 32

<210> SEQ ID NO 1901
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1901

gatcacggag gcgaatatta gatca 25

<210> SEQ ID NO 1902
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1902

cgacagacgc ctgatctaat atgccgaggt gt 32

<210> SEQ ID NO 1903
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1903

gatcacacct cggcatatta gatca 25

<210> SEQ ID NO 1904
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1904

cgacagacgc ctgatctaat agttggctcg gt 32

<210> SEQ ID NO 1905
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1905

gatcaccgag ccaactatta gatca 25

<210> SEQ ID NO 1906
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1906

cgacagacgc ctgatctaat accacctgac gt 32

<210> SEQ ID NO 1907
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1907

gatcacgtca ggtggtatta gatca 25

<210> SEQ ID NO 1908
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1908

cgacagacgc ctgatctaag ttggtgtcct gt 32

<210> SEQ ID NO 1909
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1909

gatcacagga caccaactta gatca 25

<210> SEQ ID NO 1910
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1910

cgacagacgc ctgatctaag ttgctcctgt ct 32

<210> SEQ ID NO 1911
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1911

gatcagacag gagcaactta gatca 25

<210> SEQ ID NO 1912
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1912

cgacagacgc ctgatctaag ttcggttagg ct 32

<210> SEQ ID NO 1913
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1913

gatcagccta accgaactta gatca 25

<210> SEQ ID NO 1914
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1914

cgacagacgc ctgatctaag ttcctcggtt gt 32

<210> SEQ ID NO 1915
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1915

gatcacaacc gaggaactta gatca 25

<210> SEQ ID NO 1916
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1916

cgacagacgc ctgatctaag tgtagaagcc gt 32

<210> SEQ ID NO 1917
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1917

gatcacggct tctacactta gatca 25

<210> SEQ ID NO 1918
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1918

cgacagacgc ctgatctaag tacatcaggc gt 32

<210> SEQ ID NO 1919
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1919

gatcacgcct gatgtactta gatca 25

<210> SEQ ID NO 1920

<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1920

cgacagacgc ctgatctaag gttgcttctg gt 32

<210> SEQ ID NO 1921
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1921

gatcaccaga agcaacctta gatca 25

<210> SEQ ID NO 1922
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1922

cgacagacgc ctgatctaag gttctctcac gt 32

<210> SEQ ID NO 1923
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1923

gatcacgtga gagaacctta gatca 25

<210> SEQ ID NO 1924
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1924

cgacagacgc ctgatctaag gcctttacca ct 32

<210> SEQ ID NO 1925
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1925

gatcagtggt aaaggcctta gatca 25

<210> SEQ ID NO 1926
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1926

cgacagacgc ctgatctaag gatctttcgg ct 32

<210> SEQ ID NO 1927
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1928

cgacagacgc ctgatctaag gataactcgg ct 32

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<400> SEQUENCE: 1929

gatcagccga gttatcctta gatca 25

<210> SEQ ID NO 1930
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1930

cgacagacgc ctgatctaag gaatactggc gt 32

<210> SEQ ID NO 1931
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<212> TYPE: DNA
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<400> SEQUENCE: 1931

gatcacgcca gtattcctta gatca 25

<210> SEQ ID NO 1932
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<212> TYPE: DNA
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<400> SEQUENCE: 1932

cgacagacgc ctgatctaac tttccggtct ct 32

<210> SEQ ID NO 1933
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1933

gatcagagac cggaaagtta gatca 25

<210> SEQ ID NO 1934
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1934

cgacagacgc ctgatctaac ttagagtggc gt 32

<210> SEQ ID NO 1935
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 1935

gatcacgcca ctctaagtta gatca 25

<210> SEQ ID NO 1936
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<212> TYPE: DNA
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<400> SEQUENCE: 1936

cgacagacgc ctgatctaac gtcttctcag gt 32

<210> SEQ ID NO 1937
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<400> SEQUENCE: 1937

gatcacctga gaagacgtta gatca 25

<210> SEQ ID NO 1938
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 1938

cgacagacgc ctgatctaac gtatggagag ct 32

<210> SEQ ID NO 1939
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<212> TYPE: DNA
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<400> SEQUENCE: 1939

gatcagctct ccatacgtta gatca 25

<210> SEQ ID NO 1940
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<212> TYPE: DNA
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<400> SEQUENCE: 1940

cgacagacgc ctgatctaac gaactcacct gt 32

<210> SEQ ID NO 1941
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<400> SEQUENCE: 1942

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<210> SEQ ID NO 1943
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<400> SEQUENCE: 1943

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<210> SEQ ID NO 1944
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<400> SEQUENCE: 1944

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<210> SEQ ID NO 1945
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<400> SEQUENCE: 1945

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<210> SEQ ID NO 1946
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 1946

cgacagacgc ctgatctaaa ttcggagagg ct 32

<210> SEQ ID NO 1947
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 1947

gatcagcctc tccgaattta gatca 25

<210> SEQ ID NO 1948
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1948

cgacagacgc ctgatctaaa tgacctccac gt 32

<210> SEQ ID NO 1949
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1949

gatcacgtgg aggtcattta gatca 25

<210> SEQ ID NO 1950
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<212> TYPE: DNA
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<400> SEQUENCE: 1950

cgacagacgc ctgatctaaa tcaggctcca ct 32

<210> SEQ ID NO 1951
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1951

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<210> SEQ ID NO 1952
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1952

cgacagacgc ctgatctaaa gttccagctc ct 32

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<210> SEQ ID NO 1953
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1953

gatcaggagc tggaacttta gatca 25

<210> SEQ ID NO 1954
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<212> TYPE: DNA
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<400> SEQUENCE: 1954

cgacagacgc ctgatctaaa gtaacctcgc ct 32

<210> SEQ ID NO 1955
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1955

gatcaggcga ggttacttta gatca 25

<210> SEQ ID NO 1956
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<212> TYPE: DNA
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<400> SEQUENCE: 1956

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<210> SEQ ID NO 1957
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<212> TYPE: DNA
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<400> SEQUENCE: 1957

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<210> SEQ ID NO 1958
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<400> SEQUENCE: 1958

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<210> SEQ ID NO 1959
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1959

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<210> SEQ ID NO 1960
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<212> TYPE: DNA
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<400> SEQUENCE: 1960

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<210> SEQ ID NO 1961
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<212> TYPE: DNA
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<400> SEQUENCE: 1961

gatcagaggt gtccagttta gatca 25

<210> SEQ ID NO 1962
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1962

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<210> SEQ ID NO 1963
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1963

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<210> SEQ ID NO 1964
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1964

tcgatggttt ggcgcgccgg tagtttgaac catccat 37

<210> SEQ ID NO 1965
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1965

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<210> SEQ ID NO 1966
<211> LENGTH: 18

<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 1966

tcgatggttt ggcgcgcc 18

<210> SEQ ID NO 1967
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<212> TYPE: DNA
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<400> SEQUENCE: 1967

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<210> SEQ ID NO 1968
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<400> SEQUENCE: 1968

gctagggcta atatc 15

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<400> SEQUENCE: 1969

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<210> SEQ ID NO 1970
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1970

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1971

gccatttaca aactaggtat t 21

<210> SEQ ID NO 1972
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<222> LOCATION: (28)..(41)

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

<400> SEQUENCE: 1972

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<210> SEQ ID NO 1973
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: synthetic oligonucleotide
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<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(19)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 1973

gatcannnnn nnnnnnnnna gatcaggcgt ctgtcgtgct cagtaa 46

<210> SEQ ID NO 1974
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide
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<222> LOCATION: (18)..(31)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 1974

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<210> SEQ ID NO 1975
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide
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<222> LOCATION: (6)..(19)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 1975

gatcannnnn nnnnnnnnna gatca 25

<210> SEQ ID NO 1976
<211> LENGTH: 103
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<222> LOCATION: (7)..(20)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
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<222> LOCATION: (27)..(77)
<223> OTHER INFORMATION: n is a, c, g, or t
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<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 1976

tgatctnnnn nnnnnnnnnn tgatccnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60

nnnnnnnnnn nnnnnnngga tcannnnnnn nnnnnnnaga tca 103

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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

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aaggccttca cgacagacgc ctgat 25

<210> SEQ ID NO 1978
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<222> LOCATION: (18)..(31)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 1978

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<210> SEQ ID NO 1979
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(19)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 1979

ctagannnnn nnnnnnnnna ctag 24

We claim:

1. A method for counting n wherein n is a number of molecules of a first target molecule that are present in a sample comprising: (a) attaching by a species-independent manner to each occurrence of the first target molecule a label from a set of diverse labels, wherein the set comprises m different labels, thereby generating for each occurrence of the first target molecule, a new molecule that comprises a copy of the first target molecule and a label, wherein more than 90% of the new molecules have a label that is different from the labels on the other new molecules; (b) detecting each new molecule by detecting each label present on the new molecule; and (c) counting a number of new molecules, thereby counting the number of molecules of the first target molecule in the sample.

2. The method of claim **1** wherein a ratio of m to n is greater than 50.

3. The method of claim **1** wherein a ratio of m to n is greater than 100.

4. The method of claim **1** wherein a ratio of m to n is greater than 500.

5. The method of claim **1** wherein a ratio of m to n is greater than 1000.

6. A method comprising:

(a) combining a mixture comprising at least two distinct target nucleic acid molecules with a pool of nucleic acid label-tags, wherein the pool of nucleic acid label-tags comprises a plurality of nucleic acid label-tags with different sequences;

(b) attaching at least two nucleic acid label-tags from the pool of nucleic acid label-tags to the at least two distinct target nucleic acid molecules to obtain at least two label-tag-target nucleic acid molecules, wherein the distinct target nucleic acid molecules have different sequences from one another;

(c) amplifying at least a portion of the label-tag-target nucleic acid molecules, wherein an amplified portion of the label-tag-target nucleic acid molecules comprises at least a portion of said target nucleic acid molecule; and

(d) detecting an amplified product of step (c).

7. The method of claim **6**, wherein the attaching is stochastic.

8. The method of claim **6**, wherein distinct target nucleic acid molecules are known targets.

9. The method of claim **6**, wherein the nucleic acid label-tags are designed to bind to the distinct target nucleic acid molecules.

10. The method of claim **6**, wherein an identity of the distinct target nucleic acid molecules is determined after the detecting step.

11. The method of claim **6**, wherein the nucleic acid label-tags may bind to any of the distinct target nucleic acid molecules.

12. The method of claim 6, wherein the attaching occurs on both ends of at least one of the two distinct target nucleic acid molecules.

13. The method of claim 6, wherein the detecting comprises hybridizing at least a portion of the label-tag-target nucleic acid molecules to a solid or semi-solid substrate.

14. The method of claim 6, wherein the detecting comprises hybridizing at least a portion of the target nucleic acid molecule to a solid or semi-solid substrate.

15. The method of claim 6, wherein the detecting comprises hybridizing at least a portion of the nucleic acid label-tag to a solid or semi-solid substrate.

16. The method of claim 1, wherein the attaching of step (a) is stochastic.

17. The method of claim 1, wherein the attaching of step (a) comprises ligation of the label to an occurrence of the first target molecule.

18. The method of claim 1, wherein the attaching of step (a) comprises reverse transcription of an occurrence of the first target molecule.

19. The method of claim 1, wherein the attaching of step (a) comprises use of the label for primer extension.

20. The method of claim 1, wherein the first target molecule is a nucleic acid.

21. The method of claim 1, wherein the first target molecule is RNA.

22. The method of claim 21, wherein the RNA is mRNA.

23. The method of claim 22, wherein the labels comprise an oligodT sequence.

24. The method of claim 23, wherein the labels are attached to the molecules by hybridization of the oligodT sequence of the label to a polyA tail of the mRNA.

25. The method of claim 1, wherein the first target molecule is DNA.

26. The method of claim 1, further comprising fragmenting the occurrences of the first target molecule.

27. The method of claim 26, wherein the occurrences of the first target molecule are fragmented prior to the attaching of step (a).

28. The method of claim 26, wherein fragmenting the occurrences of the first target molecule comprises restriction enzyme digestion of the occurrences of the first target molecule.

29. The method of claim 1, further comprising amplifying the new molecules.

30. The method of claim 29, wherein amplifying comprises PCR.

31. The method of claim 29, wherein amplifying comprises rolling circle amplification.

32. The method of claim 1, wherein detecting the new molecule comprises detecting at least a portion of the copy of the first target molecule.

33. The method of claim 1, wherein detecting the new molecule comprises detecting a junction formed between the label and the copy of the first target molecule.

34. The method of claim 1, wherein detecting the new molecule comprises detecting at least a portion of the copy of the first target molecule and at least a portion of the label.

35. The method of claim 1, wherein detecting the new molecule comprises hybridization of the new molecule to a solid support.

36. The method of claim 35, wherein the solid support is an array.

37. The method of claim 35, wherein the solid support comprises a plurality of probes.

38. The method of claim 37, wherein a probe of the plurality of probes comprises a sequence that is complementary to at least a portion of the copy of the first target molecule.

39. The method of claim 37, wherein a probe of the plurality of probes comprises a sequence that is complementary to at least a portion of the label.

40. The method of claim 37, wherein a probe of the plurality of probes comprises a sequence that is complementary to a junction formed between the label and the copy of the first target molecule.

41. The method of claim 37, wherein a probe of the plurality of probes comprises a sequence that is complementary to at least a portion of the label and at least a portion of the copy of the first target molecule.

42. The method of claim 1, wherein the attaching of step (a) further comprises attaching labels to occurrences of one or more additional target molecules, wherein the first target molecule is different from the one or more additional target molecules.

43. The method of claim 42, wherein the counting of step (c) further comprises counting a number of new molecules of the one or more additional target molecules, thereby counting a number of molecules of the one or more additional target molecules.

44. The method of claim 42, wherein the one or more additional target molecules comprise 2 or more target molecules.

45. The method of claim 42, wherein the one or more additional target molecules comprise 5 or more target molecules.

46. The method of claim 42, wherein the one or more additional target molecules comprise 10 or more target molecules.

47. The method of claim 42, wherein m different labels in the set of labels is constant.

48. The method of claim 42, wherein the set of labels comprises multiple copies of the same label.

49. The method of claim 48, wherein copies of a first label may attach to the occurrences of the first target molecule and the occurrences of the one or more additional target molecules.

50. The method of claim 1, wherein the attaching of step (a) occurs on one end of an occurrence of the first target molecule.

51. The method of claim 1, wherein the attaching of step (a) occurs on both ends of an occurrence of the first target molecule.

52. The method of claim 1, wherein the label comprises an adaptor.

53. The method of claim 1, wherein the label comprises a universal primer.

54. The method of claim 42, wherein the label does not comprise a sequence that is specific to one species of target molecules.

55. The method of claim 1, wherein the copy of the first target molecule is an occurrence of the first target molecule.

56. The method of claim 1, wherein the copy of the first target molecule is a copy of an occurrence of the first target molecule.

57. The method of claim 1, wherein the copy of the first target molecule is a complement or reverse complement of an occurrence of the first target molecule.

58. The method of claim 6, wherein the attaching of step (b) occurs in a species-independent manner.

59. The method of claim 6, wherein the attaching of step (b) occurs in a non-specific manner.

60. The method of claim 6, wherein the pool of nucleic acid label-tags comprises multiple copies of a nucleic acid label-tag.

61. The method of claim 60, wherein the copies of the nucleic acid label-tag may attach to copies of a first target nucleic molecule and copies of a second target nucleic acid molecule.

62. The method of claim 6, wherein the attaching of step (b) comprises ligation of the label-tags to copies of the two distinct target nucleic acid molecules.

63. The method of claim 62, wherein the copies of the two distinct target nucleic acid molecules are occurrences of the two distinct target nucleic acids molecules.

64. The method of claim 62, wherein the copies of the two distinct target nucleic acid molecules are copies of occurrences of the two distinct target nucleic acids molecules.

65. The method of claim 62, wherein the copies of the two distinct target nucleic acid molecules are complements or reverse complements of occurrences of the two distinct target nucleic acids molecules.

66. The method of claim 6, wherein the attaching of step (b) comprises reverse transcription of the two distinct target nucleic acid molecules.

67. The method of claim 6, wherein the two distinct target nucleic acid molecules are RNA.

68. The method of claim 67, wherein the RNA is mRNA.

69. The method of claim 68, wherein the label-tags comprise an oligodT sequence.

70. The method of claim 69, wherein the label-tags are attached to the two distinct target nucleic acid molecules by hybridization of the oligodT sequence of the label-tag to a polyA tail of the mRNA.

71. The method of claim 6, wherein the two distinct target nucleic acid molecules are DNA.

72. The method of claim 6, further comprising fragmenting the two distinct target nucleic acid molecules.

73. The method of claim 72, wherein the two distinct target nucleic acid molecules are fragmented prior to the attaching of step (b).

74. The method of claim 72, wherein fragmenting the two distinct target nucleic acid molecules comprises restriction enzyme digestion of the two distinct target nucleic acid molecules.

75. The method of claim 6, wherein amplifying comprises PCR.

76. The method of claim 6, wherein amplifying comprises rolling circle amplification.

77. The method of claim 6, wherein detecting the amplified product comprises detecting at least a portion of the distinct target nucleic acid molecule.

78. The method of claim 6, wherein detecting the amplified product comprises detecting at least a portion of the label-tag.

79. The method of claim 6, wherein detecting the amplified product comprises detecting a junction formed between the label-tag and the distinct target nucleic acid molecule.

80. The method of claim 6, wherein detecting the amplified product comprises detecting at least a portion of the distinct target nucleic acid molecule and at least a portion of the label.

81. The method of claim 6, wherein detecting the amplified product comprises hybridization of the amplified product to a solid support.

82. The method of claim 81, wherein the solid support is an array.

83. The method of claim 81, wherein the solid support comprises a plurality of probes.

84. The method of claim 83, wherein a probe of the plurality of probes comprises a sequence that is complementary to at least a portion of the distinct target nucleic acid molecule.

85. The method of claim 83, wherein a probe of the plurality of probes comprises a sequence that is complementary to at least a portion of the label-tag.

86. The method of claim 83, wherein a probe of the plurality of probes comprises a sequence that is complementary to a junction formed between the label-tag and the distinct target nucleic acid molecule.

87. The method of claim 83, wherein a probe of the plurality of probes comprises a sequence that is complementary to at least a portion of the label-tag and at least a portion of the distinct target nucleic acid molecule.

88. The method of claim 6, further comprising determining a count of the at least two distinct target nucleic acid molecules based on the detection of the amplified product.

89. The method of claim 88, wherein determining the count of the at least two distinct target nucleic acid molecules comprises determining the count of 5 or more distinct target nucleic acid molecules.

90. The method of claim 88, wherein determining the count of at least two distinct target nucleic acid molecules comprises determining the count of 10 or more distinct target molecules.

91. The method of claim 6, wherein the attaching of step (b) occurs on one end of the distinct target nucleic acid molecules.

92. The method of claim 6, wherein the attaching of step (b) occurs on both ends of the distinct target nucleic acid molecules.

93. The method of claim 6, wherein the label-tag comprises an adaptor.

94. The method of claim 6, wherein the label-tag comprises a universal primer.

95. The method of claim 6, wherein the label-tag does not comprise a sequence that is specific to one species of at least two distinct target nucleic acid molecules.

* * * * *