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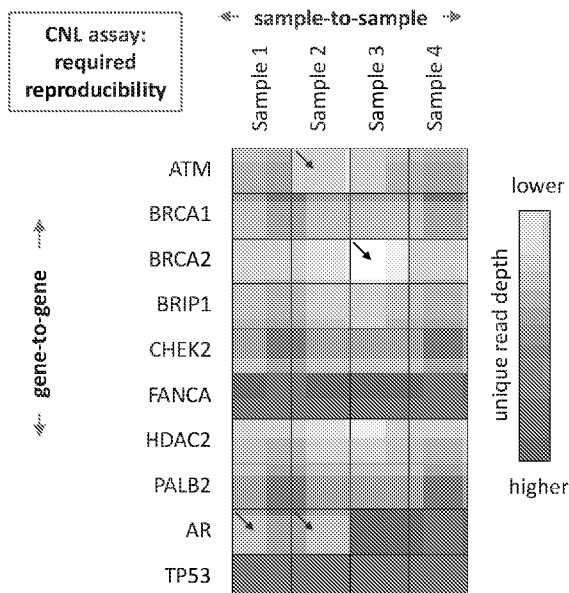
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FIG. 1



(57) Abstract: The present invention includes compositions and methods useful for the detection of a mutational change, SNP, translocation, inversion, deletion, change in copy number, or other genetic variation within a sample of cellular genomic DNA or cell-free DNA (cfDNA). In some embodiments, the compositions and methods of the present invention provide an extremely high level of resolution that is particularly useful in detecting copy number variations in a small fraction of the total cfDNA from a biological sample (e.g., blood).



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METHODS FOR THE DETECTION OF GENOMIC COPY CHANGES IN DNA SAMPLES

REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Patent Application No. 62/379,593, filed August 25, 2016, and U.S. Provisional Patent Application No. 62/481,538, filed April 4, 2017, each of which are incorporated herein by reference in their entireties.

STATEMENT REGARDING SEQUENCE LISTING

[0002] The sequence listing associated with this application is provided in text format in lieu of a paper copy, and is hereby incorporated by reference into the specification. The name of the text file containing the sequence listing is CLFK_005_02WO_ST25. The text file is 2,238 KB, was created on August 24, 2017, and is being submitted electronically via EFS-Web.

TECHNICAL FIELD

[0003] The invention relates generally to compositions and methods for the quantitative genetic analysis of biological samples, *e.g.*, direct tissue biopsies or peripheral blood. In particular, the present invention relates to methods for detection of target-specific copy number change, as well as genetic characterization and analysis, of biological samples.

BACKGROUND

[0004] It is becoming increasingly clear that most, if not all, of the most common human cancers are diseases of the human genome. It is thought that somatic mutations accumulate during an individual's lifetime, some of which increase the probability that the cell in which they are harbored can develop into a tumor. With just the wrong combination of accumulated mutational events, a precancerous growth loses constraints that keep uncontrolled proliferation in check and the resulting cell mass becomes a cancer. The constellations of mutations that are necessary and sufficient to cause cancer are often collectively referred to as "driver mutations." One of the themes that have emerged from recent and intensive molecular analysis is that cancer, once thought of as a single, tissue-specific disease, is in fact a group of related diseases, each with a unique molecular

pathology. The human genome project laid the groundwork for genome-wide analysis of cancers.

[0005] Changes in gene copy number are a fundamental driver of biological diversity. In the context of evolution, duplication of genes and divergence of function is a well-recognized driver of species diversity. In the context of human disease, gene loss and gene amplification within somatic cells are hallmarks of diseased tissues such as cancer. Certain therapeutic agents act specifically on cells with these genomic gain and/or loss mutations, however, the identification of these copy number variations is difficult because often such mutations are only present within the DNA of diseased or cancerous cells and are not found in other cells of the body. While the diseased tissue or cells is the major source of the mutated DNA, acquiring DNA through a biopsy is invasive, risky and often not possible. The observation that dying tumor or cancer cells release small pieces of their DNA into the bloodstream, termed cell free DNA or circulating DNA has allowed for the development of genetic tests that can be performed with less invasive techniques, such as a blood sample. However, only small amounts of DNA can be obtained from isolating cell free DNA from a sample, and only a portion of the total DNA will carry the mutation associated with the disease. For example, in the context of cancer genomics, diagnostically significant tumor mutations are often only found at minor allele frequencies that are significantly less than 50%. This is in contrast to conventional SNP genotyping where allele frequencies are generally ~100%, 50% or 0%.

[0006] Thus there is a need for genomic techniques capable of detecting genetic copy number changes in specific target loci.

BRIEF SUMMARY

[0007] Methods of detecting rare mutations in cfDNA have been previously described in International PCT Publication No. WO 2016/028316. However, these techniques still lack the requisite sensitivity to detect the rarest copy number losses at very minor allele frequencies. Provided herein are compositions and methods for detection of target-specific copy number change that are applicable to several sample types, including direct tissue biopsies, peripheral blood, and in particular cfDNA. The compositions and methods described herein are sensitive enough to detect changes in copy number that are present only a tiny fraction of the total DNA.

[0008] The present invention includes, *inter alia*, compositions and methods that are useful for the detection of a mutational change, SNP, translocation, inversion, deletion, change in copy number, or other genetic variation within a sample of cellular genomic DNA (*e.g.*, from a tissue biopsy sample) or cfDNA (*e.g.*, from a blood sample). In particular, the compositions and methods of the present invention provide an extremely high level of resolution that is particularly useful in detecting copy number variations in a small fraction of the total cfDNA from a biological sample (*e.g.*, blood).

[0009] Particular embodiments are drawn to a method for performing a genetic analysis on a DNA target region from a test sample comprising: (a) generating a genomic DNA library comprising a plurality of DNA library fragments, wherein each of the DNA library fragments comprises a genomic DNA fragment from the test sample and an adaptor; (b) contacting the genomic DNA library with a plurality of capture probes that specifically bind to a DNA target region, thereby forming complexes between the capture probes and DNA library fragments comprising the DNA target region; and (c) performing a quantitative genetic analysis of the genomic DNA fragments comprising the DNA target region; wherein the adaptor is a DNA polynucleotide that comprises: an amplification region, a sample tag region, and an anchor region; wherein the amplification region comprises a polynucleotide sequence capable of serving as a primer recognition site for PCR amplification; wherein the sample tag comprises a polynucleotide sequence that encodes an identity of the unique library DNA fragment and encodes an identity of the test sample; wherein the anchor region comprises a polynucleotide sequence that encodes the identity of the test sample and wherein the anchor region is capable of attaching to the genomic DNA fragment; and wherein the genetic analysis is performed to detect a genetic change indicative of a disease state.

[0010] In some embodiments, the genetic change indicative of a disease state is selected from a single nucleotide variant (SNV), an insertion less than 40 nucleotides in length, a deletion of a DNA region less than 40 nucleotides in length, and/or a change in copy number. In particular embodiments, the genetic change indicative of a disease state is a change in copy number. In some embodiments, the test sample is a tissue biopsy. In various embodiments, the tissue biopsy is taken from a tumor or a tissue suspected of being a tumor. In certain embodiments, the genomic DNA is cell free DNA (cfDNA) or cellular DNA. In particular embodiments, the genomic DNA is cfDNA is isolated from the test sample; and wherein the test sample is a biological sample selected from the group consisting of: amniotic

fluid, blood, plasma, serum, semen, lymphatic fluid, cerebral spinal fluid, ocular fluid, urine, saliva, stool, mucous, and sweat.

[0011] In certain embodiments, the genomic DNA fragments are obtained the steps comprising; (i) isolating cellular DNA from the test sample; and (ii) fragmenting the cellular DNA to obtain the genomic DNA fragments. In particular embodiments, step (ii) is performed by contacting the cellular DNA with at least one digestion enzyme. In some embodiments, step (ii) is performed by applying mechanical stress to the cellular DNA. In certain embodiments, the mechanical stress is applied by sonicating the cellular DNA.

[0012] In particular embodiments, the sample tag further comprises a unique molecule identifier (UMI) that facilitates the identification of the unique genomic DNA fragment.

[0013] In some embodiments, the amplification region is between 10 and 50 nucleotides in length. In particular embodiments, the amplification region is between 20 and 30 nucleotides in length. In certain embodiments, the amplification region is 25 nucleotides in length.

[0014] In some embodiments, the sample tag is between 5 and 50 nucleotides in length. In particular embodiments, the sample tag is between 5 and 15 nucleotides in length. In certain embodiments, the sample tag is 8 nucleotides in length. In some embodiments, the UMI multiplier is adjacent to or contained within the sample tag region.

[0015] In certain embodiments, the UMI multiplier is between 1 and 5 nucleotides in length. In particular embodiments, the UMI multiplier is 3 nucleotides in length, and comprises one of 64 possible nucleotide sequences.

[0016] In some embodiments, the anchor region is between 1 and 50 nucleotides in length. In particular embodiments, the anchor region is between 5 and 25 nucleotides in length. In certain embodiments, the anchor region is 10 nucleotides in length.

[0017] Particular embodiments of the present invention are drawn to methods where the step of (a) generating a genomic DNA library comprising a plurality of DNA library fragments, comprises attaching the genomic DNA fragments to a plurality of adaptors. In certain embodiments, the genomic DNA fragments are end repaired prior to attaching the genomic DNA fragments with a plurality of adaptors. In particular embodiments, the amplification regions of each adaptor of the plurality of adaptors comprises an identical nucleotide sequence.

[0018] In certain embodiments, the sample tag region of each adaptor of the plurality of adaptors comprise one of between 2 and 1,000 nucleotide sequences. In particular embodiments, the sample tag region of each adaptor of the plurality of adaptors comprise one of between 50 and 500 nucleotide sequences. In various embodiments, the sample tag region of each adaptor of the plurality of adaptors comprises one of between 100 and 400 nucleotide sequences. In some embodiments, the sample tag region of each adaptor of the plurality of adaptors comprises one of between 200 and 300 nucleotide sequences. In certain embodiments, the sample tag region of each adaptor of the plurality of adaptors is 8 nucleotides in length. In some embodiments, each sequence of the nucleotide sequences are discrete from any other sequence of the 240 nucleotide sequences by Hamming distance of at least two.

[0019] In particular embodiments, each of the plurality of adaptors comprises a UMI multiplier that is adjacent to or contained within the sample tag region. In some embodiments, each of the plurality of adaptors comprises a UMI multiplier that is adjacent to the sample tag region. In certain embodiments, the UMI multiplier of each adaptor of the plurality of adaptors is between 1 and 5 nucleotides in length. In some embodiments, the UMI multiplier of each adaptor of the plurality of adaptors is three nucleotides in length.

[0020] In particular embodiments, the anchor tag region of each adaptor of the plurality of adaptors comprises one of four nucleotide sequences, and each sample region of a given sequence is paired to only one of the four anchor regions of a given sequence.

[0021] In some embodiments, the amplification regions of each adaptor of the plurality of adaptors comprises an identical nucleotide sequence; the sample tag region of each adaptor of the plurality of adaptors is 8 nucleotides in length; the nucleotide sequence of each sample tag is discrete from any other nucleotide sequence of the sample tags of the plurality of adaptors by Hamming distance of at least two; each of the plurality of adaptors comprises a UMI multiplier that is adjacent to or contained within the sample tag region; the UMI multiplier of each adaptor of the plurality of adaptors is three nucleotides in length; and the UMI multiplier of each of the possible nucleotide sequences is paired to each sample tag region of the plurality of adaptors; the anchor tag region of each adaptor of the plurality of adaptors comprises one of four nucleotide sequences; and each sample region of a given sequence is paired to only one of the four anchor regions of a given sequence.

[0022] Particular embodiments of the present invention are drawn to a method where the step of attaching the genomic DNA fragments with a plurality of adaptors

comprises: (i) attaching an oligonucleotide comprising least a portion of an anchor region to each genomic DNA fragment, wherein the oligonucleotide comprising least a portion of an anchor region is a DNA duplex comprising a 5' phosphorylated attachment strand duplexed with a partner strand, wherein the partner strand is blocked from attachment by chemical modification at its 3' end, and wherein the attachment strand is attached to the genomic DNA fragment; (ii) contacting the genomic DNA fragments attached to the oligonucleotides comprising at least a portion of the anchor region with DNA oligonucleotides encoding full length adaptor sequences for each adaptor nucleotide sequence of the plurality of adaptors; and (iii) contacting the genomic DNA fragments and the DNA oligonucleotides encoding the full length adaptor sequence with T4 polynucleotide kinase, Taq DNA ligase and full-length Bst polymerase under conditions suitable for DNA ligation; thereby attaching the plurality of adaptors to the genomic DNA fragments. In some embodiments, the genomic DNA fragments are cfDNA. In certain embodiments, the DNA target region is analyzed for a change in copy number.

[0023] In particular embodiments, step (c) performing a quantitative genetic analysis of the genomic DNA fragments comprising the DNA target region comprises purification of the complexes formed between the capture probes and DNA library fragments comprising the DNA target region. In certain embodiments, step (c) comprises purification of the complexes formed between the capture probes and DNA library fragments comprising the DNA target region, performing primer extension and/or amplification of the DNA library fragments comprising the region of interest from the genomic DNA library. In some embodiments, step (c) comprises purification of the complexes formed between the capture probes and DNA library fragments comprising the DNA target region, performing primer extension and amplification of the DNA library fragments comprising the region of interest from the genomic DNA library. In certain embodiments, step (c) comprises DNA sequencing of the DNA library fragments comprising the DNA target region to generate a plurality of sequencing reads.

[0024] In some embodiments, the present invention is drawn to a method wherein the genomic analysis comprises determining a change of copy number in a DNA region of interest, and wherein step (c), performing a quantitative genetic analysis of the genomic DNA fragments comprising the DNA target region, comprises determining a copy number of the region of interest present in the genomic DNA library derived from the test sample, and comparing it to a copy number of the region of interest present in the genomic

DNA library derived from a reference sample, wherein the reference sample comprises a known copy number of the DNA target region.

[0025] In some embodiments, determining the copy number in the region of interest comprises DNA sequencing of the DNA library fragments comprising the DNA target region to generate a plurality of sequencing reads, wherein each sequencing read comprises a unique molecular identification element (UMIE). In some embodiments, the UMIE comprises sequencing information from the adaptor and at least a portion of the genomic DNA sequence. In some embodiments, sequencing reads comprising identical UMIEs are identified as a unique genomic sequence (UGS).

[0026] In some embodiments, methods of determining the copy number further comprise determining a raw genomic depth (RGD) for each of the capture probes contacted with the genomic DNA library. In some embodiments, determining the RGD comprises determining the average number of UGSs associated with each capture probe sequence within a group of sample replicates. In some embodiments, capture probes associated with a highly variable number of UGSs are identified as noisy probes and are removed from further calculations. In some embodiments, determining the RGD further comprises calculating an RGD for a sample, comprising calculating a numerical average of all RGDs for all capture probes in the sample. In some embodiments, the RGD values for noisy probes are not included in calculating an RGD for a sample.

[0027] In some embodiments, the RGDs for the capture probes are normalized across all samples in an experimental group by converting the RGD for each capture probe into a probe-specific, normalized read count comprising (i) multiplying each capture probe RGD in a sample by a normalization constant, wherein the normalization constant comprises any real number; and (ii) dividing the product of (i) by the RGD calculated for the corresponding sample; or (iii) dividing the product of (i) by an average RGD calculated from a subset of probes. In some embodiments, the subset of probes is a set of control probes.

[0028] In some embodiments, the probe-specific, normalized read counts are converted in to a copy number value comprising (i) multiplying the probe-specific, normalized read counts of probes directed to autosomal and/or X-linked regions by 2 in samples derived from females; (ii) multiplying the probe-specific, normalized read counts of probes directed to Y-linked and/or X-linked regions by 1 in samples derived from males; (iii) averaging the products of (i) and/or (ii) across all samples in an experiment; and (iv) dividing

the product of (i) and/or (ii) by the average of (iii). In some embodiments, the approximate copy number values for all probes that target a specific gene are averaged.

[0029] In some embodiments, the present invention is drawn to a method for highly sensitive detection of copy number gain and copy number loss comprising (i) determining an RGD for a capture probe; (ii) normalizing the RGD for the capture probe across all samples in an experimental group by converting the RGD for the capture probe into a probe-specific, normalized read count; (iii) calculating an approximate copy number value for each probe-specific, normalized read count; and (iv) averaging the approximate copy number values for all probes that target a specific gene.

[0030] In some embodiments, the present invention is drawn to a method for measuring chromosome stability comprising (i) designing and validating a set of one or more chromosomal stability probes, wherein the chromosomal stability probes are uniformly distributed across human chromosomes; (ii) performing targeted sequencing on patient samples using the one or more chromosomal stability probes; (iii) determining an approximate copy number value for each chromosomal probe; (iv) determining a genomic phenotype of a patient sample, wherein fluctuations in the copy number values for one or more chromosomal probes in the patient sample indicate genomic instability.

[0031] In some embodiments, the present invention is drawn to a method of treating a cancer in a subject in need thereof, wherein the subject has been identified as having a destabilized genome according to the method claim 62, wherein the method of treating the cancer comprises administering a pharmaceutically effective amount of a PARP inhibitor.

[0032] In some embodiments, the present invention is drawn to a method wherein the genomic analysis comprises determining a change of copy number in a DNA region of interest, and wherein step (c), performing a quantitative genetic analysis of the genomic DNA fragments comprising the DNA target region, comprises determining a copy number of the region of interest present in the genomic DNA library derived from the test sample, and comparing it to a copy number of the region of interest present in the genomic DNA library derived from a reference sample, wherein the reference sample comprises a known copy number of the DNA target region. In some embodiments, the region of interest is a gene or a portion of the gene. In particular embodiments, the gene is associated with a disease. In certain embodiments, the disease is a cancer. In various embodiments, the gene is BRCA2, ATM, BRCA1, BRIP1, CHEK2, FANCA, HDAC2, and/or PALB2.

[0033] Particular embodiments are drawn to a genomic DNA library comprising a plurality of DNA library fragments, wherein each of the DNA library fragments comprises an adaptor and a genomic DNA fragment; wherein the adaptor is a DNA polynucleotide that comprises: an amplification region, a sample tag region, and an anchor region; wherein the amplification region comprises a polynucleotide sequence capable of serving as a primer recognition site for PCR amplification; wherein the sample tag comprises a polynucleotide sequence that encodes an identity of the unique library DNA fragment and encodes an identity of the test sample; and wherein the anchor region comprises a polynucleotide sequence that encodes the identity of the test sample, and wherein the anchor region is capable of attaching to the genomic DNA fragment. In some embodiments, the sample tag further comprises a unique molecule identifier (UMI), wherein the UMI facilitates the identification of the unique genomic DNA fragment. In particular embodiments, the amplification region is between 10 and 50 nucleotides in length. In particular embodiments, the amplification region is 25 nucleotides in length. In particular embodiments, the sample tag is between 5 and 50 nucleotides in length. In certain embodiments, the sample tag is 8 nucleotides in length. In some embodiments, the UMI multiplier is adjacent to or contained within the sample tag region. In particular embodiments, the UMI multiplier is between 1 and 5 nucleotides in length. In certain embodiments, the anchor region is between 1 and 50 nucleotides in length. In some embodiments, the anchor region is 10 nucleotides in length. In particular embodiments, the amplification regions of each adaptor of the plurality of adaptors comprises an identical nucleotide sequence. In some embodiments, each nucleotide sequence of the sample tags are discrete from any other sequence of the nucleotide sequences of the sample by Hamming distance of at least two. In certain embodiments, each of the plurality of adaptors comprises a UMI multiplier that is adjacent to or contained within the sample tag region. In particular embodiments, each of the plurality of adaptors comprises a UMI multiplier that is adjacent to the sample tag region. In some embodiments, the anchor tag region of each adaptor of the plurality of adaptors comprises one of four nucleotide sequences, and wherein each sample region of a given sequence is paired to only one of the four anchor regions of a given sequence. In some embodiments, the genomic DNA fragment is cfDNA.

[0034] In certain embodiments, the amplification regions of each adaptor of the plurality of adaptors comprises an identical nucleotide sequence; the sample tag region of each adaptor of the plurality of adaptors is 8 nucleotides in length, the sample tag region of

each adaptor of the plurality of adaptors comprises a nucleotide sequence that is discrete from any other nucleotide sequence of the sample tags of the plurality of adaptors by Hamming distance of at least two, the each of the plurality of adaptors comprises a UMI multiplier that is adjacent to or contained within the sample tag region, the UMI multiplier of each adaptor of the plurality of adaptors is three nucleotides in length, and the UMI multiplier of each of the possible nucleotide sequences is paired to each of the sample tag regions of the plurality of adaptors, the anchor tag region of each adaptor of the plurality of adaptors comprises one of four nucleotide sequences, and each sample region of a given sequence is paired to only one of the four anchor regions of a given sequence. In some embodiments, the genomic DNA fragment is cfDNA.

[0035] Certain embodiments are drawn to a plurality of genomic DNA libraries, comprising more than one genomic library described herein. In some embodiments, the nucleic acid sequences of the sample tag regions of a genomic DNA library belonging to the plurality of genomic DNA libraries are different from the nucleic acid sequences of the sample tag regions of other genomic DNA libraries belonging to the plurality of genomic DNA libraries. In particular embodiments, the nucleic acid sequences of the amplification regions of a genomic DNA library belonging to the plurality of genomic DNA libraries are identical to the nucleic acid sequences of the amplification regions of other genomic DNA libraries belonging to the plurality of genomic DNA libraries.

[0036] Certain embodiments are drawn to a method for genetic analysis of a DNA target region of cell free DNA (cfDNA) comprising: (a) generating a DNA library as described herein; (b) contacting the cfDNA library with a plurality of capture probes that specifically bind to a DNA target region, thereby forming complexes between the capture probes and DNA library fragments comprising the DNA target region; and (c) performing a quantitative genetic analysis of the cfDNA fragments comprising the DNA target region; thereby performing genetic analysis of the DNA target region.

[0037] Certain embodiments are directed to a method of predicting, diagnosing, or monitoring a genetic disease in a subject comprising: (a) obtaining a test sample from the subject; (b) isolating genomic DNA from the test sample; (c) generating a DNA library comprising a plurality of DNA library fragments, wherein each of the DNA library fragments comprises a genomic DNA fragment from the test sample and an adaptor; (d) contacting the cfDNA library with a plurality of capture probes that specifically bind to a DNA target region, thereby forming complexes between the capture probes and DNA library

fragments comprising the DNA target region; and (e) performing a quantitative genetic analysis of one or more target genetic loci associated with the genetic disease in the cfDNA clone library, wherein the identification or detection of one or more genetic lesions in the one or more target genetic loci is prognostic for, diagnostic of, or monitors the progression of the genetic disease. In particular embodiments, the quantitative genetic analysis comprises DNA sequencing to generate a plurality of sequencing reads.

[0038] Particular embodiments are drawn to a set of adaptors that encode an identity of a unique genomic DNA fragment and an identity of a test sample, for use in generating a genomic DNA library, wherein each adaptor in said set of adaptors is a DNA polynucleotide that comprises: an amplification region, a sample tag region, and an anchor region; wherein the amplification region comprises a polynucleotide sequence capable of serving as a primer recognition site for PCR amplification; wherein the sample tag comprises a polynucleotide sequence that encodes the identity of the unique library DNA fragment and encodes the identity of the test sample; and wherein the anchor region comprises a polynucleotide sequence that encodes the identity of the test sample, and wherein the anchor region is capable of attaching to the genomic DNA fragment. In some embodiments, the sample tag further comprises a unique molecule identifier (UMI), wherein the UMI facilitates the identification of the unique genomic DNA fragment. In various embodiments, the amplification region is between 10 and 50 nucleotides in length. In certain embodiments, the amplification region is 25 nucleotides in length. In particular embodiments, the sample tag is between 5 and 50 nucleotides in length. In some embodiments, the sample tag is 8 nucleotides in length. In particular embodiments, the UMI multiplier is adjacent to or contained within the sample tag region. In some embodiments, the UMI multiplier is between 1 and 5 nucleotides in length. In particular embodiments, the anchor region is between 1 and 50 nucleotides in length. In some embodiments, the anchor region is 10 nucleotides in length. In certain embodiments, the amplification regions of each adaptor of the plurality of adaptors comprises an identical nucleotide sequence.

[0039] In some embodiments, each nucleotide sequence of the sample tags is discrete from any other nucleotide sequence of the sample tags of the set of adaptors by Hamming distance of at least two. In various embodiments, each of the plurality of adaptors comprises a UMI multiplier that is adjacent to or contained within the sample tag region. In particular embodiments, each of the plurality of adaptors comprises a UMI multiplier that is adjacent to the sample tag region.

[0040] In some embodiments, the anchor tag region of each adaptor of the plurality of adaptors comprises one of four nucleotide sequences, and wherein each sample region of a given sequence is paired to only one of the four anchor regions of a given sequence. The set of adaptors claim 75, wherein the amplification regions of each adaptor of the plurality of adaptors comprises an identical nucleotide sequence; wherein the sample tag region of each adaptor is 8 nucleotides in length, wherein each nucleotide sequence of the sample tags is discrete from any other nucleotide sequence of the sample tags of the set of adaptors by Hamming distance of at least two, wherein each of the plurality of adaptors comprises a UMI multiplier that is adjacent to or contained within the sample tag region, wherein the UMI multiplier of each adaptor of the plurality of adaptors is three nucleotides in length, wherein the UMI multiplier comprises one of 64 possible nucleotide sequences, and wherein the UMI multiplier of each of the 64 possible nucleotide sequences is paired to each of the sample tag region of the plurality of adaptors, wherein the anchor tag region of each adaptor of the plurality of adaptors comprises one of four nucleotide sequences, and wherein each sample region of a given sequence is paired to only one of the four anchor regions of a given sequence.

BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWINGS

[0041] FIG. 1 shows the framework of the copy number loss (CNL) assay. Each gene (rows) exhibits a characteristic unique read value that is represented here by a shade. Each sample (columns) is interrogated across the same panel of genes.

[0042] FIG. 2 shows a diagram illustrating the drivers of the CNL assay signal.

[0043] FIG. 3 shows a diagram illustrating steps of an illustrative CNL assay performed on cell free DNA (cfDNA).

[0044] FIG. 4A – 4E shows diagrams of an illustrative first generation adaptor (FIG. 4A and 4B) and an adaptor of the present invention (FIGs. 4C-4E). FIG. 4A shows the first generation adaptor design. FIG. 4B shows that in the first generation adaptors, there were a collection of 249 possible sequence tags, each 5 nucleotides (nt) in length that attached to a single anchor sequence. FIG. 4C shows a diagram of a second generation adaptor. FIG. 4D shows an illustrative set of adaptors that are applied to a single sample that consists of four sets of 8mer tag sequences with each set having 60 members. Each set of 60

tags is specific to one of four anchor sequences. FIG. 4E shows an illustrative DNA sequence of a 47 nt adaptor.

[0045] FIG. 5A – FIG. 5B shows a diagram illustrating that shifting the position of the UMI multiplier within the sample tag can increase the number of unique sample tags.

[0046] FIG. 6A and B shows a diagram illustrating the process of constructing genomic libraries for a CNL assay. FIG. 6A shows the step where the 10 nt anchor sequence is attached to the 3' ends of genomic fragments. FIG. 6B shows the step where the full length genomic adaptors are annealed to the initial anchor sequence.

[0047] FIG. 7 shows DNA inputs into CNL libraries. Agarose gel images are shown with the sizes of markers (bp) indicated at left.

[0048] FIG. 8A – FIG. 8C shows conventional box-and-whiskers plots of measured gene copies across eight samples as determined by CNL analysis.

[0049] FIG. 9A – FIG. 9B shows Log₁₀ P-value plots that quantify significant deviation-from-normal in CNL measurements for fragmented genomic samples. The SNP percentages at the top show the minor allele frequencies of rare, heterozygous SNPs that are present in the Δ ATM and Δ BRCA2 samples.

[0050] FIG. 10A – FIG. 10B shows Log₁₀ P-value plots that quantify significant deviation-from-normal in CNL measurements for cfDNA samples spiked with fragmented genomic DNA. The SNP percentages at the top show the minor allele frequencies of rare, heterozygous SNPs that are present in the Δ ATM and Δ BRCA2 samples.

[0051] FIG. 11A – 11D illustrate the targeted hybrid capture platform. FIG. 11A shows conversion of cfDNA to a genomic library by the addition of adaptor sequences that provide universal, single-primer PCR amplification sequences, sample multiplexing tags, and unique molecular identifiers to every genomic clone. FIG. 11B shows denatured amplified genomic hybridized with target specific capture probes and primer extension. FIG. 11C shows a schematic of asymmetric paired-end sequencing. FIG. 11D shows mapping statistics for 377,711,020 Illumina NextSeq reads from a typical targeted capture sequence run. 98.5% of reads map to their intended targets. Following de-duplication, 20.40% of reads (77,053,048) are derived from unique genomic clones.

[0052] FIG. 12A – FIG. 12H shows sequences of adaptor oligonucleotides from Pools 1 – 3.

[0053] FIG. 13A – FIG. 13H shows sequences of adaptor oligonucleotides from Pools 4 – 6.

[0054] FIG. 14A – FIG. 14I shows sequences of adaptor oligonucleotides from Pools 7 – 9.

[0055] FIG. 15A – FIG. 15H shows sequences of adaptor oligonucleotides from Pools 10 – 12.

[0056] FIG. 16A – FIG. 16H shows sequences of adaptor oligonucleotides from Pools 13 – 15.

[0057] FIG. 17A – FIG. 18H shows sequences of adaptor oligonucleotides from Pools 16 – 18.

[0058] FIG. 18A – FIG. 18H shows sequences of adaptor oligonucleotides from Pools 19 – 21.

[0059] FIG. 19A – FIG. 19H shows sequences of adaptor oligonucleotides from Pools 22 – 24.

[0060] FIG. 20A – FIG. 20H shows sequences of adaptor oligonucleotides from Pools 25 – 27.

[0061] FIG. 21A – FIG. 21H shows sequences of adaptor oligonucleotides from Pools 28 – 30.

[0062] FIG. 22A – FIG. 22H shows sequences of adaptor oligonucleotides from Pools 31 – 32.

[0063] FIG. 23A – 23C shows targeted sequencing of the TP53 gene. FIG. 23A illustrates BedFile display of capture probes. FIG. 23B illustrates coverage depth at each base position on a scale of 0 to 8000 unique reads. FIG. 23C illustrates a UCSC gene model display of known TP53 splice variants. The thicker rectangular regions represent the amino acid coding regions for the TP53-encoded protein.

[0064] FIG. 24A – 24C illustrate raw and normalized unique read density for a single probe, TP53r10_1, across 16 samples. FIG. 24A illustrates the number of raw unique reads capture by probe TP53r10_1 for 16 independent sample after removal of redundant reads by “de-duplication.” FIG. 24B shows global average of unique reads across 2596 capture probes for all 16 samples. FIG. 24C shows normalized unique read depth across 16 samples (Calculated as: [sample *n* unique reads from probe TP53r10_1 x constant ÷ global average unique reads/probe from sample *n*]).

[0065] FIG. 25 shows general consistency of the normalized unique read counts for all 16 samples within any given TP53 probe despite significant average depth variation between probes. The normalized unique read counts for all 16 samples are shown as “pillars” of tightly spaced bar graphs; the results for all 45 probes that target TP53 are shown. Two probes that exhibit “noisy” counting behavior are highlighted with arrows. Counts from such probes often appear as outliers in subsequent copy number analysis.

[0066] FIG. 26 illustrates sample-to-sample consistency of normalized probe-by-probe unique read counts across a broad panel of 2596 probes. The scatter plots from three representative samples are shown. Each dot represents a different probe. The x-axis is the normalized average unique read depth per probe across 16 samples. The y-axis is the normalized unique read depth per probe for three different individual samples. The consistent probe-by-probe unique read counts support quantitative analysis of chromosomal copy variation.

[0067] FIG. 27A – 27C illustrate copy number analysis of cfDNA from a healthy female and male donor and from an advanced stage prostate cancer patient. FIG. 27A shows analysis of a cfDNA from a healthy female donor. The x-axis is a series of control probes that target regions from all 22 autosomal chromosomes, a series of probes that target the X-linked AR gene, and a series of probes that target the coding regions of the TP53 gene. The Y-axis shows the calculated ploidy for each probe. This approximation is calculated for each probe by normalizing the observed unique read counts to a series of control samples whose ploidy is known ($[\text{unique read count for probe_Y of sample_Z}] \times 2 \div [\text{average unique read count for probe_Y for multiple control samples}]$). FIG. 27B illustrates that the X-linked AR gene exhibits a haploid copy number in healthy males. FIG. 27C illustrates copy number analysis of cfDNA from an advanced prostate cancer patient and shows evidence of very significant aneuploidy across the control probes, amplification of the AR gene, and loss of the TP53 gene.

[0068] FIG. 28 shows whole genome aneuploidy analysis of a prostate patient cfDNA library relative to a control sample. The approximate ploidy for each of 239 control probes is shown sorted by chromosome. Patient chromosome 2 probes show consistent copy loss and the majority of chromosome 5 probes show copy gain. Significant deviation of approximate ploidy are seen for many, but not all, of the patient control probes.

[0069] FIG. 29 shows analytical validation of copy number loss detection. Genomic DNA from immortalized line NA02718 (monoallelic Δ ATM) and from NA09596

(monoallelic Δ BRCA2) were spiked into the “gold standard” genomic DNA from NA12878 at 16%, resulting in the equivalent of an 8% biallelic deletion minor allele frequency. Following targeted sequencing and CNV analysis, the probe-by-probe ploidies were averaged for the two target genes. Two unperturbed control genes, BRIP1 and HDAC2, are shown for comparison.

DETAILED DESCRIPTION

A. OVERVIEW

[0070] The present invention includes, *inter alia*, compositions and methods that are useful for the detection of a mutational change, SNP, translocation, inversion, deletion, change in copy number or other genetic variation within a sample of cellular genomic DNA (*e.g.* from a tissue biopsy sample) or cfDNA (*e.g.* from a blood sample). The compositions and methods of the current invention are particularly useful in detecting incredibly hard to detect copy number variations in cfDNA from a biological sample (*e.g.* blood) with exquisite resolution. In particular, some embodiments of the present invention are drawn to a method for the detecting copy number of a DNA target region from a test sample by generating a genomic DNA library made up of genomic DNA fragments attached to an adaptor, capturing DNA target regions with a plurality of capture probes, isolating the DNA library fragments comprising the DNA target region, and performing a quantitative genetic analysis of the DNA target region to thereby determining the copy number of the DNA target region. The adaptors described herein allow for the identification of the individual DNA fragment that is being sequenced, as well as the identity of the sample or source of the genomic DNA.

[0071] The present invention contemplates, in part, compositions and methods for detection of target-specific copy number changes that are applicable to several sample types, including but not limited to direct tissue biopsies and peripheral blood. In the context of cancer genomics, and in particular cell free DNA (cfDNA) assays for the analysis of solid tumors, the amount of tumor DNA is often a very small fraction of the overall DNA. Further, copy number loss is difficult to detect in genomic DNA assays, and in particular, genomic DNA assays where copy number change may only be present in a portion of the total genomic DNA from a sample, *e.g.*, cfDNA assays. For example, most of the cell-free DNA extracted from a cancer patient will be derived from normal sources and have a diploid copy number (except for X-linked genes in male subjects). In a cancer patient, the fraction of DNA

derived from tumors often has a low minor allele frequency, such as for example, a patient in which 2% of the circulating DNA extracted from plasma is derived from the tumor. The loss of one copy of a tumor suppressor gene (for example, BRCA1 in breast cancer) means that the minor allele frequency for the absence of detectable genomic fragments is 1%. In this scenario, a copy number loss assay engineered must be able to discriminate between 100 copies (normal) and 99 copies (heterozygous gene loss). Thus, particular embodiments contemplate that the methods and compositions of the present invention allow for the detection of copy number change with sufficient resolution to detect changes in copy number at minor allele frequencies even in the context of cfDNA.

[0072] To achieve this level of discrimination, the present invention provides novel sample adaptor designs. The adaptors of the present invention are designed to include features that are critical for successful copy number loss assay performance including (i) even performance across adaptors; (ii) a high number of unique molecule identifiers (UMIs); (iii) high efficiency attachment; and (iv) accommodation of sample multiplexing. For example, the adaptors of the present invention provide the following:

[0073] Even performance across adaptors: Bioinformatics analysis often looks at intra-sample probe performance and inter-sample probe performance. Thus, it is contemplated that any performance fluctuation between adaptor pools across samples will negatively impact the ability to detect the subtle variations required by CNL analysis. In the present invention, this evenness of performance is achieved by having multiple anchor tags that are all represented in each sample tag pool, with the fixed sample tag regions (which serve to identify both the sample and the genomic fragments) being randomly selected for each pool, and a UMI multiplier that increases the unique sample tag sequences for identifying the genomic fragments.

[0074] High number of Unique Molecule Identifiers (UMIs): While adaptors must be functionally equivalent from a molecular biology perspective, they must possess a very large number of unique sequence tags ($\geq 10,000$) that augment the identification of unique genomic fragments. In this context, by “augment,” it is meant that each genomic clone fragment has a particular pair of fragmentation sites corresponding to the position in the genomic sequence where the double-strand DNA was cleaved. This cleavage site is used to differentiate unique genomic clones since each clone is likely to possess a different cleavage site. However, in libraries that possess thousands of independent clones, uniquely derived fragments will often possess the exact same cleavage sites. Genomic clones (i.e. fragments)

sharing the same cleavage site can be classified as either unique or as redundant with respect to other clone sequences derived from the same sample. By attaching adaptors that introduce a high diversity of sequence tags, different genomic clones sharing the same cleavage site are more likely to be identified as unique. In this system, the UMI is created by a combination of the sample tag region with the UMI multiplier. The combination of the UMI and the cleavage site create a unique molecular identifier element (UMIE), which facilitates the classification of sequence reads as redundant reads or unique reads. Particular embodiments contemplate that the UMI multiplier could comprise longer or shorter sequences to increase or lower the overall UMI complexity.

[0075] High efficiency attachment: Adaptors must attach to genomic fragments with high efficiency. In most oncology applications, the quantities of available cellular DNA or cfDNA are limited and therefore conversion of these genomic fragments to genomic library clones must be highly efficient. In order to achieve this, in some aspects of the present invention, the adaptor systems described herein convert about 25% to about 50% or greater of the genomic input fragments are converted into genomic library clones.

[0076] Accommodation of sample multiplexing: In general, there must be pools of different sets of adaptors where each unique adaptor of the set is attached to a different sample. At the same time, each member of the set of adaptors must possess essentially identical behavior (from a sequence counting perspective) to all other members in a set. In order to achieve this, in some embodiments, the sample tag regions have a Hamming distance of 2 between any other possible sample tag combinations reducing the chance for a read to be spuriously assigned to the wrong sample. In some embodiments, each set of adaptors is split into pools that are paired with specific anchor regions, allowing for further reduction in the possibility of an error in sample de-multiplexing. For example, in an 8mer tag with Hamming distance of 2, the total number of possible sequences is 16,384.

[0077] In a particular embodiment, pre-specified pools of adaptor oligonucleotides are provided. Such pre-specified pools are used to represent a single sample. That is, each adapter sequence in each pool of X adapter oligonucleotides (16,384 in the example given above) is distinct from each adapter sequence in every other pool used to identify other samples. One of skill in the art will recognize the number of distinct pre-specified pools that are possible for the adapter oligonucleotides will depend on the length of the sample tag and/or the UMI multiplier.

[0078] Thus, in certain embodiments the adaptors comprise a sequence, i.e., the sample tag and adjacent and/or encompassed UMI multiplier that represents or identifies both the sample and uniquely identifies the genetic fragment. This is in stark contrast to the current systems that are used in the art that use a randomly generated tag to identify the sequence and a separate barcode or sequencer indexing to allow for multiplexing.

[0079] An illustrative embodiment for detecting target-specific copy number changes within DNA obtained from a sample is shown in FIG. 3. While FIG. 3 generates a DNA library from cfDNA, this illustrative procedure could be used with DNA from other sources, e.g., fragmented cellular DNA. As shown in FIG. 3, cfDNA is collected (top panel). Next, a genomic library is generated from cfDNA by conjugating genomic library adaptors (gray circles) of the present invention to the genomic DNA. Genomic DNA fragments are captured with capture probes (black circles) that recognize the genomic region of interest. The genomic DNA of interest is sequenced, and data analysis is performed for copy loss analysis and/or characterization of the genomic DNA of interest.

[0080] The practice of particular embodiments of the invention will employ, unless indicated specifically to the contrary, conventional methods of chemistry, biochemistry, organic chemistry, molecular biology, microbiology, recombinant DNA techniques, genetics, immunology, and cell biology that are within the skill of the art, many of which are described below for the purpose of illustration. Such techniques are explained fully in the literature. See, e.g., Sambrook, *et al.*, *Molecular Cloning: A Laboratory Manual* (3rd Edition, 2001); Sambrook, *et al.*, *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); Maniatis *et al.*, *Molecular Cloning: A Laboratory Manual* (1982); Ausubel *et al.*, *Current Protocols in Molecular Biology* (John Wiley and Sons, updated July 2008); *Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology*, Greene Pub. Associates and Wiley-Interscience; Glover, *DNA Cloning: A Practical Approach*, vol. I & II (IRL Press, Oxford, 1985); Anand, *Techniques for the Analysis of Complex Genomes*, (Academic Press, New York, 1992); *Transcription and Translation* (B. Hames & S. Higgins, Eds., 1984); Perbal, *A Practical Guide to Molecular Cloning* (1984); and Harlow and Lane, *Antibodies*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1998).

B. DEFINITIONS

[0081] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by those of ordinary skill in the art to which the invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, preferred embodiments of compositions, methods and materials are described herein. For the purposes of the present invention, the following terms are defined below.

[0082] The articles “a,” “an,” and “the” are used herein to refer to one or to more than one (*i.e.* to at least one) of the grammatical object of the article. By way of example, “an element” means one element or more than one element.

[0083] The use of the alternative (*e.g.*, “or”) should be understood to mean either one, both, or any combination thereof of the alternatives.

[0084] The term “and/or” should be understood to mean either one, or both of the alternatives.

[0085] As used herein, the term “about” or “approximately” refers to a quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length that varies by as much as 15%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2% or 1% to a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length. In one embodiment, the term “about” or “approximately” refers a range of quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length $\pm 15\%$, $\pm 10\%$, $\pm 9\%$, $\pm 8\%$, $\pm 7\%$, $\pm 6\%$, $\pm 5\%$, $\pm 4\%$, $\pm 3\%$, $\pm 2\%$, or $\pm 1\%$ about a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length.

[0086] Throughout this specification, unless the context requires otherwise, the words “comprise”, “comprises,” and “comprising” will be understood to imply the inclusion of a stated step or element or group of steps or elements but not the exclusion of any other step or element or group of steps or elements. In particular embodiments, the terms “include,” “has,” “contains,” and “comprise” are used synonymously.

[0087] By “consisting of” is meant including, and limited to, whatever follows the phrase “consisting of.” Thus, the phrase “consisting of” indicates that the listed elements are required or mandatory, and that no other elements may be present.

[0088] By “consisting essentially of” is meant including any elements listed after the phrase, and limited to other elements that do not interfere with or contribute to the

activity or action specified in the disclosure for the listed elements. Thus, the phrase “consisting essentially of” indicates that the listed elements are required or mandatory, but that no other elements are optional and may or may not be present depending upon whether or not they affect the activity or action of the listed elements.

[0089] Reference throughout this specification to “one embodiment,” “an embodiment,” “a particular embodiment,” “a related embodiment,” “a certain embodiment,” “an additional embodiment,” or “a further embodiment” or combinations thereof means that a particular feature, structure or characteristic described in connection with the embodiment is included in at least one embodiment of the present invention. Thus, the appearances of the foregoing phrases in various places throughout this specification are not necessarily all referring to the same embodiment. Furthermore, the particular features, structures, or characteristics may be combined in any suitable manner in one or more embodiments.

[0090] As used herein, the term “isolated” means material that is substantially or essentially free from components that normally accompany it in its native state. In particular embodiments, the term “obtained” or “derived” is used synonymously with isolated.

[0091] As used herein, the term “DNA” refers to deoxyribonucleic acid. In various embodiments, the term DNA refers to genomic DNA, recombinant DNA, synthetic DNA, or cDNA. In one embodiment, DNA refers to genomic DNA or cDNA. In particular embodiments, the DNA comprises a “target region.” DNA libraries contemplated herein include genomic DNA libraries and cDNA libraries constructed from RNA, *e.g.*, an RNA expression library. In various embodiments, the DNA libraries comprise one or more additional DNA sequences and/or tags.

[0092] The terms “target genetic locus” and “DNA target region” are used interchangeably herein and refer to a region of interest within a DNA sequence. In various embodiments, targeted genetic analyses are performed on the target genetic locus. In particular embodiments, the DNA target region is a region of a gene that is associated with a particular genetic state, genetic condition, genetic diseases; fetal testing; genetic mosaicism, paternity testing; predicting response to drug treatment; diagnosing or monitoring a medical condition; microbiome profiling; pathogen screening; or organ transplant monitoring. In further embodiments, the DNA target region is a DNA sequence that is associated with a particular human chromosome, such as a particular autosomal or X-linked chromosome, or region thereof (*e.g.*, a unique chromosome region).

[0093] As used herein, the terms “circulating DNA,” “circulating cell-free DNA,” and “cell-free DNA” are often used interchangeably and refer to DNA that is extracellular DNA, DNA that has been extruded from cells, or DNA that has been released from necrotic or apoptotic cells. This term is often used in contrast to “cellular genomic DNA” or “cellular DNA,” which are used interchangeably herein and refer to genomic DNA that is contained within the cell (i.e. the nucleus) and is only accessible to molecular biological techniques such as those described herein, by lysing or otherwise disrupting the integrity of the cell.

[0094] A “subject,” “individual,” or “patient” as used herein, includes any animal that exhibits a symptom of a condition that can be detected or identified with compositions contemplated herein. Suitable subjects include laboratory animals (such as mouse, rat, rabbit, or guinea pig), farm animals (such as horses, cows, sheep, pigs), and domestic animals or pets (such as a cat or dog). In particular embodiments, the subject is a mammal. In certain embodiments, the subject is a non-human primate and, in preferred embodiments, the subject is a human.

[0095] As used herein, the term “paired” when used with respect to two different polynucleotide sequences or regions of DNA comprising different polynucleotide sequences, means that the two different polynucleotide sequences or regions of DNA comprising different polynucleotide sequences are present on the same polynucleotide. For example, if a particular sample tag region of DNA is said to be paired to particular amplification region of DNA, it is meant that the sample tag region and the amplification tag are present on the same DNA polynucleotide molecule.

C. METHODS OF COPY NUMBER ANALYSIS

[0096] In various embodiments, a method for copy number analysis of a DNA target region DNA is provided. In certain embodiments, copy number analysis is performed by generating a genomic DNA library of DNA library fragments that each contain genomic DNA fragment and an adaptor, isolating the DNA library fragments containing the DNA target regions, and performing a quantitative genetic analysis of the DNA target region. By “quantitative genetic analysis” it is meant an analysis performed by any molecular biological technique that is able to quantify changes in a DNA (*e.g.*, a gene, genetic locus, target region of interest, etc.) including but not limited to DNA mutations, SNPs, translocations, deletions,

and copy number variations (CNVs). In certain embodiments, the quantitative genetic analysis is performed by sequencing, for example, next generation sequencing.

[0097] Next-generation DNA sequencing (NGS) is ideally suited for two diagnostic applications. The first is the determination of DNA sequence on a vast scale. In the present context, this capability enables the search for rare, actionable variants that guide effective treatment decisions. The second is counting gene copy number. The output of millions of independent sequences can enable precise measurement of gene copy number on a genome-wide scale. The emergence of non-invasive prenatal testing for fetal trisomy from maternal blood samples is a testament to this capability. RNAseq, that is, the technology of gene expression profiling using NGS is another example, albeit the input is RNA (cDNA) rather than genomic DNA. Comparisons of current capture methods are described Samorodnitsky *et al.* J Mol Diagn. 2015 Jan;17(1):64-75.

[0098] The present invention extends NGS counting capability into the realm of targeted hybrid capture methods. The methods described here are effective for the detection of copy number variation at least in part because they possess the following four qualities:

(a) The present methods differentiate between unique clones and redundant clones. NGS sequencing of amplified genomic DNA library fragments results in a plurality of individual NGS reads, each comprising adaptor-encoded sequence information linked to a specific human genomic sequence. These elements define the identity of every clone. Because captured genomic regions are amplified by PCR, it is not uncommon for the same clone to be encountered several times in a subsequent NGS analysis. Groups of reads that are derived from a single cloning and capture process are termed “redundant reads.” Two or more redundant reads are identified as redundant reads based on the sequencing information provided by the unique molecular identification elements (UMIE). The UMIE refers to the combination of the sequence information from the adaptor tags and the start of the genomic DNA sequence. Two or more reads comprising identical UMIEs are identified as redundant reads. Redundant reads are grouped together and a single, representative consensus sequence is assembled from families of redundant reads. This consensus sequence is designated as a “unique read” or a “unique genomic sequence” (UGS). Each unique read represents a separate clone from the original DNA specimen. The process of identifying and grouping redundant clone families and of generating a single unique read representative of this family is defined as “deduplication.” The adaptors used to create genomic libraries possess a very

deep repertoire of unique sample tag information (15,360 codes per adaptor). When applied in conjunction with the exact mapping coordinates of each captured genomic clone (which can span >100 different positions relative to a capture probe), each unique clone that is generated in a genomic library and subsequently retrieved by a target-specific capture probe has an extremely high likelihood of being differentiable from all other unique clones that encompass the same capture environment. The ability to differentiate between unique clones and redundant clones is central to the methods described herein.

(b) The adaptors used to create genomic libraries permit sample multiplexing without creating adaptor-to-adaptor variability in copy number counts. A central foundation of copy number determination is the simultaneous analysis of a set of samples that have all been processed within a single sequencing run. This allows positive and negative controls to be included along with clinical samples. A major issue with previous adaptor design iterations induced subtle shifts in gene copy counts among identical control samples, in effect setting a signal-to-noise uncertainty threshold that was too high to be clinically useful in blood-based, solid tumor genotyping assays. The present invention overcomes this issue and substantially lowers the signal-to-noise threshold such that single copy gene loss is detectable at $\leq 2\%$ minor allele frequency. This improved signal recognition enables the methods of the present invention to have significant clinical utility in circulating tumor DNA assays.

(c) The proprietary targeted hybrid capture method used herein must produce highly uniform “on-target” read coverage across all targets. Methods that rely on counting of unique genomic fragments to estimate copy number, such as the ones described herein, must achieve near-saturation in terms of encountering all possible unique fragments. Near-saturation is only achieved by oversampling, that is to say, gathering more sequencing reads than the number of unique reads that will ultimately be encountered. To be practical, scalable, and economical, the unique reads in a targeted hybrid capture library must exhibit sufficient uniformity such that < 10-fold oversampling of on-target reads, and preferably < 4-fold oversampling of on-target reads will capture > 90% of unique on-target reads at all target loci.

(d) The targeted hybrid capture method (See U.S. Patent Publication No. 2014-0274731) must have high on-target capture rates. To be practical, scalable and economical, in other words to be a distinguishing feature of the present disclosure relative to other art in the field, the method must achieve >90%, preferably >95% on-target reads. With on-target

mapping rates exceeding 95%, the requirement for 4 to 10-fold oversampling of on-target reads and the requirement for overall oversampling are one in the same.

[0099] In some embodiments, the number of copies of the DNA target region present in the sample is determined by the quantitative genetic analysis. In some embodiments, the copy number of the DNA target region is determined by comparing the amount of copies of DNA target regions present in the sample and comparing it to amounts of DNA target regions present in one or more samples with known copy number.

[00100] Particular embodiments contemplate that the compositions and methods described herein are particularly useful for detecting changes in copy number in a sample of genomic DNA, where only a portion of the total genomic DNA in the sample has a change in copy number. For example, a significant tumor mutation may be present in a sample, *e.g.* a sample of cell free DNA, that is present in a minor allele frequency that is significantly less than 50% (*e.g.*, in the range of 0.1% to >20%), in contrast to conventional SNP genotyping where allele frequencies are generally ~100%, 50% or 0%. One of skill of the art will recognize that the compositions and methods of the current invention are also useful in detecting other types of mutation including single nucleotide variants (SNVs), short (*e.g.*, less than 40 base pairs (bp)) insertions, and deletions (indels), and genomic rearrangements including oncogenic gene fusions.

[00101] In certain embodiments, the compositions and/or methods of the present invention described herein are useful for, capable of, suited for, and/or able to detect, identify, observe, and/or reveal a change in copy number of one or more DNA target regions present in less than about 20%, less than about 19%, less than about 18%, less than about 17%, less than about 16%, less than about 15%, less than about 14%, less than about 13%, less than about 12%, less than about 11%, less than about 10%, less than about 9%, less than about 8%, less than about 7%, less than about 6%, less than about 5%, less than about 4%, less than about 3%, less than about 2%, less than about 1%, less than about 0.5%, less than about 0.2%, or less than about 0.1% of the total genomic DNA from the sample. In some embodiments, the methods of the present invention are useful for, capable of, suited for, and/or able to detect, identify, observe, and/or reveal a change in copy number of one or more DNA target regions present in between about 0.01% to about 100%, about 0.01% to about 50%, and or about 0.1% to about 20% of the total genomic DNA from the sample.

[00102] Particular embodiments are represented by the conceptual framework that is illustrated in FIG. 1. In FIG. 1, each gene is represented by a row and each patient

sample is represented as a column. Within any given genomic DNA sample, the number of fragments counted for each individual gene will have some variability, and that for any given DNA region of interest, *e.g.* a gene, perturbations in copy number are detected as significant fragment count deviations relative to the normalized counts to the DNA target region in other samples. Such an assay requires the gene-by-gene fragment counting profile within a sample to be reproducible, and also requires the sample-by-sample counting profiles to be highly comparable. Both assay requirements demand excellent signal-to-noise counting discrimination.

[00103] Some embodiments contemplate that the assay elements that contribute to increasing the signal to noise ratio are the genomic input, the number of probes, and the sequencing depth, as illustrated in FIG. 2.

[00104] In particular embodiments, a method for genetic analysis of cfDNA comprises: generating and amplifying a cfDNA library, determining the number of genome equivalents in the cfDNA library; and performing a quantitative genetic analysis of one or more genomic target loci.

[00105] Particular embodiments contemplate that the any of the methods and compositions described herein are effective for use to efficiently analyze, detect, diagnose, and/or monitor genetic states, genetic conditions, genetic diseases, genetic mosaicism, fetal diagnostics, paternity testing, microbiome profiling, pathogen screening, and organ transplant monitoring using genomic DNA, *e.g.*, cellular or cfDNA, where all or where only a portion of the total genomic DNA in the sample has a feature of interest, *e.g.* a genetic lesion, mutation, single nucleotide variant (SNV). In some embodiments, a feature of interest is a genetic feature associated with a disease or condition. For example, a significant tumor mutation may be present in a sample, *e.g.* a sample of cfDNA, that is present in a minor allele frequency that is significantly less than 50% (*e.g.* in the range of 0.1% to >20%), in contrast to conventional SNP genotyping where allele frequencies are generally ~100%, 50% or 0%.

[00106] In certain embodiments, the compositions and/or methods of the present invention described herein are useful for, capable of, suited for, and/or able to detect, identify, observe, and/or reveal a genetic lesion of one or more DNA target regions present in less than about 20%, less than about 19%, less than about 18%, less than about 17%, less than about 16%, less than about 15%, less than about 14%, less than about 13%, less than about 12%, less than about 11%, less than about 10%, less than about 9%, less than about 8%, less than about 7%, less than about 6%, less than about 5%, less than about 4%, less than about

3%, less than about 2%, less than about 1%, less than about 0.5%, less than about 0.2%, or less than about 0.1% of the total genomic DNA from the sample. In some embodiments, the methods of the present invention are useful for, capable of, suited for, and/or able to detect, identify, observe, and/or reveal a genetic lesion of one or more DNA target regions present in between about 0.01% to about 100%, about 0.01% to about 50%, and or about 0.1% to about 20% of the total genomic DNA from the sample.

1. GENERATING A DNA LIBRARY

[00107] In particular embodiments, methods of genetic analysis contemplated herein comprise generating a DNA library comprising treating cfDNA or fragmented cellular genomic DNA with one or more end-repair enzymes to generate end-repaired DNA and attaching one or more adaptors to each end of the end-repaired DNA to generate the DNA library. Genomic DNA

[00108] In particular embodiments, the methods and compositions contemplated herein are designed to efficiently analyze, detect, diagnose, and/or monitor change in copy number using genomic DNA as an analyte. In certain embodiments, copy number analysis is performed by generating a genomic DNA library from genomic DNA obtained from a test sample, *e.g.*, a biological sample such as a tissue biopsy. In certain embodiments, the genomic DNA is circulating or cell free DNA. In some embodiments, the genomic DNA is cellular genomic DNA.

[00109] In certain embodiments, genomic DNA is obtained from a tissue sample or biopsy taken from a tissue, including but not limited to, bone marrow, esophagus, stomach, duodenum, rectum, colon, ileum, pancreases, lung, liver, prostate, brain, nerves, meningeal tissue, renal tissue, endometrial tissue, cervical tissue, breast, lymph node, muscle, and skin. In certain embodiments, the tissue sample is a biopsy of a tumor or a suspected tumor. In particular embodiments, the tumor is cancerous or suspected of being cancerous. In particular embodiments, the tissue sample comprises cancer cells or cells suspected of being cancerous.

[00110] Methods for purifying genomic DNA from cells or from a biologic tissue comprised of cells are well known in the art, and the skilled artisan will recognize optimal procedures or commercial kits depending on the tissue and the conditions in which the tissue is obtained. Some embodiments contemplate that purifying cellular DNA from a

tissue will require cell disruption or cell lysis to expose the cellular DNA within, for example by chemical and physical methods such as blending, grinding or sonicating the tissue sample; removing membrane lipids by adding a detergent or surfactants which also serves in cell lysis, optionally removing proteins, for example by adding a protease; removing RNA, for example by adding an RNase; and DNA purification, for example from detergents, proteins, salts and reagents used during cell lysis step. DNA purification may be performed by precipitation, for example with ethanol or isopropanol; by phenol–chloroform extraction.

[00111] In particular embodiments, cellular DNA obtained from tissues and/or cells are fragmented prior to and or during obtaining, generating, making, forming, and/or producing a genomic DNA library as described herein. One of skill in the art will understand that there are several suitable techniques for DNA fragmentation, and is able to recognize and identify suitable techniques for fragmenting cellular DNA for the purposes of generating a genomic DNA library for DNA sequencing, including but not limited to next-generation sequencing. Certain embodiments contemplate that cellular DNA can be fragmented into fragments of appropriate and/or sufficient length for generating a library by methods including but not limited to physical fragmentation, enzymatic fragmentation, and chemical shearing.

[00112] Physical fragmentation can include, but is not limited to, acoustic shearing, sonication, and hydrodynamic shear. In some embodiments, cellular DNA is fragmented by physical fragmentation. In particular embodiments, cellular DNA is fragmented by acoustic shearing or sonication. Particular embodiments contemplate that acoustic shearing and sonication are common physical methods used to shear cellular DNA. The Covaris® instrument (Woburn, MA) is an acoustic device for breaking DNA into 100-5kb bp. Covaris also manufactures tubes (gTubes) which will process samples in the 6-20 kb for Mate-Pair libraries. The Bioruptor® (Denville, NJ) is a sonication device utilized for shearing chromatin, DNA and disrupting tissues. Small volumes of DNA can be sheared to 150-1kb in length. Hydroshear from Digilab (Marlborough, MA) utilizes hydrodynamic forces to shear DNA. Nebulizers (Life Tech, Grand Island, NY) can also be used to atomize liquid using compressed air, shearing DNA into 100-3kb fragments in seconds. Nebulization is low cost, but the process can cause a loss of about 30% of the cellular DNA from the original sample. In certain embodiments, cellular DNA is fragmented by sonication.

[00113] Enzymatic fragmentation can include, but is not limited to, treatment with a restriction endonuclease, *e.g.* DNase I, or treatment with a nonspecific nuclease. In

some embodiments, cellular DNA is fragmented by enzymatic fragmentation. In particular embodiments, the cellular DNA is fragmented by treatment with a restriction endonuclease. In some embodiments, the cellular DNA is fragmented by treatment with a nonspecific nuclease. In certain embodiments, the cellular DNA is fragmented by treatment with a transposase. Certain embodiments contemplate that enzymatic methods to shear cellular DNA into small pieces include DNase I, a combination of maltose binding protein (MBP)-T7 Endo I and a non-specific nuclease *Vibrio vulnificus* (Vvn) New England Biolabs's (Ipswich, MA) Fragmentase and Nextera tagmentation technology (Illumina, San Diego, CA). The combination of non-specific nuclease and T7 Endo synergistically work to produce non-specific nicks and counter nicks, generating fragments that disassociate 8 nucleotides or less from the nick site. Tagmentation uses a transposase to simultaneously fragment and insert adapters onto double stranded DNA.

[00114] Chemical fragmentation can include treatment with heat and divalent metal cation. In some embodiments, genomic DNA is fragmented by chemical fragmentation. Particular embodiments contemplate that chemical shear is more commonly used for the breakup of long RNA fragments as opposed to genomic DNA. Chemical fragmentation is typically performed through the heat digestion of DNA with a divalent metal cation (magnesium or zinc). The length of DNA fragments can be adjusted by increasing or decreasing the time of incubation.

[00115] In particular embodiments, the methods and compositions contemplated herein are designed to efficiently analyze, detect, diagnose, and/or monitor change in copy number using cell-free DNA (cfDNA) as an analyte. The size distribution of cfDNA ranges from about 150 bp to about 180 bp fragments. Fragmentation of cfDNA may be the result of endonucleolytic and/or exonucleolytic activity and presents a formidable challenge to the accurate, reliable, and robust analysis of cfDNA. Another challenge for analyzing cfDNA is its short half-life in the blood stream, on the order of about 15 minutes. Without wishing to be bound to any particular theory, the present invention contemplates, in part, that analysis of cfDNA is like a "liquid biopsy" and is a real-time snapshot of current biological processes.

[00116] Moreover, because cfDNA is not found within cells and may be obtained from a number of suitable sources including, but not limited to, biological fluids and stool samples, it is not subject to the existing limitations that plague next generation sequencing analysis, such as direct access to the tissues being analyzed.

[00117] Illustrative examples of biological fluids that are suitable sources from which to isolate cfDNA in particular embodiments include, but are not limited to amniotic fluid, blood, plasma, serum, semen, lymphatic fluid, cerebral spinal fluid, ocular fluid, urine, saliva, mucous, and sweat. In particular embodiments, the biological fluid is blood or blood plasma.

[00118] In certain embodiments, commercially available kits and other methods known to the skilled artisan can be used to isolate cfDNA directly from the biological fluids of a subject or from a previously obtained and optionally stabilized biological sample, *e.g.*, by freezing and/or addition of enzyme chelating agents including, but not limited to EDTA, EGTA, or other chelating agents specific for divalent cations.

(a) Generating End-Repaired cfDNA

[00119] In particular embodiments, generating a genomic DNA library comprises the end-repair of isolated cfDNA or fragmented cellular DNA. The fragmented cfDNA or cellular DNA is processed by end-repair enzymes to generate end-repaired cfDNA with blunt ends, 5'-overhangs, or 3'-overhangs. In some embodiments, the end-repair enzymes can yield for example. In some embodiments, the end-repaired cfDNA or cellular DNA contains blunt ends. In some embodiments, the end-repaired cellular DNA or cfDNA is processed to contain blunt ends. In some embodiments, the blunt ends of the end-repaired cfDNA or cellular DNA are further modified to contain a single base pair overhang. In some embodiments, end-repaired cfDNA or cellular DNA containing blunt ends can be further processed to contain adenine (A)/thymine (T) overhang. In some embodiments, end-repaired cfDNA or cellular DNA containing blunt ends can be further processed to contain adenine (A)/thymine (T) overhang as the single base pair overhang. In some embodiments, the end-repaired cfDNA or cellular DNA has non-templated 3' overhangs. In some embodiments, the end-repaired cfDNA or cellular DNA is processed to contain 3' overhangs. In some embodiments, the end-repaired cfDNA or cellular DNA is processed with terminal transferase (TdT) to contain 3' overhangs. In some embodiments, a G-tail can be added by TdT. In some embodiments, the end-repaired cfDNA or cellular DNA is processed to contain overhang ends using partial digestion with any known restriction enzymes (*e.g.*, with the enzyme Sau3A, and the like).

(b) Attaching Adaptor Molecules to End-Repaired cfDNA

[00120] In particular embodiments, generating a cfDNA library comprises attaching one or more adaptors to each end of the end-repaired cfDNA. The present invention contemplates, in part, an adaptor module designed to accommodate large numbers of genome equivalents in cfDNA libraries. Adaptor modules are configured to measure the number of genome equivalents present in cfDNA libraries, and, by extension, the sensitivity of sequencing assays used to identify sequence mutations.

[00121] As used herein, the terms “adaptor” and “adaptor module” are used for interchangeably, and refer to a polynucleotide comprising that comprises at least three elements: an amplification region, a sample tag region, and an anchor region. In particular embodiments, the adaptor comprises an amplification region, a sample tag region, and an anchor region. In some embodiments, the adaptor also comprises a unique molecule identifier (UMI). In particular embodiments, the adaptor comprises one or amplification regions, one or more sample tag regions, one or more UMIs, and/or one or more anchor regions. In some embodiments, the adaptor comprises, in order from 5' to 3', an amplification region, a sample tag region, a UMI, and an anchor region. In particular embodiments, the adaptor comprises, in order from 5' to 3', an amplification region, a sample tag region, a UMI, and an anchor region. In certain embodiments, the UMI is contained within the sample tag region, and the adaptor comprises, in order from 5' to 3', an amplification region, an integrated sample tag/UMI region, and an anchor region.

[00122] As used herein, the term “amplification region” refers to an element of the adaptor molecule that comprises a polynucleotide sequence capable of serving as a primer recognition site for PCR amplification. In particular embodiments, an adaptor comprises an amplification region that comprises one or more primer recognition sequences for single-primer amplification of a genomic DNA library. In some embodiments, the amplification region comprises one, two, three, four, five, six, seven, eight, nine, ten, or more primer recognition sequences for single-primer amplification of a genomic DNA library.

[00123] In some embodiments, the amplification region is about is between 5 and 50 nucleotides, between 10 and 45 nucleotides, between 15 and 40 nucleotides, or between 20 and 30 nucleotides in length. In some embodiments, the amplification region is 10 nucleotides, 11 nucleotides, 12 nucleotides, 13 nucleotides, 14 nucleotides, 15 nucleotides, 16 nucleotides, 17 nucleotides, about 18 nucleotides, 19 nucleotides, 20 nucleotides, 21 nucleotides, 22 nucleotides, 23 nucleotides, 24 nucleotides, 25 nucleotides, 26 nucleotides, 27

nucleotides, 28 nucleotides, 29 nucleotides, 30 nucleotides, 31 nucleotides, 32 nucleotides, 33 nucleotides, 34 nucleotides, 35 nucleotides, 36 nucleotides, 37 nucleotides, 38 nucleotides, 39 nucleotides, or 40 nucleotides or more. In particular embodiments, the amplification region is 25 nucleotides in length.

[00124] As used herein, the term “sample tag” or sample tag region” are used interchangeably and refer to an element of the adaptor that comprises a polynucleotide sequence that uniquely identifies the particular DNA fragment as well as the sample from which it was derived.

[00125] In certain embodiments, the sample tag region is about is between 3 and 50 nucleotides, between 3 and 25 nucleotides, or between 5 and 15 nucleotides in length. In some embodiments, the sample tag region is 3 nucleotides, 4 nucleotides, 5 nucleotides, 6 nucleotides, 7 nucleotides, 8 nucleotides, 9 nucleotides, 10 nucleotides, about 11 nucleotides, 12 nucleotides, 13 nucleotides, 14 nucleotides, 15 nucleotides, 16 nucleotides, 17 nucleotides, 18 nucleotides, 19 nucleotides, or 20 nucleotides or more in length.

[00126] In certain embodiments, the adaptor comprises a UMI multiplier, wherein the UMI multiplier is at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 nucleotides in length.

[00127] In certain embodiments, each nucleotide position of the UMI multiplier can comprise any of adenine, guanine, cytosine, or thymine. Thus, in some embodiments, a UMI multiplier comprising n number of nucleotides can comprise any of n^4 possible nucleotide sequences. In some embodiments, the UMI multiplier is one nucleotide in length and comprises one of four possible sequences. In some embodiments, the UMI multiplier is two nucleotides in length and comprises one of sixteen possible sequences. In some embodiments, the UMI multiplier is three nucleotides in length and comprises one of 64 possible sequences. In some embodiments, the UMI multiplier is four nucleotides in length and comprises one of 256 possible sequences. In some embodiments, the UMI multiplier is five nucleotides in length and comprises one of 1,024 possible sequences. In some embodiments, the UMI multiplier is six nucleotides in length and comprises one of 4,096 possible sequences. In some embodiments, the UMI multiplier is seven nucleotides in length and comprises one of 16,384 possible sequences. In some embodiments, the UMI multiplier is eight nucleotides in length and comprises one of 65,536 possible sequences. In some embodiments, the UMI multiplier is nine nucleotides in length and comprises one of 262,144

possible sequences. In some embodiments, the UMI multiplier is ten or more nucleotides in length and comprises one of 1,048,576 or more possible sequences.

[00128] In particular embodiments, the adaptor comprises a UMI multiplier, wherein the UMI multiplier is adjacent to or contained within the sample tag region (FIG. 5A). Illustrative examples of UMI multipliers adjacent or contained within the sample tag are shown in FIG. 5B. In FIG. 5B, an 8-mer sample tag region is shown with an adjacent UMI multiplier (top and bottom rows) or a UMI multiplier incorporated within the sample tag (middle 7 rows). In some embodiments, that adaptor comprises a sample tag that is eight nucleotides in length and a UMI multiplier that is three nucleotides in length and comprises one of 64 possible sequences, and wherein the UMI multiplier is adjacent to or contained within the sample tag region. In some embodiments, identical processes attach full length adaptor to the other end of the genomic fragments.

[00129] In particular embodiments, an adaptor module comprises one or more anchor sequences. As used herein, an “anchor region” and “anchor sequence” are used interchangeably and refer to a nucleotide sequence that hybridizes to a partner oligonucleotide. In some embodiments, the anchor region comprises the following three properties: (1) each anchor sequence is part of a family of two or more anchor sequences that collectively represent each of the four possible DNA bases at each site within extension; this feature, balanced base representation, is useful to calibrate proper base calling in sequencing reads in particular embodiments; (2) each anchor sequence is composed of only two of four possible bases, and these are specifically chosen to be either an equal number of A + C or an equal number of G + T; an anchor sequence formed from only two bases reduces the possibility that the anchor sequence will participate in secondary structure formation that would preclude proper adaptor function; and (3) because each anchor sequence is composed of equal numbers of A + C or G + T, each anchor sequence shares roughly the same melting temperature and duplex stability as every other anchor sequence in a set of four.

[00130] In some embodiments, the anchor sequences is between 1 and 50 nucleotides in length. In some embodiments, the anchor sequences is between 4 and 40 nucleotides in length. In certain embodiments, the anchor region is between 5 and 25 nucleotides in length. In particular embodiments, the anchor region is at least 4 nucleotides, at least six nucleotides, at least 8 nucleotides, at least 10 nucleotides, at least 12 nucleotides, at least 14 nucleotides, or at least 16 nucleotides in length. In particular embodiments, the anchor region is 10 nucleotides in length.

[00131] In particular embodiments, an attachment step comprises attaching/ligating an adaptor module to the end-repaired cfDNA or cellular DNA to generate a “tagged” genomic DNA library. In some embodiments, a single adaptor module is employed. In some embodiments, two, three, four or five adaptor modules are employed. In some embodiments, an adaptor module of identical sequence is attached to each end of the fragmented end-repaired DNA.

[00132] In some embodiments, a plurality of adaptor species is attached to an end-repaired cellular or cell free genomic DNA fragments. Each of the plurality of adaptors may comprise one or more amplification regions for the amplification of the cfDNA or cellular DNA library, one or more sample tag regions for the identification of the cfDNA or cellular genomic DNA fragment and identification of the individual sample; and one or more sequences for DNA sequencing.

[00133] In some embodiments, a plurality of adaptor species is attached to an end-repaired cellular or cell free genomic DNA fragments of a sample, and the plurality of adaptors all comprise amplification regions of an identical nucleotide sequence.

[00134] In certain embodiments, the genomic DNA from a sample is attached with a plurality of adaptors that comprise sample tag sequences that all are different from other sequences of sample tag regions in adaptors that are attached to genomic DNA fragments from other samples.

[00135] In particular embodiments, a plurality of adaptor species is attached to an end-repaired cellular or cell free genomic DNA fragments from a sample, and the plurality of adaptors all comprise one or more sample tag regions comprising one of between 2 and 10,000 nucleotide sequences, one of between 5 and 5,000 nucleotide sequences, one of between 25 and 1,000 nucleotide sequences, one of between 50 and 500 nucleotide sequences, one of between 100 and 400 nucleotide sequences, or one of between 200 and 300 nucleotide sequences. In some embodiments, the sample tag region of each adaptor is 8 nucleotides in length, and each sample tag region of the plurality of adaptors comprises one of 240 nucleotide sequences.

[00136] In certain embodiments, a plurality of adaptor species is attached to an end-repaired cellular or cell free genomic DNA fragments from a sample, and the sample tag regions of the plurality of adaptors comprises nucleotide sequences that are different from each other by a Hamming distance of 1, 2, 3, 4 or greater than 4. In particular embodiments, the Hamming distance is 2.

[00137] In particular embodiments, the sample tag regions of the plurality of adaptors that are attached to genomic DNA fragments of a sample are 8 nucleotides in length, and comprise one of 240 nucleotide sequences that are different from each other by a Hamming distance of 2.

[00138] In certain embodiments, the sample tag region serves to identify individual genomic DNA fragments and to identify the individual sample, i.e., the genomic library source. For example, when the sample tags of a plurality of adaptors attached to a sample have one of 240 possible sequences, each sample is identified as having one of 240 possible tags, and each sample receives a set of 240 tags that are discrete from any other sample by Hamming distance of two (meaning two base changes are required to change one tag into another). These same tags are used to enumerate clone diversity and thus they also serve as sequence tags, i.e., to identify genomic DNA fragments. To further augment the diversity of possible sequence tags, UMI multipliers may be added. For example, a UMI multiplier can be added to the adaptor region comprising 3 nucleotides consisting of the 64 possible combinations of 3 bases. In addition, the plurality of adaptors can comprise more than one anchor sequence. For example, a plurality of adaptors may contain 4 different anchor sequences are used simultaneously. These anchor sequences may also be used during sample de-multiplexing to lower errors.

[00139] FIG. 4 shows an illustrative comparison between a first generation adaptor (FIG. 4A and 4B) and an adaptor of the present invention (FIG. 4C – FIG. 4E). FIG. 4A and FIG. 4B show an example of first generation adaptor that is 40 nt in length and consisted of a discrete PCR amplification sequence, sequence tag, and sample tag. Here, the sample is identified by a fixed sequence (sequence tag) that is present on all adaptors that are used to generate a DNA library from the sample. Individual genomic fragments are identified by a separate and distinct sequences (sequence tag). FIG. 4C – FIG. 4E show an illustrative example of an adaptor from the present invention. The illustrative adaptor shown is 47 nucleotides in length, and the sequence tag is combined with the sample tag. There is an additional 3 nt sequence, the UMI multiplier, consisting of the 64 possible combinations of 3 bases. The 10 nt anchor sequence is one of four different distinct sequences.

[00140] Thus, in the illustrative example (*See* FIG. 4C – FIG. 4E), a set of adaptors that are used in connection with a single sample comprise 240 sample tag sequences that can be split into four sets of sample tag sequences with each set comprising 60 tags (one for each nucleotide, A, C, T and G). Thus, each set of 60 tags is specific to one of four anchor

sequences. In total, a pool of 240 possible sample tag configurations are possible per sample. Specifically, in this scenario, the 240 sample tag sequences are divided into four sets of 60 sequences, with each set directed to a specific anchor region. Therefore, the sample ID involves not only the sequence information from the eight nucleotide sample tag, but also the associated anchor sequence information. In addition, the position of sequences within the read is fixed, and therefore the sample tags and anchor sequences must have a fixed position within a sequencing read in order to pass inclusion filters for downstream consideration. Further, the inclusion of the UMI multiplier increases the sequence tag diversity from 240 to $240 \times 64 = 15,360$ possible sequence tags.

[00141] Attachment of one or more adaptors contemplated herein may be carried out by methods known to those of ordinary skill in the art. In particular embodiments, one or more adaptors contemplated herein are attached to end-repaired cfDNA that comprises blunt ends. In certain embodiments, one or more adaptors contemplated herein are attached to end-repaired cfDNA that comprises complementary ends appropriate for the attachment method employed. In certain embodiments, one or more adaptors contemplated herein are attached to end-repaired cfDNA that comprises a 3' overhang.

[00142] In some embodiments, attaching the genomic DNA fragments to a plurality of adaptors includes the steps of attaching the end repaired cfDNA or cellular DNA fragments to an oligonucleotide containing at least a portion of an anchor region. In some embodiments, the oligonucleotide contains the whole anchor region. In particular embodiments, the oligonucleotide is a DNA duplex comprising a 5' phosphorylated attachment strand duplexed with a partner strand, wherein the partner strand is blocked from attachment by chemical modification at its 3' end, and wherein the attachment strand is attached to the genomic DNA fragment. In certain embodiments, the DNA fragments attached with at least a portion of the anchor region are then annealed with DNA oligonucleotides encoding the full length adaptor sequences. In particular embodiments, one or more polynucleotide kinases, one or more DNA ligases, and/or one or more DNA polymerases are added to the genomic DNA fragments and the DNA oligonucleotides encoding the full length adaptor sequence. In some embodiments, the polynucleotide kinase is T4 polynucleotide kinase. In some embodiments, the DNA ligase is Taq DNA ligase. In certain embodiments, the DNA polymerase is Taq polymerase. In particular embodiments, the DNA polymerase is full length Bst polymerase.

[00143] FIG. 6 shows an illustrative method for attaching a plurality of adaptors to the 3' end of repaired DNA fragments. In the first step, the anchor sequence is attached to the 3' ends of genomic fragments. In this step, the anchor portion is a DNA duplex in which the ten nucleotide 5' phosphorylated "attachment strand" is duplexed with an eight nucleotide "partner strand" that is blocked from attachment by chemical modification at its 3' end. The anchor duplex is blunt-ended on the phosphorylated/blocked end and can therefore attach to blunt-ended genomic fragments. In the next step, pools of oligonucleotides encoding the full adaptor sequences are annealed to the initial anchor sequence. The combined action of T4 polynucleotide kinase, Taq DNA ligase, and full-length Bst polymerase attach this oligonucleotide via ligation as illustrated for the top strand and extend the initial anchor sequence by DNA polymerization on the bottom strand to complete the full-length adaptor sequence. Identical processes may be used to attach full length adaptors to the 5' end of the genomic fragments.

2. DNA LIBRARY AMPLIFICATION

[00144] In particular embodiments, methods of genetic analysis contemplated herein comprise amplification of a genomic DNA library, *e.g.* a cellular DNA library or a cfDNA library, to generate a DNA clone library or a library of DNA clones, *e.g.*, a cfDNA clone library or a library of cfDNA clones, or a cellular DNA clone library or a library of cellular DNA clones. Each molecule of the DNA library comprises an adaptor attached to each end of an end-repaired DNA fragments, and each adaptor comprises one or more amplification regions. In some embodiments, different adaptors are attached to different ends of the end-repaired cfDNA. In particular embodiments, different adaptors are attached to different ends of the end-repaired cellular DNA.

[00145] In some embodiments, the same adaptor is attached to both ends of the DNA fragment. Attachment of the same adaptor to both ends of end-repaired DNA allows for PCR amplification with a single primer sequence. In particular embodiments, a portion of the adaptor attached-cfDNA library will be amplified using standard PCR techniques with a single primer sequence driving amplification. In one embodiment, the single primer sequence is about 25 nucleotides, optionally with a projected T_m of $\geq 55^\circ \text{C}$ under standard ionic strength conditions.

[00146] In particular embodiments, picograms of the initial genomic DNA library, *e.g.* a cellular DNA library or cfDNA library, are amplified into micrograms of DNA clones, implying a 10,000-fold amplification. The amount of amplified product can be measured using methods known in the art, *e.g.*, quantification on a Qubit 2.0 or Nanodrop instrument.

3. DETERMINING THE NUMBER OF GENOME EQUIVALENTS

[00147] In various embodiments, a method for genetic analysis of genomic DNA comprises determining the number of genome equivalents in the DNA clone library. As used herein, the term “genome equivalent” refers to the number of genome copies in each library. An important challenge met by the compositions and methods contemplated herein is achieving sufficient assay sensitivity to detect and analysis rare genetic mutations or differences in genetic sequence. To determine assay sensitivity value on a sample-by-sample basis, the numbers of different and distinct sequences that are present in each sample are measured by measuring the number of genome equivalents that are present in a sequencing library. To establish sensitivity, the number of genome equivalents must be measured for each sample library.

[00148] The number of genome equivalents can be determined by qPCR assay or by using bioinformatics-based counting after sequencing is performed. In the process flow of clinical samples, qPCR measurement of genome equivalents is used as a QC step for DNA libraries, *e.g.*, cfDNA libraries or genomic DNA libraries. It establishes an expectation for assay sensitivity prior to sequence analysis and allows a sample to be excluded from analysis if its corresponding DNA clone library lacks the required depth of genome equivalents. Ultimately, the bioinformatics-based counting of genome equivalents is also used to identify the genome equivalents – and hence the assay sensitivity and false negative estimates – for each given DNA clone library.

[00149] The empirical qPCR assay and statistical counting assays should be well correlated. In cases where sequencing fails to reveal the sequence depth in a DNA clone library, reprocessing of the DNA clone library and/or additional sequencing may be required.

[00150] In one embodiment, the genome equivalents in a cellular DNA or cfDNA clone library are determined using a quantitative PCR (qPCR) assay. In a particular embodiment, a standard library of known concentration is used to construct a standard curve

and the measurements from the qPCR assay are fit to the resulting standard curve and a value for genome equivalents is derived from the fit. The present inventors have discovered that a qPCR “repeat-based” assay comprising one primer that specifically hybridizes to a common sequence in the genome, *e.g.*, a repeat sequence, and another primer that binds to the primer binding site in the adaptor, measured an 8-fold increase in genome equivalents compared to methods using just the adaptor specific primer (present on both ends of the cfDNA clone). The number of genome equivalents measured by the repeat-based assays provides a more consistent library-to-library performance and a better alignment between qPCR estimates of genome equivalents and bioinformatically counted tag equivalents in sequencing runs.

[00151] Illustrative examples of repeats suitable for use in the repeat-based genome equivalent assays contemplated herein include, but not limited to: short interspersed nuclear elements (SINEs), *e.g.*, Alu repeats; long interspersed nuclear elements (LINEs), *e.g.*, LINE1, LINE2, LINE3; microsatellite repeat elements, *e.g.*, short tandem repeats (STRs), simple sequence repeats (SSRs); and mammalian-wide interspersed repeats (MIRs).

[00152] In one embodiment, the repeat is an Alu repeat.

4. QUANTITATIVE GENETIC ANALYSIS

[00153] In various embodiments, a method for genetic analysis of genomic DNA, *e.g.*, genomic cellular or cfDNA, comprises quantitative genetic analysis of one or more target genetic loci of the DNA library clones. Quantitative genetic analysis comprises one or more of, or all of, the following steps: capturing DNA clones comprising a target genetic locus; amplification of the captured targeted genetic locus; sequencing of the amplified captured targeted genetic locus; and bioinformatic analysis of the resulting sequence reads. As used herein, the terms “DNA library clone” refer to a DNA library fragment wherein the combination of the adaptor and the genomic DNA fragment result in a unique DNA sequence (*e.g.*, a DNA sequence that can be distinguished from that of another DNA library clone).

(a) Capture of Target Genetic Locus

[00154] The present invention contemplates, in part, a capture probe module designed to retain the efficiency and reliability of larger probes but that minimizes

uninformative sequence generation in a genomic DNA library that comprises smaller DNA fragments, *e.g.*, a cfDNA clone library. A “capture probe” or “capture probe module” as used herein, are used interchangeably and refer to a polynucleotide that comprises a capture probe sequence and a tail sequence. In particular embodiments, the capture probe module sequence or a portion thereof serves as a primer binding site for one or more sequencing primers.

[00155] In particular embodiments, a capture probe module comprises a capture probe. As used herein a “capture probe” refers to a region capable of hybridizing to a specific DNA target region. In some embodiments, the capture probes are used with genomic DNA library constructed from cellular DNA. In particular embodiments, the capture probes are used with genomic DNA library constructed from cfDNA. Because the average size of cfDNA is about 150 to about 170 bp and is highly fragmented, certain embodiments are directed compositions and methods contemplated herein comprise the use of high density and relatively short capture probes to interrogate DNA target regions of interest. In some embodiments, the capture probes are capable of hybridizing to DNA target regions that are distributed across all chromosomal segments at a uniform density. A set of such capture probes is referred to herein as “chromosomal stability probes.” Chromosomal stability probes are used to interrogate copy number variations on a genome-wide scale in order to provide a genome-wide measurement of chromosomal copy number (*e.g.*, chromosomal ploidy).

[00156] One particular concern with using high density capture probes is that generally capture probes are designed using specific “sequence rules.” For example, regions of redundant sequence or that exhibit extreme base composition biases are generally excluded in designing capture probes. However, the present inventors have discovered that the lack of flexibility in capture probe design rules does not substantially impact probe performance. In contrast, capture probes chosen strictly by positional constraint provided on-target sequence information; exhibit very little off-target and unmappable read capture; and yield uniform, useful, on-target reads with only few exceptions. Moreover, the high redundancy at close probe spacing more than compensates for occasional poor-performing capture probes.

[00157] In particular embodiments, a target region is targeted by a plurality of capture probes, wherein any two or more capture probes are designed to bind to the target region within 10 nucleotides of each other, within 15 nucleotides of each other, within 20 nucleotides of each other, within 25 nucleotides of each other, within 30 nucleotides of each other, within 35 nucleotides of each other, within 40 nucleotides of each other, within 45

nucleotides of each other, or within 50 nucleotides or more of each other, as well as all intervening nucleotide lengths.

[00158] In one embodiment, the capture probe is about 25 nucleotides, about 26 nucleotides, about 27 nucleotides, about 28 nucleotides, about 29 nucleotides, about 30 nucleotides, about 31 nucleotides, about 32 nucleotides, about 33 nucleotides, about 34 nucleotides, about 35 nucleotides, about 36 nucleotides, about 37 nucleotides, about 38 nucleotides, about 39 nucleotides, about 40 nucleotides, about 41 nucleotides, about 42 nucleotides, about 43 nucleotides, about 44 nucleotides, or about 45 nucleotides.

[00159] In one embodiment, the capture probe is about 100 nucleotides, about 200 nucleotides, about 300 nucleotides, about 400 nucleotides, or about 100 nucleotides. In another embodiment, the capture probe is from about 100 nucleotides to about 500 nucleotides, about 200 nucleotides to about 500 nucleotides, about 300 nucleotides to about 500 nucleotides, or about 400 nucleotides to about 500 nucleotides, or any intervening range thereof.

[00160] In a particular embodiment, the capture probe is 60 nucleotides. In another embodiment, the capture probe is substantially smaller than 60 nucleotides but hybridizes comparably, as well as, or better than a 60 nucleotide capture probe targeting the same DNA target region. In a certain embodiment, the capture probe is 40 nucleotides.

[00161] In certain embodiments, a capture probe module comprises a tail sequence. As used herein, the term “tail sequence” refers to a polynucleotide at the 5' end of the capture probe module, which in particular embodiments can serve as a primer binding site. In particular embodiments, a sequencing primer binds to the primer binding site in the tail region.

[00162] In particular embodiments, the tail sequence is about 5 to about 100 nucleotides, about 10 to about 100 nucleotides, about 5 to about 75 nucleotides, about 5 to about 50 nucleotides, about 5 to about 25 nucleotides, or about 5 to about 20 nucleotides. In certain embodiments, the third region is from about 10 to about 50 nucleotides, about 15 to about 40 nucleotides, about 20 to about 30 nucleotides or about 20 nucleotides, or any intervening number of nucleotides.

[00163] In particular embodiments, the tail sequence is about 30 nucleotides, about 31 nucleotides, about 32 nucleotides, about 33 nucleotides, about 34 nucleotides, about 35 nucleotides, about 36 nucleotides, about 37 nucleotides, about 38 nucleotides, about 39 nucleotides, or about 40 nucleotides.

[00164] In various embodiments, the capture probe module comprises a specific member of a binding pair to enable isolation and/or purification of one or more captured fragments of a tagged and or amplified genomic DNA library (*e.g.*, a cellular or cfDNA library) that hybridizes to the capture probe. In particular embodiments, the capture probe module is conjugate to biotin or another suitable hapten, *e.g.*, dinitrophenol, digoxigenin.

[00165] In various embodiments, the capture probe module is hybridized to a tagged and optionally amplified DNA library to form a complex. In some embodiments, the multifunctional capture probe module substantially hybridizes to a specific genomic target region in the DNA library.

[00166] Hybridization or hybridizing conditions can include any reaction conditions where two nucleotide sequences form a stable complex; for example, the tagged DNA library and capture probe module forming a stable tagged DNA library—capture probe module complex. Such reaction conditions are well known in the art and those of skill in the art will appreciate that such conditions can be modified as appropriate, *e.g.*, decreased annealing temperatures with shorter length capture probes, and within the scope of the present invention. Substantial hybridization can occur when the second region of the capture probe complex exhibits 100%, 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 85%, 80%, 75%, or 70% sequence identity, homology or complementarity to a region of the tagged DNA library.

[00167] In particular embodiments, the capture probe is about 40 nucleotides and has an optimal annealing temperature of about 44° C to about 47° C.

[00168] In certain embodiments, the methods contemplated herein comprise isolating a tagged cfDNA library—capture probe module complex. In particular embodiments, methods for isolating DNA complexes are well known to those skilled in the art and any methods deemed appropriate by one of skill in the art can be employed with the methods of the present invention (Ausubel *et al.*, *Current Protocols in Molecular Biology*, 2007-2012). In particular embodiments, the complexes are isolated using biotin—streptavidin isolation techniques.

[00169] In particular embodiments, removal of the single stranded 3'-ends from the isolated tagged DNA library fragments-capture probe module complex is contemplated. In certain embodiments, the methods comprise 3'-5' exonuclease enzymatic processing of the

isolated tagged DNA library-multifunctional capture probe module complex to remove the single stranded 3' ends.

[00170] In certain other embodiments, the methods comprise performing 5'-3' DNA polymerase extension of multifunctional capture probe utilizing the isolated tagged DNA library fragments as template.

[00171] In certain other embodiments, the methods comprise creating a hybrid capture probe-isolated tagged DNA target molecule, *e.g.*, a tagged cfDNA target molecule or a tagged cellular DNA target molecule, through the concerted action of a 5' FLAP endonuclease, DNA polymerization and nick closure by a DNA ligase.

[00172] A variety of enzymes can be employed for the 3'-5' exonuclease enzymatic processing of the isolated tagged DNA library-multifunctional capture probe module complex. Illustrative examples of suitable enzymes, which exhibit 3'-5' exonuclease enzymatic activity, that can be employed in particular embodiments include, but are not limited to: T4 or Exonucleases I, III, V (*See also*, Shevelev IV, Hübscher U., *Nat Rev Mol Cell Biol.* 3(5):364-76 (2002)). In particular embodiments, the enzyme comprising 3'-5' exonuclease activity is T4 polymerase. In particular embodiments, an enzyme which exhibits 3'-5' exonuclease enzymatic activity and is capable of primer template extension can be employed, including for example T4 or Exonucleases I, III, V. *Id.*

[00173] In some embodiments, the methods contemplated herein comprise performing sequencing and/or PCR on the 3'-5' exonuclease enzymatically processed complex discussed *supra* and elsewhere herein. In particular embodiments, a tail portion of a capture probe molecule is copied in order to generate a hybrid nucleic acid molecule. In one embodiment, the hybrid nucleic acid molecule generated comprises the target region capable of hybridizing to the capture probe module and the complement of the capture probe module tail sequence.

[00174] In a particular embodiment, genetic analysis comprises a) hybridizing one or more capture probe modules to one or more target genetic loci in a plurality of genomic DNA library clones to form one or more capture probe module-DNA library clone complexes; b) isolating the one or more capture probe module-DNA library clone complexes from a); c) enzymatically processing the one or more isolated capture probe module-DNA library clone complexes from step b); d) performing PCR on the enzymatically processed complex from c) wherein the tail portion of the capture probe molecule is copied in order to generate amplified hybrid nucleic acid molecules, wherein the amplified hybrid nucleic acid

molecules comprise a target sequence in the target genomic locus capable of hybridizing to the capture probe and the complement of the capture probe module tail sequence; and e) performing quantitative genetic analysis on the amplified hybrid nucleic acid molecules from d).

[00175] In a particular embodiment, methods for determining copy number of a specific target genetic locus are contemplated comprising: a) hybridizing one or more capture probe modules to one or more target genetic loci in a plurality of DNA library clones to form one or more capture probe module-DNA library clone complexes; b) isolating the one or more capture probe module-DNA library clone complexes from a); c) enzymatically processing the one or more isolated capture probe module-DNA library clone complexes from step b); d) performing PCR on the enzymatically processed complex from c) wherein the tail portion of the capture probe molecule is copied in order to generate amplified hybrid nucleic acid molecules, wherein the amplified hybrid nucleic acid molecules comprise a target sequence in the target genetic locus capable of hybridizing to the capture probe and the complement of the capture probe module tail sequence; e) performing PCR amplification of the amplified hybrid nucleic acid molecules in d); and f) quantitating the PCR reaction in e), wherein the quantitation allows for a determination of copy number of the specific target region.

[00176] In one embodiment, the enzymatic processing of step c) comprises performing 3'-5' exonuclease enzymatic processing on the one or more capture probe module-DNA library clone complexes from b) using an enzyme with 3'-5' exonuclease activity to remove the single stranded 3' ends; creating one or more hybrid capture probe module-cfDNA library clone molecules through the concerted action of a 5' FLAP endonuclease, DNA polymerization and nick closure by a DNA ligase; or performing 5'-3' DNA polymerase extension of the capture probe using the isolated DNA clone in the complex as a template.

[00177] In one embodiment, the enzymatic processing of step c) comprises performing 5'-3' DNA polymerase extension of the capture probe using the isolated DNA clone in the complex as a template.

[00178] In particular embodiments, PCR can be performed using any standard PCR reaction conditions well known to those of skill in the art. In certain embodiments, the PCR reaction in e) employs two PCR primers. In one embodiment, the PCR reaction in e) employs a first PCR primer that hybridizes to a repeat within the target genetic locus. In a

particular embodiment, the PCR reaction in e) employs a second PCR primer that hybridizes to the hybrid nucleic acid molecules at the target genetic locus/tail junction. In certain embodiments, the PCR reaction in e) employs a first PCR primer that hybridizes to the target genetic locus and a second PCR primer hybridizes to the amplified hybrid nucleic acid molecules at the target genetic locus/tail junction. In particular embodiments, the second primer hybridizes to the target genetic locus/tail junction such that at least one or more nucleotides of the primer hybridize to the target genetic locus and at least one or more nucleotides of the primer hybridize to the tail sequence.

[00179] In certain embodiments, the amplified hybrid nucleic acid molecules obtained from step e) are sequenced and the sequences aligned horizontally, *i.e.*, aligned to one another but not aligned to a reference sequence. In particular embodiments, steps a) through e) are repeated one or more times with one or more capture probe modules. The capture probe modules can be the same or different and designed to target either cfDNA strand of a target genetic locus. In some embodiments, when the capture probes are different, they hybridize at overlapping or adjacent target sequences within a target genetic locus in the tagged cfDNA clone library. In one embodiment, a high density capture probe strategy is used wherein a plurality of capture probes hybridize to a target genetic locus, and wherein each of the plurality of capture probes hybridizes to the target genetic locus within about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 200 bp or more of any other capture probe that hybridizes to the target genetic locus in a tagged DNA clone library, including all intervening distances.

[00180] In some embodiments, the method can be performed using two capture probe modules per target genetic locus, wherein one hybridizes to the “Watson” strand (non-coding or template strand) upstream of the target region and one hybridizes to the “Crick” strand (coding or non-template strand) downstream of the target region.

[00181] In particular embodiments, the methods contemplated herein can further be performed multiple times with any number of capture probe modules, for example 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more capture probe modules per target genetic locus any number of which hybridize to the Watson or Crick strand in any combination. In some embodiments, the sequences obtained can be aligned to one another in order to identify any of a number of differences.

[00182] In certain embodiments, a plurality of target genetic loci are interrogated, *e.g.*, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1500, 2000, 2500, 3000,

3500, 4000, 4500, 5000, 10000, 50000, 100000, 500000 or more in a single reaction, using one or more capture probe modules.

(b) Sequencing

[00183] In particular embodiments, the quantitative genetic analysis comprises sequencing a plurality of hybrid nucleic acid molecules, as discussed elsewhere herein, *supra*, to generate sufficient sequencing depths to obtain a plurality of unique sequencing reads. The terms “unique reads” or “unique genomic sequences” (UGS) are used interchangeably herein and are identified by grouping individual redundant reads together into a “family.” Redundant reads are sequence reads that share an identical UMIE (*e.g.*, share the same read code and the same DNA sequence start position within genomic sequence) and are derived from a single attachment event and are therefore amplification-derived “siblings” of one another. A single consensus representative of a family of redundant reads is carried forward as a unique read or UGS. Each unique read or UGS is considered a unique attachment event. The sum of unique reads corresponding to a particular capture probe is referred to as the “raw genomic depth” (RGD) for that particular capture probe. Each capture probe yields a set of unique reads that are computationally distilled from total reads by grouping into families. The unique reads for a given sample (*e.g.*, raw genomic depth for a sample) are then computed as the average of all the unique reads observed on a probe-by-probe basis. Unique reads are important because each unique read must be derived from a unique genomic DNA clone. Each unique read represents the input and analysis of a haploid equivalent of genomic DNA. The sum of unique reads is the sum of haploid genomes analyzed. The number of genomes analyzed, in turn, defines the sensitivity of the sequencing assay. By way of a non-limiting example, if the average unique read count is 100 genome equivalents, then that particular assay has a sensitivity of being able to detect one mutant read in 100, or 1%. Any observation less than this is not defensible.

[00184] Cases where there is an obvious copy number change (*e.g.*, instances of noisy probes) are excluded from the data set used to compute the sample average. Herein, a “noisy probe” refers to a probe that captures a highly variable number of unique reads among a large set identical samples (*e.g.*, a highly variable number of unique reads among 12 – 16 sample replicates). In some embodiments, the number of unique reads associated with a noisy probe is increased compared to the average number of unique reads for the sample by

50% or more. In some embodiments, the number of unique reads associated with a noisy probe is decreased compared to the average number of unique reads for the sample by 50% or more. In some embodiments, about 2% to about 4% of probes used in a particular analysis are identified as noisy probes and are excluded from calculations to determine the average number of unique reads for a given sample.

[00185] In some embodiments, sequencing reads are identified as either “on-target reads” or “off-target reads.” On-target reads possess a genomic DNA sequence that maps within the vicinity of a capture probe used to create the genomic library. In some embodiments, where each genomic sequence is physically linked to a specific capture probe and where the sequence of the genomic segment and capture probe are both determined as a unified piece of information, an on-target read is defined as any genomic sequence whose starting coordinate maps within 400 bp, and more generally within 200 bp of the 3' end of the corresponding capture probe. Off-target reads are defined as having genomic sequence that aligns to the reference genome at a location ≥ 500 base pairs (and more often mapping to entirely different chromosomes) relative to the capture probe.

[00186] In particular embodiments, the quantitative genetic analysis comprises multiplex sequencing of hybrid nucleic acid molecules derived from a plurality of samples.

[00187] In various embodiments, the quantitative genetic analysis comprises obtaining one or more or a plurality of tagged DNA library clones, each clone comprising a first DNA sequence and a second DNA sequence, wherein the first DNA sequence comprises a sequence in a targeted genetic locus and the second DNA sequence comprises a capture probe sequence; performing a paired end sequencing reaction on the one or more clones and obtaining one or more sequencing reads or performing a sequencing reaction on the one or more clones in which a single long sequencing read of greater than about 100, 200, 300, 400, 500 or more nucleotides is obtained, wherein the read is sufficient to identify both the first DNA sequence and the second DNA sequence; and ordering or clustering the sequencing reads of the one or more clones according to the probe sequences of the sequencing reads.

(c) Bioinformatics Analysis

[00188] In various embodiments, the quantitative genetic analysis further comprises bioinformatic analysis of the sequencing reads. Bioinformatic analysis excludes any purely mental analysis performed in the absence of a composition or method for sequencing. In certain embodiments, bioinformatics analysis includes, but is not limited to:

sequence alignments; genome equivalents analysis; single nucleotide variant (SNV) analysis; gene copy number variation (CNV) analysis; measurement of chromosomal copy number; and detection of genetic lesions. In particular embodiments, bioinformatics analysis is useful to quantify the number of genome equivalents analyzed in the cfDNA clone library; to detect the genetic state of a target genetic locus; to detect genetic lesions in a target genetic locus; and to measure copy number fluctuations within a target genetic locus.

[00189] Sequence alignments may be performed between the sequence reads and one or more human reference DNA sequences. In particular embodiments, sequencing alignments can be used to detect genetic lesions in a target genetic locus including, but not limited to detection of a nucleotide transition or transversion, a nucleotide insertion or deletion, a genomic rearrangement, a change in copy number, or a gene fusion. Detection of genetic lesions that are causal or prognostic indicators may be useful in the diagnosis, prognosis, treatment, and/or monitoring of a particular genetic condition or disease.

[00190] Also contemplated herein, are methods for sequence alignment analysis that can be performed without the need for alignment to a reference sequence, referred to herein as horizontal sequence analysis. Such analysis can be performed on any sequences generated by the methods contemplated herein or any other methods. In particular embodiments, the sequence analysis comprises performing sequence alignments on the reads obtained by the methods contemplated herein.

[00191] In one embodiment, the genome equivalents in a cfDNA clone library are determined using bioinformatics-based counting after sequencing is performed. Each sequencing read is associated with a particular capture probe, and the collection of reads assigned to each capture probe is parsed into groups. Within a group, sets of individual reads share the same read code and the same DNA sequence start position within genomic sequence. These individual reads are grouped into a “family” and a single consensus representative of this family is carried forward as a “unique read.” All of the individual reads that constituted a family are derived from a single attachment event and thus, they are amplification-derived “siblings” of one another. Each unique read is considered a unique attachment event and the sum of unique reads is considered equivalent to the number of genome equivalents analyzed.

[00192] As the number of unique clones approaches the total number of possible sequence combinations, probability dictates that the same code and start site combinations will be created by independent events and that these independent events will be

inappropriately grouped within single families. The net result will be an underestimate of genome equivalents analyzed, and rare mutant reads may be discarded as sequencing errors because they overlap with wild-type reads bearing the same identifiers.

[00193] In particular embodiments, to provide an accurate analysis for cfDNA clone libraries, the number of genome equivalents analyzed is about 1/10, about 1/12, about 1/14, about 1/16, about 1/18, about 1/20, about 1/25 or less the number of possible unique clones. It should be understood that the procedure outlined above is merely illustrative and not limiting.

[00194] In some embodiments, the number of genome equivalents to be analyzed may need to be increased. To expand the depth of genome equivalents, at least two solutions are contemplated. The first solution is to use more than one adaptor set per sample. By combining adaptors, it is possible to multiplicatively expand the total number of possible clones and therefore, expand the comfortable limits of genomic input. The second solution is to expand the read code by 1, 2, 3, 4, or 5, or more bases. The number of possible read codes that differ by at least 2 bases from every other read code scales as $4^{(n-1)}$ where n is the number of bases within a read code. Thus, in a non-limiting example, if a read code is 5 nucleotides and $4^{(5-1)} = 256$; therefore, the inclusion of additional bases expands the available repertoire by a factor of four for each additional base.

[00195] In one embodiment, quantitative genetic analysis comprises bioinformatic analysis of sequencing reads to identify rare single nucleotide variants (SNV).

[00196] Next-generation sequencing has an inherent error rate of roughly 0.02-0.02%, meaning that anywhere from 1/200 to 1/500 base calls are incorrect. To detect variants and other mutations that occur at frequencies lower than this, for example at frequencies of 1 per 1000 sequences, it is necessary to invoke molecular annotation strategies. By way of a non-limiting example, analysis of 5000 unique molecules using targeted sequence capture technology would generate – at sufficient sequencing depths of >50,000 reads – a collection of 5000 unique reads, with each unique read belonging to a “family” of reads that all possess the same read code. A SNV that occurs within a family is a candidate for being a rare variant. When this same variant is observed in more than one family, it becomes a very strong candidate for being a rare variant that exists within the starting sample. In contrast, variants that occur sporadically within families are likely to be sequencing errors and variants that occur within one and only one family are either rare or the

result of a base alteration that occurred *ex vivo* (e.g., oxidation of a DNA base or PCR-introduced errors).

[00197] In one embodiment, the methods of detecting SNVs comprise introducing 10-fold more genomic input (genomes or genome equivalents) as the desired target sensitivity of the assay. In one non-limiting example, if the desired sensitivity is 2% (2 in 100), then the experimental target is an input of 2000 genomes.

[00198] In particular embodiments, bioinformatics analysis of sequencing data is used to detect or identify SNV associated with a genetic state, condition or disease, genetic mosaicism, fetal testing, paternity testing, predicting response to drug treatment, diagnosing or monitoring a medical condition, microbiome profiling, pathogen screening, and monitoring organ transplants.

[00199] In various embodiments, a method for copy number determination analysis is provided comprising obtaining one or more or a plurality of clones, each clone comprising a first DNA sequence and a second DNA sequence, wherein the first DNA sequence comprises a sequence in a targeted genetic locus and the second DNA sequence comprises a capture probe sequence. In related embodiments, a paired end sequencing reaction on the one or more clones is performed and one or more sequencing reads are obtained. In another embodiment, a sequencing reaction on the one or more clones is performed in which a single long sequencing read of greater than about 100 nucleotides is obtained, wherein the read is sufficient to identify both the first DNA sequence and the second DNA sequence. The sequencing reads of the one or more clones can be ordered or clustered according to the probe sequence of the sequencing reads.

[00200] Copy number analyses include, but are not limited to, analyses that examine the number of copies of a particular gene or mutation that occurs in a given genomic DNA sample and can further include quantitative determination of the number of copies of a given gene or sequence differences in a given sample. In particular embodiments, copy number analysis is used to detect or identify gene amplification associated with genetic states, conditions, or diseases, fetal testing, genetic mosaicism, paternity testing, predicting response to drug treatment, diagnosing or monitoring a medical condition, microbiome profiling, pathogen screening, and monitoring organ transplants.

[00201] In some embodiments, copy number analysis is used to measure chromosomal instability. In such embodiments, sets of capture probes that comprise chromosomal stability probes are used to determine copy number variations at a uniform

density across all sets of chromosomes. Copy number analyses are performed for each chromosomal stability probe and the chromosomal stability probes are then ordered according to their chromosomal target. This allows for visualization of copy number losses or gains across the genome and can serve as a measure of chromosomal stability.

[00202] In particular embodiments, bioinformatics analysis of sequencing data is used to detect or identify one or more sequences or genetic lesions in a target locus including, but not limited to detection of a nucleotide transition or transversion, a nucleotide insertion or deletion, a genomic rearrangement, a change in copy number, or a gene fusion. Detection of genetic lesions that are causal or prognostic indicators may be useful in the diagnosis, prognosis, treatment, and/or monitoring of a particular genetic condition or disease. In one embodiment, genetic lesions are associated with genetic states, conditions, or diseases, fetal testing, genetic mosaicism, paternity testing, predicting response to drug treatment, diagnosing or monitoring a medical condition, microbiome profiling, pathogen screening, and monitoring organ transplants.

D. CLINICAL APPLICATIONS OF QUANTITATIVE CNL ASSAYS

[00203] In various embodiments, the present invention contemplates a method of detecting, identifying, predicting, diagnosing, or monitoring a condition or disease in a subject by detecting a mutational change, SNP, translocation, inversion, deletion, change in copy number or other genetic variation in a region of interest.

E. CLINICAL APPLICATIONS OF QUANTITATIVE GENETIC ANALYSIS

[00204] In various embodiments, the present invention contemplates a method of detecting, identifying, predicting, diagnosing, or monitoring a condition or disease in a subject.

[00205] In particular embodiments, a method of detecting, identifying, predicting, diagnosing, or monitoring a genetic state, condition or disease in a subject comprises performing a quantitative genetic analysis of one or more target genetic loci in a DNA clone library to detect or identify a change in the sequence at the one or more target genetic loci. In some embodiments, the change is a change in copy number.

[00206] In one embodiment, a method of detecting, identifying, predicting, diagnosing, or monitoring a genetic state, condition or disease comprises isolating or obtaining cellular DNA or cfDNA from a biological sample of a subject; treating the cellular DNA or cfDNA with one or more end-repair enzymes to generate end-repaired DNA; attaching one or more adaptors to each end of the end-repaired DNA to generate a genomic DNA library; amplifying the DNA library to generate a DNA clone library; determining the number of genome equivalents in the DNA clone library; and performing a quantitative genetic analysis of one or more target genetic loci in a DNA clone library to detect or identify a change in the sequence, *e.g.*, an SNP, a translocation, an inversion, a deletion, or a change in copy number at of the one or more target genetic loci.

[00207] In particular embodiments, a method of detecting, identifying, predicting, diagnosing, or monitoring a genetic state, or genetic condition or disease selected from the group consisting of: genetic diseases; genetic mosaicism; fetal testing; paternity testing; paternity testing; predicting response to drug treatment; diagnosing or monitoring a medical condition; microbiome profiling; pathogen screening; and organ transplant monitoring comprising isolating or obtaining genomic DNA from a biological sample of a subject; treating the DNA with one or more end-repair enzymes to generate end-repaired DNA; attaching one or more adaptors to each end of the end-repaired DNA to generate a genomic DNA library; amplifying the genomic DNA library to generate a DNA clone library; determining the number of genome equivalents in the DNA clone library; and performing a quantitative genetic analysis of one or more target genetic loci in a DNA clone library to detect or identify a nucleotide transition or transversion, a nucleotide insertion or deletion, a genomic rearrangement, a change in copy number, or a gene fusion in the sequence at the one or more target genetic loci.

[00208] Illustrative examples of genetic diseases that can be detected, identified, predicted, diagnosed, or monitored with the compositions and methods contemplated herein include, but are not limited to cancer, Alzheimer's disease (APOE1), Charcot-Marie-Tooth disease, Leber hereditary optic neuropathy (LHON), Angelman syndrome (UBE3A, ubiquitin-protein ligase E3A), Prader-Willi syndrome (region in chromosome 15), β -Thalassaemia (HBB, β -Globin), Gaucher disease (type I) (GBA, Glucocerebrosidase), Cystic fibrosis (CFTR Epithelial chloride channel), Sickle cell disease (HBB, β -Globin), Tay-Sachs disease (HEXA, Hexosaminidase A), Phenylketonuria (PAH, Phenylalanine hydrolyase), Familial hypercholesterolaemia (LDLR, Low density lipoprotein

receptor), Adult polycystic kidney disease (PKD1, Polycystin), Huntington disease (HDD, Huntingtin), Neurofibromatosis type I (NF1, NF1 tumour suppressor gene), Myotonic dystrophy (DM, Myotonin), Tuberous sclerosis (TSC1, Tuberin), Achondroplasia (FGFR3, Fibroblast growth factor receptor), Fragile X syndrome (FMR1, RNA-binding protein), Duchenne muscular dystrophy (DMD, Dystrophin), Haemophilia A (F8C, Blood coagulation factor VIII), Lesch–Nyhan syndrome (HPRT1, Hypoxanthine guanine ribosyltransferase 1), and Adrenoleukodystrophy (ABCD1).

[00209] Illustrative examples of cancers that can be detected, identified, predicted, diagnosed, or monitored with the compositions and methods contemplated herein include, but are not limited to: B cell cancer, *e.g.*, multiple myeloma, melanomas, breast cancer, lung cancer (such as non-small cell lung carcinoma or NSCLC), bronchus cancer, colorectal cancer, prostate cancer, pancreatic cancer, stomach cancer, ovarian cancer, urinary bladder cancer, brain or central nervous system cancer, peripheral nervous system cancer, esophageal cancer, cervical cancer, uterine or endometrial cancer, cancer of the oral cavity or pharynx, liver cancer, kidney cancer, testicular cancer, biliary tract cancer, small bowel or appendix cancer, salivary gland cancer, thyroid gland cancer, adrenal gland cancer, osteosarcoma, chondrosarcoma, cancer of hematological tissues, adenocarcinomas, inflammatory myofibroblastic tumors, gastrointestinal stromal tumor (GIST), colon cancer, multiple myeloma (MM), myelodysplastic syndrome (MDS), myeloproliferative disorder (MPD), acute lymphocytic leukemia (ALL), acute myelocytic leukemia (AML), chronic myelocytic leukemia (CML), chronic lymphocytic leukemia (CLL), polycythemia Vera, Hodgkin lymphoma, non-Hodgkin lymphoma (NHL), soft-tissue sarcoma, fibrosarcoma, myxosarcoma, liposarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilms' tumor, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma, retinoblastoma, follicular lymphoma, diffuse large B-cell lymphoma, mantle cell lymphoma, hepatocellular carcinoma, thyroid cancer, gastric cancer,

head and neck cancer, small cell cancers, essential thrombocythemia, agnogenic myeloid metaplasia, hypereosinophilic syndrome, systemic mastocytosis, familial hypereosinophilia, chronic eosinophilic leukemia, neuroendocrine cancers, carcinoid tumors, and the like.

[00210] In one embodiment, the genetic lesion is a lesion annotated in the Cosmic database (the lesions and sequence data are available online and can be downloaded from the Cancer Gene Census section of the Cosmic website) or a lesion annotated in the Cancer Genome Atlas (the lesions and sequence data are available online and can be downloaded from The Cancer Genome Atlas website).

[00211] Illustrative examples of genes that harbor one or more genetic lesions associated with cancer that can be detected, identified, predicted, diagnosed, or monitored with the compositions and methods contemplated herein include, but are not limited to ABCB1, ABCC2, ABCC4, ABCG2, ABL1, ABL2, AKT1, AKT2, AKT3, ALDH4A1, ALK, APC, AR, ARAF, ARFRP1, ARID1A, ATM, ATR, AURKA, AURKB, BCL2, BCL2A1, BCL2L1, BCL2L2, BCL6, BRAF, BRCA1, BRCA2, Clorf144, CARD11, CBL, CCND1, CCND2, CCND3, CCNE1, CDH1, CDH2, CDH20, CDH5, CDK4, CDK6, CDK8, CDKN2A, CDKN2B, CDKN2C, CEBPA, CHEK1, CHEK2, CRKL, CRLF2, CTNNB1, CYP1B1, CYP2C19, CYP2C8, CYP2D6, CYP3A4, CYP3A5, DNMT3A, DOT1L, DPYD, EGFR, EPHA3, EPHA5, EPHA6, EPHA7, EPHB1, EPHB4, EPHB6, EPHX1, ERBB2, ERBB3, ERBB4, ERCC2, ERG, ESR1, ESR2, ETV1, ETV4, ETV5, ETV6, EWSR1, EZH2, FANCA, FBXW7, FCGR3A, FGFR1, FGFR2, FGFR3, FGFR4, FLT1, FLT3, FLT4, FOXP4, GATA1, GNA11, GNAQ, GNAS, GPR124, GSTP1, GUCY1A2, HOXA3, HRAS, HSP90AA1, IDH1, IDH2, IGF1R, IGF2R, IKBKE, IKZF1, INHBA, IRS2, ITPA, JAK1, JAK2, JAK3, JUN, KDR, KIT, KRAS, LRP1B, LRP2, LTK, MAN1B1, MAP2K1, MAP2K2, MAP2K4, MCL1, MDM2, MDM4, MEN1, MET, MITF, MLH1, MLL, MPL, MRE11A, MSH2, MSH6, MTHFR, MTOR, MUTYH, MYC, MYCL1, MYCN, NF1, NF2, NKX2-1, NOTCH1, NPM1, NQO1, NRAS, NRP2, NTRK1, NTRK3, PAK3, PAX5, PDGFRA, PDGFRB, PIK3CA, PIK3R1, PKHD1, PLCG1, PRKDC, PTCH1, PTEN, PTPN11, PTPRD, RAF1, RARA, RB1, RET, RICTOR, RPTOR, RUNX1, SLC19A1, SLC22A2, SLC01B3, SMAD2, SMAD3, SMAD4, SMARCA4, SMARCB1, SMO, SOD2, SOX10, SOX2, SRC, STK11, SULT1A1, TBX22, TET2, TGFB2, TMPRSS2, TNFRSF14, TOP1, TP53, TPMT, TSC1, TSC2, TYMS, UGT1A1, UMPS, USP9X, VHL, and WT1.

[00212] In particular embodiments, the genetic lesion comprises a nucleotide transition or transversion, a nucleotide insertion or deletion, a genomic rearrangement, a change in copy number, or a gene fusion.

[00213] In one embodiment, the genetic lesion is a gene fusion that fuses the 3' coding region of the ALK gene to another gene.

[00214] In one embodiment, the genetic lesion is a gene fusion that fuses the 3' coding region of the ALK gene to the EML4 gene.

[00215] Illustrative examples of conditions suitable for fetal testing that can be detected, identified, predicted, diagnosed, or monitored with the compositions and methods contemplated herein include but are not limited to: Down Syndrome (Trisomy 21), Edwards Syndrome (Trisomy 18), Patau Syndrome (Trisomy 13), Klinefelter's Syndrome (XXY), Triple X syndrome, XYY syndrome, Trisomy 8, Trisomy 16, Turner Syndrome (XO), Robertsonian translocation, DiGeorge Syndrome and Wolf-Hirschhorn Syndrome.

[00216] Illustrative examples of alleles suitable for paternity testing that can be detected, identified, predicted, diagnosed, or monitored with the compositions and methods contemplated herein include but are not limited to 16 or more of: D20S1082, D6S474, D12ATA63, D22S1045, D10S1248, D1S1677, D11S4463, D4S2364, D9S1122, D2S1776, D10S1425, D3S3053, D5S2500, D1S1627, D3S4529, D2S441, D17S974, D6S1017, D4S2408, D9S2157, Amelogenin, D17S1301, D1GATA113, D18S853, D20S482, and D14S1434.

[00217] Illustrative examples of genes suitable for predicting the response to drug treatment that can be detected, identified, predicted, diagnosed, or monitored with the compositions and methods contemplated herein include, but are not limited to, one or more of the following genes: ABCB1 (ATP-binding cassette, sub-family B (MDR/TAP), member 1), ACE (angiotensin I converting enzyme), ADH1A (alcohol dehydrogenase 1A (class I), alpha polypeptide), ADH1B (alcohol dehydrogenase 1B (class I), beta polypeptide), ADH1C (alcohol dehydrogenase 1C (class I), gamma polypeptide), ADRB1 (adrenergic, beta-1-, receptor), ADRB2 (adrenergic, beta-2-, receptor, surface), AHR (aryl hydrocarbon receptor), ALDH1A1 (aldehyde dehydrogenase 1 family, member A1), ALOX5 (arachidonate 5-lipoxygenase), BRCA1 (breast cancer 1, early onset), COMT (catechol-O-methyltransferase), CYP2A6 (cytochrome P450, family 2, subfamily A, polypeptide 6), CYP2B6 (cytochrome P450, family 2, subfamily B, polypeptide 6), CYP2C9 (cytochrome P450, family 2, subfamily C, polypeptide 9), CYP2C19 (cytochrome P450, family 2, subfamily C,

polypeptide 19), CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6), CYP2J2 (cytochrome P450, family 2, subfamily J, polypeptide 2), CYP3A4 (cytochrome P450, family 3, subfamily A, polypeptide 4), CYP3A5 (cytochrome P450, family 3, subfamily A, polypeptide 5), DPYD (dihydropyrimidine dehydrogenase), DRD2 (dopamine receptor D2), F5 (coagulation factor V), GSTP1 (glutathione S-transferase pi), HMGCR (3-hydroxy-3-methylglutaryl-Coenzyme A reductase), KCNH2 (potassium voltage-gated channel, subfamily H (eag-related), member 2), KCNJ11 (potassium inwardly-rectifying channel, subfamily J, member 11), MTHFR (5,10-methylenetetrahydrofolate reductase (NADPH)), NQO1 (NAD(P)H dehydrogenase, quinone 1), P2RY1 (purinergic receptor P2Y, G-protein coupled, 1), P2RY12 (purinergic receptor P2Y, G-protein coupled, 12), PTGIS (prostaglandin I₂ (prostacyclin) synthase), SCN5A (sodium channel, voltage-gated, type V, alpha (long QT syndrome 3)), SLC19A1 (solute carrier family 19 (folate transporter), member 1), SLCO1B1 (solute carrier organic anion transporter family, member 1B1), SULT1A1 (sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1), TPMT (thiopurine S-methyltransferase), TYMS (thymidylate synthetase), UGT1A1 (UDP glucuronosyltransferase 1 family, polypeptide A1), VDR (vitamin D (1,25- dihydroxyvitamin D₃) receptor), VKORC1 (vitamin K epoxide reductase complex, subunit 1).

[00218] Illustrative examples of medical conditions that can be detected, identified, predicted, diagnosed, or monitored with the compositions and methods contemplated herein include, but are not limited to: stroke, transient ischemic attack, traumatic brain injury, heart disease, heart attack, angina, atherosclerosis, and high blood pressure.

[00219] Illustrative examples of pathogens that can be screened for with the compositions and methods contemplated herein include, but are not limited to: bacteria fungi, and viruses.

[00220] Illustrative examples of bacterial species that can be screened for with the compositions and methods contemplated herein include, but are not limited to: a *Mycobacterium* spp., a *Pneumococcus* spp., an *Escherichia* spp., a *Campylobacter* spp., a *Corynebacterium* spp., a *Clostridium* spp., a *Streptococcus* spp., a *Staphylococcus* spp., a *Pseudomonas* spp., a *Shigella* spp., a *Treponema* spp., or a *Salmonella* spp.

[00221] Illustrative examples of fungal species that can be screened for with the compositions and methods contemplated herein include, but are not limited to: an *Aspergillus* spp., a *Blastomyces* spp., a *Candida* spp., a *Coccidioides* spp., a *Cryptococcus*

spp., dermatophytes, a *Tinea* spp., a *Trichophyton* spp., a *Microsporum* spp., a *Fusarium* spp., a *Histoplasma* spp., a *Mucoromycotina* spp., a *Pneumocystis* spp., a *Sporothrix* spp., an *Exserophilum* spp., or a *Cladosporium* spp.

[00222] Illustrative examples of viruses that can be screened for with the compositions and methods contemplated herein include, but are not limited to: Influenza A such as H1N1, H1N2, H3N2 and H5N1 (bird flu), Influenza B, Influenza C virus, Hepatitis A virus, Hepatitis B virus, Hepatitis C virus, Hepatitis D virus, Hepatitis E virus, Rotavirus, any virus of the Norwalk virus group, enteric adenoviruses, parvovirus, Dengue fever virus, Monkey pox, Mononegavirales, Lyssavirus such as rabies virus, Lagos bat virus, Mokola virus, Duvenhage virus, European bat virus 1 & 2 and Australian bat virus, Ephemero virus, Vesiculovirus, Vesicular Stomatitis Virus (VSV), Herpesviruses such as Herpes simplex virus types 1 and 2, varicella zoster, cytomegalovirus, Epstein-Bar virus (EBV), human herpesviruses (HHV), human herpesvirus type 6 and 8, Moloney murine leukemia virus (M-MuLV), Moloney murine sarcoma virus (MoMSV), Harvey murine sarcoma virus (HaMuSV), murine mammary tumor virus (MuMTV), gibbon ape leukemia virus (GaLV), feline leukemia virus (FLV), spumavirus, Friend murine leukemia virus, Murine Stem Cell Virus (MSCV) and Rous Sarcoma Virus (RSV), HIV (human immunodeficiency virus; including HIV type 1, and HIV type 2), visna-maedi virus (VMV) virus, the caprine arthritis-encephalitis virus (CAEV), equine infectious anemia virus (EIAV), feline immunodeficiency virus (FIV), bovine immune deficiency virus (BIV), and simian immunodeficiency virus (SIV), papilloma virus, murine gammaherpesvirus, Arenaviruses such as Argentine hemorrhagic fever virus, Bolivian hemorrhagic fever virus, Sabia-associated hemorrhagic fever virus, Venezuelan hemorrhagic fever virus, Lassa fever virus, Machupo virus, Lymphocytic choriomeningitis virus (LCMV), Bunyaviridae such as Crimean-Congo hemorrhagic fever virus, Hantavirus, hemorrhagic fever with renal syndrome causing virus, Rift Valley fever virus, Filoviridae (filovirus) including Ebola hemorrhagic fever and Marburg hemorrhagic fever, Flaviviridae including Kaysanur Forest disease virus, Omsk hemorrhagic fever virus, Tick-borne encephalitis causing virus and Paramyxoviridae such as Hendra virus and Nipah virus, variola major and variola minor (smallpox), alphaviruses such as Venezuelan equine encephalitis virus, eastern equine encephalitis virus, western equine encephalitis virus, SARS-associated coronavirus (SARS-CoV), West Nile virus, and any encephalitis causing virus.

[00223] Illustrative examples of genes suitable for monitoring an organ transplant in a transplant recipient that can be detected, identified, predicted, diagnosed, or monitored with the compositions and methods contemplated herein include, but are not limited to, one or more of the following genes: HLA-A, HLA-B, HLA-C, HLA-DR, HLA-DP, and HLA-DQ.

[00224] In particular embodiments, a bioinformatic analysis is used to quantify the number of genome equivalents analyzed in the cfDNA clone library; detect genetic variants in a target genetic locus; detect mutations within a target genetic locus; detect genetic fusions within a target genetic locus; or measure copy number fluctuations within a target genetic locus.

F. COMPANION DIAGNOSTICS

[00225] In various embodiments, a companion diagnostic for a genetic disease is provided, comprising: isolating or obtaining genomic DNA from a biological sample of a subject; treating the DNA with one or more end-repair enzymes to generate end-repaired DNA; attaching one or more adaptors to each end of the end-repaired DNA to generate a DNA library; amplifying the DNA library to generate a DNA clone library; determining the number of genome equivalents in the DNA clone library; and performing a quantitative genetic analysis of one or more biomarkers associated with the genetic disease in the DNA clone library, wherein detection of, or failure to detect, at least one of the one or more biomarkers indicates whether the subject should be treated for the genetic disease. In some embodiments, the DNA is cfDNA. In particular embodiments, the DNA is cellular DNA.

[00226] As used herein, the term “companion diagnostic” refers to a diagnostic test that is linked to a particular anti-cancer therapy. In a particular embodiment, the diagnostic methods comprise detection of genetic lesion in a biomarker associated with in a biological sample, thereby allowing for prompt identification of patients should or should not be treated with the anti-cancer therapy.

[00227] Anti-cancer therapy includes, but is not limited to surgery, radiation, chemotherapeutics, anti-cancer drugs, and immunomodulators.

[00228] Illustrative examples of anti-cancer drugs include, but are not limited to: alkylating agents such as thiotepa and cyclophosphamide (CYTOXAN™); alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa,

carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, trietylenephosphoramidate, triethylenethiophosphoramidate and trimethylolomelamine resins; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, ranimustine; antibiotics such as aclacinomysins, actinomycin, anthramycin, azaserine, bleomycins, cactinomycin, calicheamicin, carabycin, carminomycin, carzinophilin, chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, doxorubicin and its pegylated formulations, epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine, 5-FU; androgens such as calusterone, dromostanolone propionate, epitostanol, mepitiostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; amsacrine; bestabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elformithine; elliptinium acetate; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidamine; mitoguanzone; mitoxantrone; mopidamol; nitracrine; pentostatin; phenamet; pirarubicin; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK®; razoxane; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2, 2',2''-trichlorotriethylamine; urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; taxoids, *e.g.*, paclitaxel (TAXOL®, Bristol-Myers Squibb Oncology, Princeton, N.J.) and doxorubicin (TAXOTERE®, Rhne-Poulenc Rorer, Antony, France); chlorambucil; gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitomycin C; mitoxantrone; vincristine; vinorelbine; navelbine; novantrone; teniposide; aminopterin; xeloda; ibandronate; CPT-11; topoisomerase inhibitor RFS 2000; difluoromethylomithine (DMFO); retinoic acid derivatives such as Targretin™ (bexarotene), Panretin™ (alitretinoin);

ONTAK™ (denileukin diftitox) ; esperamicins; capecitabine; and pharmaceutically acceptable salts, acids or derivatives of any of the above. Also included in this definition are anti-hormonal agents that act to regulate or inhibit hormone action on cancers such as anti-estrogens including for example tamoxifen, raloxifene, aromatase inhibiting 4(5)-imidazoles, 4-hydroxytamoxifen, trioxifene, keoxifene, LY117018, onapristone, and toremifene (Fareston); and anti-androgens such as flutamide, nilutamide, bicalutamide, leuprolide, and goserelin; and pharmaceutically acceptable salts, acids or derivatives of any of the above.

[00229] Illustrative examples of immunomodulators include, but are not limited to: cyclosporine, tacrolimus, tresperimus, pimecrolimus, sirolimus, verolimus, laflunimus, laquinimod and imiquimod, as well as analogs, derivatives, salts, ions and complexes thereof.

[00230] In some embodiments, an anti-cancer drug may include a poly-ADP ribose polymerase (PARP) inhibitor. Illustrative examples of PARP inhibitors include, but are not limited to, olaparib (AZD-2281), rucaparib (AG014699 or PF-01367338, niraparib (MK-4827), talazoparib (BMN-673) veliparib (ABT-888), CEP 9722, E7016, BGB-290, 3-aminobenzamide.

[00231] All publications, patent applications, and issued patents cited in this specification are herein incorporated by reference as if each individual publication, patent application, or issued patent were specifically and individually indicated to be incorporated by reference. In particular, the entire contents of International PCT Publication No. WO 2016/028316 are specifically incorporated by reference.

[00232] Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to one of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims. The following examples are provided by way of illustration only and not by way of limitation. Those of skill in the art will readily recognize a variety of noncritical parameters that could be changed or modified to yield essentially similar results.

EXAMPLES

Example 1: Copy Number Analysis of Samples Containing Blends Of Fragmented Genomic DNA

[00233] Meticulous blends of fragmented genomic DNA were generated that contained DNA derived from Δ ATM or Δ BRCA2 immortalized human samples spiked into a

fragmented wild-type human gDNA sample. The advantage of this sample type is that the composition can be carefully controlled and sample availability is essentially unlimited.

[00234] Wild-type, human female genomic DNA was purified from whole blood samples donated by a healthy volunteer. Genomic DNA isolated from an immortalized cell harboring a heterozygous deletion covering the entire ATM gene (NA09596, Δ ATM) and a separate sample bearing a heterozygous deletion of BRCA2 (NA02718, Δ BRCA2) were obtained from the Coriell repository. Importantly, these samples appeared to have an otherwise normal ploidy across the remainder of the genomes. The Δ ATM sample was derived from a male donor and was therefore also hemizygous in copy number for the X-linked AR gene. Cell free DNA (cfDNA) was obtained from healthy donor plasma samples of female or male origin. For library construction, genomic DNA was sonicated on a setting of 200 bp with a Covaris instrument, then further size selected using a “two-sided” DNA bead purification. Library input DNA samples are shown in FIG. 7.

[00235] Appropriate combinations of fragmented and cfDNA samples were blended to defined percentages, end-repaired, and converted to genomic libraries. Approximately 500 ng of each library was combined in sets of eight samples and hybridized to the copy number loss (CNL) prostate probe pool that contained 2304 DNA probes. Following sample processing, each set of eight samples was sequenced on an Illumina NextSeq NGS instrument to a depth of ~480 million pass-filter reads; this corresponds to 60 million reads/sample. Roughly 95% of reads possessed legitimate sample ID tags and aligned to the human reference genome and of these, ~98% mapped to the intended target loci. The overall sequencing depth, measured as the number of reads per input genome per probe (calculated as on-target reads (60 million) divided by average genome depth (2500) and divided by probe count (2400)) was approximately 10 reads per genome per probe. A graphic representation of the copy number loss analysis is shown in FIG. 1. Copy number perturbations are highlighted by arrows. (Sample 1, 5% male DNA into female DNA; sample 2, 5% Δ ATM DNA (male) into female DNA; sample 3, 5% Δ BRCA2 DNA (female) into female DNA; sample 4, pure female DNA).

[00236] The CNL caller identifies redundant reads and condenses these into a single consensus reads that are then quantified at each probe location. This information was further condensed into gene-by-gene copy number averages. Finally, a statistical significance

was assigned to deviations detected in each CNL measurement; this is shown graphically as the $\log_{10}P$ -value of statistical significance.

[00237] FIG. 8 shows box-and-whisker plots of copy number determinations for the AR (FIG. 8B) and ATM (FIG. 8C) genes in fragmented and blended genomic libraries. Because the Δ ATM sample is male, the AR gene (X-linked, hemizygous) and the ATM gene both exhibited CNL behavior. As anticipated, the magnitude of measured copy variation was modest. The statistical analysis shown in FIG. 9B demonstrates that the observed copy fluctuation was statistically significant. Moreover, very little significant fluctuation was observed in the remaining genes that were predicted to exhibit uniform copy characteristics. These values correlated well with frequencies predicted for the various genomic blends. FIG. 10 shows that statistically significant copy fluctuation was also readily observed in samples that were primarily cfDNA with minor spike-ins of either cfDNA from the opposite sex or minor additions of fragmented gDNA. These values correlated well with frequencies predicted for the various genomic blends. The results seen with both fragmented gDNA and with cfDNA were comparable, thereby demonstrating the integrity of the assay and suggesting that the integrity will translate to clinical samples.

[00238] These data demonstrate the ability of the assay system to detect subtle changes in gene copy number down to minor allele frequencies of 2%. While the focus of demonstrated examples presented is on copy number loss, the technology is equally well suited to the detection of copy number gains, including increases in gene copy that occur through chromosomal arm duplications and focal amplifications. This assay further retains the ability to detect other types of genomic variants, including SNVs, indels and gene fusions (chromosomal rearrangements). Importantly, these data demonstrate that the method can be applied to genomic DNA derived from plasma, but also to genomic DNA derived from other sources such as tissue and other bodily sources.

Example 2: Copy number analysis of cfDNA from healthy donors and a cancer patient

[00239] The following example illustrate the manner in which the molecular features added during genomic library construction and post-hybridization processing are used to generate copy number analysis. DNA was extracted from the plasma of sixteen healthy donors and one castration-resistant prostate cancer patient using the Qiagen Circulating Nucleic Acids Extraction kit (Qiagen, Hilden, Germany). The yield of double-strand DNA was quantified using a Qubit fluorometer (Thermo Fisher, Waltham, MA) and

the corresponding hsDNA quantitation kit. Size analysis was performed using gel electrophoresis on 2% agarose gels with PCR markers as size standards (New England Biolabs, Ipswich, MA). Approximately 40 – 100 ng of cfDNA, depending on the yield of cfDNA from the sample, was used for library construction.

[00240] The basic features of library construction are illustrated in FIG. 11A – 11C. The cfDNA was first dephosphorylated and then repaired to blunt ends in a two-step process. Short, 10 nt anchor sequences consisting of a phosphorylated ligation strand and an inert partner strand were then ligated to the cfDNA. The eight oligonucleotides used to create the set of four anchor sequences are shown in Table 1.

Table 1: Ligation anchor oligonucleotides

Oligo ID	Nucleic Acid Sequence	SEQ ID NO:
Partner strand oLigation strand oligoo_16-1	GTATGCC[3-dA-Q]*	1
Partner strand oLigation strand oligoo_16-2	AGCGTTA[3-dC-Q]*	2
Partner strand oLigation strand oligoo_16-3	TCGACAT[3-dG-Q]*	3
Partner strand oLigation strand oligoo_16-4	CATCAGG[3-dT-Q]*	4
Ligation strand oligo_16-1	/5Phos/TGG CAT ACG T**	5
Ligation strand oligo_16-2	/5Phos/GTA ACG CTA G**	6
Ligation strand oligo_16-3	/5Phos/CAT GTC GAT C**	7
Ligation strand oligo_16-4	/5Phos/ACC TGA TGC A**	8

*[3-d(A, C, G, or T)-Q] denotes a modified base in which the hydroxyl group resides on the 2' position of the ribose ring

** /5Phos/ denotes the chemical addition of a 5' phosphate group to the 5' base position

[00241] The adaptor structures were completed by the addition of full-length adaptor sequences that annealed to the anchor sequence. Thirty-two sets of adaptor sequences, each composed of 240 members, are shown in FIG. 12 – FIG. 22. These adaptors were attached to the cfDNA and extended through the concerted actions of polynucleotide kinase, DNA polymerase and DNA ligase to generate genomic libraries. As a pre-sequencing quality control step, the resulting genomic libraries were quantified by qPCR for depth of coverage. The genomic libraries were then amplified and hybridized to probe sets targeting specific genes (FIG. 11B). Following hybridization, primer extension of the probe was used to copy the captured genomic sequences and the information encoded in the attached adaptor (FIG. 11C). An example of post sequencing analysis using standard next-generation analysis software is shown in FIG. 11D. This analysis was performed on a sequencing run that

contained 32 samples (28 cancer patient samples and 4 wild-type controls) and it displays the overall distribution of sequencing reads.

[00242] A central feature of the targeted hybrid capture platform described herein is that it provides multiple types of genomic information. One essential function of capture probes is to provide mutation detection across target regions at a high depth of coverage. This function is governed by the sequence context, density, and placement of the capture probes and is illustrated in FIG. 23 with the TP53 gene (TP53 probe sequences are shown in Table 2 below). Of equal significance, the targeted hybrid capture platform assay generated a readout of equal depth of coverage in regions where no significant mutations were detected. These data are critical to physicians and patients as they add statistical significance in cases where no deleterious mutations were detected.

Table 2: TP53 Probes

Name	Sequence	SEQ ID NO:
TP53_1	GGCACAGACCCTCTCACTCATGTGATGTCATCTCTCCTCC	7689
TP53_2	ATGGGGGTGGGAGGCTGTCAGTGGGGAACAAGAAGTGGAG	7690
TP53_3	GTCAGTCTGAGTCAGGCCCTTCTGTCTTGAACATGAGTTT	7691
TP53_4	CCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAA	7692
TP53_5	TCATGCTGGATCCCCACTTTTCCTCTTGACAGCCAGAC	7693
TP53_6	GTTGGGGTGGGGGTGGTGGGCCTGCCCTTCCAATGGATCC	7694
TP53_7	CAGTTTCCATAGGTCTGAAAATGTTTCCTGACTCAGAGGG	7695
TP53_8	CTGCCATGGAGGAGCCGAGTCAGATCCTAGCGTCGAGCC	7696
TP53_9	GCAGAGACCTGTGGGAAGCGAAAATTCATGGGACTGACT	7697
TP53_10	CTGGGGGGCTGGGGGGCTGAGGACCTGGTCCTCTGACTGC	7698
TP53_11	GCAGGGGGGATACGGCCAGGCATTGAAGTCTCATGGAAGCC	7699
TP53_12	GTGGCCCCTGCACCAGCAGCTCCTACACCGGCGGCCCTG	7700
TP53_13	GGGGGGAGCAGCCTCTGGCATTCTGGGAGCTTCATCTGGA	7701
TP53_14	CCGTGCAAGTCACAGACTTGGCTGTCCAGAATGCAAGAA	7702
TP53_15	CCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGG	7703
TP53_16	CCAGAAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGC	7704
TP53_17	TAGGTTTTCTGGGAAGGGACAGAAGATGACAGGGGCCAGG	7705
TP53_18	TGCTTTATCTGTTCACTTGTGCCCTGACTTTCAACTCTGT	7706
TP53_19	CCTGGGCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGC	7707
TP53_20	TTTGCCAACTGGCCAAGACCTGCCCTGTGCAGCTGTGGGT	7708
TP53_21	CCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCC	7709
TP53_22	GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGA	7710

TP53_23	CATGGCGCGGACGCGGGTGCCGGGCGGGGGTGTGGAATCA	7711
TP53_24	CCAGGGTCCCCAGGCCTCTGATTCTCACTGATTGCTCTT	7712
TP53_25	GAGGGCCACTGACAACCACCCTTAACCCCTCCTCCCAGAG	7713
TP53_26	CCTCAGGCGGCTCATAGGGCACCACCACACTATGTCGAAA	7714
TP53_27	AGGAAATTTGCGTGTGGAGTATTTGGATGACAGAAACACT	7715
TP53_28	CTTGCCACAGGTCTCCCCAAGGCGCACTGGCCTCATCTTG	7716
TP53_29	GAGGCAAGCAGAGGCTGGGGCACAGCAGGCCAGTGTGCAG	7717
TP53_30	CCTGGAGTCTTCCAGTGTGATGATGGTGAGGATGGGCCTC	7718
TP53_31	ACTACATGTGTAACAGTTCCTGCATGGGCGGCATGAACCG	7719
TP53_32	GGACAGGTAGGACCTGATTTCCCTTACTGCCTCTTGCTTCT	7720
TP53_33	CTGCACCCTTGGTCTCCTCCACCGCTTCTTGTCTGCTTG	7721
TP53_34	TCTCTTTTCTATCCTGAGTAGTGGTAATCTACTGGGACG	7722
TP53_35	CCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGCT	7723
TP53_36	GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGG	7724
TP53_37	TCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTC	7725
TP53_38	TGCCTCAGATTCACCTTTTATCACCTTTCCTTGCTCTTTC	7726
TP53_39	GGCATTTTGAGTGTTAGACTGGAACTTTCCACTTGATAA	7727
TP53_40	CCTGAAGGGTGAAATATTCTCCATCCAGTGGTTTCTTCTT	7728
TP53_41	CCTAGCACTGCCCCAACACACCAGCTCCTCTCCCCAGCCA	7729
TP53_42	CATCTTTTAACTCAGGTACTGTGTATATACTTACTTCTCC	7730
TP53_43	ATGGCTTTCCAACCTAGGAAGGCAGGGGAGTAGGGCCAGG	7731
TP53_44	CCTGGAGTGAGCCCTGCTCCCCCTGGCTCCTTCCCAGCC	7732
TP53_45	TCCGAGAGCTGAATGAGGCCTTGGAAGTCAAGGATGCCCA	7733

[00243] The linkage of the capture probe with captured genomic sequence (FIG. 11C) also facilitated measurement of genomic depth at each probe location. The number of unique reads associated with every capture probe used in the experiment was measured (FIG. 24). The data shown in FIG. 24 was derived from a sequencing run in which 16 healthy donor cfDNA samples were analyzed. The depth of unique reads encountered in each sample at one probe location in the TP53 gene were calculated (Raw unique read counts shown in FIG. 24A). Each sample comprised a unique library depth, as reflected in the broad sample-to-sample distribution of unique reads. The global average of unique read depth across all 2596 capture probes in the experiment was also calculated (FIG. 24B). Significantly, normalization of the observed read depth at the single probe site displayed in FIG. 24C by the global unique read depth measured for all probes revealed a uniform density of normalized unique reads. These data indicate that the capture performance of a particular

probe chosen for analysis was uniform from sample-to-sample and proportional to the genomic depth of each individual library.

[00244] This same normalization function was applied to the 45 TP53-specific probes shown in FIG. 23 (normalization data shown in FIG. 25). Whereas FIG. 23 shows the aggregate contribution of all probes to the sequencing depth of TP53 coding regions, FIG. 25 shows the normalized depth retrieved by each individual probe. The normalized depth retrieved by each individual probe was generally consistent from sample-to-sample for any given probe but somewhat variable when one probe was compared to another. Several factors governed the differences in the post-normalization capture depths observed between probes, the most significant being the placement of probes relative to one another and the proximity of probes to genomic repeat regions. Not all probes exhibited uniform capture behavior; two probes whose capture performance were not consistent are highlighted by arrows in FIG. 25. However, these data indicate that such probes are rare and easily identified. As such, and they can be excluded from downstream copy number analysis.

[00245] The uniform capture performance exhibited by the 45 TP53 targeting probes in FIG. 25 is a general feature of the targeted hybrid capture platform described herein. In FIG. 26, the average capture depth for each probe in a panel of 2596 capture probes was calculated for all 16 normal cfDNA libraries that were profiled in this experiment. The average was then compared individually with three representative samples using scatter plot analysis. Each dot represents a different probe and its position on the graph is a comparison of the average on the x-axis and the individual sample on the y-axis. The tight diagonal distribution of the majority of probes reflected the highly-correlated unique read capture performance of most probes (R^2 correlation ≥ 0.95 for all three graphs). Importantly, the consistency of probe-by-probe sequencing depth supports the use of the targeted hybrid capture platform in copy number measurement.

[00246] With respect to copy number, the most straightforward treatment of probe data is to further normalize the adjusted genomic depth values that occur in autosomal chromosomes to a diploid-averaged value of “2”. The same is true for probe values that occur in females for X-linked loci. For X-linked and Y-linked regions in normal males, averaged copy values are appropriately set to “1”. This numerical transformation was applied to a set of chromosomal control probes (239 probes that target select loci on all 22 autosomal chromosomes, Table 3), a set of 199 probes that target the X-linked AR gene, and the 45 TP53-specific probes considered in detail above (FIG. 27A and 27B). Each dot represents the

value for an individual probe. With the exception of infrequent “noisy” probes, the vast majority of individual probe counts in regions anticipated to be diploid possessed values that were approximately “2”. Probes for the AR gene in a healthy male fluctuated with an average value close to the anticipated “1.”

Table 3: Chromosomal Control Probes

Name	Sequence	SEQ ID NO:
Chr_1_1	GTGTCTCGGCAACCACTCTTCACCAATATCACAGTGGACA	7734
Chr_1_2	ATCCAAGGGGAGGAGATCAGTGCCCCTATTTGTATCGCAC	7735
Chr_1_3	ACTTACTGAAGCAAGAACCTCATCAAGCTGCCTCCCACCA	7736
Chr_1_4	AGTTTGTGATCCTCCTGTGGGCAACCTCAGCAGTCTGGTT	7737
Chr_1_5	GGAGAGCGGAGCTGCTCAGAGCTTGCCAGGTTCTAAGTG	7738
Chr_1_6	GACTGTGGCAATGAGGCAGCTAAGTGGTTCACCAACTTCT	7739
Chr_1_7	GGTGTATTTTGACAACGGTGGACCCAGACACTGGAGTCAT	7740
Chr_1_8	GTTGGTCTATTCTTGCGGTTGTAAAAGTGGCCCAGAGTGA	7741
Chr_1_9	GTGAGCCTTCTCTCACCATTCTGTCCAAAATAGCAGCCCT	7742
Chr_1_10	CAGCCTAGATATGATTCCTCACTACCCTGTTCCATGGTTC	7743
Chr_1_11	AAAGAATGTGTTGGCTCATGATCAGACTTGAGCACTTGGG	7744
Chr_1_12	CCTAGGCTGTTGCTGCTGGACCTGTTTGTGCTTCATCACA	7745
Chr_2_1	CAGTTGACCCTTCAGCCACAGGGGTTTGAACCTTGAAGGA	7746
Chr_2_2	AGGACCTGAGTATGCACGTTTTTGGTATACTGGGTAGGGGT	7747
Chr_2_3	TATCAGCTGGGATGGTCCGGTCAGCAGCATTACCCTGTTT	7748
Chr_2_4	TGCCTGCTCAGCCCAGATTTTCAGTCATGCTGGCCATAAAC	7749
Chr_2_5	CTGGGGGGTGAGGTTTGAGGTTTGTAGTGTGGGATGTGAGG	7750
Chr_2_6	CCAGCTTTTTTCAGAAGCTGGGAAAGTAATAACCCGTGTTG	7751
Chr_2_7	CCCAGCGCCCGTGGCTTTGGCTCCTCAGTCCCATTAAAT	7752
Chr_2_8	TATACCACCAAGTCTACCTACTGCCTGCACATGCTATGGC	7753
Chr_2_9	GGTCAATCCGGCACTACTGGTTGTCCAAAGGGAGGTTACT	7754
Chr_2_10	AATCAAACATCAGGACCGCCACAGCACAGGTCAATGAAC	7755
Chr_2_11	GTGTCTCCTGGAGGTGCATGGGTGGTTTTGAACTTCATTG	7756
Chr_2_12	GACCCATGTAAGGGGTTGGGTTATGTTCTCCTTTTGCCCA	7757
Chr_2_13	TCACTGACATGCGAAGCTGGGAACGAGAAAATGCACATCC	7758
Chr_2_14	TCCTACAGTGCTTAGGGATGAATCTGGCAAAGAAGGATGC	7759
Chr_2_15	GAAAGCAGTCCTTACCACAAGAAGACCCCGATGTGGTGGT	7760
Chr_2_16	ATTGCTCACTGGCTGGCTTGCATTGTTGATGCGATTGGGA	7761
Chr_2_17	GTCCCTGGGACCATCTGTGCATTGTTCTGTAACTGGAAA	7762
Chr_2_18	GACCGAATGGCGAACGCAGTGAATAGATCAGGAGGGAAAA	7763

Chr_3_1	GAAGGAATGGAGTGGAACAGATAGGGGTGAGGGAATAACG	7764
Chr_3_2	CCACTGCCATCCTCAGAGGGAGATTCAAGTCTCACAAT	7765
Chr_3_3	ATCCAGGCTTCATGTTCAAATGCAATGGCCCTTGCCCCAT	7766
Chr_3_4	AAATTTCCCCTGGCTCCCTACTGCTTTGCAGGCCAAGTAA	7767
Chr_3_5	ACCTTAAAGACGGGCCCACATCTCTTTGGATGGGATTAGG	7768
Chr_3_6	GGGCTTCGGTTTTTGGCGAAGGTGCTCACAATCTTGATATC	7769
Chr_3_7	TGAGCTGTCCTTCATGCCTGCATTTCCCATGTCTGTCTTC	7770
Chr_3_8	ATCTTTATCCAGGGCTACCAGTGGTGGGTCCAAAATGACT	7771
Chr_3_9	TACAGGTGAAGGATGTCAACGAGTTTGCTCCCACCTTCAA	7772
Chr_3_10	GCTGTTGTGACGGAGGGCAAGATCTATGACAGCATTCTGC	7773
Chr_3_11	AATGAAGGGGATTCAAGCCTTGCCACCGACTTACAGGAAG	7774
Chr_3_12	TGTGAGCGTACTTTCTCCCCAGGTTGAAGAGGAATGAGT	7775
Chr_4_1	ATTCCAAGTCCAGGTCCCAAATCTATCAGTACCGGCTGGC	7776
Chr_4_2	GACACAGAGTGCATGAAGACCGTTCAAATATGTCAGGGAC	7777
Chr_4_3	CATGAGTCCTTCTATGACTCCCTCTCAGACATGCAGGAAG	7778
Chr_4_4	TTTTTAGGAGACAGGTACCCACTGTCTGGTGACGAGGACT	7779
Chr_4_5	CCTTCTGTTGAGTCGCTAGGAGATGCCTCAGTTCAACAAT	7780
Chr_4_6	GACAGAACTTCATACCCAAGAGCTGCTTCTCAGCTGGA	7781
Chr_4_7	CAGGCAACTTTGGCAAGACCAAGTCAGCCTTCTCATCTCT	7782
Chr_4_8	CCCTTGCTACCATCACTGTTGTATCTGTGCTTGCATTCC	7783
Chr_5_1	AGGTCTCACTCCAAGTCCCCCTGTATTAGAGCTAGGCTGC	7784
Chr_5_2	GAAACCATGCGGGATTCATCTTTGTGTCAGAGTGGAGCGGCA	7785
Chr_5_3	TATGAAATTAGGCGGTGGTTGGACGTGACTGTGTGTTGAC	7786
Chr_5_4	TGAAACTTGTCATGACATACTGCGGCTGCCCATTCACTAGG	7787
Chr_5_5	TGCTTCTTGTTTATAACTCCCCTGGCCACCATCTCGGGCT	7788
Chr_5_6	ATTCCCTCTCATTTGTGGTTGGTGGCTGGATATCTGTTCC	7789
Chr_5_7	AGCATCAGCATTTCCCTGTGGACTTACCTCTCTCAGTAGT	7790
Chr_5_8	AAAATTTAAAGGTCGGCGGTAAGGCTGAAAGCCAACAGGC	7791
Chr_5_9	GAGTGTGTGCGTTCAGAAGGAACACCTGAGAAACCGCTTTA	7792
Chr_5_10	CATAGCAAATACCTGTCGCTGAGCCAGGAGTAAAGTCTGG	7793
Chr_5_11	AAGAGGCTCTGAGCTCTTGATAGAGGTTACATGGGGAGCA	7794
Chr_5_12	GGAGACAACCTTAGGAGGTTATCTAGACCATTCCCGCCTTC	7795
Chr_5_13	GTGTTTCCTCCCAGCATGCACTTTGTGGCTGCCTTTCTTT	7796
Chr_5_14	TGGCTTGTGTAGCGTGTTTCATTTTGGAACTTGGAGCCG	7797
Chr_5_15	GACACCTCTGGTGCAGTTTTGAGGCTGGCCGGAAGGGAT	7798
Chr_5_16	GTTTCAGATCTTGCAATGGGAGGGATCGACTCGGCCCTTT	7799
Chr_5_17	TGCCTAAATCAGAAATGGGCTACTTCCCTTGGCCACATCC	7800
Chr_5_18	CAATCTACCACCTCAAGGTTACGCGTGGATTCTACACCT	7801

Chr_6_1	GAGTTTTTCTTTCAGGTAGTCTGAGATGGCCCCGCACCAAG	7802
Chr_6_2	TACTATAAAGAAGGCACCTCTAGGCTTGGCAAGCACACGT	7803
Chr_6_3	GGCAGATTTCGATGGGACTTTAGACACTTGCTTTGCTCCCT	7804
Chr_6_4	CAAATGTCCCATGCAAACATGTCCCGCACTGTGTGGTAA	7805
Chr_6_5	ACATGTGTAATCTTCTTCTCCTAGGGCGGCAGAACTCATG	7806
Chr_6_6	CCCGAGGAAAGCTCCTCTTTGCTGACTGTAATGTACTGCA	7807
Chr_6_7	GAGGACAGCATTTCGCATATCAGGTCGAAATTTCTCCGCGA	7808
Chr_6_8	GTCCAGCTTTCATCCTTGATCCTGCTACTCTAGGCTCTCC	7809
Chr_6_9	ACTGATGGTGTTCACTTGCACCATCAGGTCTGATGGAGGA	7810
Chr_6_10	AATTGGTTCACAAAGCGTCGGGTGATCCAGTAACAGTCGA	7811
Chr_6_11	CAGAACTCTGCTCTAACGCCAAGCCTTCAATATGTCTTCG	7812
Chr_7_1	CAATTCTTACCATCCACAAAATGGATCCAGACAACTGTTC	7813
Chr_7_2	ACTACACCTCAGATATATTTCTTCATGAAGACCTCACAGT	7814
Chr_7_3	TGCTATAGACGCACAAACGACCGCGAGCCACAAATCAAGC	7815
Chr_7_4	CCATGACTTATGTGCAGCTTGCGCATCCAGGGGTAGATCT	7816
Chr_7_5	AGGAGTTGGTGGCTAAACCGCTGACTTTTCTATTGCAGAC	7817
Chr_7_6	GAAATATAACAGGACCAGAAGTGGCTCGCAGGAGACTCAT	7818
Chr_7_7	TAGCCAGACAGAAGGCGGACACTGATGATACCTCAAGACT	7819
Chr_7_8	GTTTGCCACCAGCGAAGAGAGCCATCCTGGTAGAATTGGA	7820
Chr_7_9	GGAGATATGCACTTGCCCTTTGGTAATCCTGCTCCTTCTG	7821
Chr_7_10	AAAATAACCAGTAAGTACAGGGAGGGACCGAGAGGCATC	7822
Chr_7_11	AAGAACACCAGTCCATAAAGACGCATGTCCGGTGATGCCT	7823
Chr_7_12	AATCTGTTTAGACTGAGCAACTGTGCCAGCAGAGGGACCT	7824
Chr_8_1	AAGATGGCGAAGGTCTCAGAGCTTTACGATGTCACTTGGG	7825
Chr_8_2	CCATGCCTGCCAGCTGATAAGATTTGGTTACCTTTCCATG	7826
Chr_8_3	GCTGCAAGAAAGCGTAAGATTGCCATTCGAAAAGCCCAGG	7827
Chr_8_4	ATGCAGGAGTACAATGTGGGCATGTCCACCCTCTACGACA	7828
Chr_8_5	AGAACGGCTTTGCTGTCTTCCGGCAAACCTATGGTTCTGA	7829
Chr_8_6	TGGCTTTGGCGCTTTAAGGCCAGACACGGCATTAAAAAGC	7830
Chr_8_7	GCAGGCAGAGAAAGATGGCTTTAGAAACCTCTTCCCCACC	7831
Chr_8_8	TCAGCTGTGGCCATTGGTGGATCTCATCCTTAGTACTAGT	7832
Chr_8_9	CCATGGTTCTGTGAGACTGGTAGAAAGCACAGACCCCTTA	7833
Chr_9_1	AATGTGCTTATCACTCGTGATGGGGTCTGAAGCTGGCAG	7834
Chr_9_2	AGGGTCTCATTTTAAGACAGCTTGATTTGAGGGTGAGGGG	7835
Chr_9_3	CAGTTGCAAACCATACTTCCTTCAGCCCAGTCCTGTCTAT	7836
Chr_9_4	GTCTAAGGGCATCTTACCTCCAAGAACTGCTTGAGGCGTA	7837
Chr_9_5	TACCTAGGGAATGACCACTAAGCACCATCTCCGTCACCTCT	7838
Chr_9_6	GGAAGAGAGGAGGGTCATCCAGTCAGTTTTGCAGGAATCT	7839

Chr_9_7	TGCTGCAGTGTCTGGAAGAAACCTACCTGCGTTTCTTAGAA	7840
Chr_9_8	CATCATACCTATGGCATAGCCATCAGGGCACTGCAGTTTG	7841
Chr_9_9	TATATCTCACGTGACCGAGGATGGGTCTGTTGGCATTACACA	7842
Chr_9_10	GAAATGGCCATCTATAGGTGGGAACCACTCCAGTGTACACA	7843
Chr_10_1	GGAAACCTTTTCACTCTCTACTAGAAGCGCGGAGAGAACTC	7844
Chr_10_2	TCTGGCCGGCATTTCATTTAAGGCCTAAGGATGAAGGCGGT	7845
Chr_10_3	AGATACCCTATCGTTCCTTATCTCAGCGAAACAACCTCCCC	7846
Chr_10_4	CGCAACTCCTCCAGATCGCAGTGGTGCTTCTTCACTTTCA	7847
Chr_10_5	TGATTCCATGGTTGCCCCTATACTCCATAAGGCGGTACTT	7848
Chr_10_6	ATACCATATCCGGCTTGTTAGGAGGAGGTATTACAGGGG	7849
Chr_10_7	GTACCTGTTAACCCAGACGCAATTCCTCCACAGTACACAG	7850
Chr_11_1	ATGTGACACTTGCATCCAGGGAGGTCACCATCTGTGTATG	7851
Chr_11_2	CTAGGTCCTGAAGAGGTGGCAAGGAACCAGGACAGAACAT	7852
Chr_11_3	TCTGTCATTGGTGACGCCATCTAGACTCTTGGCTTTGGGA	7853
Chr_11_4	AAGGTATAGAGCTGGGCGGCTTTCTCGTTATAGGTGGAG	7854
Chr_11_5	CTCCTACGTAGCCGGGTAGAACTTATGGCAGAAGTCAGG	7855
Chr_11_6	TGGATTCCCAGGGTTAATTGTGACCCATTGCAGGAAGGTG	7856
Chr_11_7	AATGCTGTCCTACTATGGTCTGTACCTGTCCCAGAGGTGG	7857
Chr_11_8	GTGCACCTGGAGAGCATAACAGGGCACTGACTTGTAGATCA	7858
Chr_11_9	TTCCATCTCGCATAACCTGCCCCCTAACTCTTCTCGGTTT	7859
Chr_11_10	ATGAAGGCCTGCTTTGAGTTATCAGATAGGAAGGGGCCAG	7860
Chr_11_11	AGGTCATGTCCCGCTTTTGGCTGAACCTAGTTTTGCCCCAA	7861
Chr_12_1	CTGCATTCTCCATGAGTAGAGTACGAGCCTCATGTTGGTA	7862
Chr_12_2	AAGGCTGTCTTCACCAACTGGGTAGGTGTGGATCAAGACC	7863
Chr_12_3	CTGACTTTGGTGTTGGGGAGTCGGTGGTCTTCTTCCATT	7864
Chr_12_4	ACTGCAGAGGACCAGACTGGGAAAACAACGATATGGCAGG	7865
Chr_12_5	CCTGGCTTAGAAGTCTGGCCGGTCTTCTTCAGCTTCTTA	7866
Chr_12_6	AATCTCAGAAAGAGTTTCTGGGACCATGGCAAATGGTGGC	7867
Chr_12_7	ACATTATATCCGGTCCAGGAATATCTGGCTCAGGCTGGGT	7868
Chr_12_8	AAGCACAGGAAATGTGCCTCACACGACTTCACATGCCCTT	7869
Chr_12_9	GGGGGCTTTGCGGGAAGAGGGGACTAAACAACCCTTCTGT	7870
Chr_12_10	AAAAGAAATGCGATCAGCGCAACCCATCCGGTGTGGCGCT	7871
Chr_12_11	GGCAGTGGTACCATGACATACTTAGCAGAGATGGACTACA	7872
Chr_13_1	ATTTCCCATGCGAGAGGTAGCTTGCCCAGGCTGTTGGATA	7873
Chr_13_2	TTCCATGCCGAGTCTGATGGAACTAGCACTGAAAGACC	7874
Chr_13_3	TCACGGGAGCTTCTTCACTGAGTTCTGCGAATCTGAAGC	7875
Chr_13_4	TTTCCAGAGATGAAGCACTACCCAGTCTTACCCAAGTTTCG	7876
Chr_13_5	CCACCGAGAACAGTGATGAAGGACTTAAAGTGAGAGATGG	7877

Chr_13_6	GTTCACTCGTCGGTTTTTCACCAACCACAGACTAGCCTCA	7878
Chr_13_7	ACGCAGCTGTGTTGAGTGCACAGGAAGCTCTTAGGGTTAA	7879
Chr_13_8	TCTCAGTGAACAGAGGGCTCACTGAGAGGACTTTGAATAC	7880
Chr_13_9	ATGGCACAGGCCACATACTGGAATGAATGACGGGCTTCAT	7881
Chr_13_10	TGCTGCTTGATGGTGGCATCACTGTCCCCTCATTCCATGA	7882
Chr_14_1	GGACACATGTGGACAGTGTGAAACCTCAGAACACTAACCC	7883
Chr_14_2	AAGTTCTTATCCTTAGGGACCCAGCGGAGACCTTGGTTCT	7884
Chr_14_3	CGACGATGCCTGGGAATAGGATCCATGGGATTGATGAGAA	7885
Chr_14_4	GGGAGCCATGAAGATTTCTCCCAGCTCCTGAGGAACTTTG	7886
Chr_14_5	TCTGGTCCCTCAAGTCCTCAGCTGTAGAAGTTCTCATTGCG	7887
Chr_14_6	TGCCAACCCCTGGAAACTGGCTTGTGTGTCCACAACAGAAA	7888
Chr_15_1	TAGGTGACAGCACTGTCCTTTCCCTGCCATTTGCAGGGAA	7889
Chr_15_2	TTCTTCTAGATGGCAGACATTGTTGAGGCCTCCCGTACCT	7890
Chr_15_3	AGAGAGCTGCGAGACAAGACTTGAGTGCGACAAGATTTTC	7891
Chr_15_4	TTCAATCAGGTACTCCGAGTTCCCTTGGAGGCCAAAAGGA	7892
Chr_15_5	AGGAATATGGGGTCCATCTGAGACTCGCAAGTGATGATAC	7893
Chr_15_6	GATCTCCAGGACCAGCTCTCAGAAATGCACGATGAACTGG	7894
Chr_15_7	ACAGTGTGATGGAGCAGCAGTCCAAGTTCATCCTCCAAGA	7895
Chr_15_8	AAGATGACAGGATCCAGGAAACAAGACGCATGGGCCAGAA	7896
Chr_15_9	AAAGAGTGGGTCTGTTAATAATCAGGCCGAGACCACCAGC	7897
Chr_15_10	CACCCTTGTTTCGTGGCCCTTGCTTGGTAAACTGGTATCCA	7898
Chr_15_11	CCCAAGTATGGGTGAGGATGCTAGAAATGCCACATAATG	7899
Chr_15_12	AAGACTGTCATTGGTAGGTCATGATCCTTGGCAGCATGAC	7900
Chr_16_1	GTGGGGACGGTCATTATCAGCTTTCTGGACACACAGACAG	7901
Chr_16_2	TGAGAGGCCAAAGAATATCAGTTGACTCTGGATCAGGGGC	7902
Chr_16_3	GAGGCTTTTTAGGGCAGCGAGAAAACGGGAACCTTCATTCC	7903
Chr_16_4	AGGACTTCTCTGGACCTGTGCCTCACTACTCACCTGGAT	7904
Chr_16_5	TGGCCACAAATGTTGCCTCCAGCTGCTCAATGTTCTCCAA	7905
Chr_16_6	CTGGCATTGGTGAGTAATAGGAGCCAGACGGGTCTGTGTT	7906
Chr_16_7	ATACTTACCTGCACGAGAATGAGTTTGGAGCGCAAGGGGG	7907
Chr_16_8	TTCCCCCAGAGACTCTGTCCACTATGGACATTAAAATGTG	7908
Chr_16_9	GTGCTACCCTCCTCCCTCAGGTTATGTGGTCCAGGCTTT	7909
Chr_16_10	TAAGTGGAACAACATTCCCTTCATTATAGCCCTTCGTGGG	7910
Chr_16_11	GCAACGTCAACAACACTACTACGTGCACAAGCGCCTCTACTG	7911
Chr_17_1	GCGGATGTCGTTATGGGACAGGTACAAGTAGATAAGTTGC	7912
Chr_17_2	GTGGTCACCATCTCTTCAAACCATTGACTGGGCCTGGT	7913
Chr_17_3	AAGCCAAGGAGTTCTGAGAGAGCTTAGCTAAGTTCTTCGC	7914
Chr_17_4	TTTTTTAGTACCCCAGTGTGTAAGACCAACTGAGGGTGGC	7915

Chr_17_5	GTTGTCATTGGGGCTATAGACATAAGCACCTTCCGGAATC	7916
Chr_17_6	CTGAGTGTGCGAGGGGAAGATATTGGTGAAGACCTGTTCT	7917
Chr_17_7	GTCAGACCCTGTCCTCGTCTCCTTTACCTTGTCTCGATTT	7918
Chr_17_8	TAAACTATGCTCGCCACCACTCAGCACTCACCTCTTGGGC	7919
Chr_17_9	GGCAACTTCCTGAGACAGATCGGTAAAAACAACCCCTTCT	7920
Chr_17_10	TCAACTGTATTTTCATCAGAGAGATGTGGCTTTCCAGACA	7921
Chr_17_11	GTTTCCCTCATGTTCCCCCAGGTTCTGTCAGGTGAAGCTG	7922
Chr_18_1	TTAACCCATCTCTACCCGTCCTGTGTCAAGAACGGAGGCT	7923
Chr_18_2	CTGCCCAAATAGAAACCGAGGTTCTCCGTGACCTACATC	7924
Chr_18_3	TTCCTTTGCGAGTAACAGCGGGAACATGAAGCCGCCACTCT	7925
Chr_18_4	TGGTTTGCCAGTTCAGACACCCAGCCAAATTGCCCTCTCA	7926
Chr_18_5	TAGTGCAGCTGGCTTTGAGCCTGTTCCCGAATGTTTCAGAT	7927
Chr_18_6	AGGGTAATAGCACCAAGCTCTAGTCTACCCACCTCTCTGA	7928
Chr_18_7	CCGCATCTCTGGAGTAGGAATTGATCAGCCACCATATGGG	7929
Chr_18_8	CTATGAGCATACTGGGGAGGGAAACCTCTAAGCGGAACTT	7930
Chr_18_9	AAAAACCTGCAGGAAGGAGACCTGAATGCAACTGTGGGTC	7931
Chr_18_10	CAGGTGCTCCAAACCTTCCAGTCTATGTTGTAGATTGCAG	7932
Chr_18_11	GCCATACTAACCTACTTCTCCTTGAAGCTCTTGGCCCATC	7933
Chr_19_1	ACTGTGAGATAGCCCTCATCATCTTCAACAGCGCCAACCG	7934
Chr_19_2	AGATACACGGTCACAGACGCCATGTGTTGTGGCTTCTGCA	7935
Chr_19_3	CACATCCTCTCACCTTTTCCGAAGGTTGCAGCTCCTTCTC	7936
Chr_19_4	TCTGTCTCACCGGTCCCTTCATTCTAGGCAACTGTAGAT	7937
Chr_19_5	ATATCATGGTCTGTATCCCCCAGGTACCTTGACACAGGCC	7938
Chr_19_6	CTCTCCGCCTTTCTTTAGACCTGAGCATGCAGAATTCCGA	7939
Chr_19_7	AAGGCATTTAAATGGGACAGCGTCCCATGCGTGACTTCTC	7940
Chr_19_8	TCTTTCTAACAGACGAACAGCCTACACCTACAACCCCGAG	7941
Chr_19_9	GTCCAGCCCAAAAGCATCTTGGGTAAGGATTTGGGATCA	7942
Chr_19_10	GTTGTTCTGGGCCAGTGTTAGTTGCTCACATGTCCTGTCT	7943
Chr_19_11	AACATGCCTCTTAGTCCTGGGCCATACCTTAGCCTTGTGC	7944
Chr_20_1	TAACCTCCAAAAGAGGTACCCATTGGCGCTCAACCGAATT	7945
Chr_20_2	CTATATCTCCGACTATGCCTTCTTGGGCACTGCACTGCTG	7946
Chr_20_3	TCTAGATGGAAGCTGTATCCAAGGATGCTCCGGAATGTTG	7947
Chr_20_4	ATCTTCTCTGCCTGCCGCACTAGCTTCTTGGTGACTTCTC	7948
Chr_20_5	ATCGAGTTGTGCGAGCCCCATGATTCGACACCAAGATCCCA	7949
Chr_20_6	AGGTGCTTGTGTTTACTCTCTCCAGGTGATGATGCCAGGGA	7950
Chr_20_7	GTGCACTGTCAGATCTTGAAACGGCCAAAGGATTTTTCC	7951
Chr_20_8	CATTTTGCAGGAGGCTGCTAATTAAGGCTGAGGGCCATCA	7952
Chr_20_9	TCAATGGTAGACTGGAGTACCTTGCCAGGGCAGAGAAAAA	7953

Chr_20_10	CTCCTCCAGGAGCTGGCAGCATCAAGACCCCACTTCGCTT	7954
Chr_21_1	AAATAATAGCAGGCGTTGAGATGTCCCTTCCCCAGCACTC	7955
Chr_21_2	AAGTCTGACAGCATCTGCTTGAAGTGAAGCACAGTGATGG	7956
Chr_21_3	ATTCGTGATGGCGCTCATTTCCATAAAGGACGACAGGTCA	7957
Chr_21_4	GAAGAGTGAATTCCCGCTTCTGCGCCAACATTCTGTTTCC	7958
Chr_21_5	ACAGGTGAAGTCTTTGCGTGCCTCCCTGTTGGACTCAAAT	7959
Chr_21_6	TAATGATATTCTGGCACAAGGAGCAGAGCCCCTCTTCTTC	7960
Chr_21_7	AGACCCAGCCTACCTGCATGATCTCTTGTACAGCTTTGCA	7961
Chr_21_8	TCATGGAACATGGGCCTTGCAAAGGGGTCAAGATCACAAC	7962
Chr_21_9	GTCAAAAAGGTCCAATCAGCTAGAGACTAGGCCAGACCCA	7963
Chr_22_1	TGTGACCACCCTAAAGGGAGGGCAGAAGCCGAGTCACCCT	7964
Chr_22_2	ACGCCTCCACCTGCTGCTAGGACTCCCCTCCCAAACAAAG	7965
Chr_22_3	CACAGTCTAGACCCTGATGGGCGATCTCAGTAGTGCTGTT	7966
Chr_22_4	CCTATCAACGTGCAAGTGGGATTTGTCTCCACTGGCTTTC	7967
Chr_22_5	GAAAATCATTCCCCATTCTGCAGGATCCGTTCCCCTGGCA	7968
Chr_22_6	AGTGGGACATACCAACTTGATGAGGCAGTTGTGCGAGTTC	7969
Chr_22_7	GTAAACAGCTGTCTTCTTACCCTACAGATCATTGGGCAGG	7970
Chr_22_8	CAGAAGGATACTAGAATGGAATGTCCTGCGTGACGAAAGC	7971
Chr_22_9	AGTTCACATCTGATTCTCTATGGCTGCTAGGCTCCAGGA	7972

[00247] Significantly, when the same analysis was applied to cfDNA collected from the blood plasma fraction of a castration-resistant prostate cancer patient using healthy samples as normalization controls, three prominent features emerged (FIG. 27C). First, all of the control probes exhibited noisy counting behavior. Second, the counts across all AR probes were significantly elevated from a normal value of “1” to an amplified value of approximately “5”. Amplification of the AR gene is consistently observed in advanced prostate cancer patients. Third, the TP53 probe counts, while more tightly clustered, possessed an average value far closer to “1” than the expected value of “2.” This likely reflected inactivation of one or both alleles of TP53 by copy number loss in the fraction of circulating DNA derived from tumor tissue.

[00248] These data indicated that the methods of the present invention comprise three important karyotyping aspects. Namely, the methods described herein detect generalized chromosomal aneuploidy, copy increases of specific, targeted genes, and copy losses in the same specific, targeted genes. These result further indicate that the methods and

platforms described herein can guide the use of precision therapies, as all three of these genomic abnormalities occur frequently in cancer.

[00249] Generalized chromosomal aneuploidy for castration-resistant prostate cancer patient samples (blue dots) relative to a healthy control (brown dots) was measured (FIG. 28). In this analysis, the approximate ploidy for all 239 control probes used in the experiment were ordered according to their chromosomal targets. For some chromosomes (*e.g.*, chromosome 1 and chromosome 22) a similar ploidy value of “2” was observed between patient and control samples. In other cases, deviation between the two samples was observed. The degree of information regarding overall genomic ploidy provided by these experiments was constrained by the number and density of control probes used. However, these data indicate that a denser probe panel covering all chromosomal segments at uniform density can be used – in conjunction with the additional unique features of the present invention. Such analyses will provide a higher resolution, genome-wide measurement of chromosomal copy number.

[00250] These data further highlight the capabilities of the present invention as a guide for precision therapy. For example, tumors that possess genomic deficiencies in homologous recombination repair often exhibit highly destabilized chromosomal ploidies, and patients with such tumors are good candidates for inhibitors of the PARP enzyme complex (See Popova *et al.*, Genome Biol. 2009;10(11):R128). Unlike most sequencing assays that seek to *genotype* a tumor, the assays described herein use sequencing to detect destabilized chromosomal ploidy as a *tumor phenotype*, even if the causal mutations driving this phenotype remain hidden from targeted analysis.

[00251] The ability to detect gene loss in DNA shed from solid tumors is especially significant. Mutation and deletion of tumor suppressor genes is a frequent event in cancer genomes; moreover, individuals with germline loss of tumor suppressor genes are uniquely vulnerable to developing cancer later in life. The diagnostic value of a liquid biopsy copy number loss (CNL) assay is directly proportional to its sensitivity. To determine the lower limit of detection for the invention described here, the immortalized lines described in Example 1 were systematically diluted into the “genome-in-a-bottle” reference cell line, NA12878. One line had a single copy deletion (monoallelic loss) of ATM, the other a single copy deletion of BRCA2. The experiment included four control samples of pure NA12878 and eight spike-in samples containing 16% of each monoallelic deletion line (FIG. 29). For reporting purposes, this corresponds to an 8% minor allele frequency of biallelic loss.

Averaged values for all probes targeting specific genes and two additional, undeleted control genes are shown in FIG. 29. Copy loss of ATM and BRCA2 was confined to spike-in samples only. Additional computational treatment of the data revealed confident copy loss calling of biallelic deletions down to 2% minor allele frequencies. This sensitivity indicated that the present invention required no specialized considerations in order to routinely include copy loss calls in standard blood-based genotyping assays.

[00252] These data demonstrate the use of probe-specific genomic capture data for the analysis of copy number, including both copy number gain and copy number loss of target genomic loci. Additionally, the invention described herein has been shown to possess the sensitive ability to detect single nucleotide variants, insertions and deletions ranging from single nucleotides to many thousands of base pairs, and gene fusions resulting from chromosomal rearrangement by aberrant mutational processes (See PCT Publication No. WO 2016/028316; and U.S. Patent Publication No. 2014-0274731). All of these mutational processes can contribute to the transformation of normal tissue to neoplastic cancers, and as precision therapies continue to emerge, accurate diagnosis of these diseased genomic signatures will become an increasingly indispensable feature of precision medicine.

CLAIMS

1. A method for performing a genetic analysis on a DNA target region from a test sample comprising:

(a) generating a genomic DNA library comprising a plurality of DNA library fragments, wherein each of the DNA library fragments comprises a genomic DNA fragment from the test sample and an adaptor;

(b) contacting the genomic DNA library with a plurality of capture probes that specifically bind to a DNA target region, thereby forming complexes between the capture probes and DNA library fragments comprising the DNA target region; and

(c) performing a quantitative genetic analysis of the genomic DNA fragments comprising the DNA target region;

wherein the adaptor is a DNA polynucleotide that comprises: an amplification region, a sample tag region, and an anchor region;

wherein the amplification region comprises a polynucleotide sequence capable of serving as a primer recognition site for PCR amplification;

wherein the sample tag comprises a polynucleotide sequence that encodes an identity of the unique library DNA fragment and encodes an identity of the test sample;

wherein the anchor region comprises a polynucleotide sequence that encodes the identity of the test sample and wherein the anchor region is capable of attaching to the genomic DNA fragment; and

wherein the genetic analysis is performed to detect a genetic change indicative of a disease state.

2. The method of claim 1, wherein the genetic change indicative of a disease state is selected from a single nucleotide variant (SNV), an insertion less than 40 nucleotides in length, a deletion of a DNA region less than 40 nucleotides in length, and/or a change in copy number.

3. The method of claim 1, wherein the genetic change indicative of a disease state is a change in copy number.

4. The method of any of claims 1-3, wherein the test sample is a tissue biopsy.

5. The method of claim 4, wherein the tissue biopsy is taken from a tumor or a tissue suspected of being a tumor.
6. The method of any of claims 1-3, wherein the genomic DNA is cell free DNA (cfDNA) or cellular DNA.
7. The method of claim 6, wherein the genomic DNA is cfDNA is isolated from the test sample; and wherein the test sample is a biological sample selected from the group consisting of: amniotic fluid, blood, plasma, serum, semen, lymphatic fluid, cerebral spinal fluid, ocular fluid, urine, saliva, stool, mucous, and sweat.
8. The method of any claims 1-5, wherein the genomic DNA fragments are obtained by the steps comprising:
 - (i) isolating cellular DNA from the test sample;
 - (ii) fragmenting the cellular DNA to obtain the genomic DNA fragments.
9. The method of claim 8, wherein step (ii) is performed by contacting the cellular DNA with at least one digestion enzyme.
10. The method of claim 8, wherein step (ii) is performed by applying mechanical stress to the cellular DNA.
11. The method of claim 10, where the mechanical stress is applied by sonicating the cellular DNA.
12. The method of any of the preceding claims, wherein the sample tag further comprises a unique molecule identifier (UMI) that facilitates the identification of the unique genomic DNA fragment.
13. The method of any one of the preceding claims, wherein the amplification region is between 10 and 50 nucleotides in length.

14. The method of any of any one of the preceding claims, wherein the amplification region is between 20 and 30 nucleotides in length.
15. The method of any of any one of the preceding claims, wherein the amplification region is 25 nucleotides in length.
16. The method of any one of the preceding claims, wherein the sample tag is between 5 and 50 nucleotides in length.
17. The method of claim 16, wherein the sample tag is between 5 and 15 nucleotides in length.
18. The method of claim 16, wherein the sample tag is 8 nucleotides in length.
19. The method of any one of claims 12-18, wherein the UMI multiplier is adjacent to or contained within the sample tag region.
20. The method of claim 19, wherein the UMI multiplier is between 1 and 5 nucleotides in length.
21. The method of claim 19, wherein the UMI multiplier is 3 nucleotides in length, and comprises one of 64 possible nucleotide sequences.
22. The method of any one of the previous claims, wherein the anchor region is between 1 and 50 nucleotides in length.
23. The method of claim 22, wherein the anchor region is between 5 and 25 nucleotides in length.
24. The method of claim 22 or 23, wherein the anchor region is 10 nucleotides in length.

25. The method of any one of the previous claims, wherein step (a) comprises attaching the genomic DNA fragments to a plurality of adaptors.

26. The method of claim 25, wherein the genomic DNA fragments are end repaired prior to attaching the genomic DNA fragments with a plurality of adaptors.

27. The method of claim 25, wherein the amplification regions of each adaptor of the plurality of adaptors comprises an identical nucleotide sequence.

28. The method of claim 26 or 27, wherein the sample tag region of each adaptor of the plurality of adaptors comprise one of between 2 and 1,000 nucleotide sequences.

29. The method of claim 28, wherein the sample tag region of each adaptor of the plurality of adaptors comprise one of between 50 and 500 nucleotide sequences.

30. The method of claim 28, wherein the sample tag region of each adaptor of the plurality of adaptors comprises one of between 100 and 400 nucleotide sequences.

31. The method of claim 28, wherein the sample tag region of each adaptor of the plurality of adaptors comprises one of between 200 and 300 nucleotide sequences.

32. The method of claim 28, wherein the sample tag region of each adaptor of the plurality of adaptors is 8 nucleotides in length.

33. The method of any of claims 28-32, wherein each sequence of the nucleotide sequences are discrete from any other sequence of the 240 nucleotide sequences by Hamming distance of at least two.

34. The method of any one of claims 26-33, wherein each of the plurality of adaptors comprises a UMI multiplier that is adjacent to or contained within the sample tag region.

35. The method of any one of claims 26-34, wherein each of the plurality of adaptors comprises a UMI multiplier that is adjacent to the sample tag region.

36. The method of claims 34 or 35, wherein the UMI multiplier of each adaptor of the plurality of adaptors is between 1 and 5 nucleotides in length.

37. The method of claim 36, wherein the UMI multiplier of each adaptor of the plurality of adaptors is three nucleotides in length.

38. The method of claim 26-37, wherein the anchor tag region of each adaptor of the plurality of adaptors comprises one of four nucleotide sequences, and wherein each sample region of a given sequence is paired to only one of the four anchor regions of a given sequence.

39. The method claim 25 or 26, wherein the amplification regions of each adaptor of the plurality of adaptors comprises an identical nucleotide sequence;

wherein the sample tag region of each adaptor of the plurality of adaptors is 8 nucleotides in length, wherein the nucleotide sequence of each sample tag is discrete from any other nucleotide sequence of the sample tags of the plurality of adaptors by Hamming distance of at least two,

wherein each of the plurality of adaptors comprises a UMI multiplier that is adjacent to or contained within the sample tag region, wherein the UMI multiplier of each adaptor of the plurality of adaptors is three nucleotides in length, and wherein the UMI multiplier of each of the possible nucleotide sequences is paired to each sample tag region of the plurality of adaptors,

wherein the anchor tag region of each adaptor of the plurality of adaptors comprises one of four nucleotide sequences, and wherein each sample region of a given sequence is paired to only one of the four anchor regions of a given sequence.

40. The method of any one of claims 25-39, wherein the step of attaching the genomic DNA fragments with a plurality of adaptors comprises:

(i) attaching an oligonucleotide comprising least a portion of an anchor region to each genomic DNA fragment, wherein the oligonucleotide comprising least a portion of an

anchor region is a DNA duplex comprising a 5' phosphorylated attachment strand duplexed with a partner strand, wherein the partner strand is blocked from attachment by chemical modification at its 3' end, and wherein the attachment strand is attached to the genomic DNA fragment;

(ii) contacting the genomic DNA fragments attached to the oligonucleotides comprising at least a portion of the anchor region with DNA oligonucleotides encoding full length adaptor sequences for each adaptor nucleotide sequence of the plurality of adaptors; and

(iii) contacting the genomic DNA fragments and the DNA oligonucleotides encoding the full length adaptor sequence with T4 polynucleotide kinase, Taq DNA ligase and full-length Bst polymerase under conditions suitable for DNA ligation;

thereby attaching the plurality of adaptors to the genomic DNA fragments.

41. The method of any of claims 25-40, wherein the genomic DNA fragments are cfDNA.

42. The method of any of claims 25-41, wherein the DNA target region is analyzed for a change in copy number.

43. The method of any one of the preceding claims, wherein step (c) comprises purification of the complexes formed between the capture probes and DNA library fragments comprising the DNA target region.

44. The method of any one of the preceding claims, wherein step (c) comprises purification of the complexes formed between the capture probes and DNA library fragments comprising the DNA target region, performing primer extension and/or amplification of the DNA library fragments comprising the region of interest from the genomic DNA library.

45. The method of any one of the preceding claims, wherein step (c) comprises purification of the complexes formed between the capture probes and DNA library fragments comprising the DNA target region, performing primer extension and amplification of the DNA library fragments comprising the region of interest from the genomic DNA library.

46. The method of any one of the preceding claims, wherein step (c) comprises DNA sequencing of the DNA library fragments comprising the DNA target region to generate a plurality of sequencing reads.

47. The method of any one of the preceding claims, wherein the genomic analysis comprises determining a change of a copy number in a DNA region of interest, and wherein step (c) comprises:

(i). determining a copy number of the region of interest present in the genomic DNA library derived from the test sample, and

(ii). comparing the copy number determined in step (i) to a copy number of the region of interest present in the genomic DNA library derived from a reference sample, wherein the reference sample comprises a known copy number of the DNA target region.

48. The method of claim 47, wherein determining the copy number in the region of interest comprises DNA sequencing of the DNA library fragments comprising the DNA target region to generate a plurality of sequencing reads, wherein each sequencing read comprises a unique molecular identification element (UMIE).

49. The method of claim 48, wherein the UMIE comprises sequencing information from the adaptor and at least a portion of the genomic DNA sequence.

50. The method of claim 49, wherein sequencing reads comprising identical UMIEs are identified as a unique genomic sequence (UGS).

51. The method of any of claims 47- 50, further comprising determining a raw genomic depth (RGD) for each of the capture probes contacted with the genomic DNA library.

52. The method of claim 51, wherein determining the RGD comprises determining the average number of UGSs associated with each capture probe sequence within a group of sample replicates.

53. The method of claim 52, wherein capture probes associated with a highly variable number of UGSs are identified as noisy probes and are removed from further calculations.

54. The method of claim 52, further comprising calculating an RGD for a sample, comprising calculating a numerical average of all RGDs for all capture probes in the sample.

55. The method of claim 52, wherein the RGD values for noisy probes are not included in calculating an RGD for a sample.

56. The method of any of claims 51-55, wherein the RGDs for the capture probes are normalized across all samples in an experimental group by converting the RGD for each capture probe into a probe-specific, normalized read count comprising:

- (i). multiplying each capture probe RGD in a sample by a normalization constant, wherein the normalization constant comprises any real number; and
- (ii). dividing the product of (i) by the RGD calculated for the corresponding sample; or
- (iii). dividing the product of (i) by an average RGD calculated from a subset of probes.

57. The method of claim 56, wherein the subset of probes is a set of control probes.

58. The method of claim 57, wherein the probe-specific, normalized read counts are converted in to a copy number value comprising:

- (i). multiplying the probe-specific, normalized read counts of probes directed to autosomal and/or X-linked regions by 2 in samples derived from females;
- (ii). multiplying the probe-specific, normalized read counts of probes directed to Y-linked and/or X-linked regions by 1 in samples derived from males;
- (iii). averaging the products of (i) and/or (ii) across all samples in an experiment; and
- (iv). dividing the product of (i) and/or (ii) by the average of (iii).

59. The method of claim 58, wherein the approximate copy number values for all probes that target a specific gene are averaged.

60. A method for or highly sensitive detection of copy number gain and copy number loss comprising:

- (i). determining an RGD for a capture probe;
- (ii). normalizing the RGD for the capture probe across all samples in an experimental group by converting the RGD for the capture probe into a probe-specific, normalized read count;
- (iii). calculating an approximate copy number value for each probe-specific, normalized read count; and
- (iv). averaging the approximate copy number values for all probes that target a specific gene.

61. A method for measuring chromosome stability comprising:

- (i). designing and validating a set of one or more chromosomal stability probes, wherein the chromosomal stability probes are uniformly distributed across human chromosomes;
- (ii). performing targeted sequencing on patient samples using the one or more chromosomal stability probes;
- (iii). determining an approximate copy number value for each chromosomal probe;
- (iv). determining a genomic phenotype of a patient sample, wherein fluctuations in the copy number values for one or more chromosomal probes in the patient sample indicate genomic instability.

62. A method of treating a cancer in a subject in need thereof, wherein the subject has been identified as having a destabilized genome according to the method claim 61, wherein the method of treating the cancer comprises administering a pharmaceutically effective amount of a PARP inhibitor.

63. The method of any one of the preceding claims, wherein the region of interest is a gene or a portion of the gene.

64. The method of claim 63, wherein the gene is associated with a disease.

65. The method of claim 64, wherein the disease is a cancer.

66. The method of claim 63, wherein the gene is BRCA2, ATM, BRCA1, BRIP1, CHEK2, FANCA, HDAC2, and/or PALB2.

67. A genomic DNA library comprising a plurality of DNA library fragments, wherein each of the DNA library fragments comprises an adaptor and a genomic DNA fragment,

wherein the adaptor is a DNA polynucleotide that comprises: an amplification region, a sample tag region, and an anchor region;

wherein the amplification region comprises a polynucleotide sequence capable of serving as a primer recognition site for PCR amplification;

wherein the sample tag comprises a polynucleotide sequence that encodes an identity of the unique library DNA fragment and encodes an identity of the test sample; and

wherein the anchor region comprises a polynucleotide sequence that encodes the identity of the test sample, and wherein the anchor region is capable of attaching to the genomic DNA fragment.

68. The genomic DNA library of claim 67, wherein the sample tag further comprises a unique molecule identifier (UMI), wherein the UMI facilitates the identification of the unique genomic DNA fragment.

69. The genomic DNA library of claim 67 or 68, wherein the amplification region is between 10 and 50 nucleotides in length.

70. The genomic DNA library of claim 69, wherein the amplification region is 25 nucleotides in length.

71. The genomic DNA library of any one of the preceding claims, wherein the sample tag is between 5 and 50 nucleotides in length.

72. The genomic DNA library of claim 71, wherein the sample tag is 8 nucleotides in length.

73. The genomic DNA library of any one of claims 67-72, wherein the UMI multiplier is adjacent to or contained within the sample tag region.

74. The genomic DNA library of claim 73, wherein the UMI multiplier is between 1 and 5 nucleotides in length.

75. The genomic DNA library of any one of the previous claims, wherein the anchor region is between 1 and 50 nucleotides in length.

76. The genomic DNA library of claim 75, wherein the anchor region is 10 nucleotides in length.

77. The genomic DNA library of any one of claims 67-76, wherein the amplification regions of each adaptor of the plurality of adaptors comprises an identical nucleotide sequence.

78. The genomic DNA library of any one of claims 67-77, wherein each nucleotide sequence of the sample tags are discrete from any other sequence of the nucleotide sequences of the sample by Hamming distance of at least two.

79. The genomic DNA library of any one of claims 67-78, wherein each of the plurality of adaptors comprises a UMI multiplier that is adjacent to or contained within the sample tag region.

80. The genomic DNA library of any one of claims 67-78, wherein each of the plurality of adaptors comprises a UMI multiplier that is adjacent to the sample tag region.

81. The genomic DNA library of any one of claims 67-78, wherein the anchor tag region of each adaptor of the plurality of adaptors comprises one of four nucleotide

sequences, and wherein each sample region of a given sequence is paired to only one of the four anchor regions of a given sequence.

82. The genomic DNA library of claim 67, wherein the amplification regions of each adaptor of the plurality of adaptors comprises an identical nucleotide sequence;

wherein the sample tag region of each adaptor of the plurality of adaptors is 8 nucleotides in length, wherein the sample tag region of each adaptor of the plurality of adaptors comprises a nucleotide sequence that is discrete from any other nucleotide sequence of the sample tags of the plurality of adaptors by Hamming distance of at least two;

wherein each of the plurality of adaptors comprises a UMI multiplier that is adjacent to or contained within the sample tag region, wherein the UMI multiplier of each adaptor of the plurality of adaptors is three nucleotides in length, and wherein the UMI multiplier of each of the possible nucleotide sequences is paired to each of the sample tag regions of the plurality of adaptors;

wherein the anchor tag region of each adaptor of the plurality of adaptors comprises one of four nucleotide sequences; and

wherein each sample region of a given sequence is paired to only one of the four anchor regions of a given sequence.

83. The genomic DNA library of any of claims 67-82, wherein the genomic DNA fragment is cfDNA.

84. A plurality of genomic DNA libraries, comprising more than one genomic library according to any one of claims 67-83.

85. The plurality of genomic DNA libraries of claim 84 wherein the nucleic acid sequences of the sample tag regions of a genomic DNA library belonging to the plurality of genomic DNA libraries are different from the nucleic acid sequences of the sample tag regions of other genomic DNA libraries belonging to the plurality of genomic DNA libraries.

86. The plurality of genomic DNA libraries of claim 84 or 85, wherein the nucleic acid sequences of the amplification regions of a genomic DNA library belonging to the plurality of genomic DNA libraries are identical to the nucleic acid sequences of the

amplification regions of other genomic DNA libraries belonging to the plurality of genomic DNA libraries.

87. A method for genetic analysis of a DNA target region of cell free DNA (cfDNA) comprising:

- (a) generating the DNA library of any of claims 67-86;
 - (b) contacting the cfDNA library with a plurality of capture probes that specifically bind to a DNA target region, thereby forming complexes between the capture probes and DNA library fragments comprising the DNA target region; and
 - (c) performing a quantitative genetic analysis of the cfDNA fragments comprising the DNA target region;
- thereby performing genetic analysis of the DNA target region.

88. A method of predicting, diagnosing, or monitoring a genetic disease in a subject comprising:

- (a) obtaining a test sample from the subject;
- (b) isolating genomic DNA from the test sample;
- (c) generating a DNA library comprising a plurality of DNA library fragments, wherein each of the DNA library fragments comprises a genomic DNA fragment from the test sample and an adaptor;
- (d) contacting the cfDNA library with a plurality of capture probes that specifically bind to a DNA target region, thereby forming complexes between the capture probes and DNA library fragments comprising the DNA target region; and
- (e) performing a quantitative genetic analysis of one or more target genetic loci associated with the genetic disease in the cfDNA clone library, wherein the identification or detection of one or more genetic lesions in the one or more target genetic loci is prognostic for, diagnostic of, or monitors the progression of the genetic disease.

89. The method of claim 87 or 88, wherein the quantitative genetic analysis comprises DNA sequencing to generate a plurality of sequencing reads.

90. A set of adaptors that encode an identity of a unique genomic DNA fragment and an identity of a test sample, for use in generating a genomic DNA library, wherein each

adaptor in said set of adapters is a DNA polynucleotide that comprises: an amplification region, a sample tag region, and an anchor region;

wherein the amplification region comprises a polynucleotide sequence capable of serving as a primer recognition site for PCR amplification;

wherein the sample tag comprises a polynucleotide sequence that encodes the identity of the unique library DNA fragment and encodes the identity of the test sample; and

wherein the anchor region comprises a polynucleotide sequence that encodes the identity of the test sample, and wherein the anchor region is capable of attaching to the genomic DNA fragment.

91. The set of adaptors of claim 90, wherein the sample tag further comprises a unique molecule identifier (UMI), wherein the UMI facilitates the identification of the unique genomic DNA fragment.

92. The set of adaptors of claim 90 or 91, wherein the amplification region is between 10 and 50 nucleotides in length.

93. The set of adaptors of any one of claims 90-92, wherein the amplification region is 25 nucleotides in length.

94. The set of adaptors of any one of the preceding claims, wherein the sample tag is between 5 and 50 nucleotides in length.

95. The set of adaptors of claim 94, wherein the sample tag is 8 nucleotides in length.

96. The set of adaptors of any one of claims 90-95, wherein the UMI multiplier is adjacent to or contained within the sample tag region.

97. The set of adaptors of claim 96, wherein the UMI multiplier is between 1 and 5 nucleotides in length.

98. The set of adaptors of claims 90-97, wherein the anchor region is between 1 and 50 nucleotides in length.

99. The set of adaptors of claim 98, wherein the anchor region is 10 nucleotides in length.

100. The set of adaptors of any of claims 90-99, wherein the amplification regions of each adaptor of the plurality of adaptors comprises an identical nucleotide sequence.

101. The set of adaptors of claim 100, wherein each nucleotide sequence of the sample tags is discrete from any other nucleotide sequence of the sample tags of the set of adaptors by Hamming distance of at least two.

102. The set of adaptors of any one of claims 90-101, wherein each of the plurality of adaptors comprises a UMI multiplier that is adjacent to or contained within the sample tag region.

103. The set of adaptors of any one of claims 90-101, wherein each of the plurality of adaptors comprises a UMI multiplier that is adjacent to the sample tag region.

104. The set of adaptors of claim 103, wherein the anchor tag region of each adaptor of the plurality of adaptors comprises one of four nucleotide sequences, and wherein each sample region of a given sequence is paired to only one of the four anchor regions of a given sequence.

105. The set of adaptors of any one of claims 90-104, wherein the amplification regions of each adaptor of the plurality of adaptors comprises an identical nucleotide sequence;

wherein the sample tag region of each adaptor is 8 nucleotides in length, wherein each nucleotide sequence of the sample tags is discrete from any other nucleotide sequence of the sample tags of the set of adaptors by Hamming distance of at least two;

wherein each of the plurality of adaptors comprises a UMI multiplier that is adjacent to or contained within the sample tag region, wherein the UMI multiplier of each adaptor of

the plurality of adaptors is three nucleotides in length, wherein the UMI multiplier comprises one of 64 possible nucleotide sequences, and wherein the UMI multiplier of each of the 64 possible nucleotide sequences is paired to each of the sample tag region of the plurality of adaptors;

wherein the anchor tag region of each adaptor of the plurality of adaptors comprises one of four nucleotide sequences; and

wherein each sample region of a given sequence is paired to only one of the four anchor regions of a given sequence.

FIG. 1

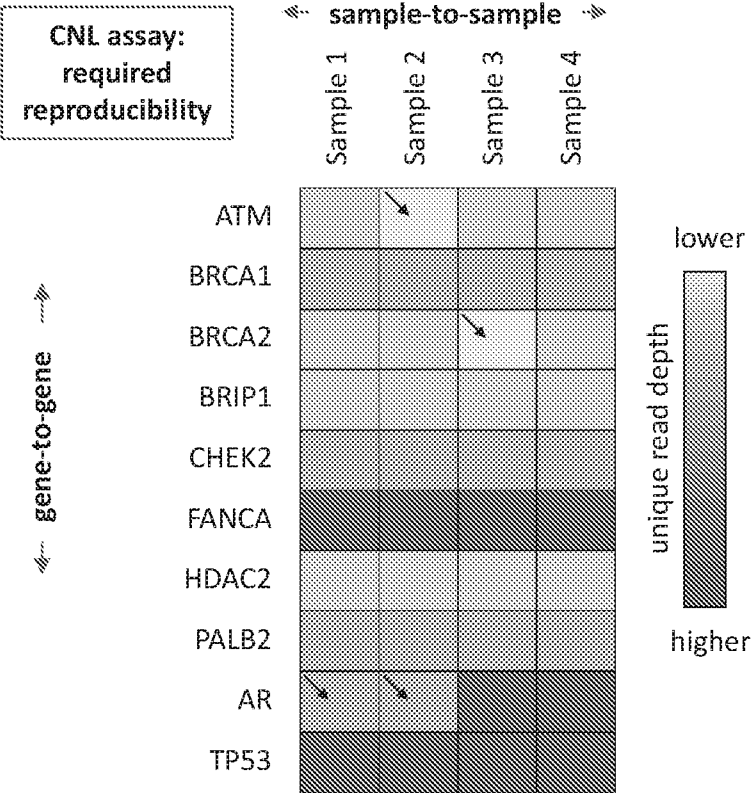


FIG. 2

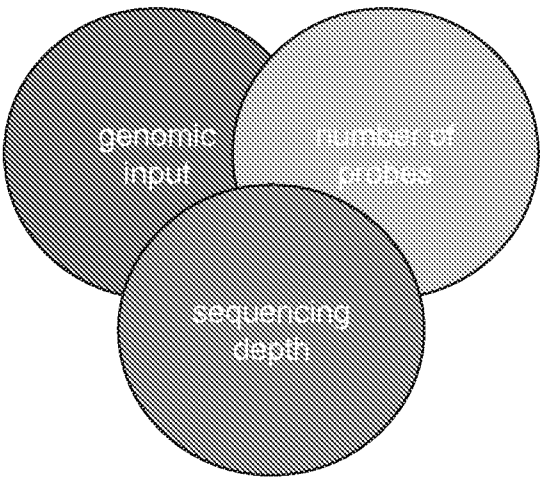


FIG. 3

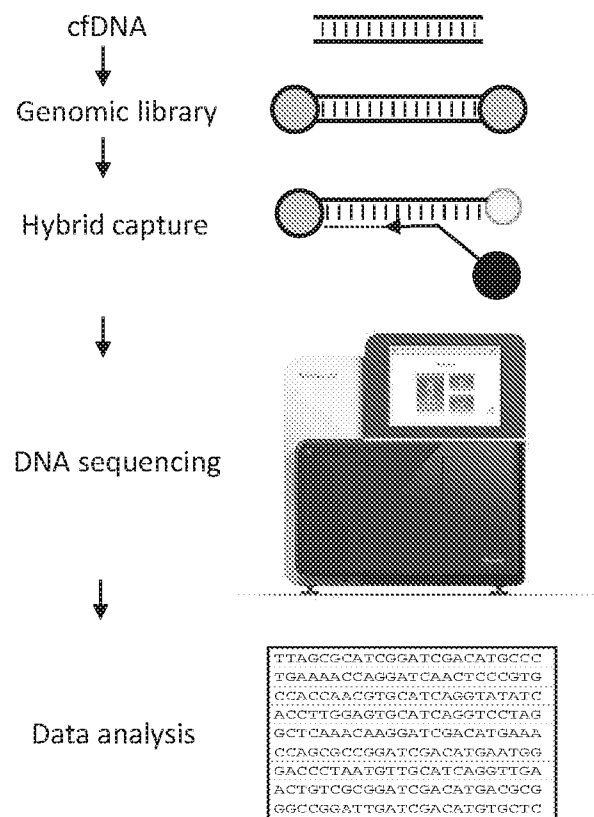


FIG. 4A

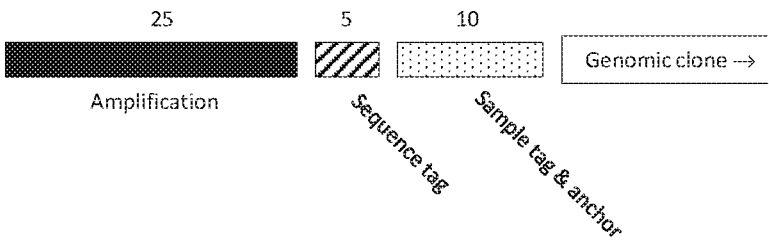
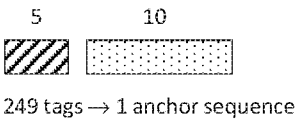


FIG. 4B



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FIG. 4C

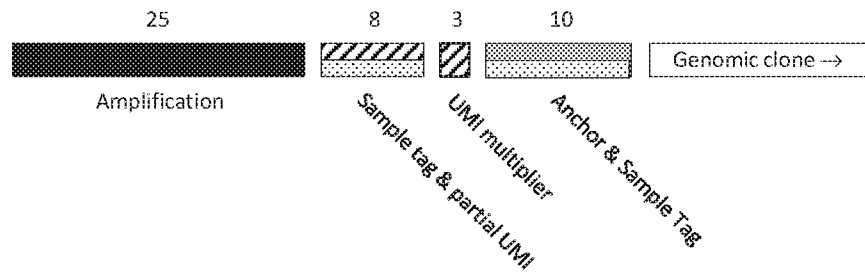


FIG. 4D

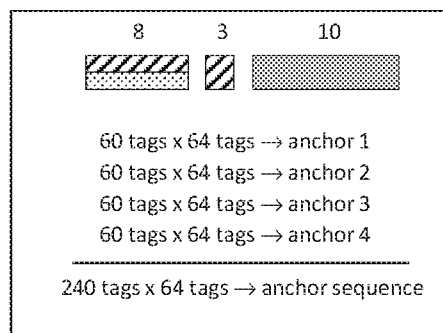


FIG. 4E



FIG. 5A

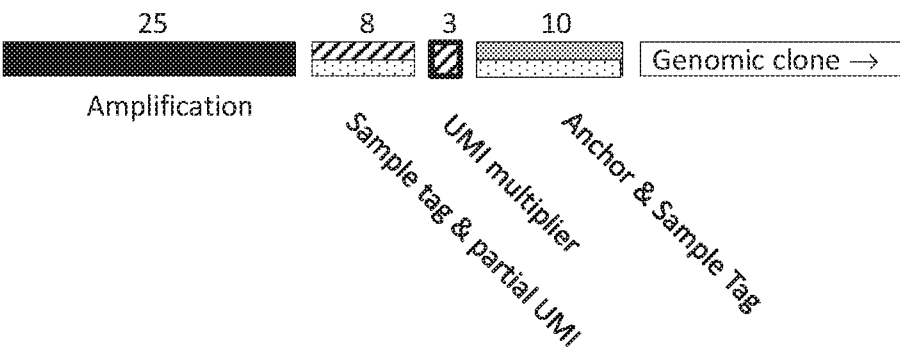
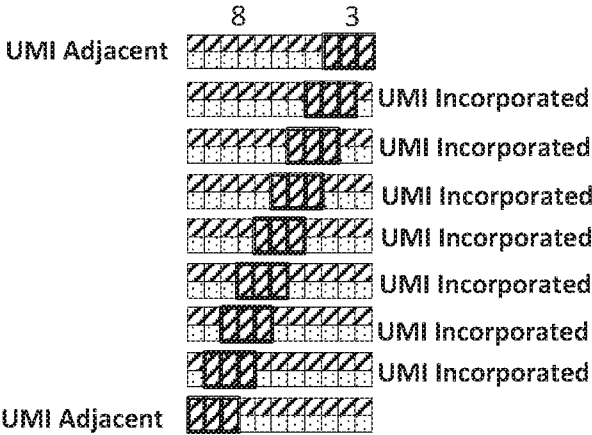


FIG. 5B

Shifting the UMI multiplier to increase the number of unique tags



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FIG. 6

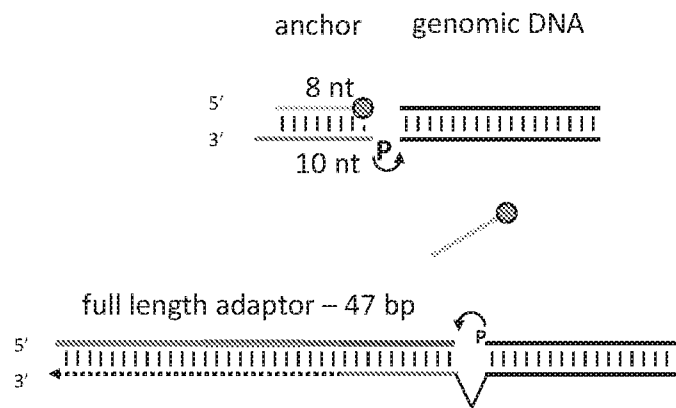


FIG. 7

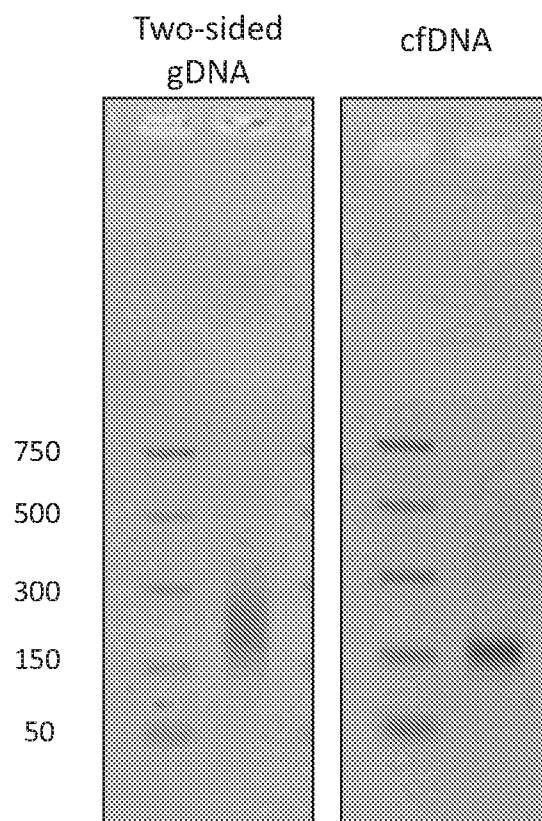


FIG. 8A

Sample	Input
Sample 1	Female gDNA + 8% BRCA2 delete
Sample 2	Female gDNA + 4% BRCA2 delete
Sample 3	Female gDNA + 2% BRCA2 delete
Sample 4	Pure Female gDNA
Sample 5	Female gDNA + 8% ATM delete
Sample 6	Female gDNA + 4% ATM delete
Sample 7	Female gDNA + 2% ATM delete
Sample 8	Pure Female gDNA

FIG. 8B

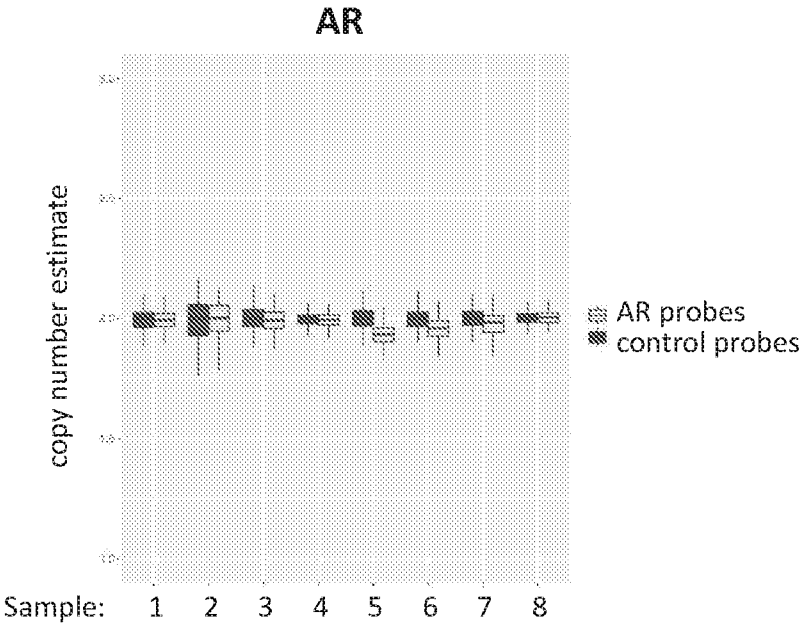


FIG. 8C

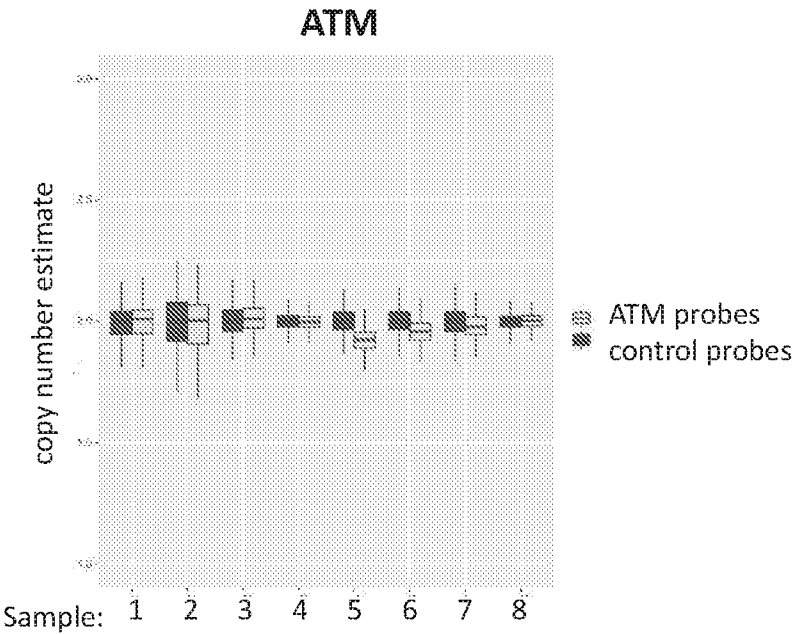


FIG. 9A

Sample	Input
Sample 1	Female gDNA + 8% BRCA2 delete
Sample 2	Female gDNA + 4% BRCA2 delete
Sample 3	Female gDNA + 2% BRCA2 delete
Sample 4	Pure Female gDNA
Sample 5	Female gDNA + 8% ATM delete
Sample 6	Female gDNA + 4% ATM delete
Sample 7	Female gDNA + 2% ATM delete
Sample 8	Pure Female gDNA

FIG. 9B

Measured Δ BRCA2 SNP frequency: 5.3 2.4 0.8
Measured Δ ATM SNP frequency: 5.2 2.2 1.3

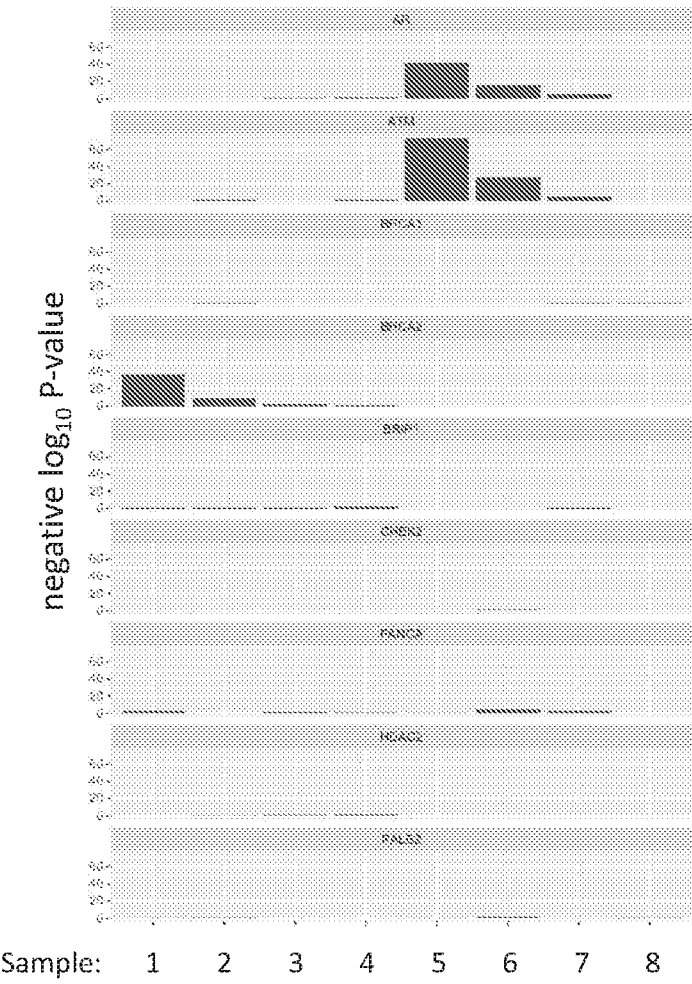


FIG. 11A

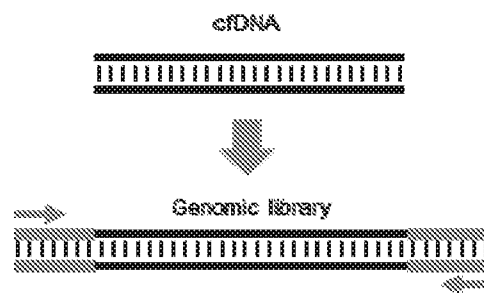


FIG. 11B

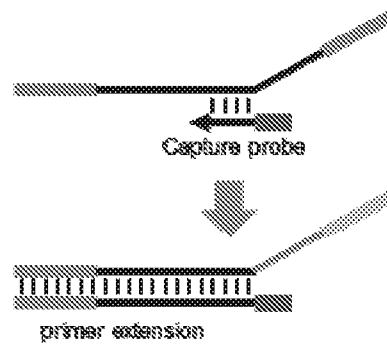


FIG. 11C

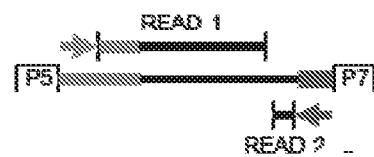


FIG. 11D ^D Distribution of targeted sequencing reads

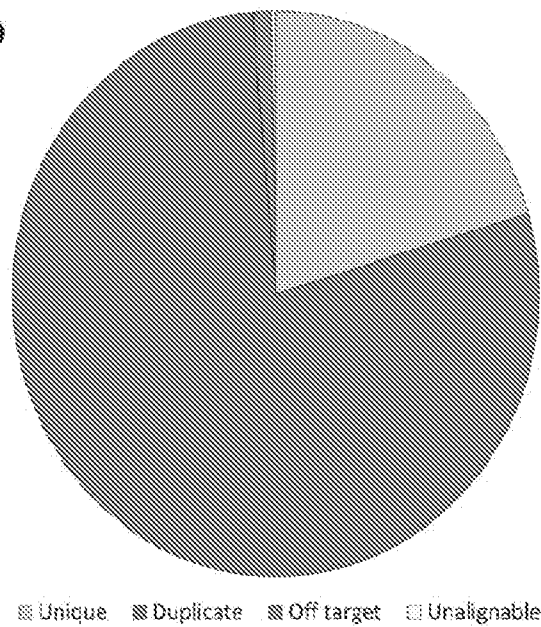


FIG. 12A

Pool-1	SEQ ID NO:	Pool-2	SEQ ID NO:	Pool-3	SEQ ID NO:
TGCAGGACCAGAGAATT CGAATA	9	TGCAGGACCAGAGAATT CGAATA	249	TGCAGGACCAGAGAATT CGAATA	489
CACGAGCTTANNNACGTATGCCA		CACCCTGTCGNNNACGTATGCCA		CAACGTCAACNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	10	TGCAGGACCAGAGAATT CGAATA	250	TGCAGGACCAGAGAATT CGAATA	490
CATTGCTCACNNNACGTATGCCA		CATATCAATGNNNACGTATGCCA		CAGTGTCTAGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	11	TGCAGGACCAGAGAATT CGAATA	251	TGCAGGACCAGAGAATT CGAATA	491
CATAATACACNNNACGTATGCCA		CACTGCAGATNNNACGTATGCCA		CAGCGCCAGTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	12	TGCAGGACCAGAGAATT CGAATA	252	TGCAGGACCAGAGAATT CGAATA	492
CATCAGCATGNNNACGTATGCCA		CAATCGGATCNNNACGTATGCCA		CAGCTCTGAANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	13	TGCAGGACCAGAGAATT CGAATA	253	TGCAGGACCAGAGAATT CGAATA	493
CAACTGTAGCNNNACGTATGCCA		CACGTGTTCCANNNACGTATGCCA		CAAGACTTGCNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	14	TGCAGGACCAGAGAATT CGAATA	254	TGCAGGACCAGAGAATT CGAATA	494
CAATTATGCAANNNACGTATGCCA		CATCACATTTNNNACGTATGCCA		CAGATGGTCTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	15	TGCAGGACCAGAGAATT CGAATA	255	TGCAGGACCAGAGAATT CGAATA	495
CATGACCTTCNNNACGTATGCCA		CAGCGTGGCTNNNACGTATGCCA		CATTGTGAATNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	16	TGCAGGACCAGAGAATT CGAATA	256	TGCAGGACCAGAGAATT CGAATA	496
CAAAAATCCTNNNACGTATGCCA		CACGGAGTAANNNACGTATGCCA		CACAGCGCTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	17	TGCAGGACCAGAGAATT CGAATA	257	TGCAGGACCAGAGAATT CGAATA	497
CAGGTTCCGGNNNACGTATGCCA		CAGTGTCCGGNNNACGTATGCCA		CATGCCAAGTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	18	TGCAGGACCAGAGAATT CGAATA	258	TGCAGGACCAGAGAATT CGAATA	498
CAACGTGCATNNNACGTATGCCA		CATATTGTAGNNNACGTATGCCA		CACGTGCTTTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	19	TGCAGGACCAGAGAATT CGAATA	259	TGCAGGACCAGAGAATT CGAATA	499
CACGCCCCATNNNACGTATGCCA		CATAGTATTGNNNACGTATGCCA		CACCAACGGCNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	20	TGCAGGACCAGAGAATT CGAATA	260	TGCAGGACCAGAGAATT CGAATA	500
CAGTAAGCCTNNNACGTATGCCA		CAAGCGCTTANNNACGTATGCCA		CACAGTTATANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	21	TGCAGGACCAGAGAATT CGAATA	261	TGCAGGACCAGAGAATT CGAATA	501
CAAGTAATAGNNNACGTATGCCA		CATGCAAGTTNNNACGTATGCCA		CACGAAGGCGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	22	TGCAGGACCAGAGAATT CGAATA	262	TGCAGGACCAGAGAATT CGAATA	502
CAAAAGTCCANNNACGTATGCCA		CACCTCCGGTNNNACGTATGCCA		CAATGGCTACNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	23	TGCAGGACCAGAGAATT CGAATA	263	TGCAGGACCAGAGAATT CGAATA	503
CAAGTGCATCANNNACGTATGCCA		CAAGACGGATNNNACGTATGCCA		CATCGCATGANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	24	TGCAGGACCAGAGAATT CGAATA	264	TGCAGGACCAGAGAATT CGAATA	504
CAGACATATTNNNACGTATGCCA		CATCTGTCTGNNNACGTATGCCA		CAATATCCTTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	25	TGCAGGACCAGAGAATT CGAATA	265	TGCAGGACCAGAGAATT CGAATA	505
CAGTCCACAANNNACGTATGCCA		CATTACCGTNNNACGTATGCCA		CATGAAGCAGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	26	TGCAGGACCAGAGAATT CGAATA	266	TGCAGGACCAGAGAATT CGAATA	506
CATCTCAGAGNNNACGTATGCCA		CACGTAAGGNNNACGTATGCCA		CAGACCACCGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	27	TGCAGGACCAGAGAATT CGAATA	267	TGCAGGACCAGAGAATT CGAATA	507
CAAAAACGTANNNACGTATGCCA		CAAGAAAGANNNACGTATGCCA		CAAGATTAGANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	28	TGCAGGACCAGAGAATT CGAATA	268	TGCAGGACCAGAGAATT CGAATA	508
CACTACCAAGNNNACGTATGCCA		CAAGTAGTTTNNNACGTATGCCA		CAAGATCTATNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	29	TGCAGGACCAGAGAATT CGAATA	269	TGCAGGACCAGAGAATT CGAATA	509
CACCTGACTTNNNACGTATGCCA		CAGGTACCTANNNACGTATGCCA		CAACGTACACNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	30	TGCAGGACCAGAGAATT CGAATA	270	TGCAGGACCAGAGAATT CGAATA	510
CACTCCTATGNNNACGTATGCCA		CAGAAGCACANNNACGTATGCCA		CACGGTTACANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	31	TGCAGGACCAGAGAATT CGAATA	271	TGCAGGACCAGAGAATT CGAATA	511
CAATCATGATNNNACGTATGCCA		CACTAATAACNNNACGTATGCCA		CAAAACCTATNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	32	TGCAGGACCAGAGAATT CGAATA	272	TGCAGGACCAGAGAATT CGAATA	512
CATGACGGTNNNACGTATGCCA		CAACGGACAANNNACGTATGCCA		CACTGATTTTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	33	TGCAGGACCAGAGAATT CGAATA	273	TGCAGGACCAGAGAATT CGAATA	513
CAGTCGGCGTNNNACGTATGCCA		CAATCCAGTNNNACGTATGCCA		CATGAATATCANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	34	TGCAGGACCAGAGAATT CGAATA	274	TGCAGGACCAGAGAATT CGAATA	514
CAGTTACCTNNNACGTATGCCA		CAGGACAACANNNACGTATGCCA		CAACTGCGCGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	35	TGCAGGACCAGAGAATT CGAATA	275	TGCAGGACCAGAGAATT CGAATA	515
CACCTTAACGNNNACGTATGCCA		CAGAAAGTTANNNACGTATGCCA		CAGAACGACANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	36	TGCAGGACCAGAGAATT CGAATA	276	TGCAGGACCAGAGAATT CGAATA	516
CACGCTCCTGNNNACGTATGCCA		CAAAACACAGNNNACGTATGCCA		CATATATTGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	37	TGCAGGACCAGAGAATT CGAATA	277	TGCAGGACCAGAGAATT CGAATA	517
CATCTCGGTNNNACGTATGCCA		CACCAGAATCANNNACGTATGCCA		CATAGATGCCNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	38	TGCAGGACCAGAGAATT CGAATA	278	TGCAGGACCAGAGAATT CGAATA	518
CAGCTCGAGCANNNACGTATGCCA		CATTCAACACNNNACGTATGCCA		CAGCAAGTAGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	39	TGCAGGACCAGAGAATT CGAATA	279	TGCAGGACCAGAGAATT CGAATA	519
CACGCTTCGNNNACGTATGCCA		CATCGAGACANNNACGTATGCCA		CAAAACGACCTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	40	TGCAGGACCAGAGAATT CGAATA	280	TGCAGGACCAGAGAATT CGAATA	520
CAATCCAGACNNNACGTATGCCA		CACGATGTANNNACGTATGCCA		CAGTACAGTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	41	TGCAGGACCAGAGAATT CGAATA	281	TGCAGGACCAGAGAATT CGAATA	521
CATAGCACTGNNNACGTATGCCA		CACGGCAGGANNNACGTATGCCA		CATATGCGGTNNNACGTATGCCA	

FIG. 12B

Pool-1	SEQ ID NO:	Pool-2	SEQ ID NO:	Pool-3	SEQ ID NO:
TGCAGGACCAGAGAATT CGAATA	42	TGCAGGACCAGAGAATT CGAATA	282	TGCAGGACCAGAGAATT CGAATA	522
CACTGGCTTTNNNACGTATGCCA		CAAGAACCAGNNNACGTATGCCA		CAATAATAGGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	43	TGCAGGACCAGAGAATT CGAATA	283	TGCAGGACCAGAGAATT CGAATA	523
CAGCAAATGGNNNACGTATGCCA		CAGATTTTGANNNACGTATGCCA		CAGTTACTAANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	44	TGCAGGACCAGAGAATT CGAATA	284	TGCAGGACCAGAGAATT CGAATA	524
CAGGATGACANNNACGTATGCCA		CAAAACACGTCNNNACGTATGCCA		CACCCCTGTANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	45	TGCAGGACCAGAGAATT CGAATA	285	TGCAGGACCAGAGAATT CGAATA	525
CAGCCCCACTNNNACGTATGCCA		CAACCTCTACNNNACGTATGCCA		CAACATTTCTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	46	TGCAGGACCAGAGAATT CGAATA	286	TGCAGGACCAGAGAATT CGAATA	526
CACTAGCCGGNNNACGTATGCCA		CAGGCGTTTANNNACGTATGCCA		CACCCGACTTTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	47	TGCAGGACCAGAGAATT CGAATA	287	TGCAGGACCAGAGAATT CGAATA	527
CACCCCTCCTCNNNACGTATGCCA		CACCCGAAGCNNNACGTATGCCA		CATATGAACCTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	48	TGCAGGACCAGAGAATT CGAATA	288	TGCAGGACCAGAGAATT CGAATA	528
CATGTAGTGCNNNACGTATGCCA		CATACCTACCNNNACGTATGCCA		CATTCTTTTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	49	TGCAGGACCAGAGAATT CGAATA	289	TGCAGGACCAGAGAATT CGAATA	529
CAGAATGTGGNNNACGTATGCCA		CATTTACGCCNNNACGTATGCCA		CAATAGGTTTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	50	TGCAGGACCAGAGAATT CGAATA	290	TGCAGGACCAGAGAATT CGAATA	530
CAAATGATCTNNNACGTATGCCA		CAAGGTATGGNNNACGTATGCCA		CACGACGTTANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	51	TGCAGGACCAGAGAATT CGAATA	291	TGCAGGACCAGAGAATT CGAATA	531
CACACTAACGNNNACGTATGCCA		CAACTACAAATNNNACGTATGCCA		CAAGCATAGGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	52	TGCAGGACCAGAGAATT CGAATA	292	TGCAGGACCAGAGAATT CGAATA	532
CACGTCGGACNNNACGTATGCCA		CACCTCCTCAANNNACGTATGCCA		CACCTGCATCTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	53	TGCAGGACCAGAGAATT CGAATA	293	TGCAGGACCAGAGAATT CGAATA	533
CAGCAACTTGNNNACGTATGCCA		CAGATACAAANNNACGTATGCCA		CACGACGCCANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	54	TGCAGGACCAGAGAATT CGAATA	294	TGCAGGACCAGAGAATT CGAATA	534
CACGGTGGAGNNNACGTATGCCA		CACCAACACANNNACGTATGCCA		CAAAACGCCGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	55	TGCAGGACCAGAGAATT CGAATA	295	TGCAGGACCAGAGAATT CGAATA	535
CAGTAACCGTNNNACGTATGCCA		CAACCCATTNNNACGTATGCCA		CACCTCTCGATNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	56	TGCAGGACCAGAGAATT CGAATA	296	TGCAGGACCAGAGAATT CGAATA	536
CATAGTTTTNNNACGTATGCCA		CATCTAAGCGNNNACGTATGCCA		CACCCCTGACNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	57	TGCAGGACCAGAGAATT CGAATA	297	TGCAGGACCAGAGAATT CGAATA	537
CACCTGTCTNNNACGTATGCCA		CACCTAAGGCGNNNACGTATGCCA		CAGTTGTAAATNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	58	TGCAGGACCAGAGAATT CGAATA	298	TGCAGGACCAGAGAATT CGAATA	538
CATTTCGAGGTNNNACGTATGCCA		CACGAATCCANNNACGTATGCCA		CAAAAAGACTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	59	TGCAGGACCAGAGAATT CGAATA	299	TGCAGGACCAGAGAATT CGAATA	539
CACCTCCACGNNNACGTATGCCA		CACAACCTAATNNNACGTATGCCA		CATCCTAGCTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	60	TGCAGGACCAGAGAATT CGAATA	300	TGCAGGACCAGAGAATT CGAATA	540
CAGAGACTAGNNNACGTATGCCA		CATCACACCTNNNACGTATGCCA		CAACCAAAGGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	61	TGCAGGACCAGAGAATT CGAATA	301	TGCAGGACCAGAGAATT CGAATA	541
CATGAACCTATNNNACGTATGCCA		CAGACCGTCGNNNACGTATGCCA		CAACGAGTTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	62	TGCAGGACCAGAGAATT CGAATA	302	TGCAGGACCAGAGAATT CGAATA	542
CAGTTGATTANNNACGTATGCCA		CACCTTTAAGANNNACGTATGCCA		CACCTATGGTGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	63	TGCAGGACCAGAGAATT CGAATA	303	TGCAGGACCAGAGAATT CGAATA	543
CATCCACTCANNNACGTATGCCA		CATGTGATTANNNACGTATGCCA		CACCACCGTCNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	64	TGCAGGACCAGAGAATT CGAATA	304	TGCAGGACCAGAGAATT CGAATA	544
CAGTGACTGTNNNACGTATGCCA		CAACCCAAATGNNNACGTATGCCA		CAGAATCGCTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	65	TGCAGGACCAGAGAATT CGAATA	305	TGCAGGACCAGAGAATT CGAATA	545
CATTACGGCANNNACGTATGCCA		CAACGTTGACNNNACGTATGCCA		CAAGTGTTATNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	66	TGCAGGACCAGAGAATT CGAATA	306	TGCAGGACCAGAGAATT CGAATA	546
CACACCTCCGNNNACGTATGCCA		CAATGAAATGNNNACGTATGCCA		CAACGCGTCGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	67	TGCAGGACCAGAGAATT CGAATA	307	TGCAGGACCAGAGAATT CGAATA	547
CAAAGAAGAANNNACGTATGCCA		CATCCTCGTANNNACGTATGCCA		CACCTCGTGTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	68	TGCAGGACCAGAGAATT CGAATA	308	TGCAGGACCAGAGAATT CGAATA	548
CAGAACCTGTNNNACGTATGCCA		CAGTAACAGGNNNACGTATGCCA		CATTGTAGATNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	69	TGCAGGACCAGAGAATT CGAATA	309	TGCAGGACCAGAGAATT CGAATA	549
CAGAATAACANNNCTAGCGTTAC		CAACTCGGTANNNCTAGCGTTAC		CAGCCGCGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	70	TGCAGGACCAGAGAATT CGAATA	310	TGCAGGACCAGAGAATT CGAATA	550
CAGCCCTCGTCNNNCTAGCGTTAC		CAACGCTTAGNNNCTAGCGTTAC		CAAGTGACGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	71	TGCAGGACCAGAGAATT CGAATA	311	TGCAGGACCAGAGAATT CGAATA	551
CACCCGCACTNNNCTAGCGTTAC		CATCAAGCTGNNNCTAGCGTTAC		CAATACCTCCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	72	TGCAGGACCAGAGAATT CGAATA	312	TGCAGGACCAGAGAATT CGAATA	552
CACCACGATANNNCTAGCGTTAC		CATAGCTAATNNNCTAGCGTTAC		CACCTTTTGTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	73	TGCAGGACCAGAGAATT CGAATA	313	TGCAGGACCAGAGAATT CGAATA	553
CACGGTACATNNNCTAGCGTTAC		CACGGCATTANNNCTAGCGTTAC		CAATATCATGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	74	TGCAGGACCAGAGAATT CGAATA	314	TGCAGGACCAGAGAATT CGAATA	554
CACCATATCCNNNCTAGCGTTAC		CAAATGATGANNNCTAGCGTTAC		CATACATATGNNNCTAGCGTTAC	

FIG. 12C

Pool-1	SEQ ID NO:	Pool-2	SEQ ID NO:	Pool-3	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA	75	TGCAGGACCAGAGAATTCGAATA	315	TGCAGGACCAGAGAATTCGAATA	555
CACATACGGTNNNCTAGCGTTAC		CATCGCGATANNNCTAGCGTTAC		CAACTTTTGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	76	TGCAGGACCAGAGAATTCGAATA	316	TGCAGGACCAGAGAATTCGAATA	556
CAAATAGCTTNNNCTAGCGTTAC		CACACAGGTTNNNCTAGCGTTAC		CATAATGTACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	77	TGCAGGACCAGAGAATTCGAATA	317	TGCAGGACCAGAGAATTCGAATA	557
CACCAGGTATNNNCTAGCGTTAC		CAACGGTGCCNNNCTAGCGTTAC		CAAACGACAGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	78	TGCAGGACCAGAGAATTCGAATA	318	TGCAGGACCAGAGAATTCGAATA	558
CACAACCTGANNNCTAGCGTTAC		CAGTTACAGCINNCTAGCGTTAC		CAGCTCCTATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	79	TGCAGGACCAGAGAATTCGAATA	319	TGCAGGACCAGAGAATTCGAATA	559
CATGATGGTCNNNCTAGCGTTAC		CATGCGATGTNNNCTAGCGTTAC		CACCGAACTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	80	TGCAGGACCAGAGAATTCGAATA	320	TGCAGGACCAGAGAATTCGAATA	560
CAGGAGCCGANNNCTAGCGTTAC		CAATGGTGCTNNNCTAGCGTTAC		CAGCTAGGAANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	81	TGCAGGACCAGAGAATTCGAATA	321	TGCAGGACCAGAGAATTCGAATA	561
CAATGCGGCCNNNCTAGCGTTAC		CAACCCAGGNNNCTAGCGTTAC		CAGCTTCCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	82	TGCAGGACCAGAGAATTCGAATA	322	TGCAGGACCAGAGAATTCGAATA	562
CATGCTGTAGNNNCTAGCGTTAC		CAGCAGACGGNNNCTAGCGTTAC		CAACAGCATCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	83	TGCAGGACCAGAGAATTCGAATA	323	TGCAGGACCAGAGAATTCGAATA	563
CAGCATTGACNNNCTAGCGTTAC		CACCTGGCAGCINNCTAGCGTTAC		CAACGAGAGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	84	TGCAGGACCAGAGAATTCGAATA	324	TGCAGGACCAGAGAATTCGAATA	564
CATTTGTACTNNNCTAGCGTTAC		CAAGAGAGTCNNNCTAGCGTTAC		CAATCATATGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	85	TGCAGGACCAGAGAATTCGAATA	325	TGCAGGACCAGAGAATTCGAATA	565
CACATATGGCINNCTAGCGTTAC		CACGTTTTATNNNCTAGCGTTAC		CATGAGATTTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	86	TGCAGGACCAGAGAATTCGAATA	326	TGCAGGACCAGAGAATTCGAATA	566
CAGCATGAAGNNNCTAGCGTTAC		CAAGAGGTCANNNCTAGCGTTAC		CAGCCGGCCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	87	TGCAGGACCAGAGAATTCGAATA	327	TGCAGGACCAGAGAATTCGAATA	567
CACAGGAAACNNNCTAGCGTTAC		CATTCTCTCINNCTAGCGTTAC		CAAGGCGCAGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	88	TGCAGGACCAGAGAATTCGAATA	328	TGCAGGACCAGAGAATTCGAATA	568
CACCTAAGACNNNCTAGCGTTAC		CACGTGTCTTNNNCTAGCGTTAC		CAGTACACACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	89	TGCAGGACCAGAGAATTCGAATA	329	TGCAGGACCAGAGAATTCGAATA	569
CAACCTAGGTNNNCTAGCGTTAC		CACCTCAGCAANNNCTAGCGTTAC		CAAGATTTTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	90	TGCAGGACCAGAGAATTCGAATA	330	TGCAGGACCAGAGAATTCGAATA	570
CACCATTTCTNNNCTAGCGTTAC		CATCTTATGTNNNCTAGCGTTAC		CATGCATCTCINNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	91	TGCAGGACCAGAGAATTCGAATA	331	TGCAGGACCAGAGAATTCGAATA	571
CATCGGTTTTNNNCTAGCGTTAC		CATCGGCACGNNNCTAGCGTTAC		CACCTCAGAGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	92	TGCAGGACCAGAGAATTCGAATA	332	TGCAGGACCAGAGAATTCGAATA	572
CACACCTGTTNNNCTAGCGTTAC		CACGTTTTCTGNNNCTAGCGTTAC		CAACTCTGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	93	TGCAGGACCAGAGAATTCGAATA	333	TGCAGGACCAGAGAATTCGAATA	573
CAAGAGAGAGNNNCTAGCGTTAC		CAATGTGAGGNNNCTAGCGTTAC		CATTATCCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	94	TGCAGGACCAGAGAATTCGAATA	334	TGCAGGACCAGAGAATTCGAATA	574
CAATGGCCCGNNNCTAGCGTTAC		CAAGAAACATNNNCTAGCGTTAC		CAGCCCTTGCCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	95	TGCAGGACCAGAGAATTCGAATA	335	TGCAGGACCAGAGAATTCGAATA	575
CATAGCGTGTNNNCTAGCGTTAC		CAGAGAGAAGNNNCTAGCGTTAC		CAAACTTCTTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	96	TGCAGGACCAGAGAATTCGAATA	336	TGCAGGACCAGAGAATTCGAATA	576
CAGAAAGACNNNCTAGCGTTAC		CACCTCAGGANNNCTAGCGTTAC		CATTGTAGGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	97	TGCAGGACCAGAGAATTCGAATA	337	TGCAGGACCAGAGAATTCGAATA	577
CATCATTTGTNNNCTAGCGTTAC		CATCCCTCGGNNNCTAGCGTTAC		CATGACCCAAANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	98	TGCAGGACCAGAGAATTCGAATA	338	TGCAGGACCAGAGAATTCGAATA	578
CATCGAAGACNNNCTAGCGTTAC		CACCTTCCTTNNNCTAGCGTTAC		CACCTCTGTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	99	TGCAGGACCAGAGAATTCGAATA	339	TGCAGGACCAGAGAATTCGAATA	579
CAAGCTTACGNNNCTAGCGTTAC		CATAGTTATGNNNCTAGCGTTAC		CAAGCCACTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	100	TGCAGGACCAGAGAATTCGAATA	340	TGCAGGACCAGAGAATTCGAATA	580
CACCTCGGTTTTNNNCTAGCGTTAC		CAGCATAGAGNNNCTAGCGTTAC		CATGTATGATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	101	TGCAGGACCAGAGAATTCGAATA	341	TGCAGGACCAGAGAATTCGAATA	581
CAAAATCGTTANNNCTAGCGTTAC		CATAGCTCCTNNNCTAGCGTTAC		CACAGGTCCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	102	TGCAGGACCAGAGAATTCGAATA	342	TGCAGGACCAGAGAATTCGAATA	582
CATAACAGTTNNNCTAGCGTTAC		CAACCCAGGTANNNCTAGCGTTAC		CATTTTTTTTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	103	TGCAGGACCAGAGAATTCGAATA	343	TGCAGGACCAGAGAATTCGAATA	583
CAATCCTGTNNNCTAGCGTTAC		CACATCGTCTNNNCTAGCGTTAC		CATTTGCGGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	104	TGCAGGACCAGAGAATTCGAATA	344	TGCAGGACCAGAGAATTCGAATA	584
CAGTAATGTTNNNCTAGCGTTAC		CAAGAGATTANNNCTAGCGTTAC		CAAGCCTGTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	105	TGCAGGACCAGAGAATTCGAATA	345	TGCAGGACCAGAGAATTCGAATA	585
CATTGCGCGNNNCTAGCGTTAC		CAATCAAGANNNCTAGCGTTAC		CAGCGGCACCTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	106	TGCAGGACCAGAGAATTCGAATA	346	TGCAGGACCAGAGAATTCGAATA	586
CAGTCAGGAANNNCTAGCGTTAC		CAGGAGTACANNNCTAGCGTTAC		CATGTTGAGCINNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	107	TGCAGGACCAGAGAATTCGAATA	347	TGCAGGACCAGAGAATTCGAATA	587
CAGTTAAAAGNNNCTAGCGTTAC		CAATAGCAGGNNNCTAGCGTTAC		CAAAAAGTTGNNNCTAGCGTTAC	

FIG. 12D

Pool-1	SEQ ID NO:	Pool-2	SEQ ID NO:	Pool-3	SEQ ID NO:
TGCAGGACCAGAGAATT CGAATA	108	TGCAGGACCAGAGAATT CGAATA	348	TGCAGGACCAGAGAATT CGAATA	588
CATGT CATAANNCTAGCGTTAC		CATCTAATT CANNCTAGCGTTAC		CACGGTGCCANNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	109	TGCAGGACCAGAGAATT CGAATA	349	TGCAGGACCAGAGAATT CGAATA	589
CAACTTGAATNNNCTAGCGTTAC		CAGTTCCCGCANNCTAGCGTTAC		CACAGCGGT CANNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	110	TGCAGGACCAGAGAATT CGAATA	350	TGCAGGACCAGAGAATT CGAATA	590
CATGTGGCATNNNCTAGCGTTAC		CATAGATTTGNNNCTAGCGTTAC		CAAGCTAACCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	111	TGCAGGACCAGAGAATT CGAATA	351	TGCAGGACCAGAGAATT CGAATA	591
CATCTACACNNNCTAGCGTTAC		CACGGCAGAGNNNCTAGCGTTAC		CAACGGCGT CANNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	112	TGCAGGACCAGAGAATT CGAATA	352	TGCAGGACCAGAGAATT CGAATA	592
CATCATGCCCTNNNCTAGCGTTAC		CACCTCGTGCNNNCTAGCGTTAC		CATAGTTCAANNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	113	TGCAGGACCAGAGAATT CGAATA	353	TGCAGGACCAGAGAATT CGAATA	593
CATCTAGCCTNNNCTAGCGTTAC		CACCCTTGATNNNCTAGCGTTAC		CAATGTAGCCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	114	TGCAGGACCAGAGAATT CGAATA	354	TGCAGGACCAGAGAATT CGAATA	594
CAATAAAGCANNNCTAGCGTTAC		CACGTCACGGNNNCTAGCGTTAC		CAAGAAGCACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	115	TGCAGGACCAGAGAATT CGAATA	355	TGCAGGACCAGAGAATT CGAATA	595
CATGCATAATNNNCTAGCGTTAC		CAGTTTGGCANNNCTAGCGTTAC		CAGAAGCGCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	116	TGCAGGACCAGAGAATT CGAATA	356	TGCAGGACCAGAGAATT CGAATA	596
CACATGACGTNNNCTAGCGTTAC		CATGCTCTGTNNNCTAGCGTTAC		CACGGTATACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	117	TGCAGGACCAGAGAATT CGAATA	357	TGCAGGACCAGAGAATT CGAATA	597
CACCTTATCATNNNCTAGCGTTAC		CATCAGTATANNNCTAGCGTTAC		CATAACATACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	118	TGCAGGACCAGAGAATT CGAATA	358	TGCAGGACCAGAGAATT CGAATA	598
CACGGCCTGANNNCTAGCGTTAC		CACCCAAGTANNNCTAGCGTTAC		CACTGCTATCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	119	TGCAGGACCAGAGAATT CGAATA	359	TGCAGGACCAGAGAATT CGAATA	599
CACGTCATGNNNCTAGCGTTAC		CAAGCTAAANNNCTAGCGTTAC		CACGGCAACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	120	TGCAGGACCAGAGAATT CGAATA	360	TGCAGGACCAGAGAATT CGAATA	600
CACCTTATACTNNNCTAGCGTTAC		CAAGATCCACNNNCTAGCGTTAC		CACAAAAACANNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	121	TGCAGGACCAGAGAATT CGAATA	361	TGCAGGACCAGAGAATT CGAATA	601
CAGGAGGTATNNNCTAGCGTTAC		CAGCATCGGCNNNCTAGCGTTAC		CACGTTAGCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	122	TGCAGGACCAGAGAATT CGAATA	362	TGCAGGACCAGAGAATT CGAATA	602
CAATTGTTCTNNNCTAGCGTTAC		CACCTCTGGAANNNCTAGCGTTAC		CACCCCTAATCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	123	TGCAGGACCAGAGAATT CGAATA	363	TGCAGGACCAGAGAATT CGAATA	603
CAAACCTCCAGNNNCTAGCGTTAC		CAAGTCTGACNNNCTAGCGTTAC		CATGTGGCCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	124	TGCAGGACCAGAGAATT CGAATA	364	TGCAGGACCAGAGAATT CGAATA	604
CACGAGGTCCNNNCTAGCGTTAC		CAGAGGCCGANNNCTAGCGTTAC		CATCTAGAGCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	125	TGCAGGACCAGAGAATT CGAATA	365	TGCAGGACCAGAGAATT CGAATA	605
CACGCGACCAANNNCTAGCGTTAC		CATGGTGGAAANNNCTAGCGTTAC		CATACGCATGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	126	TGCAGGACCAGAGAATT CGAATA	366	TGCAGGACCAGAGAATT CGAATA	606
CATGCGCGCTNNNCTAGCGTTAC		CACGGTGTANNNCTAGCGTTAC		CATTGGCCCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	127	TGCAGGACCAGAGAATT CGAATA	367	TGCAGGACCAGAGAATT CGAATA	607
CAGTTACGACNNNCTAGCGTTAC		CATCGCGCAGNNNCTAGCGTTAC		CATGGTTCCTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	128	TGCAGGACCAGAGAATT CGAATA	368	TGCAGGACCAGAGAATT CGAATA	608
CATTATCATCANNNCTAGCGTTAC		CAGCTGTGTANNNCTAGCGTTAC		CAAACGGTGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	129	TGCAGGACCAGAGAATT CGAATA	369	TGCAGGACCAGAGAATT CGAATA	609
CACCTTCTCTNNNGATCGACATG		CAACGTGCGCANNNGATCGACATG		CAGGCTATACNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	130	TGCAGGACCAGAGAATT CGAATA	370	TGCAGGACCAGAGAATT CGAATA	610
CAAACAGGTGNNNGATCGACATG		CAATCAGCCANNNGATCGACATG		CAATTGGTTANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	131	TGCAGGACCAGAGAATT CGAATA	371	TGCAGGACCAGAGAATT CGAATA	611
CAACTTGTCCNNNGATCGACATG		CAGATACTTANNNGATCGACATG		CACAGGATGANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	132	TGCAGGACCAGAGAATT CGAATA	372	TGCAGGACCAGAGAATT CGAATA	612
CATTGGTAATNNNGATCGACATG		CAATTTGCCCANNNGATCGACATG		CACGTTATCCNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	133	TGCAGGACCAGAGAATT CGAATA	373	TGCAGGACCAGAGAATT CGAATA	613
CAGGACTCGCANNNGATCGACATG		CACTTAAAGTNNNGATCGACATG		CAGTTCAATANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	134	TGCAGGACCAGAGAATT CGAATA	374	TGCAGGACCAGAGAATT CGAATA	614
CATGCCGTCAANNNGATCGACATG		CATATGCCCTNNNGATCGACATG		CACAAATCTNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	135	TGCAGGACCAGAGAATT CGAATA	375	TGCAGGACCAGAGAATT CGAATA	615
CACAGAATAANNNGATCGACATG		CAACTTGACGNNNGATCGACATG		CACTGCAAACNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	136	TGCAGGACCAGAGAATT CGAATA	376	TGCAGGACCAGAGAATT CGAATA	616
CATCCGAGGCNNNGATCGACATG		CAAGGAACANNNGATCGACATG		CAGGTGCCANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	137	TGCAGGACCAGAGAATT CGAATA	377	TGCAGGACCAGAGAATT CGAATA	617
CAATTTCTTGNNNGATCGACATG		CATGAGCGAANNNGATCGACATG		CACGATAACNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	138	TGCAGGACCAGAGAATT CGAATA	378	TGCAGGACCAGAGAATT CGAATA	618
CAACTTGTAANNNGATCGACATG		CATGCTGTGANNNGATCGACATG		CATTATGACANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	139	TGCAGGACCAGAGAATT CGAATA	379	TGCAGGACCAGAGAATT CGAATA	619
CACACGGTGCCNNNGATCGACATG		CAGGTTCTGANNNGATCGACATG		CAACCTTCACNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	140	TGCAGGACCAGAGAATT CGAATA	380	TGCAGGACCAGAGAATT CGAATA	620
CAAACCTCGGTNNNGATCGACATG		CAACAAACAANNNGATCGACATG		CATCTTCTCCNNNGATCGACATG	

FIG. 12E

Pool-1	SEQ ID NO:	Pool-2	SEQ ID NO:	Pool-3	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA	141	TGCAGGACCAGAGAATTCGAATA	381	TGCAGGACCAGAGAATTCGAATA	621
CAGCCTATTNNNGATCGACATG		CAAGCTAGAGNNNGATCGACATG		CACCCGAGCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	142	TGCAGGACCAGAGAATTCGAATA	382	TGCAGGACCAGAGAATTCGAATA	622
CACCGCTAAANNNGATCGACATG		CATTAAATATNNNGATCGACATG		CAGTGTGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	143	TGCAGGACCAGAGAATTCGAATA	383	TGCAGGACCAGAGAATTCGAATA	623
CAGTGACATGNNNGATCGACATG		CAAGGAGTCANNNGATCGACATG		CAGTTCTAAANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	144	TGCAGGACCAGAGAATTCGAATA	384	TGCAGGACCAGAGAATTCGAATA	624
CATCTCTCAGNNNGATCGACATG		CACGCACAGCANNNGATCGACATG		CAGCGTTTTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	145	TGCAGGACCAGAGAATTCGAATA	385	TGCAGGACCAGAGAATTCGAATA	625
CATCTCTAGCANNNGATCGACATG		CAGCGACAGNNNGATCGACATG		CAGTCTGCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	146	TGCAGGACCAGAGAATTCGAATA	386	TGCAGGACCAGAGAATTCGAATA	626
CACAAGCGCCNNNGATCGACATG		CACGCTCGTCNNNGATCGACATG		CAACAGAAATNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	147	TGCAGGACCAGAGAATTCGAATA	387	TGCAGGACCAGAGAATTCGAATA	627
CAGGCAGTAANNNGATCGACATG		CATCTGATGNNNGATCGACATG		CATTGCTATTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	148	TGCAGGACCAGAGAATTCGAATA	388	TGCAGGACCAGAGAATTCGAATA	628
CATTGGCTGANNNNGATCGACATG		CAGGCTAGAANNNGATCGACATG		CACCCCTGTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	149	TGCAGGACCAGAGAATTCGAATA	389	TGCAGGACCAGAGAATTCGAATA	629
CAACAGCGAANNNGATCGACATG		CAATGAGGCANNNGATCGACATG		CAGCAGTCCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	150	TGCAGGACCAGAGAATTCGAATA	390	TGCAGGACCAGAGAATTCGAATA	630
CAAAGTTTCANNNGATCGACATG		CACACCCGTCNNNGATCGACATG		CAGTAACCCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	151	TGCAGGACCAGAGAATTCGAATA	391	TGCAGGACCAGAGAATTCGAATA	631
CACGCTCTATNNNGATCGACATG		CATCATCGGANNNGATCGACATG		CAACATTGTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	152	TGCAGGACCAGAGAATTCGAATA	392	TGCAGGACCAGAGAATTCGAATA	632
CATAGGAGTGNNGATCGACATG		CAGGCAAGCGNNNGATCGACATG		CAAAACCGTCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	153	TGCAGGACCAGAGAATTCGAATA	393	TGCAGGACCAGAGAATTCGAATA	633
CATCAGCACANNNGATCGACATG		CACAGTCGATNNNGATCGACATG		CAATTCTGCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	154	TGCAGGACCAGAGAATTCGAATA	394	TGCAGGACCAGAGAATTCGAATA	634
CACGAACACTNNNGATCGACATG		CATGCTACTCNNNGATCGACATG		CATCTAGGCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	155	TGCAGGACCAGAGAATTCGAATA	395	TGCAGGACCAGAGAATTCGAATA	635
CATACTAAACNNNGATCGACATG		CATCCATACNNNGATCGACATG		CAGGTCTACANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	156	TGCAGGACCAGAGAATTCGAATA	396	TGCAGGACCAGAGAATTCGAATA	636
CAGGTACAAGNNNGATCGACATG		CAACCCGCGACNNNGATCGACATG		CAGGTGAGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	157	TGCAGGACCAGAGAATTCGAATA	397	TGCAGGACCAGAGAATTCGAATA	637
CAACAGGCTTNNNGATCGACATG		CAGGCAAGTNNNGATCGACATG		CATGTCTTTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	158	TGCAGGACCAGAGAATTCGAATA	398	TGCAGGACCAGAGAATTCGAATA	638
CAGAAACCCCTNNNGATCGACATG		CAGGATCCCGNNNGATCGACATG		CATGGCTTGANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	159	TGCAGGACCAGAGAATTCGAATA	399	TGCAGGACCAGAGAATTCGAATA	639
CATCCGCATTNNNGATCGACATG		CACCTCTCTNNNGATCGACATG		CAATTACGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	160	TGCAGGACCAGAGAATTCGAATA	400	TGCAGGACCAGAGAATTCGAATA	640
CACAATCTGNNNGATCGACATG		CATCGTCGCCNNNGATCGACATG		CATGGCTCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	161	TGCAGGACCAGAGAATTCGAATA	401	TGCAGGACCAGAGAATTCGAATA	641
CAACCTTACNNNGATCGACATG		CACCTATGTCNNNGATCGACATG		CACACTCACTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	162	TGCAGGACCAGAGAATTCGAATA	402	TGCAGGACCAGAGAATTCGAATA	642
CAGCGGTCTGNNNGATCGACATG		CAGGATGCTNNNGATCGACATG		CAGTGGAGCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	163	TGCAGGACCAGAGAATTCGAATA	403	TGCAGGACCAGAGAATTCGAATA	643
CAAAATCAGCANNNGATCGACATG		CAATTGAGAANNNGATCGACATG		CACCCCAATCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	164	TGCAGGACCAGAGAATTCGAATA	404	TGCAGGACCAGAGAATTCGAATA	644
CAAATAGTAGNNNGATCGACATG		CAGTGTGTGNNNGATCGACATG		CAACGTAACCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	165	TGCAGGACCAGAGAATTCGAATA	405	TGCAGGACCAGAGAATTCGAATA	645
CAGGCATCTANNNGATCGACATG		CAAGCAATANNNGATCGACATG		CAACCGTCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	166	TGCAGGACCAGAGAATTCGAATA	406	TGCAGGACCAGAGAATTCGAATA	646
CAAGCGCCTGNNNGATCGACATG		CATTAGCGCANNNGATCGACATG		CATTGCGGAANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	167	TGCAGGACCAGAGAATTCGAATA	407	TGCAGGACCAGAGAATTCGAATA	647
CAGACCCGGTNNNGATCGACATG		CAACCGGATGNNNGATCGACATG		CACGCACAATNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	168	TGCAGGACCAGAGAATTCGAATA	408	TGCAGGACCAGAGAATTCGAATA	648
CACGGTAAAGNNNGATCGACATG		CAGCATGGAANNNGATCGACATG		CACAATCTCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	169	TGCAGGACCAGAGAATTCGAATA	409	TGCAGGACCAGAGAATTCGAATA	649
CAAGGATGCAANNNGATCGACATG		CATCTCATANNNGATCGACATG		CATCAGAGTCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	170	TGCAGGACCAGAGAATTCGAATA	410	TGCAGGACCAGAGAATTCGAATA	650
CATTCTGGAGNNNGATCGACATG		CAGTGGCCTNNNGATCGACATG		CAAATCTGTCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	171	TGCAGGACCAGAGAATTCGAATA	411	TGCAGGACCAGAGAATTCGAATA	651
CAGCTCAACNNNGATCGACATG		CAGATTCCGANNNGATCGACATG		CAGTAACTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	172	TGCAGGACCAGAGAATTCGAATA	412	TGCAGGACCAGAGAATTCGAATA	652
CATAAGTTACNNNGATCGACATG		CAATCTATCTNNNGATCGACATG		CAGATTAACTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	173	TGCAGGACCAGAGAATTCGAATA	413	TGCAGGACCAGAGAATTCGAATA	653
CACAAGCCCTNNNGATCGACATG		CAGTCAACCCNNNGATCGACATG		CAGGCTACGNNNGATCGACATG	

FIG. 12F

Pool-1	SEQ ID NO:	Pool-2	SEQ ID NO:	Pool-3	SEQ ID NO:
TGCAGGACCAGAGAATT CGAATA	174	TGCAGGACCAGAGAATT CGAATA	414	TGCAGGACCAGAGAATT CGAATA	654
CACCTTCCGGNNNGATCGACATG		CACGTTGTGANNNGATCGACATG		CAATACGAGGNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	175	TGCAGGACCAGAGAATT CGAATA	415	TGCAGGACCAGAGAATT CGAATA	655
CAGTGGAGTNNNGATCGACATG		CAGCTCTGCCNNNGATCGACATG		CAAAATGTCTNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	176	TGCAGGACCAGAGAATT CGAATA	416	TGCAGGACCAGAGAATT CGAATA	656
CAGCGTCCAGNNNGATCGACATG		CACATCGATGNNNGATCGACATG		CAGCGCATCGNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	177	TGCAGGACCAGAGAATT CGAATA	417	TGCAGGACCAGAGAATT CGAATA	657
CATTTATTTCGNNNGATCGACATG		CAAGTCGCCGNNNGATCGACATG		CACTCCCGTGMNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	178	TGCAGGACCAGAGAATT CGAATA	418	TGCAGGACCAGAGAATT CGAATA	658
CAGTAATAAGNNNGATCGACATG		CAGATAGCGANNNGATCGACATG		CAGATAAGGCNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	179	TGCAGGACCAGAGAATT CGAATA	419	TGCAGGACCAGAGAATT CGAATA	659
CATACAAGCCNNNGATCGACATG		CATCTTTGGCNNNGATCGACATG		CAGCACATCANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	180	TGCAGGACCAGAGAATT CGAATA	420	TGCAGGACCAGAGAATT CGAATA	660
CAAAGCCGAANNNGATCGACATG		CATCTCATCGNNNGATCGACATG		CATCCTATGCNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	181	TGCAGGACCAGAGAATT CGAATA	421	TGCAGGACCAGAGAATT CGAATA	661
CAATACTTTTNNNGATCGACATG		CATGAGCGCCNNNGATCGACATG		CACGCATCCNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	182	TGCAGGACCAGAGAATT CGAATA	422	TGCAGGACCAGAGAATT CGAATA	662
CACCTGGATCANNNGATCGACATG		CAAGTCTCGANNNGATCGACATG		CAACCGGTGNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	183	TGCAGGACCAGAGAATT CGAATA	423	TGCAGGACCAGAGAATT CGAATA	663
CAAACGCCATNNNGATCGACATG		CAAAGGTATANNNGATCGACATG		CACACGATGTNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	184	TGCAGGACCAGAGAATT CGAATA	424	TGCAGGACCAGAGAATT CGAATA	664
CAGTCGAGAANNNGATCGACATG		CAGGTGTGCGNNNGATCGACATG		CAAACCTCGCANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	185	TGCAGGACCAGAGAATT CGAATA	425	TGCAGGACCAGAGAATT CGAATA	665
CATAATTCTCANNNGATCGACATG		CATCACATCCNNNGATCGACATG		CACCCCTTCCNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	186	TGCAGGACCAGAGAATT CGAATA	426	TGCAGGACCAGAGAATT CGAATA	666
CATAACCCCTCANNNGATCGACATG		CAGCATACACNNNGATCGACATG		CATCTTCGTGNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	187	TGCAGGACCAGAGAATT CGAATA	427	TGCAGGACCAGAGAATT CGAATA	667
CAGCGCTTGGNNNGATCGACATG		CATCCAACAGNNNGATCGACATG		CATATTTAAANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	188	TGCAGGACCAGAGAATT CGAATA	428	TGCAGGACCAGAGAATT CGAATA	668
CACGGACACNNNGATCGACATG		CATCTGCCTANNNGATCGACATG		CATTAAATGCANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	189	TGCAGGACCAGAGAATT CGAATA	429	TGCAGGACCAGAGAATT CGAATA	669
CATGGAAGTGNNTGCATCAGGT		CACACACCGGNNNTGCATCAGGT		CACTTTGGTGNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	190	TGCAGGACCAGAGAATT CGAATA	430	TGCAGGACCAGAGAATT CGAATA	670
CAAAGTCTATNNNTGCATCAGGT		CAGACCTCCNNNTGCATCAGGT		CATACGAAGGNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	191	TGCAGGACCAGAGAATT CGAATA	431	TGCAGGACCAGAGAATT CGAATA	671
CAATGAATAGNNNTGCATCAGGT		CATGGCAATCNNNTGCATCAGGT		CAAGTCACTGNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	192	TGCAGGACCAGAGAATT CGAATA	432	TGCAGGACCAGAGAATT CGAATA	672
CATTCTCCTCANNNTGCATCAGGT		CATCTCCGGCANNNTGCATCAGGT		CAGTTTATCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	193	TGCAGGACCAGAGAATT CGAATA	433	TGCAGGACCAGAGAATT CGAATA	673
CACCAGCCCTNNNTGCATCAGGT		CACCAGCGTGNNTGCATCAGGT		CATTTGGAANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	194	TGCAGGACCAGAGAATT CGAATA	434	TGCAGGACCAGAGAATT CGAATA	674
CAAACAAAACNNNTGCATCAGGT		CAAATATAANNNTGCATCAGGT		CACAGATCACNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	195	TGCAGGACCAGAGAATT CGAATA	435	TGCAGGACCAGAGAATT CGAATA	675
CACGCTCACNNNTGCATCAGGT		CAGCAATTTANNNTGCATCAGGT		CATTGGAAGGNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	196	TGCAGGACCAGAGAATT CGAATA	436	TGCAGGACCAGAGAATT CGAATA	676
CATGGTGATCANNNTGCATCAGGT		CAACTCAGTGNNTGCATCAGGT		CAGTGGCGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	197	TGCAGGACCAGAGAATT CGAATA	437	TGCAGGACCAGAGAATT CGAATA	677
CAGTTGCTAGNNNTGCATCAGGT		CAAGAGGCATNNNTGCATCAGGT		CATGAAGGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	198	TGCAGGACCAGAGAATT CGAATA	438	TGCAGGACCAGAGAATT CGAATA	678
CATCACCCATANNNTGCATCAGGT		CATAGGCTTGNNTGCATCAGGT		CAAAAAGTACNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	199	TGCAGGACCAGAGAATT CGAATA	439	TGCAGGACCAGAGAATT CGAATA	679
CAGACTCTGANNNTGCATCAGGT		CACACACAGTNNNTGCATCAGGT		CAGATGGAACNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	200	TGCAGGACCAGAGAATT CGAATA	440	TGCAGGACCAGAGAATT CGAATA	680
CACGTATGACNNNTGCATCAGGT		CATGATAGAANNNTGCATCAGGT		CAGCCTCGAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	201	TGCAGGACCAGAGAATT CGAATA	441	TGCAGGACCAGAGAATT CGAATA	681
CATGCACCGGNNNTGCATCAGGT		CAGACAACGANNNTGCATCAGGT		CAAAATAAATNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	202	TGCAGGACCAGAGAATT CGAATA	442	TGCAGGACCAGAGAATT CGAATA	682
CAACTGATGCNNNTGCATCAGGT		CACTGCCTCGNNNTGCATCAGGT		CATTCCCCCANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	203	TGCAGGACCAGAGAATT CGAATA	443	TGCAGGACCAGAGAATT CGAATA	683
CATACGTTCCNNNTGCATCAGGT		CAGTTTCCANNNTGCATCAGGT		CATTCTTCTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	204	TGCAGGACCAGAGAATT CGAATA	444	TGCAGGACCAGAGAATT CGAATA	684
CACGGCCGCGNNNTGCATCAGGT		CATTCAATAGNNNTGCATCAGGT		CATTGTGGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	205	TGCAGGACCAGAGAATT CGAATA	445	TGCAGGACCAGAGAATT CGAATA	685
CAATCTTTGTNNNTGCATCAGGT		CATAGCCATGNNNTGCATCAGGT		CATCCCATGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	206	TGCAGGACCAGAGAATT CGAATA	446	TGCAGGACCAGAGAATT CGAATA	686
CATTGTACTTNNNTGCATCAGGT		CAGTTGTTAANNNTGCATCAGGT		CAGTGTGTACNNNTGCATCAGGT	

FIG. 12G

Pool-1	SEQ ID NO:	Pool-2	SEQ ID NO:	Pool-3	SEQ ID NO:
TGCAGGACCAGAGAATT CGAATA	207	TGCAGGACCAGAGAATT CGAATA	447	TGCAGGACCAGAGAATT CGAATA	687
CATGTTAATGNNNTGCATCAGGT		CACCTTGCCTNNNTGCATCAGGT		CATCGCTATNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	208	TGCAGGACCAGAGAATT CGAATA	448	TGCAGGACCAGAGAATT CGAATA	688
CAACATTGTNNNTGCATCAGGT		CATTAGAGCCNNNTGCATCAGGT		CACGCTGACGNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	209	TGCAGGACCAGAGAATT CGAATA	449	TGCAGGACCAGAGAATT CGAATA	689
CACGCCCGAANNNTGCATCAGGT		CAGCCCCACNNNTGCATCAGGT		CATGGTGGTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	210	TGCAGGACCAGAGAATT CGAATA	450	TGCAGGACCAGAGAATT CGAATA	690
CACAGCGCACNNNTGCATCAGGT		CAATGACGNNNTGCATCAGGT		CACTATCTTANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	211	TGCAGGACCAGAGAATT CGAATA	451	TGCAGGACCAGAGAATT CGAATA	691
CACGAGTATCNNNTGCATCAGGT		CAAGACCTGTNNNTGCATCAGGT		CAATAACCTANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	212	TGCAGGACCAGAGAATT CGAATA	452	TGCAGGACCAGAGAATT CGAATA	692
CAATGGTGGANNNTGCATCAGGT		CACCTACATNNNTGCATCAGGT		CAAGAGTGTGNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	213	TGCAGGACCAGAGAATT CGAATA	453	TGCAGGACCAGAGAATT CGAATA	693
CATCACACTCNNNTGCATCAGGT		CATAAGAAACNNNTGCATCAGGT		CAATGGCGANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	214	TGCAGGACCAGAGAATT CGAATA	454	TGCAGGACCAGAGAATT CGAATA	694
CAGAAACGACNNNTGCATCAGGT		CAGATTCCTTNNNTGCATCAGGT		CAGTCTCTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	215	TGCAGGACCAGAGAATT CGAATA	455	TGCAGGACCAGAGAATT CGAATA	695
CAGAGTTTTANNNTGCATCAGGT		CATCTAGGTGNNNTGCATCAGGT		CATGCCCCCANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	216	TGCAGGACCAGAGAATT CGAATA	456	TGCAGGACCAGAGAATT CGAATA	696
CAGGCCCTTTNNNTGCATCAGGT		CAGTGTCTTNNNTGCATCAGGT		CACGAGCTCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	217	TGCAGGACCAGAGAATT CGAATA	457	TGCAGGACCAGAGAATT CGAATA	697
CACAACCTCTCNNNTGCATCAGGT		CATAAACTTGNNTGCATCAGGT		CAACTGAACNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	218	TGCAGGACCAGAGAATT CGAATA	458	TGCAGGACCAGAGAATT CGAATA	698
CATGTACTGGNNNTGCATCAGGT		CAGACATCCANNNTGCATCAGGT		CACTCGTATCNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	219	TGCAGGACCAGAGAATT CGAATA	459	TGCAGGACCAGAGAATT CGAATA	699
CATTTGGCTCNNNTGCATCAGGT		CATAAGTCCGNNNTGCATCAGGT		CACACTTCCANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	220	TGCAGGACCAGAGAATT CGAATA	460	TGCAGGACCAGAGAATT CGAATA	700
CAGAAGTATANNNTGCATCAGGT		CAAGGCGCGANNNTGCATCAGGT		CAGATCCTGANNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	221	TGCAGGACCAGAGAATT CGAATA	461	TGCAGGACCAGAGAATT CGAATA	701
CAGAATCACNNNTGCATCAGGT		CAGAGCTCTANNNTGCATCAGGT		CAAGAAGTATNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	222	TGCAGGACCAGAGAATT CGAATA	462	TGCAGGACCAGAGAATT CGAATA	702
CACCTTACCGTNNNTGCATCAGGT		CATCATAATGNNNTGCATCAGGT		CAAAACCCACANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	223	TGCAGGACCAGAGAATT CGAATA	463	TGCAGGACCAGAGAATT CGAATA	703
CATCTTTACANNNTGCATCAGGT		CAGGATGGTANNNTGCATCAGGT		CATGCCGAATNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	224	TGCAGGACCAGAGAATT CGAATA	464	TGCAGGACCAGAGAATT CGAATA	704
CACGAAGTGANNNTGCATCAGGT		CATAGCCCTCNNNTGCATCAGGT		CAATCAGAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	225	TGCAGGACCAGAGAATT CGAATA	465	TGCAGGACCAGAGAATT CGAATA	705
CACCTTGTGGANNNTGCATCAGGT		CAATCCCCGNNNTGCATCAGGT		CAGTCATATANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	226	TGCAGGACCAGAGAATT CGAATA	466	TGCAGGACCAGAGAATT CGAATA	706
CAGTTCTCTGNNNTGCATCAGGT		CAGATTGCTGNNNTGCATCAGGT		CAACCCACCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	227	TGCAGGACCAGAGAATT CGAATA	467	TGCAGGACCAGAGAATT CGAATA	707
CACCTTCAACNNNTGCATCAGGT		CAGTGATGAGNNNTGCATCAGGT		CACCCACAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	228	TGCAGGACCAGAGAATT CGAATA	468	TGCAGGACCAGAGAATT CGAATA	708
CAAAATGCTTNNNTGCATCAGGT		CACGGAACGNNNTGCATCAGGT		CATGCTGAACNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	229	TGCAGGACCAGAGAATT CGAATA	469	TGCAGGACCAGAGAATT CGAATA	709
CAATCGCGATNNNTGCATCAGGT		CAGCTCTTTGNNNTGCATCAGGT		CAGCAGCATNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	230	TGCAGGACCAGAGAATT CGAATA	470	TGCAGGACCAGAGAATT CGAATA	710
CAGGCTCGTGNNTGCATCAGGT		CAGTAATCGCNNNTGCATCAGGT		CAGGCGATGNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	231	TGCAGGACCAGAGAATT CGAATA	471	TGCAGGACCAGAGAATT CGAATA	711
CAGACCTAANNNTGCATCAGGT		CACCTGTTATNNNTGCATCAGGT		CATTTCGATGNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	232	TGCAGGACCAGAGAATT CGAATA	472	TGCAGGACCAGAGAATT CGAATA	712
CACAAATTTGNNNTGCATCAGGT		CACACACACANNNTGCATCAGGT		CATGGAGGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	233	TGCAGGACCAGAGAATT CGAATA	473	TGCAGGACCAGAGAATT CGAATA	713
CATTTTTCCNNNTGCATCAGGT		CATAAAATAANNNTGCATCAGGT		CAGTATTACANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	234	TGCAGGACCAGAGAATT CGAATA	474	TGCAGGACCAGAGAATT CGAATA	714
CATTTAAGCANNNTGCATCAGGT		CAAACGCATCNNNTGCATCAGGT		CACGACAATCANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	235	TGCAGGACCAGAGAATT CGAATA	475	TGCAGGACCAGAGAATT CGAATA	715
CAGTGGTCTANNNTGCATCAGGT		CACATATGACNNNTGCATCAGGT		CAGTGGCCACNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	236	TGCAGGACCAGAGAATT CGAATA	476	TGCAGGACCAGAGAATT CGAATA	716
CATTCTAATCANNNTGCATCAGGT		CAGCGTCATANNNTGCATCAGGT		CATACGCGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	237	TGCAGGACCAGAGAATT CGAATA	477	TGCAGGACCAGAGAATT CGAATA	717
CAATTGATTGNNNTGCATCAGGT		CATAAGCCTGNNNTGCATCAGGT		CACGAAGACANNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	238	TGCAGGACCAGAGAATT CGAATA	478	TGCAGGACCAGAGAATT CGAATA	718
CATGCATAGCANNNTGCATCAGGT		CATAGCAGAGNNNTGCATCAGGT		CACCAATGACNNNTGCATCAGGT	
TGCAGGACCAGAGAATT CGAATA	239	TGCAGGACCAGAGAATT CGAATA	479	TGCAGGACCAGAGAATT CGAATA	719
CAGACAGATGNNNTGCATCAGGT		CACCTTGAACNNNTGCATCAGGT		CAAGCCTTCTNNNTGCATCAGGT	

FIG. 12H

Pool-1	SEQ ID NO:	Pool-2	SEQ ID NO:	Pool-3	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATGCTCTACNNNTGCATCAGGT	240	TGCAGGACCAGAGAATTCGAATA CAACCGAGAANNNTGCATCAGGT	480	TGCAGGACCAGAGAATTCGAATA CATATCACCNNNTGCATCAGGT	720
TGCAGGACCAGAGAATTCGAATA CATGCGATACNNNTGCATCAGGT	241	TGCAGGACCAGAGAATTCGAATA CACTATCTATNNNTGCATCAGGT	481	TGCAGGACCAGAGAATTCGAATA CACCTTATGCNNNTGCATCAGGT	721
TGCAGGACCAGAGAATTCGAATA CAACACTGCANNNTGCATCAGGT	242	TGCAGGACCAGAGAATTCGAATA CACAATTTAGNNNTGCATCAGGT	482	TGCAGGACCAGAGAATTCGAATA CATTAAATGACNNNTGCATCAGGT	722
TGCAGGACCAGAGAATTCGAATA CAGTCACCTCTNNNTGCATCAGGT	243	TGCAGGACCAGAGAATTCGAATA CACTAAACGCNNNTGCATCAGGT	483	TGCAGGACCAGAGAATTCGAATA CACTACCTTGNNNTGCATCAGGT	723
TGCAGGACCAGAGAATTCGAATA CATTGTATTCNNNTGCATCAGGT	244	TGCAGGACCAGAGAATTCGAATA CATAGTAGAANNNTGCATCAGGT	484	TGCAGGACCAGAGAATTCGAATA CAAGGATCTCNNNTGCATCAGGT	724
TGCAGGACCAGAGAATTCGAATA CAAACCTAGCNNNTGCATCAGGT	245	TGCAGGACCAGAGAATTCGAATA CAGCAAAGTGNNNTGCATCAGGT	485	TGCAGGACCAGAGAATTCGAATA CAAAGATCAANNNTGCATCAGGT	725
TGCAGGACCAGAGAATTCGAATA CAGCCGGATCNNNTGCATCAGGT	246	TGCAGGACCAGAGAATTCGAATA CACAAAGTTATNNNTGCATCAGGT	486	TGCAGGACCAGAGAATTCGAATA CAGAATGAGCNNNTGCATCAGGT	726
TGCAGGACCAGAGAATTCGAATA CAAGGATCCTNNNTGCATCAGGT	247	TGCAGGACCAGAGAATTCGAATA CACAAGTACNNNTGCATCAGGT	487	TGCAGGACCAGAGAATTCGAATA CAACTAGATTNNNTGCATCAGGT	727
TGCAGGACCAGAGAATTCGAATA CATACTGGACNNNTGCATCAGGT	248	TGCAGGACCAGAGAATTCGAATA CATTCGTCGTNNNTGCATCAGGT	488	TGCAGGACCAGAGAATTCGAATA CATTTTCCGGNNNTGCATCAGGT	728

FIG. 13A

Pool-4	SEQ ID NO:	Pool-5	SEQ ID NO:	Pool-6	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATA	729	TGCAGGACCAGAGAATTCTGAATA	969	TGCAGGACCAGAGAATTCTGAATA	1209
CATATGCGCANNNNACGTATGCCA		CAGCGATTACNNNNACGTATGCCA		CACAATGACCCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	730	TGCAGGACCAGAGAATTCTGAATA	970	TGCAGGACCAGAGAATTCTGAATA	1210
CAGTTTACCTNNNNACGTATGCCA		CATAGTCCTCNNNNACGTATGCCA		CAGCTACGTANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	731	TGCAGGACCAGAGAATTCTGAATA	971	TGCAGGACCAGAGAATTCTGAATA	1211
CATCCTACACNNNNACGTATGCCA		CAGTTATAACNNNNACGTATGCCA		CAGCCAGCACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	732	TGCAGGACCAGAGAATTCTGAATA	972	TGCAGGACCAGAGAATTCTGAATA	1212
CACCTACTCTGNNNNACGTATGCCA		CATATCTTCANNNNACGTATGCCA		CACGATCCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	733	TGCAGGACCAGAGAATTCTGAATA	973	TGCAGGACCAGAGAATTCTGAATA	1213
CACCTTCCCCNNNNACGTATGCCA		CAACGTTCCGANNNNACGTATGCCA		CATTGGACACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	734	TGCAGGACCAGAGAATTCTGAATA	974	TGCAGGACCAGAGAATTCTGAATA	1214
CAGAAGATCGNNNNACGTATGCCA		CAACTCGTGANNNNACGTATGCCA		CAACAATGCCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	735	TGCAGGACCAGAGAATTCTGAATA	975	TGCAGGACCAGAGAATTCTGAATA	1215
CAGTCCGCTGNNNNACGTATGCCA		CAGGACTACTNNNNACGTATGCCA		CACCTTTATANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	736	TGCAGGACCAGAGAATTCTGAATA	976	TGCAGGACCAGAGAATTCTGAATA	1216
CATATGTCCCNNNACGTATGCCA		CATCTGTACNNNNACGTATGCCA		CAGTGGCTGCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	737	TGCAGGACCAGAGAATTCTGAATA	977	TGCAGGACCAGAGAATTCTGAATA	1217
CATATTTGCTNNNNACGTATGCCA		CACCTTAAGTNNNNACGTATGCCA		CAATCTCCGTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	738	TGCAGGACCAGAGAATTCTGAATA	978	TGCAGGACCAGAGAATTCTGAATA	1218
CAGTCCAGGCGNNNNACGTATGCCA		CATTGGAGAGNNNNACGTATGCCA		CAATGGCCATNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	739	TGCAGGACCAGAGAATTCTGAATA	979	TGCAGGACCAGAGAATTCTGAATA	1219
CAAAGATGGCANNNNACGTATGCCA		CAGAATCAAANNNNACGTATGCCA		CATTTGATAGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	740	TGCAGGACCAGAGAATTCTGAATA	980	TGCAGGACCAGAGAATTCTGAATA	1220
CAGTCCCGAGNNNNACGTATGCCA		CAGTTTCGTCCNNNNACGTATGCCA		CAGTCCCGGANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	741	TGCAGGACCAGAGAATTCTGAATA	981	TGCAGGACCAGAGAATTCTGAATA	1221
CAAGGTTTCGNNNNACGTATGCCA		CACTACACAGNNNNACGTATGCCA		CAGGCTTCAANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	742	TGCAGGACCAGAGAATTCTGAATA	982	TGCAGGACCAGAGAATTCTGAATA	1222
CATGCCAAGGNNNNACGTATGCCA		CAAGTCAGTCNNNNACGTATGCCA		CACCTTTTTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	743	TGCAGGACCAGAGAATTCTGAATA	983	TGCAGGACCAGAGAATTCTGAATA	1223
CAAGGTGTAGNNNNACGTATGCCA		CACAACGAGANNNNACGTATGCCA		CAACGCCCGANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	744	TGCAGGACCAGAGAATTCTGAATA	984	TGCAGGACCAGAGAATTCTGAATA	1224
CACACGAGTTNNNNACGTATGCCA		CATAGGCTCANNNNACGTATGCCA		CACCCCTAGCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	745	TGCAGGACCAGAGAATTCTGAATA	985	TGCAGGACCAGAGAATTCTGAATA	1225
CACACGCGCTNNNNACGTATGCCA		CAGGCCCATGNNNNACGTATGCCA		CACGGAGGCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	746	TGCAGGACCAGAGAATTCTGAATA	986	TGCAGGACCAGAGAATTCTGAATA	1226
CAAAGCTACNNNNACGTATGCCA		CAGGCAGTCCNNNNACGTATGCCA		CACCTATGAATNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	747	TGCAGGACCAGAGAATTCTGAATA	987	TGCAGGACCAGAGAATTCTGAATA	1227
CAGAACCAGANNNNACGTATGCCA		CATCGATTGGNNNNACGTATGCCA		CAGACCGCGTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	748	TGCAGGACCAGAGAATTCTGAATA	988	TGCAGGACCAGAGAATTCTGAATA	1228
CAAGTACTGCGNNNNACGTATGCCA		CATAGACAGGNNNNACGTATGCCA		CATACTAGTANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	749	TGCAGGACCAGAGAATTCTGAATA	989	TGCAGGACCAGAGAATTCTGAATA	1229
CAAACAATTCCNNNNACGTATGCCA		CAACTAAGTTNNNNACGTATGCCA		CAACCAGTGTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	750	TGCAGGACCAGAGAATTCTGAATA	990	TGCAGGACCAGAGAATTCTGAATA	1230
CAGTATTAACNNNNACGTATGCCA		CAATGTTCCGNNNNACGTATGCCA		CAGATGCCTANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	751	TGCAGGACCAGAGAATTCTGAATA	991	TGCAGGACCAGAGAATTCTGAATA	1231
CATGATTATGNNNNACGTATGCCA		CAAGCCCCAATNNNNACGTATGCCA		CACCATATTTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	752	TGCAGGACCAGAGAATTCTGAATA	992	TGCAGGACCAGAGAATTCTGAATA	1232
CAGCAAACCTNNNNACGTATGCCA		CAGTGAAGTCCNNNNACGTATGCCA		CAAAACCACCCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	753	TGCAGGACCAGAGAATTCTGAATA	993	TGCAGGACCAGAGAATTCTGAATA	1233
CAGAATCTTANNNNACGTATGCCA		CAGTGCTAACNNNNACGTATGCCA		CAGCACGAAANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	754	TGCAGGACCAGAGAATTCTGAATA	994	TGCAGGACCAGAGAATTCTGAATA	1234
CAGAGGACCGCANNNNACGTATGCCA		CAGCCACCGANNNNACGTATGCCA		CAACGACACANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	755	TGCAGGACCAGAGAATTCTGAATA	995	TGCAGGACCAGAGAATTCTGAATA	1235
CAAGCCAAAGNNNNACGTATGCCA		CAAGTCCGATNNNNACGTATGCCA		CAATACCATANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	756	TGCAGGACCAGAGAATTCTGAATA	996	TGCAGGACCAGAGAATTCTGAATA	1236
CAGGACCGCTCANNNNACGTATGCCA		CAGTTAAATCCNNNNACGTATGCCA		CACCAAGTCTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	757	TGCAGGACCAGAGAATTCTGAATA	997	TGCAGGACCAGAGAATTCTGAATA	1237
CAGCTGCCCTNNNNACGTATGCCA		CAACTGACTGNNNNACGTATGCCA		CATTGCTGGANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	758	TGCAGGACCAGAGAATTCTGAATA	998	TGCAGGACCAGAGAATTCTGAATA	1238
CACCCCTTTCCNNNNACGTATGCCA		CACTTCATGCGNNNNACGTATGCCA		CAGCCCATTTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	759	TGCAGGACCAGAGAATTCTGAATA	999	TGCAGGACCAGAGAATTCTGAATA	1239
CATCGCAGATNNNNACGTATGCCA		CAACCAGCATNNNNACGTATGCCA		CAAACAGCTCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	760	TGCAGGACCAGAGAATTCTGAATA	1000	TGCAGGACCAGAGAATTCTGAATA	1240
CAATCGCATGNNNNACGTATGCCA		CAGGCGTCCANNNNACGTATGCCA		CACGTGTTCTGNNNNACGTATGCCA	

FIG. 13B

Pool-4	SEQ ID NO:	Pool-5	SEQ ID NO:	Pool-6	SEQ ID NO:
TGCAGGACCAGAGAATT CGAATA	761	TGCAGGACCAGAGAATT CGAATA	1001	TGCAGGACCAGAGAATT CGAATA	1241
CAAGATGGCANNNACGTATGCCA		CAAACAACCCNNNACGTATGCCA		CATGGAATAANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	762	TGCAGGACCAGAGAATT CGAATA	1002	TGCAGGACCAGAGAATT CGAATA	1242
CATCATCGCTNNNACGTATGCCA		CAGGTCTTAGNNNACGTATGCCA		CATTCCCTTCNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	763	TGCAGGACCAGAGAATT CGAATA	1003	TGCAGGACCAGAGAATT CGAATA	1243
CACGTGTTCTNNNACGTATGCCA		CAGCCCGGATNNNACGTATGCCA		CACACGCAATNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	764	TGCAGGACCAGAGAATT CGAATA	1004	TGCAGGACCAGAGAATT CGAATA	1244
CAGGTTATTANNNACGTATGCCA		CAATCCCGAANNNACGTATGCCA		CAGCTTATCCNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	765	TGCAGGACCAGAGAATT CGAATA	1005	TGCAGGACCAGAGAATT CGAATA	1245
CAAGAGTTAANNNACGTATGCCA		CATTACTCANNNACGTATGCCA		CAGGCATAGANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	766	TGCAGGACCAGAGAATT CGAATA	1006	TGCAGGACCAGAGAATT CGAATA	1246
CATGAAATTCNNNACGTATGCCA		CATCCACCGCNNNACGTATGCCA		CAAGCGCCGTCNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	767	TGCAGGACCAGAGAATT CGAATA	1007	TGCAGGACCAGAGAATT CGAATA	1247
CACTTACCTGNNNACGTATGCCA		CACCAGATTGNNNACGTATGCCA		CACAAATTCANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	768	TGCAGGACCAGAGAATT CGAATA	1008	TGCAGGACCAGAGAATT CGAATA	1248
CAAACTCGTGNNNACGTATGCCA		CACATGGTCANNNACGTATGCCA		CATAATGCATNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	769	TGCAGGACCAGAGAATT CGAATA	1009	TGCAGGACCAGAGAATT CGAATA	1249
CAGGACACGGNNNACGTATGCCA		CACCATTTCGNNNACGTATGCCA		CAACTCGTCTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	770	TGCAGGACCAGAGAATT CGAATA	1010	TGCAGGACCAGAGAATT CGAATA	1250
CATCTCGCGCNNNACGTATGCCA		CATGTGCGGNNNACGTATGCCA		CAAAATTGTGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	771	TGCAGGACCAGAGAATT CGAATA	1011	TGCAGGACCAGAGAATT CGAATA	1251
CACTTCCAGTNNNACGTATGCCA		CAAACAATAGNNNACGTATGCCA		CATGAGAGGTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	772	TGCAGGACCAGAGAATT CGAATA	1012	TGCAGGACCAGAGAATT CGAATA	1252
CAATAGTTACNNNACGTATGCCA		CATTGCGAGANNNACGTATGCCA		CAGCCATACANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	773	TGCAGGACCAGAGAATT CGAATA	1013	TGCAGGACCAGAGAATT CGAATA	1253
CACGACTTGANNNACGTATGCCA		CACCTTGAGANNNACGTATGCCA		CAGTCCTTCANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	774	TGCAGGACCAGAGAATT CGAATA	1014	TGCAGGACCAGAGAATT CGAATA	1254
CATGCTTTATNNNACGTATGCCA		CAACGCTCTTNNNACGTATGCCA		CAGTGGGAGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	775	TGCAGGACCAGAGAATT CGAATA	1015	TGCAGGACCAGAGAATT CGAATA	1255
CAGCCACTTTNNNACGTATGCCA		CACACGAAGANNNACGTATGCCA		CATTTAGACANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	776	TGCAGGACCAGAGAATT CGAATA	1016	TGCAGGACCAGAGAATT CGAATA	1256
CATATCGGACNNNACGTATGCCA		CAGGCCACACNNNACGTATGCCA		CACACCGGCTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	777	TGCAGGACCAGAGAATT CGAATA	1017	TGCAGGACCAGAGAATT CGAATA	1257
CAATTCCATTNNNACGTATGCCA		CATCTGTGAGNNNACGTATGCCA		CAATTCTAGANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	778	TGCAGGACCAGAGAATT CGAATA	1018	TGCAGGACCAGAGAATT CGAATA	1258
CAAAATGCTGCNNNACGTATGCCA		CAAAAGCCAGNNNACGTATGCCA		CACGGACGAGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	779	TGCAGGACCAGAGAATT CGAATA	1019	TGCAGGACCAGAGAATT CGAATA	1259
CAACCGGATNNNACGTATGCCA		CACCAGTTGANNNACGTATGCCA		CACGACCGCANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	780	TGCAGGACCAGAGAATT CGAATA	1020	TGCAGGACCAGAGAATT CGAATA	1260
CATAGCTAGCANNNACGTATGCCA		CACCTTGTAGNNNACGTATGCCA		CACATATAGTNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	781	TGCAGGACCAGAGAATT CGAATA	1021	TGCAGGACCAGAGAATT CGAATA	1261
CAGCAACGTTNNNACGTATGCCA		CAATATGCATNNNACGTATGCCA		CATGTGATATNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	782	TGCAGGACCAGAGAATT CGAATA	1022	TGCAGGACCAGAGAATT CGAATA	1262
CACGTCCATNNNACGTATGCCA		CACCAGGCGTNNNACGTATGCCA		CAATCCTAAANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	783	TGCAGGACCAGAGAATT CGAATA	1023	TGCAGGACCAGAGAATT CGAATA	1263
CAGCCACACGNNNACGTATGCCA		CAATGTTTTAGNNNACGTATGCCA		CATGATGAGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	784	TGCAGGACCAGAGAATT CGAATA	1024	TGCAGGACCAGAGAATT CGAATA	1264
CAGGCTTCCCNNNACGTATGCCA		CACCTGTCGCGCNNNACGTATGCCA		CAGCTCGACGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	785	TGCAGGACCAGAGAATT CGAATA	1025	TGCAGGACCAGAGAATT CGAATA	1265
CAGTTGACACNNNACGTATGCCA		CATTTTACCANNNACGTATGCCA		CATTAGCTAANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	786	TGCAGGACCAGAGAATT CGAATA	1026	TGCAGGACCAGAGAATT CGAATA	1266
CAGCATCTTCNNNACGTATGCCA		CATGCCCCGCGNNNACGTATGCCA		CATGCTTTTANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	787	TGCAGGACCAGAGAATT CGAATA	1027	TGCAGGACCAGAGAATT CGAATA	1267
CAACAATTGTNNNACGTATGCCA		CACCTTTGACNNNACGTATGCCA		CAATCACAGCANNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	788	TGCAGGACCAGAGAATT CGAATA	1028	TGCAGGACCAGAGAATT CGAATA	1268
CAGATCCCCNNNACGTATGCCA		CAATTATTTTNNNACGTATGCCA		CAAAATCTCGGNNNACGTATGCCA	
TGCAGGACCAGAGAATT CGAATA	789	TGCAGGACCAGAGAATT CGAATA	1029	TGCAGGACCAGAGAATT CGAATA	1269
CAGCCCAGTGNNNCTAGCGTTAC		CAGTGTGGAANNNCTAGCGTTAC		CAACACTGGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	790	TGCAGGACCAGAGAATT CGAATA	1030	TGCAGGACCAGAGAATT CGAATA	1270
CAGCGGTGCTNNNCTAGCGTTAC		CAACTCGTAGNNNCTAGCGTTAC		CATTTGTTTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	791	TGCAGGACCAGAGAATT CGAATA	1031	TGCAGGACCAGAGAATT CGAATA	1271
CATACGTGCANNNCTAGCGTTAC		CATCGCGTCCNNNCTAGCGTTAC		CACGACACGCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATT CGAATA	792	TGCAGGACCAGAGAATT CGAATA	1032	TGCAGGACCAGAGAATT CGAATA	1272
CACACCCACNNNCTAGCGTTAC		CAGCCTAATGNNNCTAGCGTTAC		CACGCGAGAGNNNCTAGCGTTAC	

FIG. 13C

Pool-4	SEQ ID NO:	Pool-5	SEQ ID NO:	Pool-6	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATA	793	TGCAGGACCAGAGAATTCTGAATA	1033	TGCAGGACCAGAGAATTCTGAATA	1273
CACACAGAAGNNNCTAGCGTTAC		CAGCGTGTANNNNCTAGCGTTAC		CATAAGTAGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	794	TGCAGGACCAGAGAATTCTGAATA	1034	TGCAGGACCAGAGAATTCTGAATA	1274
CACGCTAACANNNNCTAGCGTTAC		CACGAGAAACNNNNCTAGCGTTAC		CAAAGACGTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	795	TGCAGGACCAGAGAATTCTGAATA	1035	TGCAGGACCAGAGAATTCTGAATA	1275
CAGACCTATGNNNNCTAGCGTTAC		CAATGCTCAGNNNNCTAGCGTTAC		CACGGAACAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	796	TGCAGGACCAGAGAATTCTGAATA	1036	TGCAGGACCAGAGAATTCTGAATA	1276
CAAAAAGGAANNNNCTAGCGTTAC		CAGTCAGCTANNNNCTAGCGTTAC		CAGTGTGGAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	797	TGCAGGACCAGAGAATTCTGAATA	1037	TGCAGGACCAGAGAATTCTGAATA	1277
CAACAGAGGTTNNNNCTAGCGTTAC		CAGGTAGCGGNNNNCTAGCGTTAC		CAAGCCTACANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	798	TGCAGGACCAGAGAATTCTGAATA	1038	TGCAGGACCAGAGAATTCTGAATA	1278
CAGCTAGCTGANNNNCTAGCGTTAC		CACCTGGTCCNNNNCTAGCGTTAC		CACCAATTGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	799	TGCAGGACCAGAGAATTCTGAATA	1039	TGCAGGACCAGAGAATTCTGAATA	1279
CATCCCAGCANNNNCTAGCGTTAC		CACAGCACCGNNNNCTAGCGTTAC		CAGAGTCTACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	800	TGCAGGACCAGAGAATTCTGAATA	1040	TGCAGGACCAGAGAATTCTGAATA	1280
CAGTACCTGANNNNCTAGCGTTAC		CACATTGTGNNNNCTAGCGTTAC		CAAATGTTACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	801	TGCAGGACCAGAGAATTCTGAATA	1041	TGCAGGACCAGAGAATTCTGAATA	1281
CAAGAGAGGANNNNCTAGCGTTAC		CAAGGAACCTGNNNNCTAGCGTTAC		CAAGTGGCAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	802	TGCAGGACCAGAGAATTCTGAATA	1042	TGCAGGACCAGAGAATTCTGAATA	1282
CAGTAACCTCGNNNNCTAGCGTTAC		CAGTTATTAGNNNNCTAGCGTTAC		CAGGTTAACCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	803	TGCAGGACCAGAGAATTCTGAATA	1043	TGCAGGACCAGAGAATTCTGAATA	1283
CAGGTACATCANNNNCTAGCGTTAC		CAAATCTTCTNNNNCTAGCGTTAC		CATTGTGGTGNNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	804	TGCAGGACCAGAGAATTCTGAATA	1044	TGCAGGACCAGAGAATTCTGAATA	1284
CAGTTAACCGNNNNCTAGCGTTAC		CAGACAATCCNNNNCTAGCGTTAC		CAAAATGGCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	805	TGCAGGACCAGAGAATTCTGAATA	1045	TGCAGGACCAGAGAATTCTGAATA	1285
CAAACGAGTGNNNNNCTAGCGTTAC		CAATCTAGATNNNNCTAGCGTTAC		CAGTGTAGGTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	806	TGCAGGACCAGAGAATTCTGAATA	1046	TGCAGGACCAGAGAATTCTGAATA	1286
CATCTCACTGNNNNCTAGCGTTAC		CAGCGACGTCNNNNCTAGCGTTAC		CACCTAAGCGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	807	TGCAGGACCAGAGAATTCTGAATA	1047	TGCAGGACCAGAGAATTCTGAATA	1287
CATACGAGCTNNNNCTAGCGTTAC		CACACCCCGTNNNNCTAGCGTTAC		CAGTTTATGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	808	TGCAGGACCAGAGAATTCTGAATA	1048	TGCAGGACCAGAGAATTCTGAATA	1288
CACAGATACCGNNNNCTAGCGTTAC		CACGCGCTCGTNNNNCTAGCGTTAC		CAACGACTGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	809	TGCAGGACCAGAGAATTCTGAATA	1049	TGCAGGACCAGAGAATTCTGAATA	1289
CATACATTTGNNNNCTAGCGTTAC		CAGTGTACACANNNNCTAGCGTTAC		CACCTAGTAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	810	TGCAGGACCAGAGAATTCTGAATA	1050	TGCAGGACCAGAGAATTCTGAATA	1290
CAGTGTAGGNNNNCTAGCGTTAC		CATGCTTTGCGNNNNCTAGCGTTAC		CAGGTTCTGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	811	TGCAGGACCAGAGAATTCTGAATA	1051	TGCAGGACCAGAGAATTCTGAATA	1291
CAGGTTGAAGNNNNCTAGCGTTAC		CAACTGTCTCANNNNCTAGCGTTAC		CATACATCCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	812	TGCAGGACCAGAGAATTCTGAATA	1052	TGCAGGACCAGAGAATTCTGAATA	1292
CACGTCCTCGNNNNCTAGCGTTAC		CATATTGTCTNNNNCTAGCGTTAC		CACCTCGGAATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	813	TGCAGGACCAGAGAATTCTGAATA	1053	TGCAGGACCAGAGAATTCTGAATA	1293
CAAATCCCTCANNNNCTAGCGTTAC		CAATTTGACANNNNCTAGCGTTAC		CATCAGTTGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	814	TGCAGGACCAGAGAATTCTGAATA	1054	TGCAGGACCAGAGAATTCTGAATA	1294
CATGCCCCACNNNNCTAGCGTTAC		CACGCACACGNNNNCTAGCGTTAC		CAAGTGCCCTANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	815	TGCAGGACCAGAGAATTCTGAATA	1055	TGCAGGACCAGAGAATTCTGAATA	1295
CAGTATTATGNNNNCTAGCGTTAC		CACCGCGAACNNNNCTAGCGTTAC		CAGTATGTATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	816	TGCAGGACCAGAGAATTCTGAATA	1056	TGCAGGACCAGAGAATTCTGAATA	1296
CATTGATTGANNNNCTAGCGTTAC		CATTAGGCGTNNNNCTAGCGTTAC		CAGCAGCAGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	817	TGCAGGACCAGAGAATTCTGAATA	1057	TGCAGGACCAGAGAATTCTGAATA	1297
CATGCGACGCGNNNNCTAGCGTTAC		CATCGGAGCCNNNNCTAGCGTTAC		CAGCAGGTCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	818	TGCAGGACCAGAGAATTCTGAATA	1058	TGCAGGACCAGAGAATTCTGAATA	1298
CAGTGGTTCAANNNNCTAGCGTTAC		CAGTCTACAGNNNNCTAGCGTTAC		CATGTAGGCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	819	TGCAGGACCAGAGAATTCTGAATA	1059	TGCAGGACCAGAGAATTCTGAATA	1299
CAGCCGGCTANNNNCTAGCGTTAC		CACCGCGCTCANNNNCTAGCGTTAC		CATAACGACCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	820	TGCAGGACCAGAGAATTCTGAATA	1060	TGCAGGACCAGAGAATTCTGAATA	1300
CACCTTGCGCANNNNCTAGCGTTAC		CATTAAACTGNNNNCTAGCGTTAC		CACGATCGCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	821	TGCAGGACCAGAGAATTCTGAATA	1061	TGCAGGACCAGAGAATTCTGAATA	1301
CAGGTAAGTGNNNNNCTAGCGTTAC		CAATAAGAACNNNNCTAGCGTTAC		CAGGCCAAGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	822	TGCAGGACCAGAGAATTCTGAATA	1062	TGCAGGACCAGAGAATTCTGAATA	1302
CAGTGTCCAAANNNNCTAGCGTTAC		CAATCATGCGNNNNCTAGCGTTAC		CAGACATAAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	823	TGCAGGACCAGAGAATTCTGAATA	1063	TGCAGGACCAGAGAATTCTGAATA	1303
CATGCACTGANNNNCTAGCGTTAC		CACCAACTAGNNNNCTAGCGTTAC		CACGCACATANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	824	TGCAGGACCAGAGAATTCTGAATA	1064	TGCAGGACCAGAGAATTCTGAATA	1304
CAGAACTTTNNNNCTAGCGTTAC		CAGTCTAGTANNNNCTAGCGTTAC		CAGCCTAGGCGNNNNCTAGCGTTAC	

FIG. 13D

Pool-4	SEQ ID NO:	Pool-5	SEQ ID NO:	Pool-6	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA	825	TGCAGGACCAGAGAATTGGAATA	1065	TGCAGGACCAGAGAATTGGAATA	1305
CATGTGTAGCANNCTAGCGTTAC		CACCTTGCCANNCTAGCGTTAC		CATCCGCAANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	826	TGCAGGACCAGAGAATTGGAATA	1066	TGCAGGACCAGAGAATTGGAATA	1306
CATCTACCTGNNCTAGCGTTAC		CAAACTCTGANNCTAGCGTTAC		CACCTTAGANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	827	TGCAGGACCAGAGAATTGGAATA	1067	TGCAGGACCAGAGAATTGGAATA	1307
CATCTCTTAANNCTAGCGTTAC		CAGATCGCATNNCTAGCGTTAC		CACGGCGGAANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	828	TGCAGGACCAGAGAATTGGAATA	1068	TGCAGGACCAGAGAATTGGAATA	1308
CAATCGAATTNNCTAGCGTTAC		CATGTGTTGNNCTAGCGTTAC		CAGTAGCACTNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	829	TGCAGGACCAGAGAATTGGAATA	1069	TGCAGGACCAGAGAATTGGAATA	1309
CATTTTTGGTNNCTAGCGTTAC		CAGTAACATTNNCTAGCGTTAC		CAGCTGTCAANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	830	TGCAGGACCAGAGAATTGGAATA	1070	TGCAGGACCAGAGAATTGGAATA	1310
CATCAGTCCTGNNCTAGCGTTAC		CAACGCATCANNCTAGCGTTAC		CAGTGGCAGCANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	831	TGCAGGACCAGAGAATTGGAATA	1071	TGCAGGACCAGAGAATTGGAATA	1311
CAGTGACATNNCTAGCGTTAC		CATAGGAAGCANNCTAGCGTTAC		CATTTCATATCANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	832	TGCAGGACCAGAGAATTGGAATA	1072	TGCAGGACCAGAGAATTGGAATA	1312
CAGTAGAAGCANNCTAGCGTTAC		CAGCAATGTCNNCTAGCGTTAC		CACCCATGCCNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	833	TGCAGGACCAGAGAATTGGAATA	1073	TGCAGGACCAGAGAATTGGAATA	1313
CACAGCATTGNNCTAGCGTTAC		CAGCCGGCATNNCTAGCGTTAC		CATTAGTTGANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	834	TGCAGGACCAGAGAATTGGAATA	1074	TGCAGGACCAGAGAATTGGAATA	1314
CACGCCTAGGNNCTAGCGTTAC		CAGTGGCGCANNCTAGCGTTAC		CAATCAGAAANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	835	TGCAGGACCAGAGAATTGGAATA	1075	TGCAGGACCAGAGAATTGGAATA	1315
CACAGTTTGGNNCTAGCGTTAC		CAGTGTCTGANNCTAGCGTTAC		CATTAGAACTNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	836	TGCAGGACCAGAGAATTGGAATA	1076	TGCAGGACCAGAGAATTGGAATA	1316
CATCCCAAGANNCTAGCGTTAC		CAGTGGCGGANNCTAGCGTTAC		CAGTGGTATGNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	837	TGCAGGACCAGAGAATTGGAATA	1077	TGCAGGACCAGAGAATTGGAATA	1317
CATTAGGACCNNCTAGCGTTAC		CAAGGCTACTNNCTAGCGTTAC		CATTGGATCGNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	838	TGCAGGACCAGAGAATTGGAATA	1078	TGCAGGACCAGAGAATTGGAATA	1318
CAACAATTTGNNCTAGCGTTAC		CAACTTTGTTNNCTAGCGTTAC		CACAAGAATANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	839	TGCAGGACCAGAGAATTGGAATA	1079	TGCAGGACCAGAGAATTGGAATA	1319
CATGCTCGAANNCTAGCGTTAC		CAGCCATATGNNCTAGCGTTAC		CAAGCACCATTNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	840	TGCAGGACCAGAGAATTGGAATA	1080	TGCAGGACCAGAGAATTGGAATA	1320
CAGCGGTAGNNCTAGCGTTAC		CAAGCCTGCGNNCTAGCGTTAC		CAACTAGACCNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	841	TGCAGGACCAGAGAATTGGAATA	1081	TGCAGGACCAGAGAATTGGAATA	1321
CAAAATTAACNNCTAGCGTTAC		CAACGTGTGNNCTAGCGTTAC		CAATCATTAGNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	842	TGCAGGACCAGAGAATTGGAATA	1082	TGCAGGACCAGAGAATTGGAATA	1322
CACGACACCGNNCTAGCGTTAC		CATTTTCATGNNCTAGCGTTAC		CAAGAACCTCNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	843	TGCAGGACCAGAGAATTGGAATA	1083	TGCAGGACCAGAGAATTGGAATA	1323
CAGTGAGGATNNCTAGCGTTAC		CAGCTGCGACNNCTAGCGTTAC		CAGATTTTCTNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	844	TGCAGGACCAGAGAATTGGAATA	1084	TGCAGGACCAGAGAATTGGAATA	1324
CAAAATTAANNCTAGCGTTAC		CACAAAATAGNNCTAGCGTTAC		CAAGTACGGANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	845	TGCAGGACCAGAGAATTGGAATA	1085	TGCAGGACCAGAGAATTGGAATA	1325
CACATGCCAANNCTAGCGTTAC		CACTAAACTANNCTAGCGTTAC		CACGCCATAAANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	846	TGCAGGACCAGAGAATTGGAATA	1086	TGCAGGACCAGAGAATTGGAATA	1326
CACCATCAGANNCTAGCGTTAC		CAAAATGATGNNCTAGCGTTAC		CAAGTTGGTCNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	847	TGCAGGACCAGAGAATTGGAATA	1087	TGCAGGACCAGAGAATTGGAATA	1327
CAATATAAANNCTAGCGTTAC		CACCTTGCTGNNCTAGCGTTAC		CATGCGCACGNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	848	TGCAGGACCAGAGAATTGGAATA	1088	TGCAGGACCAGAGAATTGGAATA	1328
CAGCCTCCGTTNNCTAGCGTTAC		CAGATAGGCANNCTAGCGTTAC		CATTGGTACGNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	849	TGCAGGACCAGAGAATTGGAATA	1089	TGCAGGACCAGAGAATTGGAATA	1329
CATCCATCCNNNGATCGACATG		CACAGATTATNNNGATCGACATG		CAATGAGATANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	850	TGCAGGACCAGAGAATTGGAATA	1090	TGCAGGACCAGAGAATTGGAATA	1330
CAAAATGCCNNNGATCGACATG		CAGTTACGGTNNNGATCGACATG		CAATCGGTACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	851	TGCAGGACCAGAGAATTGGAATA	1091	TGCAGGACCAGAGAATTGGAATA	1331
CAACTGTCCANNNGATCGACATG		CAACAGTTGCGNNNGATCGACATG		CATGTGCTCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	852	TGCAGGACCAGAGAATTGGAATA	1092	TGCAGGACCAGAGAATTGGAATA	1332
CAGCTGTTGANNNGATCGACATG		CAAACTGCCNNNGATCGACATG		CATGTGTATANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	853	TGCAGGACCAGAGAATTGGAATA	1093	TGCAGGACCAGAGAATTGGAATA	1333
CAGGTAACCTNNNGATCGACATG		CAAGAATATGNNNGATCGACATG		CAGTGGATCTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	854	TGCAGGACCAGAGAATTGGAATA	1094	TGCAGGACCAGAGAATTGGAATA	1334
CACCTTTCCNNNGATCGACATG		CATCGTCTANNNGATCGACATG		CATCTTCAATNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	855	TGCAGGACCAGAGAATTGGAATA	1095	TGCAGGACCAGAGAATTGGAATA	1335
CAGAGAGCCGNNNGATCGACATG		CACAGAATCCNNNGATCGACATG		CACGCGTGTGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	856	TGCAGGACCAGAGAATTGGAATA	1096	TGCAGGACCAGAGAATTGGAATA	1336
CACAGACAGANNNGATCGACATG		CACCTTGACAGNNNGATCGACATG		CACCTCTCGGNNNGATCGACATG	

FIG. 13E

Pool-4	SEQ ID NO:	Pool-5	SEQ ID NO:	Pool-6	SEQ ID NO:
TGCAGGACCAGAGAATT CGAATA	857	TGCAGGACCAGAGAATT CGAATA	1097	TGCAGGACCAGAGAATT CGAATA	1337
CATATATGACNNNGATCGACATG		CACTGGTAGTNNNGATCGACATG		CAGACTAATTNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	858	TGCAGGACCAGAGAATT CGAATA	1098	TGCAGGACCAGAGAATT CGAATA	1338
CAGTCCGACGNNNGATCGACATG		CACGGATCTANNNGATCGACATG		CACAATAAGANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	859	TGCAGGACCAGAGAATT CGAATA	1099	TGCAGGACCAGAGAATT CGAATA	1339
CAACTGCATGNNNGATCGACATG		CAAAAAAGAGNNNGATCGACATG		CATTTACCGCNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	860	TGCAGGACCAGAGAATT CGAATA	1100	TGCAGGACCAGAGAATT CGAATA	1340
CATACCTAAANNNGATCGACATG		CAGGAGACATNNNGATCGACATG		CAGTGTATTANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	861	TGCAGGACCAGAGAATT CGAATA	1101	TGCAGGACCAGAGAATT CGAATA	1341
CAACCAGATCNNNGATCGACATG		CATCCGGAGCNNNGATCGACATG		CAAGATGTAANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	862	TGCAGGACCAGAGAATT CGAATA	1102	TGCAGGACCAGAGAATT CGAATA	1342
CAGGCCAATTNNNGATCGACATG		CATGTTATTCNNNGATCGACATG		CATTATTCGTTNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	863	TGCAGGACCAGAGAATT CGAATA	1103	TGCAGGACCAGAGAATT CGAATA	1343
CAGAACGTCTNNNGATCGACATG		CAGCGAGACGNNNGATCGACATG		CAAGTCACACNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	864	TGCAGGACCAGAGAATT CGAATA	1104	TGCAGGACCAGAGAATT CGAATA	1344
CACCACCAANNNGATCGACATG		CATTATCGAANNNGATCGACATG		CAGTGACAACNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	865	TGCAGGACCAGAGAATT CGAATA	1105	TGCAGGACCAGAGAATT CGAATA	1345
CATTTTCCAANNNGATCGACATG		CAGTGCCAAATNNNGATCGACATG		CAACGCCGGTNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	866	TGCAGGACCAGAGAATT CGAATA	1106	TGCAGGACCAGAGAATT CGAATA	1346
CAGTTAGTTANNNGATCGACATG		CAGCTAAANNNGATCGACATG		CAGGTGACCCNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	867	TGCAGGACCAGAGAATT CGAATA	1107	TGCAGGACCAGAGAATT CGAATA	1347
CATCAGCTCTNNNGATCGACATG		CAATCCAATANNNGATCGACATG		CACCTTAGCTNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	868	TGCAGGACCAGAGAATT CGAATA	1108	TGCAGGACCAGAGAATT CGAATA	1348
CATCGCGAGGNNNGATCGACATG		CATTCAAGGCNNNGATCGACATG		CACTCGCTATNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	869	TGCAGGACCAGAGAATT CGAATA	1109	TGCAGGACCAGAGAATT CGAATA	1349
CATCTGCAAGNNNGATCGACATG		CATTATTAANNNGATCGACATG		CAAGCCTAGTNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	870	TGCAGGACCAGAGAATT CGAATA	1110	TGCAGGACCAGAGAATT CGAATA	1350
CATCTAACCNNNGATCGACATG		CAAACTCTAANNNGATCGACATG		CAGAGAGTTGNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	871	TGCAGGACCAGAGAATT CGAATA	1111	TGCAGGACCAGAGAATT CGAATA	1351
CACGTAGGAANNNGATCGACATG		CAGACTCCAANNNGATCGACATG		CATAAGAGGCNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	872	TGCAGGACCAGAGAATT CGAATA	1112	TGCAGGACCAGAGAATT CGAATA	1352
CACAAGACTCNNNGATCGACATG		CACAGCCTCCNNNGATCGACATG		CAGTTAATACNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	873	TGCAGGACCAGAGAATT CGAATA	1113	TGCAGGACCAGAGAATT CGAATA	1353
CATTCCGTGTNNNGATCGACATG		CAGAGTCACTNNNGATCGACATG		CAGGTCCGCANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	874	TGCAGGACCAGAGAATT CGAATA	1114	TGCAGGACCAGAGAATT CGAATA	1354
CAGTGAACGANNNNGATCGACATG		CAAGAACTGGNNNGATCGACATG		CATAAGCATTNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	875	TGCAGGACCAGAGAATT CGAATA	1115	TGCAGGACCAGAGAATT CGAATA	1355
CAGCTAAACNNNGATCGACATG		CAGCGTATTGNNNGATCGACATG		CAGTACGCATNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	876	TGCAGGACCAGAGAATT CGAATA	1116	TGCAGGACCAGAGAATT CGAATA	1356
CACAATTTTCNNNGATCGACATG		CACCTTAAATGNNNGATCGACATG		CAAACGAACGNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	877	TGCAGGACCAGAGAATT CGAATA	1117	TGCAGGACCAGAGAATT CGAATA	1357
CATGAGGAACNNNGATCGACATG		CATTAGCCTCNNNGATCGACATG		CAGTAGGTTCCNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	878	TGCAGGACCAGAGAATT CGAATA	1118	TGCAGGACCAGAGAATT CGAATA	1358
CAGTAATCTANNNGATCGACATG		CAACCAGAGANNNGATCGACATG		CACTTTTTCNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	879	TGCAGGACCAGAGAATT CGAATA	1119	TGCAGGACCAGAGAATT CGAATA	1359
CATATCTCCGNNNGATCGACATG		CATCAGCCAANNNGATCGACATG		CAATGACCCANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	880	TGCAGGACCAGAGAATT CGAATA	1120	TGCAGGACCAGAGAATT CGAATA	1360
CAGCTACGGCNNNGATCGACATG		CACCGAATACNNNGATCGACATG		CAATCAGTTANNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	881	TGCAGGACCAGAGAATT CGAATA	1121	TGCAGGACCAGAGAATT CGAATA	1361
CAATATCTGANNNNGATCGACATG		CAGCGGCAAGNNNGATCGACATG		CATAGTAAAGNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	882	TGCAGGACCAGAGAATT CGAATA	1122	TGCAGGACCAGAGAATT CGAATA	1362
CATACTTAGANNNGATCGACATG		CATAAATCGTNNNGATCGACATG		CACCCGATCGNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	883	TGCAGGACCAGAGAATT CGAATA	1123	TGCAGGACCAGAGAATT CGAATA	1363
CATCATTTTGNNGATCGACATG		CAAAGCTTCGNNNGATCGACATG		CACACAGCATNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	884	TGCAGGACCAGAGAATT CGAATA	1124	TGCAGGACCAGAGAATT CGAATA	1364
CAGCGTCGAGNNNGATCGACATG		CAATGCATATNNNGATCGACATG		CACAGGTACTNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	885	TGCAGGACCAGAGAATT CGAATA	1125	TGCAGGACCAGAGAATT CGAATA	1365
CATAAGACGGNNNGATCGACATG		CATCTCTCCTNNNGATCGACATG		CACATAACCGNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	886	TGCAGGACCAGAGAATT CGAATA	1126	TGCAGGACCAGAGAATT CGAATA	1366
CAAGGCCCTTANNNGATCGACATG		CATAGTGGTCNNNGATCGACATG		CAGTACTGGTNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	887	TGCAGGACCAGAGAATT CGAATA	1127	TGCAGGACCAGAGAATT CGAATA	1367
CACATCTCACNNNGATCGACATG		CAGAAACCTCNNNGATCGACATG		CAGCAAGTCTNNNGATCGACATG	
TGCAGGACCAGAGAATT CGAATA	888	TGCAGGACCAGAGAATT CGAATA	1128	TGCAGGACCAGAGAATT CGAATA	1368
CATGCGATCANNNGATCGACATG		CATGACTATANNNGATCGACATG		CACGTGCTCCNNNGATCGACATG	

FIG. 13F

Pool-4	SEQ ID NO:	Pool-5	SEQ ID NO:	Pool-6	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA	889	TGCAGGACCAGAGAATTGGAATA	1129	TGCAGGACCAGAGAATTGGAATA	1369
CACGGAGGACNNNGATCGACATG		CACATGACTGNNNGATCGACATG		CACACTACCTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	890	TGCAGGACCAGAGAATTGGAATA	1130	TGCAGGACCAGAGAATTGGAATA	1370
CAACTAATTGNNNGATCGACATG		CACCAAAGTCNNNGATCGACATG		CAGTGTATATNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	891	TGCAGGACCAGAGAATTGGAATA	1131	TGCAGGACCAGAGAATTGGAATA	1371
CATGCCCTAGANNNGATCGACATG		CACGCATTTCNNNGATCGACATG		CAATGACGCTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	892	TGCAGGACCAGAGAATTGGAATA	1132	TGCAGGACCAGAGAATTGGAATA	1372
CACATATCCGTTNNNGATCGACATG		CAACCCGCTGNNNGATCGACATG		CAAGGCACTTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	893	TGCAGGACCAGAGAATTGGAATA	1133	TGCAGGACCAGAGAATTGGAATA	1373
CATGCCAGGCGNNNGATCGACATG		CACTTGCGTTNNNGATCGACATG		CAGGCGAGGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	894	TGCAGGACCAGAGAATTGGAATA	1134	TGCAGGACCAGAGAATTGGAATA	1374
CAGCGGAGCANNNGATCGACATG		CATTATGCAANNNGATCGACATG		CACATATGTTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	895	TGCAGGACCAGAGAATTGGAATA	1135	TGCAGGACCAGAGAATTGGAATA	1375
CAAGACCCATNNNGATCGACATG		CATATTTGAGNNNGATCGACATG		CATAAATATTTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	896	TGCAGGACCAGAGAATTGGAATA	1136	TGCAGGACCAGAGAATTGGAATA	1376
CATTGACCTCANNNGATCGACATG		CATGTTGCTNNNGATCGACATG		CAGACACCATNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	897	TGCAGGACCAGAGAATTGGAATA	1137	TGCAGGACCAGAGAATTGGAATA	1377
CACTTGCTCANNNGATCGACATG		CATAGCATCGNNNGATCGACATG		CATAGATACTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	898	TGCAGGACCAGAGAATTGGAATA	1138	TGCAGGACCAGAGAATTGGAATA	1378
CAATGCTGCANNNGATCGACATG		CATTGAGCGNNNGATCGACATG		CATACCTGTTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	899	TGCAGGACCAGAGAATTGGAATA	1139	TGCAGGACCAGAGAATTGGAATA	1379
CAAACGGACANNNGATCGACATG		CAAACGCGAGANNNGATCGACATG		CAGTCGCCGANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	900	TGCAGGACCAGAGAATTGGAATA	1140	TGCAGGACCAGAGAATTGGAATA	1380
CAGCGATCATNNNGATCGACATG		CATATGGCGTNNNGATCGACATG		CACCTCTTAGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	901	TGCAGGACCAGAGAATTGGAATA	1141	TGCAGGACCAGAGAATTGGAATA	1381
CATGAGACAGNNNGATCGACATG		CAAGCCTATGNNNGATCGACATG		CATAAGATTCTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	902	TGCAGGACCAGAGAATTGGAATA	1142	TGCAGGACCAGAGAATTGGAATA	1382
CAGCCACTGGNNNGATCGACATG		CACACTCTACNNNGATCGACATG		CACGCGTACGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	903	TGCAGGACCAGAGAATTGGAATA	1143	TGCAGGACCAGAGAATTGGAATA	1383
CAGGTTTGACNNNGATCGACATG		CAAAACTGAANNNGATCGACATG		CACTGACCAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	904	TGCAGGACCAGAGAATTGGAATA	1144	TGCAGGACCAGAGAATTGGAATA	1384
CAAACCTGGCANNNGATCGACATG		CACCTCCGCGNNNGATCGACATG		CAAAGACCGANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	905	TGCAGGACCAGAGAATTGGAATA	1145	TGCAGGACCAGAGAATTGGAATA	1385
CAACCTAATANNNGATCGACATG		CAACGTCGGCANNNGATCGACATG		CAAAATGATCTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	906	TGCAGGACCAGAGAATTGGAATA	1146	TGCAGGACCAGAGAATTGGAATA	1386
CAGCAGAGAANNNGATCGACATG		CAGTACCCAAANNNGATCGACATG		CACCCCCAAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	907	TGCAGGACCAGAGAATTGGAATA	1147	TGCAGGACCAGAGAATTGGAATA	1387
CATGTGTGAGNNNGATCGACATG		CAACCGCATANNNGATCGACATG		CAGCCTGAATNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	908	TGCAGGACCAGAGAATTGGAATA	1148	TGCAGGACCAGAGAATTGGAATA	1388
CAAGTAACAANNNGATCGACATG		CAAACAGCTNNNGATCGACATG		CATCGGTAGTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	909	TGCAGGACCAGAGAATTGGAATA	1149	TGCAGGACCAGAGAATTGGAATA	1389
CATCTGAGCANNNTGCATCAGGT		CAGAGCGAGCANNNTGCATCAGGT		CATGGCTCGGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	910	TGCAGGACCAGAGAATTGGAATA	1150	TGCAGGACCAGAGAATTGGAATA	1390
CAAGTGGAAACNNNTGCATCAGGT		CATTTTATTANNNTGCATCAGGT		CACAATCCTCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	911	TGCAGGACCAGAGAATTGGAATA	1151	TGCAGGACCAGAGAATTGGAATA	1391
CAGAACTCGTNNNTGCATCAGGT		CAGCTAGGTTNNNTGCATCAGGT		CATAGAGACGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	912	TGCAGGACCAGAGAATTGGAATA	1152	TGCAGGACCAGAGAATTGGAATA	1392
CAGCAGGCGANNNTGCATCAGGT		CATTTGACTTNNNTGCATCAGGT		CAGCGGATGGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	913	TGCAGGACCAGAGAATTGGAATA	1153	TGCAGGACCAGAGAATTGGAATA	1393
CAGGGCTCTCCNNNTGCATCAGGT		CACAAACATNNNTGCATCAGGT		CACCTCACCATTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	914	TGCAGGACCAGAGAATTGGAATA	1154	TGCAGGACCAGAGAATTGGAATA	1394
CAAATACATCANNNTGCATCAGGT		CATTGCAATANNNTGCATCAGGT		CAATGGTAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	915	TGCAGGACCAGAGAATTGGAATA	1155	TGCAGGACCAGAGAATTGGAATA	1395
CAAGGTCAAGNNNTGCATCAGGT		CAACAAGGCANNNTGCATCAGGT		CATATCAACANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	916	TGCAGGACCAGAGAATTGGAATA	1156	TGCAGGACCAGAGAATTGGAATA	1396
CATGAGCCGCGNNNTGCATCAGGT		CAGGTGCTGCGNNNTGCATCAGGT		CAAAAGTCAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	917	TGCAGGACCAGAGAATTGGAATA	1157	TGCAGGACCAGAGAATTGGAATA	1397
CATTAGTTTCNNNTGCATCAGGT		CAAGGTGCTTNNNTGCATCAGGT		CACAAAGGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	918	TGCAGGACCAGAGAATTGGAATA	1158	TGCAGGACCAGAGAATTGGAATA	1398
CAGTCGTAGTNNNTGCATCAGGT		CACAACGGAAANNNTGCATCAGGT		CACGATGACTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	919	TGCAGGACCAGAGAATTGGAATA	1159	TGCAGGACCAGAGAATTGGAATA	1399
CAAAAGGATTNNNTGCATCAGGT		CAGATCCAACNNNTGCATCAGGT		CACGATTGTGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	920	TGCAGGACCAGAGAATTGGAATA	1160	TGCAGGACCAGAGAATTGGAATA	1400
CATTTTGTAGCANNNTGCATCAGGT		CAGGAAGACTNNNTGCATCAGGT		CATTATCTTGNNTGCATCAGGT	

FIG. 13G

Pool-4	SEQ ID NO:	Pool-5	SEQ ID NO:	Pool-6	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATA	921	TGCAGGACCAGAGAATTCTGAATA	1161	TGCAGGACCAGAGAATTCTGAATA	1401
CAATAACTCANNNTGCATCAGGT		CAGGTAAATANNNTGCATCAGGT		CAGTATTGATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	922	TGCAGGACCAGAGAATTCTGAATA	1162	TGCAGGACCAGAGAATTCTGAATA	1402
CATTTTAACCNNTGCATCAGGT		CAGGTAGAACNNNTGCATCAGGT		CAAGGAGGTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	923	TGCAGGACCAGAGAATTCTGAATA	1163	TGCAGGACCAGAGAATTCTGAATA	1403
CAGTGCCGACNNNTGCATCAGGT		CAATATGAGANNNTGCATCAGGT		CAACTGCCCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	924	TGCAGGACCAGAGAATTCTGAATA	1164	TGCAGGACCAGAGAATTCTGAATA	1404
CAGAAATAGATNNNTGCATCAGGT		CATGGAAATANNNTGCATCAGGT		CAAAATCTCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	925	TGCAGGACCAGAGAATTCTGAATA	1165	TGCAGGACCAGAGAATTCTGAATA	1405
CAGCTGAGCCNNNTGCATCAGGT		CATAACCAATNNNTGCATCAGGT		CACCATGTGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	926	TGCAGGACCAGAGAATTCTGAATA	1166	TGCAGGACCAGAGAATTCTGAATA	1406
CAACAGCGAACNNNTGCATCAGGT		CAGTCTGATGNNNTGCATCAGGT		CACCCCTTTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	927	TGCAGGACCAGAGAATTCTGAATA	1167	TGCAGGACCAGAGAATTCTGAATA	1407
CAGACCGCACNNNTGCATCAGGT		CATTATGAGNNNTGCATCAGGT		CAGCTAGCGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	928	TGCAGGACCAGAGAATTCTGAATA	1168	TGCAGGACCAGAGAATTCTGAATA	1408
CACCTTATTCANNNTGCATCAGGT		CAATGATTTGNNNTGCATCAGGT		CAAAACCCGTCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	929	TGCAGGACCAGAGAATTCTGAATA	1169	TGCAGGACCAGAGAATTCTGAATA	1409
CAGTGTGCTANNNTGCATCAGGT		CACCTCATCGTNNNTGCATCAGGT		CACCTGAGATCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	930	TGCAGGACCAGAGAATTCTGAATA	1170	TGCAGGACCAGAGAATTCTGAATA	1410
CAATTTAGTGNNNTGCATCAGGT		CACCTCCATCANNNTGCATCAGGT		CAAAATGCGTCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	931	TGCAGGACCAGAGAATTCTGAATA	1171	TGCAGGACCAGAGAATTCTGAATA	1411
CATCGGAGANNNTGCATCAGGT		CAGCTAGCATNNNTGCATCAGGT		CAATTGCCAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	932	TGCAGGACCAGAGAATTCTGAATA	1172	TGCAGGACCAGAGAATTCTGAATA	1412
CACGCCGAACNNNTGCATCAGGT		CAAAATCATCANNNTGCATCAGGT		CATTAATTCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	933	TGCAGGACCAGAGAATTCTGAATA	1173	TGCAGGACCAGAGAATTCTGAATA	1413
CAGCTTCGCCNNNTGCATCAGGT		CACGTCTCATNNNTGCATCAGGT		CAAGCATATTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	934	TGCAGGACCAGAGAATTCTGAATA	1174	TGCAGGACCAGAGAATTCTGAATA	1414
CAACAATCATNNNTGCATCAGGT		CAACTCGTTCCNNNTGCATCAGGT		CACCCATTACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	935	TGCAGGACCAGAGAATTCTGAATA	1175	TGCAGGACCAGAGAATTCTGAATA	1415
CATGATCGCANNNTGCATCAGGT		CAAGTTCTGNNNTGCATCAGGT		CACCTCGTTTGNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	936	TGCAGGACCAGAGAATTCTGAATA	1176	TGCAGGACCAGAGAATTCTGAATA	1416
CACACAGTACNNNTGCATCAGGT		CAACTAGTATNNNTGCATCAGGT		CAGGTATCGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	937	TGCAGGACCAGAGAATTCTGAATA	1177	TGCAGGACCAGAGAATTCTGAATA	1417
CAGTCAAGTCNNNTGCATCAGGT		CAATTGCGCANNNTGCATCAGGT		CAGTACCCCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	938	TGCAGGACCAGAGAATTCTGAATA	1178	TGCAGGACCAGAGAATTCTGAATA	1418
CAGCTCCCACNNNTGCATCAGGT		CACGAGCGCTNNNTGCATCAGGT		CACAACTTTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	939	TGCAGGACCAGAGAATTCTGAATA	1179	TGCAGGACCAGAGAATTCTGAATA	1419
CATTACTTGTNNNTGCATCAGGT		CAACGACCATTNNNTGCATCAGGT		CAGAACTTGCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	940	TGCAGGACCAGAGAATTCTGAATA	1180	TGCAGGACCAGAGAATTCTGAATA	1420
CATAATGTGTNNNTGCATCAGGT		CATAAGTGAANNNTGCATCAGGT		CATATTATGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	941	TGCAGGACCAGAGAATTCTGAATA	1181	TGCAGGACCAGAGAATTCTGAATA	1421
CATACCATTNNNTGCATCAGGT		CATCTCGCCGNNNTGCATCAGGT		CAGCCCGCGGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	942	TGCAGGACCAGAGAATTCTGAATA	1182	TGCAGGACCAGAGAATTCTGAATA	1422
CAGTCCGTAAANNNTGCATCAGGT		CAAATACTGTNNNTGCATCAGGT		CAGCAAAAGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	943	TGCAGGACCAGAGAATTCTGAATA	1183	TGCAGGACCAGAGAATTCTGAATA	1423
CAAGCGGTAAANNNTGCATCAGGT		CATATGTTCTNNNTGCATCAGGT		CAGATACGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	944	TGCAGGACCAGAGAATTCTGAATA	1184	TGCAGGACCAGAGAATTCTGAATA	1424
CAGGAAACTGNNNTGCATCAGGT		CACCAGCGGTNNNTGCATCAGGT		CACAGTATCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	945	TGCAGGACCAGAGAATTCTGAATA	1185	TGCAGGACCAGAGAATTCTGAATA	1425
CAGGCGCACGTNNNTGCATCAGGT		CACGGTTGATNNNTGCATCAGGT		CACCTACTGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	946	TGCAGGACCAGAGAATTCTGAATA	1186	TGCAGGACCAGAGAATTCTGAATA	1426
CATCATTGAANNNTGCATCAGGT		CACGCTGCAGNNNTGCATCAGGT		CACCGTCAGGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	947	TGCAGGACCAGAGAATTCTGAATA	1187	TGCAGGACCAGAGAATTCTGAATA	1427
CAGCGTCAATNNNTGCATCAGGT		CAGTCTAAATNNNTGCATCAGGT		CAGCTTCTGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	948	TGCAGGACCAGAGAATTCTGAATA	1188	TGCAGGACCAGAGAATTCTGAATA	1428
CACGGAAGCGNNNTGCATCAGGT		CAGTAATTACNNNTGCATCAGGT		CATTATATTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	949	TGCAGGACCAGAGAATTCTGAATA	1189	TGCAGGACCAGAGAATTCTGAATA	1429
CAGTTTGAACNNNTGCATCAGGT		CATTCCGGTTNNNTGCATCAGGT		CAGGTTTACGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	950	TGCAGGACCAGAGAATTCTGAATA	1190	TGCAGGACCAGAGAATTCTGAATA	1430
CAGGCCCCCTNNNTGCATCAGGT		CAGAGCGTGGNNNTGCATCAGGT		CAGGACGATANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	951	TGCAGGACCAGAGAATTCTGAATA	1191	TGCAGGACCAGAGAATTCTGAATA	1431
CAATGGCTCANNNTGCATCAGGT		CAATTTACTCANNNTGCATCAGGT		CAAGTCAGGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	952	TGCAGGACCAGAGAATTCTGAATA	1192	TGCAGGACCAGAGAATTCTGAATA	1432
CATTGACGGTNNNTGCATCAGGT		CACAACACTGNNNTGCATCAGGT		CACACGAACNNNTGCATCAGGT	

FIG. 13H

Pool-4	SEQ ID NO:	Pool-5	SEQ ID NO:	Pool-6	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA CATGGACGTTNNNTGCATCAGGT	953	TGCAGGACCAGAGAATTGGAATA CACCGCGGCGNNNTGCATCAGGT	1193	TGCAGGACCAGAGAATTGGAATA CAAGCCATGTTNNNTGCATCAGGT	1433
TGCAGGACCAGAGAATTGGAATA CATGACAGTCNNNTGCATCAGGT	954	TGCAGGACCAGAGAATTGGAATA CACTAAGCTGNNNTGCATCAGGT	1194	TGCAGGACCAGAGAATTGGAATA CATTCCACTGNNNTGCATCAGGT	1434
TGCAGGACCAGAGAATTGGAATA CACTAGCTGTTNNNTGCATCAGGT	955	TGCAGGACCAGAGAATTGGAATA CAATTCAAGTNNNTGCATCAGGT	1195	TGCAGGACCAGAGAATTGGAATA CAACCCGTGTTNNNTGCATCAGGT	1435
TGCAGGACCAGAGAATTGGAATA CAAGGTCCCGNNNTGCATCAGGT	956	TGCAGGACCAGAGAATTGGAATA CAATTGGCGTNNNTGCATCAGGT	1196	TGCAGGACCAGAGAATTGGAATA CACCCCTTCTNNNTGCATCAGGT	1436
TGCAGGACCAGAGAATTGGAATA CATTTCATCTANNNTGCATCAGGT	957	TGCAGGACCAGAGAATTGGAATA CATGATTTGANNNTGCATCAGGT	1197	TGCAGGACCAGAGAATTGGAATA CAATGTTGATNNNTGCATCAGGT	1437
TGCAGGACCAGAGAATTGGAATA CAGATAAAGTNNNTGCATCAGGT	958	TGCAGGACCAGAGAATTGGAATA CAACTGGCGTNNNTGCATCAGGT	1198	TGCAGGACCAGAGAATTGGAATA CACACTGGCGNNNTGCATCAGGT	1438
TGCAGGACCAGAGAATTGGAATA CACACGGAAANNNTGCATCAGGT	959	TGCAGGACCAGAGAATTGGAATA CATTAATCCTNNNTGCATCAGGT	1199	TGCAGGACCAGAGAATTGGAATA CATTCCGTAGNNNTGCATCAGGT	1439
TGCAGGACCAGAGAATTGGAATA CATGTGAGGANNNTGCATCAGGT	960	TGCAGGACCAGAGAATTGGAATA CACTACGCTTNNNTGCATCAGGT	1200	TGCAGGACCAGAGAATTGGAATA CAACCCGTCCNNNTGCATCAGGT	1440
TGCAGGACCAGAGAATTGGAATA CACGTGATCANNNTGCATCAGGT	961	TGCAGGACCAGAGAATTGGAATA CATAGCTATANNNTGCATCAGGT	1201	TGCAGGACCAGAGAATTGGAATA CAGTACCTAGNNNTGCATCAGGT	1441
TGCAGGACCAGAGAATTGGAATA CATGCCGTTGANNNTGCATCAGGT	962	TGCAGGACCAGAGAATTGGAATA CATGCACCTCTNNNTGCATCAGGT	1202	TGCAGGACCAGAGAATTGGAATA CACGATAATTNNNTGCATCAGGT	1442
TGCAGGACCAGAGAATTGGAATA CATCGCTCCGNNNTGCATCAGGT	963	TGCAGGACCAGAGAATTGGAATA CAGTGCTCCGNNNTGCATCAGGT	1203	TGCAGGACCAGAGAATTGGAATA CAGCCAACCGNNNTGCATCAGGT	1443
TGCAGGACCAGAGAATTGGAATA CACCAGTCAANNNTGCATCAGGT	964	TGCAGGACCAGAGAATTGGAATA CAGCCACCAGNNNTGCATCAGGT	1204	TGCAGGACCAGAGAATTGGAATA CATAACATCANNNTGCATCAGGT	1444
TGCAGGACCAGAGAATTGGAATA CACACATTCNNNTGCATCAGGT	965	TGCAGGACCAGAGAATTGGAATA CATTATGTGANNNTGCATCAGGT	1205	TGCAGGACCAGAGAATTGGAATA CAGCAAGAACNNNTGCATCAGGT	1445
TGCAGGACCAGAGAATTGGAATA CAGGTATATTNNNTGCATCAGGT	966	TGCAGGACCAGAGAATTGGAATA CAATACTCCGNNNTGCATCAGGT	1206	TGCAGGACCAGAGAATTGGAATA CAACGTGATCANNNTGCATCAGGT	1446
TGCAGGACCAGAGAATTGGAATA CATAAGATGANNNTGCATCAGGT	967	TGCAGGACCAGAGAATTGGAATA CAACTATGGCANNNTGCATCAGGT	1207	TGCAGGACCAGAGAATTGGAATA CACGTTCCCTANNNTGCATCAGGT	1447
TGCAGGACCAGAGAATTGGAATA CATTAATAATTNNNTGCATCAGGT	968	TGCAGGACCAGAGAATTGGAATA CAACGGCCTGNNNTGCATCAGGT	1208	TGCAGGACCAGAGAATTGGAATA CAATGCCAGTNNNTGCATCAGGT	1448

FIG. 14A

Pool-7	SEQ ID NO:	Pool-8	SEQ ID NO:	Pool-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACAGGCTCGNNNACGTATGCCA	1449	TGCAGGACCAGAGAATTCGAATA CAACTACCAGNNNACGTATGCCA	1689	TGCAGGACCAGAGAATTCGAATA CAGAACGCCNNNACGTATGCCA	1929
TGCAGGACCAGAGAATTCGAATA CATTGAAGCCNNNACGTATGCCA	1450	TGCAGGACCAGAGAATTCGAATA CATTATTGAGNNNACGTATGCCA	1690	TGCAGGACCAGAGAATTCGAATA CAACCAATGCNNNACGTATGCCA	1930
TGCAGGACCAGAGAATTCGAATA CACACAGAGANNNACGTATGCCA	1451	TGCAGGACCAGAGAATTCGAATA CAACTGTGTGNNNACGTATGCCA	1691	TGCAGGACCAGAGAATTCGAATA CAGACCGATTNNNACGTATGCCA	1931
TGCAGGACCAGAGAATTCGAATA CAGGACTCCGNNNACGTATGCCA	1452	TGCAGGACCAGAGAATTCGAATA CATTGATCGGNNNACGTATGCCA	1692	TGCAGGACCAGAGAATTCGAATA CAATGTTATTGNNNACGTATGCCA	1932
TGCAGGACCAGAGAATTCGAATA CATTGGTTAANNNACGTATGCCA	1453	TGCAGGACCAGAGAATTCGAATA CATTCTCGGTNNNACGTATGCCA	1693	TGCAGGACCAGAGAATTCGAATA CAGGAAGAAGNNNACGTATGCCA	1933
TGCAGGACCAGAGAATTCGAATA CATACTAACANNNACGTATGCCA	1454	TGCAGGACCAGAGAATTCGAATA CAACAGTTAGNNNACGTATGCCA	1694	TGCAGGACCAGAGAATTCGAATA CAGTTATACANNNACGTATGCCA	1934
TGCAGGACCAGAGAATTCGAATA CAGTCCAATGNNNACGTATGCCA	1455	TGCAGGACCAGAGAATTCGAATA CAAGAACAATNNNACGTATGCCA	1695	TGCAGGACCAGAGAATTCGAATA CACCTCCTAANNNACGTATGCCA	1935
TGCAGGACCAGAGAATTCGAATA CAAGGCACGGNNNACGTATGCCA	1456	TGCAGGACCAGAGAATTCGAATA CATCCGAAGTNNNACGTATGCCA	1696	TGCAGGACCAGAGAATTCGAATA CATAAACATCNNNACGTATGCCA	1936
TGCAGGACCAGAGAATTCGAATA CAATCATGTANNNACGTATGCCA	1457	TGCAGGACCAGAGAATTCGAATA CATCGGCTCCNNNACGTATGCCA	1697	TGCAGGACCAGAGAATTCGAATA CACGGCGGTNNNACGTATGCCA	1937
TGCAGGACCAGAGAATTCGAATA CAAAAAGGTTNNNACGTATGCCA	1458	TGCAGGACCAGAGAATTCGAATA CACAGTCCCCNNNACGTATGCCA	1698	TGCAGGACCAGAGAATTCGAATA CATTAACAACNNNACGTATGCCA	1938
TGCAGGACCAGAGAATTCGAATA CAAGGCACCCNNNACGTATGCCA	1459	TGCAGGACCAGAGAATTCGAATA CAGTCAACTGNNNACGTATGCCA	1699	TGCAGGACCAGAGAATTCGAATA CATGGCCATANNNACGTATGCCA	1939
TGCAGGACCAGAGAATTCGAATA CATTGAAGANNNACGTATGCCA	1460	TGCAGGACCAGAGAATTCGAATA CAGGCGGCTTNNNACGTATGCCA	1700	TGCAGGACCAGAGAATTCGAATA CAGAGTGATGNNNACGTATGCCA	1940
TGCAGGACCAGAGAATTCGAATA CACTCGACTTNNNACGTATGCCA	1461	TGCAGGACCAGAGAATTCGAATA CAATCGCTANNNACGTATGCCA	1701	TGCAGGACCAGAGAATTCGAATA CACTAATGCGNNNACGTATGCCA	1941
TGCAGGACCAGAGAATTCGAATA CAGCGAATTCNNNACGTATGCCA	1462	TGCAGGACCAGAGAATTCGAATA CAGCTCCGANNNACGTATGCCA	1702	TGCAGGACCAGAGAATTCGAATA CAAGGTTAAANNNACGTATGCCA	1942
TGCAGGACCAGAGAATTCGAATA CACCCCGCGNNNACGTATGCCA	1463	TGCAGGACCAGAGAATTCGAATA CATGCTGGCGNNNACGTATGCCA	1703	TGCAGGACCAGAGAATTCGAATA CAACAGTACCNNNACGTATGCCA	1943
TGCAGGACCAGAGAATTCGAATA CAGATAAGCGNNNACGTATGCCA	1464	TGCAGGACCAGAGAATTCGAATA CACTAACGTGNNNACGTATGCCA	1704	TGCAGGACCAGAGAATTCGAATA CAATGTGATTNNNACGTATGCCA	1944
TGCAGGACCAGAGAATTCGAATA CAGAACGATGNNNACGTATGCCA	1465	TGCAGGACCAGAGAATTCGAATA CAGAATACAANNNACGTATGCCA	1705	TGCAGGACCAGAGAATTCGAATA CAGCTGCCGANNNACGTATGCCA	1945
TGCAGGACCAGAGAATTCGAATA CAAATATTATNNNACGTATGCCA	1466	TGCAGGACCAGAGAATTCGAATA CAATGACAAANNNACGTATGCCA	1706	TGCAGGACCAGAGAATTCGAATA CACTTTTTAGNNNACGTATGCCA	1946
TGCAGGACCAGAGAATTCGAATA CATAAGCTATNNNACGTATGCCA	1467	TGCAGGACCAGAGAATTCGAATA CAACGGCTCGNNNACGTATGCCA	1707	TGCAGGACCAGAGAATTCGAATA CATCCCAAAGNNNACGTATGCCA	1947
TGCAGGACCAGAGAATTCGAATA CAACTCGCGNNNACGTATGCCA	1468	TGCAGGACCAGAGAATTCGAATA CAACAGATAANNNACGTATGCCA	1708	TGCAGGACCAGAGAATTCGAATA CAGACACTACNNNACGTATGCCA	1948
TGCAGGACCAGAGAATTCGAATA CAGGACTCGGNNNACGTATGCCA	1469	TGCAGGACCAGAGAATTCGAATA CATGTAGCCANNNACGTATGCCA	1709	TGCAGGACCAGAGAATTCGAATA CAATACCGACNNNACGTATGCCA	1949
TGCAGGACCAGAGAATTCGAATA CATCCGACTTNNNACGTATGCCA	1470	TGCAGGACCAGAGAATTCGAATA CACTTCTGCANNNACGTATGCCA	1710	TGCAGGACCAGAGAATTCGAATA CAGTTGAAAANNNACGTATGCCA	1950
TGCAGGACCAGAGAATTCGAATA CAGGAGGAGNNNACGTATGCCA	1471	TGCAGGACCAGAGAATTCGAATA CATTACCTTANNNACGTATGCCA	1711	TGCAGGACCAGAGAATTCGAATA CAATTTCTANNNACGTATGCCA	1951
TGCAGGACCAGAGAATTCGAATA CACAGGCAGNNNACGTATGCCA	1472	TGCAGGACCAGAGAATTCGAATA CATCAATTCTNNNACGTATGCCA	1712	TGCAGGACCAGAGAATTCGAATA CAACGTTCCAGNNNACGTATGCCA	1952
TGCAGGACCAGAGAATTCGAATA CAATCTCATTNNNACGTATGCCA	1473	TGCAGGACCAGAGAATTCGAATA CAAGGTTCTGNNNACGTATGCCA	1713	TGCAGGACCAGAGAATTCGAATA CAAATACGAANNNACGTATGCCA	1953
TGCAGGACCAGAGAATTCGAATA CAAGGCGATANNNACGTATGCCA	1474	TGCAGGACCAGAGAATTCGAATA CAATTTTAAANNNACGTATGCCA	1714	TGCAGGACCAGAGAATTCGAATA CACCACCTGANNNACGTATGCCA	1954
TGCAGGACCAGAGAATTCGAATA CACCTAGATTGNNNACGTATGCCA	1475	TGCAGGACCAGAGAATTCGAATA CATTGCAGACNNNACGTATGCCA	1715	TGCAGGACCAGAGAATTCGAATA CAATCCGCTNNNACGTATGCCA	1955
TGCAGGACCAGAGAATTCGAATA CACCTACCATNNNACGTATGCCA	1476	TGCAGGACCAGAGAATTCGAATA CACCCCACTGNNNACGTATGCCA	1716	TGCAGGACCAGAGAATTCGAATA CACGTCCGCTNNNACGTATGCCA	1956

FIG. 14B

Pool-7	SEQ ID NO:	Pool-8	SEQ ID NO:	Pool-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAAACGTCCANNACGTATGCCA	1477	TGCAGGACCAGAGAATTCGAATA CACTTCCTGANNACGTATGCCA	1717	TGCAGGACCAGAGAATTCGAATA CATATACACANNACGTATGCCA	1957
TGCAGGACCAGAGAATTCGAATA CAGCACTTAGNNACGTATGCCA	1478	TGCAGGACCAGAGAATTCGAATA CAAGAACTCONNNACGTATGCCA	1718	TGCAGGACCAGAGAATTCGAATA CACTCTATATNNACGTATGCCA	1958
TGCAGGACCAGAGAATTCGAATA CAGATCGGAANNACGTATGCCA	1479	TGCAGGACCAGAGAATTCGAATA CACTGTAAGCANNACGTATGCCA	1719	TGCAGGACCAGAGAATTCGAATA CACTCACAGANNACGTATGCCA	1959
TGCAGGACCAGAGAATTCGAATA CACGCCATAANNACGTATGCCA	1480	TGCAGGACCAGAGAATTCGAATA CAAGTCGATCANNACGTATGCCA	1720	TGCAGGACCAGAGAATTCGAATA CAGCCGGTGTNNACGTATGCCA	1960
TGCAGGACCAGAGAATTCGAATA CATTAAGTTGNNACGTATGCCA	1481	TGCAGGACCAGAGAATTCGAATA CAGTAATAGANNACGTATGCCA	1721	TGCAGGACCAGAGAATTCGAATA CATACGTGANNACGTATGCCA	1961
TGCAGGACCAGAGAATTCGAATA CAGCCAGCTGNNACGTATGCCA	1482	TGCAGGACCAGAGAATTCGAATA CACGGAGCTCANNACGTATGCCA	1722	TGCAGGACCAGAGAATTCGAATA CATCTGCTCANNACGTATGCCA	1962
TGCAGGACCAGAGAATTCGAATA CAAAACGCCCTNNACGTATGCCA	1483	TGCAGGACCAGAGAATTCGAATA CATTGTCTTANNACGTATGCCA	1723	TGCAGGACCAGAGAATTCGAATA CAACGTATATNNACGTATGCCA	1963
TGCAGGACCAGAGAATTCGAATA CAGTATTTCTNNACGTATGCCA	1484	TGCAGGACCAGAGAATTCGAATA CATTTTCTGANNACGTATGCCA	1724	TGCAGGACCAGAGAATTCGAATA CAGGAGCCACNNACGTATGCCA	1964
TGCAGGACCAGAGAATTCGAATA CAGGTCTCCNNACGTATGCCA	1485	TGCAGGACCAGAGAATTCGAATA CAAAACGGAACNNACGTATGCCA	1725	TGCAGGACCAGAGAATTCGAATA CATCGCTCTANNACGTATGCCA	1965
TGCAGGACCAGAGAATTCGAATA CACAACTCTGNNACGTATGCCA	1486	TGCAGGACCAGAGAATTCGAATA CAACCACGGCANNACGTATGCCA	1726	TGCAGGACCAGAGAATTCGAATA CAGGGAAGATNNACGTATGCCA	1966
TGCAGGACCAGAGAATTCGAATA CAGAGCACAAANNACGTATGCCA	1487	TGCAGGACCAGAGAATTCGAATA CAGAGTATTTNNACGTATGCCA	1727	TGCAGGACCAGAGAATTCGAATA CATTAGCGGTNNACGTATGCCA	1967
TGCAGGACCAGAGAATTCGAATA CATCAAACCGNNACGTATGCCA	1488	TGCAGGACCAGAGAATTCGAATA CACC CGCTANNACGTATGCCA	1728	TGCAGGACCAGAGAATTCGAATA CATGAGCTCANNACGTATGCCA	1968
TGCAGGACCAGAGAATTCGAATA CATTCCGCTANNACGTATGCCA	1489	TGCAGGACCAGAGAATTCGAATA CAAGTATGCCNNACGTATGCCA	1729	TGCAGGACCAGAGAATTCGAATA CATACACGTGNNACGTATGCCA	1969
TGCAGGACCAGAGAATTCGAATA CAATTGCACGNNACGTATGCCA	1490	TGCAGGACCAGAGAATTCGAATA CATAGCAGCTNNACGTATGCCA	1730	TGCAGGACCAGAGAATTCGAATA CATAGTGTATNNACGTATGCCA	1970
TGCAGGACCAGAGAATTCGAATA CAATACCTAANNACGTATGCCA	1491	TGCAGGACCAGAGAATTCGAATA CACGCGTGACNNACGTATGCCA	1731	TGCAGGACCAGAGAATTCGAATA CACATTAGGCNNACGTATGCCA	1971
TGCAGGACCAGAGAATTCGAATA CAGGACCGGANNACGTATGCCA	1492	TGCAGGACCAGAGAATTCGAATA CAAAATACGANNACGTATGCCA	1732	TGCAGGACCAGAGAATTCGAATA CAACACCAANNACGTATGCCA	1972
TGCAGGACCAGAGAATTCGAATA CATGTCCCGCANNACGTATGCCA	1493	TGCAGGACCAGAGAATTCGAATA CACTAGATATNNACGTATGCCA	1733	TGCAGGACCAGAGAATTCGAATA CAGTGCGTCGNNACGTATGCCA	1973
TGCAGGACCAGAGAATTCGAATA CAGCCCCAGANNACGTATGCCA	1494	TGCAGGACCAGAGAATTCGAATA CAATGTTGGCANNACGTATGCCA	1734	TGCAGGACCAGAGAATTCGAATA CATATGTTTCNNACGTATGCCA	1974
TGCAGGACCAGAGAATTCGAATA CACAAAGCCGNNACGTATGCCA	1495	TGCAGGACCAGAGAATTCGAATA CACTACGCAANNACGTATGCCA	1735	TGCAGGACCAGAGAATTCGAATA CAGTGGTTCGNNACGTATGCCA	1975
TGCAGGACCAGAGAATTCGAATA CAGCCATTGANNACGTATGCCA	1496	TGCAGGACCAGAGAATTCGAATA CATTTCGTANNACGTATGCCA	1736	TGCAGGACCAGAGAATTCGAATA CACTGGACCGNNACGTATGCCA	1976
TGCAGGACCAGAGAATTCGAATA CATGAACACGNNACGTATGCCA	1497	TGCAGGACCAGAGAATTCGAATA CACCTCCCTCANNACGTATGCCA	1737	TGCAGGACCAGAGAATTCGAATA CAGGCGTGTGNNACGTATGCCA	1977
TGCAGGACCAGAGAATTCGAATA CAGAATCCGTTNNACGTATGCCA	1498	TGCAGGACCAGAGAATTCGAATA CAGACTTGACNNACGTATGCCA	1738	TGCAGGACCAGAGAATTCGAATA CAAGTCTAATNNACGTATGCCA	1978
TGCAGGACCAGAGAATTCGAATA CATTAATCGANNACGTATGCCA	1499	TGCAGGACCAGAGAATTCGAATA CAGTCATCGANNACGTATGCCA	1739	TGCAGGACCAGAGAATTCGAATA CACTCATGCTNNACGTATGCCA	1979
TGCAGGACCAGAGAATTCGAATA CACGCCACTCANNACGTATGCCA	1500	TGCAGGACCAGAGAATTCGAATA CAATCTAGTANNACGTATGCCA	1740	TGCAGGACCAGAGAATTCGAATA CAAGTTCTCCNNACGTATGCCA	1980
TGCAGGACCAGAGAATTCGAATA CACCCCTTAGTNNACGTATGCCA	1501	TGCAGGACCAGAGAATTCGAATA CACGAAGATGNNACGTATGCCA	1741	TGCAGGACCAGAGAATTCGAATA CAGTGAAGGTNNACGTATGCCA	1981
TGCAGGACCAGAGAATTCGAATA CATTTCTGNNACGTATGCCA	1502	TGCAGGACCAGAGAATTCGAATA CAATTTGCAANNACGTATGCCA	1742	TGCAGGACCAGAGAATTCGAATA CAGTTTTAAGNNACGTATGCCA	1982
TGCAGGACCAGAGAATTCGAATA CATTCACCGNNACGTATGCCA	1503	TGCAGGACCAGAGAATTCGAATA CAGACCGCTNNACGTATGCCA	1743	TGCAGGACCAGAGAATTCGAATA CAAAAGCAATNNACGTATGCCA	1983
TGCAGGACCAGAGAATTCGAATA CATTGAGGAGNNACGTATGCCA	1504	TGCAGGACCAGAGAATTCGAATA CACTTGTCACNNACGTATGCCA	1744	TGCAGGACCAGAGAATTCGAATA CATGAAGCGANNACGTATGCCA	1984
TGCAGGACCAGAGAATTCGAATA CATTCACGCTNNACGTATGCCA	1505	TGCAGGACCAGAGAATTCGAATA CACTCGTAAGNNACGTATGCCA	1745	TGCAGGACCAGAGAATTCGAATA CAGTAGTGCTNNACGTATGCCA	1985

FIG. 14C

Pool-7	SEQ ID NO:	Pool-8	SEQ ID NO:	Pool-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATCGCGGTGNNNACGTATGCCA	1506	TGCAGGACCAGAGAATTCGAATA CAGCCTTACTNNNACGTATGCCA	1746	TGCAGGACCAGAGAATTCGAATA CAACTATGTANNNACGTATGCCA	1986
TGCAGGACCAGAGAATTCGAATA CAAATTCGCGNNNACGTATGCCA	1507	TGCAGGACCAGAGAATTCGAATA CAGCATGTGTNNNACGTATGCCA	1747	TGCAGGACCAGAGAATTCGAATA CAGAAGTTCNNNACGTATGCCA	1987
TGCAGGACCAGAGAATTCGAATA CACGTGATGANNNACGTATGCCA	1508	TGCAGGACCAGAGAATTCGAATA CACTACTGTGNNNACGTATGCCA	1748	TGCAGGACCAGAGAATTCGAATA CACGGTGTGNNNACGTATGCCA	1988
TGCAGGACCAGAGAATTCGAATA CACGTTTATTNNNCTAGCGTTAC	1509	TGCAGGACCAGAGAATTCGAATA CAATCTAACANNNCTAGCGTTAC	1749	TGCAGGACCAGAGAATTCGAATA CATGCAAATTNNNCTAGCGTTAC	1989
TGCAGGACCAGAGAATTCGAATA CACTGCAACGNNNCTAGCGTTAC	1510	TGCAGGACCAGAGAATTCGAATA CAACGATTGCGNNNCTAGCGTTAC	1750	TGCAGGACCAGAGAATTCGAATA CAACTTGTGNNNCTAGCGTTAC	1990
TGCAGGACCAGAGAATTCGAATA CAACCTTGTGNNNCTAGCGTTAC	1511	TGCAGGACCAGAGAATTCGAATA CAAAACCTTANNNCTAGCGTTAC	1751	TGCAGGACCAGAGAATTCGAATA CATCGCTGCCNNNCTAGCGTTAC	1991
TGCAGGACCAGAGAATTCGAATA CATCCACCCGNNNCTAGCGTTAC	1512	TGCAGGACCAGAGAATTCGAATA CACGTAAAAANNNCTAGCGTTAC	1752	TGCAGGACCAGAGAATTCGAATA CATCCCTTCTNNNCTAGCGTTAC	1992
TGCAGGACCAGAGAATTCGAATA CAAAGGCCGNNNCTAGCGTTAC	1513	TGCAGGACCAGAGAATTCGAATA CATCTGAGACNNNCTAGCGTTAC	1753	TGCAGGACCAGAGAATTCGAATA CACGGTACTANNNCTAGCGTTAC	1993
TGCAGGACCAGAGAATTCGAATA CAGGCAATAGNNNCTAGCGTTAC	1514	TGCAGGACCAGAGAATTCGAATA CATGGCGATTNNNCTAGCGTTAC	1754	TGCAGGACCAGAGAATTCGAATA CAAGATATCTNNNCTAGCGTTAC	1994
TGCAGGACCAGAGAATTCGAATA CACGCTAGCGNNNCTAGCGTTAC	1515	TGCAGGACCAGAGAATTCGAATA CACATCTTGCGNNNCTAGCGTTAC	1755	TGCAGGACCAGAGAATTCGAATA CACTCAAGTGNNNCTAGCGTTAC	1995
TGCAGGACCAGAGAATTCGAATA CATGTTCTATNNNCTAGCGTTAC	1516	TGCAGGACCAGAGAATTCGAATA CATCTTTCGNNNCTAGCGTTAC	1756	TGCAGGACCAGAGAATTCGAATA CAACCTCTANNNCTAGCGTTAC	1996
TGCAGGACCAGAGAATTCGAATA CATTAATATANNNCTAGCGTTAC	1517	TGCAGGACCAGAGAATTCGAATA CAGCGAACAANNNCTAGCGTTAC	1757	TGCAGGACCAGAGAATTCGAATA CAAGCAATTTNNNCTAGCGTTAC	1997
TGCAGGACCAGAGAATTCGAATA CAATATGGTTNNNCTAGCGTTAC	1518	TGCAGGACCAGAGAATTCGAATA CAGAGTAGACNNNCTAGCGTTAC	1758	TGCAGGACCAGAGAATTCGAATA CAGCCCCGAANNNCTAGCGTTAC	1998
TGCAGGACCAGAGAATTCGAATA CAGCTGGTTANNNCTAGCGTTAC	1519	TGCAGGACCAGAGAATTCGAATA CACTCATGGAANNNCTAGCGTTAC	1759	TGCAGGACCAGAGAATTCGAATA CACCAAATCGNNNCTAGCGTTAC	1999
TGCAGGACCAGAGAATTCGAATA CAAGACTGAGNNNCTAGCGTTAC	1520	TGCAGGACCAGAGAATTCGAATA CATTCCCGCGNNNCTAGCGTTAC	1760	TGCAGGACCAGAGAATTCGAATA CAGATCGGTTNNNCTAGCGTTAC	2000
TGCAGGACCAGAGAATTCGAATA CAGACTTGCANNNCTAGCGTTAC	1521	TGCAGGACCAGAGAATTCGAATA CATGGCCTAANNNCTAGCGTTAC	1761	TGCAGGACCAGAGAATTCGAATA CAACCCCTGCGNNNCTAGCGTTAC	2001
TGCAGGACCAGAGAATTCGAATA CAGTCTATCCNNNCTAGCGTTAC	1522	TGCAGGACCAGAGAATTCGAATA CAAGCGCAAANNNCTAGCGTTAC	1762	TGCAGGACCAGAGAATTCGAATA CAACCCACTTNNNCTAGCGTTAC	2002
TGCAGGACCAGAGAATTCGAATA CAAGCTATCGNNNCTAGCGTTAC	1523	TGCAGGACCAGAGAATTCGAATA CAATAGAAACNNNCTAGCGTTAC	1763	TGCAGGACCAGAGAATTCGAATA CAAGACCTTGNNNCTAGCGTTAC	2003
TGCAGGACCAGAGAATTCGAATA CAGGCGAACGNNNCTAGCGTTAC	1524	TGCAGGACCAGAGAATTCGAATA CATCGGTGCGNNNCTAGCGTTAC	1764	TGCAGGACCAGAGAATTCGAATA CACCTTGATCINNCTAGCGTTAC	2004
TGCAGGACCAGAGAATTCGAATA CAACGAATGNNNCTAGCGTTAC	1525	TGCAGGACCAGAGAATTCGAATA CAGTGCTGCGNNNCTAGCGTTAC	1765	TGCAGGACCAGAGAATTCGAATA CAAAGTATTNNNCTAGCGTTAC	2005
TGCAGGACCAGAGAATTCGAATA CATCATGCTCINNCTAGCGTTAC	1526	TGCAGGACCAGAGAATTCGAATA CAAATGCCACNNNCTAGCGTTAC	1766	TGCAGGACCAGAGAATTCGAATA CACATCCAAGNNNCTAGCGTTAC	2006
TGCAGGACCAGAGAATTCGAATA CATTGCTTATNNNCTAGCGTTAC	1527	TGCAGGACCAGAGAATTCGAATA CAATCACGTGNNNCTAGCGTTAC	1767	TGCAGGACCAGAGAATTCGAATA CACACAAGTCINNCTAGCGTTAC	2007
TGCAGGACCAGAGAATTCGAATA CAAAGCCAGANNNCTAGCGTTAC	1528	TGCAGGACCAGAGAATTCGAATA CATCACGACANNNCTAGCGTTAC	1768	TGCAGGACCAGAGAATTCGAATA CATAAAAATGNNNCTAGCGTTAC	2008
TGCAGGACCAGAGAATTCGAATA CAGCAGCTCGNNNCTAGCGTTAC	1529	TGCAGGACCAGAGAATTCGAATA CATGTTACGNNNCTAGCGTTAC	1769	TGCAGGACCAGAGAATTCGAATA CAATCTACAANNNCTAGCGTTAC	2009
TGCAGGACCAGAGAATTCGAATA CACCGAGTCGNNNCTAGCGTTAC	1530	TGCAGGACCAGAGAATTCGAATA CATTACCGCTNNNCTAGCGTTAC	1770	TGCAGGACCAGAGAATTCGAATA CAGCGAGAATNNNCTAGCGTTAC	2010
TGCAGGACCAGAGAATTCGAATA CAAACAGACGNNNCTAGCGTTAC	1531	TGCAGGACCAGAGAATTCGAATA CACCCCTTTAGNNNCTAGCGTTAC	1771	TGCAGGACCAGAGAATTCGAATA CAGTAGCCATNNNCTAGCGTTAC	2011
TGCAGGACCAGAGAATTCGAATA CACCCAAACANNNCTAGCGTTAC	1532	TGCAGGACCAGAGAATTCGAATA CAGTCTTGAGNNNCTAGCGTTAC	1772	TGCAGGACCAGAGAATTCGAATA CAAAGGCAGTNNNCTAGCGTTAC	2012
TGCAGGACCAGAGAATTCGAATA CAAAGGCGATNNNCTAGCGTTAC	1533	TGCAGGACCAGAGAATTCGAATA CACTTTGACNNNCTAGCGTTAC	1773	TGCAGGACCAGAGAATTCGAATA CAGTAGACTCINNCTAGCGTTAC	2013
TGCAGGACCAGAGAATTCGAATA CACCTTAAAAANNNCTAGCGTTAC	1534	TGCAGGACCAGAGAATTCGAATA CACTTCTCAGNNNCTAGCGTTAC	1774	TGCAGGACCAGAGAATTCGAATA CAGGTATGCTNNNCTAGCGTTAC	2014

FIG. 14D

Pool-7	SEQ ID NO:	Pool-8	SEQ ID NO:	Pool-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACATACCTCNNNCTAGCGTTAC	1535	TGCAGGACCAGAGAATTCGAATA CATGTTGCAGNNNCTAGCGTTAC	1775	TGCAGGACCAGAGAATTCGAATA CAGGTTTTAANNNCTAGCGTTAC	2015
TGCAGGACCAGAGAATTCGAATA CAGCCAATCANNNCTAGCGTTAC	1536	TGCAGGACCAGAGAATTCGAATA CAAACCCAAANNNCTAGCGTTAC	1776	TGCAGGACCAGAGAATTCGAATA CAACAGAAGCANNNCTAGCGTTAC	2016
TGCAGGACCAGAGAATTCGAATA CACTTAGGCCANNNCTAGCGTTAC	1537	TGCAGGACCAGAGAATTCGAATA CATAAGCACCNNNCTAGCGTTAC	1777	TGCAGGACCAGAGAATTCGAATA CACAGCACGCNNNCTAGCGTTAC	2017
TGCAGGACCAGAGAATTCGAATA CAGCGACCAGNNNCTAGCGTTAC	1538	TGCAGGACCAGAGAATTCGAATA CAGATGTAAANNNCTAGCGTTAC	1778	TGCAGGACCAGAGAATTCGAATA CAACCGTAACNNNCTAGCGTTAC	2018
TGCAGGACCAGAGAATTCGAATA CATTCOCGTANNNCTAGCGTTAC	1539	TGCAGGACCAGAGAATTCGAATA CAGTTATGCGNNNCTAGCGTTAC	1779	TGCAGGACCAGAGAATTCGAATA CAGGAAGCCGNNNCTAGCGTTAC	2019
TGCAGGACCAGAGAATTCGAATA CATTCAGAATNNNCTAGCGTTAC	1540	TGCAGGACCAGAGAATTCGAATA CAGCGCGGAANNNCTAGCGTTAC	1780	TGCAGGACCAGAGAATTCGAATA CAGAGGATCANNNCTAGCGTTAC	2020
TGCAGGACCAGAGAATTCGAATA CAGGCATTACNNNCTAGCGTTAC	1541	TGCAGGACCAGAGAATTCGAATA CAAGATTGTNNNCTAGCGTTAC	1781	TGCAGGACCAGAGAATTCGAATA CACGGTTCCGNNNCTAGCGTTAC	2021
TGCAGGACCAGAGAATTCGAATA CAAACCAAAANNNCTAGCGTTAC	1542	TGCAGGACCAGAGAATTCGAATA CACACAGCTANNNCTAGCGTTAC	1782	TGCAGGACCAGAGAATTCGAATA CAATCCACAGNNNCTAGCGTTAC	2022
TGCAGGACCAGAGAATTCGAATA CAACGCTGTANNNCTAGCGTTAC	1543	TGCAGGACCAGAGAATTCGAATA CAACGGCAGGNNNCTAGCGTTAC	1783	TGCAGGACCAGAGAATTCGAATA CAGAGACCCNNNCTAGCGTTAC	2023
TGCAGGACCAGAGAATTCGAATA CAACGATCTGNNNCTAGCGTTAC	1544	TGCAGGACCAGAGAATTCGAATA CATACGGGAAGNNNCTAGCGTTAC	1784	TGCAGGACCAGAGAATTCGAATA CACTCCGGAGNNNCTAGCGTTAC	2024
TGCAGGACCAGAGAATTCGAATA CAGCATGAGANNNCTAGCGTTAC	1545	TGCAGGACCAGAGAATTCGAATA CACTCGATGANNNCTAGCGTTAC	1785	TGCAGGACCAGAGAATTCGAATA CATCGCCTCGNNNCTAGCGTTAC	2025
TGCAGGACCAGAGAATTCGAATA CAGTAAGTCCNNNCTAGCGTTAC	1546	TGCAGGACCAGAGAATTCGAATA CATCCCCCTNNNCTAGCGTTAC	1786	TGCAGGACCAGAGAATTCGAATA CATCATTCGNNNCTAGCGTTAC	2026
TGCAGGACCAGAGAATTCGAATA CAAAGCGAGTNNNCTAGCGTTAC	1547	TGCAGGACCAGAGAATTCGAATA CACCATCTACNNNCTAGCGTTAC	1787	TGCAGGACCAGAGAATTCGAATA CAGAACTACNNNCTAGCGTTAC	2027
TGCAGGACCAGAGAATTCGAATA CAAGATCTGCNNNCTAGCGTTAC	1548	TGCAGGACCAGAGAATTCGAATA CAAAGCAGGTNNNCTAGCGTTAC	1788	TGCAGGACCAGAGAATTCGAATA CATAATTTTNNNCTAGCGTTAC	2028
TGCAGGACCAGAGAATTCGAATA CACCCTGCACNNNCTAGCGTTAC	1549	TGCAGGACCAGAGAATTCGAATA CAAAGTCAAANNNCTAGCGTTAC	1789	TGCAGGACCAGAGAATTCGAATA CAGATTGTGCNNNCTAGCGTTAC	2029
TGCAGGACCAGAGAATTCGAATA CATCCTCGCGNNNCTAGCGTTAC	1550	TGCAGGACCAGAGAATTCGAATA CAATTTCGACGNNNCTAGCGTTAC	1790	TGCAGGACCAGAGAATTCGAATA CATGGCGCACNNNCTAGCGTTAC	2030
TGCAGGACCAGAGAATTCGAATA CACATGTGANNNCTAGCGTTAC	1551	TGCAGGACCAGAGAATTCGAATA CAACCAGCCGNNNCTAGCGTTAC	1791	TGCAGGACCAGAGAATTCGAATA CAAAATCAGANNNCTAGCGTTAC	2031
TGCAGGACCAGAGAATTCGAATA CAAACGGTTCNNNCTAGCGTTAC	1552	TGCAGGACCAGAGAATTCGAATA CATAGTCGGTNNNCTAGCGTTAC	1792	TGCAGGACCAGAGAATTCGAATA CAAGGCTATCANNNCTAGCGTTAC	2032
TGCAGGACCAGAGAATTCGAATA CACCCTCAATTNNNCTAGCGTTAC	1553	TGCAGGACCAGAGAATTCGAATA CATGCGCATANNNCTAGCGTTAC	1793	TGCAGGACCAGAGAATTCGAATA CATCTTGTGCNNNCTAGCGTTAC	2033
TGCAGGACCAGAGAATTCGAATA CAACCGTTCTNNNCTAGCGTTAC	1554	TGCAGGACCAGAGAATTCGAATA CATAGAACCNNNCTAGCGTTAC	1794	TGCAGGACCAGAGAATTCGAATA CACCATTCCANNNCTAGCGTTAC	2034
TGCAGGACCAGAGAATTCGAATA CAACTCTAAANNNCTAGCGTTAC	1555	TGCAGGACCAGAGAATTCGAATA CAGGTTTGTGNNNCTAGCGTTAC	1795	TGCAGGACCAGAGAATTCGAATA CATAGATTACNNNCTAGCGTTAC	2035
TGCAGGACCAGAGAATTCGAATA CAATGAGCTCNNNCTAGCGTTAC	1556	TGCAGGACCAGAGAATTCGAATA CAAAGTTTGTNNNCTAGCGTTAC	1796	TGCAGGACCAGAGAATTCGAATA CAGTTTGCTCNNNCTAGCGTTAC	2036
TGCAGGACCAGAGAATTCGAATA CATCTAAGGCNNNCTAGCGTTAC	1557	TGCAGGACCAGAGAATTCGAATA CATTAGCGACNNNCTAGCGTTAC	1797	TGCAGGACCAGAGAATTCGAATA CATCTTCGGTNNNCTAGCGTTAC	2037
TGCAGGACCAGAGAATTCGAATA CACAATAGCCNNNCTAGCGTTAC	1558	TGCAGGACCAGAGAATTCGAATA CAGATATATCANNNCTAGCGTTAC	1798	TGCAGGACCAGAGAATTCGAATA CAAGTAGTCCNNNCTAGCGTTAC	2038
TGCAGGACCAGAGAATTCGAATA CATCTTGCGTNNNCTAGCGTTAC	1559	TGCAGGACCAGAGAATTCGAATA CAAACCTGTGCNNNCTAGCGTTAC	1799	TGCAGGACCAGAGAATTCGAATA CACGGTGTATNNNCTAGCGTTAC	2039
TGCAGGACCAGAGAATTCGAATA CACAAGAGCANNNCTAGCGTTAC	1560	TGCAGGACCAGAGAATTCGAATA CACGAATGGANNNCTAGCGTTAC	1800	TGCAGGACCAGAGAATTCGAATA CACTGTTTGCNNNCTAGCGTTAC	2040
TGCAGGACCAGAGAATTCGAATA CAGCTTGGATNNNCTAGCGTTAC	1561	TGCAGGACCAGAGAATTCGAATA CACTTCGTTGNNNCTAGCGTTAC	1801	TGCAGGACCAGAGAATTCGAATA CAAACGTTGCNNNCTAGCGTTAC	2041
TGCAGGACCAGAGAATTCGAATA CACTAAATACNNNCTAGCGTTAC	1562	TGCAGGACCAGAGAATTCGAATA CATCGTGGTANNNCTAGCGTTAC	1802	TGCAGGACCAGAGAATTCGAATA CAATAAATGNNNCTAGCGTTAC	2042
TGCAGGACCAGAGAATTCGAATA CACCTAAAAANNNCTAGCGTTAC	1563	TGCAGGACCAGAGAATTCGAATA CAGCAAAATANNNCTAGCGTTAC	1803	TGCAGGACCAGAGAATTCGAATA CAACGCGTGCNNNCTAGCGTTAC	2043

FIG. 14E

Pool-7	SEQ ID NO:	Pool-8	SEQ ID NO:	Pool-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAGAACCTCANNCTAGCGTTAC	1564	TGCAGGACCAGAGAATTCGAATA CAAGACTAAANNCTAGCGTTAC	1804	TGCAGGACCAGAGAATTCGAATA CACGTTGGTANNCTAGCGTTAC	2044
TGCAGGACCAGAGAATTCGAATA CAGAGGCCTCNNCTAGCGTTAC	1565	TGCAGGACCAGAGAATTCGAATA CATGCGAGTTNNCTAGCGTTAC	1805	TGCAGGACCAGAGAATTCGAATA CAAGGCGTAANNCTAGCGTTAC	2045
TGCAGGACCAGAGAATTCGAATA CAAGGTGATGNNCTAGCGTTAC	1566	TGCAGGACCAGAGAATTCGAATA CAGTCTGAGNNCTAGCGTTAC	1806	TGCAGGACCAGAGAATTCGAATA CATGCCTATCNNCTAGCGTTAC	2046
TGCAGGACCAGAGAATTCGAATA CAACGCGTTANNCTAGCGTTAC	1567	TGCAGGACCAGAGAATTCGAATA CATCGGCGTGNNCTAGCGTTAC	1807	TGCAGGACCAGAGAATTCGAATA CAAAAGCTCCNNCTAGCGTTAC	2047
TGCAGGACCAGAGAATTCGAATA CAGGTGCTCNNCTAGCGTTAC	1568	TGCAGGACCAGAGAATTCGAATA CAGATCCGGCNNCTAGCGTTAC	1808	TGCAGGACCAGAGAATTCGAATA CAAGGACGATNNCTAGCGTTAC	2048
TGCAGGACCAGAGAATTCGAATA CAGAGATCAGNNNGATCGACATG	1569	TGCAGGACCAGAGAATTCGAATA CAGTGTATGNNNGATCGACATG	1809	TGCAGGACCAGAGAATTCGAATA CACTTGAAGCNNNGATCGACATG	2049
TGCAGGACCAGAGAATTCGAATA CATACGTGTGNNNGATCGACATG	1570	TGCAGGACCAGAGAATTCGAATA CAAGTATTTGNNNGATCGACATG	1810	TGCAGGACCAGAGAATTCGAATA CATGCCCTCGNNNGATCGACATG	2050
TGCAGGACCAGAGAATTCGAATA CAAGTTATCANNNGATCGACATG	1571	TGCAGGACCAGAGAATTCGAATA CAAGTAAACNNNGATCGACATG	1811	TGCAGGACCAGAGAATTCGAATA CAAGCGAAACNNNGATCGACATG	2051
TGCAGGACCAGAGAATTCGAATA CACAGTGATCANNNGATCGACATG	1572	TGCAGGACCAGAGAATTCGAATA CAAGCCACCGNNNGATCGACATG	1812	TGCAGGACCAGAGAATTCGAATA CATAGAGTGGNNNGATCGACATG	2052
TGCAGGACCAGAGAATTCGAATA CATACGCGGNNNGATCGACATG	1573	TGCAGGACCAGAGAATTCGAATA CAAAGTGTCCNNNGATCGACATG	1813	TGCAGGACCAGAGAATTCGAATA CAAGCAGCAANNNGATCGACATG	2053
TGCAGGACCAGAGAATTCGAATA CAGTGTGTACNNNGATCGACATG	1574	TGCAGGACCAGAGAATTCGAATA CACTATTTGTNNNGATCGACATG	1814	TGCAGGACCAGAGAATTCGAATA CACCTATTATNNNGATCGACATG	2054
TGCAGGACCAGAGAATTCGAATA CAGTGTTTAANNNGATCGACATG	1575	TGCAGGACCAGAGAATTCGAATA CAGTGTATCGNNNGATCGACATG	1815	TGCAGGACCAGAGAATTCGAATA CAGCGACGAGNNNGATCGACATG	2055
TGCAGGACCAGAGAATTCGAATA CAGCTCTACTNNNGATCGACATG	1576	TGCAGGACCAGAGAATTCGAATA CAATAGTATCANNNGATCGACATG	1816	TGCAGGACCAGAGAATTCGAATA CAACGATTTANNNGATCGACATG	2056
TGCAGGACCAGAGAATTCGAATA CATTGTGCTCANNNGATCGACATG	1577	TGCAGGACCAGAGAATTCGAATA CACCCTGAGNNNGATCGACATG	1817	TGCAGGACCAGAGAATTCGAATA CAAATTGTTGNNNGATCGACATG	2057
TGCAGGACCAGAGAATTCGAATA CATATAAGCTNNNGATCGACATG	1578	TGCAGGACCAGAGAATTCGAATA CATTATTTTANNNGATCGACATG	1818	TGCAGGACCAGAGAATTCGAATA CACATTAAGTNNNGATCGACATG	2058
TGCAGGACCAGAGAATTCGAATA CAAGAACGACNNNGATCGACATG	1579	TGCAGGACCAGAGAATTCGAATA CAACAAGACGNNNGATCGACATG	1819	TGCAGGACCAGAGAATTCGAATA CAGACGGAGCANNNGATCGACATG	2059
TGCAGGACCAGAGAATTCGAATA CATACGATATNNNGATCGACATG	1580	TGCAGGACCAGAGAATTCGAATA CATAAGTATCANNNGATCGACATG	1820	TGCAGGACCAGAGAATTCGAATA CACCAGATAGTNNNGATCGACATG	2060
TGCAGGACCAGAGAATTCGAATA CATAAACCTANNNGATCGACATG	1581	TGCAGGACCAGAGAATTCGAATA CAGGCACACNNNGATCGACATG	1821	TGCAGGACCAGAGAATTCGAATA CAAGTATTTGNNNGATCGACATG	2061
TGCAGGACCAGAGAATTCGAATA CATAACGTTANNNGATCGACATG	1582	TGCAGGACCAGAGAATTCGAATA CAGTACCTCTNNNGATCGACATG	1822	TGCAGGACCAGAGAATTCGAATA CATTTCGGCTNNNGATCGACATG	2062
TGCAGGACCAGAGAATTCGAATA CAGCACGTGANNNGATCGACATG	1583	TGCAGGACCAGAGAATTCGAATA CACTGTGATGNNNGATCGACATG	1823	TGCAGGACCAGAGAATTCGAATA CAGTAGACAGNNNGATCGACATG	2063
TGCAGGACCAGAGAATTCGAATA CACCCTCGACNNNGATCGACATG	1584	TGCAGGACCAGAGAATTCGAATA CAACAAGGACNNNGATCGACATG	1824	TGCAGGACCAGAGAATTCGAATA CAACGAAGTGNNNGATCGACATG	2064
TGCAGGACCAGAGAATTCGAATA CATTGTCATCCNNNGATCGACATG	1585	TGCAGGACCAGAGAATTCGAATA CAAGAGGCTANNNGATCGACATG	1825	TGCAGGACCAGAGAATTCGAATA CACGTCTTTGNNNGATCGACATG	2065
TGCAGGACCAGAGAATTCGAATA CATCAACTGGNNNGATCGACATG	1586	TGCAGGACCAGAGAATTCGAATA CAATTGAGTTNNNGATCGACATG	1826	TGCAGGACCAGAGAATTCGAATA CAACACAGGANNNGATCGACATG	2066
TGCAGGACCAGAGAATTCGAATA CAATTGCCCTNNNGATCGACATG	1587	TGCAGGACCAGAGAATTCGAATA CACGTTCTCANNNGATCGACATG	1827	TGCAGGACCAGAGAATTCGAATA CAGGTCACTANNNGATCGACATG	2067
TGCAGGACCAGAGAATTCGAATA CATACATGTANNNGATCGACATG	1588	TGCAGGACCAGAGAATTCGAATA CAGGTAGCTTNNNGATCGACATG	1828	TGCAGGACCAGAGAATTCGAATA CAGAACGAACNNNGATCGACATG	2068
TGCAGGACCAGAGAATTCGAATA CAGACTTGGTNNNGATCGACATG	1589	TGCAGGACCAGAGAATTCGAATA CATCCTTGTGNNNGATCGACATG	1829	TGCAGGACCAGAGAATTCGAATA CACCTAACTCANNNGATCGACATG	2069
TGCAGGACCAGAGAATTCGAATA CAGTCCCATTTNNNGATCGACATG	1590	TGCAGGACCAGAGAATTCGAATA CAGCCGACACNNNGATCGACATG	1830	TGCAGGACCAGAGAATTCGAATA CAAGAGCTTTNNNGATCGACATG	2070
TGCAGGACCAGAGAATTCGAATA CAAGATGGTNNNGATCGACATG	1591	TGCAGGACCAGAGAATTCGAATA CAACTAGAGGNNNGATCGACATG	1831	TGCAGGACCAGAGAATTCGAATA CAGGACATCTNNNGATCGACATG	2071
TGCAGGACCAGAGAATTCGAATA CAGACACAGANNNGATCGACATG	1592	TGCAGGACCAGAGAATTCGAATA CAACAGTCGTNNNGATCGACATG	1832	TGCAGGACCAGAGAATTCGAATA CAGGCGTAAANNNGATCGACATG	2072

FIG. 14F

Pool-7	SEQ ID NO:	Pool-8	SEQ ID NO:	Pool-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACGCGTTTTNNNGATCGACATG	1593	TGCAGGACCAGAGAATTCGAATA CACGAGGCGANNNGATCGACATG	1833	TGCAGGACCAGAGAATTCGAATA CAGTACCAGTNNNGATCGACATG	2073
TGCAGGACCAGAGAATTCGAATA CACCCAGAGCANNNGATCGACATG	1594	TGCAGGACCAGAGAATTCGAATA CAACCGAAAGNNNGATCGACATG	1834	TGCAGGACCAGAGAATTCGAATA CAGAATTTACNNNGATCGACATG	2074
TGCAGGACCAGAGAATTCGAATA CACGCAGCTGNNNGATCGACATG	1595	TGCAGGACCAGAGAATTCGAATA CAGTTTGAGCANNNGATCGACATG	1835	TGCAGGACCAGAGAATTCGAATA CAACACCCANNNGATCGACATG	2075
TGCAGGACCAGAGAATTCGAATA CACTTTGGCTNNNGATCGACATG	1596	TGCAGGACCAGAGAATTCGAATA CAGTATGCGTNNNGATCGACATG	1836	TGCAGGACCAGAGAATTCGAATA CAAGTTATTGNNNGATCGACATG	2076
TGCAGGACCAGAGAATTCGAATA CAGTTGATCGNNNGATCGACATG	1597	TGCAGGACCAGAGAATTCGAATA CAATGTAACTNNNGATCGACATG	1837	TGCAGGACCAGAGAATTCGAATA CACTTCTTTNNNGATCGACATG	2077
TGCAGGACCAGAGAATTCGAATA CAGTGAAGTGNNGATCGACATG	1598	TGCAGGACCAGAGAATTCGAATA CAAGACGTAGNNNGATCGACATG	1838	TGCAGGACCAGAGAATTCGAATA CAGAGCTCCGNNNGATCGACATG	2078
TGCAGGACCAGAGAATTCGAATA CACACGTTGANNNGATCGACATG	1599	TGCAGGACCAGAGAATTCGAATA CATTTGGCGCANNNGATCGACATG	1839	TGCAGGACCAGAGAATTCGAATA CAGAACCCCGNNNGATCGACATG	2079
TGCAGGACCAGAGAATTCGAATA CACAATCCAGNNNGATCGACATG	1600	TGCAGGACCAGAGAATTCGAATA CAGGACTCATNNNGATCGACATG	1840	TGCAGGACCAGAGAATTCGAATA CAATTGTGATNNNGATCGACATG	2080
TGCAGGACCAGAGAATTCGAATA CAGCGCAGAGNNNGATCGACATG	1601	TGCAGGACCAGAGAATTCGAATA CAGTCCGGTGNNGATCGACATG	1841	TGCAGGACCAGAGAATTCGAATA CAAGTTCTTTNNNGATCGACATG	2081
TGCAGGACCAGAGAATTCGAATA CACTCTGATCANNNGATCGACATG	1602	TGCAGGACCAGAGAATTCGAATA CAGCAAGCCCGNNNGATCGACATG	1842	TGCAGGACCAGAGAATTCGAATA CAGCACGGTCNNNGATCGACATG	2082
TGCAGGACCAGAGAATTCGAATA CATATGCCAGNNNGATCGACATG	1603	TGCAGGACCAGAGAATTCGAATA CAAGCATGGANNNGATCGACATG	1843	TGCAGGACCAGAGAATTCGAATA CAGTATCCCTNNNGATCGACATG	2083
TGCAGGACCAGAGAATTCGAATA CAGTTGGTCANNNGATCGACATG	1604	TGCAGGACCAGAGAATTCGAATA CAAGCAGCCCGNNNGATCGACATG	1844	TGCAGGACCAGAGAATTCGAATA CAGCAAGTGANNNGATCGACATG	2084
TGCAGGACCAGAGAATTCGAATA CACCTCTCGGNNNGATCGACATG	1605	TGCAGGACCAGAGAATTCGAATA CAATCTCTATNNNGATCGACATG	1845	TGCAGGACCAGAGAATTCGAATA CATAAGATAGNNNGATCGACATG	2085
TGCAGGACCAGAGAATTCGAATA CATGGTACACNNNGATCGACATG	1606	TGCAGGACCAGAGAATTCGAATA CATAATGCCGNNNGATCGACATG	1846	TGCAGGACCAGAGAATTCGAATA CAGCAATCTGNNNGATCGACATG	2086
TGCAGGACCAGAGAATTCGAATA CACCTCGGCTNNNGATCGACATG	1607	TGCAGGACCAGAGAATTCGAATA CACAGGCGGANNNGATCGACATG	1847	TGCAGGACCAGAGAATTCGAATA CACTGCCAGGNNNGATCGACATG	2087
TGCAGGACCAGAGAATTCGAATA CAGCGACGANNNGATCGACATG	1608	TGCAGGACCAGAGAATTCGAATA CAGCGAATGANNNGATCGACATG	1848	TGCAGGACCAGAGAATTCGAATA CAGGTTTATANNNGATCGACATG	2088
TGCAGGACCAGAGAATTCGAATA CACCCCTGATTNNNGATCGACATG	1609	TGCAGGACCAGAGAATTCGAATA CAAGCGTACTNNNGATCGACATG	1849	TGCAGGACCAGAGAATTCGAATA CAAACCTTGGNNNGATCGACATG	2089
TGCAGGACCAGAGAATTCGAATA CAATTCTCTANNNGATCGACATG	1610	TGCAGGACCAGAGAATTCGAATA CACCCAGGCAANNNGATCGACATG	1850	TGCAGGACCAGAGAATTCGAATA CACCAACGCGNNNGATCGACATG	2090
TGCAGGACCAGAGAATTCGAATA CACTGTCAAGNNNGATCGACATG	1611	TGCAGGACCAGAGAATTCGAATA CAGGCCCTGTGNNNGATCGACATG	1851	TGCAGGACCAGAGAATTCGAATA CATGGAAGACNNNGATCGACATG	2091
TGCAGGACCAGAGAATTCGAATA CAATTACCGGNNNGATCGACATG	1612	TGCAGGACCAGAGAATTCGAATA CACCTAGGCGNNNGATCGACATG	1852	TGCAGGACCAGAGAATTCGAATA CAATTGAAGANNNGATCGACATG	2092
TGCAGGACCAGAGAATTCGAATA CATAATATCGNNNGATCGACATG	1613	TGCAGGACCAGAGAATTCGAATA CACCGTTTTGNNNGATCGACATG	1853	TGCAGGACCAGAGAATTCGAATA CATTTTCACANNNGATCGACATG	2093
TGCAGGACCAGAGAATTCGAATA CAATAGACTTNNNGATCGACATG	1614	TGCAGGACCAGAGAATTCGAATA CAGACGCACCGNNNGATCGACATG	1854	TGCAGGACCAGAGAATTCGAATA CAACGAACTCANNNGATCGACATG	2094
TGCAGGACCAGAGAATTCGAATA CACCTGATACGNNNGATCGACATG	1615	TGCAGGACCAGAGAATTCGAATA CAACTTATGANNNGATCGACATG	1855	TGCAGGACCAGAGAATTCGAATA CAAGGCCGTGNNNGATCGACATG	2095
TGCAGGACCAGAGAATTCGAATA CAGCCGCACANNNGATCGACATG	1616	TGCAGGACCAGAGAATTCGAATA CAAGATCAAANNNGATCGACATG	1856	TGCAGGACCAGAGAATTCGAATA CATTGGAGCTNNNGATCGACATG	2096
TGCAGGACCAGAGAATTCGAATA CACGAATATTNNNGATCGACATG	1617	TGCAGGACCAGAGAATTCGAATA CATACTTCCGNNNGATCGACATG	1857	TGCAGGACCAGAGAATTCGAATA CAACAGACAGNNNGATCGACATG	2097
TGCAGGACCAGAGAATTCGAATA CAGTCAATCGNNNGATCGACATG	1618	TGCAGGACCAGAGAATTCGAATA CACGTTAGACNNNGATCGACATG	1858	TGCAGGACCAGAGAATTCGAATA CAATCGTCAGNNNGATCGACATG	2098
TGCAGGACCAGAGAATTCGAATA CATCAGCCCCNNNGATCGACATG	1619	TGCAGGACCAGAGAATTCGAATA CAGGAGTTAGNNNGATCGACATG	1859	TGCAGGACCAGAGAATTCGAATA CATTATGCTNNNGATCGACATG	2099
TGCAGGACCAGAGAATTCGAATA CAGGAGTTCTNNNGATCGACATG	1620	TGCAGGACCAGAGAATTCGAATA CAGACCTCTTNNNGATCGACATG	1860	TGCAGGACCAGAGAATTCGAATA CAGTCACGATNNNGATCGACATG	2100
TGCAGGACCAGAGAATTCGAATA CAGTGAATCCNNNGATCGACATG	1621	TGCAGGACCAGAGAATTCGAATA CAGCCCCGAANNNGATCGACATG	1861	TGCAGGACCAGAGAATTCGAATA CACATTCTGNNNGATCGACATG	2101

FIG. 14G

Pool-7	SEQ ID NO:	Pool-8	SEQ ID NO:	Pool-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAACGATTATNNNGATCGACATG	1622	TGCAGGACCAGAGAATTCGAATA CAGAAGCCATNNNGATCGACATG	1862	TGCAGGACCAGAGAATTCGAATA CAGAAAACTNNNGATCGACATG	2102
TGCAGGACCAGAGAATTCGAATA CACAATCCGANNGATCGACATG	1623	TGCAGGACCAGAGAATTCGAATA CAOCCACTGCCNNNGATCGACATG	1863	TGCAGGACCAGAGAATTCGAATA CATCGTCGTTNNNGATCGACATG	2103
TGCAGGACCAGAGAATTCGAATA CAGGCAATGANNNNGATCGACATG	1624	TGCAGGACCAGAGAATTCGAATA CACTAAATTTNNNGATCGACATG	1864	TGCAGGACCAGAGAATTCGAATA CAATTGTGCCNNNGATCGACATG	2104
TGCAGGACCAGAGAATTCGAATA CACTGTCCAGNNNGATCGACATG	1625	TGCAGGACCAGAGAATTCGAATA CACGGTCCAGNNNGATCGACATG	1865	TGCAGGACCAGAGAATTCGAATA CAACTGGACTNNNGATCGACATG	2105
TGCAGGACCAGAGAATTCGAATA CACAGACCTANNNNGATCGACATG	1626	TGCAGGACCAGAGAATTCGAATA CATTTCGCACNNNGATCGACATG	1866	TGCAGGACCAGAGAATTCGAATA CACGTTGTTNNNGATCGACATG	2106
TGCAGGACCAGAGAATTCGAATA CAGATCATCGNNNGATCGACATG	1627	TGCAGGACCAGAGAATTCGAATA CAGGATAAGCNNNGATCGACATG	1867	TGCAGGACCAGAGAATTCGAATA CACAAGACCTNNNGATCGACATG	2107
TGCAGGACCAGAGAATTCGAATA CAGAACGAGTNNNGATCGACATG	1628	TGCAGGACCAGAGAATTCGAATA CACTCGCAGGNNNGATCGACATG	1868	TGCAGGACCAGAGAATTCGAATA CATACCCCGNNNGATCGACATG	2108
TGCAGGACCAGAGAATTCGAATA CATCGGTGATNNNTGCATCAGGT	1629	TGCAGGACCAGAGAATTCGAATA CAACTGAAAAANNNTGCATCAGGT	1869	TGCAGGACCAGAGAATTCGAATA CACCTACCGCNNNTGCATCAGGT	2109
TGCAGGACCAGAGAATTCGAATA CAATTGCAATNNNTGCATCAGGT	1630	TGCAGGACCAGAGAATTCGAATA CAAGTCTTTNNNTGCATCAGGT	1870	TGCAGGACCAGAGAATTCGAATA CAAGACAGTGNNTGCATCAGGT	2110
TGCAGGACCAGAGAATTCGAATA CATTAAAGATNNNTGCATCAGGT	1631	TGCAGGACCAGAGAATTCGAATA CAGGTGTTACNNNTGCATCAGGT	1871	TGCAGGACCAGAGAATTCGAATA CAGTCCTATCNNNTGCATCAGGT	2111
TGCAGGACCAGAGAATTCGAATA CATGTACGTGNNNTGCATCAGGT	1632	TGCAGGACCAGAGAATTCGAATA CATATCCGCTNNNTGCATCAGGT	1872	TGCAGGACCAGAGAATTCGAATA CACGCGCTCTNNNTGCATCAGGT	2112
TGCAGGACCAGAGAATTCGAATA CAGCGTGTGCNNNTGCATCAGGT	1633	TGCAGGACCAGAGAATTCGAATA CAGCGTGAGNNNTGCATCAGGT	1873	TGCAGGACCAGAGAATTCGAATA CATTGATTCTNNNTGCATCAGGT	2113
TGCAGGACCAGAGAATTCGAATA CACCATATAANNNTGCATCAGGT	1634	TGCAGGACCAGAGAATTCGAATA CAGCCGTTCCNNNTGCATCAGGT	1874	TGCAGGACCAGAGAATTCGAATA CAATAATGTNNNTGCATCAGGT	2114
TGCAGGACCAGAGAATTCGAATA CAAAATTTAGNNNTGCATCAGGT	1635	TGCAGGACCAGAGAATTCGAATA CATTACCCCANNNNTGCATCAGGT	1875	TGCAGGACCAGAGAATTCGAATA CAGAGTTAAANNNTGCATCAGGT	2115
TGCAGGACCAGAGAATTCGAATA CAGTATCACGNNNTGCATCAGGT	1636	TGCAGGACCAGAGAATTCGAATA CAGACCCCTCANNNTGCATCAGGT	1876	TGCAGGACCAGAGAATTCGAATA CACGACACATNNNTGCATCAGGT	2116
TGCAGGACCAGAGAATTCGAATA CACCTTAGGANNNTGCATCAGGT	1637	TGCAGGACCAGAGAATTCGAATA CATATGGAGNNNTGCATCAGGT	1877	TGCAGGACCAGAGAATTCGAATA CATTGGCCGNNNTGCATCAGGT	2117
TGCAGGACCAGAGAATTCGAATA CATAAAAGCANNNTGCATCAGGT	1638	TGCAGGACCAGAGAATTCGAATA CAGACGGTCCNNNTGCATCAGGT	1878	TGCAGGACCAGAGAATTCGAATA CAGAACTTTANNNTGCATCAGGT	2118
TGCAGGACCAGAGAATTCGAATA CATGCATCCTNNNTGCATCAGGT	1639	TGCAGGACCAGAGAATTCGAATA CACTACGACANNNTGCATCAGGT	1879	TGCAGGACCAGAGAATTCGAATA CACCAAAACNNNTGCATCAGGT	2119
TGCAGGACCAGAGAATTCGAATA CACAGCCTGNNNTGCATCAGGT	1640	TGCAGGACCAGAGAATTCGAATA CATGACTACGNNNTGCATCAGGT	1880	TGCAGGACCAGAGAATTCGAATA CAATACCAGCANNNTGCATCAGGT	2120
TGCAGGACCAGAGAATTCGAATA CACACACTAGNNNTGCATCAGGT	1641	TGCAGGACCAGAGAATTCGAATA CAGGACGTTTNNNTGCATCAGGT	1881	TGCAGGACCAGAGAATTCGAATA CAAGTAGAATNNNTGCATCAGGT	2121
TGCAGGACCAGAGAATTCGAATA CACGTATCCTNNNTGCATCAGGT	1642	TGCAGGACCAGAGAATTCGAATA CAAAGCCTCANNNTGCATCAGGT	1882	TGCAGGACCAGAGAATTCGAATA CAGTACTACGNNNTGCATCAGGT	2122
TGCAGGACCAGAGAATTCGAATA CATGGCTTAGNNNTGCATCAGGT	1643	TGCAGGACCAGAGAATTCGAATA CACTTTAAAGNNNTGCATCAGGT	1883	TGCAGGACCAGAGAATTCGAATA CATTCATGAANNNTGCATCAGGT	2123
TGCAGGACCAGAGAATTCGAATA CACTGTCATCANNNTGCATCAGGT	1644	TGCAGGACCAGAGAATTCGAATA CATTGTATTNNNTGCATCAGGT	1884	TGCAGGACCAGAGAATTCGAATA CACCTAAGGTNNNTGCATCAGGT	2124
TGCAGGACCAGAGAATTCGAATA CATCCAGAACNNNTGCATCAGGT	1645	TGCAGGACCAGAGAATTCGAATA CACTGTATTTNNNTGCATCAGGT	1885	TGCAGGACCAGAGAATTCGAATA CAACAAAGGCNNNTGCATCAGGT	2125
TGCAGGACCAGAGAATTCGAATA CACGAGTACTNNNTGCATCAGGT	1646	TGCAGGACCAGAGAATTCGAATA CATTAAATTTGNNNTGCATCAGGT	1886	TGCAGGACCAGAGAATTCGAATA CAGAGGCAGCANNNTGCATCAGGT	2126
TGCAGGACCAGAGAATTCGAATA CAGATCGAGANNNTGCATCAGGT	1647	TGCAGGACCAGAGAATTCGAATA CACAGAGTTCNNNTGCATCAGGT	1887	TGCAGGACCAGAGAATTCGAATA CACTACTCGTNNNTGCATCAGGT	2127
TGCAGGACCAGAGAATTCGAATA CAAGAATAACNNNTGCATCAGGT	1648	TGCAGGACCAGAGAATTCGAATA CAGCATCTAGNNNTGCATCAGGT	1888	TGCAGGACCAGAGAATTCGAATA CAGGTAGTGANNNTGCATCAGGT	2128
TGCAGGACCAGAGAATTCGAATA CAGCGCACANNNTGCATCAGGT	1649	TGCAGGACCAGAGAATTCGAATA CATTGTCTATNNNTGCATCAGGT	1889	TGCAGGACCAGAGAATTCGAATA CACCACCACNNNTGCATCAGGT	2129
TGCAGGACCAGAGAATTCGAATA CACAGCAACTNNNTGCATCAGGT	1650	TGCAGGACCAGAGAATTCGAATA CACATCCTGTNNNTGCATCAGGT	1890	TGCAGGACCAGAGAATTCGAATA CATGTGTGACNNNTGCATCAGGT	2130

FIG. 14H

Pool-7	SEQ ID NO:	Pool-8	SEQ ID NO:	Pool-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA	1651	TGCAGGACCAGAGAATTCGAATA	1891	TGCAGGACCAGAGAATTCGAATA	2131
CAGTGGCATANNNTGCATCAGGT		CACATTCAAANNNTGCATCAGGT		CACACCCTGCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1652	TGCAGGACCAGAGAATTCGAATA	1892	TGCAGGACCAGAGAATTCGAATA	2132
CAATCTATTNNNTGCATCAGGT		CAAAAGCCTCNNNTGCATCAGGT		CATCGCCATTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1653	TGCAGGACCAGAGAATTCGAATA	1893	TGCAGGACCAGAGAATTCGAATA	2133
CAAGTATGTTNNNTGCATCAGGT		CATGATCAATNNNTGCATCAGGT		CAACTTCGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1654	TGCAGGACCAGAGAATTCGAATA	1894	TGCAGGACCAGAGAATTCGAATA	2134
CAGGTTCTTNNNTGCATCAGGT		CAATATGATCNNNTGCATCAGGT		CATTGCTTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1655	TGCAGGACCAGAGAATTCGAATA	1895	TGCAGGACCAGAGAATTCGAATA	2135
CATAGTGGCTNNNTGCATCAGGT		CAGGACCGAGNNNTGCATCAGGT		CAGCACGAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1656	TGCAGGACCAGAGAATTCGAATA	1896	TGCAGGACCAGAGAATTCGAATA	2136
CACCAACTTNNNTGCATCAGGT		CACCCCTAATNNNTGCATCAGGT		CACGAATGTCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1657	TGCAGGACCAGAGAATTCGAATA	1897	TGCAGGACCAGAGAATTCGAATA	2137
CAAGTTCAATNNNTGCATCAGGT		CACTCAAAGCNNNTGCATCAGGT		CATGGCTAGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1658	TGCAGGACCAGAGAATTCGAATA	1898	TGCAGGACCAGAGAATTCGAATA	2138
CATTGTTCCGNNNTGCATCAGGT		CACCTTCGTACNNNTGCATCAGGT		CAGTGTATANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1659	TGCAGGACCAGAGAATTCGAATA	1899	TGCAGGACCAGAGAATTCGAATA	2139
CAGTCATGCANNNTGCATCAGGT		CAATTGGCCANNNTGCATCAGGT		CATTCCCTCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1660	TGCAGGACCAGAGAATTCGAATA	1900	TGCAGGACCAGAGAATTCGAATA	2140
CACCTGTAATANNNTGCATCAGGT		CACGAAGGTANNNTGCATCAGGT		CATCAACTAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1661	TGCAGGACCAGAGAATTCGAATA	1901	TGCAGGACCAGAGAATTCGAATA	2141
CATTTCGGCCNNNTGCATCAGGT		CAGGCCTTGGNNNTGCATCAGGT		CATTTACAAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1662	TGCAGGACCAGAGAATTCGAATA	1902	TGCAGGACCAGAGAATTCGAATA	2142
CATCTCTCTCNNNTGCATCAGGT		CAACAATATCNNNTGCATCAGGT		CATCCTGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1663	TGCAGGACCAGAGAATTCGAATA	1903	TGCAGGACCAGAGAATTCGAATA	2143
CACCTTCGCGCNNNTGCATCAGGT		CATCACAACGNNNTGCATCAGGT		CATCGGCTAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1664	TGCAGGACCAGAGAATTCGAATA	1904	TGCAGGACCAGAGAATTCGAATA	2144
CAACAGATTTNNNTGCATCAGGT		CAACTGTACGNNNTGCATCAGGT		CAAGGAGCATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1665	TGCAGGACCAGAGAATTCGAATA	1905	TGCAGGACCAGAGAATTCGAATA	2145
CACAGACAAGNNNTGCATCAGGT		CATCTCAATTNNNTGCATCAGGT		CAGGAATACGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1666	TGCAGGACCAGAGAATTCGAATA	1906	TGCAGGACCAGAGAATTCGAATA	2146
CACAGCTACANNNTGCATCAGGT		CAAGGCTCTANNNTGCATCAGGT		CATGAGACGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1667	TGCAGGACCAGAGAATTCGAATA	1907	TGCAGGACCAGAGAATTCGAATA	2147
CAGACCGAGNNNTGCATCAGGT		CACCTTAACANNNTGCATCAGGT		CACCACCGAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1668	TGCAGGACCAGAGAATTCGAATA	1908	TGCAGGACCAGAGAATTCGAATA	2148
CACCTATAAANNNTGCATCAGGT		CAGATTCTCNNNTGCATCAGGT		CAAGCTCATGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1669	TGCAGGACCAGAGAATTCGAATA	1909	TGCAGGACCAGAGAATTCGAATA	2149
CACCTAACCTNNNTGCATCAGGT		CATGCCITGTTNNNTGCATCAGGT		CATATACCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1670	TGCAGGACCAGAGAATTCGAATA	1910	TGCAGGACCAGAGAATTCGAATA	2150
CATTTAGCGGNNNTGCATCAGGT		CATCACCAGNNNTGCATCAGGT		CAGATGCCATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1671	TGCAGGACCAGAGAATTCGAATA	1911	TGCAGGACCAGAGAATTCGAATA	2151
CATAAACCATTNNNTGCATCAGGT		CACCTCCGGCNNNTGCATCAGGT		CATTGAGCTGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1672	TGCAGGACCAGAGAATTCGAATA	1912	TGCAGGACCAGAGAATTCGAATA	2152
CAGCTAACTGNNNTGCATCAGGT		CAAAACGCAGNNNTGCATCAGGT		CATAAATGGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1673	TGCAGGACCAGAGAATTCGAATA	1913	TGCAGGACCAGAGAATTCGAATA	2153
CAGTACAGANNNTGCATCAGGT		CACGCATTCTNNNTGCATCAGGT		CAACATGAAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1674	TGCAGGACCAGAGAATTCGAATA	1914	TGCAGGACCAGAGAATTCGAATA	2154
CACCGGACANNNTGCATCAGGT		CACGCCTATTNNNTGCATCAGGT		CACTCGGAGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1675	TGCAGGACCAGAGAATTCGAATA	1915	TGCAGGACCAGAGAATTCGAATA	2155
CACCTCTAGTNNNTGCATCAGGT		CATCATCATNNNTGCATCAGGT		CAGTTTCCTGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1676	TGCAGGACCAGAGAATTCGAATA	1916	TGCAGGACCAGAGAATTCGAATA	2156
CAGCCCTGTNNNTGCATCAGGT		CAAAATTCAGTNNNTGCATCAGGT		CACAACAIGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1677	TGCAGGACCAGAGAATTCGAATA	1917	TGCAGGACCAGAGAATTCGAATA	2157
CACGGACTGCNNNTGCATCAGGT		CAATTCTGCGNNNTGCATCAGGT		CATGGTGCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1678	TGCAGGACCAGAGAATTCGAATA	1918	TGCAGGACCAGAGAATTCGAATA	2158
CACCCCTCTGNNNTGCATCAGGT		CAATAGAGTANNNTGCATCAGGT		CATACGGAGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATA	1679	TGCAGGACCAGAGAATTCGAATA	1919	TGCAGGACCAGAGAATTCGAATA	2159
CAACCAAGTCNNNTGCATCAGGT		CAGAGCGGACNNNTGCATCAGGT		CAGGCGTGGANNNTGCATCAGGT	

FIG. 14I

Pool-7	SEQ ID NO:	Pool-8	SEQ ID NO:	Pool-9	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAGCGTGGTCNNNTGCATCAGGT	1680	TGCAGGACCAGAGAATTCGAATA CAACTTTTACNNNTGCATCAGGT	1920	TGCAGGACCAGAGAATTCGAATA CATCTAACGGNNNTGCATCAGGT	2160
TGCAGGACCAGAGAATTCGAATA CACCAGCGCANNNNTGCATCAGGT	1681	TGCAGGACCAGAGAATTCGAATA CAAGTCAAAANNNNTGCATCAGGT	1921	TGCAGGACCAGAGAATTCGAATA CATATAGCATNNNTGCATCAGGT	2161
TGCAGGACCAGAGAATTCGAATA CATTACCGGANNNNTGCATCAGGT	1682	TGCAGGACCAGAGAATTCGAATA CATCTAGACGNNNTGCATCAGGT	1922	TGCAGGACCAGAGAATTCGAATA CACGCTCCGTNNNTGCATCAGGT	2162
TGCAGGACCAGAGAATTCGAATA CATCTTTGCGNNNTGCATCAGGT	1683	TGCAGGACCAGAGAATTCGAATA CACAAATGTTNNNTGCATCAGGT	1923	TGCAGGACCAGAGAATTCGAATA CAATACATGTTNNNTGCATCAGGT	2163
TGCAGGACCAGAGAATTCGAATA CACACAATTANNNNTGCATCAGGT	1684	TGCAGGACCAGAGAATTCGAATA CATGGCTTTCNNNTGCATCAGGT	1924	TGCAGGACCAGAGAATTCGAATA CAGGCTCGCANNNNTGCATCAGGT	2164
TGCAGGACCAGAGAATTCGAATA CACCTACATCNNNTGCATCAGGT	1685	TGCAGGACCAGAGAATTCGAATA CAAGGCTGTTNNNTGCATCAGGT	1925	TGCAGGACCAGAGAATTCGAATA CAGTTTAGTANNNNTGCATCAGGT	2165
TGCAGGACCAGAGAATTCGAATA CAATTACTGANNNTGCATCAGGT	1686	TGCAGGACCAGAGAATTCGAATA CAAACCTATTGNNNTGCATCAGGT	1926	TGCAGGACCAGAGAATTCGAATA CACTGAAATTNNNTGCATCAGGT	2166
TGCAGGACCAGAGAATTCGAATA CATTTTTCGANNNNTGCATCAGGT	1687	TGCAGGACCAGAGAATTCGAATA CAATGTATTGNNNTGCATCAGGT	1927	TGCAGGACCAGAGAATTCGAATA CAAACACCTGNNNTGCATCAGGT	2167
TGCAGGACCAGAGAATTCGAATA CAAGGTGCTTNNNTGCATCAGGT	1688	TGCAGGACCAGAGAATTCGAATA CACGTGCGCANNNNTGCATCAGGT	1928	TGCAGGACCAGAGAATTCGAATA CAGGAAAACNNNTGCATCAGGT	2168

FIG. 15A

Pool-10	SEQ ID NO:	Pool-11	SEQ ID NO:	Pool-12	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATACAG	2169	TGCAGGACCAGAGAATTGGAATACAA	2409	TGCAGGACCAGAGAATTGGAATACAT	2649
CTTCTCANNNNACGTATGCCA		TACGTATNNNNACGTATGCCA		TGAGAAANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	2170	TGCAGGACCAGAGAATTGGAATACAA	2410	TGCAGGACCAGAGAATTGGAATACAA	2650
TGCTACGNNNNACGTATGCCA		ACTAGCCNNNNACGTATGCCA		ATATCCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2171	TGCAGGACCAGAGAATTGGAATACAC	2411	TGCAGGACCAGAGAATTGGAATACAA	2651
ACTCTCGNNNNACGTATGCCA		GGATTACNNNNACGTATGCCA		TGGACCTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	2172	TGCAGGACCAGAGAATTGGAATACAG	2412	TGCAGGACCAGAGAATTGGAATACAG	2652
GGTCGCANNNNACGTATGCCA		GACGCCNNNNACGTATGCCA		GCATACTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	2173	TGCAGGACCAGAGAATTGGAATACAC	2413	TGCAGGACCAGAGAATTGGAATACAC	2653
CGGTTACNNNNACGTATGCCA		GTTAAATNNNNACGTATGCCA		TAAAAAGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2174	TGCAGGACCAGAGAATTGGAATACAG	2414	TGCAGGACCAGAGAATTGGAATACAA	2654
GGTCTCANNNNACGTATGCCA		GCTAGTTNNNNACGTATGCCA		TACATACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	2175	TGCAGGACCAGAGAATTGGAATACAT	2415	TGCAGGACCAGAGAATTGGAATACAT	2655
GTCTCTANNNNACGTATGCCA		CAGAAAGNNNNACGTATGCCA		ATGGCCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2176	TGCAGGACCAGAGAATTGGAATACAA	2416	TGCAGGACCAGAGAATTGGAATACAA	2656
CTCCGCTNNNNACGTATGCCA		CCAAGTNNNNACGTATGCCA		TGATGCCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2177	TGCAGGACCAGAGAATTGGAATACAT	2417	TGCAGGACCAGAGAATTGGAATACAA	2657
TGGCACNNNNACGTATGCCA		CGACAACNNNNACGTATGCCA		GGTAGGTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2178	TGCAGGACCAGAGAATTGGAATACAG	2418	TGCAGGACCAGAGAATTGGAATACAT	2658
CACATATGNNNNACGTATGCCA		TCGTACANNNNACGTATGCCA		CCCTAGTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	2179	TGCAGGACCAGAGAATTGGAATACAG	2419	TGCAGGACCAGAGAATTGGAATACAG	2659
ATAACGANNNNACGTATGCCA		CCAGAGNNNNACGTATGCCA		TATTTGANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2180	TGCAGGACCAGAGAATTGGAATACAC	2420	TGCAGGACCAGAGAATTGGAATACAA	2660
GTATAGGNNNNACGTATGCCA		ATAGTATNNNNACGTATGCCA		GTGAATANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	2181	TGCAGGACCAGAGAATTGGAATACAT	2421	TGCAGGACCAGAGAATTGGAATACAA	2661
GAACCTNNNNACGTATGCCA		AAATGTNNNNACGTATGCCA		ATCGCACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2182	TGCAGGACCAGAGAATTGGAATACAG	2422	TGCAGGACCAGAGAATTGGAATACAG	2662
CCGCGTANNNNACGTATGCCA		CGTCGGTNNNNACGTATGCCA		TCCCCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2183	TGCAGGACCAGAGAATTGGAATACAT	2423	TGCAGGACCAGAGAATTGGAATACAG	2663
TCCTTGANNNNACGTATGCCA		TTGAACANNNNACGTATGCCA		CCCACCTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	2184	TGCAGGACCAGAGAATTGGAATACAT	2424	TGCAGGACCAGAGAATTGGAATACAG	2664
TGGCATCANNNNACGTATGCCA		AACTATGNNNNACGTATGCCA		AGATATANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	2185	TGCAGGACCAGAGAATTGGAATACAT	2425	TGCAGGACCAGAGAATTGGAATACAG	2665
AGGATCGNNNNACGTATGCCA		CAGATGNNNNACGTATGCCA		CACATACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2186	TGCAGGACCAGAGAATTGGAATACAC	2426	TGCAGGACCAGAGAATTGGAATACAA	2666
TGCATCANNNNACGTATGCCA		TCAACAGNNNNACGTATGCCA		CTTTGCCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2187	TGCAGGACCAGAGAATTGGAATACAA	2427	TGCAGGACCAGAGAATTGGAATACAC	2667
TCGTCTTNNNNACGTATGCCA		TAAAGTNNNNACGTATGCCA		TGAGGCCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	2188	TGCAGGACCAGAGAATTGGAATACAA	2428	TGCAGGACCAGAGAATTGGAATACAA	2668
TTGAGGTNNNNACGTATGCCA		GAGCAGTNNNNACGTATGCCA		AGTAGGCCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2189	TGCAGGACCAGAGAATTGGAATACAT	2429	TGCAGGACCAGAGAATTGGAATACAG	2669
ACATCAANNNNACGTATGCCA		ATGTCTTNNNNACGTATGCCA		CTTCTCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	2190	TGCAGGACCAGAGAATTGGAATACAG	2430	TGCAGGACCAGAGAATTGGAATACAT	2670
CGAACCGNNNNACGTATGCCA		CAGAGATNNNNACGTATGCCA		GGAGGATNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	2191	TGCAGGACCAGAGAATTGGAATACAT	2431	TGCAGGACCAGAGAATTGGAATACAG	2671
CCACACNNNNACGTATGCCA		CTCAGCANNNNACGTATGCCA		CTAACCCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	2192	TGCAGGACCAGAGAATTGGAATACAC	2432	TGCAGGACCAGAGAATTGGAATACAA	2672
CGTAAANNNNACGTATGCCA		CCCTTGGNNNNACGTATGCCA		CCCTTACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2193	TGCAGGACCAGAGAATTGGAATACAC	2433	TGCAGGACCAGAGAATTGGAATACAG	2673
TAGAGTNNNNACGTATGCCA		AGTGGCCNNNNACGTATGCCA		TCTTCTGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	2194	TGCAGGACCAGAGAATTGGAATACAC	2434	TGCAGGACCAGAGAATTGGAATACAC	2674
CACATAGNNNNACGTATGCCA		TGATCGANNNNACGTATGCCA		GGAGCCTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2195	TGCAGGACCAGAGAATTGGAATACAT	2435	TGCAGGACCAGAGAATTGGAATACAC	2675
CTGTGCTNNNNACGTATGCCA		GGTACGTNNNNACGTATGCCA		CTGATGANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2196	TGCAGGACCAGAGAATTGGAATACAG	2436	TGCAGGACCAGAGAATTGGAATACAT	2676
AGTACATNNNNACGTATGCCA		TACGGCCNNNNACGTATGCCA		CGATACGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	2197	TGCAGGACCAGAGAATTGGAATACAC	2437	TGCAGGACCAGAGAATTGGAATACAA	2677
CGGACACNNNNACGTATGCCA		CATGCGGNNNNACGTATGCCA		AGAATGTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2198	TGCAGGACCAGAGAATTGGAATACAC	2438	TGCAGGACCAGAGAATTGGAATACAT	2678
TAAGCTCANNNNACGTATGCCA		AAGTAGNNNNACGTATGCCA		GCGCTCCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	2199	TGCAGGACCAGAGAATTGGAATACAC	2439	TGCAGGACCAGAGAATTGGAATACAA	2679
CTTGGTNNNNACGTATGCCA		ATCAAATNNNNACGTATGCCA		AGTCATTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	2200	TGCAGGACCAGAGAATTGGAATACAG	2440	TGCAGGACCAGAGAATTGGAATACAT	2680
GACCTGGNNNNACGTATGCCA		ACTGGTNNNNACGTATGCCA		GTAATGTNNNNACGTATGCCA	

FIG. 15B

Pool-10	SEQ ID NO:	Pool-11	SEQ ID NO:	Pool-12	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATACAT	2201	TGCAGGACCAGAGAATTGGAATACAG	2441	TGCAGGACCAGAGAATTGGAATACAA	2681
GAGGATGNNNACGTATGCCA		CAAAATTTNNNACGTATGCCA		TCTACCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	2202	TGCAGGACCAGAGAATTGGAATACAT	2442	TGCAGGACCAGAGAATTGGAATACAT	2682
TCGTGCCNNNACGTATGCCA		TAGTGTANNNACGTATGCCA		GCCACANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2203	TGCAGGACCAGAGAATTGGAATACAG	2443	TGCAGGACCAGAGAATTGGAATACAG	2683
TGCTCGTNNNACGTATGCCA		ATGAAATNNNACGTATGCCA		AGTGTTCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	2204	TGCAGGACCAGAGAATTGGAATACAT	2444	TGCAGGACCAGAGAATTGGAATACAA	2684
CACGTGACNNNACGTATGCCA		TGCCGANNNACGTATGCCA		ACAGCCTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2205	TGCAGGACCAGAGAATTGGAATACAT	2445	TGCAGGACCAGAGAATTGGAATACAG	2685
TTGGTACNNNACGTATGCCA		CCTCCTTNNNACGTATGCCA		GACGACGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2206	TGCAGGACCAGAGAATTGGAATACAC	2446	TGCAGGACCAGAGAATTGGAATACAA	2686
TACGTCCNNNACGTATGCCA		CCCATTANNNACGTATGCCA		TTCCGGANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2207	TGCAGGACCAGAGAATTGGAATACAG	2447	TGCAGGACCAGAGAATTGGAATACAG	2687
TAACAAANNNACGTATGCCA		TTTGTTTNNNACGTATGCCA		GTCTCAANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	2208	TGCAGGACCAGAGAATTGGAATACAT	2448	TGCAGGACCAGAGAATTGGAATACAC	2688
AACTGGTNNNACGTATGCCA		ATCCGTTNNNACGTATGCCA		ACCATGANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2209	TGCAGGACCAGAGAATTGGAATACAT	2449	TGCAGGACCAGAGAATTGGAATACAC	2689
GGATACNNNACGTATGCCA		TCGGTGANNNACGTATGCCA		AAACGGANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	2210	TGCAGGACCAGAGAATTGGAATACAC	2450	TGCAGGACCAGAGAATTGGAATACAA	2690
TGCACANNNACGTATGCCA		GTAAAGANNNACGTATGCCA		GAGCGTANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	2211	TGCAGGACCAGAGAATTGGAATACAC	2451	TGCAGGACCAGAGAATTGGAATACAC	2691
CTCCTTGNNNACGTATGCCA		TTTCTTTNNNACGTATGCCA		CCTTGACNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	2212	TGCAGGACCAGAGAATTGGAATACAG	2452	TGCAGGACCAGAGAATTGGAATACAC	2692
ATAGTTCCNNNACGTATGCCA		ACTTTTNNNACGTATGCCA		CAAGTTGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2213	TGCAGGACCAGAGAATTGGAATACAG	2453	TGCAGGACCAGAGAATTGGAATACAT	2693
GAGAGCANNNACGTATGCCA		GTTAAGGNNNACGTATGCCA		GTGTAATNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2214	TGCAGGACCAGAGAATTGGAATACAA	2454	TGCAGGACCAGAGAATTGGAATACAA	2694
CACCCGNNNACGTATGCCA		TCACGGTNNNACGTATGCCA		TTTGTGANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2215	TGCAGGACCAGAGAATTGGAATACAC	2455	TGCAGGACCAGAGAATTGGAATACAG	2695
AATGGAANNNACGTATGCCA		ATTTAGANNNACGTATGCCA		TAGCGTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2216	TGCAGGACCAGAGAATTGGAATACAC	2456	TGCAGGACCAGAGAATTGGAATACAC	2696
CCAAATANNNACGTATGCCA		ACCGCANNNACGTATGCCA		ACGTGATNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2217	TGCAGGACCAGAGAATTGGAATACAC	2457	TGCAGGACCAGAGAATTGGAATACAA	2697
AGGCTCCNNNACGTATGCCA		TGAATCGNNNACGTATGCCA		ACAGCGANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2218	TGCAGGACCAGAGAATTGGAATACAT	2458	TGCAGGACCAGAGAATTGGAATACAA	2698
CCGCGTCNNNACGTATGCCA		TGTGTANNNACGTATGCCA		AATGCGGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2219	TGCAGGACCAGAGAATTGGAATACAC	2459	TGCAGGACCAGAGAATTGGAATACAT	2699
CATTGCAANNNACGTATGCCA		CGCGTGANNNACGTATGCCA		ACCAAGCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	2220	TGCAGGACCAGAGAATTGGAATACAA	2460	TGCAGGACCAGAGAATTGGAATACAC	2700
CCCTTAANNNACGTATGCCA		ACCAAGGNNNACGTATGCCA		GACCCCTCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2221	TGCAGGACCAGAGAATTGGAATACAT	2461	TGCAGGACCAGAGAATTGGAATACAA	2701
ACCGCCANNNACGTATGCCA		CGTTTGCNNNACGTATGCCA		CACCCCTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2222	TGCAGGACCAGAGAATTGGAATACAC	2462	TGCAGGACCAGAGAATTGGAATACAC	2702
ATCTGACNNNACGTATGCCA		TATTCCGNNNACGTATGCCA		TGTCGCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2223	TGCAGGACCAGAGAATTGGAATACAA	2463	TGCAGGACCAGAGAATTGGAATACAA	2703
CATGTTGNNNACGTATGCCA		ACAGATANNNACGTATGCCA		GCCGCCANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2224	TGCAGGACCAGAGAATTGGAATACAC	2464	TGCAGGACCAGAGAATTGGAATACAT	2704
AGCACGTNNNACGTATGCCA		TATTATCNNNACGTATGCCA		GTACAATNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2225	TGCAGGACCAGAGAATTGGAATACAT	2465	TGCAGGACCAGAGAATTGGAATACAG	2705
GTCCAAATNNNACGTATGCCA		CCCAATCNNNACGTATGCCA		ATCTACGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	2226	TGCAGGACCAGAGAATTGGAATACAC	2466	TGCAGGACCAGAGAATTGGAATACAC	2706
CCCTCTANNNACGTATGCCA		TAAAGTTNNNACGTATGCCA		CAGTCTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	2227	TGCAGGACCAGAGAATTGGAATACAA	2467	TGCAGGACCAGAGAATTGGAATACAG	2707
TACGACGNNNACGTATGCCA		GCTAATTNNNACGTATGCCA		CTGCAATNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	2228	TGCAGGACCAGAGAATTGGAATACAT	2468	TGCAGGACCAGAGAATTGGAATACAG	2708
ATATCGGNNNACGTATGCCA		TGTTATCNNNACGTATGCCA		AAGAGTCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	2229	TGCAGGACCAGAGAATTGGAATACAT	2469	TGCAGGACCAGAGAATTGGAATACAA	2709
CGATATCNNNCTAGCGTTAC		AGTAGCNCNNCTAGCGTTAC		CAACTCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	2230	TGCAGGACCAGAGAATTGGAATACAC	2470	TGCAGGACCAGAGAATTGGAATACAT	2710
ACGAGGANNNCTAGCGTTAC		AGGCTATNNNCTAGCGTTAC		GCGCAATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	2231	TGCAGGACCAGAGAATTGGAATACAC	2471	TGCAGGACCAGAGAATTGGAATACAT	2711
CTTACATNNNCTAGCGTTAC		ATTAGTANNNCTAGCGTTAC		AAGAACANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	2232	TGCAGGACCAGAGAATTGGAATACAC	2472	TGCAGGACCAGAGAATTGGAATACAC	2712
CGTCTCCNNNCTAGCGTTAC		CTCTAACNNNCTAGCGTTAC		GCTTGCCNNNCTAGCGTTAC	

FIG. 15C

Pool-10	SEQ ID NO:	Pool-11	SEQ ID NO:	Pool-12	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAT	2233	TGCAGGACCAGAGAATTCGAATACAT	2473	TGCAGGACCAGAGAATTCGAATACAT	2713
AATCCGNNNNCTAGCGTTAC		AGTGTGNNNNCTAGCGTTAC		TACACGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	2234	TGCAGGACCAGAGAATTCGAATACAC	2474	TGCAGGACCAGAGAATTCGAATACAC	2714
AGCATACNNNNCTAGCGTTAC		GCAGAGNNNNCTAGCGTTAC		TCCACGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	2235	TGCAGGACCAGAGAATTCGAATACAG	2475	TGCAGGACCAGAGAATTCGAATACAC	2715
TTCTCCANNNNCTAGCGTTAC		CGGTTGNNNNCTAGCGTTAC		GACCCAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	2236	TGCAGGACCAGAGAATTCGAATACAC	2476	TGCAGGACCAGAGAATTCGAATACAC	2716
GTTCCTGNNNNCTAGCGTTAC		CAGAGTTNNNNCTAGCGTTAC		GGTCAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	2237	TGCAGGACCAGAGAATTCGAATACAT	2477	TGCAGGACCAGAGAATTCGAATACAC	2717
AATCGAANNNNCTAGCGTTAC		GATGAAANNNNCTAGCGTTAC		ACTATCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	2238	TGCAGGACCAGAGAATTCGAATACAG	2478	TGCAGGACCAGAGAATTCGAATACAC	2718
GATTATCANNNNCTAGCGTTAC		GTGAATGNNNNCTAGCGTTAC		TAGTCTCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	2239	TGCAGGACCAGAGAATTCGAATACAG	2479	TGCAGGACCAGAGAATTCGAATACAT	2719
TTTCACGNNNNCTAGCGTTAC		TATGTGNNNNCTAGCGTTAC		ACCTTCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	2240	TGCAGGACCAGAGAATTCGAATACAA	2480	TGCAGGACCAGAGAATTCGAATACAA	2720
TTACATGNNNNCTAGCGTTAC		ATACTAGNNNNCTAGCGTTAC		ACCAGAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	2241	TGCAGGACCAGAGAATTCGAATACAT	2481	TGCAGGACCAGAGAATTCGAATACAT	2721
CCATCCTNNNNCTAGCGTTAC		TCGGATGNNNNCTAGCGTTAC		GACTCGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	2242	TGCAGGACCAGAGAATTCGAATACAT	2482	TGCAGGACCAGAGAATTCGAATACAA	2722
AGACTACNNNNCTAGCGTTAC		ACATTAGNNNNCTAGCGTTAC		CCCAGATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	2243	TGCAGGACCAGAGAATTCGAATACAT	2483	TGCAGGACCAGAGAATTCGAATACAT	2723
ATTGGTGNNNNNCTAGCGTTAC		GGCCCGANNNNCTAGCGTTAC		GGGCTTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	2244	TGCAGGACCAGAGAATTCGAATACAG	2484	TGCAGGACCAGAGAATTCGAATACAG	2724
AGACCTTNNNNCTAGCGTTAC		TTGAGTGNNNNNCTAGCGTTAC		GAGGACGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAT	2245	TGCAGGACCAGAGAATTCGAATACAG	2485	TGCAGGACCAGAGAATTCGAATACAT	2725
CAGGCCGNNNNCTAGCGTTAC		TTAGCACNNNNCTAGCGTTAC		CGTCCATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	2246	TGCAGGACCAGAGAATTCGAATACAA	2486	TGCAGGACCAGAGAATTCGAATACAC	2726
AACACACNNNNCTAGCGTTAC		GTTCCTTNNNNCTAGCGTTAC		GACCTCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	2247	TGCAGGACCAGAGAATTCGAATACAC	2487	TGCAGGACCAGAGAATTCGAATACAA	2727
GAOGTCGNNNNCTAGCGTTAC		ATGGAGANNNNCTAGCGTTAC		GATTCCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAT	2248	TGCAGGACCAGAGAATTCGAATACAA	2488	TGCAGGACCAGAGAATTCGAATACAA	2728
AGACTATNNNNCTAGCGTTAC		ATCGTCGNNNNCTAGCGTTAC		CTCGAACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	2249	TGCAGGACCAGAGAATTCGAATACAA	2489	TGCAGGACCAGAGAATTCGAATACAA	2729
CGAGAAANNNNCTAGCGTTAC		CTCGCAANNNNCTAGCGTTAC		GACCGATGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAT	2250	TGCAGGACCAGAGAATTCGAATACAT	2490	TGCAGGACCAGAGAATTCGAATACAG	2730
TCATATNNNNCTAGCGTTAC		CAGCCTTNNNNCTAGCGTTAC		AACTTATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	2251	TGCAGGACCAGAGAATTCGAATACAT	2491	TGCAGGACCAGAGAATTCGAATACAA	2731
CCATGATNNNNCTAGCGTTAC		TGCGCTCANNNNCTAGCGTTAC		CCAGCGCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	2252	TGCAGGACCAGAGAATTCGAATACAG	2492	TGCAGGACCAGAGAATTCGAATACAT	2732
GCGACGANNNNCTAGCGTTAC		GACCCACNNNNCTAGCGTTAC		AOCTCTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	2253	TGCAGGACCAGAGAATTCGAATACAT	2493	TGCAGGACCAGAGAATTCGAATACAC	2733
CCAGTAANNNNCTAGCGTTAC		TCTCCAGNNNNCTAGCGTTAC		GGAGCGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	2254	TGCAGGACCAGAGAATTCGAATACAG	2494	TGCAGGACCAGAGAATTCGAATACAA	2734
TCAAACGNNNNCTAGCGTTAC		TCCTCGCNNNNCTAGCGTTAC		CCGGAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	2255	TGCAGGACCAGAGAATTCGAATACAA	2495	TGCAGGACCAGAGAATTCGAATACAG	2735
AGATCTGNNNNCTAGCGTTAC		ATAGTCTNNNNCTAGCGTTAC		GATCGCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	2256	TGCAGGACCAGAGAATTCGAATACAG	2496	TGCAGGACCAGAGAATTCGAATACAA	2736
GAAAATCNNNNCTAGCGTTAC		CTGGATTNNNNCTAGCGTTAC		TCAGCACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	2257	TGCAGGACCAGAGAATTCGAATACAT	2497	TGCAGGACCAGAGAATTCGAATACAA	2737
TCCTTCANNNNCTAGCGTTAC		TCGTCACNNNNCTAGCGTTAC		ACTCTCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	2258	TGCAGGACCAGAGAATTCGAATACAA	2498	TGCAGGACCAGAGAATTCGAATACAT	2738
CCATCTANNNNCTAGCGTTAC		TTATGACNNNNCTAGCGTTAC		ATGAGTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	2259	TGCAGGACCAGAGAATTCGAATACAT	2499	TGCAGGACCAGAGAATTCGAATACAA	2739
TAAGGTGNNNNCTAGCGTTAC		TTTAGAGNNNNCTAGCGTTAC		GGCGTCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	2260	TGCAGGACCAGAGAATTCGAATACAG	2500	TGCAGGACCAGAGAATTCGAATACAA	2740
ACCGACGNNNNCTAGCGTTAC		ATATACTNNNNCTAGCGTTAC		GAATTAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	2261	TGCAGGACCAGAGAATTCGAATACAC	2501	TGCAGGACCAGAGAATTCGAATACAG	2741
TTTAGATNNNNCTAGCGTTAC		CTACCCGNNNNCTAGCGTTAC		ATTTAGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAT	2262	TGCAGGACCAGAGAATTCGAATACAA	2502	TGCAGGACCAGAGAATTCGAATACAT	2742
CCCTCCNNNNCTAGCGTTAC		ACCTTTTTNNNNCTAGCGTTAC		ATTTCTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAT	2263	TGCAGGACCAGAGAATTCGAATACAA	2503	TGCAGGACCAGAGAATTCGAATACAG	2743
TAATCAGNNNNCTAGCGTTAC		TGTGTATNNNNCTAGCGTTAC		CTGTACANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	2264	TGCAGGACCAGAGAATTCGAATACAT	2504	TGCAGGACCAGAGAATTCGAATACAG	2744
ATTGAGNNNNCTAGCGTTAC		CCCACGNNNNCTAGCGTTAC		CTTACGANNNNCTAGCGTTAC	

FIG. 15C

Pool-10	SEQ ID NO:	Pool-11	SEQ ID NO:	Pool-12	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATACAA ACCGTGTNNNCTAGCGTTAC	2265	TGCAGGACCAGAGAATTCTGAATACAC GCCTCTGNNNCTAGCGTTAC	2505	TGCAGGACCAGAGAATTCTGAATACAC CCACGGANNNCTAGCGTTAC	2745
TGCAGGACCAGAGAATTCTGAATACAC CCAAATTCNNNCTAGCGTTAC	2266	TGCAGGACCAGAGAATTCTGAATACAC TATAACANNNCTAGCGTTAC	2506	TGCAGGACCAGAGAATTCTGAATACAT GGATCTGNNNCTAGCGTTAC	2746
TGCAGGACCAGAGAATTCTGAATACAT TGGTGGTNNNCTAGCGTTAC	2267	TGCAGGACCAGAGAATTCTGAATACAG ACTGACTNNNCTAGCGTTAC	2507	TGCAGGACCAGAGAATTCTGAATACAT CCACGAANNNCTAGCGTTAC	2747
TGCAGGACCAGAGAATTCTGAATACAT GCTTAGGNNNCTAGCGTTAC	2268	TGCAGGACCAGAGAATTCTGAATACAC TGGCCAGNNNCTAGCGTTAC	2508	TGCAGGACCAGAGAATTCTGAATACAT CAAGACNNNCTAGCGTTAC	2748
TGCAGGACCAGAGAATTCTGAATACAA CACCCCNNNCTAGCGTTAC	2269	TGCAGGACCAGAGAATTCTGAATACAA AGCCAGNNNCTAGCGTTAC	2509	TGCAGGACCAGAGAATTCTGAATACAG GCAGACNNNCTAGCGTTAC	2749
TGCAGGACCAGAGAATTCTGAATACAC CATTAGGNNNCTAGCGTTAC	2270	TGCAGGACCAGAGAATTCTGAATACAC GCTTTTNNNCTAGCGTTAC	2510	TGCAGGACCAGAGAATTCTGAATACAT TTTACGNNNCTAGCGTTAC	2750
TGCAGGACCAGAGAATTCTGAATACAA CTTAAACNNNCTAGCGTTAC	2271	TGCAGGACCAGAGAATTCTGAATACAT TTCCTTCNNNCTAGCGTTAC	2511	TGCAGGACCAGAGAATTCTGAATACAG CGTTTGTANNNCTAGCGTTAC	2751
TGCAGGACCAGAGAATTCTGAATACAT ATAGTAGNNNCTAGCGTTAC	2272	TGCAGGACCAGAGAATTCTGAATACAC TTACTCGNNNCTAGCGTTAC	2512	TGCAGGACCAGAGAATTCTGAATACAA GGTACTGNNNCTAGCGTTAC	2752
TGCAGGACCAGAGAATTCTGAATACAC AGTGTACNNNCTAGCGTTAC	2273	TGCAGGACCAGAGAATTCTGAATACAA TCGAGTCNNNCTAGCGTTAC	2513	TGCAGGACCAGAGAATTCTGAATACAT TCTGTTANNNCTAGCGTTAC	2753
TGCAGGACCAGAGAATTCTGAATACAG CGTCTTTNNNCTAGCGTTAC	2274	TGCAGGACCAGAGAATTCTGAATACAT TGACGNNNCTAGCGTTAC	2514	TGCAGGACCAGAGAATTCTGAATACAC CGATGTANNNCTAGCGTTAC	2754
TGCAGGACCAGAGAATTCTGAATACAT GACTCAGNNNCTAGCGTTAC	2275	TGCAGGACCAGAGAATTCTGAATACAC ACCATTNNNCTAGCGTTAC	2515	TGCAGGACCAGAGAATTCTGAATACAG TCGGTTANNNCTAGCGTTAC	2755
TGCAGGACCAGAGAATTCTGAATACAA CTTAGTANNNCTAGCGTTAC	2276	TGCAGGACCAGAGAATTCTGAATACAC CCTCTTTNNNCTAGCGTTAC	2516	TGCAGGACCAGAGAATTCTGAATACAC GAACCCGNNNCTAGCGTTAC	2756
TGCAGGACCAGAGAATTCTGAATACAA AACATGANNNCTAGCGTTAC	2277	TGCAGGACCAGAGAATTCTGAATACAT GCATTAAANNNCTAGCGTTAC	2517	TGCAGGACCAGAGAATTCTGAATACAT TCGACTCNNNCTAGCGTTAC	2757
TGCAGGACCAGAGAATTCTGAATACAG TTAGGCTNNNCTAGCGTTAC	2278	TGCAGGACCAGAGAATTCTGAATACAC GTAGCGCNNNCTAGCGTTAC	2518	TGCAGGACCAGAGAATTCTGAATACAT TCAGCCNNNCTAGCGTTAC	2758
TGCAGGACCAGAGAATTCTGAATACAT CCGCAGNNNCTAGCGTTAC	2279	TGCAGGACCAGAGAATTCTGAATACAG TCTCTANNNCTAGCGTTAC	2519	TGCAGGACCAGAGAATTCTGAATACAC ACTTGAGNNNCTAGCGTTAC	2759
TGCAGGACCAGAGAATTCTGAATACAA GTACATTNNNCTAGCGTTAC	2280	TGCAGGACCAGAGAATTCTGAATACAT GCGCCGANNNCTAGCGTTAC	2520	TGCAGGACCAGAGAATTCTGAATACAT CACGCGNNNCTAGCGTTAC	2760
TGCAGGACCAGAGAATTCTGAATACAG GTGCTATNNNCTAGCGTTAC	2281	TGCAGGACCAGAGAATTCTGAATACAC AATGATTNNNCTAGCGTTAC	2521	TGCAGGACCAGAGAATTCTGAATACAC ACTGTAGNNNCTAGCGTTAC	2761
TGCAGGACCAGAGAATTCTGAATACAA GACGACANNNCTAGCGTTAC	2282	TGCAGGACCAGAGAATTCTGAATACAA GCGAGGCNNNCTAGCGTTAC	2522	TGCAGGACCAGAGAATTCTGAATACAA CCAAGCTNNNCTAGCGTTAC	2762
TGCAGGACCAGAGAATTCTGAATACAA AGTTCTANNNCTAGCGTTAC	2283	TGCAGGACCAGAGAATTCTGAATACAT TGAATACNNNCTAGCGTTAC	2523	TGCAGGACCAGAGAATTCTGAATACAA CTGCAACNNNCTAGCGTTAC	2763
TGCAGGACCAGAGAATTCTGAATACAA CCGAACNNNCTAGCGTTAC	2284	TGCAGGACCAGAGAATTCTGAATACAA CCGCCAGNNNCTAGCGTTAC	2524	TGCAGGACCAGAGAATTCTGAATACAT AACGGTCNNNCTAGCGTTAC	2764
TGCAGGACCAGAGAATTCTGAATACAG GCAATTCNNNCTAGCGTTAC	2285	TGCAGGACCAGAGAATTCTGAATACAG GCCAGAGNNNCTAGCGTTAC	2525	TGCAGGACCAGAGAATTCTGAATACAA GTTTGTANNNCTAGCGTTAC	2765
TGCAGGACCAGAGAATTCTGAATACAG TCACACANNNCTAGCGTTAC	2286	TGCAGGACCAGAGAATTCTGAATACAA TATCCAANNNCTAGCGTTAC	2526	TGCAGGACCAGAGAATTCTGAATACAC ACGTTTCNNNCTAGCGTTAC	2766
TGCAGGACCAGAGAATTCTGAATACAC GGAAATGNNNCTAGCGTTAC	2287	TGCAGGACCAGAGAATTCTGAATACAA TGTTGTANNNCTAGCGTTAC	2527	TGCAGGACCAGAGAATTCTGAATACAT TAAACNNNCTAGCGTTAC	2767
TGCAGGACCAGAGAATTCTGAATACAC TGTCTACNNNCTAGCGTTAC	2288	TGCAGGACCAGAGAATTCTGAATACAG ATTGTTANNNCTAGCGTTAC	2528	TGCAGGACCAGAGAATTCTGAATACAT TCGTAGGNNNCTAGCGTTAC	2768
TGCAGGACCAGAGAATTCTGAATACAG AGCCAGGNNNGATCGACATG	2289	TGCAGGACCAGAGAATTCTGAATACAG TCCACGGNNNGATCGACATG	2529	TGCAGGACCAGAGAATTCTGAATACAT GCGTAGTNNNGATCGACATG	2769
TGCAGGACCAGAGAATTCTGAATACAC ACTCCTANNNGATCGACATG	2290	TGCAGGACCAGAGAATTCTGAATACAT GACTGACNNNGATCGACATG	2530	TGCAGGACCAGAGAATTCTGAATACAG CTTTGCTNNNGATCGACATG	2770
TGCAGGACCAGAGAATTCTGAATACAC TTTCCCTNNNGATCGACATG	2291	TGCAGGACCAGAGAATTCTGAATACAT GATTAGNNNGATCGACATG	2531	TGCAGGACCAGAGAATTCTGAATACAG TAAATAGNNNGATCGACATG	2771
TGCAGGACCAGAGAATTCTGAATACAC TGAGCTANNNGATCGACATG	2292	TGCAGGACCAGAGAATTCTGAATACAA CATAGTANNNGATCGACATG	2532	TGCAGGACCAGAGAATTCTGAATACAC GCTGTCCNNNGATCGACATG	2772
TGCAGGACCAGAGAATTCTGAATACAG TCTGACANNNGATCGACATG	2293	TGCAGGACCAGAGAATTCTGAATACAA GCATCCANNNGATCGACATG	2533	TGCAGGACCAGAGAATTCTGAATACAC TTAGAGCANNNGATCGACATG	2773
TGCAGGACCAGAGAATTCTGAATACAC TGACGCGNNNGATCGACATG	2294	TGCAGGACCAGAGAATTCTGAATACAA CGGCAANNNGATCGACATG	2534	TGCAGGACCAGAGAATTCTGAATACAG GACATAGNNNGATCGACATG	2774
TGCAGGACCAGAGAATTCTGAATACAG TGATGGANNNGATCGACATG	2295	TGCAGGACCAGAGAATTCTGAATACAC TTTGCTGNNNGATCGACATG	2535	TGCAGGACCAGAGAATTCTGAATACAT CTACAGGNNNGATCGACATG	2775
TGCAGGACCAGAGAATTCTGAATACAG AATTCTANNNGATCGACATG	2296	TGCAGGACCAGAGAATTCTGAATACAT TAACTAGNNNGATCGACATG	2536	TGCAGGACCAGAGAATTCTGAATACAC AAACTCGNNNGATCGACATG	2776

FIG. 15D

Pool-10	SEQ ID NO:	Pool-11	SEQ ID NO:	Pool-12	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG	
GTGCATANNNGATCGACATG	2297	GTACTGANNNGATCGACATG	2537	CTATTCCNNNGATCGACATG	2777
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG	
GGCGTGCNNNGATCGACATG	2298	AGTATCANNNGATCGACATG	2538	TCCAGTANNNGATCGACATG	2778
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG	
CAGTCCGNNNGATCGACATG	2299	CTGACAAANNNGATCGACATG	2539	GCGAGACNNNGATCGACATG	2779
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT	
GCCCTGCNNNGATCGACATG	2300	GTGGCCANNNGATCGACATG	2540	TTCATACNNNGATCGACATG	2780
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAC	
CCGTCCGNNNGATCGACATG	2301	CGTATACNNNGATCGACATG	2541	AGCTGTANNNGATCGACATG	2781
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAA	
ACGCTCANNNGATCGACATG	2302	CGCTGCANNNGATCGACATG	2542	CTGCTCANNNGATCGACATG	2782
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAA	
CTCCATTNNNGATCGACATG	2303	CCGTAGNNNGATCGACATG	2543	AAGTTCNNNGATCGACATG	2783
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG	
ACTCCTTNNNGATCGACATG	2304	GTACTTTNNNGATCGACATG	2544	AATCGANNNGATCGACATG	2784
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC	
GTAAC TANNNGATCGACATG	2305	ATTATGANNNGATCGACATG	2545	TCCCGCANNNGATCGACATG	2785
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG	
GAGTCTCANNNGATCGACATG	2306	AGACCGCANNNGATCGACATG	2546	AAAAC TANNNGATCGACATG	2786
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA	
TTTCTAANNNGATCGACATG	2307	AGCACCANNNGATCGACATG	2547	CCCTAAGNNNGATCGACATG	2787
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG	
GAGACCCNNNGATCGACATG	2308	GGAGTGANNNGATCGACATG	2548	GTCATACNNNGATCGACATG	2788
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT	
TTTAGT CANNNGATCGACATG	2309	GACGTGGNNNGATCGACATG	2549	GGTTGTGNNNGATCGACATG	2789
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA	
TGTGCTGNNNGATCGACATG	2310	CTTACACNNNGATCGACATG	2550	AGTTCGNNNGATCGACATG	2790
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA	
CCAGGTGNNNGATCGACATG	2311	GGCAGCCNNNGATCGACATG	2551	TCAATGTNNNGATCGACATG	2791
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC	
AACCAAGNNNGATCGACATG	2312	CTTACTGNNNGATCGACATG	2552	ATTGATANNNGATCGACATG	2792
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG	
CTGAGGCNNNGATCGACATG	2313	TACTCTANNNGATCGACATG	2553	GAGGAAANNNGATCGACATG	2793
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC	
TAAGCGGNNNGATCGACATG	2314	CGCCTACNNNGATCGACATG	2554	ATTTTACNNNGATCGACATG	2794
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG	
TTGTCTANNNGATCGACATG	2315	CTTAGAGNNNGATCGACATG	2555	AACTTCGNNNGATCGACATG	2795
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC	
GCGTTTGNNGATCGACATG	2316	TCTAIGTNNNGATCGACATG	2556	GTCACCCNNNGATCGACATG	2796
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA	
CTATTTNNNGATCGACATG	2317	TTTACACNNNGATCGACATG	2557	CGTTAATNNNGATCGACATG	2797
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG	
GACACCANNNGATCGACATG	2318	TGTTTTGNNNGATCGACATG	2558	GTGTGTTNNNGATCGACATG	2798
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG	
GCTCAANNNGATCGACATG	2319	AAAGACGNNNGATCGACATG	2559	AAATAGTNNNGATCGACATG	2799
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG	
CGCATTANNNGATCGACATG	2320	CCTCCG CNNNGATCGACATG	2560	TCTATTTNNNGATCGACATG	2800
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT	
CTAAATGNNNGATCGACATG	2321	TTAACATNNNGATCGACATG	2561	AGTAGCCNNNGATCGACATG	2801
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG	
GCACTACNNNGATCGACATG	2322	GATGGCCNNNGATCGACATG	2562	TACAAAANNNGATCGACATG	2802
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA	
ATTCAGCANNNGATCGACATG	2323	CTCGAAANNNGATCGACATG	2563	GAGTACGNNNGATCGACATG	2803
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT	
TGCTCCGNNNGATCGACATG	2324	TGTCGACNNNGATCGACATG	2564	AGACTTANNNGATCGACATG	2804
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC	
CAGGATTNNNGATCGACATG	2325	AACGAC CNNNGATCGACATG	2565	GAGCAANNNGATCGACATG	2805
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAA	
TGTCATANNNGATCGACATG	2326	CGCAGTCNNNGATCGACATG	2566	GCGTCCGNNNGATCGACATG	2806
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG	
CAGGACANNNGATCGACATG	2327	TCATAACNNNGATCGACATG	2567	CTGGTCGNNNGATCGACATG	2807
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAA	
CGTAAGTNNNGATCGACATG	2328	AGGTCTCNNNGATCGACATG	2568	GTCCACANNNGATCGACATG	2808

FIG. 15E

Pool-10	SEQ ID NO:	Pool-11	SEQ ID NO:	Pool-12	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT	
AAGAATCANNNGATCGACATG	2329	AAATACANNNGATCGACATG	2569	CCCTTAGNNNGATCGACATG	2809
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC	
AAGCCTANNNGATCGACATG	2330	CGTACTGNNNGATCGACATG	2570	CGGATGNNNGATCGACATG	2810
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT	
TAACATAANNNGATCGACATG	2331	TTAAGTCNNNGATCGACATG	2571	CTATATCANNNGATCGACATG	2811
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAA	
GCGTAATNNNGATCGACATG	2332	GTCAAAGNNNGATCGACATG	2572	GACCCCTANNNGATCGACATG	2812
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG	
AGGTCTTNNNGATCGACATG	2333	GTTAATTNNNGATCGACATG	2573	GCTGGTCNNNGATCGACATG	2813
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG	
ACCGCTGNNNGATCGACATG	2334	GACAGGTNNNGATCGACATG	2574	ACGATGANNNGATCGACATG	2814
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG	
CTCAACANNNGATCGACATG	2335	CCAGTGGNNNGATCGACATG	2575	CCCATAAANNNGATCGACATG	2815
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA	
TCAGGAGNNNGATCGACATG	2336	CCAAGGTNNNGATCGACATG	2576	CTTTCATNNNGATCGACATG	2816
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAT	
CCGAGGNNNGATCGACATG	2337	GAGTATTNNNGATCGACATG	2577	CGACTTCNNNGATCGACATG	2817
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC	
AGGTGGCNNNGATCGACATG	2338	GTACGGTNNNGATCGACATG	2578	GCTACTTNNNGATCGACATG	2818
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC	
CCAAGCCNNNGATCGACATG	2339	GCGTCAGNNNGATCGACATG	2579	GAAAACGNNNGATCGACATG	2819
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT	
TGGTGGCNNNGATCGACATG	2340	GGATGTTNNNGATCGACATG	2580	TATGGCCNNNGATCGACATG	2820
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG	
GTATGTGNNNGATCGACATG	2341	ACAAGGTNNNGATCGACATG	2581	CTATTAANNNGATCGACATG	2821
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG	
GCGTTTCNNNGATCGACATG	2342	TTAAAAANNNGATCGACATG	2582	GCCCCGNNNGATCGACATG	2822
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG	
AAATTTANNNGATCGACATG	2343	CGACCCGNNNGATCGACATG	2583	ACGCTGCNNNGATCGACATG	2823
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA	
CGGACATNNNGATCGACATG	2344	CAAACCTANNNGATCGACATG	2584	CGAGCCCNNGATCGACATG	2824
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT	
AAACACTNNNGATCGACATG	2345	ACGCCGANNNGATCGACATG	2585	TCATCGCNNNGATCGACATG	2825
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC	
TAGGCCANNNGATCGACATG	2346	GATCAGTNNNGATCGACATG	2586	ATAAAAGNNNGATCGACATG	2826
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC	
GCCCTCCNNNGATCGACATG	2347	ACTTTGNNNGATCGACATG	2587	TCGCGCTNNNGATCGACATG	2827
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG	
GGAAAACNNNGATCGACATG	2348	CCTGATCNNNGATCGACATG	2588	ACATGTGNNNGATCGACATG	2828
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAC	
GCCGGTTNNNTGCATCAGGT	2349	AACTCCANNNTGCATCAGGT	2589	TCACCCGNNNTGCATCAGGT	2829
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAC	
AGGCTACNNNTGCATCAGGT	2350	GTCAATCNNNTGCATCAGGT	2590	ACGTCTTNNNTGCATCAGGT	2830
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA	
CACCTTGTNNNTGCATCAGGT	2351	ATGCAGCNNNTGCATCAGGT	2591	CTGCGTANNNTGCATCAGGT	2831
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT	
ATAGAGCNNNTGCATCAGGT	2352	CACCTCCNNNTGCATCAGGT	2592	AAATTATNNNTGCATCAGGT	2832
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAT	
GTCCAGTNNNTGCATCAGGT	2353	CAAGTGCNNNTGCATCAGGT	2593	AGTCTAANNNTGCATCAGGT	2833
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC	
TCATCAGNNNTGCATCAGGT	2354	TGCCGTTNNNTGCATCAGGT	2594	AAACTATNNNTGCATCAGGT	2834
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT	
TTCCGAGNNNTGCATCAGGT	2355	TGGAGTANNNTGCATCAGGT	2595	CACCTGTCNNNTGCATCAGGT	2835
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAA	
TCAGGATNNNTGCATCAGGT	2356	CCTCACNNNTGCATCAGGT	2596	ACAAATGNNNTGCATCAGGT	2836
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT	
CTATCCANNNTGCATCAGGT	2357	CACACANNNTGCATCAGGT	2597	TTTCTTCNNNTGCATCAGGT	2837
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC	
AATGCTGNNNTGCATCAGGT	2358	CCCCATTNNNTGCATCAGGT	2598	TTCACTCNNNTGCATCAGGT	2838
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAA	
GGTGAAANNNTGCATCAGGT	2359	TAGTCTANNNTGCATCAGGT	2599	GGTCTGNNNTGCATCAGGT	2839
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG	
TTGCAACNNNTGCATCAGGT	2360	AATGTCCNNNTGCATCAGGT	2600	CAAACGNNNTGCATCAGGT	2840

FIG. 15F

Pool-10	SEQ ID NO:	Pool-11	SEQ ID NO:	Pool-12	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAG	2361	TGCAGGACCAGAGAATTCGAATACAC	2601	TGCAGGACCAGAGAATTCGAATACAC	2841
AGAGCTANNNTGCATCAGGT		TAGATCGNNNTGCATCAGGT		CGAGAGGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	2362	TGCAGGACCAGAGAATTCGAATACAG	2602	TGCAGGACCAGAGAATTCGAATACAA	2842
CCTAACANNNTGCATCAGGT		GCAACCCNNNTGCATCAGGT		TATTGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	2363	TGCAGGACCAGAGAATTCGAATACAG	2603	TGCAGGACCAGAGAATTCGAATACAT	2843
TGAGACTNNNTGCATCAGGT		GAGAGAANNNTGCATCAGGT		CTCTGGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAA	2364	TGCAGGACCAGAGAATTCGAATACAG	2604	TGCAGGACCAGAGAATTCGAATACAA	2844
CGTTGCGNNNTGCATCAGGT		TTGTCGCTNNNTGCATCAGGT		TTGGAGGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	2365	TGCAGGACCAGAGAATTCGAATACAT	2605	TGCAGGACCAGAGAATTCGAATACAC	2845
GAAGCTANNNTGCATCAGGT		GGCATACNNNTGCATCAGGT		ATCATTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	2366	TGCAGGACCAGAGAATTCGAATACAG	2606	TGCAGGACCAGAGAATTCGAATACAG	2846
CCTGTATNNNTGCATCAGGT		AGGCAATNNNTGCATCAGGT		AGGTGATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	2367	TGCAGGACCAGAGAATTCGAATACAT	2607	TGCAGGACCAGAGAATTCGAATACAC	2847
AGCCTCTNNNTGCATCAGGT		CTCAGGTNNNTGCATCAGGT		CCCGTCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAA	2368	TGCAGGACCAGAGAATTCGAATACAC	2608	TGCAGGACCAGAGAATTCGAATACAG	2848
GGTACCTNNNTGCATCAGGT		TGCGGCANNNTGCATCAGGT		ACAGGTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	2369	TGCAGGACCAGAGAATTCGAATACAC	2609	TGCAGGACCAGAGAATTCGAATACAG	2849
GTATCTNNNTGCATCAGGT		TTAATGANNNTGCATCAGGT		CCTTAGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	2370	TGCAGGACCAGAGAATTCGAATACAA	2610	TGCAGGACCAGAGAATTCGAATACAC	2850
ACTTACGNNNTGCATCAGGT		ACTCAGNNNTGCATCAGGT		CTTCTAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAA	2371	TGCAGGACCAGAGAATTCGAATACAA	2611	TGCAGGACCAGAGAATTCGAATACAA	2851
CTTCCANNNTGCATCAGGT		GCAGTGANNNTGCATCAGGT		GGCTTGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	2372	TGCAGGACCAGAGAATTCGAATACAT	2612	TGCAGGACCAGAGAATTCGAATACAT	2852
CTTCTGANNNTGCATCAGGT		AATAGTNNNTGCATCAGGT		GGAGTTCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	2373	TGCAGGACCAGAGAATTCGAATACAA	2613	TGCAGGACCAGAGAATTCGAATACAC	2853
GACACTANNNTGCATCAGGT		AAGTCCCNNTGCATCAGGT		CACCGAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	2374	TGCAGGACCAGAGAATTCGAATACAG	2614	TGCAGGACCAGAGAATTCGAATACAG	2854
TGTGAGTNNNTGCATCAGGT		CTGGAAANNNTGCATCAGGT		GAATGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAA	2375	TGCAGGACCAGAGAATTCGAATACAA	2615	TGCAGGACCAGAGAATTCGAATACAA	2855
GAGACACNNNTGCATCAGGT		AGAGGAGNNNTGCATCAGGT		CATTACANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	2376	TGCAGGACCAGAGAATTCGAATACAG	2616	TGCAGGACCAGAGAATTCGAATACAA	2856
AATTGTGNNNTGCATCAGGT		TGCAAGTNNNTGCATCAGGT		GTCTCTCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	2377	TGCAGGACCAGAGAATTCGAATACAC	2617	TGCAGGACCAGAGAATTCGAATACAT	2857
TAATTTGNNNTGCATCAGGT		GCGGACTNNNTGCATCAGGT		AGTGCCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	2378	TGCAGGACCAGAGAATTCGAATACAT	2618	TGCAGGACCAGAGAATTCGAATACAG	2858
ATACTATNNNTGCATCAGGT		ACTTGTNNNTGCATCAGGT		CAATGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAA	2379	TGCAGGACCAGAGAATTCGAATACAA	2619	TGCAGGACCAGAGAATTCGAATACAG	2859
GTGGATGNNNTGCATCAGGT		ACTGACNNNTGCATCAGGT		TTGAATTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	2380	TGCAGGACCAGAGAATTCGAATACAT	2620	TGCAGGACCAGAGAATTCGAATACAC	2860
TAATAGACNNNTGCATCAGGT		GCTGGTANNNTGCATCAGGT		CACCTTCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	2381	TGCAGGACCAGAGAATTCGAATACAA	2621	TGCAGGACCAGAGAATTCGAATACAT	2861
AGTTTTCGNNNTGCATCAGGT		TATTTTNNNTGCATCAGGT		CCATTTCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	2382	TGCAGGACCAGAGAATTCGAATACAT	2622	TGCAGGACCAGAGAATTCGAATACAC	2862
AGAGATGNNNTGCATCAGGT		CCCCATANNNTGCATCAGGT		ACTCTCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	2383	TGCAGGACCAGAGAATTCGAATACAC	2623	TGCAGGACCAGAGAATTCGAATACAG	2863
ACTCAACNNNTGCATCAGGT		AAGTTGCGNNNTGCATCAGGT		ACCTGATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	2384	TGCAGGACCAGAGAATTCGAATACAT	2624	TGCAGGACCAGAGAATTCGAATACAA	2864
TCGCTGTNNNTGCATCAGGT		GAACCGTNNNTGCATCAGGT		GAGCTCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	2385	TGCAGGACCAGAGAATTCGAATACAC	2625	TGCAGGACCAGAGAATTCGAATACAC	2865
GTCCGAGNNNTGCATCAGGT		GCATTGANNNTGCATCAGGT		TGGATTGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	2386	TGCAGGACCAGAGAATTCGAATACAC	2626	TGCAGGACCAGAGAATTCGAATACAT	2866
CATGCATNNNTGCATCAGGT		GGCGTTGNNNTGCATCAGGT		GCTATCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAA	2387	TGCAGGACCAGAGAATTCGAATACAC	2627	TGCAGGACCAGAGAATTCGAATACAG	2867
AAGTGCGNNNTGCATCAGGT		CCGCCGNNNTGCATCAGGT		ACGTTGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	2388	TGCAGGACCAGAGAATTCGAATACAC	2628	TGCAGGACCAGAGAATTCGAATACAA	2868
AAAGCACNNNTGCATCAGGT		AAGCTACNNNTGCATCAGGT		TTTATCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	2389	TGCAGGACCAGAGAATTCGAATACAC	2629	TGCAGGACCAGAGAATTCGAATACAC	2869
GGTGTGNNNTGCATCAGGT		GGTTCAANNNTGCATCAGGT		GATTCAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	2390	TGCAGGACCAGAGAATTCGAATACAC	2630	TGCAGGACCAGAGAATTCGAATACAT	2870
CGGAAGCANNNTGCATCAGGT		AACGTTGNNNTGCATCAGGT		GGTGCATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAA	2391	TGCAGGACCAGAGAATTCGAATACAG	2631	TGCAGGACCAGAGAATTCGAATACAT	2871
TCACATANNNTGCATCAGGT		TACTAGCANNNTGCATCAGGT		GTGTTTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAA	2392	TGCAGGACCAGAGAATTCGAATACAT	2632	TGCAGGACCAGAGAATTCGAATACAT	2872
CTCTCTGNNNTGCATCAGGT		GAGTGTGNNNTGCATCAGGT		GGCATCANNNTGCATCAGGT	

FIG. 15G

Pool-10	SEQ ID NO:	Pool-11	SEQ ID NO:	Pool-12	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACACGCCCCGNNNTGCATCAGGT	2393	TGCAGGACCAGAGAATTCGAATACACAAACAGGNNNTGCATCAGGT	2633	TGCAGGACCAGAGAATTCGAATACATAAGCTGCGNNNTGCATCAGGT	2873
TGCAGGACCAGAGAATTCGAATACATTAAATCCNNNTGCATCAGGT	2394	TGCAGGACCAGAGAATTCGAATACAGCATGCTANNNTGCATCAGGT	2634	TGCAGGACCAGAGAATTCGAATACAA CGGACTTNNNTGCATCAGGT	2874
TGCAGGACCAGAGAATTCGAATACACCGTCGGANNNTGCATCAGGT	2395	TGCAGGACCAGAGAATTCGAATACAGATTACAGNNNTGCATCAGGT	2635	TGCAGGACCAGAGAATTCGAATACATGAATTACNNNTGCATCAGGT	2875
TGCAGGACCAGAGAATTCGAATACATGAGAAATNNNTGCATCAGGT	2396	TGCAGGACCAGAGAATTCGAATACAGTAGATCCNNNTGCATCAGGT	2636	TGCAGGACCAGAGAATTCGAATACAAACAGAGCNNNTGCATCAGGT	2876
TGCAGGACCAGAGAATTCGAATACACGTATAANNNTGCATCAGGT	2397	TGCAGGACCAGAGAATTCGAATACACGCCACGNNNTGCATCAGGT	2637	TGCAGGACCAGAGAATTCGAATACACATGTTCCNNNTGCATCAGGT	2877
TGCAGGACCAGAGAATTCGAATACATCTAAACNNNTGCATCAGGT	2398	TGCAGGACCAGAGAATTCGAATACAGAGCATAGNNNTGCATCAGGT	2638	TGCAGGACCAGAGAATTCGAATACATCGTCTACNNNTGCATCAGGT	2878
TGCAGGACCAGAGAATTCGAATACAACTCTCGANNNTGCATCAGGT	2399	TGCAGGACCAGAGAATTCGAATACAGGTGTCATNNNTGCATCAGGT	2639	TGCAGGACCAGAGAATTCGAATACAGTAGAGACNNNTGCATCAGGT	2879
TGCAGGACCAGAGAATTCGAATACAGCATCGTANNNTGCATCAGGT	2400	TGCAGGACCAGAGAATTCGAATACATCTTCGACNNNTGCATCAGGT	2640	TGCAGGACCAGAGAATTCGAATACATATAGTGTNNNTGCATCAGGT	2880
TGCAGGACCAGAGAATTCGAATACAGTAAGACGNNNTGCATCAGGT	2401	TGCAGGACCAGAGAATTCGAATACAGATCAGCTNNNTGCATCAGGT	2641	TGCAGGACCAGAGAATTCGAATACAGGAGAGTTNNNTGCATCAGGT	2881
TGCAGGACCAGAGAATTCGAATACAAAGCCCTNNNTGCATCAGGT	2402	TGCAGGACCAGAGAATTCGAATACATCGACCTTNNNTGCATCAGGT	2642	TGCAGGACCAGAGAATTCGAATACATACATTCNNNTGCATCAGGT	2882
TGCAGGACCAGAGAATTCGAATACACCATGGTANNNTGCATCAGGT	2403	TGCAGGACCAGAGAATTCGAATACAA GCCCAGGNNNTGCATCAGGT	2643	TGCAGGACCAGAGAATTCGAATACACACAATGCGNNNTGCATCAGGT	2883
TGCAGGACCAGAGAATTCGAATACACGAAATAANNNTGCATCAGGT	2404	TGCAGGACCAGAGAATTCGAATACAGAGATCTCNNNTGCATCAGGT	2644	TGCAGGACCAGAGAATTCGAATACAGATATTACNNNTGCATCAGGT	2884
TGCAGGACCAGAGAATTCGAATACAGATCAAAANNNTGCATCAGGT	2405	TGCAGGACCAGAGAATTCGAATACATCTTTAACNNNTGCATCAGGT	2645	TGCAGGACCAGAGAATTCGAATACACGGCTTTNNNTGCATCAGGT	2885
TGCAGGACCAGAGAATTCGAATACAA GTCCGCGNNNTGCATCAGGT	2406	TGCAGGACCAGAGAATTCGAATACATCCCTAACNNNTGCATCAGGT	2646	TGCAGGACCAGAGAATTCGAATACAGCTGCTGNNNTGCATCAGGT	2886
TGCAGGACCAGAGAATTCGAATACACCTGGCTNNNTGCATCAGGT	2407	TGCAGGACCAGAGAATTCGAATACAACTCGACANNNTGCATCAGGT	2647	TGCAGGACCAGAGAATTCGAATACAAAGGCGCGNNNTGCATCAGGT	2887
TGCAGGACCAGAGAATTCGAATACACAAGTTCGNNNTGCATCAGGT	2408	TGCAGGACCAGAGAATTCGAATACATGAGAGACNNNTGCATCAGGT	2648	TGCAGGACCAGAGAATTCGAATACAA CGGTGAANNNTGCATCAGGT	2888

FIG. 16A

Pool-13	SEQ ID NO.	Pool-14	SEQ ID NO.	Pool-15	SEQ ID NO.
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG	
CACGGACNNNACGTATGCCA	2889	ATGCGTANNNNACGTATGCCA	3129	TGTGATCNNNACGTATGCCA	3369
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA	
ATCCTCCNNNACGTATGCCA	2890	CGTGGGNNNACGTATGCCA	3130	AAGCGCANNNACGTATGCCA	3370
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
TGGCCGTNNNACGTATGCCA	2891	TAGTGGANNNACGTATGCCA	3131	CGTGGATNNNACGTATGCCA	3371
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
GAGTAGCANNNACGTATGCCA	2892	TTGTTGGNNNACGTATGCCA	3132	CACCGAANNNACGTATGCCA	3372
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
CCTGCGCNNNACGTATGCCA	2893	GAGCTTCNNNACGTATGCCA	3133	CGGTTGGNNNACGTATGCCA	3373
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
TCTCGTGNNNACGTATGCCA	2894	TACTGTGNNNACGTATGCCA	3134	CACGGTTNNNACGTATGCCA	3374
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
GGTATGCNNNACGTATGCCA	2895	GCAACCTNNNACGTATGCCA	3135	CTCAGGNNNACGTATGCCA	3375
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC	
TCACTCCNNNACGTATGCCA	2896	CCCTGCTNNNACGTATGCCA	3136	AATCGCANNNACGTATGCCA	3376
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT	
ACAAGGCNNNACGTATGCCA	2897	TCTCGCGNNNACGTATGCCA	3137	AATATATNNNACGTATGCCA	3377
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC	
CGTCTTANNNACGTATGCCA	2898	TACTTGCNNNACGTATGCCA	3138	ATTACCCNNNACGTATGCCA	3378
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
AAAATTANNNACGTATGCCA	2899	TAATGAGNNNACGTATGCCA	3139	ACTACTGNNNACGTATGCCA	3379
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG	
CACAGAGNNNACGTATGCCA	2900	CGTAGTANNNACGTATGCCA	3140	TGCAGGACCAGAGAATTGGAATACAG	
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
GTGCGCTNNNACGTATGCCA	2901	GCAACAGNNNACGTATGCCA	3141	GCTATTGNNNACGTATGCCA	3381
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG	
GTGACGCGNNNACGTATGCCA	2902	TGTGTCTNNNACGTATGCCA	3142	GTGGTGGNNNACGTATGCCA	3382
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
ACCCCTNNNACGTATGCCA	2903	CCAACGNNNACGTATGCCA	3143	GGGTACANNNACGTATGCCA	3383
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA	
CATTGANNNACGTATGCCA	2904	GTCAAGCANNNACGTATGCCA	3144	TTCTTCANNNACGTATGCCA	3384
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT	
GTGGCAGNNNACGTATGCCA	2905	GTGTACANNNACGTATGCCA	3145	CTGGTCTNNNACGTATGCCA	3385
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG	
AGGCCAGNNNACGTATGCCA	2906	CTCAAGANNNACGTATGCCA	3146	CGAGCCCTNNNACGTATGCCA	3386
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
CTCGAGTNNNACGTATGCCA	2907	TGAAGCANNNACGTATGCCA	3147	GCCGTGCGNNNACGTATGCCA	3387
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
CAAAAGNNNACGTATGCCA	2908	TGCGCCNNNACGTATGCCA	3148	ATAACCCNNNACGTATGCCA	3388
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC	
AGCAACGNNNACGTATGCCA	2909	TATTGCGNNNACGTATGCCA	3149	GGAACCCNNNACGTATGCCA	3389
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
CGTTTGTNNNACGTATGCCA	2910	CAAATAGNNNACGTATGCCA	3150	TCAGCGCANNNACGTATGCCA	3390
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC	
GGATGCTNNNACGTATGCCA	2911	TACGCGGNNNACGTATGCCA	3151	GTGAGCCNNNACGTATGCCA	3391
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
CAATGGCANNNACGTATGCCA	2912	GTATACANNNACGTATGCCA	3152	CGGCCAGNNNACGTATGCCA	3392
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC	
ACTACTANNNACGTATGCCA	2913	GACCTACNNNACGTATGCCA	3153	CGCCAAGNNNACGTATGCCA	3393
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
TGCGATGNNNACGTATGCCA	2914	TCCCATGNNNACGTATGCCA	3154	GCTGTTANNNACGTATGCCA	3394
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
AGATACGNNNACGTATGCCA	2915	AGCCCTTNNNACGTATGCCA	3155	GAAAATGNNNACGTATGCCA	3395
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC	
CCTTTTTNNNACGTATGCCA	2916	GTTTCACANNNACGTATGCCA	3156	TTCTATANNNACGTATGCCA	3396
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
TTAGCGTNNNACGTATGCCA	2917	ACGTTTGNNNACGTATGCCA	3157	CCCCGCANNNACGTATGCCA	3397
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
CGGCGCCNNNACGTATGCCA	2918	GTTTGATANNNACGTATGCCA	3158	GTCTACCCNNNACGTATGCCA	3398
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT	
TGCTCTCANNNACGTATGCCA	2919	GTATTACNNNACGTATGCCA	3159	GTAGTTANNNACGTATGCCA	3399
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
TATCTACNNNACGTATGCCA	2920	AGAACACNNNACGTATGCCA	3160	GGTTTAANNNACGTATGCCA	3400
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG	
TCTATTGNNNACGTATGCCA	2921	CTAATANNNACGTATGCCA	3161	AGACGGCANNNACGTATGCCA	3401

FIG. 16B

Pool-13	SEQ ID NO:	Pool-14	SEQ ID NO:	Pool-15	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATACAC	2922	TGCAGGACCAGAGAATTGGAATACAA	3162	TGCAGGACCAGAGAATTGGAATACAC	3402
CAGTACANNNACGTATGCCA	2923	TTTCACTNNNACGTATGCCA	3163	GTGAGCANNNACGTATGCCA	3403
TGCAGGACCAGAGAATTGGAATACAA	2924	TGCAGGACCAGAGAATTGGAATACAG	3164	TGCAGGACCAGAGAATTGGAATACAC	3404
CAGAATANNNACGTATGCCA	2925	TCAACGTNNNACGTATGCCA	3165	AACAGTCNNNACGTATGCCA	3405
TGCAGGACCAGAGAATTGGAATACAG	2926	TGCAGGACCAGAGAATTGGAATACAG	3166	GTGCGANNNACGTATGCCA	3406
TATATACNNNACGTATGCCA	2927	CGTGTGNNNACGTATGCCA	3167	TGCAGGACCAGAGAATTGGAATACAT	3407
TGCAGGACCAGAGAATTGGAATACAT	2928	TGCAGGACCAGAGAATTGGAATACAA	3168	TGCAGGACCAGAGAATTGGAATACAC	3408
ATTAAACNNNACGTATGCCA	2929	AACCCACNNNACGTATGCCA	3169	GTATTTNNNACGTATGCCA	3409
TGCAGGACCAGAGAATTGGAATACAG	2930	TGCAGGACCAGAGAATTGGAATACAC	3170	TGCAGGACCAGAGAATTGGAATACAG	3410
GTTAGANNNACGTATGCCA	2931	CCCTGTNNNACGTATGCCA	3171	AGCATGTNNNACGTATGCCA	3411
TGCAGGACCAGAGAATTGGAATACAC	2932	TGCAGGACCAGAGAATTGGAATACAG	3172	TGCAGGACCAGAGAATTGGAATACAA	3412
TAGGATCANNNACGTATGCCA	2933	GTAGCCTNNNACGTATGCCA	3173	GCTTAATNNNACGTATGCCA	3413
TGCAGGACCAGAGAATTGGAATACAG	2934	TCCATGNNNACGTATGCCA	3174	TGCAGGACCAGAGAATTGGAATACAC	3414
ACTAGANNNACGTATGCCA	2935	TGCAGGACCAGAGAATTGGAATACAA	3175	TCACCCGNNNACGTATGCCA	3415
TGCAGGACCAGAGAATTGGAATACAA	2936	GAATCCNNNACGTATGCCA	3176	TGCAGGACCAGAGAATTGGAATACAG	3416
CTTATCTNNNACGTATGCCA	2937	TGCAGGACCAGAGAATTGGAATACAC	3177	CGGACGNNNACGTATGCCA	3417
TGCAGGACCAGAGAATTGGAATACAG	2938	GCATCTNNNACGTATGCCA	3178	TGCAGGACCAGAGAATTGGAATACAA	3418
ACGTCCGNNNACGTATGCCA	2939	GAATCCNNNACGTATGCCA	3179	GGAGTACNNNACGTATGCCA	3419
TGCAGGACCAGAGAATTGGAATACAA	2940	CTTGTGNNNACGTATGCCA	3180	TGCAGGACCAGAGAATTGGAATACAC	3420
TGCAGGACCAGAGAATTGGAATACAT	2941	TGCAGGACCAGAGAATTGGAATACAG	3181	TGCAGGACCAGAGAATTGGAATACAA	3421
TGCAGGACCAGAGAATTGGAATACAG	2942	AAACCAGNNNACGTATGCCA	3182	AGAGCACNNNACGTATGCCA	3422
GCATCGNNNACGTATGCCA	2943	TGCAGGACCAGAGAATTGGAATACAG	3183	GTGGAATNNNACGTATGCCA	3423
TGCAGGACCAGAGAATTGGAATACAT	2944	GATACTCANNNACGTATGCCA	3184	TGCAGGACCAGAGAATTGGAATACAC	3424
TATGGATNNNACGTATGCCA	2945	TGCAGGACCAGAGAATTGGAATACAA	3185	ATGGCAANNNACGTATGCCA	3425
TGCAGGACCAGAGAATTGGAATACAA	2946	GGCCGAGNNNACGTATGCCA	3186	AGGTGGANNNACGTATGCCA	3426
CATCGTNNNACGTATGCCA	2947	TGCAGGACCAGAGAATTGGAATACAG	3187	TGCAGGACCAGAGAATTGGAATACAG	3427
TGCAGGACCAGAGAATTGGAATACAA	2948	ACTGTTNNNACGTATGCCA	3188	CTCTGTNNNACGTATGCCA	3428
AAGTAGTNNNACGTATGCCA	2949	TGCAGGACCAGAGAATTGGAATACAG	3189	TGCAGGACCAGAGAATTGGAATACAA	3429
TGCAGGACCAGAGAATTGGAATACAT	2950	GTATCGCANNNACGTATGCCA	3190	GCCAACTNNNACGTATGCCA	3430
AATAACNNNACGTATGCCA	2951	TGCAGGACCAGAGAATTGGAATACAG	3191	TGCAGGACCAGAGAATTGGAATACAG	3431
TGCAGGACCAGAGAATTGGAATACAA	2952	CGAGATCANNNACGTATGCCA	3192	GTCCATGNNNACGTATGCCA	3432
TTCTCATNNNACGTATGCCA	2953	TGCAGGACCAGAGAATTGGAATACAT	3193	TGCAGGACCAGAGAATTGGAATACAG	3433
TGCAGGACCAGAGAATTGGAATACAA	2954	CGAGATCANNNACGTATGCCA	3194	GTCCATGNNNACGTATGCCA	3434
GTTCCTNNNACGTATGCCA		TGCAGGACCAGAGAATTGGAATACAG			
GAAAGTANNNACGTATGCCA		GGTAGTNNNACGTATGCCA			
TGCAGGACCAGAGAATTGGAATACAG		CGTATCTNNNACGTATGCCA			
ACATTATNNNACGTATGCCA		TGCAGGACCAGAGAATTGGAATACAA			
TGCAGGACCAGAGAATTGGAATACAG		ACGCACTNNNACGTATGCCA			
GATACGANNNACGTATGCCA		TGCAGGACCAGAGAATTGGAATACAG			
TGCAGGACCAGAGAATTGGAATACAG		CGATTGANNNACGTATGCCA			
TACATATNNNACGTATGCCA		TGCAGGACCAGAGAATTGGAATACAG			
TGCAGGACCAGAGAATTGGAATACAT		CTCTAAGNNNACGTATGCCA			
CATAGCGNNNACGTATGCCA		TGCAGGACCAGAGAATTGGAATACAG			
TTGAACGNNNACGTATGCCA		GTGAGTANNNACGTATGCCA			
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG			
TTGACGNNNACGTATGCCA		CCTATGANNNACGTATGCCA			
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA			
TTCCCAANNNACGTATGCCA		CGGAGCGNNNACGTATGCCA			
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG			
GAGCCCCNNNACGTATGCCA		TGTGACANNNACGTATGCCA			
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG			
TAATCACNNNACGTATGCCA		GTCCGTNNNACGTATGCCA			
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA			
ACGACAANNNCTAGCGTTAC		TCGTTGACNNNCTAGCGTTAC			
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG			
GAATTATNNNCTAGCGTTAC		CATGTCNNNCTAGCGTTAC			
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG			
GGCGTGANNNCTAGCGTTAC		CTTTTGGNNNCTAGCGTTAC			
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG			
CAATTAGNNNCTAGCGTTAC		GCGTCGANNNCTAGCGTTAC			
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG			
TGAGCAGNNNCTAGCGTTAC		CCCCATNNNCTAGCGTTAC			
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG			
GACTTAANNNCTAGCGTTAC		TCTTTGNNNCTAGCGTTAC			

FIG. 16C

Pool-13	SEQ ID NO:	Pool-14	SEQ ID NO:	Pool-15	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC	
GAGAATANNNNCTAGCGTTAC	2955	TCCACGANNNNCTAGCGTTAC	3195	TATTCATNNNNCTAGCGTTAC	3435
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
TTTTCTNNNNCTAGCGTTAC	2956	ATGCATANNNNCTAGCGTTAC	3196	TCGTTCTNNNNCTAGCGTTAC	3436
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC	
TCGCAATNNNNCTAGCGTTAC	2957	AGAAATNNNNCTAGCGTTAC	3197	GTTGTAGNNNNCTAGCGTTAC	3437
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG	
TCATCCNNNNCTAGCGTTAC	2958	CTCAATCNNNNCTAGCGTTAC	3198	ACAGCGNNNNCTAGCGTTAC	3438
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT	
GATATGANNNNCTAGCGTTAC	2959	AAAACAANNNNCTAGCGTTAC	3199	ACACCCNNNNCTAGCGTTAC	3439
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC	
AGCTACGNNNNCTAGCGTTAC	2960	TGATGTCNNNNCTAGCGTTAC	3200	GTTAAGCNNNNCTAGCGTTAC	3440
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA	
TACAGGCNNNNCTAGCGTTAC	2961	GCCGTAANNNNCTAGCGTTAC	3201	TGCGCTNNNNCTAGCGTTAC	3441
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
ACTACACNNNNCTAGCGTTAC	2962	GCTCTAGNNNNCTAGCGTTAC	3202	CTATGCANNNNCTAGCGTTAC	3442
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
TTTAGGNNNNCTAGCGTTAC	2963	GCGTGCTNNNNCTAGCGTTAC	3203	CGCAGCNNNNCTAGCGTTAC	3443
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC	
TTTCAGTNNNNCTAGCGTTAC	2964	ACGTGTCNNNNCTAGCGTTAC	3204	GTCACAANNNNCTAGCGTTAC	3444
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAC	
CAGAACANNNNCTAGCGTTAC	2965	GTATTAGNNNNCTAGCGTTAC	3205	GCGATCGNNNNCTAGCGTTAC	3445
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
GAGTAGANNNNCTAGCGTTAC	2966	TGATTACNNNNCTAGCGTTAC	3206	TTAGACNNNNCTAGCGTTAC	3446
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT	
TCGGAGGNNNNCTAGCGTTAC	2967	CTCCGAANNNNCTAGCGTTAC	3207	CGCGAGCNNNNCTAGCGTTAC	3447
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
TGTAATANNNNCTAGCGTTAC	2968	TCTTCCNNNNCTAGCGTTAC	3208	GTAAACTNNNNCTAGCGTTAC	3448
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
ACTCCGNNNNCTAGCGTTAC	2969	CTCCTAGNNNNCTAGCGTTAC	3209	GCCATAGNNNNCTAGCGTTAC	3449
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
ACATTGGNNNNCTAGCGTTAC	2970	ACTTATANNNNCTAGCGTTAC	3210	AATTACGNNNNCTAGCGTTAC	3450
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC	
TAGCAATNNNNCTAGCGTTAC	2971	GAGTGAANNNNCTAGCGTTAC	3211	CCGCGCCNNNNCTAGCGTTAC	3451
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAC	
CCAACGANNNNCTAGCGTTAC	2972	ATAAATNNNNCTAGCGTTAC	3212	AATATCANNNNCTAGCGTTAC	3452
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
TGATCCNNNNCTAGCGTTAC	2973	CGGTGAGNNNNCTAGCGTTAC	3213	TTAAGGANNNNCTAGCGTTAC	3453
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA	
ATTAATANNNNCTAGCGTTAC	2974	GTCCTGNNNNCTAGCGTTAC	3214	TATACACNNNNCTAGCGTTAC	3454
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT	
AAGTTTGNNNNNCTAGCGTTAC	2975	GACTTATNNNNCTAGCGTTAC	3215	ATTGACANNNNCTAGCGTTAC	3455
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA	
GCGCGCANNNNCTAGCGTTAC	2976	GCGACTANNNNCTAGCGTTAC	3216	CGAAATNNNNCTAGCGTTAC	3456
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
CACACGANNNNCTAGCGTTAC	2977	TTCCATANNNNCTAGCGTTAC	3217	TAGGACANNNNCTAGCGTTAC	3457
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC	
AGTCGTTNNNNCTAGCGTTAC	2978	TGATATANNNNCTAGCGTTAC	3218	CCCCAGTNNNNCTAGCGTTAC	3458
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC	
GAGCCTTNNNNCTAGCGTTAC	2979	AAGCACTNNNNCTAGCGTTAC	3219	CTACGTTNNNNCTAGCGTTAC	3459
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
CTTGCTANNNNCTAGCGTTAC	2980	CGCATGNNNNCTAGCGTTAC	3220	GGTGAGANNNNCTAGCGTTAC	3460
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAC	
TCATAGTNNNNCTAGCGTTAC	2981	TCTCAATNNNNCTAGCGTTAC	3221	TAGCACANNNNCTAGCGTTAC	3461
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
AGCAATNNNNCTAGCGTTAC	2982	CGCCACNNNNCTAGCGTTAC	3222	CATGTAANNNNCTAGCGTTAC	3462
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG	
AATTGTANNNNCTAGCGTTAC	2983	GACGGACNNNNCTAGCGTTAC	3223	GACGAATNNNNCTAGCGTTAC	3463
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG	
TCGGCAANNNNCTAGCGTTAC	2984	GAACAGANNNNCTAGCGTTAC	3224	GATGGCANNNNCTAGCGTTAC	3464
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
CTAGTCTNNNNCTAGCGTTAC	2985	ATCTCGCANNNNCTAGCGTTAC	3225	CCCAGTTNNNNCTAGCGTTAC	3465
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAC	
TAGGCTANNNNCTAGCGTTAC	2986	GCATCAGNNNNCTAGCGTTAC	3226	GAGACAANNNNCTAGCGTTAC	3466
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC	
ATCAATCNNNNCTAGCGTTAC	2987	CTAAGCANNNNCTAGCGTTAC	3227	AATACCGNNNNCTAGCGTTAC	3467

FIG. 16D

Pool-13	SEQ ID NO.	Pool-14	SEQ ID NO.	Pool-15	SEQ ID NO.
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
CCCTCGTNNNCTAGCGTTAC	2988	TTGACAANNNCTAGCGTTAC	3228	TTATGTCNNNCTAGCGTTAC	3468
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT	
GGTTGAGNNNCTAGCGTTAC	2989	CCGCCATNNNCTAGCGTTAC	3229	GGTAACNNNCTAGCGTTAC	3469
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA	
AGCCAGCNNNCTAGCGTTAC	2990	TGCATAANNNCTAGCGTTAC	3230	GCCCATANNNCTAGCGTTAC	3470
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA	
CTAATGTNNNCTAGCGTTAC	2991	CAGAGCANNNCTAGCGTTAC	3231	TCTCCANNNCTAGCGTTAC	3471
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
GTAAGCANNNCTAGCGTTAC	2992	GTACGTTNNNCTAGCGTTAC	3232	TTTTGACNNNCTAGCGTTAC	3472
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
TGCGGAGNNNCTAGCGTTAC	2993	ATGCACTNNNCTAGCGTTAC	3233	TAGCCTGNNNCTAGCGTTAC	3473
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
TGCCGCTNNNCTAGCGTTAC	2994	TCTAAACNNNCTAGCGTTAC	3234	GAGTCTNNNCTAGCGTTAC	3474
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA	
CTGCGCANNNCTAGCGTTAC	2995	CGAGAACNNNCTAGCGTTAC	3235	CCCCACNNNCTAGCGTTAC	3475
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC	
CTCTACANNNCTAGCGTTAC	2996	CGCAAGCANNNCTAGCGTTAC	3236	GCGGCATNNNCTAGCGTTAC	3476
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT	
GGCCACGNNNCTAGCGTTAC	2997	CGACAAGNNNCTAGCGTTAC	3237	CCAGACANNNCTAGCGTTAC	3477
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA	
CGCAATCANNNCTAGCGTTAC	2998	GCCGATGNNNCTAGCGTTAC	3238	AATGCAANNNCTAGCGTTAC	3478
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA	
GTTTGACNNNCTAGCGTTAC	2999	ATCCAGCANNNCTAGCGTTAC	3239	ATTGCGCANNNCTAGCGTTAC	3479
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
GTTAGGANNNCTAGCGTTAC	3000	TTAATGANNNCTAGCGTTAC	3240	TGTCCTTNNNCTAGCGTTAC	3480
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC	
CCTCGGCNNNCTAGCGTTAC	3001	CGCTTCCNNNCTAGCGTTAC	3241	ATGTAATNNNCTAGCGTTAC	3481
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA	
AACACGNNNCTAGCGTTAC	3002	ACAATTGNNNCTAGCGTTAC	3242	CGCATACNNNCTAGCGTTAC	3482
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
AAATCANNNCTAGCGTTAC	3003	TGGAACANNNCTAGCGTTAC	3243	TGCCCCNNNCTAGCGTTAC	3483
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC	
GTATCTCANNNCTAGCGTTAC	3004	TCTGTGTNNNCTAGCGTTAC	3244	TCCCCAGNNNCTAGCGTTAC	3484
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
GGCCACANNNCTAGCGTTAC	3005	GCAGTACNNNCTAGCGTTAC	3245	CTACTTANNNCTAGCGTTAC	3485
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
CATTCTANNNCTAGCGTTAC	3006	ACAAGTANNNCTAGCGTTAC	3246	ACCGGTANNNCTAGCGTTAC	3486
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA	
TAGATGANNNCTAGCGTTAC	3007	GAGAGCANNNCTAGCGTTAC	3247	ACCTATANNNCTAGCGTTAC	3487
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG	
CACTGCGNNNCTAGCGTTAC	3008	TAAATGTNNNCTAGCGTTAC	3248	CGACTGNNNCTAGCGTTAC	3488
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC	
CTCCCTANNNGATCGACATG	3009	GCTACGNNNGATCGACATG	3249	GAGTCTANNNGATCGACATG	3489
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT	
CAAAACANNNGATCGACATG	3010	CGTTTCCNNNGATCGACATG	3250	ATGAAAGNNNGATCGACATG	3490
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA	
ATGTACANNNGATCGACATG	3011	GCCAGTANNNGATCGACATG	3251	CTGGCCGNNNGATCGACATG	3491
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC	
CGGTCTTNNNGATCGACATG	3012	TAAGTGGNNNGATCGACATG	3252	AACCATGNNNGATCGACATG	3492
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA	
CCATATTNNNGATCGACATG	3013	ACCTACTNNNGATCGACATG	3253	AGGTAGCNNNGATCGACATG	3493
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
TGACTCGNNNGATCGACATG	3014	ATTTTGATNNNGATCGACATG	3254	TCTCAGCNNNGATCGACATG	3494
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT	
AATCTCTNNNGATCGACATG	3015	ACTACATNNNGATCGACATG	3255	TCAGGTGNNNGATCGACATG	3495
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC	
AATACTTNNNGATCGACATG	3016	CCTTGAANNNGATCGACATG	3256	CAATCCTNNNGATCGACATG	3496
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
CACTAGANNNGATCGACATG	3017	AATATTNNNGATCGACATG	3257	ACAGTTTNNNGATCGACATG	3497
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
TTGGACGNNNGATCGACATG	3018	GTTTAAATNNNGATCGACATG	3258	TCTTTACNNNGATCGACATG	3498
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG	
AAGTCTTNNNGATCGACATG	3019	CCACCGTNNNGATCGACATG	3259	CAATATTNNNGATCGACATG	3499
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
CTATGCTNNNGATCGACATG	3020	TACTTCGNNNGATCGACATG	3260	TCTCCATNNNGATCGACATG	3500

FIG. 16E

Pool-13	SEQ ID NO:	Pool-14	SEQ ID NO:	Pool-15	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATACATCGATGTGNNNGATCGACATG	3021	TGCAGGACCAGAGAATTGGAATACAAATGCGTCANNNNGATCGACATG	3261	TGCAGGACCAGAGAATTGGAATACACAAACAATTNNNGATCGACATG	3501
TGCAGGACCAGAGAATTGGAATACATGTACACGNNNGATCGACATG	3022	TGCAGGACCAGAGAATTGGAATACAAACATGTTNNNGATCGACATG	3262	TGCAGGACCAGAGAATTGGAATACATCGTAGACNNNGATCGACATG	3502
TGCAGGACCAGAGAATTGGAATACATCTTTAGTNNNGATCGACATG	3023	TGCAGGACCAGAGAATTGGAATACACCTGTTTNNNGATCGACATG	3263	TGCAGGACCAGAGAATTGGAATACAGTAGATAANNNGATCGACATG	3503
TGCAGGACCAGAGAATTGGAATACACGTAGGCCNNNGATCGACATG	3024	TGCAGGACCAGAGAATTGGAATACACACAAGCTNNNGATCGACATG	3264	TGCAGGACCAGAGAATTGGAATACAAATATACNNNGATCGACATG	3504
TGCAGGACCAGAGAATTGGAATACAACTTTTATNNNGATCGACATG	3025	TGCAGGACCAGAGAATTGGAATACAGATAAGATTNNNGATCGACATG	3265	TGCAGGACCAGAGAATTGGAATACACACGACGNNNGATCGACATG	3505
TGCAGGACCAGAGAATTGGAATACACGTCTATCNNNGATCGACATG	3026	TGCAGGACCAGAGAATTGGAATACAAAGACCTCANNNNGATCGACATG	3266	TGCAGGACCAGAGAATTGGAATACACACAAAAANNNGATCGACATG	3506
TGCAGGACCAGAGAATTGGAATACAGTAGAAATNNNGATCGACATG	3027	TGCAGGACCAGAGAATTGGAATACACGCCAAGANNNGATCGACATG	3267	TGCAGGACCAGAGAATTGGAATACACGTACCCGNNNGATCGACATG	3507
TGCAGGACCAGAGAATTGGAATACACGTACCAANNNGATCGACATG	3028	TGCAGGACCAGAGAATTGGAATACAGGTATTGNNNGATCGACATG	3268	TGCAGGACCAGAGAATTGGAATACACACCAATGNNNGATCGACATG	3508
TGCAGGACCAGAGAATTGGAATACACACCCCCNNNGATCGACATG	3029	TGCAGGACCAGAGAATTGGAATACAACTCGGATNNNGATCGACATG	3269	TGCAGGACCAGAGAATTGGAATACACGCTCTGNNNGATCGACATG	3509
TGCAGGACCAGAGAATTGGAATACATGCGGCGTNNNGATCGACATG	3030	TGCAGGACCAGAGAATTGGAATACATATATCGANNNGATCGACATG	3270	TGCAGGACCAGAGAATTGGAATACAGTCAAGCTNNNGATCGACATG	3510
TGCAGGACCAGAGAATTGGAATACAGCCCCCGNNNGATCGACATG	3031	TGCAGGACCAGAGAATTGGAATACAACTCCACTCANNNGATCGACATG	3271	TGCAGGACCAGAGAATTGGAATACAACTCTTCGNNNGATCGACATG	3511
TGCAGGACCAGAGAATTGGAATACATAGTAAGANNNGATCGACATG	3032	TGCAGGACCAGAGAATTGGAATACAGAACTGGANNNGATCGACATG	3272	TGCAGGACCAGAGAATTGGAATACAAACACGGANNNGATCGACATG	3512
TGCAGGACCAGAGAATTGGAATACATCTGAATANNNGATCGACATG	3033	TGCAGGACCAGAGAATTGGAATACAGATCAGAGNNNGATCGACATG	3273	TGCAGGACCAGAGAATTGGAATACAAACCGCGCANNNGATCGACATG	3513
TGCAGGACCAGAGAATTGGAATACACATAACANNNGATCGACATG	3034	TGCAGGACCAGAGAATTGGAATACATGAACTANNNGATCGACATG	3274	TGCAGGACCAGAGAATTGGAATACACACCTTGTNNNGATCGACATG	3514
TGCAGGACCAGAGAATTGGAATACAAATGTCACGNNNGATCGACATG	3035	TGCAGGACCAGAGAATTGGAATACAGCCAGCCANNNGATCGACATG	3275	TGCAGGACCAGAGAATTGGAATACATATATCGGNNNGATCGACATG	3515
TGCAGGACCAGAGAATTGGAATACAAACAGAAATNNNGATCGACATG	3036	TGCAGGACCAGAGAATTGGAATACATTTACTGTNNNGATCGACATG	3276	TGCAGGACCAGAGAATTGGAATACAGACTCTTCNNNGATCGACATG	3516
TGCAGGACCAGAGAATTGGAATACAGCCAGGTTNNNGATCGACATG	3037	TGCAGGACCAGAGAATTGGAATACATGTCCAGGTTNNNGATCGACATG	3277	TGCAGGACCAGAGAATTGGAATACAGAGTCTTNNNGATCGACATG	3517
TGCAGGACCAGAGAATTGGAATACAGCTCATGANNNGATCGACATG	3038	TGCAGGACCAGAGAATTGGAATACACAGCGTTANNNGATCGACATG	3278	TGCAGGACCAGAGAATTGGAATACATAGAATCTNNNGATCGACATG	3518
TGCAGGACCAGAGAATTGGAATACACCGGTTCGANNNGATCGACATG	3039	TGCAGGACCAGAGAATTGGAATACATGTGATCGNNNGATCGACATG	3279	TGCAGGACCAGAGAATTGGAATACACGACCAACNNNGATCGACATG	3519
TGCAGGACCAGAGAATTGGAATACACAAATTCNNNGATCGACATG	3040	TGCAGGACCAGAGAATTGGAATACAGCTCGTAANNNGATCGACATG	3280	TGCAGGACCAGAGAATTGGAATACATGGATTTCNNNGATCGACATG	3520
TGCAGGACCAGAGAATTGGAATACACAGGCCANNNGATCGACATG	3041	TGCAGGACCAGAGAATTGGAATACAAATTTCTACTNNNGATCGACATG	3281	TGCAGGACCAGAGAATTGGAATACACGACTAGTNNNGATCGACATG	3521
TGCAGGACCAGAGAATTGGAATACACCTGCGGANNNGATCGACATG	3042	TGCAGGACCAGAGAATTGGAATACAGATCAGTCNNNGATCGACATG	3282	TGCAGGACCAGAGAATTGGAATACACCCAAAACNNNGATCGACATG	3522
TGCAGGACCAGAGAATTGGAATACAGCTAAAGGNNNGATCGACATG	3043	TGCAGGACCAGAGAATTGGAATACAGGATTATTNNNGATCGACATG	3283	TGCAGGACCAGAGAATTGGAATACATGACCCCCNNNGATCGACATG	3523
TGCAGGACCAGAGAATTGGAATACATTTAAGGTNNNGATCGACATG	3044	TGCAGGACCAGAGAATTGGAATACACCATTCGTNNNGATCGACATG	3284	TGCAGGACCAGAGAATTGGAATACAGCATTAGCANNNGATCGACATG	3524
TGCAGGACCAGAGAATTGGAATACAAACGCTAANNNGATCGACATG	3045	TGCAGGACCAGAGAATTGGAATACAGTACATGCNNNGATCGACATG	3285	TGCAGGACCAGAGAATTGGAATACAGCCAGATTNNNGATCGACATG	3525
TGCAGGACCAGAGAATTGGAATACAAATTTGGTNNNGATCGACATG	3046	TGCAGGACCAGAGAATTGGAATACACGTCCGAGNNNGATCGACATG	3286	TGCAGGACCAGAGAATTGGAATACAACTACTATNNNGATCGACATG	3526
TGCAGGACCAGAGAATTGGAATACAAAGTTAGCANNNGATCGACATG	3047	TGCAGGACCAGAGAATTGGAATACATATTTGTCTNNNGATCGACATG	3287	TGCAGGACCAGAGAATTGGAATACAGTAGGTCTNNNGATCGACATG	3527
TGCAGGACCAGAGAATTGGAATACAAAGTTTGGNNNGATCGACATG	3048	TGCAGGACCAGAGAATTGGAATACAAAGTTCANNNGATCGACATG	3288	TGCAGGACCAGAGAATTGGAATACAAATTAAGGTNNNGATCGACATG	3528
TGCAGGACCAGAGAATTGGAATACAAAGCCTTCANNNGATCGACATG	3049	TGCAGGACCAGAGAATTGGAATACAGCGATTGTNNNGATCGACATG	3289	TGCAGGACCAGAGAATTGGAATACAAAGAGAAANNNGATCGACATG	3529
TGCAGGACCAGAGAATTGGAATACAGGACTTGTNNNGATCGACATG	3050	TGCAGGACCAGAGAATTGGAATACACCTGGAAATNNNGATCGACATG	3290	TGCAGGACCAGAGAATTGGAATACATTTTGTGTNNNGATCGACATG	3530
TGCAGGACCAGAGAATTGGAATACACGTCCAGATNNNGATCGACATG	3051	TGCAGGACCAGAGAATTGGAATACAAACGAGCAANNNGATCGACATG	3291	TGCAGGACCAGAGAATTGGAATACAAAGCGTTTNNNGATCGACATG	3531
TGCAGGACCAGAGAATTGGAATACACAGAAGANNNGATCGACATG	3052	TGCAGGACCAGAGAATTGGAATACAAACACCAACNNNGATCGACATG	3292	TGCAGGACCAGAGAATTGGAATACAAATAAGCTANNNGATCGACATG	3532
TGCAGGACCAGAGAATTGGAATACAGCGATCTANNNGATCGACATG	3053	TGCAGGACCAGAGAATTGGAATACATTTAGTCTNNNGATCGACATG	3293	TGCAGGACCAGAGAATTGGAATACAAACCGGATTNNNGATCGACATG	3533

FIG. 16F

Pool-13	SEQ ID NO.	Pool-14	SEQ ID NO.	Pool-15	SEQ ID NO.
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC	
TCACCGANNNGATCGACATG	3054	GTAGCTGNNNGATCGACATG	3294	TCAAAATANNNGATCGACATG	3534
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAC	
CACCTAATNNNGATCGACATG	3055	GCTTACANNNGATCGACATG	3295	GAGAACANNNGATCGACATG	3535
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC	
TATGAAGNNNGATCGACATG	3056	GACCAGCANNNGATCGACATG	3296	CCAGGACNNNGATCGACATG	3536
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAC	
GTAAGCGNNNGATCGACATG	3057	CCAAAGNNNGATCGACATG	3297	CAGCTCCNNNGATCGACATG	3537
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT	
ACGCTATNNNGATCGACATG	3058	GAGGTAANNNGATCGACATG	3298	ATACATGNNNGATCGACATG	3538
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT	
GACATCGNNNGATCGACATG	3059	AGTCATGNNNGATCGACATG	3299	ATAGTTGNNNGATCGACATG	3539
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC	
CAGAAACNNNGATCGACATG	3060	GACCACANNNGATCGACATG	3300	ATAGTTANNNGATCGACATG	3540
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT	
TTTTGCANNNGATCGACATG	3061	GAACACANNNGATCGACATG	3301	TCATTACNNNGATCGACATG	3541
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAT	
TACCCGCGNNNGATCGACATG	3062	AGTAATCANNNGATCGACATG	3302	GCTACCTNNNGATCGACATG	3542
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG	
TAATGCTNNNGATCGACATG	3063	CGACGGTNNNGATCGACATG	3303	TAGCTTGNNGATCGACATG	3543
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC	
AGCAGTGNNNGATCGACATG	3064	TGCCCTGNNNGATCGACATG	3304	CGGATATNNNGATCGACATG	3544
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAC	
CACGTCANNNGATCGACATG	3065	AGCGGCANNNGATCGACATG	3305	AGCCGCGANNNGATCGACATG	3545
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG	
TAATACTNNNGATCGACATG	3066	GCCTGCANNNGATCGACATG	3306	ATCCTCTNNNGATCGACATG	3546
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA	
ACAAACANNNGATCGACATG	3067	CGTCAAGNNNGATCGACATG	3307	GTACCCANNNGATCGACATG	3547
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAA	
ACATGGCANNNGATCGACATG	3068	GACGGCANNNGATCGACATG	3308	CGGAGTANNNGATCGACATG	3548
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG	
GTGTCANNNTGCATCAGGT	3069	CATGCCGNNNTGCATCAGGT	3309	TAAAGTNNNTGCATCAGGT	3549
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT	
TTTAACNNNTGCATCAGGT	3070	GTCTAAGNNNTGCATCAGGT	3310	AGGTGTNNNTGCATCAGGT	3550
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT	
TAAGGTGNNNTGCATCAGGT	3071	CGTGATTNNNTGCATCAGGT	3311	AGACCGTNNNTGCATCAGGT	3551
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG	
AATAGCGNNNTGCATCAGGT	3072	TAGTCCCNNNTGCATCAGGT	3312	CTCGTTNNNTGCATCAGGT	3552
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA	
AATTAATNNNTGCATCAGGT	3073	GGCATTGNNNTGCATCAGGT	3313	AATCTTNNNTGCATCAGGT	3553
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG	
TCCTGTGNNNTGCATCAGGT	3074	ACGGTGGNNNTGCATCAGGT	3314	ACCAACTNNNTGCATCAGGT	3554
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT	
GCGCGTNNNTGCATCAGGT	3075	CGCTTTNNNTGCATCAGGT	3315	CACCTACNNNTGCATCAGGT	3555
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG	
ACGAAACNNNTGCATCAGGT	3076	GTGGACNNNTGCATCAGGT	3316	TTAATTGNNNTGCATCAGGT	3556
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG	
GTTTAGGNNNTGCATCAGGT	3077	TGCTTTNNNTGCATCAGGT	3317	CAATTATNNNTGCATCAGGT	3557
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA	
TAGCCTANNNTGCATCAGGT	3078	GAAAGCGNNNTGCATCAGGT	3318	ACGAGACNNNTGCATCAGGT	3558
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA	
TTCCCTGNNNTGCATCAGGT	3079	CGTGCGANNNTGCATCAGGT	3319	TCGGCATNNNTGCATCAGGT	3559
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC	
ACGAAATNNNTGCATCAGGT	3080	ACAACATNNNTGCATCAGGT	3320	CACACGNNNTGCATCAGGT	3560
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG	
ACCCCCNNNTGCATCAGGT	3081	TTACTCTNNNTGCATCAGGT	3321	GCCAGGANNNTGCATCAGGT	3561
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG	
TATGATANNNTGCATCAGGT	3082	TTCCCTANNNTGCATCAGGT	3322	AGGAGTTNNNTGCATCAGGT	3562
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC	
ACATGATNNNTGCATCAGGT	3083	ACACGGCNNNTGCATCAGGT	3323	CACCGCTNNNTGCATCAGGT	3563
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA	
GTACATANNNTGCATCAGGT	3084	AGAATTCNNNTGCATCAGGT	3324	CGATGAGNNNTGCATCAGGT	3564
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT	
ACGAAAANNNTGCATCAGGT	3085	TTGAAGNNNTGCATCAGGT	3325	TAGCATANNNTGCATCAGGT	3565
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA	
ATAACATNNNTGCATCAGGT	3086	TTAECTNNNTGCATCAGGT	3326	GTCCCAANNNTGCATCAGGT	3566

FIG. 16G

Pool-13	SEQ ID NO:	Pool-14	SEQ ID NO:	Pool-15	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA	
GAGAATCANNNTGCATCAGGT	3087	CTTACCCNNNTGCATCAGGT	3327	GCCTCTNNNTGCATCAGGT	3567
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
CTTGTCGNNNTGCATCAGGT	3088	AGTTGCTNNNTGCATCAGGT	3328	CACCATCANNNTGCATCAGGT	3568
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAC	
AAGCGCTNNNTGCATCAGGT	3089	TTCCAATNNNTGCATCAGGT	3329	TCATCANNNTGCATCAGGT	3569
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA	
TCAGAAANNNTGCATCAGGT	3090	TAAGTTNNNTGCATCAGGT	3330	CGGCGAGNNNTGCATCAGGT	3570
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC	
TGCTTGNNNTGCATCAGGT	3091	ATGTACTNNNTGCATCAGGT	3331	TCGGACGNNNTGCATCAGGT	3571
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
AGCGTATNNNTGCATCAGGT	3092	TCCAAGTNNNTGCATCAGGT	3332	ACGGCATNNNTGCATCAGGT	3572
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
AGGAGCTNNNTGCATCAGGT	3093	CGACCAANNNTGCATCAGGT	3333	TTAGTAGNNNTGCATCAGGT	3573
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA	
ATGCCTTNNNTGCATCAGGT	3094	TCGATAGNNNTGCATCAGGT	3334	GGAGAGNNNTGCATCAGGT	3574
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC	
GCGGTGTNNNTGCATCAGGT	3095	CTTCCANNNTGCATCAGGT	3335	CGCGCAANNNTGCATCAGGT	3575
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG	
TGAAAGGNNNTGCATCAGGT	3096	TAGATTGNNNTGCATCAGGT	3336	TCGTGGCNNNTGCATCAGGT	3576
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA	
GTIACGNNNTGCATCAGGT	3097	ATTGCGANNNTGCATCAGGT	3337	TACACTANNNTGCATCAGGT	3577
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC	
CTAAGCTNNNTGCATCAGGT	3098	AGCACATNNNTGCATCAGGT	3338	CACGCCCTNNNTGCATCAGGT	3578
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT	
CCGAGTANNNTGCATCAGGT	3099	CCGGCAANNNTGCATCAGGT	3339	GAAGTGGNNNTGCATCAGGT	3579
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG	
AGATCGTNNNTGCATCAGGT	3100	CAGATGGNNNTGCATCAGGT	3340	AGTTGTCNNNTGCATCAGGT	3580
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAC	
GAAAAATNNNTGCATCAGGT	3101	GCGTATGNNNTGCATCAGGT	3341	CCGGCTTNNNTGCATCAGGT	3581
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC	
CCAGACNNNTGCATCAGGT	3102	CAGGAGTNNNTGCATCAGGT	3342	AGATAGGNNNTGCATCAGGT	3582
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA	
CTGCACGNNNTGCATCAGGT	3103	ATCCATCANNNTGCATCAGGT	3343	AGTCCGTNNNTGCATCAGGT	3583
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA	
TGGAATNNNTGCATCAGGT	3104	TACGCCNNNTGCATCAGGT	3344	ATCAGANNNTGCATCAGGT	3584
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC	
TAGCAANNNTGCATCAGGT	3105	ACCTACANNNTGCATCAGGT	3345	ACTCAGANNNTGCATCAGGT	3585
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAT	
AGCTATCANNNTGCATCAGGT	3106	CCCACGNNNTGCATCAGGT	3346	TATTTCCANNNTGCATCAGGT	3586
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA	
GGTATCANNNTGCATCAGGT	3107	ATTTCGCTNNNTGCATCAGGT	3347	AGTAACANNNTGCATCAGGT	3587
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAT	
TGGATCANNNTGCATCAGGT	3108	ATCTGGTNNNTGCATCAGGT	3348	TGTGCTCANNNTGCATCAGGT	3588
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA	
GGCTTCCNNNTGCATCAGGT	3109	ATCGTTTNNNTGCATCAGGT	3349	AGAGTCGNNNTGCATCAGGT	3589
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
CAGGTTGNNNTGCATCAGGT	3110	GATTCTGNNNTGCATCAGGT	3350	GCTGTTGNNNTGCATCAGGT	3590
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA	
GGCGCGCANNNTGCATCAGGT	3111	CGCATCANNNTGCATCAGGT	3351	TATTGACNNNTGCATCAGGT	3591
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAA	
TGTGTCGNNNTGCATCAGGT	3112	ACTAAAANNNTGCATCAGGT	3352	AATATTTNNNTGCATCAGGT	3592
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC	
TTTGGAGNNNTGCATCAGGT	3113	TGGATGTNNNTGCATCAGGT	3353	TCAAGACNNNTGCATCAGGT	3593
TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA	
GCCCACTNNNTGCATCAGGT	3114	CGTTTACNNNTGCATCAGGT	3354	GACGAACNNNTGCATCAGGT	3594
TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAA	
ACACTGCNNNTGCATCAGGT	3115	ATTATCGNNNTGCATCAGGT	3355	GGCAGGNNNTGCATCAGGT	3595
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC		TGCAGGACCAGAGAATTGGAATACAA	
CGCCGTANNNTGCATCAGGT	3116	ACTCGAANNNTGCATCAGGT	3356	CTTATAGNNNTGCATCAGGT	3596
TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC	
TAGCATCANNNTGCATCAGGT	3117	AACGTTNNNTGCATCAGGT	3357	TACTAAANNNTGCATCAGGT	3597
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAA		TGCAGGACCAGAGAATTGGAATACAT	
GCAGCATNNNTGCATCAGGT	3118	CCCGCAGNNNTGCATCAGGT	3358	TTAGAGTNNNTGCATCAGGT	3598
TGCAGGACCAGAGAATTGGAATACAT		TGCAGGACCAGAGAATTGGAATACAG		TGCAGGACCAGAGAATTGGAATACAC	
GCAGACTNNNTGCATCAGGT	3119	TCTCTGNNNTGCATCAGGT	3359	TGCTTCANNNTGCATCAGGT	3599

FIG. 16H

Pool-13	SEQ ID NO:	Pool-14	SEQ ID NO:	Pool-15	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATACAA AGATGCGNNNTGCATCAGGT	3120	TGCAGGACCAGAGAATTCTGAATACAA TTGATCANNNTGCATCAGGT	3360	TGCAGGACCAGAGAATTCTGAATACAA GGTTCTGNNNTGCATCAGGT	3600
TGCAGGACCAGAGAATTCTGAATACAA ACATATCANNNTGCATCAGGT	3121	TGCAGGACCAGAGAATTCTGAATACAA AGTTTACNNNTGCATCAGGT	3361	TGCAGGACCAGAGAATTCTGAATACAA GTAGGTGNNNTGCATCAGGT	3601
TGCAGGACCAGAGAATTCTGAATACAT GGAACGANNNTGCATCAGGT	3122	TGCAGGACCAGAGAATTCTGAATACAT GTTGTAANNNTGCATCAGGT	3362	TGCAGGACCAGAGAATTCTGAATACAC CCGATAANNNTGCATCAGGT	3602
TGCAGGACCAGAGAATTCTGAATACAT GCTCTTGNNTGCATCAGGT	3123	TGCAGGACCAGAGAATTCTGAATACAC TCTCAACNNNTGCATCAGGT	3363	TGCAGGACCAGAGAATTCTGAATACAC AGAGTGANNNTGCATCAGGT	3603
TGCAGGACCAGAGAATTCTGAATACAA CTCCTGTNNNTGCATCAGGT	3124	TGCAGGACCAGAGAATTCTGAATACAA ACGGCCNNNTGCATCAGGT	3364	TGCAGGACCAGAGAATTCTGAATACAG TTGCTTNNNTGCATCAGGT	3604
TGCAGGACCAGAGAATTCTGAATACAA AACGTGNNNTGCATCAGGT	3125	TGCAGGACCAGAGAATTCTGAATACAA ATGGTAANNNTGCATCAGGT	3365	TGCAGGACCAGAGAATTCTGAATACAG TTATCAANNNTGCATCAGGT	3605
TGCAGGACCAGAGAATTCTGAATACAT GTCCCTANNNTGCATCAGGT	3126	TGCAGGACCAGAGAATTCTGAATACAT ACAACCGNNNTGCATCAGGT	3366	TGCAGGACCAGAGAATTCTGAATACAA GATGCTCANNNTGCATCAGGT	3606
TGCAGGACCAGAGAATTCTGAATACAA ATCGCTGNNNTGCATCAGGT	3127	TGCAGGACCAGAGAATTCTGAATACAA TACGGTCNNNTGCATCAGGT	3367	TGCAGGACCAGAGAATTCTGAATACAA ACGTAAANNNTGCATCAGGT	3607
TGCAGGACCAGAGAATTCTGAATACAG AAGCATGNNNTGCATCAGGT	3128	TGCAGGACCAGAGAATTCTGAATACAT GCGCTGNNNTGCATCAGGT	3368	TGCAGGACCAGAGAATTCTGAATACAG CATTTCCNNNTGCATCAGGT	3608

FIG. 17A

Pool-16	SEQ ID NO:	Pool-17	SEQ ID NO:	Pool-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACATGATTCAANNACGTATGCCA	3609	TGCAGGACCAGAGAATTCGAATACAA TTCCCGNNNACGTATGCCA	3849	TGCAGGACCAGAGAATTCGAATACAA CGAGACANNACGTATGCCA	4089
TGCAGGACCAGAGAATTCGAATACAA CAAGTAANNACGTATGCCA	3610	TGCAGGACCAGAGAATTCGAATACAA TCCCAGANNACGTATGCCA	3850	TGCAGGACCAGAGAATTCGAATACAC GCTAATGNNNACGTATGCCA	4090
TGCAGGACCAGAGAATTCGAATACAA TGACCGTNNNACGTATGCCA	3611	TGCAGGACCAGAGAATTCGAATACAC GGAGACGNNNACGTATGCCA	3851	TGCAGGACCAGAGAATTCGAATACAT ACGTCGANNNACGTATGCCA	4091
TGCAGGACCAGAGAATTCGAATACAA TCTCGTCNNNACGTATGCCA	3612	TGCAGGACCAGAGAATTCGAATACAC GATACGTNNNACGTATGCCA	3852	TGCAGGACCAGAGAATTCGAATACAA TTCGTGGNNNACGTATGCCA	4092
TGCAGGACCAGAGAATTCGAATACAG GCAACAANNACGTATGCCA	3613	TGCAGGACCAGAGAATTCGAATACAT CCTGCTANNNACGTATGCCA	3853	TGCAGGACCAGAGAATTCGAATACAG TAGAGGTNNNACGTATGCCA	4093
TGCAGGACCAGAGAATTCGAATACAA GGCGCCTNNNACGTATGCCA	3614	TGCAGGACCAGAGAATTCGAATACAA ATTACACNNNACGTATGCCA	3854	TGCAGGACCAGAGAATTCGAATACAG GCGGTTTNNNACGTATGCCA	4094
TGCAGGACCAGAGAATTCGAATACAT GCTTACNNNACGTATGCCA	3615	TGCAGGACCAGAGAATTCGAATACAT TTCCGACNNNACGTATGCCA	3855	TGCAGGACCAGAGAATTCGAATACAA TAGGCTNNNACGTATGCCA	4095
TGCAGGACCAGAGAATTCGAATACAC GCACGACNNNACGTATGCCA	3616	TGCAGGACCAGAGAATTCGAATACAC TCCCCTNNNACGTATGCCA	3856	TGCAGGACCAGAGAATTCGAATACAT CCAATTTNNNACGTATGCCA	4096
TGCAGGACCAGAGAATTCGAATACAG AGGCTTTNNNACGTATGCCA	3617	TGCAGGACCAGAGAATTCGAATACAA CAATTCTANNNACGTATGCCA	3857	TGCAGGACCAGAGAATTCGAATACAC TGCCGAGNNNACGTATGCCA	4097
TGCAGGACCAGAGAATTCGAATACAC ATTCAATNNNACGTATGCCA	3618	TGCAGGACCAGAGAATTCGAATACAA GCAGCGGNNNACGTATGCCA	3858	TGCAGGACCAGAGAATTCGAATACAC TGTAGTGNNNACGTATGCCA	4098
TGCAGGACCAGAGAATTCGAATACAC AATCATANNNACGTATGCCA	3619	TGCAGGACCAGAGAATTCGAATACAA TCCGATGNNNACGTATGCCA	3859	TGCAGGACCAGAGAATTCGAATACAA ACGGTCNNNACGTATGCCA	4099
TGCAGGACCAGAGAATTCGAATACAC TACGATGNNNACGTATGCCA	3620	TGCAGGACCAGAGAATTCGAATACAT ACGCACANNNACGTATGCCA	3860	TGCAGGACCAGAGAATTCGAATACAC AGGCGTCNNNACGTATGCCA	4100
TGCAGGACCAGAGAATTCGAATACAG AGGTACANNNACGTATGCCA	3621	TGCAGGACCAGAGAATTCGAATACAC CACCATNNNACGTATGCCA	3861	TGCAGGACCAGAGAATTCGAATACAC TTGCCTANNNACGTATGCCA	4101
TGCAGGACCAGAGAATTCGAATACAC TCGTCTANNNACGTATGCCA	3622	TGCAGGACCAGAGAATTCGAATACAA AAGGTCGNNNACGTATGCCA	3862	TGCAGGACCAGAGAATTCGAATACAC TTCCGTANNNACGTATGCCA	4102
TGCAGGACCAGAGAATTCGAATACAA GAAGGAGNNNACGTATGCCA	3623	TGCAGGACCAGAGAATTCGAATACAG CAGTGTTNNNACGTATGCCA	3863	TGCAGGACCAGAGAATTCGAATACAC AGACGTTNNNACGTATGCCA	4103
TGCAGGACCAGAGAATTCGAATACAG TGACATCNNNACGTATGCCA	3624	TGCAGGACCAGAGAATTCGAATACAT CGAACTGNNNACGTATGCCA	3864	TGCAGGACCAGAGAATTCGAATACAA GGAACGTNNNACGTATGCCA	4104
TGCAGGACCAGAGAATTCGAATACAG CGGTGGANNNACGTATGCCA	3625	TGCAGGACCAGAGAATTCGAATACAT TCGCTACNNNACGTATGCCA	3865	TGCAGGACCAGAGAATTCGAATACAT TCGCTAGNNNACGTATGCCA	4105
TGCAGGACCAGAGAATTCGAATACAC ACAAAATNNNACGTATGCCA	3626	TGCAGGACCAGAGAATTCGAATACAT ATTCACTNNNACGTATGCCA	3866	TGCAGGACCAGAGAATTCGAATACAG CCCGATGNNNACGTATGCCA	4106
TGCAGGACCAGAGAATTCGAATACAC CGTGACGNNNACGTATGCCA	3627	TGCAGGACCAGAGAATTCGAATACAA AACTACTNNNACGTATGCCA	3867	TGCAGGACCAGAGAATTCGAATACAA ACGTCTGNNNACGTATGCCA	4107
TGCAGGACCAGAGAATTCGAATACAA AATTACNNNACGTATGCCA	3628	TGCAGGACCAGAGAATTCGAATACAG CCCGTAGNNNACGTATGCCA	3868	TGCAGGACCAGAGAATTCGAATACAC TCTACANNNACGTATGCCA	4108
TGCAGGACCAGAGAATTCGAATACAG CAGACAANNNACGTATGCCA	3629	TGCAGGACCAGAGAATTCGAATACAA GTCGTTGNNNACGTATGCCA	3869	TGCAGGACCAGAGAATTCGAATACAA CGCGGTCNNNACGTATGCCA	4109
TGCAGGACCAGAGAATTCGAATACAT TCTAAGANNNACGTATGCCA	3630	TGCAGGACCAGAGAATTCGAATACAT GACAGCTNNNACGTATGCCA	3870	TGCAGGACCAGAGAATTCGAATACAC ATTCCAGANNNACGTATGCCA	4110
TGCAGGACCAGAGAATTCGAATACAC ATTGAGCNNNACGTATGCCA	3631	TGCAGGACCAGAGAATTCGAATACAT CAGCGATNNNACGTATGCCA	3871	TGCAGGACCAGAGAATTCGAATACAA AGTCGAGNNNACGTATGCCA	4111
TGCAGGACCAGAGAATTCGAATACAA TGAGAGCNNNACGTATGCCA	3632	TGCAGGACCAGAGAATTCGAATACAG AGTAAATNNNACGTATGCCA	3872	TGCAGGACCAGAGAATTCGAATACAG GCAGCCTNNNACGTATGCCA	4112
TGCAGGACCAGAGAATTCGAATACAT TTCCCGANNNACGTATGCCA	3633	TGCAGGACCAGAGAATTCGAATACAG CTGCGTCNNNACGTATGCCA	3873	TGCAGGACCAGAGAATTCGAATACAT TATACAGNNNACGTATGCCA	4113
TGCAGGACCAGAGAATTCGAATACAT TCGGAACNNNACGTATGCCA	3634	TGCAGGACCAGAGAATTCGAATACAC TTGACGANNNACGTATGCCA	3874	TGCAGGACCAGAGAATTCGAATACAC COGTCTGNNNACGTATGCCA	4114
TGCAGGACCAGAGAATTCGAATACAT GGAGATGNNNACGTATGCCA	3635	TGCAGGACCAGAGAATTCGAATACAC CTCTTTNNNACGTATGCCA	3875	TGCAGGACCAGAGAATTCGAATACAT AATTTAANNNACGTATGCCA	4115
TGCAGGACCAGAGAATTCGAATACAC CAACCCNNNACGTATGCCA	3636	TGCAGGACCAGAGAATTCGAATACAA CACAGGNNNACGTATGCCA	3876	TGCAGGACCAGAGAATTCGAATACAT TCATCATNNNACGTATGCCA	4116
TGCAGGACCAGAGAATTCGAATACAG ACAATGNNNACGTATGCCA	3637	TGCAGGACCAGAGAATTCGAATACAT CTCCAGTNNNACGTATGCCA	3877	TGCAGGACCAGAGAATTCGAATACAC ATGTATANNNACGTATGCCA	4117
TGCAGGACCAGAGAATTCGAATACAC AGAGCCNNNACGTATGCCA	3638	TGCAGGACCAGAGAATTCGAATACAT ATTGGTANNNACGTATGCCA	3878	TGCAGGACCAGAGAATTCGAATACAG TAGTTATNNNACGTATGCCA	4118
TGCAGGACCAGAGAATTCGAATACAA AGAATACNNNACGTATGCCA	3639	TGCAGGACCAGAGAATTCGAATACAG CTTTCATNNNACGTATGCCA	3879	TGCAGGACCAGAGAATTCGAATACAT GTATCGGNNNACGTATGCCA	4119
TGCAGGACCAGAGAATTCGAATACAA GGTAAATNNNACGTATGCCA	3640	TGCAGGACCAGAGAATTCGAATACAT TCGTTTANNNACGTATGCCA	3880	TGCAGGACCAGAGAATTCGAATACAA GAGGTTGNNNACGTATGCCA	4120

FIG. 17B

Pool-16	SEQ ID NO:	Pool-17	SEQ ID NO:	Pool-18	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATACAG	3641	TGCAGGACCAGAGAATTGGAATACAT	3881	TGCAGGACCAGAGAATTGGAATACAG	4121
CCCCAAGNNNACGTATGCCA		ACGTGACNNNACGTATGCCA		CACAAGANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	3642	TGCAGGACCAGAGAATTGGAATACAT	3882	TGCAGGACCAGAGAATTGGAATACAA	4122
TGCTTGTNNNACGTATGCCA		GTTCGGTNNNACGTATGCCA		ACCCGGCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	3643	TGCAGGACCAGAGAATTGGAATACAC	3883	TGCAGGACCAGAGAATTGGAATACAT	4123
CACGGCCNNNACGTATGCCA		ATCACAGNNNACGTATGCCA		GTGGCTANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	3644	TGCAGGACCAGAGAATTGGAATACAA	3884	TGCAGGACCAGAGAATTGGAATACAG	4124
CGACCTANNNACGTATGCCA		ACGGCGNNNACGTATGCCA		TAGCTCANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	3645	TGCAGGACCAGAGAATTGGAATACAA	3885	TGCAGGACCAGAGAATTGGAATACAG	4125
TTAGAAGNNNACGTATGCCA		ATGTGAANNNACGTATGCCA		GOTGGCTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	3646	TGCAGGACCAGAGAATTGGAATACAG	3886	TGCAGGACCAGAGAATTGGAATACAT	4126
CCGTACGNNNACGTATGCCA		TAGCCGNNNACGTATGCCA		ACAGCTGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	3647	TGCAGGACCAGAGAATTGGAATACAT	3887	TGCAGGACCAGAGAATTGGAATACAC	4127
AGAAAGCNNNACGTATGCCA		GTGAATTNNNACGTATGCCA		TTGTGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	3648	TGCAGGACCAGAGAATTGGAATACAC	3888	TGCAGGACCAGAGAATTGGAATACAA	4128
CACCTTANNNACGTATGCCA		GGTAAGANNNACGTATGCCA		GCATCGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	3649	TGCAGGACCAGAGAATTGGAATACAT	3889	TGCAGGACCAGAGAATTGGAATACAA	4129
AGGATTANNNACGTATGCCA		CTGGTGANNNACGTATGCCA		ATAAAGCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	3650	TGCAGGACCAGAGAATTGGAATACAG	3890	TGCAGGACCAGAGAATTGGAATACAC	4130
GCATAANNNACGTATGCCA		TCCGTTTNNNACGTATGCCA		TATCGGANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	3651	TGCAGGACCAGAGAATTGGAATACAC	3891	TGCAGGACCAGAGAATTGGAATACAC	4131
ACTTCGNNNACGTATGCCA		CGTCGAGNNNACGTATGCCA		CGCCCGCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	3652	TGCAGGACCAGAGAATTGGAATACAT	3892	TGCAGGACCAGAGAATTGGAATACAT	4132
TTCTGTCNNNACGTATGCCA		CGATCCTNNNACGTATGCCA		CGTTTCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	3653	TGCAGGACCAGAGAATTGGAATACAT	3893	TGCAGGACCAGAGAATTGGAATACAC	4133
TCTTGGCNNNACGTATGCCA		TTGGCTCNNNACGTATGCCA		CTAGCAANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	3654	TGCAGGACCAGAGAATTGGAATACAC	3894	TGCAGGACCAGAGAATTGGAATACAT	4134
TGGCTCTNNNACGTATGCCA		TCCGCTCNNNACGTATGCCA		GAACATTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	3655	TGCAGGACCAGAGAATTGGAATACAT	3895	TGCAGGACCAGAGAATTGGAATACAT	4135
GAGACTANNNACGTATGCCA		CCACGCCNNNACGTATGCCA		GTAACTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	3656	TGCAGGACCAGAGAATTGGAATACAA	3896	TGCAGGACCAGAGAATTGGAATACAG	4136
ATACTTGNNNACGTATGCCA		CGTGCCGNNNACGTATGCCA		TCGGAAANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	3657	TGCAGGACCAGAGAATTGGAATACAT	3897	TGCAGGACCAGAGAATTGGAATACAG	4137
CTGTTAGNNNACGTATGCCA		GTGGTACNNNACGTATGCCA		TTGGCCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	3658	TGCAGGACCAGAGAATTGGAATACAA	3898	TGCAGGACCAGAGAATTGGAATACAG	4138
CAACCTGNNNACGTATGCCA		GCCGAAANNNACGTATGCCA		CGATAGANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	3659	TGCAGGACCAGAGAATTGGAATACAC	3899	TGCAGGACCAGAGAATTGGAATACAT	4139
CGTGCCNNNACGTATGCCA		TCCTAACNNNACGTATGCCA		TAACGTANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	3660	TGCAGGACCAGAGAATTGGAATACAG	3900	TGCAGGACCAGAGAATTGGAATACAC	4140
ACTCTCTNNNACGTATGCCA		AAGGCGCNNNACGTATGCCA		CTTATATNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	3661	TGCAGGACCAGAGAATTGGAATACAC	3901	TGCAGGACCAGAGAATTGGAATACAA	4141
ATAACACNNNACGTATGCCA		GTTCACCTNNNACGTATGCCA		AACAGATNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	3662	TGCAGGACCAGAGAATTGGAATACAG	3902	TGCAGGACCAGAGAATTGGAATACAT	4142
GAGCCTANNNACGTATGCCA		AGATGTGNNNACGTATGCCA		ACCCATCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	3663	TGCAGGACCAGAGAATTGGAATACAG	3903	TGCAGGACCAGAGAATTGGAATACAA	4143
AGACGAANNNACGTATGCCA		CTCACTTNNNACGTATGCCA		AAAGAGANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	3664	TGCAGGACCAGAGAATTGGAATACAC	3904	TGCAGGACCAGAGAATTGGAATACAC	4144
GGAAATGANNNACGTATGCCA		GAAGCTTNNNACGTATGCCA		GTTTGAANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	3665	TGCAGGACCAGAGAATTGGAATACAT	3905	TGCAGGACCAGAGAATTGGAATACAA	4145
GTGATGANNNACGTATGCCA		ACTCGAGNNNACGTATGCCA		TGGATCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	3666	TGCAGGACCAGAGAATTGGAATACAT	3906	TGCAGGACCAGAGAATTGGAATACAG	4146
ACCTCTANNNACGTATGCCA		TCTTGTANNNACGTATGCCA		CTCGATANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	3667	TGCAGGACCAGAGAATTGGAATACAG	3907	TGCAGGACCAGAGAATTGGAATACAT	4147
CTGGTACNNNACGTATGCCA		AAGAAGNNNACGTATGCCA		GTAAACCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	3668	TGCAGGACCAGAGAATTGGAATACAA	3908	TGCAGGACCAGAGAATTGGAATACAA	4148
CAAATCCNNNACGTATGCCA		GCCACGCNNNACGTATGCCA		TCTACTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	3669	TGCAGGACCAGAGAATTGGAATACAC	3909	TGCAGGACCAGAGAATTGGAATACAG	4149
ATATAAANNNCTAGCGTTAC		TATAGCGNNNCTAGCGTTAC		ATCGTACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	3670	TGCAGGACCAGAGAATTGGAATACAA	3910	TGCAGGACCAGAGAATTGGAATACAT	4150
GGTTATANNNCTAGCGTTAC		GATCTTANNNCTAGCGTTAC		GAACGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	3671	TGCAGGACCAGAGAATTGGAATACAA	3911	TGCAGGACCAGAGAATTGGAATACAT	4151
CCCGCTCNNNCTAGCGTTAC		CAACCCANNNCTAGCGTTAC		CCAACCTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	3672	TGCAGGACCAGAGAATTGGAATACAT	3912	TGCAGGACCAGAGAATTGGAATACAG	4152
GGCAAAGNNNCTAGCGTTAC		GCTAACGNNNCTAGCGTTAC		CGGAGGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	3673	TGCAGGACCAGAGAATTGGAATACAT	3913	TGCAGGACCAGAGAATTGGAATACAT	4153
GTCTGCCNNNCTAGCGTTAC		GTAGTCGNNNCTAGCGTTAC		GCCCATNNNCTAGCGTTAC	

FIG. 17C

Pool-16	SEQ ID NO:	Pool-17	SEQ ID NO:	Pool-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAA	3674	TGCAGGACCAGAGAATTCGAATACAA	3914	TGCAGGACCAGAGAATTCGAATACAA	4154
GTGTATNNNCTAGCGTTAC		TGGTCGTNNNCTAGCGTTAC		CGATCACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	3675	TGCAGGACCAGAGAATTCGAATACAA	3915	TGCAGGACCAGAGAATTCGAATACAT	4155
GCTACTANNNCTAGCGTTAC		GTAGGACNNNCTAGCGTTAC		AAGGTAANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3676	TGCAGGACCAGAGAATTCGAATACAA	3916	TGCAGGACCAGAGAATTCGAATACAA	4156
CATCATANNNCTAGCGTTAC		AAAAAANNNCTAGCGTTAC		CCTACGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3677	TGCAGGACCAGAGAATTCGAATACAA	3917	TGCAGGACCAGAGAATTCGAATACAC	4157
TTCCAGGNNNCTAGCGTTAC		GTTCAIANNNCTAGCGTTAC		ACACCAANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAT	3678	TGCAGGACCAGAGAATTCGAATACAG	3918	TGCAGGACCAGAGAATTCGAATACAT	4158
TTTGTTGNNNCTAGCGTTAC		AAGGTCANNNCTAGCGTTAC		GGTCGGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3679	TGCAGGACCAGAGAATTCGAATACAT	3919	TGCAGGACCAGAGAATTCGAATACAT	4159
GTGGACANNNCTAGCGTTAC		GAATGCCNNNCTAGCGTTAC		TATCTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	3680	TGCAGGACCAGAGAATTCGAATACAA	3920	TGCAGGACCAGAGAATTCGAATACAT	4160
AGAGGTTNNNCTAGCGTTAC		CACCCGNNNCTAGCGTTAC		CGAGCCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3681	TGCAGGACCAGAGAATTCGAATACAC	3921	TGCAGGACCAGAGAATTCGAATACAT	4161
TTCCCGNNNCTAGCGTTAC		TAACGCANNNCTAGCGTTAC		ACCGATGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3682	TGCAGGACCAGAGAATTCGAATACAA	3922	TGCAGGACCAGAGAATTCGAATACAG	4162
CCCTCATNNNCTAGCGTTAC		CCCTATNNNCTAGCGTTAC		AACGGATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3683	TGCAGGACCAGAGAATTCGAATACAA	3923	TGCAGGACCAGAGAATTCGAATACAT	4163
AAGAGGTTNNNCTAGCGTTAC		GATAGATNNNCTAGCGTTAC		TGTTCTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	3684	TGCAGGACCAGAGAATTCGAATACAG	3924	TGCAGGACCAGAGAATTCGAATACAG	4164
AAAGTCGNNNCTAGCGTTAC		GAGTGATNNNCTAGCGTTAC		GTGCTCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3685	TGCAGGACCAGAGAATTCGAATACAA	3925	TGCAGGACCAGAGAATTCGAATACAA	4165
GCAGAAANNNCTAGCGTTAC		TAGAGGCNNNCTAGCGTTAC		TGCTTCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3686	TGCAGGACCAGAGAATTCGAATACAC	3926	TGCAGGACCAGAGAATTCGAATACAT	4166
CTGGCAGNNNCTAGCGTTAC		CCCGCGNNNCTAGCGTTAC		CAGGACTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3687	TGCAGGACCAGAGAATTCGAATACAC	3927	TGCAGGACCAGAGAATTCGAATACAA	4167
GCAGATGNNNCTAGCGTTAC		CATAGTCNNNCTAGCGTTAC		AGACATANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3688	TGCAGGACCAGAGAATTCGAATACAT	3928	TGCAGGACCAGAGAATTCGAATACAC	4168
GAGGCCGNNNCTAGCGTTAC		GATTCCNNNCTAGCGTTAC		CATCGTTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3689	TGCAGGACCAGAGAATTCGAATACAA	3929	TGCAGGACCAGAGAATTCGAATACAT	4169
GTGCGTGNNNCTAGCGTTAC		GAACGGTNNNCTAGCGTTAC		AACACCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAT	3690	TGCAGGACCAGAGAATTCGAATACAG	3930	TGCAGGACCAGAGAATTCGAATACAC	4170
GGTAGGANNNCTAGCGTTAC		CTTCAAGNNNCTAGCGTTAC		CTCCTCCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3691	TGCAGGACCAGAGAATTCGAATACAA	3931	TGCAGGACCAGAGAATTCGAATACAT	4171
GCCCAANNNCTAGCGTTAC		AATATCCNNNCTAGCGTTAC		CGGACTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAT	3692	TGCAGGACCAGAGAATTCGAATACAC	3932	TGCAGGACCAGAGAATTCGAATACAG	4172
GAGCACTNNNCTAGCGTTAC		GTCCCCANNNCTAGCGTTAC		GCAACANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAT	3693	TGCAGGACCAGAGAATTCGAATACAA	3933	TGCAGGACCAGAGAATTCGAATACAG	4173
CATCGTGNNNCTAGCGTTAC		CTAATCANNNCTAGCGTTAC		GAAACACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3694	TGCAGGACCAGAGAATTCGAATACAT	3934	TGCAGGACCAGAGAATTCGAATACAT	4174
GCCAAGANNNCTAGCGTTAC		GACGCCGNNNCTAGCGTTAC		ACACTCCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3695	TGCAGGACCAGAGAATTCGAATACAG	3935	TGCAGGACCAGAGAATTCGAATACAC	4175
GAGGACGNNNCTAGCGTTAC		CGTGCCANNNCTAGCGTTAC		GGACCTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAT	3696	TGCAGGACCAGAGAATTCGAATACAA	3936	TGCAGGACCAGAGAATTCGAATACAA	4176
GTGACTGNNNCTAGCGTTAC		AAATTGGANNNCTAGCGTTAC		TOCTGAGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3697	TGCAGGACCAGAGAATTCGAATACAT	3937	TGCAGGACCAGAGAATTCGAATACAC	4177
CCTTGAGNNNCTAGCGTTAC		GTTCAACNNNCTAGCGTTAC		CCGTCTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	3698	TGCAGGACCAGAGAATTCGAATACAA	3938	TGCAGGACCAGAGAATTCGAATACAG	4178
TTAAGTTNNNCTAGCGTTAC		TCCGCAANNNCTAGCGTTAC		GCTCAATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3699	TGCAGGACCAGAGAATTCGAATACAT	3939	TGCAGGACCAGAGAATTCGAATACAG	4179
CCCAGGCNNNCTAGCGTTAC		CAGATTANNNCTAGCGTTAC		TGCTTGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3700	TGCAGGACCAGAGAATTCGAATACAC	3940	TGCAGGACCAGAGAATTCGAATACAA	4180
CGATGATNNNCTAGCGTTAC		GCTAAGTNNNCTAGCGTTAC		TTAACTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	3701	TGCAGGACCAGAGAATTCGAATACAC	3941	TGCAGGACCAGAGAATTCGAATACAT	4181
ATCTCGANNNCTAGCGTTAC		ACACGTTNNNCTAGCGTTAC		CCAGATGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	3702	TGCAGGACCAGAGAATTCGAATACAA	3942	TGCAGGACCAGAGAATTCGAATACAC	4182
GAGATGTNNNCTAGCGTTAC		AGCCTGTNNNCTAGCGTTAC		CGCGCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAT	3703	TGCAGGACCAGAGAATTCGAATACAG	3943	TGCAGGACCAGAGAATTCGAATACAC	4183
AGGTAAANNNCTAGCGTTAC		GTCCAGCANNNCTAGCGTTAC		CATAAGCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3704	TGCAGGACCAGAGAATTCGAATACAT	3944	TGCAGGACCAGAGAATTCGAATACAG	4184
CTCAGCANNNCTAGCGTTAC		GTGCGTTNNNCTAGCGTTAC		GTTGGTTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3705	TGCAGGACCAGAGAATTCGAATACAG	3945	TGCAGGACCAGAGAATTCGAATACAG	4185
GATAGCCNNNCTAGCGTTAC		AAATTTNNNCTAGCGTTAC		GCAGATANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3706	TGCAGGACCAGAGAATTCGAATACAT	3946	TGCAGGACCAGAGAATTCGAATACAA	4186
GAATTGCNNNCTAGCGTTAC		ACGGTGTNNNCTAGCGTTAC		TGCAACNNNCTAGCGTTAC	

FIG. 17D

Pool-16	SEQ ID NO:	Pool-17	SEQ ID NO:	Pool-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAT	3707	TGCAGGACCAGAGAATTCGAATACAC	3947	TGCAGGACCAGAGAATTCGAATACAG	4187
ACCAGGTNNNNCTAGCGTTAC		CGACCAGNNNNCTAGCGTTAC		CGCGCCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAT	3708	TGCAGGACCAGAGAATTCGAATACAT	3948	TGCAGGACCAGAGAATTCGAATACAC	4188
ATACTCTNNNNCTAGCGTTAC		GATAAAGNNNNCTAGCGTTAC		AAAGTGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3709	TGCAGGACCAGAGAATTCGAATACAT	3949	TGCAGGACCAGAGAATTCGAATACAT	4189
GCTTCTCNNNNCTAGCGTTAC		ATGGCTGNNNNCTAGCGTTAC		AAAAGCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3710	TGCAGGACCAGAGAATTCGAATACAC	3950	TGCAGGACCAGAGAATTCGAATACAA	4190
CCTGAGTNNNNCTAGCGTTAC		CCCTCCTNNNNCTAGCGTTAC		TCTGTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3711	TGCAGGACCAGAGAATTCGAATACAT	3951	TGCAGGACCAGAGAATTCGAATACAC	4191
ATAGATTNNNNCTAGCGTTAC		CTTACCNNNNCTAGCGTTAC		GTATATANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3712	TGCAGGACCAGAGAATTCGAATACAG	3952	TGCAGGACCAGAGAATTCGAATACAG	4192
GCAGATNNNNCTAGCGTTAC		CAATCGTNNNNCTAGCGTTAC		GTATTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	3713	TGCAGGACCAGAGAATTCGAATACAC	3953	TGCAGGACCAGAGAATTCGAATACAT	4193
GCATGCCNNNNCTAGCGTTAC		TAGCCGNNNNCTAGCGTTAC		ACAAACTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	3714	TGCAGGACCAGAGAATTCGAATACAT	3954	TGCAGGACCAGAGAATTCGAATACAC	4194
ATATCCGNNNNCTAGCGTTAC		ACTCTGCNNNNCTAGCGTTAC		TCTTAATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	3715	TGCAGGACCAGAGAATTCGAATACAA	3955	TGCAGGACCAGAGAATTCGAATACAG	4195
CTCAGCGNNNNCTAGCGTTAC		TGGCAGANNNNCTAGCGTTAC		GTCTGATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3716	TGCAGGACCAGAGAATTCGAATACAC	3956	TGCAGGACCAGAGAATTCGAATACAT	4196
TTCAAGGNNNNCTAGCGTTAC		GAGGTTTNNNNCTAGCGTTAC		CAGGAAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAT	3717	TGCAGGACCAGAGAATTCGAATACAC	3957	TGCAGGACCAGAGAATTCGAATACAC	4197
CAGTAATNNNNCTAGCGTTAC		CAGCTAANNNNCTAGCGTTAC		ACGCTTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3718	TGCAGGACCAGAGAATTCGAATACAT	3958	TGCAGGACCAGAGAATTCGAATACAG	4198
CGGCCAANNNNCTAGCGTTAC		GTGCCGNNNNCTAGCGTTAC		GGGGCAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3719	TGCAGGACCAGAGAATTCGAATACAT	3959	TGCAGGACCAGAGAATTCGAATACAG	4199
TGATCATNNNNCTAGCGTTAC		GCCGTTTNNNNCTAGCGTTAC		AAGTTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAG	3720	TGCAGGACCAGAGAATTCGAATACAC	3960	TGCAGGACCAGAGAATTCGAATACAG	4200
GCCTGTTNNNNCTAGCGTTAC		TCCGTGNNNNCTAGCGTTAC		CAGGTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3721	TGCAGGACCAGAGAATTCGAATACAG	3961	TGCAGGACCAGAGAATTCGAATACAT	4201
GTCCGCGNNNNCTAGCGTTAC		CACAATCNNNNCTAGCGTTAC		GTAAATCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3722	TGCAGGACCAGAGAATTCGAATACAC	3962	TGCAGGACCAGAGAATTCGAATACAG	4202
ACTGGTANNNNCTAGCGTTAC		ATCGTGANNNNCTAGCGTTAC		TCAACANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3723	TGCAGGACCAGAGAATTCGAATACAC	3963	TGCAGGACCAGAGAATTCGAATACAG	4203
TAAGACNNNNCTAGCGTTAC		AAGGTTNNNNCTAGCGTTAC		AGCAACANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3724	TGCAGGACCAGAGAATTCGAATACAG	3964	TGCAGGACCAGAGAATTCGAATACAA	4204
CGCTACANNNNCTAGCGTTAC		AAAGGTCNNNNCTAGCGTTAC		CCGTCCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3725	TGCAGGACCAGAGAATTCGAATACAA	3965	TGCAGGACCAGAGAATTCGAATACAT	4205
CCAAAAANNNNCTAGCGTTAC		GAAGGTCNNNNCTAGCGTTAC		AGGCGCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3726	TGCAGGACCAGAGAATTCGAATACAC	3966	TGCAGGACCAGAGAATTCGAATACAG	4206
GAGTGCCNNNNCTAGCGTTAC		CATGCTTNNNNCTAGCGTTAC		AAGCAGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3727	TGCAGGACCAGAGAATTCGAATACAT	3967	TGCAGGACCAGAGAATTCGAATACAT	4207
ACCGGAANNNNCTAGCGTTAC		TCAACTTNNNNCTAGCGTTAC		TGGTATANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAA	3728	TGCAGGACCAGAGAATTCGAATACAT	3968	TGCAGGACCAGAGAATTCGAATACAG	4208
AAAGCATNNNNCTAGCGTTAC		CTGGCAANNNNCTAGCGTTAC		AAGTGTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATACAC	3729	TGCAGGACCAGAGAATTCGAATACAG	3969	TGCAGGACCAGAGAATTCGAATACAC	4209
CCCCGGCNNNGATCGACATG		TTTACAANNNGATCGACATG		TGCTTTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3730	TGCAGGACCAGAGAATTCGAATACAA	3970	TGCAGGACCAGAGAATTCGAATACAG	4210
TGGTTGGNNNGATCGACATG		CCCACAANNNGATCGACATG		TTCCGCGCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3731	TGCAGGACCAGAGAATTCGAATACAG	3971	TGCAGGACCAGAGAATTCGAATACAC	4211
CCACGTTNNNGATCGACATG		GCTCATANNNGATCGACATG		GACTATGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	3732	TGCAGGACCAGAGAATTCGAATACAA	3972	TGCAGGACCAGAGAATTCGAATACAC	4212
TGAAGTANNNGATCGACATG		GCATTGNNNGATCGACATG		TGTAGCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	3733	TGCAGGACCAGAGAATTCGAATACAA	3973	TGCAGGACCAGAGAATTCGAATACAC	4213
CAATAAGNNNGATCGACATG		ACCCGATNNNGATCGACATG		GGGGTCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	3734	TGCAGGACCAGAGAATTCGAATACAT	3974	TGCAGGACCAGAGAATTCGAATACAT	4214
ATGTTTTNNNGATCGACATG		GACCAACNNNGATCGACATG		CCATGAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3735	TGCAGGACCAGAGAATTCGAATACAG	3975	TGCAGGACCAGAGAATTCGAATACAG	4215
CCGGTCCNNNGATCGACATG		CCGAGGANNNGATCGACATG		GCTCCCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3736	TGCAGGACCAGAGAATTCGAATACAA	3976	TGCAGGACCAGAGAATTCGAATACAA	4216
TTACGTGNNNGATCGACATG		ATATGGANNNGATCGACATG		GCTTAACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3737	TGCAGGACCAGAGAATTCGAATACAT	3977	TGCAGGACCAGAGAATTCGAATACAC	4217
GTCTTGNNNGATCGACATG		TTCCGTCNNNGATCGACATG		GAGGAATNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	3738	TGCAGGACCAGAGAATTCGAATACAT	3978	TGCAGGACCAGAGAATTCGAATACAC	4218
GTACAGNNNGATCGACATG		TAGGTTANNNGATCGACATG		CCGAGCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	3739	TGCAGGACCAGAGAATTCGAATACAA	3979	TGCAGGACCAGAGAATTCGAATACAT	4219
ATAAGTTNNNGATCGACATG		ACCGGTTNNNGATCGACATG		ACAATACNNNGATCGACATG	

FIG. 17E

Pool-16	SEQ ID NO:	Pool-17	SEQ ID NO:	Pool-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAA	3740	TGCAGGACCAGAGAATTCGAATACAA	3980	TGCAGGACCAGAGAATTCGAATACAT	4220
AATCCTANNNGATCGACATG		GGTAAGCANNNGATCGACATG		AACATGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	3741	TGCAGGACCAGAGAATTCGAATACAA	3981	TGCAGGACCAGAGAATTCGAATACAG	4221
ATCATGGNNNGATCGACATG		ATTGACTNNNGATCGACATG		TTGCGGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3742	TGCAGGACCAGAGAATTCGAATACAT	3982	TGCAGGACCAGAGAATTCGAATACAA	4222
TCACTGCNNNGATCGACATG		ACTGTAAANNNGATCGACATG		TCTGCAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3743	TGCAGGACCAGAGAATTCGAATACAT	3983	TGCAGGACCAGAGAATTCGAATACAG	4223
TGCGCCGNNNGATCGACATG		TCTCTGGNNNGATCGACATG		GTTAGTCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3744	TGCAGGACCAGAGAATTCGAATACAA	3984	TGCAGGACCAGAGAATTCGAATACAC	4224
GTCTGTNNNGATCGACATG		GAAGAAANNNGATCGACATG		TTAAGATNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3745	TGCAGGACCAGAGAATTCGAATACAA	3985	TGCAGGACCAGAGAATTCGAATACAC	4225
GGCGTCTNNNGATCGACATG		AATGAACNNNGATCGACATG		TCTACANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	3746	TGCAGGACCAGAGAATTCGAATACAA	3986	TGCAGGACCAGAGAATTCGAATACAG	4226
CCACGGNNNGATCGACATG		ACACACNNNGATCGACATG		CTCAGTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3747	TGCAGGACCAGAGAATTCGAATACAT	3987	TGCAGGACCAGAGAATTCGAATACAG	4227
CCTTTAANNNGATCGACATG		AAATGCTNNNGATCGACATG		GTACTACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3748	TGCAGGACCAGAGAATTCGAATACAA	3988	TGCAGGACCAGAGAATTCGAATACAT	4228
TACAAGTNNNGATCGACATG		CCGCTTANNNGATCGACATG		AGTATGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3749	TGCAGGACCAGAGAATTCGAATACAC	3989	TGCAGGACCAGAGAATTCGAATACAA	4229
CGAGGAANNNGATCGACATG		CGCGGTANNNGATCGACATG		AGCATCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3750	TGCAGGACCAGAGAATTCGAATACAC	3990	TGCAGGACCAGAGAATTCGAATACAA	4230
ACACTCANNNGATCGACATG		GTAGACTNNNGATCGACATG		CTAAAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	3751	TGCAGGACCAGAGAATTCGAATACAG	3991	TGCAGGACCAGAGAATTCGAATACAA	4231
CTTAGGNNNGATCGACATG		GAAGTCAANNNGATCGACATG		CTTTAAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	3752	TGCAGGACCAGAGAATTCGAATACAA	3992	TGCAGGACCAGAGAATTCGAATACAA	4232
CTTACTNNNGATCGACATG		GAATTGANNNNGATCGACATG		CGAATAANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	3753	TGCAGGACCAGAGAATTCGAATACAA	3993	TGCAGGACCAGAGAATTCGAATACAT	4233
AAGAGAANNNGATCGACATG		CCCCGTANNNGATCGACATG		AGCGTCAANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	3754	TGCAGGACCAGAGAATTCGAATACAT	3994	TGCAGGACCAGAGAATTCGAATACAA	4234
CAGCAGANNNGATCGACATG		ACAGACNNNGATCGACATG		TCATCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3755	TGCAGGACCAGAGAATTCGAATACAA	3995	TGCAGGACCAGAGAATTCGAATACAA	4235
GAGTACNNNGATCGACATG		TTAGACTNNNGATCGACATG		AAACAACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3756	TGCAGGACCAGAGAATTCGAATACAC	3996	TGCAGGACCAGAGAATTCGAATACAC	4236
ACTGTCAANNNGATCGACATG		ACTAGACNNNGATCGACATG		TATCAGGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3757	TGCAGGACCAGAGAATTCGAATACAG	3997	TGCAGGACCAGAGAATTCGAATACAT	4237
CGAGGCCNNNGATCGACATG		CCCTAAANNNGATCGACATG		ACTGTCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3758	TGCAGGACCAGAGAATTCGAATACAA	3998	TGCAGGACCAGAGAATTCGAATACAA	4238
TCATAGNNNGATCGACATG		GAGTGGTNNNGATCGACATG		GGACACANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3759	TGCAGGACCAGAGAATTCGAATACAA	3999	TGCAGGACCAGAGAATTCGAATACAG	4239
ACTGTTGNNNGATCGACATG		TCTGAATNNNGATCGACATG		TGACGTTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	3760	TGCAGGACCAGAGAATTCGAATACAA	4000	TGCAGGACCAGAGAATTCGAATACAC	4240
CACACTGNNNGATCGACATG		GCATCACNNNGATCGACATG		TTGTACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	3761	TGCAGGACCAGAGAATTCGAATACAA	4001	TGCAGGACCAGAGAATTCGAATACAG	4241
GGTGACANNNGATCGACATG		ATTGGAANNNGATCGACATG		GATGCGGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	3762	TGCAGGACCAGAGAATTCGAATACAC	4002	TGCAGGACCAGAGAATTCGAATACAC	4242
AACAATGNNNGATCGACATG		TAGCCCCNNNGATCGACATG		TGATTGGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3763	TGCAGGACCAGAGAATTCGAATACAT	4003	TGCAGGACCAGAGAATTCGAATACAG	4243
ATTTGTANNNGATCGACATG		CTTGCTGNNNGATCGACATG		CAACTCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	3764	TGCAGGACCAGAGAATTCGAATACAC	4004	TGCAGGACCAGAGAATTCGAATACAT	4244
CCCCGATNNNGATCGACATG		CGTCTGNNNGATCGACATG		ACCTCACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	3765	TGCAGGACCAGAGAATTCGAATACAC	4005	TGCAGGACCAGAGAATTCGAATACAT	4245
GGAGCGCANNNGATCGACATG		CTAAGCANNNGATCGACATG		GCACCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	3766	TGCAGGACCAGAGAATTCGAATACAA	4006	TGCAGGACCAGAGAATTCGAATACAG	4246
CCTGGAGNNNGATCGACATG		AAATAGCNNNGATCGACATG		TTCTACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	3767	TGCAGGACCAGAGAATTCGAATACAA	4007	TGCAGGACCAGAGAATTCGAATACAT	4247
GCACTCCNNNGATCGACATG		AGCACTCANNNGATCGACATG		ACTGTTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3768	TGCAGGACCAGAGAATTCGAATACAG	4008	TGCAGGACCAGAGAATTCGAATACAC	4248
AAGTCAGNNNGATCGACATG		TTCAACGNNNGATCGACATG		TTCATATNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3769	TGCAGGACCAGAGAATTCGAATACAC	4009	TGCAGGACCAGAGAATTCGAATACAT	4249
GGCTCGTNNNGATCGACATG		GTCTGTTNNNGATCGACATG		CTGCTGTTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	3770	TGCAGGACCAGAGAATTCGAATACAG	4010	TGCAGGACCAGAGAATTCGAATACAT	4250
ATGTGTCNNNGATCGACATG		CACGGCTNNNGATCGACATG		GGTATTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3771	TGCAGGACCAGAGAATTCGAATACAA	4011	TGCAGGACCAGAGAATTCGAATACAA	4251
AGTAACTNNNGATCGACATG		CCCAACNNNGATCGACATG		GAATGTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3772	TGCAGGACCAGAGAATTCGAATACAC	4012	TGCAGGACCAGAGAATTCGAATACAG	4252
AGATGTTNNNGATCGACATG		ATAAACTNNNGATCGACATG		GCGAGCANNNGATCGACATG	

FIG. 17F

Pool-16	SEQ ID NO:	Pool-17	SEQ ID NO:	Pool-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAA	3773	TGCAGGACCAGAGAATTCGAATACAT	4013	TGCAGGACCAGAGAATTCGAATACAG	4253
ATGAGCGNNNGATCGACATG		CGTAAGCNNNGATCGACATG		CCACAATNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	3774	TGCAGGACCAGAGAATTCGAATACAG	4014	TGCAGGACCAGAGAATTCGAATACAT	4254
CTTGCGANNNGATCGACATG		AGCTTGNNNGATCGACATG		ATTCTCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3775	TGCAGGACCAGAGAATTCGAATACAG	4015	TGCAGGACCAGAGAATTCGAATACAA	4255
GGGTACCCNNNGATCGACATG		TTTTGTTNNNGATCGACATG		AGACCTCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3776	TGCAGGACCAGAGAATTCGAATACAT	4016	TGCAGGACCAGAGAATTCGAATACAC	4256
GTACATNNNGATCGACATG		GAGTAGNNNGATCGACATG		ACATAATNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	3777	TGCAGGACCAGAGAATTCGAATACAT	4017	TGCAGGACCAGAGAATTCGAATACAA	4257
ACTTAAANNNGATCGACATG		GAGTCTGNNNGATCGACATG		COCTGAANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3778	TGCAGGACCAGAGAATTCGAATACAA	4018	TGCAGGACCAGAGAATTCGAATACAG	4258
TTACCTANNNGATCGACATG		GAAGCTGNNNGATCGACATG		TAGACCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	3779	TGCAGGACCAGAGAATTCGAATACAT	4019	TGCAGGACCAGAGAATTCGAATACAC	4259
GTCTGGCANNNGATCGACATG		AGAAGCANNNGATCGACATG		CCTACCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3780	TGCAGGACCAGAGAATTCGAATACAG	4020	TGCAGGACCAGAGAATTCGAATACAT	4260
AGACATGNNNGATCGACATG		CTTATGNNNGATCGACATG		ATCCCACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3781	TGCAGGACCAGAGAATTCGAATACAG	4021	TGCAGGACCAGAGAATTCGAATACAA	4261
AGGCATANNNGATCGACATG		GCATATCANNNGATCGACATG		GTCTATTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	3782	TGCAGGACCAGAGAATTCGAATACAT	4022	TGCAGGACCAGAGAATTCGAATACAG	4262
CTGCTCGNNNGATCGACATG		CCGCTTANNNGATCGACATG		GAACAACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3783	TGCAGGACCAGAGAATTCGAATACAT	4023	TGCAGGACCAGAGAATTCGAATACAA	4263
TGCTAGGNNNGATCGACATG		TTATAGGNNNGATCGACATG		TCTCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3784	TGCAGGACCAGAGAATTCGAATACAA	4024	TGCAGGACCAGAGAATTCGAATACAC	4264
CCCGACNNNGATCGACATG		TGCTTAANNNGATCGACATG		TGTACCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	3785	TGCAGGACCAGAGAATTCGAATACAT	4025	TGCAGGACCAGAGAATTCGAATACAG	4265
ACGAATCANNNGATCGACATG		GACGTACNNNGATCGACATG		ATCCAGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	3786	TGCAGGACCAGAGAATTCGAATACAA	4026	TGCAGGACCAGAGAATTCGAATACAT	4266
CGTCGCANNNGATCGACATG		GAGAAAANNNGATCGACATG		AAGTTCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	3787	TGCAGGACCAGAGAATTCGAATACAT	4027	TGCAGGACCAGAGAATTCGAATACAC	4267
ATCCAATNNNGATCGACATG		GTCTCGTNNNGATCGACATG		CGTTAGANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	3788	TGCAGGACCAGAGAATTCGAATACAC	4028	TGCAGGACCAGAGAATTCGAATACAA	4268
GCGAACCNNNGATCGACATG		GTTATGGNNNGATCGACATG		AGAGACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	3789	TGCAGGACCAGAGAATTCGAATACAT	4029	TGCAGGACCAGAGAATTCGAATACAC	4269
ATGATCANNNTGCATCAGGT		ATTGAGTNNNTGCATCAGGT		GCCCTACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	3790	TGCAGGACCAGAGAATTCGAATACAA	4030	TGCAGGACCAGAGAATTCGAATACAG	4270
TGGCACANNNTGCATCAGGT		ATAGAGTNNNTGCATCAGGT		ACGGCCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	3791	TGCAGGACCAGAGAATTCGAATACAC	4031	TGCAGGACCAGAGAATTCGAATACAC	4271
TACACCTNNNTGCATCAGGT		AGACATCANNNTGCATCAGGT		GCGGAGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	3792	TGCAGGACCAGAGAATTCGAATACAG	4032	TGCAGGACCAGAGAATTCGAATACAG	4272
TAGAGTTNNNTGCATCAGGT		AAGCCAANNNTGCATCAGGT		CGATAAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	3793	TGCAGGACCAGAGAATTCGAATACAC	4033	TGCAGGACCAGAGAATTCGAATACAA	4273
GTGTTGTTNNNTGCATCAGGT		AGTCCAANNNTGCATCAGGT		CGCTAGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	3794	TGCAGGACCAGAGAATTCGAATACAT	4034	TGCAGGACCAGAGAATTCGAATACAT	4274
CAGACGCNNNTGCATCAGGT		TCCGACTNNNTGCATCAGGT		TTGAATGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	3795	TGCAGGACCAGAGAATTCGAATACAA	4035	TGCAGGACCAGAGAATTCGAATACAT	4275
GTITGGCANNNTGCATCAGGT		CAGTATTNNNTGCATCAGGT		ATTAAATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	3796	TGCAGGACCAGAGAATTCGAATACAG	4036	TGCAGGACCAGAGAATTCGAATACAC	4276
CTTCCTCANNNTGCATCAGGT		AGAATATNNNTGCATCAGGT		GTGTTGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	3797	TGCAGGACCAGAGAATTCGAATACAA	4037	TGCAGGACCAGAGAATTCGAATACAA	4277
AAGATAANNNTGCATCAGGT		GTAAGGCNNNTGCATCAGGT		AGCTTATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	3798	TGCAGGACCAGAGAATTCGAATACAA	4038	TGCAGGACCAGAGAATTCGAATACAC	4278
ACTAGCGNNNTGCATCAGGT		GCGTATCANNNTGCATCAGGT		CCCAGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	3799	TGCAGGACCAGAGAATTCGAATACAT	4039	TGCAGGACCAGAGAATTCGAATACAG	4279
ACACAAGNNNTGCATCAGGT		ACGGTTGNNNTGCATCAGGT		TCGTCAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	3800	TGCAGGACCAGAGAATTCGAATACAA	4040	TGCAGGACCAGAGAATTCGAATACAT	4280
TTACCTCANNNTGCATCAGGT		AGGAAGGNNNTGCATCAGGT		ACATCGGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	3801	TGCAGGACCAGAGAATTCGAATACAC	4041	TGCAGGACCAGAGAATTCGAATACAG	4281
CTACCACNNNTGCATCAGGT		ATTGGACNNNTGCATCAGGT		ACTTTCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	3802	TGCAGGACCAGAGAATTCGAATACAT	4042	TGCAGGACCAGAGAATTCGAATACAT	4282
AGTCGTGNNNTGCATCAGGT		AAGGCTCANNNTGCATCAGGT		GCCCTATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAA	3803	TGCAGGACCAGAGAATTCGAATACAC	4043	TGCAGGACCAGAGAATTCGAATACAT	4283
ATGCAGGNNNTGCATCAGGT		GAAGCGGNNNTGCATCAGGT		GACGGAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	3804	TGCAGGACCAGAGAATTCGAATACAG	4044	TGCAGGACCAGAGAATTCGAATACAG	4284
ATGGACTNNNTGCATCAGGT		ACGATTNNNTGCATCAGGT		CTGCCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	3805	TGCAGGACCAGAGAATTCGAATACAG	4045	TGCAGGACCAGAGAATTCGAATACAT	4285
TGCGAGTNNNTGCATCAGGT		TCGATACNNNTGCATCAGGT		CATATAGNNNTGCATCAGGT	

FIG. 17G

Pool-16	SEQ ID NO:	Pool-17	SEQ ID NO:	Pool-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT	
TGCAAGCANNNTGCATCAGGT	3806	ATCAATANNNTGCATCAGGT	4046	GTGCGATNNNTGCATCAGGT	4286
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC	
CTCGGAGNNNTGCATCAGGT	3807	ACACATGNNNTGCATCAGGT	4047	ACGATCANNNTGCATCAGGT	4287
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG	
AACATTGNNNTGCATCAGGT	3808	CAGCGAGNNNTGCATCAGGT	4048	ACTGCCGNNNTGCATCAGGT	4288
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG	
AGGTTAGNNNTGCATCAGGT	3809	ACGGCTANNNTGCATCAGGT	4049	TGGTCATNNNTGCATCAGGT	4289
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT	
GAAACTANNNTGCATCAGGT	3810	AGCAGAANNNTGCATCAGGT	4050	GTGAGCTNNNTGCATCAGGT	4290
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAA	
CCACCTANNNTGCATCAGGT	3811	AGATTAGNNNTGCATCAGGT	4051	ACCGTCANNNTGCATCAGGT	4291
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAA	
CCTTCCTNNNTGCATCAGGT	3812	CAAAGACNNNTGCATCAGGT	4052	TTACAGTNNNTGCATCAGGT	4292
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG	
ACTCCGANNNTGCATCAGGT	3813	TAAACAGNNNTGCATCAGGT	4053	CAATAAANNNTGCATCAGGT	4293
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA	
ATAGCTNNNTGCATCAGGT	3814	TCCAAAANNNTGCATCAGGT	4054	GCTTAGCANNNTGCATCAGGT	4294
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAT	
TAGTAAGNNNTGCATCAGGT	3815	GGTATCGNNNTGCATCAGGT	4055	CATTGCCNNNTGCATCAGGT	4295
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC	
TTTTACTNNNTGCATCAGGT	3816	ACACTTANNNTGCATCAGGT	4056	ACTATAANNNTGCATCAGGT	4296
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC	
GCAATTGNNNTGCATCAGGT	3817	CCGTGGCNNNTGCATCAGGT	4057	TGCGTCCNNNTGCATCAGGT	4297
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC	
GAGGCGTNNNTGCATCAGGT	3818	GTCTAGCNNNTGCATCAGGT	4058	GATGAGANNNTGCATCAGGT	4298
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT	
TAAGTGCNNNTGCATCAGGT	3819	GACTCCANNNTGCATCAGGT	4059	AGAAGGCNNNTGCATCAGGT	4299
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA	
GTCAACGNNNTGCATCAGGT	3820	CAGGATTNNNTGCATCAGGT	4060	TACACCGNNNTGCATCAGGT	4300
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT	
GATTTTTNNNTGCATCAGGT	3821	GAATGATNNNTGCATCAGGT	4061	CCAGCAANNNTGCATCAGGT	4301
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG	
CGTATTNNNTGCATCAGGT	3822	CGACATCNNNTGCATCAGGT	4062	TGTTCCCTNNNTGCATCAGGT	4302
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG	
CCGCGATNNNTGCATCAGGT	3823	TAAAAACNNNTGCATCAGGT	4063	AAACGTGNNNTGCATCAGGT	4303
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC	
GCCCTAGNNNTGCATCAGGT	3824	TTAACACNNNTGCATCAGGT	4064	CCTCTAANNNTGCATCAGGT	4304
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAA	
ACAGGCANNNTGCATCAGGT	3825	CAAAATCNNNTGCATCAGGT	4065	CCGAGCCNNNTGCATCAGGT	4305
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAG	
CCTATGNNNTGCATCAGGT	3826	GTCCATTNNNTGCATCAGGT	4066	CGCCCTTNNNTGCATCAGGT	4306
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAA	
GTGTGANNNTGCATCAGGT	3827	GAAATCANNNTGCATCAGGT	4067	AATAGACNNNTGCATCAGGT	4307
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT	
TGGATTNNNTGCATCAGGT	3828	AATCACTNNNTGCATCAGGT	4068	GACACTGNNNTGCATCAGGT	4308
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAA	
CGGACCGNNNTGCATCAGGT	3829	TCCACGCGNNNTGCATCAGGT	4069	GCGCGAGNNNTGCATCAGGT	4309
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAG	
AACATAGNNNTGCATCAGGT	3830	AATAATGNNNTGCATCAGGT	4070	CAGAAGTNNNTGCATCAGGT	4310
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG	
GAAGCGTNNNTGCATCAGGT	3831	GTGACCAANNNTGCATCAGGT	4071	GCTGATTNNNTGCATCAGGT	4311
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG	
CCTCACGNNNTGCATCAGGT	3832	CGATTAAANNNTGCATCAGGT	4072	TAGAATANNNTGCATCAGGT	4312
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAC	
ACTGTGCGNNNTGCATCAGGT	3833	GCCAAATNNNTGCATCAGGT	4073	CATCGAANNNTGCATCAGGT	4313
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT	
CTTGGAGNNNTGCATCAGGT	3834	TTGTAAANNNTGCATCAGGT	4074	TGCCTACNNNTGCATCAGGT	4314
TGCAGGACCAGAGAATTCGAATACAG		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAA	
TGAAATANNNTGCATCAGGT	3835	ATTAGAGNNNTGCATCAGGT	4075	CTCCCATNNNTGCATCAGGT	4315
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAG	
GCTTCTGNNNTGCATCAGGT	3836	AGCTTGGNNNTGCATCAGGT	4076	TTTCCACNNNTGCATCAGGT	4316
TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAG	
GACTTCCNNNTGCATCAGGT	3837	TAGGAGCNNNTGCATCAGGT	4077	ATATTGNNNTGCATCAGGT	4317
TGCAGGACCAGAGAATTCGAATACAC		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAA	
CCGGATGNNNTGCATCAGGT	3838	TATACTCNNNTGCATCAGGT	4078	CTGAGGANNNTGCATCAGGT	4318

FIG. 17H

Pool-16	SEQ ID NO:	Pool-17	SEQ ID NO:	Pool-18	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAG AGGACATNNNTGCATCAGGT	3839	TGCAGGACCAGAGAATTCGAATACAT TGTTGCCNNNTGCATCAGGT	4079	TGCAGGACCAGAGAATTCGAATACAG TAGTCTGNNNTGCATCAGGT	4319
TGCAGGACCAGAGAATTCGAATACAC AGGTATCNNNTGCATCAGGT	3840	TGCAGGACCAGAGAATTCGAATACAT TCCGAGANNNTGCATCAGGT	4080	TGCAGGACCAGAGAATTCGAATACAT GTAAATCNNNTGCATCAGGT	4320
TGCAGGACCAGAGAATTCGAATACAG TAGTATTNNNTGCATCAGGT	3841	TGCAGGACCAGAGAATTCGAATACAA TCCCATCNNNTGCATCAGGT	4081	TGCAGGACCAGAGAATTCGAATACAG CATATGNNNTGCATCAGGT	4321
TGCAGGACCAGAGAATTCGAATACAA AGGAGANNNTGCATCAGGT	3842	TGCAGGACCAGAGAATTCGAATACAT TTGCCACNNNTGCATCAGGT	4082	TGCAGGACCAGAGAATTCGAATACAA TTCGTAANNNTGCATCAGGT	4322
TGCAGGACCAGAGAATTCGAATACAA AGAGCCANNNTGCATCAGGT	3843	TGCAGGACCAGAGAATTCGAATACAG TGAGCGNNNTGCATCAGGT	4083	TGCAGGACCAGAGAATTCGAATACAA ATCCACGNNNTGCATCAGGT	4323
TGCAGGACCAGAGAATTCGAATACAG TCTCTCANNNTGCATCAGGT	3844	TGCAGGACCAGAGAATTCGAATACAT CGCATCTNNNTGCATCAGGT	4084	TGCAGGACCAGAGAATTCGAATACAG CGCCGCGNNNTGCATCAGGT	4324
TGCAGGACCAGAGAATTCGAATACAA CGGTGTTNNNTGCATCAGGT	3845	TGCAGGACCAGAGAATTCGAATACAT CTGCAGANNNTGCATCAGGT	4085	TGCAGGACCAGAGAATTCGAATACAG GCTCGACNNNTGCATCAGGT	4325
TGCAGGACCAGAGAATTCGAATACAC GTACGATNNNTGCATCAGGT	3846	TGCAGGACCAGAGAATTCGAATACAG CCCAAGCNNNTGCATCAGGT	4086	TGCAGGACCAGAGAATTCGAATACAA CCCCGAGNNNTGCATCAGGT	4326
TGCAGGACCAGAGAATTCGAATACAG AGGTGTANNNTGCATCAGGT	3847	TGCAGGACCAGAGAATTCGAATACAT TTCTCGGNNNTGCATCAGGT	4087	TGCAGGACCAGAGAATTCGAATACAA GTCACCCANNNTGCATCAGGT	4327
TGCAGGACCAGAGAATTCGAATACAC ACCAACAANNNTGCATCAGGT	3848	TGCAGGACCAGAGAATTCGAATACAG GCCTACGNNNTGCATCAGGT	4088	TGCAGGACCAGAGAATTCGAATACAA AAATTCNNNTGCATCAGGT	4328

FIG. 18A

Poel-19	SEQ ID NO:	Poel-20	SEQ ID NO:	Poel-21	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA	4329	TGCAGGACCAGAGAATTGGAATA	4569	TGCAGGACCAGAGAATTGGAATA	4809
CAGCCCTCTGNNNACGTATGCCA		CATGTTGTCCNNNACGTATGCCA		CATGAACAANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4330	TGCAGGACCAGAGAATTGGAATA	4570	TGCAGGACCAGAGAATTGGAATA	4810
CAGCAAAGGTNNNACGTATGCCA		CATAACCAGCINNACGTATGCCA		CACCGTTGCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4331	TGCAGGACCAGAGAATTGGAATA	4571	TGCAGGACCAGAGAATTGGAATA	4811
CATTTCTATGNNNACGTATGCCA		CATGCCGCGCINNACGTATGCCA		CAGCATTGGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4332	TGCAGGACCAGAGAATTGGAATA	4572	TGCAGGACCAGAGAATTGGAATA	4812
CACGTGCCAATNNNACGTATGCCA		CAATCGTCTCINNACGTATGCCA		CATAGGCCATNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4333	TGCAGGACCAGAGAATTGGAATA	4573	TGCAGGACCAGAGAATTGGAATA	4813
CAGTTTAGCINNACGTATGCCA		CATCCGACCCINNACGTATGCCA		CAACTCCTCANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4334	TGCAGGACCAGAGAATTGGAATA	4574	TGCAGGACCAGAGAATTGGAATA	4814
CAAAAAATGACINNACGTATGCCA		CATTACTGAANNNACGTATGCCA		CAC TAGGCGCINNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4335	TGCAGGACCAGAGAATTGGAATA	4575	TGCAGGACCAGAGAATTGGAATA	4815
CAC TACTAGGNNNACGTATGCCA		CAAGGTTGCGCINNACGTATGCCA		CAAGTTTAGCINNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4336	TGCAGGACCAGAGAATTGGAATA	4576	TGCAGGACCAGAGAATTGGAATA	4816
CACACCCAGGNNNACGTATGCCA		CAGTGCCCTCINNACGTATGCCA		CATTGATACANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4337	TGCAGGACCAGAGAATTGGAATA	4577	TGCAGGACCAGAGAATTGGAATA	4817
CAGCCGCCCTNNNACGTATGCCA		CAGCGTAGCCINNACGTATGCCA		CAACAAATACINNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4338	TGCAGGACCAGAGAATTGGAATA	4578	TGCAGGACCAGAGAATTGGAATA	4818
CACAACGTCAINNACGTATGCCA		CATAGCCCAACINNACGTATGCCA		CAATACCGGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4339	TGCAGGACCAGAGAATTGGAATA	4579	TGCAGGACCAGAGAATTGGAATA	4819
CATCTCAAGGNNNACGTATGCCA		CAATATACCCANNNACGTATGCCA		CATGAAGCCTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4340	TGCAGGACCAGAGAATTGGAATA	4580	TGCAGGACCAGAGAATTGGAATA	4820
CATCATAAACNNNACGTATGCCA		CATAAAATCCINNACGTATGCCA		CATTACCTGCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4341	TGCAGGACCAGAGAATTGGAATA	4581	TGCAGGACCAGAGAATTGGAATA	4821
CATCCTCCCCNNNACGTATGCCA		CAGATGGTGANNNACGTATGCCA		CATATCAGATTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4342	TGCAGGACCAGAGAATTGGAATA	4582	TGCAGGACCAGAGAATTGGAATA	4822
CAAGTAACCCNNNACGTATGCCA		CAGAACGTAGNNNACGTATGCCA		CAGAAGAATTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4343	TGCAGGACCAGAGAATTGGAATA	4583	TGCAGGACCAGAGAATTGGAATA	4823
CAGTGACAAGNNNACGTATGCCA		CAATATTAAATNNNACGTATGCCA		CAGATCAGCTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4344	TGCAGGACCAGAGAATTGGAATA	4584	TGCAGGACCAGAGAATTGGAATA	4824
CAGCAATACCCNNNACGTATGCCA		CATACCTGAATNNNACGTATGCCA		CAAGGTAGACNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4345	TGCAGGACCAGAGAATTGGAATA	4585	TGCAGGACCAGAGAATTGGAATA	4825
CAAAATACGTTNNNACGTATGCCA		CAGTCCGAGCINNACGTATGCCA		CATTGACCCANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4346	TGCAGGACCAGAGAATTGGAATA	4586	TGCAGGACCAGAGAATTGGAATA	4826
CACCATGTAGNNNACGTATGCCA		CACCTGGTAANNNACGTATGCCA		CACCACTGTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4347	TGCAGGACCAGAGAATTGGAATA	4587	TGCAGGACCAGAGAATTGGAATA	4827
CACCCAACGGNNNACGTATGCCA		CACCCTAGAANNNACGTATGCCA		CAGTCAGAAGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4348	TGCAGGACCAGAGAATTGGAATA	4588	TGCAGGACCAGAGAATTGGAATA	4828
CAGCGGTTGCNNNACGTATGCCA		CATTAAAGTCCINNACGTATGCCA		CACCGACCTCINNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4349	TGCAGGACCAGAGAATTGGAATA	4589	TGCAGGACCAGAGAATTGGAATA	4829
CAGTGATCTGNNNACGTATGCCA		CAACGTTGCCINNACGTATGCCA		CAATTAGTGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4350	TGCAGGACCAGAGAATTGGAATA	4590	TGCAGGACCAGAGAATTGGAATA	4830
CATAAGCCGTNNNACGTATGCCA		CAGCTATCCTNNNACGTATGCCA		CAGCATAACANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4351	TGCAGGACCAGAGAATTGGAATA	4591	TGCAGGACCAGAGAATTGGAATA	4831
CATGTTTGTNNNACGTATGCCA		CAAGCGTTGTNNNACGTATGCCA		CAAGTTTTTCCINNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4352	TGCAGGACCAGAGAATTGGAATA	4592	TGCAGGACCAGAGAATTGGAATA	4832
CAACGAGCGGNNNACGTATGCCA		CACCTTCGCTANNNACGTATGCCA		CATTCCGCTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4353	TGCAGGACCAGAGAATTGGAATA	4593	TGCAGGACCAGAGAATTGGAATA	4833
CATAGATCGCINNACGTATGCCA		CACATTTTTGNNNACGTATGCCA		CATGGAGCCCCINNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4354	TGCAGGACCAGAGAATTGGAATA	4594	TGCAGGACCAGAGAATTGGAATA	4834
CATGATACGCCNNNACGTATGCCA		CAAACTTCGNNNACGTATGCCA		CACGTGGCACNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4355	TGCAGGACCAGAGAATTGGAATA	4595	TGCAGGACCAGAGAATTGGAATA	4835
CATAGTTACANNNACGTATGCCA		CATACCGTGANNNACGTATGCCA		CATCTTACTANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4356	TGCAGGACCAGAGAATTGGAATA	4596	TGCAGGACCAGAGAATTGGAATA	4836
CACCTTGGTGANNNACGTATGCCA		CAAGCTTTTTNNNACGTATGCCA		CAATCCGGTANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4357	TGCAGGACCAGAGAATTGGAATA	4597	TGCAGGACCAGAGAATTGGAATA	4837
CATTAAATCTCINNACGTATGCCA		CATGTTCTCGNNNACGTATGCCA		CAGACACCTANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4358	TGCAGGACCAGAGAATTGGAATA	4598	TGCAGGACCAGAGAATTGGAATA	4838
CATTAGACGCCNNNACGTATGCCA		CAAAATCGGCTNNNACGTATGCCA		CATCCGTCTANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4359	TGCAGGACCAGAGAATTGGAATA	4599	TGCAGGACCAGAGAATTGGAATA	4839
CAACACCAGTNNNACGTATGCCA		CATGAACCAACNNNACGTATGCCA		CAAGATTACTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4360	TGCAGGACCAGAGAATTGGAATA	4600	TGCAGGACCAGAGAATTGGAATA	4840
CAACCAGGAANNNACGTATGCCA		CAATTTTCATCINNACGTATGCCA		CAAGATTGAANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	4361	TGCAGGACCAGAGAATTGGAATA	4601	TGCAGGACCAGAGAATTGGAATA	4841
CAATGCATGCNNNACGTATGCCA		CACAGTCACANNNACGTATGCCA		CATTTAAAGCINNACGTATGCCA	

FIG. 18B

Poel-19	SEQ ID NO:	Poel-20	SEQ ID NO:	Poel-21	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATA	4362	TGCAGGACCAGAGAATTCTGAATA	4602	TGCAGGACCAGAGAATTCTGAATA	4842
CATACACATANNNNACGTATGCCA		CACCCATAGANNNNACGTATGCCA		CAGAATTGCCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4363	TGCAGGACCAGAGAATTCTGAATA	4603	TGCAGGACCAGAGAATTCTGAATA	4843
CATCTTTCAANNNNACGTATGCCA		CACAGAATTGNNNNACGTATGCCA		CATTAGCTCCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4364	TGCAGGACCAGAGAATTCTGAATA	4604	TGCAGGACCAGAGAATTCTGAATA	4844
CACATCAAAANNNNACGTATGCCA		CAGTATGAAANNNNACGTATGCCA		CAATGAGGACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4365	TGCAGGACCAGAGAATTCTGAATA	4605	TGCAGGACCAGAGAATTCTGAATA	4845
CATTACCAAAANNNNACGTATGCCA		CAGTTTAAGTNNNNACGTATGCCA		CAATTGTTAGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4366	TGCAGGACCAGAGAATTCTGAATA	4606	TGCAGGACCAGAGAATTCTGAATA	4846
CACCGGCGATTNNNNACGTATGCCA		CAGCGTTATGNNNNACGTATGCCA		CAGCTTGAGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4367	TGCAGGACCAGAGAATTCTGAATA	4607	TGCAGGACCAGAGAATTCTGAATA	4847
CAGTTTGTATANNNNACGTATGCCA		CATCCGTTACNNNNACGTATGCCA		CATTGCTTCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4368	TGCAGGACCAGAGAATTCTGAATA	4608	TGCAGGACCAGAGAATTCTGAATA	4848
CAATACGGCTTNNNNACGTATGCCA		CACGGAACCTNNNNACGTATGCCA		CAAAAGGCTGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4369	TGCAGGACCAGAGAATTCTGAATA	4609	TGCAGGACCAGAGAATTCTGAATA	4849
CATGGCAACTNNNNACGTATGCCA		CACGGCCATGNNNNACGTATGCCA		CACTTACGAGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4370	TGCAGGACCAGAGAATTCTGAATA	4610	TGCAGGACCAGAGAATTCTGAATA	4850
CAGATTTCAANNNNACGTATGCCA		CACGAAAGCANNNNACGTATGCCA		CAATCTATGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4371	TGCAGGACCAGAGAATTCTGAATA	4611	TGCAGGACCAGAGAATTCTGAATA	4851
CAGTATCTTTNNNNACGTATGCCA		CAAGGTTGTNNNNACGTATGCCA		CAGGTACACTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4372	TGCAGGACCAGAGAATTCTGAATA	4612	TGCAGGACCAGAGAATTCTGAATA	4852
CAGCAACAGANNNNACGTATGCCA		CAACGAAGGTNNNNACGTATGCCA		CACCGCCTCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4373	TGCAGGACCAGAGAATTCTGAATA	4613	TGCAGGACCAGAGAATTCTGAATA	4853
CAGCGTTCAANNNNACGTATGCCA		CATCCCCGANNNNACGTATGCCA		CACAGGACGGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4374	TGCAGGACCAGAGAATTCTGAATA	4614	TGCAGGACCAGAGAATTCTGAATA	4854
CAGTATTCGGNNNNACGTATGCCA		CAAGCGATCTNNNNACGTATGCCA		CAATCATGGCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4375	TGCAGGACCAGAGAATTCTGAATA	4615	TGCAGGACCAGAGAATTCTGAATA	4855
CATCCTATATNNNNACGTATGCCA		CACATATAATGNNNNACGTATGCCA		CATATAGGTTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4376	TGCAGGACCAGAGAATTCTGAATA	4616	TGCAGGACCAGAGAATTCTGAATA	4856
CAAGTCGTACNNNNACGTATGCCA		CATTCGTCTGNNNNACGTATGCCA		CAGATTTAACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4377	TGCAGGACCAGAGAATTCTGAATA	4617	TGCAGGACCAGAGAATTCTGAATA	4857
CACCTAGACANNNNACGTATGCCA		CAGCGCCTCTNNNNACGTATGCCA		CAATGGAACGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4378	TGCAGGACCAGAGAATTCTGAATA	4618	TGCAGGACCAGAGAATTCTGAATA	4858
CAATTGGTTCGNNNNACGTATGCCA		CACGCAATCANNNNACGTATGCCA		CAGCTTTACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4379	TGCAGGACCAGAGAATTCTGAATA	4619	TGCAGGACCAGAGAATTCTGAATA	4859
CAGGTACGCGNNNNACGTATGCCA		CAGTCCGTCGNNNNACGTATGCCA		CAGTCCGTCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4380	TGCAGGACCAGAGAATTCTGAATA	4620	TGCAGGACCAGAGAATTCTGAATA	4860
CACACCAAAACNNNNACGTATGCCA		CATAGCAGGANNNNACGTATGCCA		CATACTCCCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4381	TGCAGGACCAGAGAATTCTGAATA	4621	TGCAGGACCAGAGAATTCTGAATA	4861
CAGAATTCATNNNNACGTATGCCA		CAGATGGAGTNNNNACGTATGCCA		CAGCCGCTCTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4382	TGCAGGACCAGAGAATTCTGAATA	4622	TGCAGGACCAGAGAATTCTGAATA	4862
CATTTCGCACCTNNNNACGTATGCCA		CAAGACCTNNNNACGTATGCCA		CAGTCTCAGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4383	TGCAGGACCAGAGAATTCTGAATA	4623	TGCAGGACCAGAGAATTCTGAATA	4863
CACCGTTAAGNNNNACGTATGCCA		CAAGCGGCTNNNNACGTATGCCA		CAAGCCGAGGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4384	TGCAGGACCAGAGAATTCTGAATA	4624	TGCAGGACCAGAGAATTCTGAATA	4864
CACGCTGTCTNNNNACGTATGCCA		CACGTTTGTCTNNNNACGTATGCCA		CAGCTATATANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4385	TGCAGGACCAGAGAATTCTGAATA	4625	TGCAGGACCAGAGAATTCTGAATA	4865
CAAAAACAGTNNNNACGTATGCCA		CACCTGCATTNNNNACGTATGCCA		CATCTCTCGANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4386	TGCAGGACCAGAGAATTCTGAATA	4626	TGCAGGACCAGAGAATTCTGAATA	4866
CAGAGATTTNNNNACGTATGCCA		CAATTGAATCANNNNACGTATGCCA		CAACAATAGANNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4387	TGCAGGACCAGAGAATTCTGAATA	4627	TGCAGGACCAGAGAATTCTGAATA	4867
CAACCGAGTTGNNNNACGTATGCCA		CATCCGTTGCCNNNNACGTATGCCA		CAGAGAGCATNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4388	TGCAGGACCAGAGAATTCTGAATA	4628	TGCAGGACCAGAGAATTCTGAATA	4868
CAAGTTCCGANNNNACGTATGCCA		CATCTCAGGANNNNACGTATGCCA		CACGATATGCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4389	TGCAGGACCAGAGAATTCTGAATA	4629	TGCAGGACCAGAGAATTCTGAATA	4869
CAGATGACCTNNNNACGTATGCCA		CAAAGCGGTTNNNNACGTATGCCA		CACTTCCTCTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4390	TGCAGGACCAGAGAATTCTGAATA	4630	TGCAGGACCAGAGAATTCTGAATA	4870
CACACGTATGNNNNACGTATGCCA		CACACCCCTCGNNNNACGTATGCCA		CAAAACAGTTTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4391	TGCAGGACCAGAGAATTCTGAATA	4631	TGCAGGACCAGAGAATTCTGAATA	4871
CATGTCCGCGNNNNACGTATGCCA		CAGCTAGTTGNNNNACGTATGCCA		CATGTGGACTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4392	TGCAGGACCAGAGAATTCTGAATA	4632	TGCAGGACCAGAGAATTCTGAATA	4872
CAGACCAAAGNNNNACGTATGCCA		CACCGTTACTNNNNACGTATGCCA		CACCTCGACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4393	TGCAGGACCAGAGAATTCTGAATA	4633	TGCAGGACCAGAGAATTCTGAATA	4873
CACCTGCTACTNNNNACGTATGCCA		CATAAGCGCTNNNNACGTATGCCA		CACCGTTTCTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATA	4394	TGCAGGACCAGAGAATTCTGAATA	4634	TGCAGGACCAGAGAATTCTGAATA	4874
CACCTCAACTNNNNACGTATGCCA		CAGGTAACGNNNNACGTATGCCA		CAACGTCGATNNNNACGTATGCCA	

FIG. 18C

Poal-19	SEQ ID NO:	Poal-20	SEQ ID NO:	Poal-21	SEQ ID NO:
TGCAGGACCAGAGAATTTCGAATA	4395	TGCAGGACCAGAGAATTTCGAATA	4635	TGCAGGACCAGAGAATTTCGAATA	4875
CACAATCCCTNNNNCTAGCGTTAC		CAGAACCAGANNNNCTAGCGTTAC		CATTGGCTTCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4396	TGCAGGACCAGAGAATTTCGAATA	4636	TGCAGGACCAGAGAATTTCGAATA	4876
CATCGTGCAANNNNCTAGCGTTAC		CAGGACTGTTNNNNCTAGCGTTAC		CAATGGACGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4397	TGCAGGACCAGAGAATTTCGAATA	4637	TGCAGGACCAGAGAATTTCGAATA	4877
CAAAGCCATCANNNNCTAGCGTTAC		CAATCGTGTGNNNNCTAGCGTTAC		CATGCAAGAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4398	TGCAGGACCAGAGAATTTCGAATA	4638	TGCAGGACCAGAGAATTTCGAATA	4878
CAATGAACTTNNNNCTAGCGTTAC		CAGTCACGGCANNNNCTAGCGTTAC		CAGAAATATGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4399	TGCAGGACCAGAGAATTTCGAATA	4639	TGCAGGACCAGAGAATTTCGAATA	4879
CATGGCCGGTNNNNCTAGCGTTAC		CATCTCGTACNNNNCTAGCGTTAC		CAACACATATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4400	TGCAGGACCAGAGAATTTCGAATA	4640	TGCAGGACCAGAGAATTTCGAATA	4880
CATGCCACGGNNNNCTAGCGTTAC		CAAGTCGGCANNNNCTAGCGTTAC		CAGTAGCAGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4401	TGCAGGACCAGAGAATTTCGAATA	4641	TGCAGGACCAGAGAATTTCGAATA	4881
CAGTCTTCGTTNNNNCTAGCGTTAC		CACATGTCGNNNNCTAGCGTTAC		CACGCCCGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4402	TGCAGGACCAGAGAATTTCGAATA	4642	TGCAGGACCAGAGAATTTCGAATA	4882
CAAACGTAGGNNNNCTAGCGTTAC		CACATGTACGNNNNCTAGCGTTAC		CATAGTGCAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4403	TGCAGGACCAGAGAATTTCGAATA	4643	TGCAGGACCAGAGAATTTCGAATA	4883
CAATGGAGCANNNNCTAGCGTTAC		CAGCGTATCANNNNCTAGCGTTAC		CATCAATGCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4404	TGCAGGACCAGAGAATTTCGAATA	4644	TGCAGGACCAGAGAATTTCGAATA	4884
CATGACGGCCNNNNCTAGCGTTAC		CACAATTCTTNNNNCTAGCGTTAC		CAATGTAAGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4405	TGCAGGACCAGAGAATTTCGAATA	4645	TGCAGGACCAGAGAATTTCGAATA	4885
CACCTTAGGACNNNNCTAGCGTTAC		CAACTCTATTNNNNCTAGCGTTAC		CATATGTTAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4406	TGCAGGACCAGAGAATTTCGAATA	4646	TGCAGGACCAGAGAATTTCGAATA	4886
CAGACAGAGTNNNNCTAGCGTTAC		CATCATCCANNNNCTAGCGTTAC		CATCAATCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4407	TGCAGGACCAGAGAATTTCGAATA	4647	TGCAGGACCAGAGAATTTCGAATA	4887
CAAAGTCGTCTNNNNCTAGCGTTAC		CAGGCTTGCGNNNNCTAGCGTTAC		CACACTTAGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4408	TGCAGGACCAGAGAATTTCGAATA	4648	TGCAGGACCAGAGAATTTCGAATA	4888
CATACAAAAGNNNNCTAGCGTTAC		CAGTTCCTTGNNNNCTAGCGTTAC		CATAGGATAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4409	TGCAGGACCAGAGAATTTCGAATA	4649	TGCAGGACCAGAGAATTTCGAATA	4889
CATCTCCTGANNNNCTAGCGTTAC		CAATGAGAATNNNNCTAGCGTTAC		CAATCCGCTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4410	TGCAGGACCAGAGAATTTCGAATA	4650	TGCAGGACCAGAGAATTTCGAATA	4890
CAAGCTTGGTNNNNCTAGCGTTAC		CACGTGTATCCNNNNCTAGCGTTAC		CAACATCCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4411	TGCAGGACCAGAGAATTTCGAATA	4651	TGCAGGACCAGAGAATTTCGAATA	4891
CAAAATCAAGANNNNCTAGCGTTAC		CATAGCCCCNNNNCTAGCGTTAC		CACATATTAAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4412	TGCAGGACCAGAGAATTTCGAATA	4652	TGCAGGACCAGAGAATTTCGAATA	4892
CAACCACAACNNNNCTAGCGTTAC		CATGGCCGACNNNNCTAGCGTTAC		CAGCGTATGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4413	TGCAGGACCAGAGAATTTCGAATA	4653	TGCAGGACCAGAGAATTTCGAATA	4893
CAGCTATAATNNNNCTAGCGTTAC		CACCGCTGCTNNNNCTAGCGTTAC		CAATTGGTATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4414	TGCAGGACCAGAGAATTTCGAATA	4654	TGCAGGACCAGAGAATTTCGAATA	4894
CAGGACCGCTNNNNCTAGCGTTAC		CAGGTAGCCNNNNCTAGCGTTAC		CATTTCTGCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4415	TGCAGGACCAGAGAATTTCGAATA	4655	TGCAGGACCAGAGAATTTCGAATA	4895
CAGTCCCTATNNNNCTAGCGTTAC		CATGACGTTGNNNNCTAGCGTTAC		CAGAATCCCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4416	TGCAGGACCAGAGAATTTCGAATA	4656	TGCAGGACCAGAGAATTTCGAATA	4896
CATTGCTGAGNNNNCTAGCGTTAC		CACCCACTATNNNNCTAGCGTTAC		CACTTTCACGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4417	TGCAGGACCAGAGAATTTCGAATA	4657	TGCAGGACCAGAGAATTTCGAATA	4897
CATTGGCCCTNNNNCTAGCGTTAC		CAAAGTGTAANNNNCTAGCGTTAC		CACGGATCATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4418	TGCAGGACCAGAGAATTTCGAATA	4658	TGCAGGACCAGAGAATTTCGAATA	4898
CAATCATTTTNNNNCTAGCGTTAC		CAGGAGTATGNNNNCTAGCGTTAC		CAACAGTGCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4419	TGCAGGACCAGAGAATTTCGAATA	4659	TGCAGGACCAGAGAATTTCGAATA	4899
CAGATGTATTNNNNCTAGCGTTAC		CAAGTGATAANNNNCTAGCGTTAC		CACCTTAGTCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4420	TGCAGGACCAGAGAATTTCGAATA	4660	TGCAGGACCAGAGAATTTCGAATA	4900
CAGATCATATNNNNCTAGCGTTAC		CATAATTTCGANNNNCTAGCGTTAC		CAAGTGCCCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4421	TGCAGGACCAGAGAATTTCGAATA	4661	TGCAGGACCAGAGAATTTCGAATA	4901
CACCCCGCTANNNNCTAGCGTTAC		CAAGCTTTGNNNNCTAGCGTTAC		CATGAAATCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4422	TGCAGGACCAGAGAATTTCGAATA	4662	TGCAGGACCAGAGAATTTCGAATA	4902
CAAAAAATCGANNNNCTAGCGTTAC		CAACATGTCGNNNNCTAGCGTTAC		CATCAGTTAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4423	TGCAGGACCAGAGAATTTCGAATA	4663	TGCAGGACCAGAGAATTTCGAATA	4903
CAATGTACATNNNNCTAGCGTTAC		CATCAGCGCGNNNNCTAGCGTTAC		CAAACCTCGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4424	TGCAGGACCAGAGAATTTCGAATA	4664	TGCAGGACCAGAGAATTTCGAATA	4904
CAGCCATCTTNNNNCTAGCGTTAC		CAGCCCGGTANNNNCTAGCGTTAC		CATCATGATANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4425	TGCAGGACCAGAGAATTTCGAATA	4665	TGCAGGACCAGAGAATTTCGAATA	4905
CAAATGCTCGNNNNCTAGCGTTAC		CACCATTTCANNNNCTAGCGTTAC		CAAAGCCTTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4426	TGCAGGACCAGAGAATTTCGAATA	4666	TGCAGGACCAGAGAATTTCGAATA	4906
CACACGTCCGNNNNCTAGCGTTAC		CATTCCCTTNNNNCTAGCGTTAC		CAAGCATACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4427	TGCAGGACCAGAGAATTTCGAATA	4667	TGCAGGACCAGAGAATTTCGAATA	4907
CACATATGCGANNNNCTAGCGTTAC		CAACCTCCGNNNNCTAGCGTTAC		CAGGCATTGNNNNCTAGCGTTAC	

FIG. 18D

Pool-19	SEQ ID NO:	Pool-20	SEQ ID NO:	Pool-21	SEQ ID NO:
TGCAGGACCAGAGAATTTCGAATA	4428	TGCAGGACCAGAGAATTTCGAATA	4668	TGCAGGACCAGAGAATTTCGAATA	4908
CAGTCTGGTANNNNCTAGCGTTAC		CACACCTTACNNNNCTAGCGTTAC		CAGCGAGTCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4429	TGCAGGACCAGAGAATTTCGAATA	4669	TGCAGGACCAGAGAATTTCGAATA	4909
CAGTCAGTGTNNNNCTAGCGTTAC		CAGGAGTTGANNNCTAGCGTTAC		CATTTTGAGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4430	TGCAGGACCAGAGAATTTCGAATA	4670	TGCAGGACCAGAGAATTTCGAATA	4910
CACCTCCAGTNNNNCTAGCGTTAC		CAGACAAGACNNNNCTAGCGTTAC		CAATCCTTATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4431	TGCAGGACCAGAGAATTTCGAATA	4671	TGCAGGACCAGAGAATTTCGAATA	4911
CAGATGAAGCANNNNCTAGCGTTAC		CAGTCTACGANNNCTAGCGTTAC		CATCGAAAAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4432	TGCAGGACCAGAGAATTTCGAATA	4672	TGCAGGACCAGAGAATTTCGAATA	4912
CAAAACCATNNNNCTAGCGTTAC		CATCGCTCATNNNNCTAGCGTTAC		CAGTCCGTCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4433	TGCAGGACCAGAGAATTTCGAATA	4673	TGCAGGACCAGAGAATTTCGAATA	4913
CACCTGCGCTNNNNCTAGCGTTAC		CACCAAGCCGNNNNCTAGCGTTAC		CACCAGTTTCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4434	TGCAGGACCAGAGAATTTCGAATA	4674	TGCAGGACCAGAGAATTTCGAATA	4914
CACACCCGAGNNNNCTAGCGTTAC		CACCTCGGTNNNNCTAGCGTTAC		CACTTGGCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4435	TGCAGGACCAGAGAATTTCGAATA	4675	TGCAGGACCAGAGAATTTCGAATA	4915
CATACTACAANNNNCTAGCGTTAC		CAAACTAGTNNNNCTAGCGTTAC		CACCGCCATCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4436	TGCAGGACCAGAGAATTTCGAATA	4676	TGCAGGACCAGAGAATTTCGAATA	4916
CATAACCGACNNNNCTAGCGTTAC		CAGATGAGTNNNNCTAGCGTTAC		CAGATCGATCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4437	TGCAGGACCAGAGAATTTCGAATA	4677	TGCAGGACCAGAGAATTTCGAATA	4917
CATCTATAGANNNNCTAGCGTTAC		CACAATACTANNNNCTAGCGTTAC		CAACGCGGCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4438	TGCAGGACCAGAGAATTTCGAATA	4678	TGCAGGACCAGAGAATTTCGAATA	4918
CAGGTGAGGCNNNNCTAGCGTTAC		CACCTTTGGTNNNNCTAGCGTTAC		CATCTCGAGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4439	TGCAGGACCAGAGAATTTCGAATA	4679	TGCAGGACCAGAGAATTTCGAATA	4919
CACATACTCCNNNNCTAGCGTTAC		CATTCACACNNNNCTAGCGTTAC		CAATTGGCACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4440	TGCAGGACCAGAGAATTTCGAATA	4680	TGCAGGACCAGAGAATTTCGAATA	4920
CATAAGAGTANNNNCTAGCGTTAC		CAGTTATCCCNNNCTAGCGTTAC		CACGCGGAGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4441	TGCAGGACCAGAGAATTTCGAATA	4681	TGCAGGACCAGAGAATTTCGAATA	4921
CAGTGTGAGANNNNCTAGCGTTAC		CAAAACTTGTNNNNCTAGCGTTAC		CACTTCAGCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4442	TGCAGGACCAGAGAATTTCGAATA	4682	TGCAGGACCAGAGAATTTCGAATA	4922
CATTCCGATNNNNCTAGCGTTAC		CACAACCCANNNNCTAGCGTTAC		CAAAATAAGCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4443	TGCAGGACCAGAGAATTTCGAATA	4683	TGCAGGACCAGAGAATTTCGAATA	4923
CAAGTACGAGNNNNCTAGCGTTAC		CAGTTACAGANNNNCTAGCGTTAC		CAGCCTAAGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4444	TGCAGGACCAGAGAATTTCGAATA	4684	TGCAGGACCAGAGAATTTCGAATA	4924
CAGGTGAACANNNNCTAGCGTTAC		CAGTCTACTNNNNCTAGCGTTAC		CAGATGCTTCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4445	TGCAGGACCAGAGAATTTCGAATA	4685	TGCAGGACCAGAGAATTTCGAATA	4925
CACACTAGCANNNNNCTAGCGTTAC		CATCAACAGCANNNNCTAGCGTTAC		CAAACGAGGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4446	TGCAGGACCAGAGAATTTCGAATA	4686	TGCAGGACCAGAGAATTTCGAATA	4926
CAAGCAGAACNNNNCTAGCGTTAC		CATGAGTCGNNNNCTAGCGTTAC		CAATAGACANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4447	TGCAGGACCAGAGAATTTCGAATA	4687	TGCAGGACCAGAGAATTTCGAATA	4927
CATTTTAAANNNNCTAGCGTTAC		CAGCATCTGANNNNNCTAGCGTTAC		CATATTGGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4448	TGCAGGACCAGAGAATTTCGAATA	4688	TGCAGGACCAGAGAATTTCGAATA	4928
CACTTCGAGANNNNCTAGCGTTAC		CATGGCAGTTNNNNCTAGCGTTAC		CATCCGTGTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	4449	TGCAGGACCAGAGAATTTCGAATA	4689	TGCAGGACCAGAGAATTTCGAATA	4929
CATGCAATGCNNNGATCGACATG		CAGATCTCTCANNNGATCGACATG		CATCCTCGATNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	4450	TGCAGGACCAGAGAATTTCGAATA	4690	TGCAGGACCAGAGAATTTCGAATA	4930
CAGACGCCACNNNGATCGACATG		CAGAGCGCGANNNGATCGACATG		CATTTGGAGCANNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	4451	TGCAGGACCAGAGAATTTCGAATA	4691	TGCAGGACCAGAGAATTTCGAATA	4931
CAGTTTTTCANNNGATCGACATG		CACTCTCTAGNNNGATCGACATG		CACTTCCACANNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	4452	TGCAGGACCAGAGAATTTCGAATA	4692	TGCAGGACCAGAGAATTTCGAATA	4932
CAGTTTTATCANNNGATCGACATG		CACGTGGCGTNNNGATCGACATG		CAAATTTGCANNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	4453	TGCAGGACCAGAGAATTTCGAATA	4693	TGCAGGACCAGAGAATTTCGAATA	4933
CAACACCGGCNNNGATCGACATG		CAAGCTAGTCNNNGATCGACATG		CAAATCTGATNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	4454	TGCAGGACCAGAGAATTTCGAATA	4694	TGCAGGACCAGAGAATTTCGAATA	4934
CACGCTTTACNNNGATCGACATG		CAGCTATGTGNNNGATCGACATG		CATCCACTTGNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	4455	TGCAGGACCAGAGAATTTCGAATA	4695	TGCAGGACCAGAGAATTTCGAATA	4935
CAGTAAATGANNNGATCGACATG		CATCTGCTTGNNNGATCGACATG		CATGGTTAGCANNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	4456	TGCAGGACCAGAGAATTTCGAATA	4696	TGCAGGACCAGAGAATTTCGAATA	4936
CATTTGAAGTNNNGATCGACATG		CAGTACGCTANNNGATCGACATG		CACTGTAAACGNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	4457	TGCAGGACCAGAGAATTTCGAATA	4697	TGCAGGACCAGAGAATTTCGAATA	4937
CACACCACTTNNNGATCGACATG		CAGACCCGTTGNNNGATCGACATG		CATATTAGTGNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	4458	TGCAGGACCAGAGAATTTCGAATA	4698	TGCAGGACCAGAGAATTTCGAATA	4938
CATGTAAGAANNNGATCGACATG		CAGTCATGACNNNGATCGACATG		CATGCACATGNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	4459	TGCAGGACCAGAGAATTTCGAATA	4699	TGCAGGACCAGAGAATTTCGAATA	4939
CACGCTGAATNNNGATCGACATG		CACGCTAGATNNNGATCGACATG		CAACCTTCGTNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	4460	TGCAGGACCAGAGAATTTCGAATA	4700	TGCAGGACCAGAGAATTTCGAATA	4940
CACCTTATGTNNNGATCGACATG		CAGTAATGAANNNGATCGACATG		CAGCGTGCANNNGATCGACATG	

FIG. 18E

Pool-19	SEQ ID NO:	Pool-20	SEQ ID NO:	Pool-21	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA	4461	TGCAGGACCAGAGAATTCGAATA	4701	TGCAGGACCAGAGAATTCGAATA	4941
CACGTGAGAAANNNGATCGACATG		CATCGTATTNNNGATCGACATG		CACGCCTTTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4462	TGCAGGACCAGAGAATTCGAATA	4702	TGCAGGACCAGAGAATTCGAATA	4942
CAACCGGCTGNNNGATCGACATG		CACACGTACANNNGATCGACATG		CATTGTAAACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4463	TGCAGGACCAGAGAATTCGAATA	4703	TGCAGGACCAGAGAATTCGAATA	4943
CACAAAATTCNNNGATCGACATG		CATGACTAATNNNGATCGACATG		CAAAACGCAAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4464	TGCAGGACCAGAGAATTCGAATA	4704	TGCAGGACCAGAGAATTCGAATA	4944
CAACTAAAGANNNGATCGACATG		CACCTACCGCCNNNGATCGACATG		CAGTAATCATNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4465	TGCAGGACCAGAGAATTCGAATA	4705	TGCAGGACCAGAGAATTCGAATA	4945
CATAGTCTCCNNNGATCGACATG		CAGGCCTATTNNNGATCGACATG		CAGTCTGCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4466	TGCAGGACCAGAGAATTCGAATA	4706	TGCAGGACCAGAGAATTCGAATA	4946
CACCTAACATANNNGATCGACATG		CATCCTTAGCNNNGATCGACATG		CAGATGGTTCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4467	TGCAGGACCAGAGAATTCGAATA	4707	TGCAGGACCAGAGAATTCGAATA	4947
CATGCACGCGNNNGATCGACATG		CAGCTATAGCNNNGATCGACATG		CACCTGGCAGANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4468	TGCAGGACCAGAGAATTCGAATA	4708	TGCAGGACCAGAGAATTCGAATA	4948
CAACTGGAAGNNNGATCGACATG		CAAAATGAACANNNGATCGACATG		CATACCGAACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4469	TGCAGGACCAGAGAATTCGAATA	4709	TGCAGGACCAGAGAATTCGAATA	4949
CAGCAATCCANNNGATCGACATG		CAGTAGTAANNNGATCGACATG		CAGTGAGTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4470	TGCAGGACCAGAGAATTCGAATA	4710	TGCAGGACCAGAGAATTCGAATA	4950
CAAATCCTAANNNGATCGACATG		CATAGTTCCGNNNGATCGACATG		CACAGGTGAANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4471	TGCAGGACCAGAGAATTCGAATA	4711	TGCAGGACCAGAGAATTCGAATA	4951
CAAAGCGGTANNNGATCGACATG		CAGTTGTGACNNNGATCGACATG		CAAGGTGAGANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4472	TGCAGGACCAGAGAATTCGAATA	4712	TGCAGGACCAGAGAATTCGAATA	4952
CAGTCAGAGANNNGATCGACATG		CACGCGTAGCNNNGATCGACATG		CAGAGCGTTTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4473	TGCAGGACCAGAGAATTCGAATA	4713	TGCAGGACCAGAGAATTCGAATA	4953
CATCGGATGTNNNGATCGACATG		CACCTATGTGNNNGATCGACATG		CAGAAATGGCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4474	TGCAGGACCAGAGAATTCGAATA	4714	TGCAGGACCAGAGAATTCGAATA	4954
CATCAGGCTTNNNGATCGACATG		CATTTGGCGTANNNGATCGACATG		CAGAGTGTCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4475	TGCAGGACCAGAGAATTCGAATA	4715	TGCAGGACCAGAGAATTCGAATA	4955
CATTAGGTGCNNNGATCGACATG		CAATTATCCTNNNGATCGACATG		CAAAACATCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4476	TGCAGGACCAGAGAATTCGAATA	4716	TGCAGGACCAGAGAATTCGAATA	4956
CATCCGACGGNNNGATCGACATG		CACCTTTGAAANNNGATCGACATG		CATAAGCTTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4477	TGCAGGACCAGAGAATTCGAATA	4717	TGCAGGACCAGAGAATTCGAATA	4957
CAAAAGCAGCANNNGATCGACATG		CACCTAGTAGCNNNGATCGACATG		CATTAGTGCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4478	TGCAGGACCAGAGAATTCGAATA	4718	TGCAGGACCAGAGAATTCGAATA	4958
CAGTGCCGGTNNNGATCGACATG		CATCCCACATNNNGATCGACATG		CAGTTGCCCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4479	TGCAGGACCAGAGAATTCGAATA	4719	TGCAGGACCAGAGAATTCGAATA	4959
CAACGATATTNNNGATCGACATG		CAGTATGCACNNNGATCGACATG		CAGTGACCTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4480	TGCAGGACCAGAGAATTCGAATA	4720	TGCAGGACCAGAGAATTCGAATA	4960
CAACAAACAGGNNNGATCGACATG		CAGGCCTCAGNNNGATCGACATG		CAGGACAATGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4481	TGCAGGACCAGAGAATTCGAATA	4721	TGCAGGACCAGAGAATTCGAATA	4961
CACCTCGAAANNNGATCGACATG		CACGGCTTAANNNGATCGACATG		CATATAGGAANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4482	TGCAGGACCAGAGAATTCGAATA	4722	TGCAGGACCAGAGAATTCGAATA	4962
CATCAAGCCANNNGATCGACATG		CACATAGCACNNNGATCGACATG		CACCTAGCGCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4483	TGCAGGACCAGAGAATTCGAATA	4723	TGCAGGACCAGAGAATTCGAATA	4963
CACATTAACANNNGATCGACATG		CACCACTTTGNNNGATCGACATG		CAGCGTTTAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4484	TGCAGGACCAGAGAATTCGAATA	4724	TGCAGGACCAGAGAATTCGAATA	4964
CAAACACGAGNNNGATCGACATG		CATGTGATGCNNNGATCGACATG		CAGTATGTGCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4485	TGCAGGACCAGAGAATTCGAATA	4725	TGCAGGACCAGAGAATTCGAATA	4965
CATCCATCACNNNGATCGACATG		CAATCGCTAGNNNGATCGACATG		CACATGTGACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4486	TGCAGGACCAGAGAATTCGAATA	4726	TGCAGGACCAGAGAATTCGAATA	4966
CAGTCGCACGNNNGATCGACATG		CAGAATTAGANNNGATCGACATG		CAATCAAAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4487	TGCAGGACCAGAGAATTCGAATA	4727	TGCAGGACCAGAGAATTCGAATA	4967
CATGGCAGCANNNGATCGACATG		CAGCGGCTGNNNGATCGACATG		CAATAAACTCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4488	TGCAGGACCAGAGAATTCGAATA	4728	TGCAGGACCAGAGAATTCGAATA	4968
CATTTTCAGAAANNNGATCGACATG		CAAATTCGATNNNGATCGACATG		CACCGGATCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4489	TGCAGGACCAGAGAATTCGAATA	4729	TGCAGGACCAGAGAATTCGAATA	4969
CATACGTCTCANNNGATCGACATG		CATGGAACCTNNNGATCGACATG		CACCGGCTAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4490	TGCAGGACCAGAGAATTCGAATA	4730	TGCAGGACCAGAGAATTCGAATA	4970
CACCGGATCTNNNGATCGACATG		CAAGCGCATNNNGATCGACATG		CACCTGTGGTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4491	TGCAGGACCAGAGAATTCGAATA	4731	TGCAGGACCAGAGAATTCGAATA	4971
CAATTAAGCTNNNGATCGACATG		CATTCCTCTNNNGATCGACATG		CAGAACGTGANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4492	TGCAGGACCAGAGAATTCGAATA	4732	TGCAGGACCAGAGAATTCGAATA	4972
CAAACCTCCNNNGATCGACATG		CAATTGTGCGNNNGATCGACATG		CACGGCTGACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	4493	TGCAGGACCAGAGAATTCGAATA	4733	TGCAGGACCAGAGAATTCGAATA	4973
CAGTCGCTTTNNNGATCGACATG		CATAATGCGCANNNGATCGACATG		CAGGCATCATNNNGATCGACATG	

FIG. 18F

Poel-19	SEQ ID NO:	Poel-20	SEQ ID NO:	Poel-21	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATA	4494	TGCAGGACCAGAGAATTCTGAATA	4734	TGCAGGACCAGAGAATTCTGAATA	4974
CAGCCAGTATNNNGATCGACATG		CAACGCATTGNNNGATCGACATG		CACCGCAGGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4495	TGCAGGACCAGAGAATTCTGAATA	4735	TGCAGGACCAGAGAATTCTGAATA	4975
CAGAGAAAAANNNGATCGACATG		CATGTCGGTANNNGATCGACATG		CATCCTACTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4496	TGCAGGACCAGAGAATTCTGAATA	4736	TGCAGGACCAGAGAATTCTGAATA	4976
CAATAGCCCNNGATCGACATG		CATTTTCAACNNNGATCGACATG		CATCCCGACNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4497	TGCAGGACCAGAGAATTCTGAATA	4737	TGCAGGACCAGAGAATTCTGAATA	4977
CACACGTCCCNNGATCGACATG		CATAAGTACTNNNGATCGACATG		CATGTAGGTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4498	TGCAGGACCAGAGAATTCTGAATA	4738	TGCAGGACCAGAGAATTCTGAATA	4978
CAAGTTTATGNNNGATCGACATG		CAATATAGTGNNGATCGACATG		CACGGCGCTANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4499	TGCAGGACCAGAGAATTCTGAATA	4739	TGCAGGACCAGAGAATTCTGAATA	4979
CACCTTTTCGNNNGATCGACATG		CAGGAAATATNNNGATCGACATG		CACCTATTTANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4500	TGCAGGACCAGAGAATTCTGAATA	4740	TGCAGGACCAGAGAATTCTGAATA	4980
CACAATCGTGNNGATCGACATG		CATTTTCAACNNNGATCGACATG		CAGAACAACNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4501	TGCAGGACCAGAGAATTCTGAATA	4741	TGCAGGACCAGAGAATTCTGAATA	4981
CAGGACGTAAANNNGATCGACATG		CACACGTAAACNNNGATCGACATG		CATCCCATTTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4502	TGCAGGACCAGAGAATTCTGAATA	4742	TGCAGGACCAGAGAATTCTGAATA	4982
CACCCGAACGNNNGATCGACATG		CAGTTTCCGTGNNNGATCGACATG		CATACTGTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4503	TGCAGGACCAGAGAATTCTGAATA	4743	TGCAGGACCAGAGAATTCTGAATA	4983
CATCCGTATCANNNGATCGACATG		CAAGTATCTANNNGATCGACATG		CAGCGGTTAANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4504	TGCAGGACCAGAGAATTCTGAATA	4744	TGCAGGACCAGAGAATTCTGAATA	4984
CATTTTCGTTANNNGATCGACATG		CATCTAGTGGNNNGATCGACATG		CAGCCTCCANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4505	TGCAGGACCAGAGAATTCTGAATA	4745	TGCAGGACCAGAGAATTCTGAATA	4985
CATGCTACAGNNNGATCGACATG		CAGAGTACAGNNNGATCGACATG		CACACGATACNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4506	TGCAGGACCAGAGAATTCTGAATA	4746	TGCAGGACCAGAGAATTCTGAATA	4986
CAGTTACTTTNNNGATCGACATG		CAACTCCAGANNNGATCGACATG		CAGTGTCAACNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4507	TGCAGGACCAGAGAATTCTGAATA	4747	TGCAGGACCAGAGAATTCTGAATA	4987
CAAAATGCCTGNNNGATCGACATG		CAAAACACAANNNGATCGACATG		CATACGCCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4508	TGCAGGACCAGAGAATTCTGAATA	4748	TGCAGGACCAGAGAATTCTGAATA	4988
CACCAGGCACNNNGATCGACATG		CAGCCGCCAACNNNGATCGACATG		CAAAATCCGACNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	4509	TGCAGGACCAGAGAATTCTGAATA	4749	TGCAGGACCAGAGAATTCTGAATA	4989
CATGGCGACNNNTGCATCAGGT		CAGATCTTAANNNTGCATCAGGT		CAGCCGCCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4510	TGCAGGACCAGAGAATTCTGAATA	4750	TGCAGGACCAGAGAATTCTGAATA	4990
CAAAAGGCTNNNTGCATCAGGT		CACCTAGCTNNNTGCATCAGGT		CACCTGCCGTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4511	TGCAGGACCAGAGAATTCTGAATA	4751	TGCAGGACCAGAGAATTCTGAATA	4991
CATTACCCACNNNTGCATCAGGT		CAGCATTTCTNNNTGCATCAGGT		CACGTTACCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4512	TGCAGGACCAGAGAATTCTGAATA	4752	TGCAGGACCAGAGAATTCTGAATA	4992
CATCCGGATTNNNTGCATCAGGT		CAGCAGCCACNNNTGCATCAGGT		CACGATTAGCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4513	TGCAGGACCAGAGAATTCTGAATA	4753	TGCAGGACCAGAGAATTCTGAATA	4993
CACAGGTTGTNNNTGCATCAGGT		CAAGCTGCGCNNNTGCATCAGGT		CAAACCTAATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4514	TGCAGGACCAGAGAATTCTGAATA	4754	TGCAGGACCAGAGAATTCTGAATA	4994
CAAAACATAGANNNTGCATCAGGT		CACCCGCTACNNNTGCATCAGGT		CAATCGGCTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4515	TGCAGGACCAGAGAATTCTGAATA	4755	TGCAGGACCAGAGAATTCTGAATA	4995
CAGAAATGATNNNTGCATCAGGT		CACAAGGCAANNNTGCATCAGGT		CAGGAACCCCNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4516	TGCAGGACCAGAGAATTCTGAATA	4756	TGCAGGACCAGAGAATTCTGAATA	4996
CATGTGCTGANNNNTGCATCAGGT		CAGATGTTATNNNTGCATCAGGT		CATCACACAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4517	TGCAGGACCAGAGAATTCTGAATA	4757	TGCAGGACCAGAGAATTCTGAATA	4997
CAAGGCAGATNNNTGCATCAGGT		CACGGTATTGNNNTGCATCAGGT		CACTATTGAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4518	TGCAGGACCAGAGAATTCTGAATA	4758	TGCAGGACCAGAGAATTCTGAATA	4998
CATAGGTTATNNNTGCATCAGGT		CAGTATTTAGNNNTGCATCAGGT		CACGCGATATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4519	TGCAGGACCAGAGAATTCTGAATA	4759	TGCAGGACCAGAGAATTCTGAATA	4999
CATTTTGTGNNNTGCATCAGGT		CAGGATCAGANNNTGCATCAGGT		CACCTTATGTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4520	TGCAGGACCAGAGAATTCTGAATA	4760	TGCAGGACCAGAGAATTCTGAATA	5000
CAAAACAAGTNNNTGCATCAGGT		CAATCGAAANNNTGCATCAGGT		CAATTTGGTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4521	TGCAGGACCAGAGAATTCTGAATA	4761	TGCAGGACCAGAGAATTCTGAATA	5001
CACGTGGTTANNNTGCATCAGGT		CAGCCATTTNNNTGCATCAGGT		CAAGGCAACANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4522	TGCAGGACCAGAGAATTCTGAATA	4762	TGCAGGACCAGAGAATTCTGAATA	5002
CACCTTCGACNNNTGCATCAGGT		CATCAGACANNNTGCATCAGGT		CAGACCTTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4523	TGCAGGACCAGAGAATTCTGAATA	4763	TGCAGGACCAGAGAATTCTGAATA	5003
CATAGACGTCNNNTGCATCAGGT		CATTTGTTCAANNNTGCATCAGGT		CAGGAACCAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4524	TGCAGGACCAGAGAATTCTGAATA	4764	TGCAGGACCAGAGAATTCTGAATA	5004
CATCTAGTCCNNNTGCATCAGGT		CAACCTATCANNNTGCATCAGGT		CACGTGTAACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4525	TGCAGGACCAGAGAATTCTGAATA	4765	TGCAGGACCAGAGAATTCTGAATA	5005
CAAAACAAGATNNNTGCATCAGGT		CAAAAAGCCGNNNTGCATCAGGT		CACAGATCCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	4526	TGCAGGACCAGAGAATTCTGAATA	4766	TGCAGGACCAGAGAATTCTGAATA	5006
CATAATGAAGNNNTGCATCAGGT		CAGAGTGGCANNNTGCATCAGGT		CACCAGCAGCANNNTGCATCAGGT	

FIG. 18G

Poel-19	SEQ ID NO:	Poel-20	SEQ ID NO:	Poel-21	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA	4527	TGCAGGACCAGAGAATTGGAATA	4767	TGCAGGACCAGAGAATTGGAATA	5007
CATATTGCGCCNNNTGCATCAGGT		CAATCATACANNNTGCATCAGGT		CACGAGTCCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4528	TGCAGGACCAGAGAATTGGAATA	4768	TGCAGGACCAGAGAATTGGAATA	5008
CATTGCACGANNNTGCATCAGGT		CACAGATGAGNNNTGCATCAGGT		CAGTCGAATCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4529	TGCAGGACCAGAGAATTGGAATA	4769	TGCAGGACCAGAGAATTGGAATA	5009
CAACTACTAANNNTGCATCAGGT		CACAGCTTAGNNNTGCATCAGGT		CATCCATAAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4530	TGCAGGACCAGAGAATTGGAATA	4770	TGCAGGACCAGAGAATTGGAATA	5010
CAACTCATANNNTGCATCAGGT		CAACTTCTTANNNTGCATCAGGT		CAGTCCCACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4531	TGCAGGACCAGAGAATTGGAATA	4771	TGCAGGACCAGAGAATTGGAATA	5011
CAAGGACTGANNNTGCATCAGGT		CACAACACGANNNTGCATCAGGT		CATGGTTGACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4532	TGCAGGACCAGAGAATTGGAATA	4772	TGCAGGACCAGAGAATTGGAATA	5012
CACACATCCTNNNTGCATCAGGT		CACGTAGATCANNNTGCATCAGGT		CAAGACAACGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4533	TGCAGGACCAGAGAATTGGAATA	4773	TGCAGGACCAGAGAATTGGAATA	5013
CAATAGCGAGNNNTGCATCAGGT		CACCTCCGANNNTGCATCAGGT		CAATATTGAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4534	TGCAGGACCAGAGAATTGGAATA	4774	TGCAGGACCAGAGAATTGGAATA	5014
CAAGGAAGTCNNNTGCATCAGGT		CAGACTTTGGNNNTGCATCAGGT		CAGAGGAACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4535	TGCAGGACCAGAGAATTGGAATA	4775	TGCAGGACCAGAGAATTGGAATA	5015
CAGAAGCCTTNNNTGCATCAGGT		CAGAAGATCCNNNTGCATCAGGT		CAGAAGAACCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4536	TGCAGGACCAGAGAATTGGAATA	4776	TGCAGGACCAGAGAATTGGAATA	5016
CACCCCTCTNNNTGCATCAGGT		CACAGCATCANNNTGCATCAGGT		CAGCAACAAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4537	TGCAGGACCAGAGAATTGGAATA	4777	TGCAGGACCAGAGAATTGGAATA	5017
CAAGAAACGNNNTGCATCAGGT		CACCTTCTGACNNNTGCATCAGGT		CACATAAACGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4538	TGCAGGACCAGAGAATTGGAATA	4778	TGCAGGACCAGAGAATTGGAATA	5018
CAGACATCTGNNNTGCATCAGGT		CATCCCGTTANNNTGCATCAGGT		CAGGAGGTCCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4539	TGCAGGACCAGAGAATTGGAATA	4779	TGCAGGACCAGAGAATTGGAATA	5019
CAACGCCCTCANNNTGCATCAGGT		CATTTCATANNNTGCATCAGGT		CACGCGCTTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4540	TGCAGGACCAGAGAATTGGAATA	4780	TGCAGGACCAGAGAATTGGAATA	5020
CAGTCACCGGNNNTGCATCAGGT		CACGTGCGACNNNTGCATCAGGT		CACCGAGTGCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4541	TGCAGGACCAGAGAATTGGAATA	4781	TGCAGGACCAGAGAATTGGAATA	5021
CAAGAGCGATNNNTGCATCAGGT		CAACGCTGGCNNNTGCATCAGGT		CAGTTCAAGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4542	TGCAGGACCAGAGAATTGGAATA	4782	TGCAGGACCAGAGAATTGGAATA	5022
CAATGGCTTGNNTGCATCAGGT		CAGAGATCCNNNTGCATCAGGT		CACAGCCGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4543	TGCAGGACCAGAGAATTGGAATA	4783	TGCAGGACCAGAGAATTGGAATA	5023
CACCTGCAANNNTGCATCAGGT		CAGAGACTANNNTGCATCAGGT		CACCTTGACTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4544	TGCAGGACCAGAGAATTGGAATA	4784	TGCAGGACCAGAGAATTGGAATA	5024
CAGTCGAATCANNNTGCATCAGGT		CATTGATTAGNNNTGCATCAGGT		CAGACGCAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4545	TGCAGGACCAGAGAATTGGAATA	4785	TGCAGGACCAGAGAATTGGAATA	5025
CATGTGGAGANNNTGCATCAGGT		CACATGCATGNNNTGCATCAGGT		CATGATCCTCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4546	TGCAGGACCAGAGAATTGGAATA	4786	TGCAGGACCAGAGAATTGGAATA	5026
CAAACGTGCTNNNTGCATCAGGT		CATTGACCTCANNNTGCATCAGGT		CAAGAAATTGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4547	TGCAGGACCAGAGAATTGGAATA	4787	TGCAGGACCAGAGAATTGGAATA	5027
CAAAGATTGANNNTGCATCAGGT		CAGGCCACTGNNNTGCATCAGGT		CAGTGTGGCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4548	TGCAGGACCAGAGAATTGGAATA	4788	TGCAGGACCAGAGAATTGGAATA	5028
CAACGTTATANNNTGCATCAGGT		CATTCTCTCANNNTGCATCAGGT		CACATGTAGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4549	TGCAGGACCAGAGAATTGGAATA	4789	TGCAGGACCAGAGAATTGGAATA	5029
CACCGCATANNNTGCATCAGGT		CAGCATTGAGNNNTGCATCAGGT		CATAGCCCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4550	TGCAGGACCAGAGAATTGGAATA	4790	TGCAGGACCAGAGAATTGGAATA	5030
CACGATTTCCNNNTGCATCAGGT		CAGTAACCTANNNTGCATCAGGT		CAGTCTTGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4551	TGCAGGACCAGAGAATTGGAATA	4791	TGCAGGACCAGAGAATTGGAATA	5031
CAGTAAACANNNTGCATCAGGT		CAACTATGATNNNTGCATCAGGT		CATGTAAGCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4552	TGCAGGACCAGAGAATTGGAATA	4792	TGCAGGACCAGAGAATTGGAATA	5032
CAGGTGGTCCNNNTGCATCAGGT		CAACTAAGAANNNTGCATCAGGT		CAACAGAGACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4553	TGCAGGACCAGAGAATTGGAATA	4793	TGCAGGACCAGAGAATTGGAATA	5033
CAATGTCTGNNNTGCATCAGGT		CATAGGTTTANNNTGCATCAGGT		CAAGTTGAGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4554	TGCAGGACCAGAGAATTGGAATA	4794	TGCAGGACCAGAGAATTGGAATA	5034
CACGTAAATNNNTGCATCAGGT		CACCTCGTCGNNNTGCATCAGGT		CACCTGCTTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4555	TGCAGGACCAGAGAATTGGAATA	4795	TGCAGGACCAGAGAATTGGAATA	5035
CAACTCGCTTNNNTGCATCAGGT		CAGGCTAGCCNNNTGCATCAGGT		CAACACCTCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4556	TGCAGGACCAGAGAATTGGAATA	4796	TGCAGGACCAGAGAATTGGAATA	5036
CACCATACGANNNTGCATCAGGT		CAGGTTGTACNNNTGCATCAGGT		CATATTGACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4557	TGCAGGACCAGAGAATTGGAATA	4797	TGCAGGACCAGAGAATTGGAATA	5037
CACGGACAAANNNTGCATCAGGT		CATAAAGCGGNNNTGCATCAGGT		CAGATTGGTCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4558	TGCAGGACCAGAGAATTGGAATA	4798	TGCAGGACCAGAGAATTGGAATA	5038
CACGCTGTTTTNNNTGCATCAGGT		CAAAATCTTCCNNNTGCATCAGGT		CAAAAGAAAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	4559	TGCAGGACCAGAGAATTGGAATA	4799	TGCAGGACCAGAGAATTGGAATA	5039
CACCTCCATANNNTGCATCAGGT		CACCAAGGAANNNTGCATCAGGT		CATAAAATANNNTGCATCAGGT	

FIG. 18H

Poel-19	SEQ ID NO:	Poel-20	SEQ ID NO:	Poel-21	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CAGGCTTGCGNNNTGCATCAGGT	4560	TGCAGGACCAGAGAATTCGAATA CAACAAAAGTNNNTGCATCAGGT	4800	TGCAGGACCAGAGAATTCGAATA CATGTCCAGANNNTGCATCAGGT	5040
TGCAGGACCAGAGAATTCGAATA CAAAATTCGNNNTGCATCAGGT	4561	TGCAGGACCAGAGAATTCGAATA CAGGCCCGGNNNTGCATCAGGT	4801	TGCAGGACCAGAGAATTCGAATA CATTTGAGGCNNNTGCATCAGGT	5041
TGCAGGACCAGAGAATTCGAATA CATACCTAGGNNNTGCATCAGGT	4562	TGCAGGACCAGAGAATTCGAATA CAAACATGCCNNNTGCATCAGGT	4802	TGCAGGACCAGAGAATTCGAATA CACCATCCTANNNTGCATCAGGT	5042
TGCAGGACCAGAGAATTCGAATA CACACGCACGNNNTGCATCAGGT	4563	TGCAGGACCAGAGAATTCGAATA CATCGGAGTTNNNTGCATCAGGT	4803	TGCAGGACCAGAGAATTCGAATA CACTCCAGANNNTGCATCAGGT	5043
TGCAGGACCAGAGAATTCGAATA CACATTGCAGNNNTGCATCAGGT	4564	TGCAGGACCAGAGAATTCGAATA CATAGCGGAANNNTGCATCAGGT	4804	TGCAGGACCAGAGAATTCGAATA CACAGATGGANNNTGCATCAGGT	5044
TGCAGGACCAGAGAATTCGAATA CAGCATTAAATNNNTGCATCAGGT	4565	TGCAGGACCAGAGAATTCGAATA CAGTCTACTCNNNTGCATCAGGT	4805	TGCAGGACCAGAGAATTCGAATA CATAATCCCCNNNTGCATCAGGT	5045
TGCAGGACCAGAGAATTCGAATA CAAGACGCCCCNNNTGCATCAGGT	4566	TGCAGGACCAGAGAATTCGAATA CATTTGACCCNNNTGCATCAGGT	4806	TGCAGGACCAGAGAATTCGAATA CAAGGCGCTCNNNTGCATCAGGT	5046
TGCAGGACCAGAGAATTCGAATA CACACACGATNNNTGCATCAGGT	4567	TGCAGGACCAGAGAATTCGAATA CAAAGGAGAGNNNTGCATCAGGT	4807	TGCAGGACCAGAGAATTCGAATA CAATTGTCAANNNTGCATCAGGT	5047
TGCAGGACCAGAGAATTCGAATA CATGATTGTANNNTGCATCAGGT	4568	TGCAGGACCAGAGAATTCGAATA CATTTGCCANNNTGCATCAGGT	4808	TGCAGGACCAGAGAATTCGAATA CACGCGTTAANNNTGCATCAGGT	5048

FIG. 19A

Pool-22	SEQ ID NO:	Pool-23	SEQ ID NO:	Pool-24	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA	5049	TGCAGGACCAGAGAATTCGAATA	5289	TGCAGGACCAGAGAATTCGAATA	5529
CATTGATGCCNNNACGTATGCCA		CATAACTAACNNNACGTATGCCA		CAGTTGCGCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5050	TGCAGGACCAGAGAATTCGAATA	5290	TGCAGGACCAGAGAATTCGAATA	5530
CACCCTACGCGNNNACGTATGCCA		CAAAACTCGCINNACGTATGCCA		CAGGAACATGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5051	TGCAGGACCAGAGAATTCGAATA	5291	TGCAGGACCAGAGAATTCGAATA	5531
CAGCGGCGAANNNACGTATGCCA		CATGAGTTGCNNNACGTATGCCA		CACGGTAACINNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5052	TGCAGGACCAGAGAATTCGAATA	5292	TGCAGGACCAGAGAATTCGAATA	5532
CATAGCCGCGNNNACGTATGCCA		CAACAACAANNNACGTATGCCA		CAATGTGTGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5053	TGCAGGACCAGAGAATTCGAATA	5293	TGCAGGACCAGAGAATTCGAATA	5533
CAGAAGCGATNNNACGTATGCCA		CAGCCCTACNNNACGTATGCCA		CACGAGTTGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5054	TGCAGGACCAGAGAATTCGAATA	5294	TGCAGGACCAGAGAATTCGAATA	5534
CAGACAGTGANNNACGTATGCCA		CAGTTGAGAGNNNACGTATGCCA		CATGAACTCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5055	TGCAGGACCAGAGAATTCGAATA	5295	TGCAGGACCAGAGAATTCGAATA	5535
CACCTTTATCANNNACGTATGCCA		CACAGTGACTNNNACGTATGCCA		CAACATCGCANNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5056	TGCAGGACCAGAGAATTCGAATA	5296	TGCAGGACCAGAGAATTCGAATA	5536
CACAGGAAGTNNNACGTATGCCA		CATGAAGACGNNNACGTATGCCA		CAGAATTGTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5057	TGCAGGACCAGAGAATTCGAATA	5297	TGCAGGACCAGAGAATTCGAATA	5537
CAGTATTGCCNNNACGTATGCCA		CACCCATGTGNNNACGTATGCCA		CAAAACACTINNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5058	TGCAGGACCAGAGAATTCGAATA	5298	TGCAGGACCAGAGAATTCGAATA	5538
CATCAGCCGCGNNNACGTATGCCA		CATGGTTTGGNNNACGTATGCCA		CATGTTTGCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5059	TGCAGGACCAGAGAATTCGAATA	5299	TGCAGGACCAGAGAATTCGAATA	5539
CAAGCAGGATNNNACGTATGCCA		CAGCACTCGGNNNACGTATGCCA		CACGCGTGCCANNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5060	TGCAGGACCAGAGAATTCGAATA	5300	TGCAGGACCAGAGAATTCGAATA	5540
CAGTTAGTGCCNNNACGTATGCCA		CAAAAGAGTTNNNACGTATGCCA		CAGTAATGCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5061	TGCAGGACCAGAGAATTCGAATA	5301	TGCAGGACCAGAGAATTCGAATA	5541
CAATTGTAGTNNNACGTATGCCA		CAGTTCTGTGANNNACGTATGCCA		CAGTTGAGACNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5062	TGCAGGACCAGAGAATTCGAATA	5302	TGCAGGACCAGAGAATTCGAATA	5542
CAAGCAGCTTNNNACGTATGCCA		CATCCCCACGNNNACGTATGCCA		CATAATCAGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5063	TGCAGGACCAGAGAATTCGAATA	5303	TGCAGGACCAGAGAATTCGAATA	5543
CACCCCGGTTNNNACGTATGCCA		CAAAATTTGNNNACGTATGCCA		CATTCCCAACNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5064	TGCAGGACCAGAGAATTCGAATA	5304	TGCAGGACCAGAGAATTCGAATA	5544
CAATATCTCTNNNACGTATGCCA		CATCCACAGANNNACGTATGCCA		CACCTAGTAGCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5065	TGCAGGACCAGAGAATTCGAATA	5305	TGCAGGACCAGAGAATTCGAATA	5545
CAATCTTCATNNNACGTATGCCA		CAAGAGTTTNNNACGTATGCCA		CATTAAATACGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5066	TGCAGGACCAGAGAATTCGAATA	5306	TGCAGGACCAGAGAATTCGAATA	5546
CAGGTACTCANNNACGTATGCCA		CATGGAGCGGNNNACGTATGCCA		CATACAGAGGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5067	TGCAGGACCAGAGAATTCGAATA	5307	TGCAGGACCAGAGAATTCGAATA	5547
CACCACCTATNNNACGTATGCCA		CACCTTTAATCINNACGTATGCCA		CACGGCACCANNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5068	TGCAGGACCAGAGAATTCGAATA	5308	TGCAGGACCAGAGAATTCGAATA	5548
CAATAATAANNNACGTATGCCA		CAACGTCAGTNNNACGTATGCCA		CATCTCCCAANNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5069	TGCAGGACCAGAGAATTCGAATA	5309	TGCAGGACCAGAGAATTCGAATA	5549
CAACATAATCANNNACGTATGCCA		CATGGAGCTTNNNACGTATGCCA		CAGTAGTGCANNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5070	TGCAGGACCAGAGAATTCGAATA	5310	TGCAGGACCAGAGAATTCGAATA	5550
CACCTTCGTANNNACGTATGCCA		CAGCACACCGNNNACGTATGCCA		CAGTAGTACCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5071	TGCAGGACCAGAGAATTCGAATA	5311	TGCAGGACCAGAGAATTCGAATA	5551
CAGGATCTTGNNNACGTATGCCA		CATTTGCTGCNNNACGTATGCCA		CATAACCGTGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5072	TGCAGGACCAGAGAATTCGAATA	5312	TGCAGGACCAGAGAATTCGAATA	5552
CAGAGCGGTTNNNACGTATGCCA		CACAGCGAANNNACGTATGCCA		CACGGATAGANNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5073	TGCAGGACCAGAGAATTCGAATA	5313	TGCAGGACCAGAGAATTCGAATA	5553
CACCTCAAAATNNNACGTATGCCA		CAACGATTGCNNNACGTATGCCA		CAGGAATAGCINNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5074	TGCAGGACCAGAGAATTCGAATA	5314	TGCAGGACCAGAGAATTCGAATA	5554
CACAACATGCANNNACGTATGCCA		CATAGCGTTGNNNACGTATGCCA		CAGGAGTCAANNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5075	TGCAGGACCAGAGAATTCGAATA	5315	TGCAGGACCAGAGAATTCGAATA	5555
CACGGTTCNNNACGTATGCCA		CAACGCTGCGNNNACGTATGCCA		CAATTAGCTANNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5076	TGCAGGACCAGAGAATTCGAATA	5316	TGCAGGACCAGAGAATTCGAATA	5556
CAGTGTAGANNNACGTATGCCA		CACCTTTATGNNNACGTATGCCA		CAAGACATTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5077	TGCAGGACCAGAGAATTCGAATA	5317	TGCAGGACCAGAGAATTCGAATA	5557
CATCTGAGTGNNNACGTATGCCA		CAGCGAAATGNNNACGTATGCCA		CATCTACGCTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5078	TGCAGGACCAGAGAATTCGAATA	5318	TGCAGGACCAGAGAATTCGAATA	5558
CACAGCCTTTNNNACGTATGCCA		CATTTATTGNNNACGTATGCCA		CATGCCTTCANNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5079	TGCAGGACCAGAGAATTCGAATA	5319	TGCAGGACCAGAGAATTCGAATA	5559
CAGTGTGTTGNNNACGTATGCCA		CATCCAGCGGNNNACGTATGCCA		CAAGATCACNNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5080	TGCAGGACCAGAGAATTCGAATA	5320	TGCAGGACCAGAGAATTCGAATA	5560
CAATTGTAACNNNACGTATGCCA		CACGCATGCGNNNACGTATGCCA		CAATCCTTTANNNACGTATGCCA	
TGCAGGACCAGAGAATTCGAATA	5081	TGCAGGACCAGAGAATTCGAATA	5321	TGCAGGACCAGAGAATTCGAATA	5561
CAAGTTTCATNNNACGTATGCCA		CAATGCTGGTNNNACGTATGCCA		CAGTAGTTCGNNNACGTATGCCA	

FIG. 19B

Pool-22	SEQ ID NO:	Pool-23	SEQ ID NO:	Pool-24	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA	5082	TGCAGGACCAGAGAATTGGAATA	5322	TGCAGGACCAGAGAATTGGAATA	5562
CAAAGTCGCTNNNNACGTATGCCA		CAAATGGCCTNNNNACGTATGCCA		CAGGCCCGGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5083	TGCAGGACCAGAGAATTGGAATA	5323	TGCAGGACCAGAGAATTGGAATA	5563
CAATATCAGTNNNNACGTATGCCA		CAGGTTTAGCNNNNACGTATGCCA		CAAGGCCAGGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5084	TGCAGGACCAGAGAATTGGAATA	5324	TGCAGGACCAGAGAATTGGAATA	5564
CATTCTCCGANNNNACGTATGCCA		CATTCCCGAGTNNNNACGTATGCCA		CATTGTGAGGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5085	TGCAGGACCAGAGAATTGGAATA	5325	TGCAGGACCAGAGAATTGGAATA	5565
CATCTTGAAANNNNACGTATGCCA		CAAGCGATGANNNNACGTATGCCA		CAAAATCTGTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5086	TGCAGGACCAGAGAATTGGAATA	5326	TGCAGGACCAGAGAATTGGAATA	5566
CATTACCGAGNNNNACGTATGCCA		CACCGGTGAGNNNNACGTATGCCA		CAATAAAATNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5087	TGCAGGACCAGAGAATTGGAATA	5327	TGCAGGACCAGAGAATTGGAATA	5567
CAACTTAGATNNNNACGTATGCCA		CAAGTATACTNNNNACGTATGCCA		CATGTGACAGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5088	TGCAGGACCAGAGAATTGGAATA	5328	TGCAGGACCAGAGAATTGGAATA	5568
CACATCGGTANNNNACGTATGCCA		CAGACTGAGANNNNACGTATGCCA		CATCTGACGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5089	TGCAGGACCAGAGAATTGGAATA	5329	TGCAGGACCAGAGAATTGGAATA	5569
CACCAGCGCANNNNACGTATGCCA		CATCACGTTCNNNNACGTATGCCA		CAGAACGCTTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5090	TGCAGGACCAGAGAATTGGAATA	5330	TGCAGGACCAGAGAATTGGAATA	5570
CATATCGATANNNNACGTATGCCA		CACCTGACTACNNNNACGTATGCCA		CATCTGACGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5091	TGCAGGACCAGAGAATTGGAATA	5331	TGCAGGACCAGAGAATTGGAATA	5571
CAAGACTCTGNNNNACGTATGCCA		CAGAAGAGAGNNNNACGTATGCCA		CAGATGCGAANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5092	TGCAGGACCAGAGAATTGGAATA	5332	TGCAGGACCAGAGAATTGGAATA	5572
CAAGAGCACANNNNACGTATGCCA		CACCGTGCACNNNNACGTATGCCA		CACCTGATCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5093	TGCAGGACCAGAGAATTGGAATA	5333	TGCAGGACCAGAGAATTGGAATA	5573
CATACCGTAGNNNNACGTATGCCA		CAGCAACGAANNNNACGTATGCCA		CAGACGGTAANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5094	TGCAGGACCAGAGAATTGGAATA	5334	TGCAGGACCAGAGAATTGGAATA	5574
CAGAAGGTGTNNNNACGTATGCCA		CAGCTACCTTNNNNACGTATGCCA		CATATATTTTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5095	TGCAGGACCAGAGAATTGGAATA	5335	TGCAGGACCAGAGAATTGGAATA	5575
CATTGGACANNNNACGTATGCCA		CAACACCTTCNNNNACGTATGCCA		CATGCATTCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5096	TGCAGGACCAGAGAATTGGAATA	5336	TGCAGGACCAGAGAATTGGAATA	5576
CAGCAATCACNNNNACGTATGCCA		CACCTGTTAAANNNNACGTATGCCA		CATATATCTCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5097	TGCAGGACCAGAGAATTGGAATA	5337	TGCAGGACCAGAGAATTGGAATA	5577
CATTGAGCGTNNNNACGTATGCCA		CAATCTCGGANNNNACGTATGCCA		CACCGGCTGANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5098	TGCAGGACCAGAGAATTGGAATA	5338	TGCAGGACCAGAGAATTGGAATA	5578
CACAAGTGTGNNNNACGTATGCCA		CAATGTTGCGNNNNACGTATGCCA		CAGAATCAGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5099	TGCAGGACCAGAGAATTGGAATA	5339	TGCAGGACCAGAGAATTGGAATA	5579
CAGTCTAATANNNNACGTATGCCA		CAGCACATGTNNNNACGTATGCCA		CATCCTAGAGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5100	TGCAGGACCAGAGAATTGGAATA	5340	TGCAGGACCAGAGAATTGGAATA	5580
CAAGAAATCGNNNNACGTATGCCA		CAATCCGGTNNNNACGTATGCCA		CACCGTGTGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5101	TGCAGGACCAGAGAATTGGAATA	5341	TGCAGGACCAGAGAATTGGAATA	5581
CAGCTAGATCNNNNACGTATGCCA		CACATTTTACNNNNACGTATGCCA		CATAGTTTCTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5102	TGCAGGACCAGAGAATTGGAATA	5342	TGCAGGACCAGAGAATTGGAATA	5582
CAGATAAGTANNNNACGTATGCCA		CACGTGCCAGNNNNACGTATGCCA		CAGATACCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5103	TGCAGGACCAGAGAATTGGAATA	5343	TGCAGGACCAGAGAATTGGAATA	5583
CAGGTTTCAGTNNNNACGTATGCCA		CACCGGTAGCNNNNACGTATGCCA		CACCTGTACTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5104	TGCAGGACCAGAGAATTGGAATA	5344	TGCAGGACCAGAGAATTGGAATA	5584
CAAGCTGACTNNNNACGTATGCCA		CAACATATGTNNNNACGTATGCCA		CAGCACTTTCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5105	TGCAGGACCAGAGAATTGGAATA	5345	TGCAGGACCAGAGAATTGGAATA	5585
CATGCGCCAGNNNNACGTATGCCA		CATGGTGGCCNNNNACGTATGCCA		CAGTTCTCGTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5106	TGCAGGACCAGAGAATTGGAATA	5346	TGCAGGACCAGAGAATTGGAATA	5586
CATGTGAGTNNNNACGTATGCCA		CACAACCTCAGNNNNACGTATGCCA		CACCTTACGTCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5107	TGCAGGACCAGAGAATTGGAATA	5347	TGCAGGACCAGAGAATTGGAATA	5587
CAGAATCGTCNNNNACGTATGCCA		CACCAATTTTNNNNACGTATGCCA		CACAGAAGACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5108	TGCAGGACCAGAGAATTGGAATA	5348	TGCAGGACCAGAGAATTGGAATA	5588
CACCCATGCGNNNNACGTATGCCA		CAAACTGAGGNNNNACGTATGCCA		CATAAGTCTANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5109	TGCAGGACCAGAGAATTGGAATA	5349	TGCAGGACCAGAGAATTGGAATA	5589
CACATTAGCGNNNNACGTATGCCA		CAACGTAGTCNNNNACGTATGCCA		CACATACTAANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5110	TGCAGGACCAGAGAATTGGAATA	5350	TGCAGGACCAGAGAATTGGAATA	5590
CAATCCACCTNNNNACGTATGCCA		CAGCATGGCCNNNNACGTATGCCA		CACCGAATCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5111	TGCAGGACCAGAGAATTGGAATA	5351	TGCAGGACCAGAGAATTGGAATA	5591
CAACATGCGTNNNNACGTATGCCA		CAAGTCAGAGNNNNACGTATGCCA		CACATATTTTGNNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5112	TGCAGGACCAGAGAATTGGAATA	5352	TGCAGGACCAGAGAATTGGAATA	5592
CAGCTTTACCCNNNNACGTATGCCA		CATGAATACTNNNNACGTATGCCA		CACCCGACAGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5113	TGCAGGACCAGAGAATTGGAATA	5353	TGCAGGACCAGAGAATTGGAATA	5593
CAAACTCCTNNNNACGTATGCCA		CAGTATGAGNNNNACGTATGCCA		CAACTTCGAGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	5114	TGCAGGACCAGAGAATTGGAATA	5354	TGCAGGACCAGAGAATTGGAATA	5594
CACCTTTATGTNNNNACGTATGCCA		CAGACTTGTGNNNNACGTATGCCA		CATGATGCTGNNNNACGTATGCCA	

FIG. 19C

Poal-22	SEQ ID NO:	Poal-23	SEQ ID NO:	Poal-24	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATA	5115	TGCAGGACCAGAGAATTCTGAATA	5355	TGCAGGACCAGAGAATTCTGAATA	5595
CACTCGCCTGNNNCTAGCGTTAC		CAAATTAAGGNNNCTAGCGTTAC		CAGCGCAGGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5116	TGCAGGACCAGAGAATTCTGAATA	5356	TGCAGGACCAGAGAATTCTGAATA	5596
CAATGATGTNNNCTAGCGTTAC		CACGGTTGTANNNCTAGCGTTAC		CATTCAAAAANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5117	TGCAGGACCAGAGAATTCTGAATA	5357	TGCAGGACCAGAGAATTCTGAATA	5597
CAGAGTTGGANNNCTAGCGTTAC		CACCTGTCCGNNNCTAGCGTTAC		CAATGCACTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5118	TGCAGGACCAGAGAATTCTGAATA	5358	TGCAGGACCAGAGAATTCTGAATA	5598
CAACAACCAACNNNCTAGCGTTAC		CAGTGACGCCNNNCTAGCGTTAC		CAGTTGCCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5119	TGCAGGACCAGAGAATTCTGAATA	5359	TGCAGGACCAGAGAATTCTGAATA	5599
CATACCGCAANNNCTAGCGTTAC		CAGTGTGCAANNNCTAGCGTTAC		CAATTTCCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5120	TGCAGGACCAGAGAATTCTGAATA	5360	TGCAGGACCAGAGAATTCTGAATA	5600
CAGGTTAAANNNCTAGCGTTAC		CACCCGATTNNNCTAGCGTTAC		CACCAGCAGCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5121	TGCAGGACCAGAGAATTCTGAATA	5361	TGCAGGACCAGAGAATTCTGAATA	5601
CACGGAAAGTNNNCTAGCGTTAC		CATTCCCGTNNNCTAGCGTTAC		CACGGACAGCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5122	TGCAGGACCAGAGAATTCTGAATA	5362	TGCAGGACCAGAGAATTCTGAATA	5602
CAGTGTGTCGNNNCTAGCGTTAC		CAAGGTCCTNNNCTAGCGTTAC		CATCTGCGTTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5123	TGCAGGACCAGAGAATTCTGAATA	5363	TGCAGGACCAGAGAATTCTGAATA	5603
CAGGTGTCCGNNNCTAGCGTTAC		CAGAGCCAAANNNCTAGCGTTAC		CATTTGCTATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5124	TGCAGGACCAGAGAATTCTGAATA	5364	TGCAGGACCAGAGAATTCTGAATA	5604
CATCGCACTNNNCTAGCGTTAC		CACCCCTTCAANNNCTAGCGTTAC		CATTTCCCTTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5125	TGCAGGACCAGAGAATTCTGAATA	5365	TGCAGGACCAGAGAATTCTGAATA	5605
CATTCCGTCTNNNCTAGCGTTAC		CAGCGCGGTNNNCTAGCGTTAC		CACGAGACTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5126	TGCAGGACCAGAGAATTCTGAATA	5366	TGCAGGACCAGAGAATTCTGAATA	5606
CAACGAGGATNNNCTAGCGTTAC		CACCTTCTAGCANNNCTAGCGTTAC		CAAACTAGAAANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5127	TGCAGGACCAGAGAATTCTGAATA	5367	TGCAGGACCAGAGAATTCTGAATA	5607
CAGTAGATGNNNCTAGCGTTAC		CAGTGTAAAANNNCTAGCGTTAC		CACCTCGACTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5128	TGCAGGACCAGAGAATTCTGAATA	5368	TGCAGGACCAGAGAATTCTGAATA	5608
CACCACACTNNNCTAGCGTTAC		CAACTATGCGNNNCTAGCGTTAC		CAGTGAAGACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5129	TGCAGGACCAGAGAATTCTGAATA	5369	TGCAGGACCAGAGAATTCTGAATA	5609
CAGTTTGGANNNCTAGCGTTAC		CACGCCAGACNNNCTAGCGTTAC		CAACGTTACGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5130	TGCAGGACCAGAGAATTCTGAATA	5370	TGCAGGACCAGAGAATTCTGAATA	5610
CAACGGTATCANNNCTAGCGTTAC		CAATCAGTGCNNNCTAGCGTTAC		CACGTCTGCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5131	TGCAGGACCAGAGAATTCTGAATA	5371	TGCAGGACCAGAGAATTCTGAATA	5611
CAATGATAGANNNCTAGCGTTAC		CAGTTCTACNNNCTAGCGTTAC		CAACTCCTACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5132	TGCAGGACCAGAGAATTCTGAATA	5372	TGCAGGACCAGAGAATTCTGAATA	5612
CACAATAACTNNNCTAGCGTTAC		CACACCATAGNNNCTAGCGTTAC		CAGTTAGGTCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5133	TGCAGGACCAGAGAATTCTGAATA	5373	TGCAGGACCAGAGAATTCTGAATA	5613
CAGATCCTAGANNNCTAGCGTTAC		CACAAGATANNNCTAGCGTTAC		CACCTCATGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5134	TGCAGGACCAGAGAATTCTGAATA	5374	TGCAGGACCAGAGAATTCTGAATA	5614
CAATTACCCNNNCTAGCGTTAC		CACAAGGCTTNNNCTAGCGTTAC		CATATTACCCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5135	TGCAGGACCAGAGAATTCTGAATA	5375	TGCAGGACCAGAGAATTCTGAATA	5615
CAGTGTGCGGNNNCTAGCGTTAC		CAGTCCGTAGNNNCTAGCGTTAC		CACCTTCACTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5136	TGCAGGACCAGAGAATTCTGAATA	5376	TGCAGGACCAGAGAATTCTGAATA	5616
CATATGTGTANNNCTAGCGTTAC		CAAAAGTTCGNNNCTAGCGTTAC		CAGGACTAGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5137	TGCAGGACCAGAGAATTCTGAATA	5377	TGCAGGACCAGAGAATTCTGAATA	5617
CAGCTCCTTANNNCTAGCGTTAC		CAATGGCTGTNNNCTAGCGTTAC		CAGTGGCAAAANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5138	TGCAGGACCAGAGAATTCTGAATA	5378	TGCAGGACCAGAGAATTCTGAATA	5618
CAAAAAGCGCANNNCTAGCGTTAC		CAATTCTATCANNNCTAGCGTTAC		CAAAATAAACGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5139	TGCAGGACCAGAGAATTCTGAATA	5379	TGCAGGACCAGAGAATTCTGAATA	5619
CATGGTATATNNNCTAGCGTTAC		CAGGTAGCAANNNCTAGCGTTAC		CAGTATACCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5140	TGCAGGACCAGAGAATTCTGAATA	5380	TGCAGGACCAGAGAATTCTGAATA	5620
CACATCAGCANNNCTAGCGTTAC		CATGGTGACTNNNCTAGCGTTAC		CACCAAAATTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5141	TGCAGGACCAGAGAATTCTGAATA	5381	TGCAGGACCAGAGAATTCTGAATA	5621
CACCTCATTCGNNNCTAGCGTTAC		CATCCTAATTNNNCTAGCGTTAC		CATTCTTTAGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5142	TGCAGGACCAGAGAATTCTGAATA	5382	TGCAGGACCAGAGAATTCTGAATA	5622
CAGGCGCATCANNNCTAGCGTTAC		CAGCCCGCGCANNNCTAGCGTTAC		CATGTTTCGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5143	TGCAGGACCAGAGAATTCTGAATA	5383	TGCAGGACCAGAGAATTCTGAATA	5623
CAAAAGATTGNNNCTAGCGTTAC		CACCCGCAAGNNNCTAGCGTTAC		CACCGGCTCTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5144	TGCAGGACCAGAGAATTCTGAATA	5384	TGCAGGACCAGAGAATTCTGAATA	5624
CATGAAAGATNNNCTAGCGTTAC		CATCCCTGGCANNNCTAGCGTTAC		CACGAGTGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5145	TGCAGGACCAGAGAATTCTGAATA	5385	TGCAGGACCAGAGAATTCTGAATA	5625
CACAGGCTTANNNCTAGCGTTAC		CAGATCCCTTNNNCTAGCGTTAC		CAGCGGTATTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5146	TGCAGGACCAGAGAATTCTGAATA	5386	TGCAGGACCAGAGAATTCTGAATA	5626
CACGAATTGNNNCTAGCGTTAC		CATAGATGAANNNCTAGCGTTAC		CAAAGTCTCGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATA	5147	TGCAGGACCAGAGAATTCTGAATA	5387	TGCAGGACCAGAGAATTCTGAATA	5627
CATAACCAACGNNNCTAGCGTTAC		CAAGGCAAGTNNNCTAGCGTTAC		CAGTAGCAAGNNNCTAGCGTTAC	

FIG. 19D

Pool-22	SEQ ID NO:	Pool-23	SEQ ID NO:	Pool-24	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA	5148	TGCAGGACCAGAGAATTCGAATA	5388	TGCAGGACCAGAGAATTCGAATA	5628
CAAGCAGGTANNNNCTAGCGTTAC		CATAATCTGANNNCTAGCGTTAC		CACGGAGAGCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5149	TGCAGGACCAGAGAATTCGAATA	5389	TGCAGGACCAGAGAATTCGAATA	5629
CACACAAGGANNNNCTAGCGTTAC		CAGGCCAAAANNNNCTAGCGTTAC		CAGCTTTTGCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5150	TGCAGGACCAGAGAATTCGAATA	5390	TGCAGGACCAGAGAATTCGAATA	5630
CAACTAGCCANNNNCTAGCGTTAC		CAAAGCGCTCTNNNNCTAGCGTTAC		CATATGTAGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5151	TGCAGGACCAGAGAATTCGAATA	5391	TGCAGGACCAGAGAATTCGAATA	5631
CACACCTGGCANNNNCTAGCGTTAC		CACATGGCCGNNNNCTAGCGTTAC		CAATCTCTCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5152	TGCAGGACCAGAGAATTCGAATA	5392	TGCAGGACCAGAGAATTCGAATA	5632
CACCACTCGGNNNNCTAGCGTTAC		CAGGAAGATCANNNNCTAGCGTTAC		CAGTGTITCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5153	TGCAGGACCAGAGAATTCGAATA	5393	TGCAGGACCAGAGAATTCGAATA	5633
CACACCCCTGNNNNCTAGCGTTAC		CATCAGCTAGNNNNCTAGCGTTAC		CACGTAGTACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5154	TGCAGGACCAGAGAATTCGAATA	5394	TGCAGGACCAGAGAATTCGAATA	5634
CACAAATACATNNNNCTAGCGTTAC		CACCTGCTAAGNNNNCTAGCGTTAC		CAGCGGAATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5155	TGCAGGACCAGAGAATTCGAATA	5395	TGCAGGACCAGAGAATTCGAATA	5635
CACTGCATAGNNNNCTAGCGTTAC		CACACTTGGANNNNCTAGCGTTAC		CATAATTCAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5156	TGCAGGACCAGAGAATTCGAATA	5396	TGCAGGACCAGAGAATTCGAATA	5636
CAGTGAAANNNNNCTAGCGTTAC		CACCTCGAATGNNNNCTAGCGTTAC		CACGCGCGCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5157	TGCAGGACCAGAGAATTCGAATA	5397	TGCAGGACCAGAGAATTCGAATA	5637
CAGTCCATTCTNNNNCTAGCGTTAC		CACGCTTAAAGNNNNCTAGCGTTAC		CACGAAGAGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5158	TGCAGGACCAGAGAATTCGAATA	5398	TGCAGGACCAGAGAATTCGAATA	5638
CATTAGTGGCANNNNCTAGCGTTAC		CAATATTGTGNNNNCTAGCGTTAC		CAAGCGGTGTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5159	TGCAGGACCAGAGAATTCGAATA	5399	TGCAGGACCAGAGAATTCGAATA	5639
CAACTGGCATNNNNCTAGCGTTAC		CATTTCACGANNNNCTAGCGTTAC		CACGAAGCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5160	TGCAGGACCAGAGAATTCGAATA	5400	TGCAGGACCAGAGAATTCGAATA	5640
CAATGGTTGCGNNNNCTAGCGTTAC		CATTCCATCGNNNNCTAGCGTTAC		CAGTCTACCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5161	TGCAGGACCAGAGAATTCGAATA	5401	TGCAGGACCAGAGAATTCGAATA	5641
CATGGCTCCGNNNNCTAGCGTTAC		CAATGAGCCNNNNCTAGCGTTAC		CACATGCGGCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5162	TGCAGGACCAGAGAATTCGAATA	5402	TGCAGGACCAGAGAATTCGAATA	5642
CAGATTTTCTNNNNCTAGCGTTAC		CAATCAGTCGNNNNCTAGCGTTAC		CATGACCGCGCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5163	TGCAGGACCAGAGAATTCGAATA	5403	TGCAGGACCAGAGAATTCGAATA	5643
CAGCCTACAANNNNCTAGCGTTAC		CACCTCTGAAGNNNNCTAGCGTTAC		CAACTTTAGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5164	TGCAGGACCAGAGAATTCGAATA	5404	TGCAGGACCAGAGAATTCGAATA	5644
CAGGATTCACNNNNCTAGCGTTAC		CAAAAGTATGANNNNCTAGCGTTAC		CAAGCTCGCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5165	TGCAGGACCAGAGAATTCGAATA	5405	TGCAGGACCAGAGAATTCGAATA	5645
CAATTGCGAGNNNNCTAGCGTTAC		CATCAACCTCANNNNCTAGCGTTAC		CAAGAGATCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5166	TGCAGGACCAGAGAATTCGAATA	5406	TGCAGGACCAGAGAATTCGAATA	5646
CACGGCTACGNNNNCTAGCGTTAC		CAGCTAATGCGNNNNCTAGCGTTAC		CACCTCAATGCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5167	TGCAGGACCAGAGAATTCGAATA	5407	TGCAGGACCAGAGAATTCGAATA	5647
CAATCCTAGGNNNNCTAGCGTTAC		CATATTGGCGNNNNCTAGCGTTAC		CATATTCCGCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5168	TGCAGGACCAGAGAATTCGAATA	5408	TGCAGGACCAGAGAATTCGAATA	5648
CATCGTACCTNNNNCTAGCGTTAC		CATACTATCTNNNNCTAGCGTTAC		CATTCACTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCGAATA	5169	TGCAGGACCAGAGAATTCGAATA	5409	TGCAGGACCAGAGAATTCGAATA	5649
CACATCTAAANNNGATCGACATG		CAGACTCGGCGNNNGATCGACATG		CACCTGTGTACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5170	TGCAGGACCAGAGAATTCGAATA	5410	TGCAGGACCAGAGAATTCGAATA	5650
CAAGTGAACGNNNGATCGACATG		CAGCTGTATGNNNGATCGACATG		CATTGATTTCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5171	TGCAGGACCAGAGAATTCGAATA	5411	TGCAGGACCAGAGAATTCGAATA	5651
CACCTGAACTGNNNGATCGACATG		CAAAATTGCTNNNGATCGACATG		CAGCAGATACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5172	TGCAGGACCAGAGAATTCGAATA	5412	TGCAGGACCAGAGAATTCGAATA	5652
CAGATACGAGNNNGATCGACATG		CAACATGTTANNNGATCGACATG		CAGCTTGTGANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5173	TGCAGGACCAGAGAATTCGAATA	5413	TGCAGGACCAGAGAATTCGAATA	5653
CATTTCCTAANNNGATCGACATG		CAAGATGGACNNNGATCGACATG		CATACGGTACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5174	TGCAGGACCAGAGAATTCGAATA	5414	TGCAGGACCAGAGAATTCGAATA	5654
CATAGTCTTTNNNGATCGACATG		CATGTCTCCANNNGATCGACATG		CACACGGTCCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5175	TGCAGGACCAGAGAATTCGAATA	5415	TGCAGGACCAGAGAATTCGAATA	5655
CAAGTTGCCANNNGATCGACATG		CATTGGCTAGNNNGATCGACATG		CACCAAGGTTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5176	TGCAGGACCAGAGAATTCGAATA	5416	TGCAGGACCAGAGAATTCGAATA	5656
CAAGCGACAANNNGATCGACATG		CATAATTTCCNNNGATCGACATG		CAGTTTCGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5177	TGCAGGACCAGAGAATTCGAATA	5417	TGCAGGACCAGAGAATTCGAATA	5657
CAGGATAAATNNNGATCGACATG		CAGTGTTAATNNNGATCGACATG		CAACGCGAGCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5178	TGCAGGACCAGAGAATTCGAATA	5418	TGCAGGACCAGAGAATTCGAATA	5658
CATTTGAAACNNNGATCGACATG		CATGAGCAAGNNNGATCGACATG		CACCCCGAGANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5179	TGCAGGACCAGAGAATTCGAATA	5419	TGCAGGACCAGAGAATTCGAATA	5659
CAGAGGATACNNNGATCGACATG		CACGCCCCCTANNNGATCGACATG		CACCTCCATGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5180	TGCAGGACCAGAGAATTCGAATA	5420	TGCAGGACCAGAGAATTCGAATA	5660
CAACTGGATCANNNGATCGACATG		CAGTCACAGTNNNGATCGACATG		CATTTGCACCCNNNGATCGACATG	

FIG. 19E

Poel-22	SEQ ID NO:	Poel-23	SEQ ID NO:	Poel-24	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA	5181	TGCAGGACCAGAGAATTCGAATA	5421	TGCAGGACCAGAGAATTCGAATA	5661
CAAAATGGATNNNGATCGACATG		CAGTTGGTGTNNNGATCGACATG		CAATTACAACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5182	TGCAGGACCAGAGAATTCGAATA	5422	TGCAGGACCAGAGAATTCGAATA	5662
CACGCATGATNNNGATCGACATG		CACTTATTACNNNGATCGACATG		CATGCCACCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5183	TGCAGGACCAGAGAATTCGAATA	5423	TGCAGGACCAGAGAATTCGAATA	5663
CATACGAATTNNNGATCGACATG		CACCTCGCAAANNNGATCGACATG		CAGATTGGAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5184	TGCAGGACCAGAGAATTCGAATA	5424	TGCAGGACCAGAGAATTCGAATA	5664
CAGGAAAGCTNNNGATCGACATG		CACTAGGTGTNNNGATCGACATG		CATCATACCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5185	TGCAGGACCAGAGAATTCGAATA	5425	TGCAGGACCAGAGAATTCGAATA	5665
CACCAACAACNNNGATCGACATG		CACAACATACNNNGATCGACATG		CAGGTGGATNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5186	TGCAGGACCAGAGAATTCGAATA	5426	TGCAGGACCAGAGAATTCGAATA	5666
CAACCGGACCCNNNGATCGACATG		CAACCGATTACNNNGATCGACATG		CAGACATTCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5187	TGCAGGACCAGAGAATTCGAATA	5427	TGCAGGACCAGAGAATTCGAATA	5667
CAGGAGTCCCNNGATCGACATG		CACCGACTGGNNNGATCGACATG		CAATCTCGANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5188	TGCAGGACCAGAGAATTCGAATA	5428	TGCAGGACCAGAGAATTCGAATA	5668
CACCACGCGAGNNNGATCGACATG		CACAACGCATTNNNGATCGACATG		CAGGCCACCCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5189	TGCAGGACCAGAGAATTCGAATA	5429	TGCAGGACCAGAGAATTCGAATA	5669
CAACTCGCCCNNGATCGACATG		CATTTAATTNNNGATCGACATG		CAAAATGTTTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5190	TGCAGGACCAGAGAATTCGAATA	5430	TGCAGGACCAGAGAATTCGAATA	5670
CACCTGAAGAGNNNGATCGACATG		CAAGTGTATTNNNGATCGACATG		CAACCTGGTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5191	TGCAGGACCAGAGAATTCGAATA	5431	TGCAGGACCAGAGAATTCGAATA	5671
CAGGAGCACGNNNGATCGACATG		CAACTTCAGGNNNGATCGACATG		CAACTGAGAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5192	TGCAGGACCAGAGAATTCGAATA	5432	TGCAGGACCAGAGAATTCGAATA	5672
CAGGAGCGACNNNGATCGACATG		CAAGGCCGCCNNNGATCGACATG		CAGAATTAAAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5193	TGCAGGACCAGAGAATTCGAATA	5433	TGCAGGACCAGAGAATTCGAATA	5673
CAGGAACCTTNNNGATCGACATG		CACCACGGTGNNGATCGACATG		CAATTACGCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5194	TGCAGGACCAGAGAATTCGAATA	5434	TGCAGGACCAGAGAATTCGAATA	5674
CAGCCCTGTNNNGATCGACATG		CAGGCTCTTNNNGATCGACATG		CACAGTCTAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5195	TGCAGGACCAGAGAATTCGAATA	5435	TGCAGGACCAGAGAATTCGAATA	5675
CAAGTAATCTNNNGATCGACATG		CACCTTAGCTNNNGATCGACATG		CAATCCCTTGNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5196	TGCAGGACCAGAGAATTCGAATA	5436	TGCAGGACCAGAGAATTCGAATA	5676
CACGCTCGAGNNNGATCGACATG		CAATTAGCATNNNGATCGACATG		CATGTCCACTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5197	TGCAGGACCAGAGAATTCGAATA	5437	TGCAGGACCAGAGAATTCGAATA	5677
CAGTCATGGTNNNGATCGACATG		CAGCAGCTTANNNGATCGACATG		CAGGTACGCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5198	TGCAGGACCAGAGAATTCGAATA	5438	TGCAGGACCAGAGAATTCGAATA	5678
CAGATTCCAGNNNGATCGACATG		CAACATACGCCNNNGATCGACATG		CATGAGCAGANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5199	TGCAGGACCAGAGAATTCGAATA	5439	TGCAGGACCAGAGAATTCGAATA	5679
CACTATTACTNNNGATCGACATG		CAGTCGAAAGNNNGATCGACATG		CAGATCCGTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5200	TGCAGGACCAGAGAATTCGAATA	5440	TGCAGGACCAGAGAATTCGAATA	5680
CAAGGTCTACNNNGATCGACATG		CATTCCTAGTTNNNGATCGACATG		CATCAGTAANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5201	TGCAGGACCAGAGAATTCGAATA	5441	TGCAGGACCAGAGAATTCGAATA	5681
CACCTGTAGANNNGATCGACATG		CACACGCTCCNNNGATCGACATG		CAAAATAGATGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5202	TGCAGGACCAGAGAATTCGAATA	5442	TGCAGGACCAGAGAATTCGAATA	5682
CATCCTGTCAANNNGATCGACATG		CACCGAGGTCCNNNGATCGACATG		CATCGCGCTCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5203	TGCAGGACCAGAGAATTCGAATA	5443	TGCAGGACCAGAGAATTCGAATA	5683
CACCCCTGCGTNNNGATCGACATG		CACATTTCAGGNNNGATCGACATG		CAACCGACGCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5204	TGCAGGACCAGAGAATTCGAATA	5444	TGCAGGACCAGAGAATTCGAATA	5684
CAACAATGAANNNGATCGACATG		CATCCATAGGNNNGATCGACATG		CACACGGACCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5205	TGCAGGACCAGAGAATTCGAATA	5445	TGCAGGACCAGAGAATTCGAATA	5685
CAGGTGGAGCANNNGATCGACATG		CATTACTCATNNNGATCGACATG		CAATATCGATNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5206	TGCAGGACCAGAGAATTCGAATA	5446	TGCAGGACCAGAGAATTCGAATA	5686
CAGGATAGACNNNGATCGACATG		CAATCTGATANNNGATCGACATG		CATACCACGANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5207	TGCAGGACCAGAGAATTCGAATA	5447	TGCAGGACCAGAGAATTCGAATA	5687
CAGAGTGCCCNNGATCGACATG		CAGTCCACTTNNNGATCGACATG		CAAAGAACGCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5208	TGCAGGACCAGAGAATTCGAATA	5448	TGCAGGACCAGAGAATTCGAATA	5688
CAAAACGGTGNNGATCGACATG		CACAGGAACANNNGATCGACATG		CAAGTACCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5209	TGCAGGACCAGAGAATTCGAATA	5449	TGCAGGACCAGAGAATTCGAATA	5689
CAAATAGCAANNNGATCGACATG		CACCTAGCTTCCNNNGATCGACATG		CAGTTTGTAGANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5210	TGCAGGACCAGAGAATTCGAATA	5450	TGCAGGACCAGAGAATTCGAATA	5690
CATCAATTGANNNGATCGACATG		CATTTGGCGANNNGATCGACATG		CAGGATTTTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5211	TGCAGGACCAGAGAATTCGAATA	5451	TGCAGGACCAGAGAATTCGAATA	5691
CAAGCAATGGNNNGATCGACATG		CACCGGAAGGNNNGATCGACATG		CATAGTATACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5212	TGCAGGACCAGAGAATTCGAATA	5452	TGCAGGACCAGAGAATTCGAATA	5692
CAGTAGTGAGNNNGATCGACATG		CATCCCACTNNNGATCGACATG		CACGTATGGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATA	5213	TGCAGGACCAGAGAATTCGAATA	5453	TGCAGGACCAGAGAATTCGAATA	5693
CACACTGCGGNNNGATCGACATG		CATTTCAGGANNNGATCGACATG		CATCCCGGCTNNNGATCGACATG	

FIG. 19F

Poel-22	SEQ ID NO:	Poel-23	SEQ ID NO:	Poel-24	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA	5214	TGCAGGACCAGAGAATTGGAATA	5454	TGCAGGACCAGAGAATTGGAATA	5694
CAACCGCTCCNNNGATCGACATG		CAATTTTACNNNGATCGACATG		CAGCGCTCTCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5215	TGCAGGACCAGAGAATTGGAATA	5455	TGCAGGACCAGAGAATTGGAATA	5695
CACTAGGTTGNNNGATCGACATG		CATGGAGTCTNNNGATCGACATG		CACATTCCCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5216	TGCAGGACCAGAGAATTGGAATA	5456	TGCAGGACCAGAGAATTGGAATA	5696
CATAAAATAANNNGATCGACATG		CACGACGCCNNNGATCGACATG		CATCGCCCCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5217	TGCAGGACCAGAGAATTGGAATA	5457	TGCAGGACCAGAGAATTGGAATA	5697
CAGTCAAGTANNNGATCGACATG		CATCCCATACNNNGATCGACATG		CATGCATTGGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5218	TGCAGGACCAGAGAATTGGAATA	5458	TGCAGGACCAGAGAATTGGAATA	5698
CAGGTTTTCATNNNGATCGACATG		CAGCCCTTATNNNGATCGACATG		CAATCAGATTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5219	TGCAGGACCAGAGAATTGGAATA	5459	TGCAGGACCAGAGAATTGGAATA	5699
CACAATGGAGNNNGATCGACATG		CAGTCCCGCTNNNGATCGACATG		CACTTTATGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5220	TGCAGGACCAGAGAATTGGAATA	5460	TGCAGGACCAGAGAATTGGAATA	5700
CACCGAGCGTNNNGATCGACATG		CACGCGCTTNNNGATCGACATG		CAAAAGTCCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5221	TGCAGGACCAGAGAATTGGAATA	5461	TGCAGGACCAGAGAATTGGAATA	5701
CACAAACGAGNNNGATCGACATG		CATCAGCTCTNNNGATCGACATG		CAACGAGTGANNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5222	TGCAGGACCAGAGAATTGGAATA	5462	TGCAGGACCAGAGAATTGGAATA	5702
CAGATATGTTNNNGATCGACATG		CAGGCTCGGTNNNGATCGACATG		CAGAATATGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5223	TGCAGGACCAGAGAATTGGAATA	5463	TGCAGGACCAGAGAATTGGAATA	5703
CAGTTCTGTNNNGATCGACATG		CAAGATTGCGNNNGATCGACATG		CAATTATCTCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5224	TGCAGGACCAGAGAATTGGAATA	5464	TGCAGGACCAGAGAATTGGAATA	5704
CATCTTTTCTNNNGATCGACATG		CAACCGCGCANNNGATCGACATG		CAGCTCGGCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5225	TGCAGGACCAGAGAATTGGAATA	5465	TGCAGGACCAGAGAATTGGAATA	5705
CAAAAGACATNNNGATCGACATG		CATTAATCTCNNNGATCGACATG		CAGTTAGAGGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5226	TGCAGGACCAGAGAATTGGAATA	5466	TGCAGGACCAGAGAATTGGAATA	5706
CAACCCATGANNNNGATCGACATG		CATTCAAGATNNNGATCGACATG		CAACGAGTANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5227	TGCAGGACCAGAGAATTGGAATA	5467	TGCAGGACCAGAGAATTGGAATA	5707
CATCCTCACANNNGATCGACATG		CACTCAGTTCTNNNGATCGACATG		CAGGAGTGCNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5228	TGCAGGACCAGAGAATTGGAATA	5468	TGCAGGACCAGAGAATTGGAATA	5708
CATTGAGGTCTNNNGATCGACATG		CAAGAATTGNNNGATCGACATG		CATCGATATANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5229	TGCAGGACCAGAGAATTGGAATA	5469	TGCAGGACCAGAGAATTGGAATA	5709
CAGCGTACTANNNGATCGACATG		CAGACTACANNNGATCGACATG		CAGCGGTAGCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5230	TGCAGGACCAGAGAATTGGAATA	5470	TGCAGGACCAGAGAATTGGAATA	5710
CAAGGTTAGGNNNGATCGACATG		CACAGCTTAANNNGATCGACATG		CAGTGAATTAANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5231	TGCAGGACCAGAGAATTGGAATA	5471	TGCAGGACCAGAGAATTGGAATA	5711
CACTCCACATNNNGATCGACATG		CAAGTCAATANNNGATCGACATG		CACACITCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5232	TGCAGGACCAGAGAATTGGAATA	5472	TGCAGGACCAGAGAATTGGAATA	5712
CACGATCTAGNNNGATCGACATG		CATCAGGACNNNGATCGACATG		CATAGGCGTTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5233	TGCAGGACCAGAGAATTGGAATA	5473	TGCAGGACCAGAGAATTGGAATA	5713
CATCGATAATNNNGATCGACATG		CAAGAATCTNNNGATCGACATG		CAATATGTCANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5234	TGCAGGACCAGAGAATTGGAATA	5474	TGCAGGACCAGAGAATTGGAATA	5714
CACCAAGGCGNNNGATCGACATG		CAACCACTGANNNNGATCGACATG		CAGTCAATGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5235	TGCAGGACCAGAGAATTGGAATA	5475	TGCAGGACCAGAGAATTGGAATA	5715
CAGTGGAAATGNNNGATCGACATG		CAACACGATCANNNGATCGACATG		CAATAGAGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5236	TGCAGGACCAGAGAATTGGAATA	5476	TGCAGGACCAGAGAATTGGAATA	5716
CAAAAAATGCGNNNGATCGACATG		CAGTTACAGNNNGATCGACATG		CAGACTAAGGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5237	TGCAGGACCAGAGAATTGGAATA	5477	TGCAGGACCAGAGAATTGGAATA	5717
CAGACTAGTCTNNNGATCGACATG		CACGCTACCCNNNGATCGACATG		CACCTACCTANNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5238	TGCAGGACCAGAGAATTGGAATA	5478	TGCAGGACCAGAGAATTGGAATA	5718
CACGTAGAAGNNNGATCGACATG		CAAGAGGTACNNNGATCGACATG		CATAGGAGACNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5239	TGCAGGACCAGAGAATTGGAATA	5479	TGCAGGACCAGAGAATTGGAATA	5719
CAGTGTGAAGNNNGATCGACATG		CAAAATCTCTNNNGATCGACATG		CACCGTCATTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5240	TGCAGGACCAGAGAATTGGAATA	5480	TGCAGGACCAGAGAATTGGAATA	5720
CAAAGTACTTTNNNGATCGACATG		CAATATTTAANNNGATCGACATG		CAGTGTTCAGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5241	TGCAGGACCAGAGAATTGGAATA	5481	TGCAGGACCAGAGAATTGGAATA	5721
CACGAACGTTNNNGATCGACATG		CATATCGAATNNNGATCGACATG		CAAGCGGTTTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5242	TGCAGGACCAGAGAATTGGAATA	5482	TGCAGGACCAGAGAATTGGAATA	5722
CAATTGCTGGNNNGATCGACATG		CAGCTAAATTTNNNGATCGACATG		CAAACTCTTTNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5243	TGCAGGACCAGAGAATTGGAATA	5483	TGCAGGACCAGAGAATTGGAATA	5723
CATGTGTGTGNNNGATCGACATG		CATTTACGCCNNNGATCGACATG		CATAACGTATNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5244	TGCAGGACCAGAGAATTGGAATA	5484	TGCAGGACCAGAGAATTGGAATA	5724
CAACATCTTTNNNGATCGACATG		CAGTTACAGNNNGATCGACATG		CAAAAGGACTGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5245	TGCAGGACCAGAGAATTGGAATA	5485	TGCAGGACCAGAGAATTGGAATA	5725
CACGATGCTANNNGATCGACATG		CAGCATTCCTNNNGATCGACATG		CAAGGAGAAGNNNGATCGACATG	
TGCAGGACCAGAGAATTGGAATA	5246	TGCAGGACCAGAGAATTGGAATA	5486	TGCAGGACCAGAGAATTGGAATA	5726
CATAGTCCAGNNNGATCGACATG		CATTACACCCNNNGATCGACATG		CATCGAACGTNNNGATCGACATG	

FIG. 19G

Poel-22	SEQ ID NO:	Poel-23	SEQ ID NO:	Poel-24	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA	5247	TGCAGGACCAGAGAATTGGAATA	5487	TGCAGGACCAGAGAATTGGAATA	5727
CACAGTAATTNNNTGCATCAGGT		CATATTTTATNNNTGCATCAGGT		CACGGACATTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5248	TGCAGGACCAGAGAATTGGAATA	5488	TGCAGGACCAGAGAATTGGAATA	5728
CAAAGGTGGTNNNTGCATCAGGT		CATGTCCGCCNNNTGCATCAGGT		CATTCCGCATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5249	TGCAGGACCAGAGAATTGGAATA	5489	TGCAGGACCAGAGAATTGGAATA	5729
CACGGTGGTNNNTGCATCAGGT		CAAACCCGTTNNNTGCATCAGGT		CACGGGCTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5250	TGCAGGACCAGAGAATTGGAATA	5490	TGCAGGACCAGAGAATTGGAATA	5730
CAGTGGTTGTNNNTGCATCAGGT		CAGTACCGATNNNTGCATCAGGT		CAGTTTCTGCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5251	TGCAGGACCAGAGAATTGGAATA	5491	TGCAGGACCAGAGAATTGGAATA	5731
CATGTATTTCTNNNTGCATCAGGT		CACGGTTCCNNNTGCATCAGGT		CAAGACAGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5252	TGCAGGACCAGAGAATTGGAATA	5492	TGCAGGACCAGAGAATTGGAATA	5732
CATAAGTCGCNNNTGCATCAGGT		CACCTCAATCNNNTGCATCAGGT		CAGACCCCTCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5253	TGCAGGACCAGAGAATTGGAATA	5493	TGCAGGACCAGAGAATTGGAATA	5733
CATAGGAGCANNNTGCATCAGGT		CACCGCAGACNNNTGCATCAGGT		CATACTCGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5254	TGCAGGACCAGAGAATTGGAATA	5494	TGCAGGACCAGAGAATTGGAATA	5734
CACATAAATCNNNTGCATCAGGT		CACGCTTAGANNNTGCATCAGGT		CATTCTGATTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5255	TGCAGGACCAGAGAATTGGAATA	5495	TGCAGGACCAGAGAATTGGAATA	5735
CAAGCTGTACNNNTGCATCAGGT		CAGAAAGCCNNNTGCATCAGGT		CATACTTAAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5256	TGCAGGACCAGAGAATTGGAATA	5496	TGCAGGACCAGAGAATTGGAATA	5736
CATTGCGCTTNNNTGCATCAGGT		CACCTCATCCANNNTGCATCAGGT		CAGACTACGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5257	TGCAGGACCAGAGAATTGGAATA	5497	TGCAGGACCAGAGAATTGGAATA	5737
CAAGGCGTGGNNNTGCATCAGGT		CAAGAGATATNNNTGCATCAGGT		CAACGAGTCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5258	TGCAGGACCAGAGAATTGGAATA	5498	TGCAGGACCAGAGAATTGGAATA	5738
CAGTCTAGGTNNNTGCATCAGGT		CAATTTGTCCANNNTGCATCAGGT		CAGATCGTTGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5259	TGCAGGACCAGAGAATTGGAATA	5499	TGCAGGACCAGAGAATTGGAATA	5739
CATCCGTAAGNNNTGCATCAGGT		CAATAATACCCNNNTGCATCAGGT		CAGATGGACANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5260	TGCAGGACCAGAGAATTGGAATA	5500	TGCAGGACCAGAGAATTGGAATA	5740
CATATCGGCANNNTGCATCAGGT		CAATTTTGGNNNTGCATCAGGT		CATCGTAGTGNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5261	TGCAGGACCAGAGAATTGGAATA	5501	TGCAGGACCAGAGAATTGGAATA	5741
CAATCATCGNNNTGCATCAGGT		CAGCAGAGTNNNTGCATCAGGT		CACCACATCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5262	TGCAGGACCAGAGAATTGGAATA	5502	TGCAGGACCAGAGAATTGGAATA	5742
CAACGTCTGANNNTGCATCAGGT		CATTAAACCCANNNTGCATCAGGT		CAGTGTACANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5263	TGCAGGACCAGAGAATTGGAATA	5503	TGCAGGACCAGAGAATTGGAATA	5743
CAACGGTACTNNNTGCATCAGGT		CAATGGAGACNNNTGCATCAGGT		CATTCTTCAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5264	TGCAGGACCAGAGAATTGGAATA	5504	TGCAGGACCAGAGAATTGGAATA	5744
CATGCAAGGANNNTGCATCAGGT		CAAAGAGCCNNNTGCATCAGGT		CATTAGAGTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5265	TGCAGGACCAGAGAATTGGAATA	5505	TGCAGGACCAGAGAATTGGAATA	5745
CAAGAGCTCACNNNTGCATCAGGT		CAATCCGAACNNNTGCATCAGGT		CAAGAGCCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5266	TGCAGGACCAGAGAATTGGAATA	5506	TGCAGGACCAGAGAATTGGAATA	5746
CACAATCAGCANNNTGCATCAGGT		CAGTTAGGAGNNNTGCATCAGGT		CAGGAGCTCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5267	TGCAGGACCAGAGAATTGGAATA	5507	TGCAGGACCAGAGAATTGGAATA	5747
CATGGCTGTANNNTGCATCAGGT		CATGGCCAGCANNNTGCATCAGGT		CAATTAACCCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5268	TGCAGGACCAGAGAATTGGAATA	5508	TGCAGGACCAGAGAATTGGAATA	5748
CAGTTTACCCNNNTGCATCAGGT		CAATGTGCACNNNTGCATCAGGT		CAATCGAGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5269	TGCAGGACCAGAGAATTGGAATA	5509	TGCAGGACCAGAGAATTGGAATA	5749
CACGTCACTANNNTGCATCAGGT		CAGTACAACCCNNNTGCATCAGGT		CAGGAAACGTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5270	TGCAGGACCAGAGAATTGGAATA	5510	TGCAGGACCAGAGAATTGGAATA	5750
CACGACGGAGNNNTGCATCAGGT		CAGTGGCCAGNNNTGCATCAGGT		CATGAAGAGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5271	TGCAGGACCAGAGAATTGGAATA	5511	TGCAGGACCAGAGAATTGGAATA	5751
CAATATGCGCANNNTGCATCAGGT		CAAGCTCTCTNNNTGCATCAGGT		CAATCCGGATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5272	TGCAGGACCAGAGAATTGGAATA	5512	TGCAGGACCAGAGAATTGGAATA	5752
CAGCTGGCCANNNTGCATCAGGT		CAACCTCTGNNNTGCATCAGGT		CAGTTGTCTCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5273	TGCAGGACCAGAGAATTGGAATA	5513	TGCAGGACCAGAGAATTGGAATA	5753
CACGCGTCTCANNNTGCATCAGGT		CATCAGCGTANNNTGCATCAGGT		CATGGATAGGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5274	TGCAGGACCAGAGAATTGGAATA	5514	TGCAGGACCAGAGAATTGGAATA	5754
CAATAAGTGANNNTGCATCAGGT		CATCAGACGTTNNNTGCATCAGGT		CAAAACCCAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5275	TGCAGGACCAGAGAATTGGAATA	5515	TGCAGGACCAGAGAATTGGAATA	5755
CAGACAGTCTNNNTGCATCAGGT		CATATAGATCANNNTGCATCAGGT		CACGGCGACTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5276	TGCAGGACCAGAGAATTGGAATA	5516	TGCAGGACCAGAGAATTGGAATA	5756
CAGCAAGGTANNNTGCATCAGGT		CAACCCGCTNNNTGCATCAGGT		CATTATCGCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5277	TGCAGGACCAGAGAATTGGAATA	5517	TGCAGGACCAGAGAATTGGAATA	5757
CACACGAATNNNTGCATCAGGT		CAGCAGGATANNNTGCATCAGGT		CAAGCCACATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5278	TGCAGGACCAGAGAATTGGAATA	5518	TGCAGGACCAGAGAATTGGAATA	5758
CATACACTGGNNNTGCATCAGGT		CAAGAATGCGNNNTGCATCAGGT		CATGCTCATCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	5279	TGCAGGACCAGAGAATTGGAATA	5519	TGCAGGACCAGAGAATTGGAATA	5759
CAATTTCTGTTNNNTGCATCAGGT		CAACAAGTGGNNNTGCATCAGGT		CAGCTGGAGNNNTGCATCAGGT	

FIG. 19H

Poel-22	SEQ ID NO:	Poel-23	SEQ ID NO:	Poel-24	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CATCTGCGCCNNNTGCATCAGGT	5280	TGCAGGACCAGAGAATTCGAATA CAGTCCGGCANNNTGCATCAGGT	5520	TGCAGGACCAGAGAATTCGAATA CAAAAGATGTNNNTGCATCAGGT	5760
TGCAGGACCAGAGAATTCGAATA CAGGAGCTATNNNTGCATCAGGT	5281	TGCAGGACCAGAGAATTCGAATA CAGCCCTGAGNNNTGCATCAGGT	5521	TGCAGGACCAGAGAATTCGAATA CATCAGAAAANNNTGCATCAGGT	5761
TGCAGGACCAGAGAATTCGAATA CAACGCCATANNNTGCATCAGGT	5282	TGCAGGACCAGAGAATTCGAATA CAAACATATGTNNNTGCATCAGGT	5522	TGCAGGACCAGAGAATTCGAATA CAGTCCTGAANNNTGCATCAGGT	5762
TGCAGGACCAGAGAATTCGAATA CATCCTCTGANNNTGCATCAGGT	5283	TGCAGGACCAGAGAATTCGAATA CATCTGATCCNNNTGCATCAGGT	5523	TGCAGGACCAGAGAATTCGAATA CAGCTAGGCCNNNTGCATCAGGT	5763
TGCAGGACCAGAGAATTCGAATA CAAATTCAGNNNTGCATCAGGT	5284	TGCAGGACCAGAGAATTCGAATA CATAATAGAGNNNTGCATCAGGT	5524	TGCAGGACCAGAGAATTCGAATA CACTCCTGTANNNTGCATCAGGT	5764
TGCAGGACCAGAGAATTCGAATA CACCTCAGCCNNNTGCATCAGGT	5285	TGCAGGACCAGAGAATTCGAATA CAGGCCGTTGNNNTGCATCAGGT	5525	TGCAGGACCAGAGAATTCGAATA CATTGATCAANNNTGCATCAGGT	5765
TGCAGGACCAGAGAATTCGAATA CAACCCCGGANNNTGCATCAGGT	5286	TGCAGGACCAGAGAATTCGAATA CACAAACAAGNNNTGCATCAGGT	5526	TGCAGGACCAGAGAATTCGAATA CACTGTTCGTNNNTGCATCAGGT	5766
TGCAGGACCAGAGAATTCGAATA CAGTGATAGGNNNTGCATCAGGT	5287	TGCAGGACCAGAGAATTCGAATA CACCTGAAANNNTGCATCAGGT	5527	TGCAGGACCAGAGAATTCGAATA CATCTTATCANNNTGCATCAGGT	5767
TGCAGGACCAGAGAATTCGAATA CATTGAATTGNNNTGCATCAGGT	5288	TGCAGGACCAGAGAATTCGAATA CACTGCTGTTNNNTGCATCAGGT	5528	TGCAGGACCAGAGAATTCGAATA CATACTGGCANNNTGCATCAGGT	5768

FIG. 20A

Pool-25	SEQ ID NO:	Pool-26	SEQ ID NO:	Pool-27	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAC	5769	TGCAGGACCAGAGAATTCGAATACAC	6009	TGCAGGACCAGAGAATTCGAATACAT	6249
GGCAGCTNNNACGTATGCCA	5770	TCTGTANNNNACGTATGCCA	6010	GTACGCANNNACGTATGCCA	6250
TGCAGGACCAGAGAATTCGAATACAC	5771	TGCAGGACCAGAGAATTCGAATACAT	6011	TGCAGGACCAGAGAATTCGAATACAG	6251
GCATCAANNNACGTATGCCA	5772	TACATGANNNNACGTATGCCA	6012	ATGTGTNNNACGTATGCCA	6252
TGCAGGACCAGAGAATTCGAATACAG	5773	TGCAGGACCAGAGAATTCGAATACAC	6013	TGCAGGACCAGAGAATTCGAATACAC	6253
GCATCTNNNACGTATGCCA	5774	GAGGATANNNNACGTATGCCA	6014	TAGACTGNNNACGTATGCCA	6254
TGCAGGACCAGAGAATTCGAATACAC	5775	TGCAGGACCAGAGAATTCGAATACAC	6015	TGCAGGACCAGAGAATTCGAATACAG	6255
TAGGAGANNNACGTATGCCA	5776	GACATGTNNNACGTATGCCA	6016	ATCGTGTNNNACGTATGCCA	6256
TGCAGGACCAGAGAATTCGAATACAT	5777	TGCAGGACCAGAGAATTCGAATACAC	6017	TGCAGGACCAGAGAATTCGAATACAT	6257
TGATAACNNNACGTATGCCA	5778	CTTGAAGNNNACGTATGCCA	6018	TATCTCANNNACGTATGCCA	6258
TGCAGGACCAGAGAATTCGAATACAG	5779	TGCAGGACCAGAGAATTCGAATACAC	6019	TGCAGGACCAGAGAATTCGAATACAA	6259
AGTACTCNNNACGTATGCCA	5780	AACGATCNNNACGTATGCCA	6020	ACCCTAGNNNACGTATGCCA	6260
TGCAGGACCAGAGAATTCGAATACAA	5781	TGCAGGACCAGAGAATTCGAATACAG	6021	TGCAGGACCAGAGAATTCGAATACAT	6261
TGCCGCGNNNACGTATGCCA	5782	ACTAGAGNNNACGTATGCCA	6022	ATCATAGNNNACGTATGCCA	6262
TGCAGGACCAGAGAATTCGAATACAA	5783	TGCAGGACCAGAGAATTCGAATACAC	6023	TGCAGGACCAGAGAATTCGAATACAG	6263
AAATAGCANNNACGTATGCCA	5784	GCCGTGANNNACGTATGCCA	6024	GTTCGTNNNACGTATGCCA	6264
TGCAGGACCAGAGAATTCGAATACAA	5785	TGCAGGACCAGAGAATTCGAATACAC	6025	TGCAGGACCAGAGAATTCGAATACAA	6265
TCAGACNNNACGTATGCCA	5786	TGTGACNNNACGTATGCCA	6026	TACAAAGNNNACGTATGCCA	6266
TGCAGGACCAGAGAATTCGAATACAG	5787	TGCAGGACCAGAGAATTCGAATACAA	6027	TGCAGGACCAGAGAATTCGAATACAG	6267
GTGCGTNNNACGTATGCCA	5788	CGAATTTNNNACGTATGCCA	6028	TCCTCATNNNACGTATGCCA	6268
TGCAGGACCAGAGAATTCGAATACAT	5789	TGCAGGACCAGAGAATTCGAATACAA	6029	TGCAGGACCAGAGAATTCGAATACAA	6269
CTTTCCNNNACGTATGCCA	5790	TTGTTTCNNNACGTATGCCA	6030	GTAGCAGNNNACGTATGCCA	6270
TGCAGGACCAGAGAATTCGAATACAA	5791	TGCAGGACCAGAGAATTCGAATACAC	6031	TGCAGGACCAGAGAATTCGAATACAG	6271
AAATTCANNNACGTATGCCA	5792	GGCCTGANNNACGTATGCCA	6032	AAAACATNNNACGTATGCCA	6272
TGCAGGACCAGAGAATTCGAATACAG	5793	TGCAGGACCAGAGAATTCGAATACAC	6033	TGCAGGACCAGAGAATTCGAATACAT	6273
ATGTGCCNNNACGTATGCCA	5794	CCATTATNNNACGTATGCCA	6034	TGCAGGACCAGAGAATTCGAATACAC	6274
TGCAGGACCAGAGAATTCGAATACAC	5795	TGCAGGACCAGAGAATTCGAATACAA	6035	TGCAGGACCAGAGAATTCGAATACAA	6275
ACATGACNNNACGTATGCCA	5796	ATTGCTANNNACGTATGCCA	6036	TGCAGGACCAGAGAATTCGAATACAG	6276
TGCAGGACCAGAGAATTCGAATACAG	5797	TGCAGGACCAGAGAATTCGAATACAC	6037	TGCAGGACCAGAGAATTCGAATACAT	6277
ACCTGGCNNNACGTATGCCA	5798	CGGCCCCNNNACGTATGCCA	6038	TGCAGGACCAGAGAATTCGAATACAG	6278
TGCAGGACCAGAGAATTCGAATACAA	5799	TGCAGGACCAGAGAATTCGAATACAT	6039	TGCAGGACCAGAGAATTCGAATACAA	6279
CGAAATTNNNACGTATGCCA	5800	AGGATGGNNNACGTATGCCA	6040	CCATTAGNNNACGTATGCCA	6280
TGCAGGACCAGAGAATTCGAATACAA		TGCAGGACCAGAGAATTCGAATACAT		TGCAGGACCAGAGAATTCGAATACAC	
GCTGCCGNNNACGTATGCCA		TGGACGTNNNACGTATGCCA		GTTCGTNNNACGTATGCCA	
				TGCAGGACCAGAGAATTCGAATACAT	
				CCGCGCTGNNNACGTATGCCA	
				CTACACTNNNACGTATGCCA	
				TGCAGGACCAGAGAATTCGAATACAA	
				GAAGATTNNNACGTATGCCA	
				GTCCCTCNNNACGTATGCCA	
				TGCAGGACCAGAGAATTCGAATACAG	
				CATTATANNNACGTATGCCA	
				TGCAGGACCAGAGAATTCGAATACAG	
				TGGCATNNNACGTATGCCA	
				ACGTCACNNNACGTATGCCA	
				TGCAGGACCAGAGAATTCGAATACAG	
				TTAACTANNNACGTATGCCA	

FIG. 20B

Pool-25	SEQ ID NO:	Pool-26	SEQ ID NO:	Pool-27	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATACAT	5801	TGCAGGACCAGAGAATTGGAATACAT	6041	TGCAGGACCAGAGAATTGGAATACAT	6281
CACCTCGTNNNNACGTATGCCA		CGTGAGTNNNNACGTATGCCA		AAAGATGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	5802	TGCAGGACCAGAGAATTGGAATACAG	6042	TGCAGGACCAGAGAATTGGAATACAA	6282
TTACCGANNNNACGTATGCCA		GAACCTTCNNNNACGTATGCCA		ATTTCCTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	5803	TGCAGGACCAGAGAATTGGAATACAA	6043	TGCAGGACCAGAGAATTGGAATACAC	6283
TTAGATANNNNACGTATGCCA		TGTGCCANNNNACGTATGCCA		GGCAAANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	5804	TGCAGGACCAGAGAATTGGAATACAC	6044	TGCAGGACCAGAGAATTGGAATACAT	6284
GGCTAGANNNNACGTATGCCA		CGGTGCANNNNACGTATGCCA		CGCACANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	5805	TGCAGGACCAGAGAATTGGAATACAC	6045	TGCAGGACCAGAGAATTGGAATACAA	6285
CACAGGTNNNNACGTATGCCA		TATTGCCNNNNACGTATGCCA		GGTCGCCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	5806	TGCAGGACCAGAGAATTGGAATACAT	6046	TGCAGGACCAGAGAATTGGAATACAG	6286
ATATTTGNNNNACGTATGCCA		TAAGGCCNNNNACGTATGCCA		GATTCGTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	5807	TGCAGGACCAGAGAATTGGAATACAT	6047	TGCAGGACCAGAGAATTGGAATACAA	6287
TGTGTTTNNNNACGTATGCCA		GTTAAACNNNNACGTATGCCA		GCATCTGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	5808	TGCAGGACCAGAGAATTGGAATACAC	6048	TGCAGGACCAGAGAATTGGAATACAC	6288
AAAAAAGNNNNACGTATGCCA		TTGGTTTCNNNNACGTATGCCA		CCACAAANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	5809	TGCAGGACCAGAGAATTGGAATACAG	6049	TGCAGGACCAGAGAATTGGAATACAA	6289
GCATGTTNNNNACGTATGCCA		GTAATTTNNNNACGTATGCCA		GTTATACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	5810	TGCAGGACCAGAGAATTGGAATACAA	6050	TGCAGGACCAGAGAATTGGAATACAT	6290
GCTTTTCNNNNACGTATGCCA		TTATCAGNNNNACGTATGCCA		CTATCATNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	5811	TGCAGGACCAGAGAATTGGAATACAT	6051	TGCAGGACCAGAGAATTGGAATACAC	6291
CTAATACNNNNACGTATGCCA		GCGTTCTNNNNACGTATGCCA		GGCTCTCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	5812	TGCAGGACCAGAGAATTGGAATACAT	6052	TGCAGGACCAGAGAATTGGAATACAG	6292
TAGCCCCGNNNNACGTATGCCA		GATCCAGNNNNACGTATGCCA		TGATTATNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	5813	TGCAGGACCAGAGAATTGGAATACAC	6053	TGCAGGACCAGAGAATTGGAATACAT	6293
AACGTCGNNNNACGTATGCCA		AGTTCCAGNNNNACGTATGCCA		AGACTCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	5814	TGCAGGACCAGAGAATTGGAATACAT	6054	TGCAGGACCAGAGAATTGGAATACAA	6294
TTCAAGANNNNACGTATGCCA		GCGACATNNNNACGTATGCCA		ACGTTTANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	5815	TGCAGGACCAGAGAATTGGAATACAA	6055	TGCAGGACCAGAGAATTGGAATACAA	6295
ACAAGAGNNNNACGTATGCCA		GCAGTAGNNNNACGTATGCCA		AGTAAGTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	5816	TGCAGGACCAGAGAATTGGAATACAT	6056	TGCAGGACCAGAGAATTGGAATACAA	6296
CCGTTTANNNNACGTATGCCA		TAGTGATNNNNACGTATGCCA		TGTTAACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	5817	TGCAGGACCAGAGAATTGGAATACAC	6057	TGCAGGACCAGAGAATTGGAATACAT	6297
TTAAGAAANNNNACGTATGCCA		ACATTAAANNNNACGTATGCCA		AATCACANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	5818	TGCAGGACCAGAGAATTGGAATACAA	6058	TGCAGGACCAGAGAATTGGAATACAC	6298
AACCTACNNNNACGTATGCCA		GCTGCCNNNNACGTATGCCA		ATGCTTCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	5819	TGCAGGACCAGAGAATTGGAATACAA	6059	TGCAGGACCAGAGAATTGGAATACAA	6299
GCGACTTNNNNACGTATGCCA		CCTGGCGNNNNACGTATGCCA		GCATTATNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	5820	TGCAGGACCAGAGAATTGGAATACAC	6060	TGCAGGACCAGAGAATTGGAATACAA	6300
GCACTAANNNNACGTATGCCA		GGCGATCANNNNACGTATGCCA		GGCATANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	5821	TGCAGGACCAGAGAATTGGAATACAT	6061	TGCAGGACCAGAGAATTGGAATACAC	6301
GTGTTTCANNNNACGTATGCCA		AGACCTGNNNNACGTATGCCA		ATACGCCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	5822	TGCAGGACCAGAGAATTGGAATACAA	6062	TGCAGGACCAGAGAATTGGAATACAA	6302
TTTTCAANNNNACGTATGCCA		GACTACNNNNACGTATGCCA		GACCCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	5823	TGCAGGACCAGAGAATTGGAATACAC	6063	TGCAGGACCAGAGAATTGGAATACAT	6303
ATTTCATANNNNACGTATGCCA		TTAGACGNNNNACGTATGCCA		TCCTTAGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	5824	TGCAGGACCAGAGAATTGGAATACAC	6064	TGCAGGACCAGAGAATTGGAATACAA	6304
TGACGACNNNNACGTATGCCA		GGCGGCCNNNNACGTATGCCA		GTGTGCTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	5825	TGCAGGACCAGAGAATTGGAATACAG	6065	TGCAGGACCAGAGAATTGGAATACAC	6305
CTTGTTACNNNNACGTATGCCA		CCGATATNNNNACGTATGCCA		CTGTACTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	5826	TGCAGGACCAGAGAATTGGAATACAC	6066	TGCAGGACCAGAGAATTGGAATACAC	6306
GTGCGGANNNNACGTATGCCA		CCGGCCNNNNACGTATGCCA		ACACCCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	5827	TGCAGGACCAGAGAATTGGAATACAC	6067	TGCAGGACCAGAGAATTGGAATACAT	6307
CATGAATNNNNACGTATGCCA		CTCGCTGNNNNACGTATGCCA		TTGGTGGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	5828	TGCAGGACCAGAGAATTGGAATACAC	6068	TGCAGGACCAGAGAATTGGAATACAG	6308
CGAAAGTNNNNACGTATGCCA		AGCCATANNNNACGTATGCCA		TTAGCCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAA	5829	TGCAGGACCAGAGAATTGGAATACAA	6069	TGCAGGACCAGAGAATTGGAATACAA	6309
AAATAATNNNNACGTATGCCA		ATGGAGCNNNNACGTATGCCA		CGACACTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	5830	TGCAGGACCAGAGAATTGGAATACAT	6070	TGCAGGACCAGAGAATTGGAATACAG	6310
TCGTGTCNNNNACGTATGCCA		CACAGACNNNNACGTATGCCA		CATGACTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAT	5831	TGCAGGACCAGAGAATTGGAATACAT	6071	TGCAGGACCAGAGAATTGGAATACAT	6311
CGTCTTGNNNNACGTATGCCA		CCGTCCGNNNNACGTATGCCA		AGTTGTANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAG	5832	TGCAGGACCAGAGAATTGGAATACAG	6072	TGCAGGACCAGAGAATTGGAATACAC	6312
ACTGTGTNNNNACGTATGCCA		AATGGACNNNNACGTATGCCA		CTGTTTANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATACAC	5833	TGCAGGACCAGAGAATTGGAATACAG	6073	TGCAGGACCAGAGAATTGGAATACAC	6313
CATTGGANNNNACGTATGCCA		TGCTCAANNNNACGTATGCCA		TGAGTCAANNNNACGTATGCCA	

FIG. 20C

Pool-25	SEQ ID NO:	Pool-26	SEQ ID NO:	Pool-27	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATACAC	5834	TGCAGGACCAGAGAATTGGAATACAT	6074	TGCAGGACCAGAGAATTGGAATACAT	6314
ACAGCGCANNCTAGCGTTAC		GTTCGGANNCTAGCGTTAC		CATCTTANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	5835	TGCAGGACCAGAGAATTGGAATACAC	6075	TGCAGGACCAGAGAATTGGAATACAC	6315
CCCCGTGANNCTAGCGTTAC		TGCGTGGNNCTAGCGTTAC		ACATTTNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	5836	TGCAGGACCAGAGAATTGGAATACAA	6076	TGCAGGACCAGAGAATTGGAATACAG	6316
CACCTTGNNNCTAGCGTTAC		CCGTCAANNCTAGCGTTAC		CCACATANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	5837	TGCAGGACCAGAGAATTGGAATACAG	6077	TGCAGGACCAGAGAATTGGAATACAT	6317
GTACCACNNCTAGCGTTAC		GTAACGANNCTAGCGTTAC		AAACAGANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	5838	TGCAGGACCAGAGAATTGGAATACAA	6078	TGCAGGACCAGAGAATTGGAATACAG	6318
CAATGANNCTAGCGTTAC		TCCGAGTNNCTAGCGTTAC		GTACCATTNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	5839	TGCAGGACCAGAGAATTGGAATACAA	6079	TGCAGGACCAGAGAATTGGAATACAA	6319
TTGTTGANNCTAGCGTTAC		CCAACANNCTAGCGTTAC		GAAAAAGNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	5840	TGCAGGACCAGAGAATTGGAATACAC	6080	TGCAGGACCAGAGAATTGGAATACAG	6320
CGGAAACNNCTAGCGTTAC		AGTATATNNCTAGCGTTAC		CTCTCATNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	5841	TGCAGGACCAGAGAATTGGAATACAT	6081	TGCAGGACCAGAGAATTGGAATACAA	6321
AGAACGTNNCTAGCGTTAC		CCGATAGNNCTAGCGTTAC		GGCACAANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	5842	TGCAGGACCAGAGAATTGGAATACAT	6082	TGCAGGACCAGAGAATTGGAATACAG	6322
ACCATGNNCTAGCGTTAC		TAGTATGNNCTAGCGTTAC		CGATGAANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	5843	TGCAGGACCAGAGAATTGGAATACAA	6083	TGCAGGACCAGAGAATTGGAATACAT	6323
AAAACGGNNCTAGCGTTAC		CATTCAANNCTAGCGTTAC		CACCTATNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	5844	TGCAGGACCAGAGAATTGGAATACAG	6084	TGCAGGACCAGAGAATTGGAATACAT	6324
AGTGAGNNCTAGCGTTAC		TACTGACNNCTAGCGTTAC		AGGCCGNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	5845	TGCAGGACCAGAGAATTGGAATACAC	6085	TGCAGGACCAGAGAATTGGAATACAA	6325
GTGATACNNCTAGCGTTAC		CTCATTGNNCTAGCGTTAC		TTTAAATNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	5846	TGCAGGACCAGAGAATTGGAATACAA	6086	TGCAGGACCAGAGAATTGGAATACAT	6326
TGCCCCNNCTAGCGTTAC		TGGCACTNNCTAGCGTTAC		CTGTTTANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	5847	TGCAGGACCAGAGAATTGGAATACAC	6087	TGCAGGACCAGAGAATTGGAATACAA	6327
GACAGTANNCTAGCGTTAC		CCCACGTNNCTAGCGTTAC		GTTGAAANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	5848	TGCAGGACCAGAGAATTGGAATACAC	6088	TGCAGGACCAGAGAATTGGAATACAA	6328
TAGTATANNCTAGCGTTAC		AAACCTGNNCTAGCGTTAC		TATGACTNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	5849	TGCAGGACCAGAGAATTGGAATACAC	6089	TGCAGGACCAGAGAATTGGAATACAG	6329
AACTTGNNNCTAGCGTTAC		GGCCAGTNNCTAGCGTTAC		AAGACTGNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	5850	TGCAGGACCAGAGAATTGGAATACAG	6090	TGCAGGACCAGAGAATTGGAATACAG	6330
TGTTTATNNCTAGCGTTAC		ACAACCTNNCTAGCGTTAC		TGCGTGNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	5851	TGCAGGACCAGAGAATTGGAATACAT	6091	TGCAGGACCAGAGAATTGGAATACAA	6331
ATAGGATNNCTAGCGTTAC		GGCAGATNNCTAGCGTTAC		TGTCCGANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	5852	TGCAGGACCAGAGAATTGGAATACAC	6092	TGCAGGACCAGAGAATTGGAATACAT	6332
GTCAAGTNNCTAGCGTTAC		CAAGTACNNCTAGCGTTAC		GTATAGNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	5853	TGCAGGACCAGAGAATTGGAATACAC	6093	TGCAGGACCAGAGAATTGGAATACAT	6333
CTGTTTCNNCTAGCGTTAC		ACGACGNNCTAGCGTTAC		GTCTGANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	5854	TGCAGGACCAGAGAATTGGAATACAC	6094	TGCAGGACCAGAGAATTGGAATACAG	6334
CCGTGCGNNCTAGCGTTAC		CGTGATANNCTAGCGTTAC		ACGCTTANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	5855	TGCAGGACCAGAGAATTGGAATACAC	6095	TGCAGGACCAGAGAATTGGAATACAG	6335
AGCTGCGNNCTAGCGTTAC		ATTGCTNNCTAGCGTTAC		AATTACTNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	5856	TGCAGGACCAGAGAATTGGAATACAT	6096	TGCAGGACCAGAGAATTGGAATACAT	6336
CCTTACGNNCTAGCGTTAC		GTGTTTNNCTAGCGTTAC		CGACCCNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAA	5857	TGCAGGACCAGAGAATTGGAATACAT	6097	TGCAGGACCAGAGAATTGGAATACAG	6337
ACGAGCANNCTAGCGTTAC		GTTTTTNNCTAGCGTTAC		CCTCCGANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	5858	TGCAGGACCAGAGAATTGGAATACAG	6098	TGCAGGACCAGAGAATTGGAATACAC	6338
AAGTTTTNNCTAGCGTTAC		CTCCTCGNNCTAGCGTTAC		TGTATAANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	5859	TGCAGGACCAGAGAATTGGAATACAC	6099	TGCAGGACCAGAGAATTGGAATACAT	6339
CCGTTAANNCTAGCGTTAC		CACCTGNNCTAGCGTTAC		TGAGTGNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	5860	TGCAGGACCAGAGAATTGGAATACAG	6100	TGCAGGACCAGAGAATTGGAATACAT	6340
GTCCCAANNCTAGCGTTAC		AGCGGTGNNCTAGCGTTAC		AAGTGCCNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAG	5861	TGCAGGACCAGAGAATTGGAATACAA	6101	TGCAGGACCAGAGAATTGGAATACAC	6341
CAAAACGNNCTAGCGTTAC		ACAACGNNCTAGCGTTAC		AGATAAANNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	5862	TGCAGGACCAGAGAATTGGAATACAA	6102	TGCAGGACCAGAGAATTGGAATACAC	6342
GTAAGAGNNCTAGCGTTAC		TTGCTTTNNCTAGCGTTAC		GAATCACNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	5863	TGCAGGACCAGAGAATTGGAATACAC	6103	TGCAGGACCAGAGAATTGGAATACAG	6343
GACGTCANNCTAGCGTTAC		CAGAGAANNCTAGCGTTAC		AGCTTACNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	5864	TGCAGGACCAGAGAATTGGAATACAG	6104	TGCAGGACCAGAGAATTGGAATACAT	6344
TCCCTAANNCTAGCGTTAC		ATACCTGNNCTAGCGTTAC		CATCTGNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAT	5865	TGCAGGACCAGAGAATTGGAATACAA	6105	TGCAGGACCAGAGAATTGGAATACAC	6345
ATTGAGANNCTAGCGTTAC		CTTATTCNNCTAGCGTTAC		CACGTGNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATACAC	5866	TGCAGGACCAGAGAATTGGAATACAA	6106	TGCAGGACCAGAGAATTGGAATACAC	6346
TAGCAACNNCTAGCGTTAC		GTTGTTANNCTAGCGTTAC		GTGTATGNNCTAGCGTTAC	

FIG. 20D

Pool-25	SEQ ID NO:	Pool-26	SEQ ID NO:	Pool-27	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATACAG	5867	TGCAGGACCAGAGAATTCTGAATACAA	6107	TGCAGGACCAGAGAATTCTGAATACAC	6347
AATGCCCTNNNNCTAGCGTTAC		TGACTGCNNNNCTAGCGTTAC		TCTCCGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAG	5868	TGCAGGACCAGAGAATTCTGAATACAA	6108	TGCAGGACCAGAGAATTCTGAATACAC	6348
ACTTCTCNNNNCTAGCGTTAC		GCAAACGNNNNCTAGCGTTAC		AAGAGTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAT	5869	TGCAGGACCAGAGAATTCTGAATACAA	6109	TGCAGGACCAGAGAATTCTGAATACAT	6349
AATTAGCNNNNCTAGCGTTAC		GACTATTNNNNCTAGCGTTAC		AGCTCTCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAC	5870	TGCAGGACCAGAGAATTCTGAATACAC	6110	TGCAGGACCAGAGAATTCTGAATACAG	6350
GTGTGGCNNNNCTAGCGTTAC		TGAAACCCNNNNCTAGCGTTAC		TGGCAGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAG	5871	TGCAGGACCAGAGAATTCTGAATACAA	6111	TGCAGGACCAGAGAATTCTGAATACAT	6351
ATCTGATNNNNCTAGCGTTAC		GGAAGGNNNNCTAGCGTTAC		GCATCGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAG	5872	TGCAGGACCAGAGAATTCTGAATACAC	6112	TGCAGGACCAGAGAATTCTGAATACAC	6352
CGATCGCNNNNCTAGCGTTAC		CCTAGTTNNNNCTAGCGTTAC		GGTCCGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAA	5873	TGCAGGACCAGAGAATTCTGAATACAC	6113	TGCAGGACCAGAGAATTCTGAATACAA	6353
CTGTACNNNNCTAGCGTTAC		AAACCACNNNNCTAGCGTTAC		AGCCACTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAG	5874	TGCAGGACCAGAGAATTCTGAATACAT	6114	TGCAGGACCAGAGAATTCTGAATACAG	6354
GAAGGCCNNNNCTAGCGTTAC		TGTAGTANNNNCTAGCGTTAC		ATCTTTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAC	5875	TGCAGGACCAGAGAATTCTGAATACAG	6115	TGCAGGACCAGAGAATTCTGAATACAG	6355
ATATTAGNNNNCTAGCGTTAC		TACAGCTNNNNCTAGCGTTAC		GCTCTAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAC	5876	TGCAGGACCAGAGAATTCTGAATACAA	6116	TGCAGGACCAGAGAATTCTGAATACAT	6356
GGTGACCNNNNCTAGCGTTAC		GTGTACCNNNNCTAGCGTTAC		CTATGTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAG	5877	TGCAGGACCAGAGAATTCTGAATACAT	6117	TGCAGGACCAGAGAATTCTGAATACAA	6357
TGCATGTNNNNCTAGCGTTAC		TTTATGCNNNNCTAGCGTTAC		COGCGTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAT	5878	TGCAGGACCAGAGAATTCTGAATACAA	6118	TGCAGGACCAGAGAATTCTGAATACAG	6358
AAGTGTNNNNCTAGCGTTAC		ATCCGTGNNNNCTAGCGTTAC		TACTCCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAA	5879	TGCAGGACCAGAGAATTCTGAATACAC	6119	TGCAGGACCAGAGAATTCTGAATACAG	6359
CCTTATTNNNNCTAGCGTTAC		GATCTGANNNNCTAGCGTTAC		GAGCCCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAA	5880	TGCAGGACCAGAGAATTCTGAATACAG	6120	TGCAGGACCAGAGAATTCTGAATACAT	6360
CTCCACTNNNNCTAGCGTTAC		ATAGATANNNNCTAGCGTTAC		ATCGAGCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAC	5881	TGCAGGACCAGAGAATTCTGAATACAG	6121	TGCAGGACCAGAGAATTCTGAATACAC	6361
CAATATNNNNCTAGCGTTAC		AGTCTTANNNNCTAGCGTTAC		CGTTGAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAC	5882	TGCAGGACCAGAGAATTCTGAATACAC	6122	TGCAGGACCAGAGAATTCTGAATACAC	6362
AAGATGNNNNCTAGCGTTAC		ATGTGGTNNNNCTAGCGTTAC		GAAAGACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAC	5883	TGCAGGACCAGAGAATTCTGAATACAG	6123	TGCAGGACCAGAGAATTCTGAATACAA	6363
CCAAGGCCNNNNCTAGCGTTAC		ATCGCGCNNNNCTAGCGTTAC		GTGATCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAT	5884	TGCAGGACCAGAGAATTCTGAATACAA	6124	TGCAGGACCAGAGAATTCTGAATACAG	6364
AAGCGGANNNNNCTAGCGTTAC		CCACATGNNNNCTAGCGTTAC		GTCAACTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAG	5885	TGCAGGACCAGAGAATTCTGAATACAT	6125	TGCAGGACCAGAGAATTCTGAATACAT	6365
AGGCCCTNNNNCTAGCGTTAC		GCCGATANNNNCTAGCGTTAC		GACGTGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAC	5886	TGCAGGACCAGAGAATTCTGAATACAC	6126	TGCAGGACCAGAGAATTCTGAATACAT	6366
TTCTAGNNNNCTAGCGTTAC		AAAGCCTNNNNCTAGCGTTAC		TACAACANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAC	5887	TGCAGGACCAGAGAATTCTGAATACAA	6127	TGCAGGACCAGAGAATTCTGAATACAA	6367
GCAGAAANNNNCTAGCGTTAC		CTGACGTNNNNCTAGCGTTAC		AATGTTCCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAT	5888	TGCAGGACCAGAGAATTCTGAATACAA	6128	TGCAGGACCAGAGAATTCTGAATACAT	6368
TGCGGTANNNNCTAGCGTTAC		AGCTCGTNNNNCTAGCGTTAC		TATAACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAC	5889	TGCAGGACCAGAGAATTCTGAATACAG	6129	TGCAGGACCAGAGAATTCTGAATACAT	6369
GATGGAAANNNGATCGACATG		GATCGAANNNGATCGACATG		CCGGATANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATACAC	5890	TGCAGGACCAGAGAATTCTGAATACAT	6130	TGCAGGACCAGAGAATTCTGAATACAA	6370
CAATTAANNNGATCGACATG		CGCACANNNGATCGACATG		GCCCTTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATACAC	5891	TGCAGGACCAGAGAATTCTGAATACAC	6131	TGCAGGACCAGAGAATTCTGAATACAG	6371
ATAGGCTNNNGATCGACATG		CGACTAANNNGATCGACATG		TACACTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATACAA	5892	TGCAGGACCAGAGAATTCTGAATACAG	6132	TGCAGGACCAGAGAATTCTGAATACAC	6372
AAAAATTNNNGATCGACATG		ACCGTTANNNGATCGACATG		GTGTAGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATACAA	5893	TGCAGGACCAGAGAATTCTGAATACAA	6133	TGCAGGACCAGAGAATTCTGAATACAG	6373
ATACACTNNNGATCGACATG		TGCCCTTNNNGATCGACATG		GAAAGTCNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATACAA	5894	TGCAGGACCAGAGAATTCTGAATACAT	6134	TGCAGGACCAGAGAATTCTGAATACAT	6374
ATCGAAANNNGATCGACATG		CGAAACCCNNNGATCGACATG		TCTGCGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATACAT	5895	TGCAGGACCAGAGAATTCTGAATACAG	6135	TGCAGGACCAGAGAATTCTGAATACAT	6375
CTATTACNNNGATCGACATG		ACCTTCTNNNGATCGACATG		ACTCGGANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATACAA	5896	TGCAGGACCAGAGAATTCTGAATACAC	6136	TGCAGGACCAGAGAATTCTGAATACAC	6376
CCCGATANNNGATCGACATG		TACCTTANNNGATCGACATG		GTCCAAANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATACAG	5897	TGCAGGACCAGAGAATTCTGAATACAA	6137	TGCAGGACCAGAGAATTCTGAATACAT	6377
AAACGCANNNGATCGACATG		TGCCCTCANNNGATCGACATG		TGAACCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATACAG	5898	TGCAGGACCAGAGAATTCTGAATACAG	6138	TGCAGGACCAGAGAATTCTGAATACAG	6378
TGATCGTNNNGATCGACATG		CGACTATNNNGATCGACATG		GCCGCTANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATACAC	5899	TGCAGGACCAGAGAATTCTGAATACAG	6139	TGCAGGACCAGAGAATTCTGAATACAG	6379
GCAGCCANNNGATCGACATG		GCATTCANNNGATCGACATG		ATACGTCNNNGATCGACATG	

FIG. 20E

Pool-25	SEQ ID NO:	Pool-26	SEQ ID NO:	Pool-27	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAT	5900	TGCAGGACCAGAGAATTCGAATACAG	6140	TGCAGGACCAGAGAATTCGAATACAA	6380
GACCATGNNNGATCGACATG		CTAGAAGNNNGATCGACATG		TTCAACANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	5901	TGCAGGACCAGAGAATTCGAATACAT	6141	TGCAGGACCAGAGAATTCGAATACAG	6381
GTCCACGNNNGATCGACATG		TTATAAANNNGATCGACATG		TGTGCATNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	5902	TGCAGGACCAGAGAATTCGAATACAT	6142	TGCAGGACCAGAGAATTCGAATACAG	6382
AGCATAANNNGATCGACATG		CCCTACANNNGATCGACATG		CCATAGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	5903	TGCAGGACCAGAGAATTCGAATACAA	6143	TGCAGGACCAGAGAATTCGAATACAC	6383
ACAGGCGNNNGATCGACATG		CGTCTAGNNNGATCGACATG		TCATCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	5904	TGCAGGACCAGAGAATTCGAATACAG	6144	TGCAGGACCAGAGAATTCGAATACAA	6384
CGGTAGANNNGATCGACATG		AGCTTTGNNNGATCGACATG		ACCGACTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	5905	TGCAGGACCAGAGAATTCGAATACAA	6145	TGCAGGACCAGAGAATTCGAATACAC	6385
CATTACTNNNGATCGACATG		GAGCGGCGNNNGATCGACATG		ATCGCCCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5906	TGCAGGACCAGAGAATTCGAATACAC	6146	TGCAGGACCAGAGAATTCGAATACAT	6386
GAAAATANNNGATCGACATG		ATATACANNNGATCGACATG		AGGATCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	5907	TGCAGGACCAGAGAATTCGAATACAA	6147	TGCAGGACCAGAGAATTCGAATACAA	6387
GGAGGTNNNGATCGACATG		AGGCTAGNNNGATCGACATG		TGGCGTTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5908	TGCAGGACCAGAGAATTCGAATACAT	6148	TGCAGGACCAGAGAATTCGAATACAC	6388
TGTTTTANNNGATCGACATG		ATCGACGNNNGATCGACATG		TAAATTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5909	TGCAGGACCAGAGAATTCGAATACAA	6149	TGCAGGACCAGAGAATTCGAATACAA	6389
GGATTTGNNNGATCGACATG		GACGCTCANNNGATCGACATG		CTACATANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5910	TGCAGGACCAGAGAATTCGAATACAT	6150	TGCAGGACCAGAGAATTCGAATACAC	6390
GTGGTGCGNNNGATCGACATG		GTTACCCNNNGATCGACATG		ATCCTCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	5911	TGCAGGACCAGAGAATTCGAATACAG	6151	TGCAGGACCAGAGAATTCGAATACAG	6391
TGCGCTCANNNGATCGACATG		CCTGCAGNNNGATCGACATG		ATGTGAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	5912	TGCAGGACCAGAGAATTCGAATACAC	6152	TGCAGGACCAGAGAATTCGAATACAA	6392
GAGAAGGNNNGATCGACATG		GTAACGTTNNNGATCGACATG		GGCCAAANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	5913	TGCAGGACCAGAGAATTCGAATACAA	6153	TGCAGGACCAGAGAATTCGAATACAC	6393
CATGGTGNNNGATCGACATG		TCTTATCANNNGATCGACATG		CAAGCTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5914	TGCAGGACCAGAGAATTCGAATACAA	6154	TGCAGGACCAGAGAATTCGAATACAA	6394
TGAGGCCNNNGATCGACATG		CGTTTGGNNNGATCGACATG		GGAGATCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5915	TGCAGGACCAGAGAATTCGAATACAG	6155	TGCAGGACCAGAGAATTCGAATACAC	6395
TGTTAGGNNNGATCGACATG		ATTAAAGNNNGATCGACATG		CTCCGACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5916	TGCAGGACCAGAGAATTCGAATACAT	6156	TGCAGGACCAGAGAATTCGAATACAC	6396
TGTTCTNNNGATCGACATG		TGCCAGANNNGATCGACATG		GCTGTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5917	TGCAGGACCAGAGAATTCGAATACAC	6157	TGCAGGACCAGAGAATTCGAATACAT	6397
AAAGTCCNNNGATCGACATG		GGCATATNNNGATCGACATG		ACCGCCCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5918	TGCAGGACCAGAGAATTCGAATACAG	6158	TGCAGGACCAGAGAATTCGAATACAC	6398
GTAGCCGNNNGATCGACATG		GTACGCCNNNGATCGACATG		GTCCGCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	5919	TGCAGGACCAGAGAATTCGAATACAC	6159	TGCAGGACCAGAGAATTCGAATACAC	6399
GGCTGAANNNGATCGACATG		TACCATNNNGATCGACATG		CTCACCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5920	TGCAGGACCAGAGAATTCGAATACAC	6160	TGCAGGACCAGAGAATTCGAATACAG	6400
TAATCTTNNNGATCGACATG		GCACGGTNNNGATCGACATG		CCTGGACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	5921	TGCAGGACCAGAGAATTCGAATACAT	6161	TGCAGGACCAGAGAATTCGAATACAA	6401
ACTTAATNNNGATCGACATG		GCTTCGTNNNGATCGACATG		CTTGGACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	5922	TGCAGGACCAGAGAATTCGAATACAA	6162	TGCAGGACCAGAGAATTCGAATACAT	6402
TCACAATNNNGATCGACATG		GCACGTGNNNGATCGACATG		GTGCGCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	5923	TGCAGGACCAGAGAATTCGAATACAC	6163	TGCAGGACCAGAGAATTCGAATACAC	6403
AGCCTGCGNNNGATCGACATG		TTACAANNNGATCGACATG		GGCACGCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5924	TGCAGGACCAGAGAATTCGAATACAC	6164	TGCAGGACCAGAGAATTCGAATACAA	6404
CTAGGANNNGATCGACATG		GATGGCCNNNGATCGACATG		GGTGTGANNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	5925	TGCAGGACCAGAGAATTCGAATACAC	6165	TGCAGGACCAGAGAATTCGAATACAA	6405
GTGAGATNNNGATCGACATG		ACCGGCANNNGATCGACATG		ACGACGANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	5926	TGCAGGACCAGAGAATTCGAATACAG	6166	TGCAGGACCAGAGAATTCGAATACAC	6406
GGTTGCTNNNGATCGACATG		CCATAACNNNGATCGACATG		ATCACTCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	5927	TGCAGGACCAGAGAATTCGAATACAT	6167	TGCAGGACCAGAGAATTCGAATACAT	6407
AGGTGCGNNNGATCGACATG		GAAGTCCNNNGATCGACATG		AATGCTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	5928	TGCAGGACCAGAGAATTCGAATACAG	6168	TGCAGGACCAGAGAATTCGAATACAC	6408
CTCAGACNNNGATCGACATG		CAACACTNNNGATCGACATG		GCCTTGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5929	TGCAGGACCAGAGAATTCGAATACAA	6169	TGCAGGACCAGAGAATTCGAATACAT	6409
AATGTATNNNGATCGACATG		CGCTTCTNNNGATCGACATG		GATCAGCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	5930	TGCAGGACCAGAGAATTCGAATACAT	6170	TGCAGGACCAGAGAATTCGAATACAC	6410
ACCATTANNNGATCGACATG		ACCGGCGNNNGATCGACATG		TTCCGGAANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	5931	TGCAGGACCAGAGAATTCGAATACAT	6171	TGCAGGACCAGAGAATTCGAATACAC	6411
GGCGCTGNNNGATCGACATG		GCTAATANNNGATCGACATG		GCAAATCANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5932	TGCAGGACCAGAGAATTCGAATACAT	6172	TGCAGGACCAGAGAATTCGAATACAA	6412
GCCCTGTNNNGATCGACATG		AAGGAGCANNNGATCGACATG		GAGAACCNNNGATCGACATG	

FIG. 20F

Pool-25	SEQ ID NO:	Pool-26	SEQ ID NO:	Pool-27	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATACAT	5933	TGCAGGACCAGAGAATTCGAATACAT	6173	TGCAGGACCAGAGAATTCGAATACAT	6413
AGCCGTANNNGATCGACATG		AGTCCGANNNGATCGACATG		CGACGATNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	5934	TGCAGGACCAGAGAATTCGAATACAC	6174	TGCAGGACCAGAGAATTCGAATACAC	6414
GATAGTGNNGATCGACATG		TATCCTGNNGATCGACATG		AGCAAGANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	5935	TGCAGGACCAGAGAATTCGAATACAT	6175	TGCAGGACCAGAGAATTCGAATACAC	6415
AAGGCAGNNNGATCGACATG		TTGGTCCNNNGATCGACATG		AAAGTAANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	5936	TGCAGGACCAGAGAATTCGAATACAG	6176	TGCAGGACCAGAGAATTCGAATACAG	6416
GGTCCTANNNGATCGACATG		CCTTTCANNNGATCGACATG		AAATCAANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	5937	TGCAGGACCAGAGAATTCGAATACAG	6177	TGCAGGACCAGAGAATTCGAATACAC	6417
ACTGGAGNNNGATCGACATG		TGTTTCGANNNGATCGACATG		TCTGTANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	5938	TGCAGGACCAGAGAATTCGAATACAA	6178	TGCAGGACCAGAGAATTCGAATACAA	6418
TGTTGTNNNGATCGACATG		CTGTGAGNNNGATCGACATG		CTATAGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	5939	TGCAGGACCAGAGAATTCGAATACAA	6179	TGCAGGACCAGAGAATTCGAATACAG	6419
CGAAGCGNNNGATCGACATG		TCTGACGNNNGATCGACATG		GTAGTTCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	5940	TGCAGGACCAGAGAATTCGAATACAT	6180	TGCAGGACCAGAGAATTCGAATACAC	6420
GATCCGTNNNGATCGACATG		ACCTCGTNNNGATCGACATG		GGAACCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	5941	TGCAGGACCAGAGAATTCGAATACAT	6181	TGCAGGACCAGAGAATTCGAATACAG	6421
TACCGTGNNGATCGACATG		GCATACGNNNGATCGACATG		GATCTGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAA	5942	TGCAGGACCAGAGAATTCGAATACAC	6182	TGCAGGACCAGAGAATTCGAATACAA	6422
ATCATGTNNNGATCGACATG		AGGTAAGNNNGATCGACATG		TTCCGCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAT	5943	TGCAGGACCAGAGAATTCGAATACAG	6183	TGCAGGACCAGAGAATTCGAATACAT	6423
GTTTGTNNNGATCGACATG		GACCAANNNGATCGACATG		TTCTACANNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	5944	TGCAGGACCAGAGAATTCGAATACAG	6184	TGCAGGACCAGAGAATTCGAATACAT	6424
GATACAGNNNGATCGACATG		GTCCGCCANNNGATCGACATG		CCCAGCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	5945	TGCAGGACCAGAGAATTCGAATACAA	6185	TGCAGGACCAGAGAATTCGAATACAC	6425
TTCGTAGNNNGATCGACATG		TGGAAGCNNNGATCGACATG		TTACCACNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	5946	TGCAGGACCAGAGAATTCGAATACAC	6186	TGCAGGACCAGAGAATTCGAATACAA	6426
GAGATCANNNGATCGACATG		ATACGACNNNGATCGACATG		CCTTCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5947	TGCAGGACCAGAGAATTCGAATACAT	6187	TGCAGGACCAGAGAATTCGAATACAC	6427
TTTGTTANNNGATCGACATG		TCAGCGANNNGATCGACATG		GTGGTCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAG	5948	TGCAGGACCAGAGAATTCGAATACAC	6188	TGCAGGACCAGAGAATTCGAATACAC	6428
TGAACCTNNNGATCGACATG		TGCGGTGNNNGATCGACATG		CAAACCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCGAATACAC	5949	TGCAGGACCAGAGAATTCGAATACAC	6189	TGCAGGACCAGAGAATTCGAATACAC	6429
CTACAGANNNTGCATCAGGT		AGTACTGNNNTGCATCAGGT		TCACGCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	5950	TGCAGGACCAGAGAATTCGAATACAG	6190	TGCAGGACCAGAGAATTCGAATACAG	6430
CTCGATNNNTGCATCAGGT		ATCGAAGNNNTGCATCAGGT		ACGAGCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	5951	TGCAGGACCAGAGAATTCGAATACAT	6191	TGCAGGACCAGAGAATTCGAATACAA	6431
ACTGCTCANNNTGCATCAGGT		CAAACGCNNNTGCATCAGGT		GAATGGCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	5952	TGCAGGACCAGAGAATTCGAATACAT	6192	TGCAGGACCAGAGAATTCGAATACAC	6432
CTGTTGTNNNTGCATCAGGT		TTCAATCANNNTGCATCAGGT		CAGTCCCNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	5953	TGCAGGACCAGAGAATTCGAATACAG	6193	TGCAGGACCAGAGAATTCGAATACAA	6433
AGTCGAANNNTGCATCAGGT		AGATGGTNNNTGCATCAGGT		AAGTATGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	5954	TGCAGGACCAGAGAATTCGAATACAA	6194	TGCAGGACCAGAGAATTCGAATACAC	6434
TGACCAANNNTGCATCAGGT		GGCTCATNNNTGCATCAGGT		GTACGTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAA	5955	TGCAGGACCAGAGAATTCGAATACAT	6195	TGCAGGACCAGAGAATTCGAATACAC	6435
TGGTTATNNNTGCATCAGGT		GGCCGCANNNTGCATCAGGT		AGCGCCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	5956	TGCAGGACCAGAGAATTCGAATACAT	6196	TGCAGGACCAGAGAATTCGAATACAG	6436
CGCTCAGNNNTGCATCAGGT		AACTGCGNNNTGCATCAGGT		CTCTCCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	5957	TGCAGGACCAGAGAATTCGAATACAA	6197	TGCAGGACCAGAGAATTCGAATACAG	6437
GGACCCGNNNTGCATCAGGT		TCCTTGCNNNTGCATCAGGT		GCCGTACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	5958	TGCAGGACCAGAGAATTCGAATACAA	6198	TGCAGGACCAGAGAATTCGAATACAG	6438
TACCACNNNTGCATCAGGT		CTTAATGNNNTGCATCAGGT		AGAGTGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	5959	TGCAGGACCAGAGAATTCGAATACAC	6199	TGCAGGACCAGAGAATTCGAATACAA	6439
TATAACTNNNTGCATCAGGT		ACCTGCCNNNTGCATCAGGT		TGGAGTGNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAG	5960	TGCAGGACCAGAGAATTCGAATACAT	6200	TGCAGGACCAGAGAATTCGAATACAT	6440
CCCGTGANNNTGCATCAGGT		ATGCTTTNNNTGCATCAGGT		CGGCCGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	5961	TGCAGGACCAGAGAATTCGAATACAA	6201	TGCAGGACCAGAGAATTCGAATACAA	6441
TGATGACNNNTGCATCAGGT		GGTGCAANNNTGCATCAGGT		TOGATTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	5962	TGCAGGACCAGAGAATTCGAATACAC	6202	TGCAGGACCAGAGAATTCGAATACAC	6442
ATGGCATNNNTGCATCAGGT		GGCTAATNNNTGCATCAGGT		CCAACAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAA	5963	TGCAGGACCAGAGAATTCGAATACAT	6203	TGCAGGACCAGAGAATTCGAATACAT	6443
TGATATCANNNTGCATCAGGT		AGCAAAANNNTGCATCAGGT		GTAGATTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAT	5964	TGCAGGACCAGAGAATTCGAATACAA	6204	TGCAGGACCAGAGAATTCGAATACAA	6444
GTAAAAGNNNTGCATCAGGT		GCAAGCANNNTGCATCAGGT		CCGGAGGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCGAATACAC	5965	TGCAGGACCAGAGAATTCGAATACAA	6205	TGCAGGACCAGAGAATTCGAATACAC	6445
CTTGCCGNNNTGCATCAGGT		TAGTACTNNNTGCATCAGGT		ACCTGAANNNTGCATCAGGT	

FIG. 20G

Pool-25	SEQ ID NO:	Pool-26	SEQ ID NO:	Pool-27	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAA	
AGGCACGNNNTGCATCAGGT	5966	CCATGTTNNNTGCATCAGGT	6206	CATGTGNNNTGCATCAGGT	6446
TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAC	
CTGAGCGNNNTGCATCAGGT	5967	AGCAATGNNNTGCATCAGGT	6207	AGGATCTNNNTGCATCAGGT	6447
TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAC	
GTGCTANNNNTGCATCAGGT	5968	ATACCTANNNNTGCATCAGGT	6208	GTTTGTNNNTGCATCAGGT	6448
TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAA	
TCAAAGNNNTGCATCAGGT	5969	ATATTGNNNTGCATCAGGT	6209	AATCAAGNNNTGCATCAGGT	6449
TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAT	
CGTATGNNNTGCATCAGGT	5970	ATCCATANNNNTGCATCAGGT	6210	CAACATANNNNTGCATCAGGT	6450
TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAT		TGCAGGACCAGAGAATTCTGAATACAA	
GAGCGGANNNTGCATCAGGT	5971	CCATTANNNNTGCATCAGGT	6211	TGAAGGNNNTGCATCAGGT	6451
TGCAGGACCAGAGAATTCTGAATACAT		TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAC	
TTTGGCGNNNTGCATCAGGT	5972	AGGTTCTNNNTGCATCAGGT	6212	AAGTGGANNNTGCATCAGGT	6452
TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAA	
AGTCTGNNNTGCATCAGGT	5973	TGATACNNNTGCATCAGGT	6213	GCAAAATNNNTGCATCAGGT	6453
TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAA	
TTCTTCTNNNTGCATCAGGT	5974	CCTTGTNNNTGCATCAGGT	6214	CAGATCCNNNTGCATCAGGT	6454
TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAT		TGCAGGACCAGAGAATTCTGAATACAT	
TGTGAANNNTGCATCAGGT	5975	ATCAAGTNNNTGCATCAGGT	6215	ACGCCTNNNTGCATCAGGT	6455
TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAA	
CCGTGGTNNNTGCATCAGGT	5976	CTTAGGCGNNNTGCATCAGGT	6216	GCGCTATNNNTGCATCAGGT	6456
TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAA	
AGAGGCGNNNTGCATCAGGT	5977	CTGTTCCNNNTGCATCAGGT	6217	GTGATGNNNTGCATCAGGT	6457
TGCAGGACCAGAGAATTCTGAATACAT		TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAC	
TTGATCTNNNTGCATCAGGT	5978	GATCCATNNNTGCATCAGGT	6218	GGATGAANNNTGCATCAGGT	6458
TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAG	
CGTCGACNNNTGCATCAGGT	5979	CACTCCGNNNTGCATCAGGT	6219	ACATAGNNNTGCATCAGGT	6459
TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAA	
GATATAANNNTGCATCAGGT	5980	CAAGAGTNNNTGCATCAGGT	6220	TTGCGTNNNTGCATCAGGT	6460
TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAC	
AATTTTANNNTGCATCAGGT	5981	CCGCTCTNNNTGCATCAGGT	6221	TACAGTNNNTGCATCAGGT	6461
TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAC	
GCCCCGNNNTGCATCAGGT	5982	GCTTAGTNNNTGCATCAGGT	6222	CGTCCACNNNTGCATCAGGT	6462
TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAA	
AATAAGNNNTGCATCAGGT	5983	CTAAGCANNNTGCATCAGGT	6223	AGCCCATNNNTGCATCAGGT	6463
TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAC	
CGACATTNNNTGCATCAGGT	5984	CGCGAAGNNNTGCATCAGGT	6224	GAGGCCCTNNNTGCATCAGGT	6464
TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAA	
AGAGAGTNNNTGCATCAGGT	5985	ATTCTTANNNTGCATCAGGT	6225	CCTATCCNNNTGCATCAGGT	6465
TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAA	
TTACACNNNTGCATCAGGT	5986	CTACGGTNNNTGCATCAGGT	6226	GGCGAGNNNTGCATCAGGT	6466
TGCAGGACCAGAGAATTCTGAATACAT		TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAG	
TAAGCTANNNTGCATCAGGT	5987	CGGAGCTNNNTGCATCAGGT	6227	AGAACTNNNTGCATCAGGT	6467
TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAT	
TGACCGCNNNTGCATCAGGT	5988	TACTTAANNNTGCATCAGGT	6228	GGTGTGNNNTGCATCAGGT	6468
TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAT		TGCAGGACCAGAGAATTCTGAATACAC	
CGATATGNNNTGCATCAGGT	5989	GCCGGCTNNNTGCATCAGGT	6229	TAAATCANNNTGCATCAGGT	6469
TGCAGGACCAGAGAATTCTGAATACAT		TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAA	
AGCATTANNNTGCATCAGGT	5990	CGACTTANNNTGCATCAGGT	6230	TTCCGCGNNNTGCATCAGGT	6470
TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAC	
TAGGCCGNNNTGCATCAGGT	5991	TGGCAAGNNNTGCATCAGGT	6231	CTCCATANNNTGCATCAGGT	6471
TGCAGGACCAGAGAATTCTGAATACAT		TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAT	
TACTAACNNNTGCATCAGGT	5992	GGAGGTGNNNTGCATCAGGT	6232	TACTACTNNNTGCATCAGGT	6472
TGCAGGACCAGAGAATTCTGAATACAT		TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAT	
ATCACGNNNTGCATCAGGT	5993	CATTAAACNNNTGCATCAGGT	6233	CGTTTATNNNTGCATCAGGT	6473
TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAT		TGCAGGACCAGAGAATTCTGAATACAA	
GATTCTCNNNTGCATCAGGT	5994	AGGAAATNNNTGCATCAGGT	6234	TTCAATGNNNTGCATCAGGT	6474
TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAC		TGCAGGACCAGAGAATTCTGAATACAA	
AGGAAGANNNTGCATCAGGT	5995	CTAAGTNNNTGCATCAGGT	6235	ACCACACNNNTGCATCAGGT	6475
TGCAGGACCAGAGAATTCTGAATACAT		TGCAGGACCAGAGAATTCTGAATACAT		TGCAGGACCAGAGAATTCTGAATACAT	
GTCTGCTNNNTGCATCAGGT	5996	AGACGCTNNNTGCATCAGGT	6236	AOCGCGCNNNTGCATCAGGT	6476
TGCAGGACCAGAGAATTCTGAATACAA		TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAC	
ATACTCANNNTGCATCAGGT	5997	TGAAGCANNNTGCATCAGGT	6237	CATGGCGNNNTGCATCAGGT	6477
TGCAGGACCAGAGAATTCTGAATACAT		TGCAGGACCAGAGAATTCTGAATACAG		TGCAGGACCAGAGAATTCTGAATACAC	
AGTTCCNNNTGCATCAGGT	5998	GACGCAGNNNTGCATCAGGT	6238	CTGAGTANNNTGCATCAGGT	6478

FIG. 20H

Pool-25	SEQ ID NO:	Pool-26	SEQ ID NO:	Pool-27	SEQ ID NO:
TGCAGGACCAGAGAATT CGAATACAA ATTCGTANNNTGCATCAGGT	5999	TGCAGGACCAGAGAATT CGAATACAT TTTACGTNNNTGCATCAGGT	6239	TGCAGGACCAGAGAATT CGAATACAG GATGTCTNNNTGCATCAGGT	6479
TGCAGGACCAGAGAATT CGAATACAG CTGATTGNNNTGCATCAGGT	6000	TGCAGGACCAGAGAATT CGAATACAG ATGATTTNNNTGCATCAGGT	6240	TGCAGGACCAGAGAATT CGAATACAA AGACCCTNNNTGCATCAGGT	6480
TGCAGGACCAGAGAATT CGAATACAT ACCCGAANNNTGCATCAGGT	6001	TGCAGGACCAGAGAATT CGAATACAA CGGAATGNNNTGCATCAGGT	6241	TGCAGGACCAGAGAATT CGAATACAG TACTTGNNNTGCATCAGGT	6481
TGCAGGACCAGAGAATT CGAATACAA GGCCATTNNNTGCATCAGGT	6002	TGCAGGACCAGAGAATT CGAATACAA ATGGCAGNNNTGCATCAGGT	6242	TGCAGGACCAGAGAATT CGAATACAT CCCTCTNNNTGCATCAGGT	6482
TGCAGGACCAGAGAATT CGAATACAG CTCCCCANNNTGCATCAGGT	6003	TGCAGGACCAGAGAATT CGAATACAC GACTGATNNNTGCATCAGGT	6243	TGCAGGACCAGAGAATT CGAATACAT ACTTACTNNNTGCATCAGGT	6483
TGCAGGACCAGAGAATT CGAATACAT GAACGCTNNNTGCATCAGGT	6004	TGCAGGACCAGAGAATT CGAATACAA AAGATACNNNTGCATCAGGT	6244	TGCAGGACCAGAGAATT CGAATACAG GTTTTCCNNNTGCATCAGGT	6484
TGCAGGACCAGAGAATT CGAATACAC GAGGCAGNNNTGCATCAGGT	6005	TGCAGGACCAGAGAATT CGAATACAA CGGCATTNNNTGCATCAGGT	6245	TGCAGGACCAGAGAATT CGAATACAG GATCACTNNNTGCATCAGGT	6485
TGCAGGACCAGAGAATT CGAATACAG GTGCTATNNNTGCATCAGGT	6006	TGCAGGACCAGAGAATT CGAATACAC CACGCTCNNNTGCATCAGGT	6246	TGCAGGACCAGAGAATT CGAATACAT TGATGGCNNNTGCATCAGGT	6486
TGCAGGACCAGAGAATT CGAATACAA ATTGCCGNNNTGCATCAGGT	6007	TGCAGGACCAGAGAATT CGAATACAA ACCACTGNNNTGCATCAGGT	6247	TGCAGGACCAGAGAATT CGAATACAC CACATTCNNNTGCATCAGGT	6487
TGCAGGACCAGAGAATT CGAATACAG GCCGACTNNNTGCATCAGGT	6008	TGCAGGACCAGAGAATT CGAATACAG TCGAGTTNNNTGCATCAGGT	6248	TGCAGGACCAGAGAATT CGAATACAC AAAAAGTNNNTGCATCAGGT	6488

FIG. 21A

Pool-28	SEQ ID NO:	Pool-29	SEQ ID NO:	Pool-30	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA	6489	TGCAGGACCAGAGAATTGGAATA	6729	TGCAGGACCAGAGAATTGGAATA	6969
CACAGTATTANNNNACGTATGCCA		CAGCTGACCGNNNNACGTATGCCA		CATATTGCTTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6490	TGCAGGACCAGAGAATTGGAATA	6730	TGCAGGACCAGAGAATTGGAATA	6970
CAGTACTAAANNNNACGTATGCCA		CACCAGCATANNNNACGTATGCCA		CACCATTAAANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6491	TGCAGGACCAGAGAATTGGAATA	6731	TGCAGGACCAGAGAATTGGAATA	6971
CATTTATGCTNNNNACGTATGCCA		CACGAAGGATNNNNACGTATGCCA		CAGTTGGCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6492	TGCAGGACCAGAGAATTGGAATA	6732	TGCAGGACCAGAGAATTGGAATA	6972
CAGTCATCCTNNNNACGTATGCCA		CACGACGAGGNNNNACGTATGCCA		CAGTTGGCGTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6493	TGCAGGACCAGAGAATTGGAATA	6733	TGCAGGACCAGAGAATTGGAATA	6973
CACGAATAAANNNNACGTATGCCA		CATATAAAGCANNNNACGTATGCCA		CAAAATACCCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6494	TGCAGGACCAGAGAATTGGAATA	6734	TGCAGGACCAGAGAATTGGAATA	6974
CAGACGTATCANNNNACGTATGCCA		CAGTGGTTTGNNNACGTATGCCA		CACACAAACCCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6495	TGCAGGACCAGAGAATTGGAATA	6735	TGCAGGACCAGAGAATTGGAATA	6975
CAAAATTCANNNNACGTATGCCA		CAGTTGGCATNNNNACGTATGCCA		CAATTAAATCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6496	TGCAGGACCAGAGAATTGGAATA	6736	TGCAGGACCAGAGAATTGGAATA	6976
CAAAATCCGANNNNACGTATGCCA		CAATACCTCTNNNNACGTATGCCA		CAGATTAGCCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6497	TGCAGGACCAGAGAATTGGAATA	6737	TGCAGGACCAGAGAATTGGAATA	6977
CACCTTATTNNNNACGTATGCCA		CAGTGGAGTNNNNACGTATGCCA		CAGACAAAAATNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6498	TGCAGGACCAGAGAATTGGAATA	6738	TGCAGGACCAGAGAATTGGAATA	6978
CAGCTTACTCANNNNACGTATGCCA		CACAGGCGGTNNNNACGTATGCCA		CAAAATATTTANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6499	TGCAGGACCAGAGAATTGGAATA	6739	TGCAGGACCAGAGAATTGGAATA	6979
CATTGGATGCNNNNACGTATGCCA		CAATAGTCATNNNNACGTATGCCA		CAAAAAGTCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6500	TGCAGGACCAGAGAATTGGAATA	6740	TGCAGGACCAGAGAATTGGAATA	6980
CAGCGGACGANNNNACGTATGCCA		CAGTCCGTCGNNNNACGTATGCCA		CAGTCTATAANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6501	TGCAGGACCAGAGAATTGGAATA	6741	TGCAGGACCAGAGAATTGGAATA	6981
CAACAAGTTTNNNNACGTATGCCA		CAGTGGCGTGNNNACGTATGCCA		CAAAAAGTCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6502	TGCAGGACCAGAGAATTGGAATA	6742	TGCAGGACCAGAGAATTGGAATA	6982
CATATCTCATNNNNACGTATGCCA		CAAGTAAAGTNNNNACGTATGCCA		CATTGGTCTGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6503	TGCAGGACCAGAGAATTGGAATA	6743	TGCAGGACCAGAGAATTGGAATA	6983
CAGGTTTGGTNNNNACGTATGCCA		CATATTGCAANNNNACGTATGCCA		CAATGATGAANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6504	TGCAGGACCAGAGAATTGGAATA	6744	TGCAGGACCAGAGAATTGGAATA	6984
CATAATTCCTNNNNACGTATGCCA		CAACCCAGCGNNNNACGTATGCCA		CATCCGTGTANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6505	TGCAGGACCAGAGAATTGGAATA	6745	TGCAGGACCAGAGAATTGGAATA	6985
CAACGTCGTANNNNACGTATGCCA		CATGTCAAAATNNNNACGTATGCCA		CAACATCCGANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6506	TGCAGGACCAGAGAATTGGAATA	6746	TGCAGGACCAGAGAATTGGAATA	6986
CAGAAGCTAGNNNNACGTATGCCA		CAGTGAAGCGNNNNACGTATGCCA		CATTAGATCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6507	TGCAGGACCAGAGAATTGGAATA	6747	TGCAGGACCAGAGAATTGGAATA	6987
CAACGAATCCNNNNACGTATGCCA		CAAGCGGATANNNNACGTATGCCA		CACGCCATCCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6508	TGCAGGACCAGAGAATTGGAATA	6748	TGCAGGACCAGAGAATTGGAATA	6988
CATCTTAATCANNNNACGTATGCCA		CAACGCGAGTTNNNNACGTATGCCA		CACTCTAACCNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6509	TGCAGGACCAGAGAATTGGAATA	6749	TGCAGGACCAGAGAATTGGAATA	6989
CAGCTTTTCGNNNNACGTATGCCA		CATAGGATANNNNACGTATGCCA		CACGTCACTCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6510	TGCAGGACCAGAGAATTGGAATA	6750	TGCAGGACCAGAGAATTGGAATA	6990
CATGCTGAGTNNNNACGTATGCCA		CATAGTGGAGNNNNACGTATGCCA		CACACCTATCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6511	TGCAGGACCAGAGAATTGGAATA	6751	TGCAGGACCAGAGAATTGGAATA	6991
CACGTTGCAANNNNACGTATGCCA		CATGTGGAAGNNNNACGTATGCCA		CATCGGTATCANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6512	TGCAGGACCAGAGAATTGGAATA	6752	TGCAGGACCAGAGAATTGGAATA	6992
CACAGTACGTTNNNNACGTATGCCA		CACCCACGTCNNNNACGTATGCCA		CAGAAGGCCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6513	TGCAGGACCAGAGAATTGGAATA	6753	TGCAGGACCAGAGAATTGGAATA	6993
CATGGATTTANNNNACGTATGCCA		CAGTAACGGANNNNACGTATGCCA		CAGTTTTTCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6514	TGCAGGACCAGAGAATTGGAATA	6754	TGCAGGACCAGAGAATTGGAATA	6994
CAGTGTAGAGNNNNACGTATGCCA		CATTCTACATNNNNACGTATGCCA		CAAGTGGCCGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6515	TGCAGGACCAGAGAATTGGAATA	6755	TGCAGGACCAGAGAATTGGAATA	6995
CACCTTTAGANNNNACGTATGCCA		CATCAATGATNNNNACGTATGCCA		CAAGCCATACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6516	TGCAGGACCAGAGAATTGGAATA	6756	TGCAGGACCAGAGAATTGGAATA	6996
CAATATAGTCNNNNACGTATGCCA		CATCGCGAATNNNNACGTATGCCA		CAATTCCGAGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6517	TGCAGGACCAGAGAATTGGAATA	6757	TGCAGGACCAGAGAATTGGAATA	6997
CAGTAGACGANNNNACGTATGCCA		CATAATGACTNNNNACGTATGCCA		CACAACCGATNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6518	TGCAGGACCAGAGAATTGGAATA	6758	TGCAGGACCAGAGAATTGGAATA	6998
CATAAATACNNNNACGTATGCCA		CACAGGTTTGNNNACGTATGCCA		CAAAGTATGANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6519	TGCAGGACCAGAGAATTGGAATA	6759	TGCAGGACCAGAGAATTGGAATA	6999
CACAGGACAAANNNNACGTATGCCA		CATTCCGCTTNNNNACGTATGCCA		CAATCTGCCTNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6520	TGCAGGACCAGAGAATTGGAATA	6760	TGCAGGACCAGAGAATTGGAATA	7000
CAATATCACANNNNACGTATGCCA		CACCTTAATTANNNNACGTATGCCA		CACTCATTTANNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6521	TGCAGGACCAGAGAATTGGAATA	6761	TGCAGGACCAGAGAATTGGAATA	7001
CATGAATCATNNNNACGTATGCCA		CATAGCATGCMNNNNACGTATGCCA		CATAAATCACNNNNACGTATGCCA	

FIG. 21B

Poel-28	SEQ ID NO:	Poel-29	SEQ ID NO:	Poel-30	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA	6522	TGCAGGACCAGAGAATTGGAATA	6762	TGCAGGACCAGAGAATTGGAATA	7002
CACCTACGTAGNNNACGTATGCCA		CAAAAACGCGNNNACGTATGCCA		CACCGAGACNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6523	TGCAGGACCAGAGAATTGGAATA	6763	TGCAGGACCAGAGAATTGGAATA	7003
CAGTACATCGNNNACGTATGCCA		CATAGCTGACNNNACGTATGCCA		CATCGCCACNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6524	TGCAGGACCAGAGAATTGGAATA	6764	TGCAGGACCAGAGAATTGGAATA	7004
CACGCAGTGCNNNACGTATGCCA		CACCTACCCGNNNACGTATGCCA		CAACGACTGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6525	TGCAGGACCAGAGAATTGGAATA	6765	TGCAGGACCAGAGAATTGGAATA	7005
CAAAACAAGTNNNACGTATGCCA		CAAGCTGTCAANNACGTATGCCA		CAGTTTAGCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6526	TGCAGGACCAGAGAATTGGAATA	6766	TGCAGGACCAGAGAATTGGAATA	7006
CAAAACTTCANNNACGTATGCCA		CACCTCAGCANNNACGTATGCCA		CAGTTTCAANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6527	TGCAGGACCAGAGAATTGGAATA	6767	TGCAGGACCAGAGAATTGGAATA	7007
CAAGGAGCCGNNNACGTATGCCA		CACACGTTCTNNNACGTATGCCA		CAGAATGCGANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6528	TGCAGGACCAGAGAATTGGAATA	6768	TGCAGGACCAGAGAATTGGAATA	7008
CACGTGACATCANNNACGTATGCCA		CAACGGAACANNNACGTATGCCA		CAACCGCTAANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6529	TGCAGGACCAGAGAATTGGAATA	6769	TGCAGGACCAGAGAATTGGAATA	7009
CAATACATCANNNACGTATGCCA		CAGATCATTANNNACGTATGCCA		CAGTCAACAANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6530	TGCAGGACCAGAGAATTGGAATA	6770	TGCAGGACCAGAGAATTGGAATA	7010
CAAAATAACCTNNNACGTATGCCA		CACCTAACCCNNNACGTATGCCA		CATTGGACTGNNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6531	TGCAGGACCAGAGAATTGGAATA	6771	TGCAGGACCAGAGAATTGGAATA	7011
CACCAGCTTTNNNACGTATGCCA		CATTAGGTANNNACGTATGCCA		CAAAGCTTGCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6532	TGCAGGACCAGAGAATTGGAATA	6772	TGCAGGACCAGAGAATTGGAATA	7012
CATCCGTTTGGNNNACGTATGCCA		CATGATATTGNNNACGTATGCCA		CATTATTATNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6533	TGCAGGACCAGAGAATTGGAATA	6773	TGCAGGACCAGAGAATTGGAATA	7013
CACAGTCGGCANNNACGTATGCCA		CAGCGAAAACNNNACGTATGCCA		CATACAATGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6534	TGCAGGACCAGAGAATTGGAATA	6774	TGCAGGACCAGAGAATTGGAATA	7014
CATGATCGGTNNNACGTATGCCA		CAACTAACCCNNNACGTATGCCA		CAAAAGTGCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6535	TGCAGGACCAGAGAATTGGAATA	6775	TGCAGGACCAGAGAATTGGAATA	7015
CAACACACACNNNACGTATGCCA		CATACTTGCCNNNACGTATGCCA		CAGCTGCTCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6536	TGCAGGACCAGAGAATTGGAATA	6776	TGCAGGACCAGAGAATTGGAATA	7016
CATCAGCGAANNNACGTATGCCA		CACGTGCTAANNNACGTATGCCA		CAGCTGATACNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6537	TGCAGGACCAGAGAATTGGAATA	6777	TGCAGGACCAGAGAATTGGAATA	7017
CATCGTACTCANNNACGTATGCCA		CAAAACAGTANNNACGTATGCCA		CACCTTGATTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6538	TGCAGGACCAGAGAATTGGAATA	6778	TGCAGGACCAGAGAATTGGAATA	7018
CATTTCAGACNNNACGTATGCCA		CAGCATCATGNNNACGTATGCCA		CACCTTGTGAGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6539	TGCAGGACCAGAGAATTGGAATA	6779	TGCAGGACCAGAGAATTGGAATA	7019
CAGCGCACGTNNNACGTATGCCA		CAACCTCGAANNNACGTATGCCA		CAACTTCCGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6540	TGCAGGACCAGAGAATTGGAATA	6780	TGCAGGACCAGAGAATTGGAATA	7020
CACCAGACATCANNNACGTATGCCA		CAACAGCTACNNNACGTATGCCA		CACAAGATCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6541	TGCAGGACCAGAGAATTGGAATA	6781	TGCAGGACCAGAGAATTGGAATA	7021
CATATTGATGNNNACGTATGCCA		CACGTCAACANNNACGTATGCCA		CAGTCGCCTCANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6542	TGCAGGACCAGAGAATTGGAATA	6782	TGCAGGACCAGAGAATTGGAATA	7022
CACGAGATAGNNNACGTATGCCA		CACCGGCCNNNACGTATGCCA		CAGTGGTGAANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6543	TGCAGGACCAGAGAATTGGAATA	6783	TGCAGGACCAGAGAATTGGAATA	7023
CAATACGAAANNNACGTATGCCA		CATCGCGTGGNNNACGTATGCCA		CAAGTAAGTANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6544	TGCAGGACCAGAGAATTGGAATA	6784	TGCAGGACCAGAGAATTGGAATA	7024
CAGATGAGACNNNACGTATGCCA		CAAAAGACTGGNNNACGTATGCCA		CAATTTATTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6545	TGCAGGACCAGAGAATTGGAATA	6785	TGCAGGACCAGAGAATTGGAATA	7025
CATACAAATCANNNACGTATGCCA		CAGCAATGAGNNNACGTATGCCA		CAGGAATCGANNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6546	TGCAGGACCAGAGAATTGGAATA	6786	TGCAGGACCAGAGAATTGGAATA	7026
CATTTAATAANNNACGTATGCCA		CAAGGAGCTANNNACGTATGCCA		CACGTGCTTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6547	TGCAGGACCAGAGAATTGGAATA	6787	TGCAGGACCAGAGAATTGGAATA	7027
CAGCGCGTCAANNNACGTATGCCA		CACCTGAGATTNNNACGTATGCCA		CAGTTAACTNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6548	TGCAGGACCAGAGAATTGGAATA	6788	TGCAGGACCAGAGAATTGGAATA	7028
CACGATGATCANNNACGTATGCCA		CAACGGAGCCNNNACGTATGCCA		CAATCTTAAGNNNACGTATGCCA	
TGCAGGACCAGAGAATTGGAATA	6549	TGCAGGACCAGAGAATTGGAATA	6789	TGCAGGACCAGAGAATTGGAATA	7029
CACCGAAGCCNNNCTAGCGTTAC		CAGATCGGCCNNNCTAGCGTTAC		CAAACTCAGCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6550	TGCAGGACCAGAGAATTGGAATA	6790	TGCAGGACCAGAGAATTGGAATA	7030
CACCAAACACNNNCTAGCGTTAC		CATGCTGCAANNNCTAGCGTTAC		CAACGAAAGCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6551	TGCAGGACCAGAGAATTGGAATA	6791	TGCAGGACCAGAGAATTGGAATA	7031
CAGGTCTTCTNNNCTAGCGTTAC		CATCGGAATCANNNCTAGCGTTAC		CAGCGTAATCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6552	TGCAGGACCAGAGAATTGGAATA	6792	TGCAGGACCAGAGAATTGGAATA	7032
CACCTCGGTNNNCTAGCGTTAC		CAGACGGCTCANNNCTAGCGTTAC		CAAGGTGGTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6553	TGCAGGACCAGAGAATTGGAATA	6793	TGCAGGACCAGAGAATTGGAATA	7033
CACCGCTGGANNNCTAGCGTTAC		CAAGTTGGAGNNNCTAGCGTTAC		CACCTTGAGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTGGAATA	6554	TGCAGGACCAGAGAATTGGAATA	6794	TGCAGGACCAGAGAATTGGAATA	7034
CAACCACCTTNNNCTAGCGTTAC		CAAGTACGTNNNCTAGCGTTAC		CACCTCGCGTNNNCTAGCGTTAC	

FIG. 21C

Poel-28	SEQ ID NO:	Poel-29	SEQ ID NO:	Poel-30	SEQ ID NO:
TGCAGGACCAGAGAATTTCGAATA	6555	TGCAGGACCAGAGAATTTCGAATA	6795	TGCAGGACCAGAGAATTTCGAATA	7035
CATCTAAGTANNNNCTAGCGTTAC		CACGATTAAATNNNNCTAGCGTTAC		CAGGCCATAATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6556	TGCAGGACCAGAGAATTTCGAATA	6796	TGCAGGACCAGAGAATTTCGAATA	7036
CAATTATAATNNNNCTAGCGTTAC		CATTACGCCCTNNNNCTAGCGTTAC		CAACCCCTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6557	TGCAGGACCAGAGAATTTCGAATA	6797	TGCAGGACCAGAGAATTTCGAATA	7037
CATGGACCGNNNNCTAGCGTTAC		CAAGGAGTTGNNNNCTAGCGTTAC		CACCCATCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6558	TGCAGGACCAGAGAATTTCGAATA	6798	TGCAGGACCAGAGAATTTCGAATA	7038
CACTTCATTANNNNCTAGCGTTAC		CAGTACACCANNNNCTAGCGTTAC		CATAGAACAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6559	TGCAGGACCAGAGAATTTCGAATA	6799	TGCAGGACCAGAGAATTTCGAATA	7039
CAACCGCACTANNNNCTAGCGTTAC		CAGGAAATATNNNNCTAGCGTTAC		CACCGGAGGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6560	TGCAGGACCAGAGAATTTCGAATA	6800	TGCAGGACCAGAGAATTTCGAATA	7040
CATCATGGCANNNNCTAGCGTTAC		CACGGTTCTTNNNNCTAGCGTTAC		CAATGAACAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6561	TGCAGGACCAGAGAATTTCGAATA	6801	TGCAGGACCAGAGAATTTCGAATA	7041
CAGGCTTAACNNNNCTAGCGTTAC		CAGGTCCAGCANNNNCTAGCGTTAC		CATTTCGAAGCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6562	TGCAGGACCAGAGAATTTCGAATA	6802	TGCAGGACCAGAGAATTTCGAATA	7042
CAATGGTATTNNNNCTAGCGTTAC		CATTCCGCTCANNNNCTAGCGTTAC		CAAAACAACAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6563	TGCAGGACCAGAGAATTTCGAATA	6803	TGCAGGACCAGAGAATTTCGAATA	7043
CAGTATGCTGNNNNCTAGCGTTAC		CACCGCAGGTTNNNNCTAGCGTTAC		CATCCCTTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6564	TGCAGGACCAGAGAATTTCGAATA	6804	TGCAGGACCAGAGAATTTCGAATA	7044
CAATCGTGGTNNNNCTAGCGTTAC		CAGGTGTGCGNNNNCTAGCGTTAC		CAAAACGAATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6565	TGCAGGACCAGAGAATTTCGAATA	6805	TGCAGGACCAGAGAATTTCGAATA	7045
CAGCTTAGGTTNNNNCTAGCGTTAC		CACACAGTANNNNCTAGCGTTAC		CATCCAGTGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6566	TGCAGGACCAGAGAATTTCGAATA	6806	TGCAGGACCAGAGAATTTCGAATA	7046
CATCTGTATTNNNNCTAGCGTTAC		CAATCATTTGANNNNCTAGCGTTAC		CACTTCAAAAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6567	TGCAGGACCAGAGAATTTCGAATA	6807	TGCAGGACCAGAGAATTTCGAATA	7047
CAGGATAGCANNNNCTAGCGTTAC		CATAATCATGNNNNCTAGCGTTAC		CATATCTAGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6568	TGCAGGACCAGAGAATTTCGAATA	6808	TGCAGGACCAGAGAATTTCGAATA	7048
CATTCACTCGNNNNCTAGCGTTAC		CAGTTGACCANNNNCTAGCGTTAC		CAAAACGGCTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6569	TGCAGGACCAGAGAATTTCGAATA	6809	TGCAGGACCAGAGAATTTCGAATA	7049
CATTCCGACANNNNCTAGCGTTAC		CAACTCTTGGNNNNCTAGCGTTAC		CAACTTTTCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6570	TGCAGGACCAGAGAATTTCGAATA	6810	TGCAGGACCAGAGAATTTCGAATA	7050
CACGGTCGGTNNNNCTAGCGTTAC		CACCCAGTTTNNNNCTAGCGTTAC		CAAGTGCTTGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6571	TGCAGGACCAGAGAATTTCGAATA	6811	TGCAGGACCAGAGAATTTCGAATA	7051
CAAGATCGCTNNNNCTAGCGTTAC		CATCAAGGAGNNNNCTAGCGTTAC		CAATGGTCCANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6572	TGCAGGACCAGAGAATTTCGAATA	6812	TGCAGGACCAGAGAATTTCGAATA	7052
CAGCATTTCGANNNNCTAGCGTTAC		CAAAACGCTTGGNNNNCTAGCGTTAC		CAGCCCTTANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6573	TGCAGGACCAGAGAATTTCGAATA	6813	TGCAGGACCAGAGAATTTCGAATA	7053
CACGCTGATANNNNCTAGCGTTAC		CACCTTATATCANNNNCTAGCGTTAC		CAGTTGCTCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6574	TGCAGGACCAGAGAATTTCGAATA	6814	TGCAGGACCAGAGAATTTCGAATA	7054
CACGGTTAACNNNNCTAGCGTTAC		CAAGTGTCCANNNNCTAGCGTTAC		CAGCATATATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6575	TGCAGGACCAGAGAATTTCGAATA	6815	TGCAGGACCAGAGAATTTCGAATA	7055
CAAAATGTCAATNNNNCTAGCGTTAC		CAAGCGACGNNNNCTAGCGTTAC		CAGGTGTTGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6576	TGCAGGACCAGAGAATTTCGAATA	6816	TGCAGGACCAGAGAATTTCGAATA	7056
CAGCAAGACANNNNCTAGCGTTAC		CACCTGTCCGNNNNCTAGCGTTAC		CAACTATTTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6577	TGCAGGACCAGAGAATTTCGAATA	6817	TGCAGGACCAGAGAATTTCGAATA	7057
CACCAGCCTCNNNNCTAGCGTTAC		CAACTCACCTNNNNCTAGCGTTAC		CACCTTAAACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6578	TGCAGGACCAGAGAATTTCGAATA	6818	TGCAGGACCAGAGAATTTCGAATA	7058
CACCTTGTTCGNNNNCTAGCGTTAC		CAAAATTCGANNNNCTAGCGTTAC		CATCGCAGCGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6579	TGCAGGACCAGAGAATTTCGAATA	6819	TGCAGGACCAGAGAATTTCGAATA	7059
CATATCGGTGNNNNCTAGCGTTAC		CAGTAATATCANNNNCTAGCGTTAC		CAGATTTCGACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6580	TGCAGGACCAGAGAATTTCGAATA	6820	TGCAGGACCAGAGAATTTCGAATA	7060
CACCTGGCATANNNNCTAGCGTTAC		CACAGAAATNNNNCTAGCGTTAC		CATGGCCGTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6581	TGCAGGACCAGAGAATTTCGAATA	6821	TGCAGGACCAGAGAATTTCGAATA	7061
CATGACGCCNNNNCTAGCGTTAC		CAATTCCCCANNNNCTAGCGTTAC		CAAAGGCATGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6582	TGCAGGACCAGAGAATTTCGAATA	6822	TGCAGGACCAGAGAATTTCGAATA	7062
CATTCTCTTNNNNCTAGCGTTAC		CACCTCTTAGCANNNNCTAGCGTTAC		CAATGATCTANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6583	TGCAGGACCAGAGAATTTCGAATA	6823	TGCAGGACCAGAGAATTTCGAATA	7063
CATAACGGAGNNNNCTAGCGTTAC		CATACCAGCANNNNCTAGCGTTAC		CATCGCAATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6584	TGCAGGACCAGAGAATTTCGAATA	6824	TGCAGGACCAGAGAATTTCGAATA	7064
CAGAGTGGATNNNNCTAGCGTTAC		CACACGCCCTCNNNNCTAGCGTTAC		CAATCCGCTTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6585	TGCAGGACCAGAGAATTTCGAATA	6825	TGCAGGACCAGAGAATTTCGAATA	7065
CATCGTAAATNNNNCTAGCGTTAC		CAAAATCGAGNNNNCTAGCGTTAC		CAGAAGTGGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6586	TGCAGGACCAGAGAATTTCGAATA	6826	TGCAGGACCAGAGAATTTCGAATA	7066
CACAACGACTNNNNCTAGCGTTAC		CACATACAATNNNNCTAGCGTTAC		CAGGAACAGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6587	TGCAGGACCAGAGAATTTCGAATA	6827	TGCAGGACCAGAGAATTTCGAATA	7067
CAGCACCCCTNNNNCTAGCGTTAC		CATTATGTTCTNNNNCTAGCGTTAC		CACTAAACATNNNNCTAGCGTTAC	

FIG. 21D

Poal-28	SEQ ID NO:	Poal-29	SEQ ID NO:	Poal-30	SEQ ID NO:
TGCAGGACCAGAGAATTTCGAATA	6588	TGCAGGACCAGAGAATTTCGAATA	6828	TGCAGGACCAGAGAATTTCGAATA	7068
CAGATAATTCNNNCTAGCGTTAC		CAGTCTGTCTNNNCTAGCGTTAC		CAAAGGAGTCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6589	TGCAGGACCAGAGAATTTCGAATA	6829	TGCAGGACCAGAGAATTTCGAATA	7069
CAAACCTCAAANNCTAGCGTTAC		CAGTCTGAACNNNCTAGCGTTAC		CATCCATGTCTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6590	TGCAGGACCAGAGAATTTCGAATA	6830	TGCAGGACCAGAGAATTTCGAATA	7070
CATCAAACTNNNCTAGCGTTAC		CAAGGTGCGGNNNCTAGCGTTAC		CAGTACGAGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6591	TGCAGGACCAGAGAATTTCGAATA	6831	TGCAGGACCAGAGAATTTCGAATA	7071
CAATTATTCNNNCTAGCGTTAC		CACAGAAACGNNNCTAGCGTTAC		CAGGCCAGCTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6592	TGCAGGACCAGAGAATTTCGAATA	6832	TGCAGGACCAGAGAATTTCGAATA	7072
CACCTTCCTGNNNCTAGCGTTAC		CATCTGTTCGNNNCTAGCGTTAC		CAGTCCGATANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6593	TGCAGGACCAGAGAATTTCGAATA	6833	TGCAGGACCAGAGAATTTCGAATA	7073
CATAAGTAAGNNNCTAGCGTTAC		CACGATGGTTNNNCTAGCGTTAC		CATGTTACAANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6594	TGCAGGACCAGAGAATTTCGAATA	6834	TGCAGGACCAGAGAATTTCGAATA	7074
CACATAACCTNNNCTAGCGTTAC		CAATAATATTNNNCTAGCGTTAC		CACATTCACANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6595	TGCAGGACCAGAGAATTTCGAATA	6835	TGCAGGACCAGAGAATTTCGAATA	7075
CAATAGCGTCNNNCTAGCGTTAC		CAATCGAGCTNNNCTAGCGTTAC		CATGTTGAATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6596	TGCAGGACCAGAGAATTTCGAATA	6836	TGCAGGACCAGAGAATTTCGAATA	7076
CAAAGGTAATNNNCTAGCGTTAC		CAGAGAAAGNNNCTAGCGTTAC		CAAGAAACGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6597	TGCAGGACCAGAGAATTTCGAATA	6837	TGCAGGACCAGAGAATTTCGAATA	7077
CATCAGCTAGNNNCTAGCGTTAC		CAATTACACANNNCTAGCGTTAC		CATCCGACCCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6598	TGCAGGACCAGAGAATTTCGAATA	6838	TGCAGGACCAGAGAATTTCGAATA	7078
CAAACCATATNNNCTAGCGTTAC		CAGGACCTGCGNNNCTAGCGTTAC		CACACTAGTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6599	TGCAGGACCAGAGAATTTCGAATA	6839	TGCAGGACCAGAGAATTTCGAATA	7079
CAGACGAGTANNNCTAGCGTTAC		CAACGTAGAGNNNCTAGCGTTAC		CAACCGGCGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6600	TGCAGGACCAGAGAATTTCGAATA	6840	TGCAGGACCAGAGAATTTCGAATA	7080
CAATAAATTTNNNCTAGCGTTAC		CACACGGCGTNNNCTAGCGTTAC		CACCTTGCTACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6601	TGCAGGACCAGAGAATTTCGAATA	6841	TGCAGGACCAGAGAATTTCGAATA	7081
CAGAGCTAAGNNNCTAGCGTTAC		CAATTACGTANNNCTAGCGTTAC		CATTGCGAGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6602	TGCAGGACCAGAGAATTTCGAATA	6842	TGCAGGACCAGAGAATTTCGAATA	7082
CAGCGGATCCNNNCTAGCGTTAC		CATATGTTGANNNCTAGCGTTAC		CAAATGAAGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6603	TGCAGGACCAGAGAATTTCGAATA	6843	TGCAGGACCAGAGAATTTCGAATA	7083
CATTTCATAGANNNCTAGCGTTAC		CACAGACTCANNNCTAGCGTTAC		CACTCGCCCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6604	TGCAGGACCAGAGAATTTCGAATA	6844	TGCAGGACCAGAGAATTTCGAATA	7084
CATTAAGCATNNNCTAGCGTTAC		CACGGATGCCNNNCTAGCGTTAC		CAGTGGACCCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6605	TGCAGGACCAGAGAATTTCGAATA	6845	TGCAGGACCAGAGAATTTCGAATA	7085
CATCGAGCGCANNNCTAGCGTTAC		CATACATCTTNNNCTAGCGTTAC		CAACGACTCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6606	TGCAGGACCAGAGAATTTCGAATA	6846	TGCAGGACCAGAGAATTTCGAATA	7086
CATCGCAGCCNNNCTAGCGTTAC		CACCTTCGTGNNNCTAGCGTTAC		CAACAACTTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6607	TGCAGGACCAGAGAATTTCGAATA	6847	TGCAGGACCAGAGAATTTCGAATA	7087
CACCTTGACANNNCTAGCGTTAC		CAGAACGCGGNNNCTAGCGTTAC		CATCTGGTAGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6608	TGCAGGACCAGAGAATTTCGAATA	6848	TGCAGGACCAGAGAATTTCGAATA	7088
CATTCCAGTCNNNCTAGCGTTAC		CATCGGATTTGNNNCTAGCGTTAC		CACATGGCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATA	6609	TGCAGGACCAGAGAATTTCGAATA	6849	TGCAGGACCAGAGAATTTCGAATA	7089
CAGTTTTTACNNNGATCGACATG		CAAGACAAATNNNGATCGACATG		CAACCCGCGANNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	6610	TGCAGGACCAGAGAATTTCGAATA	6850	TGCAGGACCAGAGAATTTCGAATA	7090
CAAACCTTAGTNNNGATCGACATG		CACGAAGTAGNNNGATCGACATG		CACGCGGTACNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	6611	TGCAGGACCAGAGAATTTCGAATA	6851	TGCAGGACCAGAGAATTTCGAATA	7091
CACGCGCGCGNNNGATCGACATG		CAAAAGAGCCNNNGATCGACATG		CACACATCAGNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	6612	TGCAGGACCAGAGAATTTCGAATA	6852	TGCAGGACCAGAGAATTTCGAATA	7092
CAAACCTGTTANNNGATCGACATG		CATGAGTGGANNNGATCGACATG		CATAGACACCCNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	6613	TGCAGGACCAGAGAATTTCGAATA	6853	TGCAGGACCAGAGAATTTCGAATA	7093
CAGTAAGTTTNNNGATCGACATG		CACGCTCCCANNNGATCGACATG		CAATGTAAGNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	6614	TGCAGGACCAGAGAATTTCGAATA	6854	TGCAGGACCAGAGAATTTCGAATA	7094
CACCTTAGCAGNNNGATCGACATG		CAACACTTCCNNNGATCGACATG		CAATCCTCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	6615	TGCAGGACCAGAGAATTTCGAATA	6855	TGCAGGACCAGAGAATTTCGAATA	7095
CAACTTCCGNNNGATCGACATG		CAGCAGTCATNNNGATCGACATG		CAGTCGTCCCNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	6616	TGCAGGACCAGAGAATTTCGAATA	6856	TGCAGGACCAGAGAATTTCGAATA	7096
CACCTCCTCTTNNNGATCGACATG		CACCATATGGNNNGATCGACATG		CAACTTGCAGNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	6617	TGCAGGACCAGAGAATTTCGAATA	6857	TGCAGGACCAGAGAATTTCGAATA	7097
CAAGATAATGNNNGATCGACATG		CAATGCGCCGNNNGATCGACATG		CAGAGCGCTCANNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	6618	TGCAGGACCAGAGAATTTCGAATA	6858	TGCAGGACCAGAGAATTTCGAATA	7098
CACAGCCCTCANNNGATCGACATG		CAGTTGAACNNNGATCGACATG		CATCGCCAGGNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	6619	TGCAGGACCAGAGAATTTCGAATA	6859	TGCAGGACCAGAGAATTTCGAATA	7099
CACGTAATTANNNGATCGACATG		CAAAGGTTGNNNGATCGACATG		CACGATCCCGNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATA	6620	TGCAGGACCAGAGAATTTCGAATA	6860	TGCAGGACCAGAGAATTTCGAATA	7100
CAGTTCGTTCCNNNGATCGACATG		CAGCAGCGCTGNNNGATCGACATG		CAACCCACANNNGATCGACATG	

FIG. 21E

Pool-28	SEQ ID NO:	Pool-29	SEQ ID NO:	Pool-30	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATA	6621	TGCAGGACCAGAGAATTCTGAATA	6861	TGCAGGACCAGAGAATTCTGAATA	7101
CATTCCGTCANNNNGATCGACATG		CAGCTCATAGNNNGATCGACATG		CATCATTTTCANNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6622	TGCAGGACCAGAGAATTCTGAATA	6862	TGCAGGACCAGAGAATTCTGAATA	7102
CAACGACGTTNNNGATCGACATG		CAACAGTCTGNNNGATCGACATG		CATGCCGCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6623	TGCAGGACCAGAGAATTCTGAATA	6863	TGCAGGACCAGAGAATTCTGAATA	7103
CAAAGTAGCCNNNGATCGACATG		CATTTAAGTGNNGATCGACATG		CACGCAAGANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6624	TGCAGGACCAGAGAATTCTGAATA	6864	TGCAGGACCAGAGAATTCTGAATA	7104
CAAGTGAAGCANNNGATCGACATG		CAGATTAATCANNNGATCGACATG		CATAGACCACNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6625	TGCAGGACCAGAGAATTCTGAATA	6865	TGCAGGACCAGAGAATTCTGAATA	7105
CATTCTCATANNNGATCGACATG		CAGAGAAAGGNNNGATCGACATG		CAACCGAAGANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6626	TGCAGGACCAGAGAATTCTGAATA	6866	TGCAGGACCAGAGAATTCTGAATA	7106
CAAGTAGAGCANNNGATCGACATG		CAACATTTCGNNNGATCGACATG		CATCTTGTANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6627	TGCAGGACCAGAGAATTCTGAATA	6867	TGCAGGACCAGAGAATTCTGAATA	7107
CATCCCGATGNNNGATCGACATG		CATTGCCGCTNNNGATCGACATG		CACAGACTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6628	TGCAGGACCAGAGAATTCTGAATA	6868	TGCAGGACCAGAGAATTCTGAATA	7108
CACAAGGTCTNNNGATCGACATG		CAGCTCACANNNGATCGACATG		CAGATCTGCANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6629	TGCAGGACCAGAGAATTCTGAATA	6869	TGCAGGACCAGAGAATTCTGAATA	7109
CAGAGTATGNNNGATCGACATG		CACGTTAAGCANNNGATCGACATG		CATCGAAGANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6630	TGCAGGACCAGAGAATTCTGAATA	6870	TGCAGGACCAGAGAATTCTGAATA	7110
CACCCGAGTGNNGATCGACATG		CAGTACGTTGNNGATCGACATG		CACGGAGCAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6631	TGCAGGACCAGAGAATTCTGAATA	6871	TGCAGGACCAGAGAATTCTGAATA	7111
CAGAAGCTCTNNNGATCGACATG		CATGCTCAGANNNGATCGACATG		CACACCGGACNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6632	TGCAGGACCAGAGAATTCTGAATA	6872	TGCAGGACCAGAGAATTCTGAATA	7112
CAGTGAAGANNNGATCGACATG		CATACCAAAATNNNGATCGACATG		CAATAACGTTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6633	TGCAGGACCAGAGAATTCTGAATA	6873	TGCAGGACCAGAGAATTCTGAATA	7113
CAAACGGTAGNNNGATCGACATG		CACCATGATGNNNGATCGACATG		CATGTCGANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6634	TGCAGGACCAGAGAATTCTGAATA	6874	TGCAGGACCAGAGAATTCTGAATA	7114
CACCTTCGACTNNNGATCGACATG		CATATATGCANNNGATCGACATG		CATATGGACNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6635	TGCAGGACCAGAGAATTCTGAATA	6875	TGCAGGACCAGAGAATTCTGAATA	7115
CACCGACGACNNNGATCGACATG		CACCGCTTATNNNGATCGACATG		CACAACCTTGGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6636	TGCAGGACCAGAGAATTCTGAATA	6876	TGCAGGACCAGAGAATTCTGAATA	7116
CACTACACTCANNNGATCGACATG		CAGGCGTCACNNNGATCGACATG		CACAATCGACNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6637	TGCAGGACCAGAGAATTCTGAATA	6877	TGCAGGACCAGAGAATTCTGAATA	7117
CAAGCTAAGGNNNGATCGACATG		CAGGCAATAAGNNNGATCGACATG		CAGCAAGGACNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6638	TGCAGGACCAGAGAATTCTGAATA	6878	TGCAGGACCAGAGAATTCTGAATA	7118
CAGAGTATCCNNNGATCGACATG		CAGAATTTGNNNGATCGACATG		CAGCCAACGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6639	TGCAGGACCAGAGAATTCTGAATA	6879	TGCAGGACCAGAGAATTCTGAATA	7119
CATCCTACANNNGATCGACATG		CATCTTGACNNNGATCGACATG		CATCGTTAAANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6640	TGCAGGACCAGAGAATTCTGAATA	6880	TGCAGGACCAGAGAATTCTGAATA	7120
CATTTTCTCANNNGATCGACATG		CAACACCTAGNNNGATCGACATG		CACTAGCGTANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6641	TGCAGGACCAGAGAATTCTGAATA	6881	TGCAGGACCAGAGAATTCTGAATA	7121
CACGGATAAGNNNGATCGACATG		CAATCTCACNNNGATCGACATG		CACTGAGTTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6642	TGCAGGACCAGAGAATTCTGAATA	6882	TGCAGGACCAGAGAATTCTGAATA	7122
CACAAATCGCANNNGATCGACATG		CATTGAGATTNNNGATCGACATG		CATGGCGCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6643	TGCAGGACCAGAGAATTCTGAATA	6883	TGCAGGACCAGAGAATTCTGAATA	7123
CAGTGTCCGNNNGATCGACATG		CATCAACCAGNNNGATCGACATG		CAGTGACTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6644	TGCAGGACCAGAGAATTCTGAATA	6884	TGCAGGACCAGAGAATTCTGAATA	7124
CAAAGCTATTNNNGATCGACATG		CATTTGACGNNNGATCGACATG		CACTGCCAATNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6645	TGCAGGACCAGAGAATTCTGAATA	6885	TGCAGGACCAGAGAATTCTGAATA	7125
CAACCGGACNNNGATCGACATG		CAGTTCAFTTNNNGATCGACATG		CACATGACACNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6646	TGCAGGACCAGAGAATTCTGAATA	6886	TGCAGGACCAGAGAATTCTGAATA	7126
CATTAAATGCNNNGATCGACATG		CAGAGTGGTANNNGATCGACATG		CAGCGATTTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6647	TGCAGGACCAGAGAATTCTGAATA	6887	TGCAGGACCAGAGAATTCTGAATA	7127
CACTGCAAGTNNNGATCGACATG		CAAGTTGCTGNNNGATCGACATG		CAACTAGGAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6648	TGCAGGACCAGAGAATTCTGAATA	6888	TGCAGGACCAGAGAATTCTGAATA	7128
CACCCCTAACNNNGATCGACATG		CAGATTTTAGNNNGATCGACATG		CAGCGCAGCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6649	TGCAGGACCAGAGAATTCTGAATA	6889	TGCAGGACCAGAGAATTCTGAATA	7129
CAAGTGAGACNNNGATCGACATG		CACCTAACAAATNNNGATCGACATG		CACACAGCCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6650	TGCAGGACCAGAGAATTCTGAATA	6890	TGCAGGACCAGAGAATTCTGAATA	7130
CATATTAGACNNNGATCGACATG		CAAGCTGATCANNNGATCGACATG		CAGCCTTGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6651	TGCAGGACCAGAGAATTCTGAATA	6891	TGCAGGACCAGAGAATTCTGAATA	7131
CAGTTGGCTANNNGATCGACATG		CACGACGGCTNNNGATCGACATG		CAAATATCGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6652	TGCAGGACCAGAGAATTCTGAATA	6892	TGCAGGACCAGAGAATTCTGAATA	7132
CATCGCTAAGNNNGATCGACATG		CACGGCGTACNNNGATCGACATG		CACCGAAAGANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6653	TGCAGGACCAGAGAATTCTGAATA	6893	TGCAGGACCAGAGAATTCTGAATA	7133
CAAGCCCTCANNNGATCGACATG		CATTGCAAGTNNNGATCGACATG		CACAAAGGTGNNNGATCGACATG	

FIG. 21F

Poal-28	SEQ ID NO:	Poal-29	SEQ ID NO:	Poal-30	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATA	6654	TGCAGGACCAGAGAATTCTGAATA	6894	TGCAGGACCAGAGAATTCTGAATA	7134
CATTACGAATNNNGATCGACATG		CATGAGCTGTNNNGATCGACATG		CAAAATCCATNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6655	TGCAGGACCAGAGAATTCTGAATA	6895	TGCAGGACCAGAGAATTCTGAATA	7135
CAGGCCACCCNNNGATCGACATG		CAAGTCTCAGNNNGATCGACATG		CAAACAATCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6656	TGCAGGACCAGAGAATTCTGAATA	6896	TGCAGGACCAGAGAATTCTGAATA	7136
CATCCTTATANNNGATCGACATG		CAATTCCCTANNNGATCGACATG		CACATTGGCANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6657	TGCAGGACCAGAGAATTCTGAATA	6897	TGCAGGACCAGAGAATTCTGAATA	7137
CATCAGTCTCANNNGATCGACATG		CAGAGAGAGANNNGATCGACATG		CACTACAACGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6658	TGCAGGACCAGAGAATTCTGAATA	6898	TGCAGGACCAGAGAATTCTGAATA	7138
CACGACTTCTNNNGATCGACATG		CAGCAGAGCGNNNGATCGACATG		CAATCGAGGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6659	TGCAGGACCAGAGAATTCTGAATA	6899	TGCAGGACCAGAGAATTCTGAATA	7139
CAAGGTAACGNNNGATCGACATG		CAGGCACATANNNGATCGACATG		CACGCGTCTCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6660	TGCAGGACCAGAGAATTCTGAATA	6900	TGCAGGACCAGAGAATTCTGAATA	7140
CAAGACACTCANNNGATCGACATG		CAGACCTCAANNNGATCGACATG		CATTACGTTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6661	TGCAGGACCAGAGAATTCTGAATA	6901	TGCAGGACCAGAGAATTCTGAATA	7141
CAGGCTTCGGNNNGATCGACATG		CAATAACTCANNNGATCGACATG		CAGTAGTCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6662	TGCAGGACCAGAGAATTCTGAATA	6902	TGCAGGACCAGAGAATTCTGAATA	7142
CACAATTTCGGNNNGATCGACATG		CATCATATTCTNNNGATCGACATG		CATGCGTCTCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6663	TGCAGGACCAGAGAATTCTGAATA	6903	TGCAGGACCAGAGAATTCTGAATA	7143
CAGGCTCTGGNNNGATCGACATG		CAGATAGAAATNNNGATCGACATG		CAATACATTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6664	TGCAGGACCAGAGAATTCTGAATA	6904	TGCAGGACCAGAGAATTCTGAATA	7144
CATCTCTGACNNNGATCGACATG		CACCTGGACGNNNGATCGACATG		CATATAAAAAANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6665	TGCAGGACCAGAGAATTCTGAATA	6905	TGCAGGACCAGAGAATTCTGAATA	7145
CAGAGTAGGTNNNGATCGACATG		CATAACCCAGNNNGATCGACATG		CATACCTGCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6666	TGCAGGACCAGAGAATTCTGAATA	6906	TGCAGGACCAGAGAATTCTGAATA	7146
CAATTTTANNNGATCGACATG		CAGCAGCGCTNNNGATCGACATG		CATGAGAACGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6667	TGCAGGACCAGAGAATTCTGAATA	6907	TGCAGGACCAGAGAATTCTGAATA	7147
CAATTTCTACNNNGATCGACATG		CACAGACCGCANNNGATCGACATG		CAGGAACTGANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6668	TGCAGGACCAGAGAATTCTGAATA	6908	TGCAGGACCAGAGAATTCTGAATA	7148
CAAACGCTGTNNNGATCGACATG		CATTAAGAAGNNNGATCGACATG		CAAGAGCGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATA	6669	TGCAGGACCAGAGAATTCTGAATA	6909	TGCAGGACCAGAGAATTCTGAATA	7149
CAATCGACTGNNNTGCATCAGGT		CATTCTATAAGNNNTGCATCAGGT		CAACGCCACGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6670	TGCAGGACCAGAGAATTCTGAATA	6910	TGCAGGACCAGAGAATTCTGAATA	7150
CATAACGATTNNNTGCATCAGGT		CACCACAGCGNNNTGCATCAGGT		CATCCCTTAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6671	TGCAGGACCAGAGAATTCTGAATA	6911	TGCAGGACCAGAGAATTCTGAATA	7151
CAGCCCAGCANNNTGCATCAGGT		CAGTCAGGCCNNNTGCATCAGGT		CATCGGCATANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6672	TGCAGGACCAGAGAATTCTGAATA	6912	TGCAGGACCAGAGAATTCTGAATA	7152
CAACAAACGNNNTGCATCAGGT		CAGTCGGCACNNNTGCATCAGGT		CACGCCCTCCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6673	TGCAGGACCAGAGAATTCTGAATA	6913	TGCAGGACCAGAGAATTCTGAATA	7153
CAAGAGTGCANNNTGCATCAGGT		CATAGTCTGNNNTGCATCAGGT		CAAGGTGGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6674	TGCAGGACCAGAGAATTCTGAATA	6914	TGCAGGACCAGAGAATTCTGAATA	7154
CACGGATCGCANNNTGCATCAGGT		CACATTATCTNNNTGCATCAGGT		CAAGGTTCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6675	TGCAGGACCAGAGAATTCTGAATA	6915	TGCAGGACCAGAGAATTCTGAATA	7155
CAGGAATCCTNNNTGCATCAGGT		CAGAAGACCANNNTGCATCAGGT		CACGGAAGGCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6676	TGCAGGACCAGAGAATTCTGAATA	6916	TGCAGGACCAGAGAATTCTGAATA	7156
CAACCTAAATNNNTGCATCAGGT		CAAATTCCTNNNTGCATCAGGT		CAAGGCATTCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6677	TGCAGGACCAGAGAATTCTGAATA	6917	TGCAGGACCAGAGAATTCTGAATA	7157
CACGTATCGANNNTGCATCAGGT		CAGCCATCGGNNNTGCATCAGGT		CACACCAGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6678	TGCAGGACCAGAGAATTCTGAATA	6918	TGCAGGACCAGAGAATTCTGAATA	7158
CATCAGATATNNNTGCATCAGGT		CATATAATTANNNTGCATCAGGT		CATATGCGTGNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6679	TGCAGGACCAGAGAATTCTGAATA	6919	TGCAGGACCAGAGAATTCTGAATA	7159
CAGCGACCGTNNNTGCATCAGGT		CAACGAACAGNNNTGCATCAGGT		CAGCATAGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6680	TGCAGGACCAGAGAATTCTGAATA	6920	TGCAGGACCAGAGAATTCTGAATA	7160
CATCAGACTGNNNTGCATCAGGT		CAAGGCCGCTNNNTGCATCAGGT		CATCAGTAGGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6681	TGCAGGACCAGAGAATTCTGAATA	6921	TGCAGGACCAGAGAATTCTGAATA	7161
CAATGCACGTNNNTGCATCAGGT		CACAAAGAGCANNNTGCATCAGGT		CAGCCGAGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6682	TGCAGGACCAGAGAATTCTGAATA	6922	TGCAGGACCAGAGAATTCTGAATA	7162
CATCTACTGCGNNNTGCATCAGGT		CATTTCAGGACNNNTGCATCAGGT		CAACTGCCAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6683	TGCAGGACCAGAGAATTCTGAATA	6923	TGCAGGACCAGAGAATTCTGAATA	7163
CACTCGTTGTNNNTGCATCAGGT		CAAGCACGCCNNNTGCATCAGGT		CACCGACAATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6684	TGCAGGACCAGAGAATTCTGAATA	6924	TGCAGGACCAGAGAATTCTGAATA	7164
CACTGTGTAGNNNTGCATCAGGT		CAGACACATCANNNTGCATCAGGT		CACAGGCCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6685	TGCAGGACCAGAGAATTCTGAATA	6925	TGCAGGACCAGAGAATTCTGAATA	7165
CAGCTTGCTNNNTGCATCAGGT		CACGATACACNNNTGCATCAGGT		CACAACCCCNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATA	6686	TGCAGGACCAGAGAATTCTGAATA	6926	TGCAGGACCAGAGAATTCTGAATA	7166
CACTTTTCTNNNTGCATCAGGT		CAATACGCGTNNNTGCATCAGGT		CAAAGACGACNNNTGCATCAGGT	

FIG. 21G

Poel-28	SEQ ID NO:	Poel-29	SEQ ID NO:	Poel-30	SEQ ID NO:
TGCAGGACCAGAGAATTGGAATA	6687	TGCAGGACCAGAGAATTGGAATA	6927	TGCAGGACCAGAGAATTGGAATA	7167
CATCAACTCCNNNTGCATCAGGT		CATACACGCCANNNTGCATCAGGT		CATACAAGAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6688	TGCAGGACCAGAGAATTGGAATA	6928	TGCAGGACCAGAGAATTGGAATA	7168
CAATCCAGCANNNTGCATCAGGT		CACCTCTCTCNNNTGCATCAGGT		CAATAGCCCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6689	TGCAGGACCAGAGAATTGGAATA	6929	TGCAGGACCAGAGAATTGGAATA	7169
CAAACCGCTANNNTGCATCAGGT		CACAATGAGGNNNTGCATCAGGT		CATTGGATATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6690	TGCAGGACCAGAGAATTGGAATA	6930	TGCAGGACCAGAGAATTGGAATA	7170
CACGCCCTGTNNNTGCATCAGGT		CACACAGTGTNNNTGCATCAGGT		CACATATCGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6691	TGCAGGACCAGAGAATTGGAATA	6931	TGCAGGACCAGAGAATTGGAATA	7171
CATAAGGCTCNNNTGCATCAGGT		CAACATACTNNNTGCATCAGGT		CACCTCTGACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6692	TGCAGGACCAGAGAATTGGAATA	6932	TGCAGGACCAGAGAATTGGAATA	7172
CATGTCTATGNNNTGCATCAGGT		CACGCCATCGNNNTGCATCAGGT		CAAAATAGGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6693	TGCAGGACCAGAGAATTGGAATA	6933	TGCAGGACCAGAGAATTGGAATA	7173
CATAGCAGTGNNTGCATCAGGT		CAAGTAGATANNNTGCATCAGGT		CACGTTGCTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6694	TGCAGGACCAGAGAATTGGAATA	6934	TGCAGGACCAGAGAATTGGAATA	7174
CAGCGCTGACNNNTGCATCAGGT		CAGCGATCCGNNNTGCATCAGGT		CATTTCCCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6695	TGCAGGACCAGAGAATTGGAATA	6935	TGCAGGACCAGAGAATTGGAATA	7175
CATATATCCTNNNTGCATCAGGT		CAATTAAGTTNNNTGCATCAGGT		CAACTACTCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6696	TGCAGGACCAGAGAATTGGAATA	6936	TGCAGGACCAGAGAATTGGAATA	7176
CACACGAAAGNNNTGCATCAGGT		CAAGATTCTANNNTGCATCAGGT		CAACTCTGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6697	TGCAGGACCAGAGAATTGGAATA	6937	TGCAGGACCAGAGAATTGGAATA	7177
CAATAAGTCTNNNTGCATCAGGT		CATCACCTGTNNNTGCATCAGGT		CACCTACTCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6698	TGCAGGACCAGAGAATTGGAATA	6938	TGCAGGACCAGAGAATTGGAATA	7178
CAGCTGTCCNNNTGCATCAGGT		CACAAATACTNNNTGCATCAGGT		CAACTGCTAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6699	TGCAGGACCAGAGAATTGGAATA	6939	TGCAGGACCAGAGAATTGGAATA	7179
CAATGACCTGNNNTGCATCAGGT		CATTTAGCAANNNTGCATCAGGT		CACGCCGATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6700	TGCAGGACCAGAGAATTGGAATA	6940	TGCAGGACCAGAGAATTGGAATA	7180
CAATACCCCTNNNTGCATCAGGT		CATCCTAGTCTNNNTGCATCAGGT		CAGGCTTTCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6701	TGCAGGACCAGAGAATTGGAATA	6941	TGCAGGACCAGAGAATTGGAATA	7181
CATGAGGTAGNNNTGCATCAGGT		CATAAAGAGTNNNTGCATCAGGT		CACCTGCACTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6702	TGCAGGACCAGAGAATTGGAATA	6942	TGCAGGACCAGAGAATTGGAATA	7182
CACGAATCTGNNNTGCATCAGGT		CACATGCACANNNTGCATCAGGT		CAACATCAGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6703	TGCAGGACCAGAGAATTGGAATA	6943	TGCAGGACCAGAGAATTGGAATA	7183
CAGCCGACCTGNNNTGCATCAGGT		CATTTCAACTNNNTGCATCAGGT		CATCAGTTCTCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6704	TGCAGGACCAGAGAATTGGAATA	6944	TGCAGGACCAGAGAATTGGAATA	7184
CATTCAAACANNNTGCATCAGGT		CACCTGATGTGNNNTGCATCAGGT		CATCAGGATGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6705	TGCAGGACCAGAGAATTGGAATA	6945	TGCAGGACCAGAGAATTGGAATA	7185
CAAGGCTTACNNNTGCATCAGGT		CACCCGTTCGNNNTGCATCAGGT		CAGTATGCACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6706	TGCAGGACCAGAGAATTGGAATA	6946	TGCAGGACCAGAGAATTGGAATA	7186
CAAAAACCGCANNNTGCATCAGGT		CACATAAGAANNNTGCATCAGGT		CATCAGGCCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6707	TGCAGGACCAGAGAATTGGAATA	6947	TGCAGGACCAGAGAATTGGAATA	7187
CAGATAGGACNNNTGCATCAGGT		CAGATTACGNNNTGCATCAGGT		CAGTTTTCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6708	TGCAGGACCAGAGAATTGGAATA	6948	TGCAGGACCAGAGAATTGGAATA	7188
CAATGGCGAANNNTGCATCAGGT		CACCTGACGATNNNTGCATCAGGT		CAGGTCCGAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6709	TGCAGGACCAGAGAATTGGAATA	6949	TGCAGGACCAGAGAATTGGAATA	7189
CAACCAAGAGNNNTGCATCAGGT		CAACTTTCTANNNTGCATCAGGT		CAATAAGGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6710	TGCAGGACCAGAGAATTGGAATA	6950	TGCAGGACCAGAGAATTGGAATA	7190
CACAAACGCTNNNTGCATCAGGT		CACACATAGCANNNTGCATCAGGT		CAAGCCGACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6711	TGCAGGACCAGAGAATTGGAATA	6951	TGCAGGACCAGAGAATTGGAATA	7191
CACGCTTTCAANNNTGCATCAGGT		CATTAGTCAANNNTGCATCAGGT		CACATGTGAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6712	TGCAGGACCAGAGAATTGGAATA	6952	TGCAGGACCAGAGAATTGGAATA	7192
CATCCAGGCCGNNNTGCATCAGGT		CATGGTCGCGNNNTGCATCAGGT		CATTTTAGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6713	TGCAGGACCAGAGAATTGGAATA	6953	TGCAGGACCAGAGAATTGGAATA	7193
CATTGAAATCANNNTGCATCAGGT		CATTCTGACNNNTGCATCAGGT		CATCGAGTTGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6714	TGCAGGACCAGAGAATTGGAATA	6954	TGCAGGACCAGAGAATTGGAATA	7194
CACCTGCTGCGNNNTGCATCAGGT		CATAAAACCTNNNTGCATCAGGT		CAGCCACCTCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6715	TGCAGGACCAGAGAATTGGAATA	6955	TGCAGGACCAGAGAATTGGAATA	7195
CACGAATGAGNNNTGCATCAGGT		CAACTATAACNNNTGCATCAGGT		CATGTTGTGGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6716	TGCAGGACCAGAGAATTGGAATA	6956	TGCAGGACCAGAGAATTGGAATA	7196
CATGTGTAAANNNTGCATCAGGT		CATATGATGTNNNTGCATCAGGT		CAGTTGTGTGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6717	TGCAGGACCAGAGAATTGGAATA	6957	TGCAGGACCAGAGAATTGGAATA	7197
CATTCAAACNNNTGCATCAGGT		CATCACCGCCNNNTGCATCAGGT		CACGTGAACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6718	TGCAGGACCAGAGAATTGGAATA	6958	TGCAGGACCAGAGAATTGGAATA	7198
CACAGCCAGNNNTGCATCAGGT		CAAGGTTATTNNNTGCATCAGGT		CAAAGGCTCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTGGAATA	6719	TGCAGGACCAGAGAATTGGAATA	6959	TGCAGGACCAGAGAATTGGAATA	7199
CAGACAGTAGNNNTGCATCAGGT		CAAGCAGCTNNNTGCATCAGGT		CATATTCTGNNNTGCATCAGGT	

FIG. 21H

Poal-28	SEQ ID NO:	Poal-29	SEQ ID NO:	Poal-30	SEQ ID NO:
TGCAGGACCAGAGAATTCGAATA CACATTGTNNNTGCATCAGGT	6720	TGCAGGACCAGAGAATTCGAATA CATCGAGACTNNNTGCATCAGGT	6960	TGCAGGACCAGAGAATTCGAATA CACATTACTNNNTGCATCAGGT	7200
TGCAGGACCAGAGAATTCGAATA CATAATCCAANNNTGCATCAGGT	6721	TGCAGGACCAGAGAATTCGAATA CACACACTTCNNNTGCATCAGGT	6961	TGCAGGACCAGAGAATTCGAATA CACCAGACTNNNTGCATCAGGT	7201
TGCAGGACCAGAGAATTCGAATA CACGTACAACNNNTGCATCAGGT	6722	TGCAGGACCAGAGAATTCGAATA CAAAAAACNNNTGCATCAGGT	6962	TGCAGGACCAGAGAATTCGAATA CAAGTCCAGNNNTGCATCAGGT	7202
TGCAGGACCAGAGAATTCGAATA CAATATTCGANNNTGCATCAGGT	6723	TGCAGGACCAGAGAATTCGAATA CATACAGCCANNNTGCATCAGGT	6963	TGCAGGACCAGAGAATTCGAATA CAAACCAGTCNNNTGCATCAGGT	7203
TGCAGGACCAGAGAATTCGAATA CATAATTATANNNTGCATCAGGT	6724	TGCAGGACCAGAGAATTCGAATA CAATGAAAACNNNTGCATCAGGT	6964	TGCAGGACCAGAGAATTCGAATA CATGGCTCAANNNTGCATCAGGT	7204
TGCAGGACCAGAGAATTCGAATA CAGATGCAGANNNTGCATCAGGT	6725	TGCAGGACCAGAGAATTCGAATA CAGTGATGCTNNNTGCATCAGGT	6965	TGCAGGACCAGAGAATTCGAATA CATCTTTATGNNNTGCATCAGGT	7205
TGCAGGACCAGAGAATTCGAATA CAGGAGCCAGNNNTGCATCAGGT	6726	TGCAGGACCAGAGAATTCGAATA CATTAACAGTNNNTGCATCAGGT	6966	TGCAGGACCAGAGAATTCGAATA CAGGTGACTTNNNTGCATCAGGT	7206
TGCAGGACCAGAGAATTCGAATA CAGCGAGTTTNNNTGCATCAGGT	6727	TGCAGGACCAGAGAATTCGAATA CACAAACGCGNNNTGCATCAGGT	6967	TGCAGGACCAGAGAATTCGAATA CATCCTAACCNNNTGCATCAGGT	7207
TGCAGGACCAGAGAATTCGAATA CAAAGTGACGNNNTGCATCAGGT	6728	TGCAGGACCAGAGAATTCGAATA CATGTGCCCCNNNTGCATCAGGT	6968	TGCAGGACCAGAGAATTCGAATA CAGCGTAAAGNNNTGCATCAGGT	7208

FIG. 22A

Pool-31	SEQ ID NO:	Pool-32	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATAC	7209	TGCAGGACCAGAGAATTCTGAATA	7449
ATGGTCCAANNACGTATGCCA		CATTCCAATTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7210	TGCAGGACCAGAGAATTCTGAATA	7450
AGTACTCAGNNACGTATGCCA		CATGTACAGCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7211	TGCAGGACCAGAGAATTCTGAATA	7451
AGAAGCCCCNNNACGTATGCCA		CACAGGAGCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7212	TGCAGGACCAGAGAATTCTGAATA	7452
ATTAAACCGNNNACGTATGCCA		CAATGCGTTGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7213	TGCAGGACCAGAGAATTCTGAATA	7453
ATAACCTGGNNNACGTATGCCA		CATATTTTTCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7214	TGCAGGACCAGAGAATTCTGAATA	7454
AGTCGACTANNNACGTATGCCA		CAAAATTCGCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7215	TGCAGGACCAGAGAATTCTGAATA	7455
ACCAAACGTNNNACGTATGCCA		CATCTGACGANNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7216	TGCAGGACCAGAGAATTCTGAATA	7456
AACGTATCGNNNACGTATGCCA		CACCGCGCTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7217	TGCAGGACCAGAGAATTCTGAATA	7457
ACACGGCCANNNACGTATGCCA		CAAAACACCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7218	TGCAGGACCAGAGAATTCTGAATA	7458
AAGGTTTGCNNNACGTATGCCA		CAGGTTGTGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7219	TGCAGGACCAGAGAATTCTGAATA	7459
ACGACGCGTNNNACGTATGCCA		CAACTAACCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7220	TGCAGGACCAGAGAATTCTGAATA	7460
ACCGACGTGNNNACGTATGCCA		CATCAGGAGANNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7221	TGCAGGACCAGAGAATTCTGAATA	7461
ACAGTTTNTNNNACGTATGCCA		CAGTCTGCGGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7222	TGCAGGACCAGAGAATTCTGAATA	7462
ATGCCCGGANNNACGTATGCCA		CAACTGGCGCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7223	TGCAGGACCAGAGAATTCTGAATA	7463
AGCCACTCCNNNACGTATGCCA		CACCACTCTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7224	TGCAGGACCAGAGAATTCTGAATA	7464
AGACGAAGTNNNACGTATGCCA		CAGCGAAGCGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7225	TGCAGGACCAGAGAATTCTGAATA	7465
AGGTTCCCTTNNNACGTATGCCA		CAGGCGCCCGCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7226	TGCAGGACCAGAGAATTCTGAATA	7466
ACCGGAATTNNNACGTATGCCA		CAGAGCACCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7227	TGCAGGACCAGAGAATTCTGAATA	7467
ATCGGCAGCNNNACGTATGCCA		CACCCAAAGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7228	TGCAGGACCAGAGAATTCTGAATA	7468
AGCTAGAGANNNACGTATGCCA		CACCGAATAGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7229	TGCAGGACCAGAGAATTCTGAATA	7469
ACCACTTACNNNACGTATGCCA		CAAGTAAGATNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7230	TGCAGGACCAGAGAATTCTGAATA	7470
AACCACCGNNNACGTATGCCA		CATCTCACACNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7231	TGCAGGACCAGAGAATTCTGAATA	7471
AGAAACATANNNACGTATGCCA		CAGGCCCAANNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7232	TGCAGGACCAGAGAATTCTGAATA	7472
AGCTGAAAGNNNACGTATGCCA		CAGGATTTGCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7233	TGCAGGACCAGAGAATTCTGAATA	7473
ATAAGAAGTNNNACGTATGCCA		CAAATGACAANNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7234	TGCAGGACCAGAGAATTCTGAATA	7474
ACGTGACTANNNACGTATGCCA		CATAAAAAATNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7235	TGCAGGACCAGAGAATTCTGAATA	7475
ATTAAAGATCNNNACGTATGCCA		CATAATGGCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7236	TGCAGGACCAGAGAATTCTGAATA	7476
ATGGATCACNNNACGTATGCCA		CAGTTGCTTCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7237	TGCAGGACCAGAGAATTCTGAATA	7477
ACCGAGCTGNNNACGTATGCCA		CACGTTTCACNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7238	TGCAGGACCAGAGAATTCTGAATA	7478
ACTCATAAANNNACGTATGCCA		CAGAACAAATNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7239	TGCAGGACCAGAGAATTCTGAATA	7479
ACTCTACTGNNNACGTATGCCA		CAATAGAAGTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7240	TGCAGGACCAGAGAATTCTGAATA	7480
AAGGTGAGTNNNACGTATGCCA		CAGTAAGGCANNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7241	TGCAGGACCAGAGAATTCTGAATA	7481
AGAACACTCNNNACGTATGCCA		CAGAGATGCANNNACGTATGCCA	

FIG. 22B

Pool-31	SEQ ID NO:	Pool-32	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATAC	7242	TGCAGGACCAGAGAATTCTGAATA	7482
AGGCAGAGCANNACGTATGCCA		CACACCATCTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7243	TGCAGGACCAGAGAATTCTGAATA	7483
ATTTCCAGCANNACGTATGCCA		CAGATACACCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7244	TGCAGGACCAGAGAATTCTGAATA	7484
ACCCATCATNNNACGTATGCCA		CAGATACTGCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7245	TGCAGGACCAGAGAATTCTGAATA	7485
AATCAGCGTNNNACGTATGCCA		CACGTAACCTGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7246	TGCAGGACCAGAGAATTCTGAATA	7486
ATGAAACACNNNACGTATGCCA		CATCCTCTTCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7247	TGCAGGACCAGAGAATTCTGAATA	7487
AATGCGGAANNACGTATGCCA		CATGCGGTGCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7248	TGCAGGACCAGAGAATTCTGAATA	7488
ACGGATTTCANNNACGTATGCCA		CAACAGGAACNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7249	TGCAGGACCAGAGAATTCTGAATA	7489
AGTCATACGNNNACGTATGCCA		CAAAAATTTTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7250	TGCAGGACCAGAGAATTCTGAATA	7490
AACCTGCTTNNNACGTATGCCA		CAAAAGTCACNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7251	TGCAGGACCAGAGAATTCTGAATA	7491
AGTTGTGCANNNACGTATGCCA		CATCTACGAGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7252	TGCAGGACCAGAGAATTCTGAATA	7492
AGAAATCGGNNNACGTATGCCA		CAGATCTTCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7253	TGCAGGACCAGAGAATTCTGAATA	7493
AAAGTTAGANNNACGTATGCCA		CAGGACACCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7254	TGCAGGACCAGAGAATTCTGAATA	7494
ATGTAACGCNNNACGTATGCCA		CAATAGGTGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7255	TGCAGGACCAGAGAATTCTGAATA	7495
AGTTTTGAANNNACGTATGCCA		CACCATCGCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7256	TGCAGGACCAGAGAATTCTGAATA	7496
ACAAACTGCNNNACGTATGCCA		CATGATCTCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7257	TGCAGGACCAGAGAATTCTGAATA	7497
AGCCTGAGCANNNACGTATGCCA		CACGCGAATTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7258	TGCAGGACCAGAGAATTCTGAATA	7498
ATCTTCCAGNNNACGTATGCCA		CATATATAATNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7259	TGCAGGACCAGAGAATTCTGAATA	7499
ATACCCCTACNNNACGTATGCCA		CATATCGCCTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7260	TGCAGGACCAGAGAATTCTGAATA	7500
ATCATAGATNNNACGTATGCCA		CATTACGAGCANNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7261	TGCAGGACCAGAGAATTCTGAATA	7501
AGTATAGAANNNACGTATGCCA		CAGGTTTCTCANNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7262	TGCAGGACCAGAGAATTCTGAATA	7502
ACCCCTAAAGNNNACGTATGCCA		CACCTGCGAANNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7263	TGCAGGACCAGAGAATTCTGAATA	7503
AGCGGTTTANNNACGTATGCCA		CAGACATTTANNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7264	TGCAGGACCAGAGAATTCTGAATA	7504
ATAGCTCAGNNNACGTATGCCA		CAACACGAGANNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7265	TGCAGGACCAGAGAATTCTGAATA	7505
ACCGTCCCANNNACGTATGCCA		CATTGCCCGCANNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7266	TGCAGGACCAGAGAATTCTGAATA	7506
AAGTGCGAANNNACGTATGCCA		CACAGTCCCTNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7267	TGCAGGACCAGAGAATTCTGAATA	7507
ATGAGCTTGNNNACGTATGCCA		CAGCATTTGNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7268	TGCAGGACCAGAGAATTCTGAATA	7508
ATATCGTGGNNNACGTATGCCA		CAGGATATCCNNNACGTATGCCA	
TGCAGGACCAGAGAATTCTGAATAC	7269	TGCAGGACCAGAGAATTCTGAATA	7509
ATCAGACACNNNCTAGCGTTAC		CACCAGGAGGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7270	TGCAGGACCAGAGAATTCTGAATA	7510
ATACCCCTTGNNNCTAGCGTTAC		CATCGCCTTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7271	TGCAGGACCAGAGAATTCTGAATA	7511
ACATCGAGTNNNCTAGCGTTAC		CATTACCCGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7272	TGCAGGACCAGAGAATTCTGAATA	7512
ATGAATCTANNNCTAGCGTTAC		CAATCACCTCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7273	TGCAGGACCAGAGAATTCTGAATA	7513
AAGTGAGTNNNCTAGCGTTAC		CACCAATTCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7274	TGCAGGACCAGAGAATTCTGAATA	7514
ACTGAAGGANNNCTAGCGTTAC		CATGCGTGATNNNCTAGCGTTAC	

FIG. 22C

Pool-31	SEQ ID NO:	Pool-32	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATAC	7275	TGCAGGACCAGAGAATTCTGAATA	7515
AAATCAGTTNNNCTAGCGTTAC		CACCTCGGCTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7276	TGCAGGACCAGAGAATTCTGAATA	7516
ACGCAGGCTNNNCTAGCGTTAC		CAAGGAATTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7277	TGCAGGACCAGAGAATTCTGAATA	7517
ACGGTGCACNNNCTAGCGTTAC		CACCGTACATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7278	TGCAGGACCAGAGAATTCTGAATA	7518
ACGTATCAGNNNCTAGCGTTAC		CACGGTTTAGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7279	TGCAGGACCAGAGAATTCTGAATA	7519
ATAACGCTGNNNCTAGCGTTAC		CATCGTATAANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7280	TGCAGGACCAGAGAATTCTGAATA	7520
AACCGTACANNNCTAGCGTTAC		CATAAGCAAANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7281	TGCAGGACCAGAGAATTCTGAATA	7521
AGCTTAGTGNNNCTAGCGTTAC		CACGGTCTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7282	TGCAGGACCAGAGAATTCTGAATA	7522
ACGAACGCCNNNCTAGCGTTAC		CACCACAGTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7283	TGCAGGACCAGAGAATTCTGAATA	7523
AGTATCGTGNNNCTAGCGTTAC		CAACCACTAGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7284	TGCAGGACCAGAGAATTCTGAATA	7524
ATACAAATCINNCTAGCGTTAC		CACGCAAACTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7285	TGCAGGACCAGAGAATTCTGAATA	7525
ACGTCTTTANNNCTAGCGTTAC		CACCTCAACNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7286	TGCAGGACCAGAGAATTCTGAATA	7526
AAGACCACTNNNCTAGCGTTAC		CAGAGAGGCCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7287	TGCAGGACCAGAGAATTCTGAATA	7527
AACAAGGTGNNNCTAGCGTTAC		CAATATTGGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7288	TGCAGGACCAGAGAATTCTGAATA	7528
AATACTTGANNNCTAGCGTTAC		CACATATGANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7289	TGCAGGACCAGAGAATTCTGAATA	7529
ACTTCGATNNNCTAGCGTTAC		CAATCTTGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7290	TGCAGGACCAGAGAATTCTGAATA	7530
ACGTCTTGTNNNCTAGCGTTAC		CATAAAGGCCNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7291	TGCAGGACCAGAGAATTCTGAATA	7531
AAAGTGGTGNNNCTAGCGTTAC		CACCATTTGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7292	TGCAGGACCAGAGAATTCTGAATA	7532
ATCGGTGGCINNCTAGCGTTAC		CATACCCCTANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7293	TGCAGGACCAGAGAATTCTGAATA	7533
AAAAATCAGNNNCTAGCGTTAC		CAAGAACCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7294	TGCAGGACCAGAGAATTCTGAATA	7534
ATCCCGGTNNNCTAGCGTTAC		CAACGATAGGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7295	TGCAGGACCAGAGAATTCTGAATA	7535
AGGCCAGCTNNNCTAGCGTTAC		CAGGCGCCATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7296	TGCAGGACCAGAGAATTCTGAATA	7536
AGCTGTCTTNNNCTAGCGTTAC		CAAAAATCTCINNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7297	TGCAGGACCAGAGAATTCTGAATA	7537
AAGCATAAANNNCTAGCGTTAC		CAGACTAGCTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7298	TGCAGGACCAGAGAATTCTGAATA	7538
ATGCGAATCINNCTAGCGTTAC		CACGTGAGTTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7299	TGCAGGACCAGAGAATTCTGAATA	7539
ACGTTTCGTNNNCTAGCGTTAC		CACCCGCTGTNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7300	TGCAGGACCAGAGAATTCTGAATA	7540
AGCACTCTTNNNCTAGCGTTAC		CAAAAACCTCINNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7301	TGCAGGACCAGAGAATTCTGAATA	7541
ACTCGCTGCNNNCTAGCGTTAC		CAAGTAACGNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7302	TGCAGGACCAGAGAATTCTGAATA	7542
ACATACAGCINNCTAGCGTTAC		CAATCAACATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7303	TGCAGGACCAGAGAATTCTGAATA	7543
AGAGCAACNNNCTAGCGTTAC		CACCTTTGATNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7304	TGCAGGACCAGAGAATTCTGAATA	7544
AGCTTCCATNNNCTAGCGTTAC		CAGTGTACCANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7305	TGCAGGACCAGAGAATTCTGAATA	7545
ACCTAATTTNNNCTAGCGTTAC		CATGCACACANNNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7306	TGCAGGACCAGAGAATTCTGAATA	7546
AAGCCCGACNNNCTAGCGTTAC		CATATACTTCINNCTAGCGTTAC	
TGCAGGACCAGAGAATTCTGAATAC	7307	TGCAGGACCAGAGAATTCTGAATA	7547
ATGGTGAAGNNNCTAGCGTTAC		CAGAAACTAANNNCTAGCGTTAC	

FIG. 22D

Pool-31	SEQ ID NO:	Pool-32	SEQ ID NO:
TGCAGGACCAGAGAATTTCGAATAC	7308	TGCAGGACCAGAGAATTTCGAATA	7548
AATCGCTGANNNNCTAGCGTTAC		CAATCTCGAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7309	TGCAGGACCAGAGAATTTCGAATA	7549
ATTACTGCCNNNNCTAGCGTTAC		CAATGTCTGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7310	TGCAGGACCAGAGAATTTCGAATA	7550
AGGAGGCCANNNNCTAGCGTTAC		CAAGACATGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7311	TGCAGGACCAGAGAATTTCGAATA	7551
ATACCTGTCCNNNNCTAGCGTTAC		CACGGCAATTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7312	TGCAGGACCAGAGAATTTCGAATA	7552
AATATGCTANNNNCTAGCGTTAC		CATAATGTTGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7313	TGCAGGACCAGAGAATTTCGAATA	7553
AGATCACCANNNNCTAGCGTTAC		CAGCGAGGACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7314	TGCAGGACCAGAGAATTTCGAATA	7554
AGCGGAACGNNNNCTAGCGTTAC		CACGAACATCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7315	TGCAGGACCAGAGAATTTCGAATA	7555
AAATCCTTTNNNNCTAGCGTTAC		CAGCATGTACNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7316	TGCAGGACCAGAGAATTTCGAATA	7556
ATACTATAGNNNNCTAGCGTTAC		CAGCAACTGTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7317	TGCAGGACCAGAGAATTTCGAATA	7557
AGTCTGTAGNNNNCTAGCGTTAC		CAGTACTCTCNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7318	TGCAGGACCAGAGAATTTCGAATA	7558
AGACTATCGNNNNCTAGCGTTAC		CAGGCTAAAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7319	TGCAGGACCAGAGAATTTCGAATA	7559
AAGGATTAAANNNNCTAGCGTTAC		CACCTTTTGANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7320	TGCAGGACCAGAGAATTTCGAATA	7560
ATTACATCTNNNNCTAGCGTTAC		CACGCGAGGAGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7321	TGCAGGACCAGAGAATTTCGAATA	7561
ATTTGGCAGNNNNCTAGCGTTAC		CAGTAAGAATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7322	TGCAGGACCAGAGAATTTCGAATA	7562
ACAGTATGCNNNNCTAGCGTTAC		CATGATTACANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7323	TGCAGGACCAGAGAATTTCGAATA	7563
ATTCGATCCNNNNCTAGCGTTAC		CACAAAAATGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7324	TGCAGGACCAGAGAATTTCGAATA	7564
AAATCCCTTNNNNCTAGCGTTAC		CACCGTGGTGNNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7325	TGCAGGACCAGAGAATTTCGAATA	7565
ACTCTCCCCNNNNCTAGCGTTAC		CAAACGTTATNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7326	TGCAGGACCAGAGAATTTCGAATA	7566
ACAAATTAACNNNNCTAGCGTTAC		CAGCTTGCAANNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7327	TGCAGGACCAGAGAATTTCGAATA	7567
AATTTTGCTNNNNCTAGCGTTAC		CATTAGTCGGNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7328	TGCAGGACCAGAGAATTTCGAATA	7568
AATAAATCCNNNNCTAGCGTTAC		CAACGCCCTNNNNCTAGCGTTAC	
TGCAGGACCAGAGAATTTCGAATAC	7329	TGCAGGACCAGAGAATTTCGAATA	7569
ATACTCGTCNNNGATCGACATG		CAGCGTGAANNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATAC	7330	TGCAGGACCAGAGAATTTCGAATA	7570
AATGCCAAGNNNGATCGACATG		CATGCCTGCCNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATAC	7331	TGCAGGACCAGAGAATTTCGAATA	7571
ATGCGCAGCNNNGATCGACATG		CATCGACGCGNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATAC	7332	TGCAGGACCAGAGAATTTCGAATA	7572
ATGGTAAAAANNNGATCGACATG		CATCATCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATAC	7333	TGCAGGACCAGAGAATTTCGAATA	7573
ACACTCCATTNNNGATCGACATG		CAGTCAGTCANNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATAC	7334	TGCAGGACCAGAGAATTTCGAATA	7574
ACCTATGGANNNGATCGACATG		CACCGGTGACNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATAC	7335	TGCAGGACCAGAGAATTTCGAATA	7575
AATGCTCCTNNNGATCGACATG		CATATCGCGANNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATAC	7336	TGCAGGACCAGAGAATTTCGAATA	7576
AGATTGAAANNNGATCGACATG		CAGACGCGTCNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATAC	7337	TGCAGGACCAGAGAATTTCGAATA	7577
AACACCCAANNNGATCGACATG		CAGAACAGACNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATAC	7338	TGCAGGACCAGAGAATTTCGAATA	7578
ACCGGCATGNNNGATCGACATG		CAGTGTGTGNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATAC	7339	TGCAGGACCAGAGAATTTCGAATA	7579
ATCCGATTCCNNNGATCGACATG		CAGATTGCCGNNNGATCGACATG	
TGCAGGACCAGAGAATTTCGAATAC	7340	TGCAGGACCAGAGAATTTCGAATA	7580
AGAATCCTGNNNGATCGACATG		CAGTAGATTNNNGATCGACATG	

FIG. 22E

Pool-31	SEQ ID NO:	Pool-32	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATAC	7341	TGCAGGACCAGAGAATTCTGAATA	7581
ATTTCGTTCGNNNGATCGACATG		CAGCTTGAGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7342	TGCAGGACCAGAGAATTCTGAATA	7582
ACTTCACTGNNNGATCGACATG		CACGCAACGCNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7343	TGCAGGACCAGAGAATTCTGAATA	7583
ACCCTATTGNNNGATCGACATG		CACCTAATGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7344	TGCAGGACCAGAGAATTCTGAATA	7584
AAGTAGTAANNNGATCGACATG		CAGACAGGATNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7345	TGCAGGACCAGAGAATTCTGAATA	7585
ACACCGTAANNNGATCGACATG		CACTTCCCTTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7346	TGCAGGACCAGAGAATTCTGAATA	7586
ATGTTTCCGNNNGATCGACATG		CATAAGAGATNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7347	TGCAGGACCAGAGAATTCTGAATA	7587
AGCTGGACNNNGATCGACATG		CAACCGAATCNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7348	TGCAGGACCAGAGAATTCTGAATA	7588
AGTAATGTNNNGATCGACATG		CAGCCAACATNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7349	TGCAGGACCAGAGAATTCTGAATA	7589
AAGCTTATANNNGATCGACATG		CATGGCTAACNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7350	TGCAGGACCAGAGAATTCTGAATA	7590
AGCTACCAANNNGATCGACATG		CATCGTTCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7351	TGCAGGACCAGAGAATTCTGAATA	7591
AGATAATGANNNNGATCGACATG		CACAGTTGCANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7352	TGCAGGACCAGAGAATTCTGAATA	7592
AAAATCATCNNNGATCGACATG		CAACTAGCTGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7353	TGCAGGACCAGAGAATTCTGAATA	7593
AAATAGCCNNNGATCGACATG		CAAACTAAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7354	TGCAGGACCAGAGAATTCTGAATA	7594
ATGCTGCTTNNNGATCGACATG		CAGTTTCGAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7355	TGCAGGACCAGAGAATTCTGAATA	7595
ATTACGCAGNNNGATCGACATG		CACTCATAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7356	TGCAGGACCAGAGAATTCTGAATA	7596
ACCCAGCCTNNNGATCGACATG		CAGCAGTATCNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7357	TGCAGGACCAGAGAATTCTGAATA	7597
ACCATTATANNNGATCGACATG		CATATAGTCANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7358	TGCAGGACCAGAGAATTCTGAATA	7598
AGTGCAATCNNNGATCGACATG		CAGGTGTAAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7359	TGCAGGACCAGAGAATTCTGAATA	7599
ACATCAGGTNNNGATCGACATG		CAAGTGAAATNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7360	TGCAGGACCAGAGAATTCTGAATA	7600
AGGCCACANNNGATCGACATG		CAGGTGCTTANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7361	TGCAGGACCAGAGAATTCTGAATA	7601
AAAGCACGANNNGATCGACATG		CATCGCGCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7362	TGCAGGACCAGAGAATTCTGAATA	7602
ACACAGGAANNNGATCGACATG		CAAAGAACTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7363	TGCAGGACCAGAGAATTCTGAATA	7603
AGCAGCCTGNNNGATCGACATG		CATCCTTTCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7364	TGCAGGACCAGAGAATTCTGAATA	7604
AGGCTGCGTNNNGATCGACATG		CATGGCGTCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7365	TGCAGGACCAGAGAATTCTGAATA	7605
ACTCTAGCTNNNGATCGACATG		CAGGCTGTCGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7366	TGCAGGACCAGAGAATTCTGAATA	7606
AGAAGGCTANNNGATCGACATG		CATGTCCATCNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7367	TGCAGGACCAGAGAATTCTGAATA	7607
ATATCTGAANNNGATCGACATG		CAGTTGGAAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7368	TGCAGGACCAGAGAATTCTGAATA	7608
ATACTATTNNNGATCGACATG		CAGTGGACGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7369	TGCAGGACCAGAGAATTCTGAATA	7609
ACATGACCANNNGATCGACATG		CATCCTGGCCNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7370	TGCAGGACCAGAGAATTCTGAATA	7610
AATTCAGGCNNNGATCGACATG		CAATAGGCCANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7371	TGCAGGACCAGAGAATTCTGAATA	7611
AAACCAACNNNGATCGACATG		CAATCCGTGANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7372	TGCAGGACCAGAGAATTCTGAATA	7612
ATTACTGTTNNNGATCGACATG		CAGTAGCTGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7373	TGCAGGACCAGAGAATTCTGAATA	7613
AGGTTCCCCNNNGATCGACATG		CAGAAGACGTNNNGATCGACATG	

FIG. 22F

Pool-31	SEQ ID NO:	Pool-32	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATAC	7374	TGCAGGACCAGAGAATTCTGAATA	7614
AATAAACCTNNNGATCGACATG		CATCCGTACTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7375	TGCAGGACCAGAGAATTCTGAATA	7615
ATTTTCGTGCNNNGATCGACATG		CATGAGGCAANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7376	TGCAGGACCAGAGAATTCTGAATA	7616
AGTGACCATNNNGATCGACATG		CATGAGTTATNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7377	TGCAGGACCAGAGAATTCTGAATA	7617
ACCCTATACNNNGATCGACATG		CAATTGGTGCNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7378	TGCAGGACCAGAGAATTCTGAATA	7618
ACCCCATATNNNGATCGACATG		CAGGCGTTGCNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7379	TGCAGGACCAGAGAATTCTGAATA	7619
AGATAGGTGNNNGATCGACATG		CAGCATCTCTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7380	TGCAGGACCAGAGAATTCTGAATA	7620
AAAATAACGNNNGATCGACATG		CAACTCTCCANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7381	TGCAGGACCAGAGAATTCTGAATA	7621
AATAATCGTNNNGATCGACATG		CAATAAGTAGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7382	TGCAGGACCAGAGAATTCTGAATA	7622
AGTGGACTTNNNGATCGACATG		CAGATTGCCANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7383	TGCAGGACCAGAGAATTCTGAATA	7623
AGTTACTGGNNNGATCGACATG		CAGTTCAGANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7384	TGCAGGACCAGAGAATTCTGAATA	7624
ATCCTAGGANNNGATCGACATG		CAAACCGTACNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7385	TGCAGGACCAGAGAATTCTGAATA	7625
AAAACCTTACNNNGATCGACATG		CACGCGTTGGNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7386	TGCAGGACCAGAGAATTCTGAATA	7626
AAAGTGTCNNNGATCGACATG		CAAATTCCANNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7387	TGCAGGACCAGAGAATTCTGAATA	7627
AGTATTTTCNNNGATCGACATG		CATGACCAGTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7388	TGCAGGACCAGAGAATTCTGAATA	7628
AGAAAGCTGNNNGATCGACATG		CAATGGATTNNNGATCGACATG	
TGCAGGACCAGAGAATTCTGAATAC	7389	TGCAGGACCAGAGAATTCTGAATA	7629
AATCAGCAGNNNTGCATCAGGT		CAAAGTCCACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7390	TGCAGGACCAGAGAATTCTGAATA	7630
AAGGACCTTNNNTGCATCAGGT		CAGTGGCGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7391	TGCAGGACCAGAGAATTCTGAATA	7631
AGAATGTAANNNTGCATCAGGT		CATCTGGATGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7392	TGCAGGACCAGAGAATTCTGAATA	7632
AAAACCTGCCNNNTGCATCAGGT		CACCGATGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7393	TGCAGGACCAGAGAATTCTGAATA	7633
AATACAATCANNNTGCATCAGGT		CAAGTGCTCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7394	TGCAGGACCAGAGAATTCTGAATA	7634
AGAGCAGCGNNNTGCATCAGGT		CACAAATAGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7395	TGCAGGACCAGAGAATTCTGAATA	7635
ATCGTGTTCCNNNTGCATCAGGT		CATACAGGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7396	TGCAGGACCAGAGAATTCTGAATA	7636
ACTGAGCCGNNNTGCATCAGGT		CATATACCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7397	TGCAGGACCAGAGAATTCTGAATA	7637
ACAAGCAGANNNTGCATCAGGT		CAGGAGTAACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7398	TGCAGGACCAGAGAATTCTGAATA	7638
AGTCTTACNNNTGCATCAGGT		CAGCTATGACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7399	TGCAGGACCAGAGAATTCTGAATA	7639
ACGTCTCCGNNNTGCATCAGGT		CAGTTACACGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7400	TGCAGGACCAGAGAATTCTGAATA	7640
AGGCGTTCGNNNTGCATCAGGT		CAGAAGGAAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7401	TGCAGGACCAGAGAATTCTGAATA	7641
ACCGCACCTNNNTGCATCAGGT		CAATGACTTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7402	TGCAGGACCAGAGAATTCTGAATA	7642
AAGTGGTTCNNNTGCATCAGGT		CATCTCTAATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7403	TGCAGGACCAGAGAATTCTGAATA	7643
AGTTGCGTANNNTGCATCAGGT		CAGGAATAATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7404	TGCAGGACCAGAGAATTCTGAATA	7644
ACCAATGCNNNTGCATCAGGT		CAATTATACGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7405	TGCAGGACCAGAGAATTCTGAATA	7645
AGCTTTGTCNNNTGCATCAGGT		CACAAAGGACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7406	TGCAGGACCAGAGAATTCTGAATA	7646
ACTTCAATTNNNTGCATCAGGT		CAATAGAATGNNNTGCATCAGGT	

FIG. 22G

Pool-31	SEQ ID NO:	Pool-32	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATAC	7407	TGCAGGACCAGAGAATTCTGAATA	7647
AGAATCTGCNNNTGCATCAGGT		CAGGTCTGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7408	TGCAGGACCAGAGAATTCTGAATA	7648
ACCAGGACCNNTGCATCAGGT		CACATTTTCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7409	TGCAGGACCAGAGAATTCTGAATA	7649
AAGAGCATGNNNTGCATCAGGT		CAGCAGAGCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7410	TGCAGGACCAGAGAATTCTGAATA	7650
AACGGCCACNNNTGCATCAGGT		CAGCGGTAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7411	TGCAGGACCAGAGAATTCTGAATA	7651
ACCTAAACGNNNTGCATCAGGT		CAGGAGTCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7412	TGCAGGACCAGAGAATTCTGAATA	7652
AGGTAACTCANNNTGCATCAGGT		CAACCATTCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7413	TGCAGGACCAGAGAATTCTGAATA	7653
ATGGCTGATNNNTGCATCAGGT		CATCAAATGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7414	TGCAGGACCAGAGAATTCTGAATA	7654
AGCCGTAGCANNNTGCATCAGGT		CACAGTTCGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7415	TGCAGGACCAGAGAATTCTGAATA	7655
ATATCATTCNNNTGCATCAGGT		CAGATCTAATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7416	TGCAGGACCAGAGAATTCTGAATA	7656
AGAGCAGTANNNTGCATCAGGT		CATTTCAGTTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7417	TGCAGGACCAGAGAATTCTGAATA	7657
AGCGTAAGANNNTGCATCAGGT		CAGACAATTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7418	TGCAGGACCAGAGAATTCTGAATA	7658
ATCGCAAACNNNTGCATCAGGT		CAGCGGTAATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7419	TGCAGGACCAGAGAATTCTGAATA	7659
AGAAGCTTCNNNTGCATCAGGT		CAAAATACAAGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7420	TGCAGGACCAGAGAATTCTGAATA	7660
ATATTACCTNNNTGCATCAGGT		CAGTCCGCGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7421	TGCAGGACCAGAGAATTCTGAATA	7661
ATGCATGTGNNNTGCATCAGGT		CACCATCATCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7422	TGCAGGACCAGAGAATTCTGAATA	7662
AGCTTTGAGNNNTGCATCAGGT		CACCTGTCTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7423	TGCAGGACCAGAGAATTCTGAATA	7663
ATCCTATTANNNTGCATCAGGT		CAGCTTCCTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7424	TGCAGGACCAGAGAATTCTGAATA	7664
ACGTACAGGCNNNTGCATCAGGT		CAACCCAACANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7425	TGCAGGACCAGAGAATTCTGAATA	7665
ACCGCGATGNNNTGCATCAGGT		CAAAACCGGANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7426	TGCAGGACCAGAGAATTCTGAATA	7666
AGGTTGTCAANNNTGCATCAGGT		CATCTGCATCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7427	TGCAGGACCAGAGAATTCTGAATA	7667
AGCAGCAAAANNNTGCATCAGGT		CAATTCCAANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7428	TGCAGGACCAGAGAATTCTGAATA	7668
AGCGTAACCTNNNTGCATCAGGT		CACACCAAGTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7429	TGCAGGACCAGAGAATTCTGAATA	7669
AGAGAGTCANNNTGCATCAGGT		CAGCACAACTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7430	TGCAGGACCAGAGAATTCTGAATA	7670
ACTATGCCTNNNTGCATCAGGT		CAAGGTGGATNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7431	TGCAGGACCAGAGAATTCTGAATA	7671
AAACCGAAGNNNTGCATCAGGT		CATGCTAGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7432	TGCAGGACCAGAGAATTCTGAATA	7672
ACGGCCCGGNNNTGCATCAGGT		CATTGTGAGCANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7433	TGCAGGACCAGAGAATTCTGAATA	7673
AAAGCGCCNNNTGCATCAGGT		CAAGTTTCGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7434	TGCAGGACCAGAGAATTCTGAATA	7674
AATAAGGATNNNTGCATCAGGT		CAGCTAGTACNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7435	TGCAGGACCAGAGAATTCTGAATA	7675
AAGCTGAGANNNTGCATCAGGT		CATAGGTGCTNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7436	TGCAGGACCAGAGAATTCTGAATA	7676
ACTCTGACTNNNTGCATCAGGT		CACATTACGNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7437	TGCAGGACCAGAGAATTCTGAATA	7677
ATCGCAGGCNNNTGCATCAGGT		CATGCAATTANNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7438	TGCAGGACCAGAGAATTCTGAATA	7678
AATATTAGCANNNTGCATCAGGT		CATGGCCCCNNNTGCATCAGGT	
TGCAGGACCAGAGAATTCTGAATAC	7439	TGCAGGACCAGAGAATTCTGAATA	7679
AACCGTATGNNNTGCATCAGGT		CAGCTGCAGCANNNTGCATCAGGT	

FIG. 22H

Pool-31	SEQ ID NO:	Pool-32	SEQ ID NO:
TGCAGGACCAGAGAATTCTGAATAC AGGTCGGTCNNNTGCATCAGGT	7440	TGCAGGACCAGAGAATTCTGAATA CATTTGCCCANNNNTGCATCAGGT	7680
TGCAGGACCAGAGAATTCTGAATAC AATATCGTANNNNTGCATCAGGT	7441	TGCAGGACCAGAGAATTCTGAATA CAGACCATTGNNNTGCATCAGGT	7681
TGCAGGACCAGAGAATTCTGAATAC AACCTCTCANNNNTGCATCAGGT	7442	TGCAGGACCAGAGAATTCTGAATA CACC GCTAGNNNTGCATCAGGT	7682
TGCAGGACCAGAGAATTCTGAATAC AGTCGGTGCNNNTGCATCAGGT	7443	TGCAGGACCAGAGAATTCTGAATA CATTAGCTGNNNTGCATCAGGT	7683
TGCAGGACCAGAGAATTCTGAATAC ATTCGCCCGNNNTGCATCAGGT	7444	TGCAGGACCAGAGAATTCTGAATA CATCTGATTNNNTGCATCAGGT	7684
TGCAGGACCAGAGAATTCTGAATAC ACAGGCTGCNNNTGCATCAGGT	7445	TGCAGGACCAGAGAATTCTGAATA CATCATAGGNNNTGCATCAGGT	7685
TGCAGGACCAGAGAATTCTGAATAC ATCGCTTACNNNTGCATCAGGT	7446	TGCAGGACCAGAGAATTCTGAATA CATGGAGGTANNNNTGCATCAGGT	7686
TGCAGGACCAGAGAATTCTGAATAC ACGGATTGTNNNTGCATCAGGT	7447	TGCAGGACCAGAGAATTCTGAATA CAGTCTCTACNNNTGCATCAGGT	7687
TGCAGGACCAGAGAATTCTGAATAC ACAAGCTGTNNNTGCATCAGGT	7448	TGCAGGACCAGAGAATTCTGAATA CAGCCTGGTNNNTGCATCAGGT	7688

FIG. 23

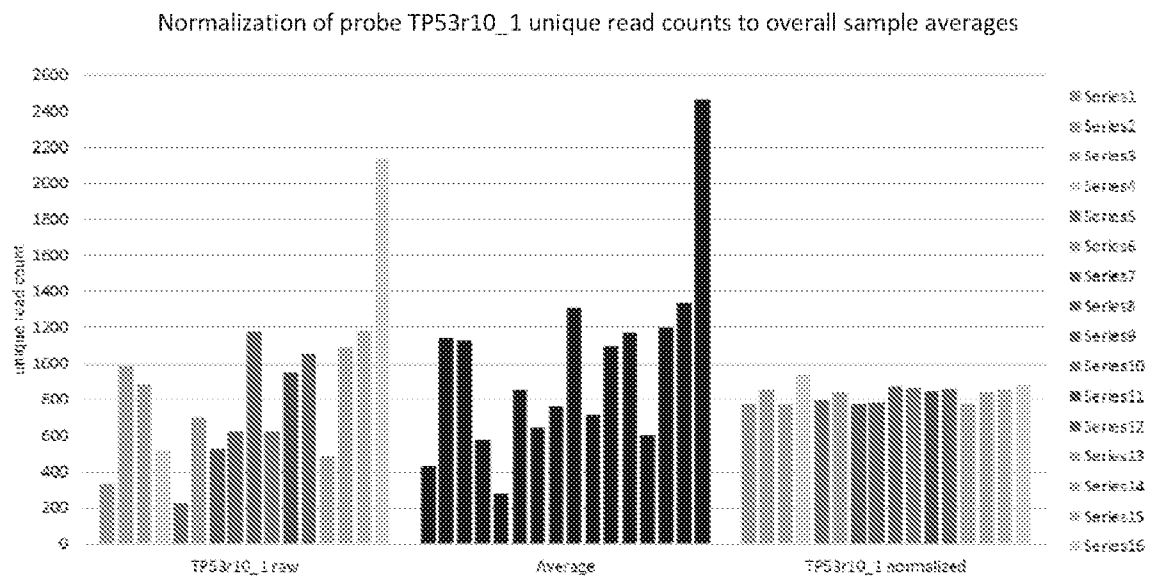
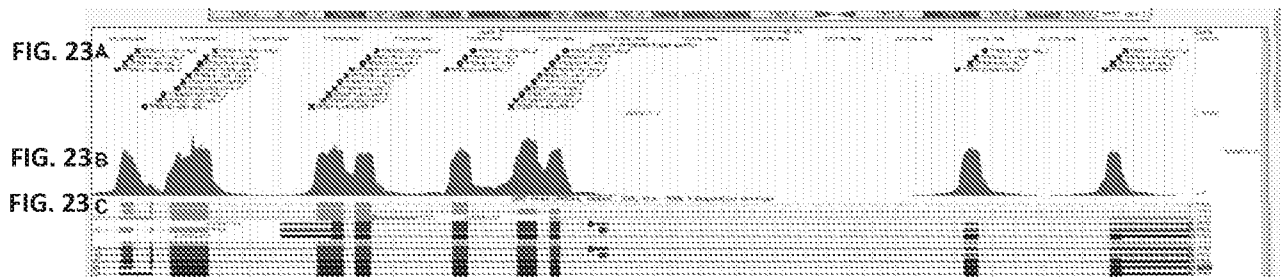


FIG. 24A

FIG. 24B

FIG. 24C

FIG. 25

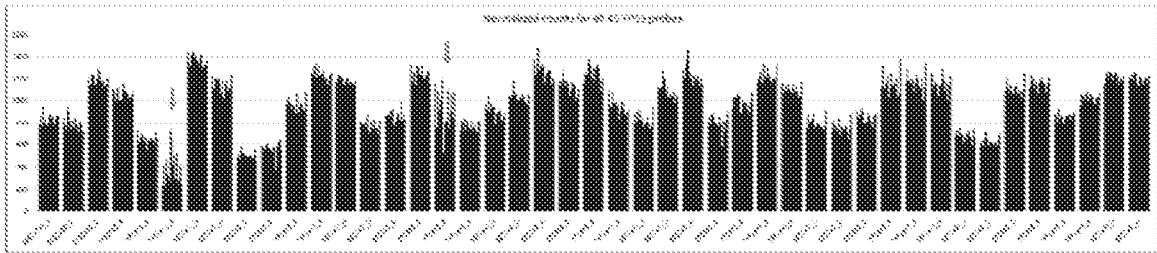


FIG. 26

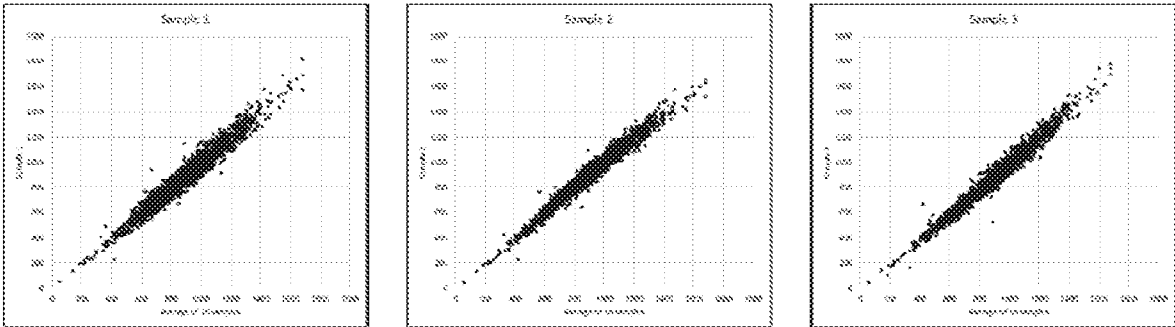


FIG. 27A

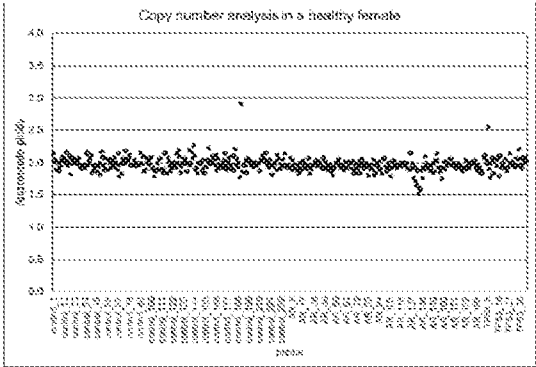


FIG. 27B

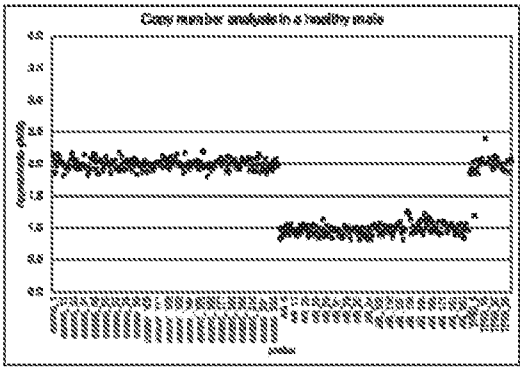


FIG. 27C

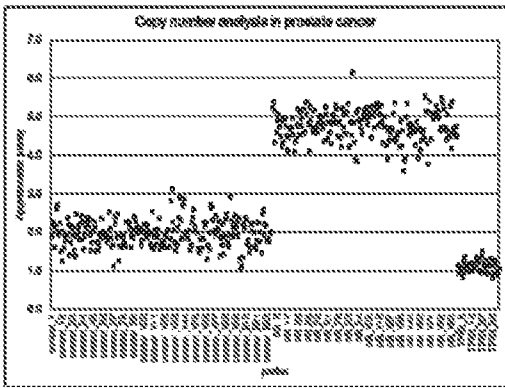


FIG. 28

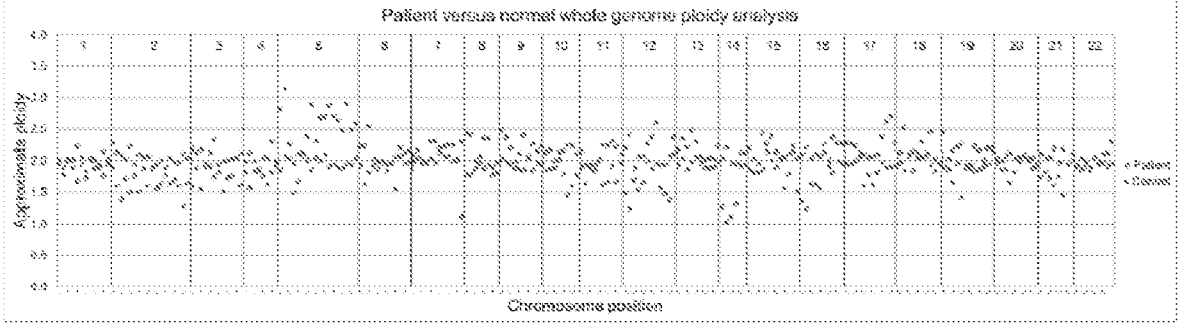
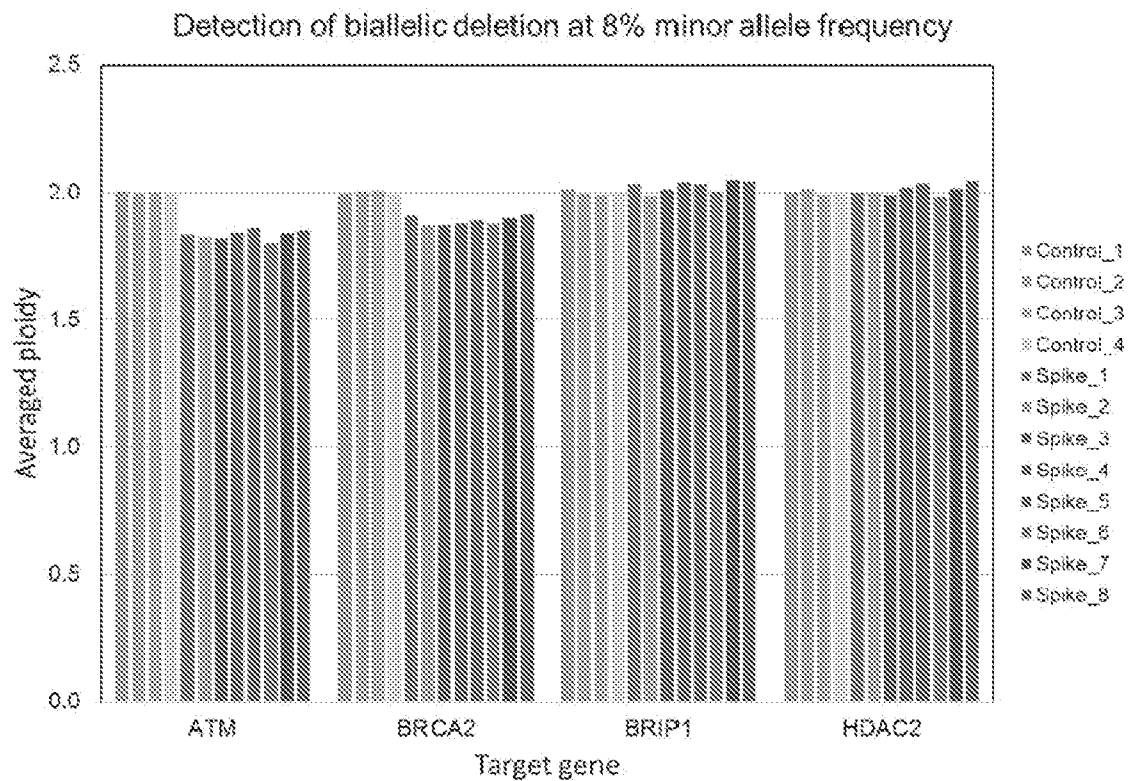


FIG. 29



INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 17/48434

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☒ Claims Nos.: 8-59, 63-66, 71-81, 83-87, 89, 93-105
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claims 1-7 and 88, directed to a method for performing a genetic analysis on a DNA target region from a test sample comprising generating a DNA library.

Group II, claims 60-62, directed to a method for or highly sensitive detection of copy number gain and copy number loss, measuring chromosome stability, and treating a subject identified as having a destabilized genome.

Group III, claims 67-70, 82 and 90-92, directed to a genomic DNA library comprising a plurality of DNA library fragments, and a set of adaptors that encode an identity of a unique genomic DNA fragment and an identity of a test sample.

--continued on first extra sheet--

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-7, 88

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 17/48434

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - C12Q 1/68, G06F 19/00, G06F 19/20 (2017.01)

CPC - C12Q 1/6806, G06F 19/22, G06F 19/345, G06F 19/18

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History Document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

See Search History Document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History Document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2016/0053301 A1 (CLEARFORK BIOSCIENCE, INC.) 25 February 2016 (25.02.2016) para [0010]-[0022]; [0031]; [0032]; [0040]; [0046]; [0062]; [0081]; [0100]; [0114]; [0123]; [0195]; [0312]; [0320].	1-3, 6, 7, 88
X	US 2014/274731 A1 (CLEARFORK BIOSCIENCE, INC.) 18 September 2014 (18.09.2014) para [0007]-[0009]; [0012]; [0022]; [0031]; [0046]; [0090]; [0171]; [0224]; [0234]; [0328]; [0678].	1-5

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

28 November 2017

Date of mailing of the international search report

26 DEC 2017

Name and mailing address of the ISA/US

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P.O. Box 1450, Alexandria, Virginia 22313-1450

Facsimile No. 571-273-8300

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PCT OSP: 571-272-7774

--continued from Box III: Observations where unity of invention is lacking--

The inventions listed as Groups I-III do not relate to a single special technical feature under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Special technical features:

Group I has the special technical feature of performing a genetic analysis using a genomic DNA library, that is not required by Groups II-III.

Group II has the special technical feature of determining copy number values using genomic DNA, that is not required by Groups I and III.

Group II also has the special technical feature of determining an RGD (raw genomic depth) for a capture probe and normalizing the RGD, that is not required by Groups I and III. (see instant Specification, para [00183]. Each capture probe yields a set of unique reads that are computationally distilled from total reads by grouping into families. The unique reads for a given sample (e.g., raw genomic depth for a sample) are then computed as the average of all the unique reads observed on a probe-by-probe basis.).

Group III has the special technical feature of a composition comprising a genomic DNA library comprising a plurality of DNA library fragments, and a set of adaptors, that is not required by Groups I-II.

Common technical features:

Groups I and III share the common technical feature of a genomic DNA library comprising a plurality of DNA library fragments, wherein each of the DNA library fragments comprises an adaptor and a genomic DNA fragment, wherein the adaptor is a DNA polynucleotide that comprises: an amplification region, a sample tag region, and an anchor region; wherein the amplification region comprises a polynucleotide sequence capable of serving as a primer recognition site for PCR amplification; wherein the sample tag comprises a polynucleotide sequence that encodes an identity of the unique library DNA fragment and encodes an identity of the test sample; and wherein the anchor region comprises a polynucleotide sequence that encodes the identity of the test sample and wherein the anchor region is capable of attaching to the genomic DNA fragment.

Groups I-III further share the common technical feature of performing a quantitative genetic analysis of the genomic DNA from a sample.

However, these shared technical features do not represent a contribution over prior art, because these shared technical features are anticipated by US 2014/274731 A1 to CLEARFORK BIOSCIENCE, INC., (hereinafter Clearfork).

Clearfork teaches a genomic DNA library comprising a plurality of DNA library fragments (para [0009] "a method for generating a tagged DNA library comprising treating fragmented DNA"), wherein each of the DNA library fragments comprises an adaptor and a genomic DNA fragment (para [0046] "and ligating a random nucleic acid tag sequence, and optionally a sample code sequence and/or a PCR primer sequence to the fragmented end-repaired DNA to generate the tagged DNA library"), wherein the adaptor is a DNA polynucleotide that comprises: an amplification region, a sample tag region, and an anchor region (para [0012] "the ligating comprises ligating a multifunctional adaptor module to the fragmented end-repaired DNA to generate the tagged DNA library, wherein the multifunctional adaptor molecule comprises: i) a first region comprising a random nucleic acid tag sequence; ii) a second region comprising a sample code sequence; and iii) a third region comprising a PCR primer sequence"; [0090] "wherein each hybrid tagged cDNA sequence comprises: fragmented end-repaired cDNA; a random nucleotide tag sequence; a sample code sequence; a PCR primer sequence; a cDNA target region; and a multifunctional capture probe module tail sequence"; [0678] For total RNA libraries...an adaptor design was created in which the first 8 bases were random and the next 12 served as a "code" and an anchor sequence for a 12 mer partner strand oligo that could therefore form a ligatable duplex"); wherein the amplification region comprises a polynucleotide sequence capable of serving as a primer recognition site for PCR amplification (para [0012] "a third region comprising a PCR primer sequence"); wherein the sample tag comprises a polynucleotide sequence that encodes an identity of the unique library DNA fragment and encodes an identity of the test sample (para [0012] "a second region comprising a sample code sequence"; [0224] "the term "sample code sequence" refers to a polynucleotide that is used to identify the sample"); wherein the anchor region comprises a polynucleotide sequence that encodes the identity of the test sample and wherein the anchor region is capable of attaching to the genomic DNA fragment (para [0090] "and a multifunctional capture probe module tail sequence"; [0234] "a multifunctional capture probe module comprises a region capable of hybridizing to a partner oligonucleotide and a region capable of hybridizing to a genomic target sequence...the partner oligo may also function as a tail sequence or primer binding site"; [0678] For total RNA libraries the poly-dT primer: TTTTTTTTTTTTTTTVN (SEQ ID NO: 722) was used. For targeted RNA-seq, an adaptor design was created in which the first 8 bases were random and the next 12 served as a "code" and an anchor sequence for a 12 mer partner strand oligo that could therefore form a ligatable duplex").

Clearfork teaches performing a quantitative genetic analysis on a DNA target region from a test sample to determine an approximate copy number value for specific probes (para [0022] "hybridizing a tagged DNA library with a multifunctional capture probe module complex, wherein the multifunctional capture probe module selectively hybridizes to a specific target region in the DNA library...performing PCR amplification of the hybrid nucleic acid in d); and e) quantitating the PCR reaction in d), wherein the quantitation allows for a determination of copy number of the specific target region").

As the technical features were known in the art at the time of the invention, they cannot be considered special technical features that would otherwise unify the groups.

Therefore, Group I-III inventions lack unity under PCT Rule 13 because they do not share the same or corresponding special technical feature.

NOTE, claims 8-59, 63-66, 71-81, 83-87, 89, 93-105 are held unsearchable because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).