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(54) Title: HIGH EFFICIENCY CONSTRUCTION OF DNA LIBRARIES

(57) Abstract: The disclosure provides a method for efficient DNA library construction and targeted genetic analyses of the libraries. Libraries are useful for predicting, diagnosing, or monitoring a genetic disease in a subject.

HIGH EFFICIENCY CONSTRUCTION OF DNA LIBRARIES

BACKGROUND

Cross Reference to Related Application

This application claims priority to U.S. Provisional Application No. 62/254,110, filed November 11, 2015, and is incorporated by reference herein in its entirety.

Description of the Text File Submitted Electronically

The contents of the text file submitted electronically herewith are incorporated herein by reference in their entirety: A computer readable format copy of the Sequence Listing (file name: CLFK_003_01WO_ST25, date recorded: November 10, 2016, file size: 23 kB).

Technical Field

The invention relates generally to improved compositions and methods for constructing DNA libraries. In particular, the present invention relates to efficiently constructing DNA clone libraries for quantitative genetic analyses.

Description of the Related Art

Various DNA specimens that are of interest for downstream analysis are collected in minute quantities. By way of example, cell-free DNA (cfDNA) collected from the plasma fraction of whole blood is generally present in nanogram quantities per mL of plasma. Given that one diploid human genome weighs 6 picograms, this means there are a few hundred to a few thousand total genomes of information that can be isolated from a single blood draw.

In cancer patients, tumor DNA is shed into the bloodstream in highly variable quantities ranging from $\leq 0.1\%$ to $\geq 10\%$ total circulating DNA. Blood draws contain only a few nanograms of DNA and if tumor genomes are present at 0.1% of the total circulating DNA, then only 1 to 10 total copies of the tumor genome are present. To unambiguously identify tumor DNA by sequence analysis, it is necessary to observe two or more copies of a

tumor-specific genetic lesion. However, the need to maximize the detection sensitivity of DNA, meaning accurate detection of tumor DNA in the 0.1% range has yet to be achieved.

These considerations illuminate the fundamental problem that reliable genetic analysis of solid tumors using blood is governed, in part, by the ability isolate and analyze rare genomic fragments. Moreover, many therapeutically actionable tumor lesions involve gene fusions, significant insertions or deletions of DNA sequence and/or changes in gene copy number. Such alterations are refractory to analysis by PCR, where two adjacent primer binding sites must be known and where copy variation is obscured by many rounds of target amplification.

At present, target retrieval methods are used for comprehensive analysis of potential lesions in circulating tumor DNA. Such retrieval methods rely on the creation of DNA clone libraries. Unfortunately, current methods for creating these DNA libraries are inefficient, with only a small percentage of DNA fragments being successfully converted to useful library clones.

Any reference to or discussion of any document, act or item of knowledge in this specification is included solely for the purpose of providing a context for the present invention. It is not suggested or represented that any of these matters or any combination thereof formed at the priority date part of the common general knowledge, or was known to be relevant to an attempt to solve any problem with which this specification is concerned.

BRIEF SUMMARY

The invention relates generally to compositions and methods for high efficiency attachment of DNA adaptors to DNA fragments to generate DNA libraries for quantitative genetic analyses.

In one aspect, the invention relates to a method for adaptor ligation to one or more DNA fragments comprising:

(a) removing the terminal phosphate residues of the one or more DNA fragments;

(b) treating the dephosphorylated DNA fragments with one or more end-repair enzymes to generate end-repaired DNA fragments;

(c) using a ligase to ligate one or more double-stranded DNA (dsDNA) pre-adaptors to the 3' end of each strand of the end-repaired DNA fragments to form pre-adaptor/end-repaired DNA complexes, wherein each dsDNA pre-adaptor comprises

(i) a ligation strand oligonucleotide that is ligated to the 3' end of each strand of the end-repaired DNA fragments and comprises an anchor sequence; and

(ii) a non-ligation partner strand oligonucleotide;

(d) displacing the non-ligation partner strand oligonucleotide from the pre-adaptor/end-repaired DNA complexes with a repair oligonucleotide, wherein the repair oligonucleotide is longer than the ligation strand oligonucleotide, and wherein the 3' end of the repair oligonucleotide is complementary to the 5' end of the ligation strand oligonucleotide;

(e) ligating the repair oligonucleotide to the 5' end of the end-repaired DNA fragments using a kinase ligase strategy to form adaptor/end-repaired DNA complexes, wherein each adaptor comprises the ligation strand oligonucleotide and the repair oligonucleotide; wherein the kinase ligase strategy comprises contacting the adaptor/end repaired DNA complexes with a kinase and a ligase, wherein the kinase adds a phosphate group to the 5' terminal nucleotide of each strand of the end repaired DNA fragments, and wherein the ligase ligates the repair oligonucleotide to the phosphorylated 5' end of each strand of the end repaired DNA fragments; and

(f) extending the ligation strand oligonucleotide at the 3' end using the repair oligonucleotide as a template to form one or more contiguous, dsDNA fragments each comprising an adaptor molecule ligated to each end of the DNA fragment.

In various embodiments, a method for increasing the efficiency of adaptor ligation to one or more DNA fragments comprising: removing the terminal phosphate residues of one or more DNA fragments; treating the dephosphorylated DNA fragments with one or more end-repair enzymes to generate end-repaired DNA; ligating one or more double-stranded DNA (dsDNA) pre-adaptors to the 3′ end of each strand of the end-repaired DNA to form pre-adaptor/end-repaired DNA complexes, wherein each dsDNA pre-adaptor comprises a ligation strand oligonucleotide that is ligated to the 3′ end of each strand of the end-repaired DNA, and a non-ligation partner strand oligonucleotide; displacing the non-ligation partner strand oligonucleotide from the pre-adaptor/end-repaired DNA complexes with a repair oligonucleotide, to form adaptor/end-repaired DNA complexes, wherein each adaptor

comprises the ligation strand oligonucleotide and the repair oligonucleotide; and treating the adaptor/end-repaired DNA complexes with one or more enzymes to form a contiguous, double-stranded, DNA library; wherein the efficiency of adapter ligation is increased compared to a method wherein dephosphorylated adapter molecules are ligated to phosphorylated DNA fragments is provided.

In various embodiments, a method for constructing a DNA library comprising: removing the terminal phosphate residues of one or more DNA fragments; treating the dephosphorylated DNA fragments with one or more end-repair enzymes to generate end-repaired DNA; ligating one or more double-stranded DNA (dsDNA) pre-adaptors to the 3′ end of each strand of the end-repaired DNA to form pre-adaptor/end-repaired DNA complexes, wherein each dsDNA pre-adaptor comprises a ligation strand oligonucleotide that is ligated to the 3′ end of each strand of the end-repaired DNA, and a non-ligation partner strand oligonucleotide; displacing the non-ligation partner strand oligonucleotide from the pre-adaptor/end-repaired DNA complexes with a repair oligonucleotide, to form adaptor/end-repaired DNA complexes, wherein each adaptor comprises the ligation strand oligonucleotide and the repair oligonucleotide; and treating the adaptor/end-repaired DNA complexes with one or more enzymes to form a contiguous, double-stranded, DNA library is provided.

In particular embodiments, the non-ligation partner strand oligonucleotide comprises a modification at the 3′ terminus that prevents its ligation to the 5′ end of the end-repaired DNA and/or adaptor dimer formation.

In certain embodiments, the source of the one or more DNA fragments is DNA selected from the group consisting of: genomic DNA (gDNA), complementary DNA (cDNA), and cell-free DNA (cfDNA).

In further embodiments, the source of the DNA is a biological sample selected from the group consisting of: blood, skin, hair, hair follicles, saliva, oral mucous, vaginal mucous, sweat, tears, epithelial tissues, urine, semen, seminal fluid, seminal plasma, prostatic fluid, pre-ejaculatory fluid (Cowper's fluid), excreta, biopsy, ascites, cerebrospinal fluid, lymph, and tissue extract sample or biopsy sample.

In particular embodiments, the source of the DNA 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.

In further embodiments, the methods further comprise isolating the DNA from a biological sample of a subject.

In some embodiments, the methods further comprise fragmenting the DNA from a biological sample of a subject.

In certain embodiments, the methods further comprise repairing damage of the one or more DNA fragments prior to ligation.

In particular embodiments, the damage is a deaminated cytosine (Uracil), an abasic site, methylation of guanine to O6MeG, DNA nicks, gaps, or a thymine dimer.

In various embodiments, a method constructing a cfDNA library comprising: isolating or obtaining cfDNA from a biological sample of a subject; removing the terminal phosphate residues of the cfDNA; treating the dephosphorylated cfDNA with one or more end-repair enzymes to generate end-repaired cfDNA, and optionally to repair DNA damage; ligating one or more double-stranded DNA (dsDNA) pre-adaptors to the 3′ end of each strand of the end-repaired cfDNA to form pre-adaptor/end-repaired cfDNA complexes, wherein each dsDNA pre-adaptor comprises a ligation strand oligonucleotide that is ligated to the 3′ end of each strand of the end-repaired cfDNA, and a non-ligation partner strand oligonucleotide; displacing the non-ligation partner strand oligonucleotide from the pre-adaptor/end-repaired cfDNA complexes with a repair oligonucleotide, to form adaptor/end-repaired cfDNA complexes, wherein each adaptor comprises the ligation strand oligonucleotide and the repair oligonucleotide; treating the adaptor/end-repaired cfDNA complexes with one or more enzymes to form a contiguous, double-stranded, cfDNA library; and amplifying the cfDNA library to generate a cell-free DNA clone library is provided.

In particular embodiments, the ligation strand oligonucleotide comprises one or more modifications to prevent adaptor dimer formation, optionally wherein the modification of the 3′ end of the no-ligation partner strand oligonucleotide prevents adaptor dimer formation.

In certain embodiments, the ligation strand oligonucleotide comprises an anchor sequence, a read code, or a PCR primer binding site.

In further embodiments, the ligation strand oligonucleotide comprises an anchor sequence, a read code, and a PCR primer binding site.

In some embodiments, the ligation strand oligonucleotide comprises one or more PCR primer binding sites for PCR amplification of the one or more contiguous, double-stranded, DNA library molecules.

In particular embodiments, the ligation strand oligonucleotide comprises one or more unique read codes.

In particular embodiments, the ligation strand oligonucleotide comprises one or more sample codes for sample multiplexing.

In certain embodiments, the ligation strand oligonucleotide comprises one or more sequences for DNA sequencing.

In further embodiments, the ligation strand oligonucleotide comprises an anchor sequence.

In further embodiments, the repair oligonucleotide comprises an anchor sequence, a read code, or a PCR primer binding site.

In certain embodiments, the repair oligonucleotide comprises an anchor sequence, a read code, and a PCR primer binding site.

In particular embodiments, the repair oligonucleotide comprises one or more primer binding sites for PCR amplification of the one or more contiguous, double-stranded, DNA library molecules.

In some embodiments, the repair oligonucleotide comprises one or more unique read codes.

In certain embodiments, the repair oligonucleotide comprises one or more sample codes for sample multiplexing.

In particular embodiments, the repair oligonucleotide comprises one or more sequences for DNA sequencing.

In further embodiments, the ligation strand oligonucleotide is complementary to the repair oligonucleotide.

In particular embodiments, the anchor sequence of the ligation strand oligonucleotide is complementary to the anchor sequence of the repair oligonucleotide.

In further embodiments, the PCR primer binding site of the ligation strand oligonucleotide is complementary to the PCR primer binding site of the repair oligonucleotide.

In particular embodiments, the one or more adaptors comprises a plurality of ligation strand oligonucleotide species.

In some embodiments, the one or more adaptors comprises a plurality of repair oligonucleotide species.

In particular embodiments, the primer binding site of the ligation strand oligonucleotide is not complementary to the primer binding site of the repair oligonucleotide.

In certain embodiments, the primer binding site of the ligation strand oligonucleotide is substantially different from the primer binding site of the repair oligonucleotide.

In certain embodiments, a primer that binds the primer binding site of the ligation strand oligonucleotide does not substantially bind the primer binding site of the repair oligonucleotide.

In particular embodiments, the DNA library is amplified to generate a DNA clone library.

In further embodiments, qPCR is performed on the DNA clone library and a qPCR measurement is compared to standards of known genome equivalents to determine the genome equivalents of the DNA clone library.

In particular embodiments, the qPCR is performed with a primer that binds to an Alu sequence and a primer that binds to a sequence in an adaptor.

In some embodiments, quantitative genetic analysis is performed on a plurality of genetic loci in the DNA clone library.

In particular embodiments, quantitative genetic analysis is performed on a plurality of genetic loci in a plurality of DNA clone libraries.

In particular embodiments, quantitative genetic analysis comprises hybridizing one or more capture probes to a target genetic locus to form capture probe module-DNA clone complexes.

In certain embodiments, quantitative genetic analysis comprises isolating the capture probe -DNA clone complexes.

In further embodiments, the quantitative genetic analysis comprises amplification of the DNA clone sequence in the isolated capture probe-DNA clone complexes.

In particular embodiments, quantitative genetic analysis comprises DNA sequencing to generate a plurality of sequencing reads.

In further embodiments, the methods further comprise bioinformatic analysis of the plurality of sequencing reads.

In particular embodiments, quantitative genetic analysis is performed on a plurality of genetic loci in the DNA clone library and wherein bioinformatic analysis is used: to quantify the number of genome equivalents analyzed in the DNA clone library; to detect genetic variants in a target genetic locus; to detect mutations within a target genetic locus; to detect genetic fusions within a target genetic locus; and/or to measure copy number fluctuations within a target genetic locus.

In certain embodiments, the quantitative genetic analysis is used to identify or detect one or more genetic lesions that cause or associated with the genetic disease.

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.

In certain embodiments, the genetic disease is cancer.

In further embodiments, the quantitative genetic analysis is used to identify or detect one or more genetic variants or genetic lesions of one or more target genetic loci in fetal cfDNA.

In some embodiments, the capture probe is a component of a capture probe module that is optionally duplexed with a hapten-labeled partner oligonucleotide that hybridizes to a tail sequence in the capture probe module.

In various embodiments, a method of predicting, diagnosing, or monitoring a genetic disease in a subject comprising: isolating or obtaining DNA from a biological sample of a subject; removing the terminal phosphate residues of the DNA; treating the dephosphorylated DNA with one or more end-repair enzymes to generate end-repaired DNA; ligating one or more double-stranded DNA (dsDNA) pre-adaptors to the 3′ end of each strand of the end-repaired DNA to form pre-adaptor/end-repaired DNA complexes, wherein each dsDNA pre-adaptor comprises a ligation strand oligonucleotide that is ligated to the 3′ end of each strand of the end-repaired DNA, and a non-ligation partner strand oligonucleotide; displacing the non-ligation partner strand oligonucleotide from the pre-adaptor/end-repaired DNA complexes with a repair oligonucleotide, to form adaptor/end-repaired DNA complexes, wherein each adaptor comprises the ligation strand oligonucleotide and the repair oligonucleotide; treating the adaptor/end-repaired DNA complexes with one or more enzymes to form a contiguous, double-stranded, 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 associated with the genetic disease in the DNA 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 is provided.

In certain embodiments, the DNA is genomic DNA, DNA from formalin-fixed, paraffin embedded (FFPE) samples, cDNA, or cfDNA.

In particular embodiments, the cfDNA is isolated from a biological sample selected from the group of: amniotic fluid, blood, plasma, serum, semen, lymphatic fluid, cerebral spinal fluid, ocular fluid, urine, saliva, stool, mucous, and sweat.

In further 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.

In particular embodiments, the genetic disease is cancer.

In various embodiments, a companion diagnostic for a genetic disease comprising: isolating or obtaining DNA from a biological sample of a subject; removing the terminal

phosphate residues of the DNA; treating the dephosphorylated DNA with one or more end-repair enzymes to generate end-repaired DNA; ligating one or more double-stranded DNA (dsDNA) pre-adaptors to the 3′ end of each strand of the end-repaired DNA to form pre-adaptor/end-repaired DNA complexes, wherein each dsDNA pre-adaptor comprises a ligation strand oligonucleotide that is ligated to the 3′ end of each strand of the end-repaired DNA, and a non-ligation partner strand oligonucleotide; displacing the non-ligation partner strand oligonucleotide from the pre-adaptor/end-repaired DNA complexes with a repair oligonucleotide, to form adaptor/end-repaired DNA complexes, wherein each adaptor comprises the ligation strand oligonucleotide and the repair oligonucleotide; treating the adaptor/end-repaired DNA complexes with one or more enzymes to form a contiguous, double-stranded, 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 is provided.

In further embodiments, the DNA is genomic DNA, DNA from formalin-fixed, paraffin embedded (FFPE) samples, cDNA, or cfDNA.

In particular embodiments, the cfDNA is isolated from 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.

In particular embodiments, the biomarker is a genetic lesion.

In further 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.

In certain embodiments, the genetic disease is cancer.

BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWINGS

Figure 1 shows conventional versus high efficiency (HE) ligation technology. (A) Target DNA fragments are 5′ phosphorylated prior to DNA ligation with unphosphorylated duplex adapters. (B) A common inefficiency with conventional ligation approaches is that 5′ target DNA fragment ends lacking a phosphate group fails to ligate with unphosphorylated duplex adapters. (C) Ligation of target DNA fragments to one another. (D) Duplex adaptor comprising a 5′ phosphate group required is ligated to 3′ end of target DNA fragment The hatched circle one the partner strand oligonucleotide of the adaptor represents a 3′ blocking group. (E) The 3′ blocking group also prevents adaptors from ligating to one another. (F) Occasional adaptor duplexes lacking a 5′ phosphate fail to ligate to target fragments.

Figure 2 shows a representative image of an agarose gel of the complete ligation of RsaI digested, dephosphorylated pUC19 plasmid to a series of nine different HE adaptors. Unligated fragments are indicated in the control lane, which is next to the molecular weight (MW) markers of 740, 500, 300, and 150 bp (top to bottom). The complete shift in the mobility of the three vector fragments (arrows) indicates the complete ligation of adaptors to both ends across all nine adaptors. These results show that the HE ligation technology is generalizable.

Figure 3 shows exemplary methods of completing HE ligated constructs. (A) The HE ligation product is a 3′ extended adaptor oligonucleotide attached to the 3′ end of fragments. (B) One strategy for "repairing" the initial ligation product is to add a repair oligonucleotide (top strand; green); T4 polynucleotide kinase can add a phosphate (P) to the 5′ end of the target fragment, and a nick sealing ligase such as *Taq* DNA ligase can be used to ligate the repair oligonucleotide to the target fragment. (C) An alternative strategy is to combine the complementary adaptor oligonucleotide, a DNA polymerase that has 5′ to 3′ exonuclease activity (*e.g., BstI* DNA polymerase), and a *Taq* DNA ligase. The *BstI* DNA polymerase extends the repair oligonucleotide by removing 5′ bases from the target fragment to expose 5′ phosphates that enable nick-sealing ligation by the *Taq* DNA ligase. (D) Complementary adaptor oligonucleotides can also be designed to introduce additional sequence features into the original HE ligation strand with the *BstI* DNA polymerase.

Figure 4 shows the preparation of DNA libraries using HE ligation technology. (A) DNA fragments can possess heterogeneous, "ragged" ends that may or may not possess phosphate groups (P). Treatment of the DNA fragments with a phosphatase removes exposed 5′ and 3′ phosphates. The DNA can then be treated with enzymes that repair DNA damage such as deaminated cytosines (U), abasic sites (↑), and thymine dimers, and that "polish" 5′ or 3′ overhangs to blunt ends. (B) Adaptors are added to DNA fragments in two steps. First, a duplex adaptor comprising a 5′ phosphorylated ligation strand and a 3′ blocked partner strand is ligated to the target fragments. The partner strand, which has a melting temperature of ~ 30°C, is removed in subsequent steps that occur at temperatures ≥ 37°C. Second, repair oligonucleotides are annealed to the adaptor ligated fragments; the repair oligonucleotides become covalently attached to the 5′ end of the target fragment either using a kinase/ligase strategy or a polymerase/exonuclease/ligase strategy (Figure 3). Primer extension of the initial ligation strand copies the repair oligo information into a full-length adaptor duplex that is suitable for downstream analysis.

Figure 5 shows a HE ligation technology strategy for generating dual PCR primer adapted DNA fragments. In this scheme, the ligation strand carries additional sequences (primer 2) that serve as an independent primer binding site. The repair oligonucleotide, while complementary to a portion of the ligation strand, has its own divergent sequence that serves as a second PCR primer binding site (primer 1). The fully completed adaptors allow amplification of the DNA specimen fragments using more conventional, universal dual-primer PCR methods.

DETAILED DESCRIPTION

A. OVERVIEW

The present invention contemplates, in part, compositions and methods to address the acute need in the field of quantitative genetic analyses for improved, highly-efficient methods to clone such DNA fragments for downstream analysis.

Current methods for DNA analysis comprise ligation of specialized adaptors to DNA fragments (Figure 1). In conventional techniques, target DNA fragments are 5′ phosphorylated prior to DNA ligation to enable covalent ligation with unphosphorylated duplex adapters. The target DNA fragment and adaptor may be blunt-ended, or they may share complementary overhangs (*e.g.*, T/A). (Figure 1A). This is a serious drawback because it is not possible to ensure that both ends of all target DNA fragments are phosphorylated, and unphosphorylated ends are incapable of ligation and these target fragments are lost from subsequent libraries. (Figure 1B). By way of a non-limiting example, if 70% of target DNA fragment ends possess a 5′ phosphate, then only 49% of fragments (0.7 x 0.7 x 100%) at the maximum, could be ligated on both ends of the fragment and ligation to both ends is required for cloning. Additionally, the presence of 5′ phosphates on target DNA fragments promotes a separate undesirable artifact in which DNA fragments can ligate to one another (Figure 1C). This creates artifactual chromosomal sequence fusion events that can confound detection of disease-specific chromosomal rearrangements.

In various embodiments, the present invention contemplates, in part, compositions and methods for efficiently attaching adaptor sequences to target DNA fragments. In particular embodiments, phosphates are removed from both the 5′ and 3′ termini of target DNA fragments. These dephosphorylated fragments are then treated with enzymes that create blunt DNA ends and optionally with enzymes that that repair many types of DNA damage that may have been inflicted on the DNA, *e.g.*, deaminated cytosine (Uracil), an abasic site, methylation of guanine to O^6MeG, nicks, double strand breaks, or a thymine dimer. The adaptor comprises a ligation strand oligonucleotide duplexed with a non-ligation partner strand oligonucleotide. The ligation strand of the adaptor carries the 5′ phosphate group required for ligation to target DNA fragments and the partner strand comprises a 3′ blocking group (Figure 1D). The 3′ blocking group prevents the formation of adaptor:adaptor dimers (Figure 1E). As with DNA fragments, not all adaptor sequences will possess a 5’ phosphate (solvent exposed terminal phosphate bonds are inherently chemically labile). While such unphosphorylated adaptors will be present, they will only transiently engage the ligation machinery (Figure 1F); unproductive pairing of such adaptors with fragments rapidly

dissociate and are replaced by adaptor:target DNA fragment pairings that can provide productive covalent attachment. Eventually ~100% of target DNA fragments become attached on both ends with adaptor molecules, which illustrates the high efficiency of the compositions and methods contemplated herein for constructing DNA libraries.

In various embodiments, compositions and methods contemplated herein for high efficiency construction of DNA libraries provide a novel comprehensive framework address molecular genetic analysis using DNA available from a variety of biological sources. Cloning of purified DNA introduces tagged DNA sequences that inform downstream analysis and enable amplification of the resulting clone libraries. Hybrid capture with target specific oligonucleotides is used to retrieve specific sequences for subsequent analysis. Independent measurements of the number of genomes present in the library are applied to each sample, and these assays provide a means to estimate the assay's sensitivity. The assays contemplated herein provide reliable, reproducible, and robust methods for the analysis, detection, diagnosis, or monitoring of genetic states, conditions, or disease.

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, T*echniques for the Analysis of Complex Genomes*, (Academic Press, New York, 1992); T*ranscription 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

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.

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.

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

The term "and/or" should be understood to mean either one, or both of the alternatives.

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 ± 15%, ± 10%, ± 9%, ± 8%, ± 7%, ± 6%, ± 5%, ± 4%, ± 3%, ± 2%, or ± 1% about a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length.

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.

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.

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.

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.

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.

As used herein, the term "DNA" refers to deoxyribonucleic acid. In various embodiments, the term DNA refers to genomic DNA, recombinant DNA, synthetic DNA, complementary DNA (cDNA), or cell-free DNA (cfDNA). In one embodiment, DNA refers to genomic DNA or cDNA. In one embodiment, DNA refers to cfDNA. In particular embodiments, the DNA is a DNA fragment that comprises a "target region," which is also referred to as a target DNA fragment in certain embodiments. DNA libraries contemplated herein include genomic DNA libraries, cfDNA 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.

A "target genetic locus" or "DNA target region" refers 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.

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.

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.

A "reaction vessel" means a container suitable for carrying out one of the reactions contemplated herein. Illustrative examples of reaction vessels suitable for use in particular embodiments include, but are not limited to test tubes, microfuge tubes (*e.g.,* PCR tubes), microtitre plates (*e.g.,* 96 well plates, 384 well plates, 1536 well plates), slides, plates, arrays, and microarrays.

C. HIGH EFFICIENCY CONSTRUCTION OF DNA LIBRARY

In particular embodiments, methods of constructing DNA libraries contemplated herein comprise high efficiency ligation of adaptors to target DNA fragments.

(a) DNA source

The methods and compositions contemplated herein are designed 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 DNA as an analyte. DNA suitable for use in

the compositions and methods contemplated herein can come from any source known to those of skill in the art. In particular embodiments, the DNA is genomic DNA isolated from any source, copy DNA (cDNA) synthesized from RNA, or cell-free DNA (cfDNA).

In some embodiments, the DNA is high molecular weight DNA (>1000 bp). Use of high molecular weight DNA in the compositions and methods contemplated herein often comprises a fragmentation step. The high molecular weight DNA can be fragmented to about 25 to about 750 base pairs, about 25 to about 500 base pairs, about 25 to about 250 base pairs, about 25 to about 200 base pairs, about 25 to about 150 base pairs, about 25 to about 100 base pairs, about 25 to about 50 base pairs, about 100 to about 200 base pairs, about 150 to about 180 base pairs, about 150 base pairs, about 155 base pairs, about 160 base pairs, about 165 base pairs, about 170 base pairs, about 175 base pairs, or about , about 180 base pairs.

Illustrative methods for fragmenting DNA suitable for use in particular embodiments of the compositions and methods contemplated herein include, but are not limited to: shearing, sonication, enzymatic digestion; including restriction digests, as well as other methods. In particular embodiments, any method known in the art for fragmenting DNA can be employed with the present invention.

Illustrative sources of genomic DNA and RNA (to generate cDNA) suitable for use in particular embodiments of the compositions and methods contemplated herein include, but are not limited to biological samples selected from the group consisting of: brain tissue, bone tissue, ocular tissue, olfactory tissue, muscles tissue, heart tissue, lung tissue, liver tissue, pancreatic tissue, kidney tissue, gastric tissue, intestinal tissue, colon tissue, blood, skin, hair, hair follicles, saliva, oral mucous, vaginal mucous, sweat, tears, epithelial tissues, urine, semen, seminal fluid, seminal plasma, prostatic fluid, pre-ejaculatory fluid (Cowper's fluid), excreta, biopsy, ascites, cerebrospinal fluid, lymph, and tissue extract sample or biopsy sample, and the like.

In particular embodiments, the DNA is cfDNA. The size distribution of cfDNA ranges from about 150 bp to about 180 bp fragments. Fragmentation 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.

In some embodiments, cfDNA isolated from the blood plasma fraction can be substantially contaminated with long (>10 kilobase pair), high-molecular weight genomic DNA that is liberated from nucleated blood cells that lyse during the collection protocol. This long, contaminating DNA, if left unfragmented, does not clone and amplify well and is therefore lost during downstream library preparation. However, in particular embodiments, in the absence of DNA fragmentation, the high-efficiency DNA library construction methods contemplated herein selectively clones shorter (<1000 bp) fragments from a collection of fragment sizes present in a DNA specimen. Without wishing to be bound by any particular theory, the selective cloning of short cfDNA fragments from a DNA specimen that is a blend of long and short fragments is advantageous in the construction of a liquid biopsy.

Illustrative examples of biological samples 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 sample is blood or blood plasma.

In certain embodiments, the DNA sample could be derived from embedded tissues such as FFPE or fine needle aspirates, from swabs intended to interrogate microbiome sequences present, from forensic samples such as hair, clothing, fingerprints, *etc.* or from any other source of DNA requiring the library construction methods contemplated herein that are especially efficient for constructing libraries from low-input DNA samples.

In certain embodiments, commercially available kits and other methods known to the skilled artisan can used to isolate cfDNA directly from the biological samples of a patient 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.

(b) Dephosphorylation of Input DNA

In particular embodiments, the input DNA, *e.g.,* target DNA fragments, is first treated with a thermo-labile phosphatase that removes terminal phosphate residues. *See, e.g.,* Figure 4A.

Illustrative examples of thermo-labile phosphatases that are suitable for use in particular embodiments of the compositions and methods contemplated herein include, but are not limited to APex™ Heat-Labile Alkaline Phosphatase (Epicentre Biotechnologies), NTPhos™ Thermolabile Phosphatase (Epicentre Biotechnologies), HK™ Thermolabile Phosphatase (Epicentre Biotechnologies), and Shrimp Alkaline Phosphatase (SAP; NEB).

In one embodiment, the thermo-labile phosphatase is SAP.

(c) Reversing DNA Damage in the Target DNA Fragments

In particular embodiments, the input DNA or dephosphorylated DNA is also treated with one or more enzymes that reverse common sources of DNA damage such as deamination of cytosines to uracil, oxidative addition to guanines, thymidine dimers, loss of bases leading to abasic sites, nicks or gaps on one strand of duplex DNA, etc. *See, e.g.,* Figure 4A.

In one embodiment, the internal damage to the DNA is reversed using a composition comprising one or more of the following enzymes: Taq DNA Ligase, Endonuclease IV, Bst DNA Polymerase, Fpg (8-oxoguanine DNA glycosylase), Uracil-DNA Glycosylase (UDG), T4 PDG (T4 Endonuclease V), Endonuclease VIII, and T4 DNA polymerase.

In one embodiment, the internal damage to the DNA is reversed using a composition comprising Taq DNA Ligase, Endonuclease IV, Bst DNA Polymerase, Fpg, Uracil-DNA Glycosylase (UDG), T4 PDG (T4 Endonuclease V), Endonuclease VIII, and T4 DNA polymerase.

(d) Generating End-Repaired DNA

In particular embodiments, the compositions and methods contemplated herein comprise generating end-repaired DNA fragments. In certain embodiments, the DNA fragments are end-repaired to generate end-repaired DNA fragments with blunt ends, 5′-

overhangs, or 3′-overhangs. *See, e.g.,* Figure 4A. In particular embodiments, the DNA is cfDNA.

In some embodiments, the end-repaired DNA contains blunt ends. In some embodiments, the end-repaired DNA is processed to contain blunt ends. In preferred embodiments, the DNA fragments are end-repaired by one or more end-repair enzymes to generate end-repaired DNA fragments with blunt ends.

Illustrative examples of end-repair enzymes suitable for generating blunt-ended DNA fragments in particular embodiments of the compositions and methods contemplated herein include DNA polymerases which retains polymerization activity and 3′→ 5′ exonuclease activity, but that lacks 5′→ 3′ exonuclease activity (*e.g.*, T4 DNA polymerase, Klenow fragment of DNA polymerase I, *etc.*). The DNA polymerase is used to either fill in 5′ overhangs or "chew back" 3′ overhangs, leaving the DNA fragments with blunt ends.

In some embodiments, the blunt ends of the end-repaired DNA are further modified to contain a single base pair overhang. In some embodiments, end-repaired DNA containing blunt ends can be further processed to contain adenine (A)/thymine (T) overhang. In some embodiments, end-repaired 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 DNA has non-templated 3′ overhangs. In some embodiments, the end-repaired DNA is processed to contain 3′ overhangs. In some embodiments, the end-repaired 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 DNA is processed to contain overhang ends using partial digestion with any known restriction enzymes (*e.g.*, with the enzyme Sau3A, and the like).

(e) Ligating Pre-Adaptors to End-Repaired DNA

In particular embodiments, the compositions and methods contemplated herein comprise ligating a duplex DNA pre-adaptor to each end of the end-repaired DNA.

As used herein, the term "pre-adaptor" refers to a double-stranded DNA molecule or DNA duplex that comprises a ligation strand oligonucleotide and a partner strand oligonucleotide. The pre-adapter may be ligated to the end–repaired DNA fragments using

any suitable ligase. In one embodiment, the ligase is T4 DNA ligase. *See, e.g.,* Figures 4B and 5.

The "ligation strand oligonucleotide" is a polynucleotide that comprises a 5′ phosphate and is capable of being ligated to each 3′ end of the end-repaired DNA fragment.

The "partner strand oligonucleotide" is complementary to, and anneals to, a portion of, or to all of, the nucleotides of the ligation strand oligonucleotide. The partner strand oligonucleotide comprises a modification at its 3′ end that prevents or substantially inhibits the partner strand oligonucleotide from being ligated to another adapter or to a phosphorylated 5′ end of a target DNA fragment. Chemical modifications of the 3′ end of the partner stand that can block ligation include, but are not limited to dideoxy ribose nucleotide analogs, 2-hydroxyl deoxyribose ribose analogs, and a broad variety of chemical modification to the ribose sugar.

Several considerations go into the sequence design and content of the ligation strand oligonucleotides used in the pre-adaptor. The ligation strand oligonucleotide can vary in length from the minimum length required to form a stable DNA duplex at temperatures where DNA ligase is active (~5 nt) to oligonucleotides that push the limits of current synthesis capabilities (>200 nt). In particular embodiments, the ligation strand oligonucleotide is about 8 to about 60 nucleotides or about 8 to about 15 nucleotides.

As an additional consideration related to the NGS analysis of DNA fragments, the DNA bases incorporated by the ligation strand are used by the sequencing instrument to calibrate DNA base calls throughout the DNA sequencing run. The instrument and software of these instruments require that all four DNA bases be present at every base position throughout the length of the initial 8 – 15 nucleotides sequenced, and this often includes bases embedded in the ligation adaptor strand. For this reason, sets of four ligation strands that mutually possess all four bases across the length of the ligation strand sequence are often used. Non-limiting examples of such ligation strand oligonucleotides are shown in Tables 1 and 2.

In various other embodiments, the ligation strand oligonucleotide comprises the following elements: (i) a PCR primer binding site for the single-primer library amplification;

(ii) a 5 nucleotide read code that acts to uniquely identified each sequencing read; (iii) an 8 to 15 nucleotide anchor sequence that acts as a sample identification sequence, enables sample multiplexing within a sequencing run; enables calibration of proper base calls in sequencing reads, and acts as an anchor for hybridization to a partner strand oligonucleotide.

In various other embodiments, the ligation strand oligonucleotide comprises an 8 to 15 nucleotide anchor sequence that acts as a sample identification sequence, enables sample multiplexing within a sequencing run; enables calibration of proper base calls in sequencing reads, and acts as an anchor for hybridization to a partner strand oligonucleotide.

In particular embodiments, a ligation strand oligonucleotide comprises one or more PCR primer sequences, one or more read codes, one or more sample codes, one or more anchor sequences, or two or more 3´nucleotides that are efficient ligation substrates. In additional embodiments, the ligation strand oligonucleotide further comprises one or more sequencing primer binding sites.

In particular embodiments, a ligation strand oligonucleotide comprises one or more PCR primer binding sequences for amplification of a DNA library. In one embodiment, the PCR primer binding sequence is about 12 to about 40 nucleotides, about 18 to about 40 nucleotides, about 20 to about 35 nucleotides, or about 20 to about 30 nucleotides. In another embodiment, the PCR primer binding sequence is about 12 nucleotides, about 13 nucleotides, about 14 nucleotides, about 15 nucleotides, about 16 nucleotides, about 17 nucleotides, about 18 nucleotides, about 19 nucleotides, about 20 nucleotides, about 21 nucleotides, about 22 nucleotides, about 23 nucleotides, about 24 nucleotides, 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, or about 40 nucleotides or more.

In one embodiment, the PCR primer binding sequence is about 25 nucleotides.

In particular embodiments, a ligation strand oligonucleotide comprises one or more read code sequences. As used herein, the term “read code” refers to a polynucleotide that is used to identify unique sequencing reads. In one embodiment, the read code is a random

sequence of nucleotides. In one embodiment, the read code is about 1 nucleotide, about 2 nucleotides, about 3 nucleotides, about 4 nucleotides, about 5 nucleotides, about 6 nucleotides, about 7 nucleotides, about 8 nucleotides, about 9 nucleotides, about 10 nucleotides, or more.

By way of a non-limiting example, a 5 nucleotide read code consists of 256 possible unique sequences where each code chosen is 2 nucleotides different from every other code in the set. This feature enables unique and distinct reads to be differentiated from reads that appear to be unique owing to a sequencing error in the code region. In particular embodiments, codes that have been empirically determined to interfere with adaptor function, owing to particular sequence combinations, may be excluded from use, *e.g.*, seven codes of the 256 had an overrepresentation of G nucleotides and were excluded.

In other embodiments, each read code of 5, 6, 7, 8, 9, 10 or more nucleotides may differ by 2, 3, 4, or 5 nucleotides from every other read code.

In one embodiment, the read code is about 5 nucleotides and optionally, differs from every other read code by 2 nucleotides.

In particular embodiments, a ligation strand oligonucleotide comprises one or more sample code sequences. As used herein, the term "sample code" refers to a polynucleotide that is used to identify the sample. The sample code is also useful in establishing multiplex sequencing reactions because each sample code is unique to the sample and thus, can be used to identify a read from a particular sample within a multiplexed sequencing reaction.

In one embodiment, the sample code comprises sequence that is about 1, about 2 nucleotides, about 3 nucleotides, about 4 nucleotides, or about 5 nucleotides, or more. In another embodiment, each sample code of 2, 3, 4, 5 or more nucleotides may differ from every other sample code by 2, 3, 4, or 5 nucleotides.

In one embodiment, the sample code is about three nucleotides and differs from every other sample code used in other samples by two nucleotides.

In particular embodiments, a ligation strand oligonucleotide comprises a one or more anchor sequences. As used herein, an "anchor sequence" refers to a nucleotide sequence of at least 8 nucleotides, at least 10 nucleotides, at least 12 nucleotides, at least 14 nucleotides, or at

least 16 nucleotides that hybridizes to a partner strand oligonucleotide and that comprises the following properties: (1) each anchor sequence is part of a family of four 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; and (2) each anchor sequence is composed of equal numbers of A+C and G+T, and thus, each anchor sequence shares roughly the same melting temperature and duplex stability as every other anchor sequence in a set of four. In one embodiment, the anchor sequence or a portion thereof also serves to identify the sample, enables sample multiplexing within a sequencing run, enable calibration of proper base calls in sequencing reads, and act as an anchor for hybridization to a partner strand oligonucleotide.

In addition, several considerations are involved in the design of the non-ligating partner strand oligonucleotide. The partner strand oligonucleotide is at least partially complementary (>5 nt) to the ligation strand oligonucleotide in the region that forms the phosphorylated blunt end. Second, the 3′ end of the partner strand oligonucleotide is modified to block or substantially inhibit the oligonucleotide from becoming a ligation substrate, particular in the formation of self-ligated adaptor dimers. The partner strand oligonucleotide is designed to form a stable duplex with the ligation strand at temperatures where ligations are performed ($\leq$ 22°C) but is also designed to dissociate from the ligation strand oligonucleotide at temperatures where a repair oligonucleotide is incorporated into the adaptor ($\geq$ 37°C). This design consideration is depicted as the dissociated partner strand oligonucleotide shown in Figures 4B and 5 in the generation of the adaptor/end-repaired DNA complexes, as the reaction is shifted from ligation to the adaptor completion step that is mediated by repair oligonucleotides.

In particular embodiments, the compositions and methods contemplated herein comprise a ligation step wherein a pre-adaptor is ligated to the end-repaired DNA to generate a “tagged” DNA library. In some embodiments, a single species of pre-adaptor is employed. In some embodiments, two, three, four or five species of pre-adaptors are employed. In some embodiments, a pre-adaptor of identical sequence is ligated to each end of the fragmented end-repaired DNA.

In one embodiment, a plurality of pre-adaptor species is ligated to an end-repaired DNA library. Each of the plurality of pre-adaptors may comprise one or more primer binding site for amplification of the DNA library, one or more read code sequences, one or more sequences for sample multiplexing, one or more anchor sequences, or one or more sequences for DNA sequencing.

(f) Formation of Adaptor/End-Repaired DNA Complexes

In particular embodiments, the compositions and methods contemplated herein comprise displacing the partner strand oligonucleotide from the pre-adaptor/end-repaired DNA complex and replacing the displaced partner strand oligonucleotide with a repair oligonucleotide to generate an adaptor/end-repaired DNA complex. *See, e.g.,* Figure 3. In particular embodiments, the design of the adaptor can be manipulated to enable single primer or dual primer amplification strategies. *See, e.g.,* Figures 4A, and 5.

In particular embodiments, the compositions and methods contemplated herein comprise a ligation step wherein an adaptor comprising a ligation strand oligonucleotide and a repair oligonucleotide is ligated to the end-repaired DNA to generate a "tagged" DNA library. In some embodiments, a single species of adaptor is employed. In some embodiments, two, three, four or five species of adaptors are employed. In some embodiments, an adaptor of identical sequence is ligated to each end of the fragmented end-repaired DNA.

The design considerations of the partner strand oligonucleotide allow it to be displaced from the pre-adaptor/end-repaired DNA complex because it dissociates from the ligation strand oligonucleotide at temperatures at which the repair oligonucleotide anneals to the ligation strand oligonucleotide (*e.g.,* > 37°C) and at temperatures at which the enzymatic steps are carried out to incorporate the repair oligonucleotide into an adaptor/end-repaired DNA complex generate a contiguous, double-stranded, DNA library molecule (*e.g.,* > 37°C).

As used herein, the term "repair oligonucleotide" refers to a polynucleotide sequence that is complementary to, and anneals to, a portion of, or to all of, the nucleotides of the ligation strand oligonucleotide. The repair oligonucleotide can vary in length from the minimum length required to form a stable DNA duplex at temperatures where DNA ligase is active (~8 nt) to oligonucleotides that push the limits of current synthesis capabilities (>200

nt). In particular embodiments, the "repair oligonucleotide" includes additional, functional DNA sequences that are not necessarily present in the ligation strand oligonucleotide.

In particular embodiments, the ligation strand oligonucleotide is about 8 to about 15 nucleotides and the repair oligonucleotide is 35 to 60 nucleotides. In this design, the sequence of the ligand strand oligonucleotide is extended by primer extension and generates a nucleotide sequence complementary to the repair oligonucleotide. This design would yield identical PCR primer binding sites. Identical PCR primer binding sites allows for a single primer library amplification strategy. *See, e.g.,* Figures 3D and 4A.

In particular embodiments, the ligation strand oligonucleotide is about 35 to about 60 nucleotides and the repair oligonucleotide is completely complementary to the ligation strand oligonucleotide. Identical PCR primer binding sites allows for a single primer library amplification strategy. *See, e.g.,* Figure 4A.

In particular embodiments, the ligation strand oligonucleotide is about 35 to about 60 nucleotides and the repair oligonucleotide is about 35 to about 60 nucleotides and the two oligonucleotides are complementary but for the PCR primer binding sites. Different PCR primer binding sites allows for a dual primer library amplification strategy. *See, e.g.,* Figure 5.

In preferred embodiments, the ligation strand oligonucleotide comprises the following elements: (i) a PCR primer binding site for the single-primer library amplification; (ii) a 5 nucleotide read code that acts to uniquely identified each sequencing read; (iii) an 8 to 15 nucleotide anchor sequence that is partially or completely complementary to the anchor sequence of the ligation strand oligonucleotide.

In other embodiments, the ligation strand oligonucleotide comprises an 8 to 15 nucleotide anchor sequence that is partially or completely complementary to the anchor sequence of the ligation strand oligonucleotide.

In particular embodiments, a repair oligonucleotide comprises one or more PCR primer sequences, one or more read codes, one or more sample codes, one or more anchor sequences, or two or more 3´nucleotides that are efficient ligation substrates. In additional

embodiments, the repair oligonucleotide further comprises one or more sequencing primer binding sites.

In particular embodiments, a repair oligonucleotide comprises (i) one or more PCR primer binding sequences that are complementary to the PCR primer binding sites in the ligation strand oligonucleotide (enables single-primer DNA library amplification) or (ii) one or more PCR primer binding sequences that are not complementary to the PCR primer binding sites in the ligation strand oligonucleotide (enables dual-primer DNA library amplification. In one embodiment, the PCR primer binding sequence is about 12 to about 40 nucleotides, about 18 to about 40 nucleotides, about 20 to about 35 nucleotides, or about 20 to about 30 nucleotides. In another embodiment, the PCR primer binding sequence is about 12 nucleotides, about 13 nucleotides, about 14 nucleotides, about 15 nucleotides, about 16 nucleotides, about 17 nucleotides, about 18 nucleotides, about 19 nucleotides, about 20 nucleotides, about 21 nucleotides, about 22 nucleotides, about 23 nucleotides, about 24 nucleotides, 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, or about 40 nucleotides or more.

In one embodiment, the PCR primer binding sequence is about 25 nucleotides.

In particular embodiments, a repair oligonucleotide comprises one or more read code sequences. In one embodiment, the read code is a random sequence of nucleotides. In one embodiment, the read code is about 1 nucleotide, about 2 nucleotides, about 3 nucleotides, about 4 nucleotides, about 5 nucleotides, about 6 nucleotides, about 7 nucleotides, about 8 nucleotides, about 9 nucleotides, about 10 nucleotides, or more.

By way of a non-limiting example, a 5 nucleotide read code consists of 256 possible unique sequences where each code chosen is 2 nucleotides different from every other code in the set. This feature enables unique and distinct reads to be differentiated from reads that appear to be unique owing to a sequencing error in the code region. In particular embodiments, codes that have been empirically determined to interfere with adaptor function,

owing to particular sequence combinations, may be excluded from use, *e.g.,* seven codes of the 256 had an overrepresentation of G nucleotides and were excluded.

In other embodiments, each read code of 5, 6, 7, 8, 9, 10 or more nucleotides may differ by 2, 3, 4, or 5 nucleotides from every other read code.

In one embodiment, the read code is about 5 nucleotides and optionally, differs from every other read code by 2 nucleotides.

In particular embodiments, a repair oligonucleotide comprises one or more sample code sequences. In one embodiment, the sample code comprises sequence that is about 1, about 2 nucleotides, about 3 nucleotides, about 4 nucleotides, or about 5 nucleotides, or more. In another embodiment, each sample code of 2, 3, 4, 5 or more nucleotides may differ from every other sample code by 2, 3, 4, or 5 nucleotides.

In one embodiment, the sample code is about three nucleotides and differs from every other sample code used in other samples by two nucleotides.

In particular embodiments, a repair oligonucleotide comprises a one or more anchor sequences complementary to the one or more anchor sequences of the ligation strand oligonucleotide.

Without wishing to be bound by any particular theory, at least two exemplary strategies are contemplated for incorporating the repair oligonucleotide into an adaptor/end-repair DNA complex.

In one embodiment, the partner strand oligonucleotide is displaced from the pre-adaptor/end-repaired DNA complex; repair oligonucleotide is added and allowed to anneal to the ligation strand; polynucleotide kinase, *e.g.,* T4 polynucleotide kinase, is used to add a phosphate group to the 5′ end of the end-repaired DNA fragment; and DNA ligase is used to repair the nick that exists between the 5′ end of the repair oligonucleotide and the 3′ end of the end-repaired DNA fragment. In particular embodiments, the DNA ligase is a thermo-stable nick-specific ligase that has activity across a broad range of temperatures, including, but not limited to Taq DNA ligase, *E. coli* DNA ligase, 9° North ligase (NEB), and any other ligase that can seal a phosphorylated nick. *See, e.g.,* Figures 3A and 3B.

In another embodiment, the partner strand oligonucleotide is displaced from the pre-adaptor/end-repaired DNA complex; repair oligonucleotide is added and allowed to anneal to the ligation strand; a low processivity DNA polymerase that has a 5′ → 3′ exonuclease activity (and no intrinsic 3′ → 5′ exonuclease activity) extends the 3′ end of ligation strand oligonucleotide and in addition, removes the dephosphorylated 5′ terminal nucleotide and adjacent nucleotides with a 5′ → 3′ exonuclease activity thereby exposing ligatable 5′ phosphate groups and replacing them with incorporated bases that leave behind a nick when the enzyme dissociates; and DNA ligase, *e.g., Taq* DNA ligase, is used to repair the nicks.

Illustrative examples of low processivity DNA polymerases suitable for use in particular embodiments of the compositions and methods contemplated herein include, but are not limited to *Taq* DNA polymerase, and *BstI* DNA polymerase.

D. DNA LIBRARY AMPLIFICATION

In particular embodiments, methods contemplated herein comprise amplification of a DNA library to generate a DNA clone library or a library of DNA clones. In particular embodiments, the DNA is cfDNA. Each molecule of the DNA library comprises an adaptor ligated to each end of an end-repaired DNA, and each adaptor comprises one or more PCR primer binding sites. In one embodiment, different adaptors are ligated to different ends of the end-repaired DNA.

In one embodiment, the same adaptor is ligated to both ends of the DNA. Ligation 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 ligated-DNA 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 Tm of $\geq$ 55° C under standard ionic strength conditions.

In one embodiment, the adaptor ligated to the 3′ end of an end-repaired DNA fragment comprises a different PCR primer binding site from the adaptor ligated to the 5′ end of the end-repaired DNA fragment. In particular embodiments, a portion of the adaptor ligated-

DNA library will be amplified using standard PCR techniques with two primers riving amplification.

In particular embodiments, picograms of the initial DNA 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.

E. METHODS OF GENETIC ANALYSIS OF DNA

In various embodiments, a method for genetic analysis of DNA is provided. In particular embodiments, the DNA is cfDNA. cfDNA is cell-free DNA that is found in plasma or other bodily fluids.

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

1. DETERMINING THE NUMBER OF GENOME EQUIVALENTS

In various embodiments, a method for genetic analysis of 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.

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.

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.

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.

In one embodiment, the genome equivalents in a DNA 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 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.

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).

In one embodiment, the repeat is an Alu repeat.

2. QUANTITATIVE GENETIC ANALYSIS

In various embodiments, a method for genetic analysis of DNA 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.

(a) Capture of Target Genetic Locus

The present invention contemplates, in part, a capture probe module that is multifunctional and designed to retain the efficiency and reliability of larger probes but that minimizes uninformative sequence generation in a DNA clone library. A "capture probe module" refers 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.

In particular embodiments, a capture probe module comprises a capture probe. As used herein a "capture probe" refers to a polynucleotide comprising a region capable of hybridizing to a specific DNA target region. Because the average size of DNA is relatively small and is highly fragmented, the compositions and methods contemplated herein comprise the use of high density and relatively short capture probes to interrogate DNA target regions of interest.

In particular embodiments, a capture probe module is combined with a partner oligonucleotide that optionally comprises a hapten and that hybridizes the tail sequence to generate a capture probe module duplex.

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.

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.

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.

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.

In a particular embodiment, the capture probe is 60 nucleotides.

In a particular embodiment, the capture probe is not 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.

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.

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.

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.

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 DNA 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.

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.

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 appreciated 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.

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

In certain embodiments, the methods contemplated herein comprise isolating a tagged DNA 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. In some embodiments, the capture partner oligonucleotide capable of hybridizing to the tail sequence of the multifunctional capture probe module is modified to contain a biotin at the 5′-end or 3′-end which is capable of interacting with streptavidin linked to a column, bead or other substrate for use in DNA complex isolation methods.

In one embodiment, the capture partner oligonucleotide capable of hybridizing to the tail sequence of the multifunctional capture probe module is modified to contain a biotin at the 3′-end which is capable of interacting with streptavidin linked to a column, bead or other substrate for use in DNA complex isolation methods.

In particular embodiments, a tail sequence of a multifunctional capture probe module is bound to a capture partner oligonucleotide. In some embodiments, the multifunctional capture probe module is bound to the capture partner oligonucleotide prior to formation of a tagged DNA library—multifunctional capture probe module complex. In some embodiments, the multifunctional capture probe module is bound to the capture partner oligonucleotide after the formation of a tagged DNA library—multifunctional capture probe module complex. In some embodiments, the multifunctional capture probe module is bound to the capture partner oligonucleotide simultaneously with the formation of a tagged DNA library—multifunctional capture probe module complex. In some embodiments, the capture partner oligonucleotide is chemically modified. In one embodiment, the capture partner oligonucleotide is modified by adding a hapten to the 5′ or 3′ end. In one embodiment the hapten is biotin.

In particular embodiments, removal of the single stranded 3′-ends from the isolated tagged DNA library- 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.

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.

In certain other embodiments, the methods comprise creating a hybrid capture probe-isolated tagged DNA target molecule through the concerted action of a 5' FLAP endonuclease, DNA polymerization and nick closure by a DNA ligase.

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., "The 3′ 5′ exonucleases," *Nat Rev Mol Cell Biol.* 3(5):364-76 (2002)). In particular embodiments, the enzyme comprising 3′-5′ exonuclease activity is T4. 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.*

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.

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 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).

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.

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-DNA 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.

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.

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.

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 DNA 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 DNA 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 of any other capture probe that hybridizes to the target genetic locus in a tagged DNA clone library, including all intervening distances.

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.

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.

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

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. A unique read is defined as the single consensus read from a "family" of reads that all share the same read code and sequence start point within DNA. 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 are then computed as the average of all the unique reads observed on a probe-by-probe basis. Cases where there is an obvious copy number change are excluded from the data set used to compute the average. Unique reads are important because each unique read must be derived from a unique 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.

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

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

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; and detection of genetic lesions. In particular embodiments, bioinformatics analysis is useful to quantify the number of genome equivalents analyzed in the DNA 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.

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.

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.

In one embodiment, the genome equivalents in a DNA 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 ligation event and thus, they are amplification-derived "siblings" of one another. Each unique read is considered a unique ligation event and the sum of unique reads is considered equivalent to the number of genome equivalents analyzed.

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.

In particular embodiments, to provide an accurate analysis for DNA 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.

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.

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

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).

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.

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.

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.

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.

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.

F. CLINICAL APPLICATIONS OF QUANTITATIVE GENETIC ANALYSIS

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

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 one embodiment, the DNA is cfDNA.

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 comprises 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.

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).

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, familiar hypereosinophilia, chronic eosinophilic leukemia, neuroendocrine cancers, carcinoid tumors, and the like.

In one embodiment, the genetic lesion is a lesion annotated in the Cosmic database (the lesions and sequence data can be downloaded from cancer.sanger.ac.uk/cosmic/census) or a lesion annotated in the Cancer Genome Atlas (the lesions and sequence data can be downloaded from tcga-data.nci.nih.gov/tcga/tcgaDownload.jsp).

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, SLCO1B3, SMAD2, SMAD3, SMAD4, SMARCA4, SMARCB1, SMO, SOD2, SOX10, SOX2, SRC, STK11, SULT1A1,

TBX22, TET2, TGFBR2, TMPRSS2, TNFRSF14, TOP1, TP53, TPMT, TSC1, TSC2, TYMS, UGT1A1, UMPS, USP9X, VHL, and WT1.

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.

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

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

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.

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.

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 IB (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).

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.

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.

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.

Illustrative examples of fungal species that can be screened for with the compositions and methods contemplated herein include, but are not limited to: an Aspergillis spp., a Blastomyces spp., a Candida spp., a Coccicioides 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.

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, Ephemerovirus, 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), Bunyaviridiae 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 encephaliltis causing virus.

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.

In particular embodiments, a bioinformatic analysis is used to quantify the number of genome equivalents analyzed in the DNA 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.

G. COMPANION DIAGNOSTICS

In various embodiments, a companion diagnostic for a genetic disease is provided, comprising: isolating or obtaining DNA, *e.g.,* cfDNA from a biological sample of a subject; removing the terminal phosphate residues of the DNA; treating the dephosphorylated DNA with one or more end-repair enzymes to generate end-repaired DNA; ligating one or more double-stranded DNA (dsDNA) pre-adaptors to the 3′ end of each strand of the end-repaired DNA to form pre-adaptor/end-repaired DNA complexes, wherein each dsDNA pre-adaptor comprises a ligation strand oligonucleotide that is ligated to the 3′ end of each strand of the end-repaired DNA, and a non-ligation partner strand oligonucleotide; displacing the non-ligation partner strand oligonucleotide from the pre-adaptor/end-repaired DNA complexes

with a repair oligonucleotide, to form adaptor/end-repaired DNA complexes, wherein each adaptor comprises the ligation strand oligonucleotide and the repair oligonucleotide; and treating the adaptor/end-repaired DNA complexes with one or more enzymes to form a contiguous, double-stranded, 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.

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.

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

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, trietylenephosphoramide, triethylenethiophosphaoramide and trimethylolomelamine resume; 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, authramycin, azaserine, bleomycins, cactinomycin, calicheamicin, carabicin, 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, epitiostanol, mepitiostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elformithine; elliptinium acetate; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidamine; mitoguazone; 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 doxetaxel (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.

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.

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. U.S. Patent Application Nos: 14/102,285, filed December 10, 2013, and 14/466,741, filed August 22, 2014, are each incorporated by reference herein, in its entirety.

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

PROOF OF PRINCIPLE FOR HIGH EFFICIENCY ADAPTOR LIGATION

This example provides direct quantitatively evidence that the high efficiency ligation strategies contemplated herein result in ligation to both ends of the DNA fragment in the absence of adaptor dimer formation (Figure 2).

Plasmid DNA from the cloning vector pUC19 was digested with the restriction enzyme RsaI to generate blunt ends and dephosphorylated with Antarctic Alkaline Phosphatase. These blunt-ended, dephosphorylated DNA fragments were ligated to a collection of nine different high-efficiency adaptors (Table 1). In all cases, a quantitative shift in fragment mobility was observed following the ligation reaction (arrows), and the shift in mobility was equivalent to the attachment of an adaptor to each end of each DNA fragment. This example provides a proof of principle that the compositions and methods contemplated herein result in high efficiency ligation of adapters to DNA fragments, thereby increasing the overall efficiency of constructing DNA libraries.

Table 1 Ligation strand and partner strand oligonucleotide sequences used to create test he adaptors

SEQ ID NO:	Adaptor ID	Ligation strand (5'phosphate, 5' to 3')	SEQ ID NO:	Partner strand (5' to 3', 3' ddC)
1	1	GAGGGTCTACCTTCTTNNNNNTGTATTCGAATTCTCTGGTCCTGCA	10	AAGGTAGACCCT
2	2	GCTCTAGACGTCATCGNNNNNTGTATTCGAATTCTCTGGTCCTGCA	11	TGACGTCTAGAG
3	3	GGATACTCGTAGCGGCNNNNNTGTATTCGAATTCTCTGGTCCTGCA	12	GCTACGAGTATC
4	4	GTCACGAGTAGAGAAANNNNNTGTATTCGAATTCTCTGGTCCTGCA	13	CTCTACTCGTGA
5	5	GAGGGTCTACCTTAGTNNNNNTGTATTCGAATTCTCTGGTCCTGCA	14	AAGGTAGACCCT
6	6	GCTCTAGACGTCAGAGNNNNNTGTATTCGAATTCTCTGGTCCTGCA	15	TGACGTCTAGAG
7	7	GGATACTCGTAGCTTCNNNNNTGTATTCGAATTCTCTGGTCCTGCA	16	GCTACGAGTATC
8	8	GTCACGAGTAGAGCCANNNNNTGTATTCGAATTCTCTGGTCCTGCA	17	CTCTACTCGTGA
9	9	GAGGGTCTACCTTGCTNNNNNTGTATTCGAATTCTCTGGTCCTGCA	18	AAGGTAGACCCT

EXAMPLE 2

HIGH EFFICIENCY DNA LIBRARY CONSTRUCTION

I. FRAGMENT END REPAIR

Cell-free DNA (cfDNA) fragment ends were dephosphorylated, internal damage to the DNA duplex was repaired and DNA termini was "polished" to blunt-ends. The resulting fragments are referred to as "end-repaired fragments."

The cfDNA fragment ends were dephosphorylated by combining 81 µl of purified cfDNA, 10 µl of New England Biolabs (NEB) CutSmart buffer (B7204S), and 5 µl of NEB Shrimp Alkaline Phosphatase (M0371). The reaction mixture was incubated at 37°C for 15 min. and then at 65°C for 5 min.

The internal damage to dephosphorylated cfDNA fragments was repaired by adding 4 µl of the following mixture, prepared on ice: 1.1 µl of 10 mM dNTP mix (NEB N0447), 2.2 µl of PreCR enzyme mix (M0309) and 1.1 µl of T4 DNA polymerase (M0203). This reaction mixture was incubated at 20°C for 15 min. and then at 70°C for 10 min. cfDNA fragments repaired and polished in this manner are ready for direct use in a DNA ligation reaction.

II. PRE-ADAPTOR DESIGN

Several design considerations were used to generate the pre-adaptors, which are made up of a ligation strand oligonucleotide and a complementary partner strand oligonucleotide with a blocked 3′ end.

The pre-adaptors used in this example were designed to have the following features: a ligation strand oligonucleotide that is 10 nt in length; an equal balance of A/T or G/C residues; each of the four DNA bases represented at each base position within each set of pre-adaptors; a predicted melting temperature of the 10 base sequence that is ~37°C in 50 mM Na^+ (or K^+), 10 mM $MgCl_2$; both an A/T and a G/C nt as the first two bases of each pre-adaptor sequence; a complementary partner oligonucleotide sequence that is 8 nt in length, that is chemically blocked with by using 2-hydroxyl ribose-modified DNA bases (MWG Eurofins), and that has a melting temperature of ~25°C in 50 mM Na^+ or K^+, 10 mM $MgCl_2$.

Even with design constrains in place, empirical performance screening of adaptor sets was performed. In the current experiment, five sets of four adaptors having acceptable performance were identified (*see, e.g.,* Table 2). The column labeled "score" shows the percent cloning efficiency of each adaptor relative to the best performing adaptor (set 6-2).

Table 2. Empirically validated adaptor sets.

SEQ ID NO:	Ligation strand oligonucleotides		Partner strand oligonucleotides		
	Name	Sequence	Name	Sequence	Score
19	he_lig_5-1	/5Phos/CTGAGCTAGT	he_part_5-1	TAGCTCA[3-dG-Q]	60
20	he_lig_5-2	/5Phos/GACTCGATAG	he_part_5-2	ATCGAGT[3-dC-Q]	97
21	he_lig_5-3	/5Phos/TCAGATCGTC	he_part_5-3	CGATCTG[3-dA-Q]	27
22	he_lig_5-4	/5Phos/AGTCTAGCCA	he_part_5-4	GCTAGAC[3-dT-Q]	84
23	he_lig_6-1	/5Phos/GGATTACCCT	he_part_6-1	GGTAATC[3-dC-Q]	70
24	he_lig_6-2	/5Phos/CTTACGGATG	he_part_6-2	TCCGTAA[3-dG-Q]	100
25	he_lig_6-3	/5Phos/ACCGATTGAC	he_part_6-3	CAATCGG[3-dT-Q]	74
26	he_lig_6-4	/5Phos/TAGCGCATGA	he_part_6-4	ATGCGCT[3-dA-Q]	48
27	he_lig_8-1	/5Phos/ATGTCCAGCT	he_part_8-1	CTGGACA[3-dT-Q]	24
28	he_lig_8-2	/5Phos/CACAGGTTAG	he_part_8-2	AACCTGT[3-dG-Q]	46
29	he_lig_8-3	/5Phos/TGACATGCTC	he_part_8-3	GCATGTC[3-dA-Q]	53
30	he_lig_8-4	/5Phos/GCTGTACAGA	he_part_8-4	TGTACAG[3-dC-Q]	48
31	he_lig_11-1	/5Phos/TCAAGTCGGT	he_part_11-1	CGACTTG[3-dA-Q]	83
32	he_lig_11-2	/5Phos/GTTCAGACTG	he_part_11-2	GTCTGAA[3-dC-Q]	95
33	he_lig_11-3	/5Phos/CAGGTCTAAC	he_part_11-3	TAGACCT[3-dG-Q]	33
34	he_lig_11-4	/5Phos/AGCTCAGTCA	he_part_11-4	ACTGAGC[3-dT-Q]	98
35	he_lig_12-1	/5Phos/GATCCGTACT	he_part_12-1	TACGGAT[3-dC-Q]	91
36	he_lig_12-2	/5Phos/ACAGTCGTAG	he_part_12-2	ACGACTG[3-dT-Q]	98
37	he_lig_12-3	/5Phos/TGGTAACCTC	he_part_12-3	GGTTACC[3-dA-Q]	85
38	he_lig_12-4	/5Phos/CTCAGTAGGA	he_part_12-4	CTACTGA[3-dG-Q]	93

III. Ligation of Pre-Adaptors

A pre-adaptor was ligated to end-repaired fragments generated in step I of this example. 25 µl of end-repaired fragment was combined with 10 µl of 10 µM adaptor. Typically, 1 to 4 ligation reactions were performed depending on the number of separate adaptors added to the reaction. 15 µl of ligation cocktail (5 µl of 10X T4-DNA ligation buffer, 7.5 µl of 50% PEG8000, and 2.5 µl of HC T4 DNA ligase (NEB; M0202)) was added

to each ligation reaction in a final volume of 50 µl. The reaction was mixed and incubated at 20°C for 60 min., then at 65°C for 10 min, then cooled to room temperature.

After the ligation reaction, 50 ul of TEzero (10 mM Tris pH 8.0, 0.1 mM EDTA, 0.05% Tween 20). and 120 ul of DNA purification beads were added to each reaction and mixed well. The reaction was incubated for 10 min. at room temperature, then the beads were washed two times with 200 µl of 70% ethanol/water (v/v), air-dried briefly (~5 min.), and eluted with 20 µl of TEzero.

IV. REPAIR OLIGONUCLEOTIDES

A complete listing of repair oligonucleotides used in this example is shown in Table 3. Each repair oligonucleotide is a pool of 249 individual oligonucleotides. The invariant sequence in each repair oligonucleotide represents a PCR primer binding site and is shown in the left hand portion of Table 3.

Each of the 249 oligonucleotides comprises a 5 nucleotide sample code, shown as an "XXXXX" in repair oligonucleotide sequence. The 5 nucleotide sample are shown in the right hand portion of Table 3. The 5 nucleotide codes consist of 256 possible unique sequences that were chosen to be 2 base changes different from every other code in the set. This feature enabled unique and distinct reads to be differentiated from reads that appeared to be unique owing to a sequencing error in the code region. Seven codes in which G residues are over-represented and that were shown empirically to interfere with adaptor function were removed, leaving 249 random codes.

Table 3. Repair oligos and their associated read codes

SEQ ID NO:	Full length repair oligos (RO) compatible with ligation oligos	
	Name	Sequence
39	RO_5-1	TGCAGGACCAGAGAATTCGAATACAXXXXXACTAGCTCAG
40	RO_5-2	TGCAGGACCAGAGAATTCGAATACAXXXXXCTATCGAGTC
41	RO_5-3	TGCAGGACCAGAGAATTCGAATACAXXXXXGACGATCTGA
42	RO_5-4	TGCAGGACCAGAGAATTCGAATACAXXXXXTGGCTAGACT
43	RO_6-1	TGCAGGACCAGAGAATTCGAATACAXXXXXAGGGTAATCC
44	RO_6-2	TGCAGGACCAGAGAATTCGAATACAXXXXXCATCCGTAAG
45	RO_6-3	TGCAGGACCAGAGAATTCGAATACAXXXXXGTCAATCGGT

46	RO_6-4	TGCAGGACCAGAGAATTCGAATACAXXXXXTCATGCGCTA
47	RO_7-1	TGCAGGACCAGAGAATTCGAATACAXXXXXACTGCTAGCA
48	RO_7-2	TGCAGGACCAGAGAATTCGAATACAXXXXXCAGCGATCAT
49	RO_7-3	TGCAGGACCAGAGAATTCGAATACAXXXXXGTCATCGATG
50	RO_7-4	TGCAGGACCAGAGAATTCGAATACAXXXXXTGATAGCTGC
51	RO_8-1	TGCAGGACCAGAGAATTCGAATACAXXXXXAGCTGGACAT
52	RO_8-2	TGCAGGACCAGAGAATTCGAATACAXXXXXCTAACCTGTG
53	RO_8-3	TGCAGGACCAGAGAATTCGAATACAXXXXXGAGCATGTCA
54	RO_8-4	TGCAGGACCAGAGAATTCGAATACAXXXXXTCTGTACAGC
55	RO_11-1	TGCAGGACCAGAGAATTCGAATACAXXXXXACCGACTTGA
56	RO_11-2	TGCAGGACCAGAGAATTCGAATACAXXXXXCAGTCTGAAC
57	RO_11-3	TGCAGGACCAGAGAATTCGAATACAXXXXXGTTAGACCTG
58	RO_11-4	TGCAGGACCAGAGAATTCGAATACAXXXXXTGACTGAGCT
59	RO_12-1	TGCAGGACCAGAGAATTCGAATACAXXXXXAGTACGGATC
60	RO_12-2	TGCAGGACCAGAGAATTCGAATACAXXXXXCTACGACTGT
61	RO_12-3	TGCAGGACCAGAGAATTCGAATACAXXXXXGAGGTTACCA
62	RO_12-4	TGCAGGACCAGAGAATTCGAATACAXXXXXTCCTACTGAG

	XXXXX - Difference 2 sequence codes						
	Seq	**Seq**	**Seq**	**Seq**	**Seq**	**Seq**	**Seq**
	CGGGT	CACGG	GTGAT	ATCAG	GATAC	TGTCT	CCAAA
	CGGTG	CAGCG	GTGTA	ATCGA	GATCA	TGTTC	CCACC
	CGTGG	CAGGC	GTTAG	ATGAC	GCAAT	TTCGT	CCATT
	GCGGT	CCAGG	GTTGA	ATGCA	GCATA	TTCTG	CCCAC
	GCGTG	CCGAG	TAGGT	CAAGT	GCCCT	TTGCT	CCCCA
	GCTGG	CCGGA	TAGTG	CAATG	GCCTC	TTGTC	CCTAT
	GGCGT	CGACG	TATGG	CAGAT	GCTAA	TTTCG	CCTTA
	GGCTG	CGAGC	TGAGT	CAGTA	GCTCC	TTTGC	CTACT
	GGGCT	CGCAG	TGATG	CATAG	GCTTT	AAAAA	CTATC
	GGGTC	CGCGA	TGGAT	CATGA	GTAAC	AAACC	CTCAT
	GGTCG	CGGAC	TGGTA	CCCGT	GTACA	AAATT	CTCTA
	GGTGC	CGGCA	TGTAG	CCCTG	GTCAA	AACAC	CTTAC
	GTCGG	GAAAG	TGTGA	CCGCT	GTCCC	AACCA	CTTCA
	GTGCG	GAAGA	TTAGG	CCGTC	GTCTT	AATAT	TAAAT
	GTGGC	GACCG	TTGAG	CCTCG	GTTCT	AATTA	TAATA
	TGCGG	GACGC	TTGGA	CCTGC	GTTTC	ACAAC	TACCT
	TGGCG	GAGAA	AACGT	CGAAT	TAACG	ACACA	TACTC
	TGGGC	GAGCC	AACTG	CGATA	TAAGC	ACCAA	TATAA
	AAAGG	GAGTT	AAGCT	CGCCT	TACAG	ACCCC	TATCC
	AAGAG	GATGT	AAGTC	CGCTC	TACGA	ACCTT	TATTT
	AAGGA	GATTG	AATCG	CGTAA	TAGAC	ACTCT	TCACT

	ACCGG	GCACG	AATGC	CGTCC	TAGCA	ACTTC	TCATC
	ACGCG	GCAGC	ACAGT	CGTTT	TCAAG	ATAAT	TCCAT
	ACGGC	GCCAG	ACATG	CTAAG	TCAGA	ATATA	TCCTA
	AGAAG	GCCGA	ACGAT	CTAGA	TCCCG	ATCCT	TCTAC
	AGAGA	GCGAC	ACGTA	CTCCG	TCCGC	ATCTC	TCTCA
	AGCCG	GCGCA	ACTAG	CTCGC	TCGAA	ATTAA	TTAAA
	AGCGC	GGAAA	ACTGA	CTGAA	TCGCC	ATTCC	TTACC
	AGGAA	GGACC	AGACT	CTGCC	TCGTT	ATTTT	TTATT
	AGGCC	GGATT	AGATC	CTGTT	TCTGT	CAAAC	TTCAC
	AGGTT	GGCAC	AGCAT	CTTGT	TCTTG	CAACA	TTCCA
	AGTGT	GGCCA	AGCTA	CTTTG	TGAAC	CACAA	TTTAT
	AGTTG	GGTAT	AGTAC	GAACT	TGACA	CACCC	TTTTA
	ATGGT	GGTTA	AGTCA	GAATC	TGCAA	CACTT	
	ATGTG	GTAGT	ATACG	GACAT	TGCCC	CATCT	
	ATTGG	GTATG	ATAGC	GACTA	TGCTT	CATTC	

V. ADDITION OF REPAIR OLIGONUCLEOTIDES TO PRE-ADAPTOR LIBRARIES

Library construction was completed by adding repair oligonucleotides to the adaptor. The repair oligonucleotides illustrated in this example contain a PCR primer binding site; sample codes; and an anchor sequence, which is a random sequence label that acts as a means to identify the sequence, that enables calibration of proper base calls in sequencing reads, and that acts as an anchor for hybridization to the ligation strand oligonucleotide.

4 µl of a 1 µM pool of repair oligonucleotide (*see, e.g.,* Table 3) was added to 20 µl of purified ligation mix from step III of this example.

Next, a 40 µl repair oligonucleotide reaction was prepared by combining 24 µl repair oligonucleotide/ligase mixture with 16 µl of the following mixture, on ice: 11 µl of water, 4.4 µl of buffer "B" (190 µl of CutSmart buffer (NEB; B7204) and 10 µl of 1M dithiothreitol (DTT; Sigma-Aldrich 646563), 1.32 µl of nucleotide mix "N" (combine 50 µl of 10 mM dNTP mixture (NEB; N0447) with 25 µl of 100X NAD+(NEB; B9007) and 0.88 µl of enzyme mix "E" (combine 20 µl of T4 polynucleotide kinase (NEB; M0201), 10 µl of full-length *BstI* polymerase (NEB; M0328) and 10 µl of *Taq* DNA ligase (NEB; M0208). The reaction was mixed and incubated at 37°C for 15 min. then at 60°C for 15 min.

The reactions were removed from the thermal cycler and 48 ul of bead resuspension solution (19% PEG8000, 2M NaCl, 10 mM Tris pH 8.0, 10 mM EDTA, 0.1% Tween 20) was added to the reaction and incubated at room temperature for 10 min. The beads were washed twice with 200 µl of 70% ethanol, air-dried briefly (~5 min.) and resuspended in 25 µl of TEzero. A magnet was used to localize the beads and the clarified DNA library was transferred to a fresh reaction vessel.

VI. SUMMARY

The resulting DNA libraries constructed using the methods contemplated herein throughout and described in Example 1 are amplification ready and suitable for next generation sequencing, qPCR analysis, and other quantitative genetic analyses of one or more target genetic loci.

In general, in the following claims, the terms used should not be construed to limit the claims to the specific embodiments disclosed in the specification and the claims, but should be construed to include all possible embodiments along with the full scope of equivalents to which such claims are entitled. Accordingly, the claims are not limited by the disclosure.

The claims defining the invention are as follows:

1. A method for adaptor ligation to one or more DNA fragments comprising:

(a) removing the terminal phosphate residues of the one or more DNA fragments;

(b) treating the dephosphorylated DNA fragments with one or more end-repair enzymes to generate end-repaired DNA fragments;

(c) using a ligase to ligate one or more double-stranded DNA (dsDNA) pre-adaptors to the 3' end of each strand of the end-repaired DNA fragments to form pre-adaptor/end-repaired DNA complexes, wherein each dsDNA pre-adaptor comprises

(i) a ligation strand oligonucleotide that is ligated to the 3' end of each strand of the end-repaired DNA fragments and comprises an anchor sequence; and

(ii) a non-ligation partner strand oligonucleotide;

(d) displacing the non-ligation partner strand oligonucleotide from the pre-adaptor/end-repaired DNA complexes with a repair oligonucleotide, wherein the repair oligonucleotide is longer than the ligation strand oligonucleotide, and wherein the 3' end of the repair oligonucleotide is complementary to the 5' end of the ligation strand oligonucleotide;

(e) ligating the repair oligonucleotide to the 5' end of the end-repaired DNA fragments using a kinase ligase strategy to form adaptor/end-repaired DNA complexes, wherein each adaptor comprises the ligation strand oligonucleotide and the repair oligonucleotide; wherein the kinase ligase strategy comprises contacting the adaptor/end repaired DNA complexes with a kinase and a ligase, wherein the kinase adds a phosphate group to the 5' terminal nucleotide of each strand of the end repaired DNA fragments, and wherein the ligase ligates the repair oligonucleotide to the phosphorylated 5' end of each strand of the end repaired DNA fragments; and

(f) extending the ligation strand oligonucleotide at the 3' end using the repair oligonucleotide as a template to form one or more contiguous, dsDNA fragments each comprising an adaptor molecule ligated to each end of the DNA fragment.

2. The method of claim 1, wherein the non-ligation partner strand oligonucleotide comprises a modification at its 3′ terminus that prevents ligation to the 5′ end of the end-repaired DNA fragments or adaptor dimer formation.

3. The method of claim 1 or 2, wherein the source of the one or more DNA fragments is selected from the group consisting of genomic DNA (gDNA), complementary DNA (cDNA), and cell-free DNA (cfDNA).

4. The method of claim 3, wherein the DNA is isolated from a biological sample selected from the group consisting of an amniotic fluid sample, a blood sample, a skin sample, a hair sample, a hair follicle sample, a saliva sample, a mucous sample, a sweat sample, a tear sample, an epithelial tissue sample, a urine sample, a semen sample, a seminal plasma sample, a serum sample, a prostatic fluid sample, a pre-ejaculatory fluid (Cowper's fluid) sample, an ocular fluid sample, an excreta sample, a biopsy sample, an ascites sample, a cerebrospinal fluid sample, a lymph sample, a tissue extract sample, a stool sample, and a formalin-fixed, paraffin embedded (FFPE) sample.

5. The method of any one of claims 1-4, further comprising repairing damage of the one or more DNA fragments prior to step (c).

6. The method of claim 5, wherein the damage is a deaminated cytosine (Uracil), an abasic site, methylation of guanine to O^6MeG, one or more DNA nicks, one or more DNA gaps, or a thymine dimer.

7. The method of any one of claims 1-6, wherein the ligation strand oligonucleotide further comprises one or more of

(i) one or more unique read codes;

(ii) a PCR primer binding site for PCR amplification of the one or more contiguous dsDNA fragments;

(iii) one or more sample codes for sample multiplexing; or

(iv) one or more primer binding sites for DNA sequencing.

8. The method of any one of claims 1-7, wherein the repair oligonucleotide comprises an anchor sequence.

9. The method of claim 8, wherein the repair oligonucleotide further comprises one or more of:

(i) one or more unique read codes;

(ii) a PCR primer binding site for PCR amplification of the one or more contiguous dsDNA fragments;

(iii) one or more sample codes for sample multiplexing; or

(iv) one or more primer binding sites for DNA sequencing.

10. The method of any one of claims 1-9, wherein each of the ligation strand oligonucleotide and the repair oligonucleotide comprise an anchor sequence and wherein the anchor sequence of the ligation strand oligonucleotide is at least partially complementary to the anchor sequence of the repair oligonucleotide.

11. The method of claim 10, wherein each of the ligation strand oligonucleotide and the repair oligonucleotide further comprise a PCR primer binding site for amplification of the one or more contiguous dsDNA fragments, wherein the PCR primer binding site of the ligation strand oligonucleotide is complementary to the PCR primer binding site of the repair oligonucleotide.

12. The method of claim 10, wherein each of the ligation strand oligonucleotide and the repair oligonucleotide further comprise a PCR primer binding site for amplification of the one or more contiguous dsDNA fragments, and wherein the PCR primer binding site of the ligation strand oligonucleotide is not complementary to the PCR primer binding site of the repair oligonucleotide.

13. The method of claim 12, wherein a primer that binds the PCR primer binding site of the ligation strand oligonucleotide does not substantially bind the PCR primer binding site of the repair oligonucleotide.

14. The method of any one of claims 1-13, wherein step (c) is performed at a first temperature and step (d) is performed at a second temperature, wherein the second

temperature is higher than the first temperature and results in the displacement of the partner strand oligonucleotide from the ligation strand oligonucleotide.

15. The method of claim 14, wherein the first temperature is 22° C or lower and the second temperature is 37° C or higher.

16. The method of any one of claims 1-15, wherein the kinase/ligase strategy of step (e) does not comprise removal of the 5′ terminal nucleotide of the end-repaired DNA fragment.

17. The method of any one of claims 1-16, wherein the ligase used in step (c) is different from the ligase used in step (e).

18. The method of any one of claims 1-17, wherein the ligase used in step (c) is capable of ligating DNA fragments with blunt ends.

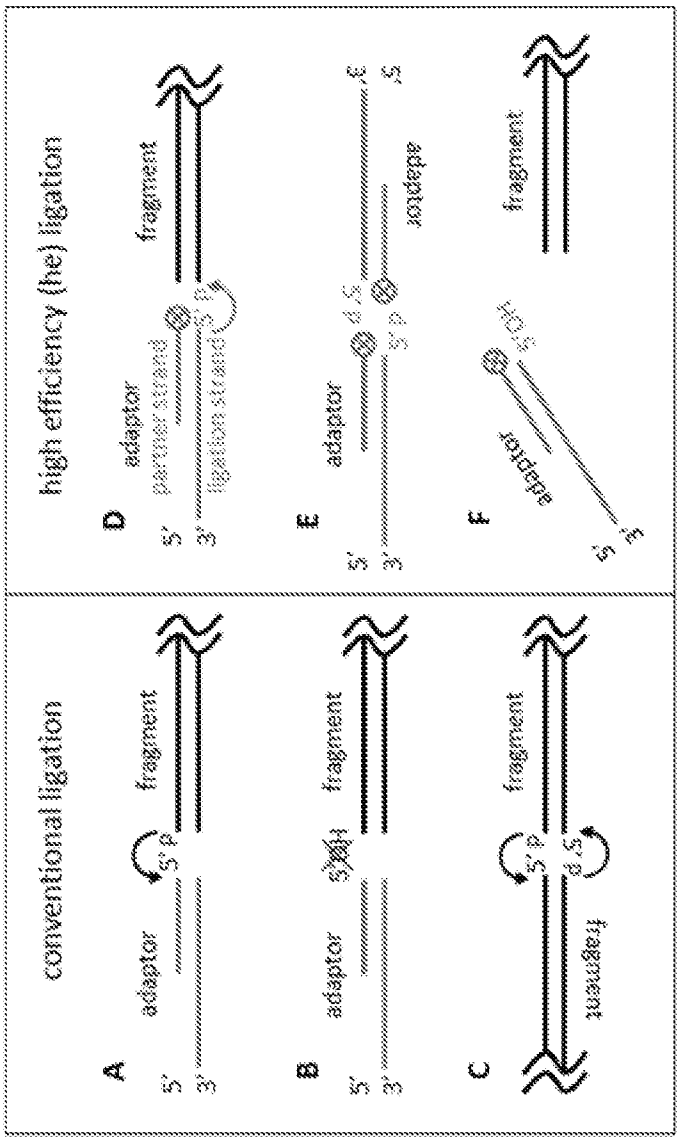
19. The method of any one of claims 1-17, wherein the ligase used in step (c) is capable of ligating DNA fragments with 5′ or 3′ overhangs.

20. The method of any one of claims 1-17, wherein the ligase used in step (c) is a T4 DNA ligase.

21. The method of any one of claims 1-20, wherein the ligase used in step (e) is a thermo-stable nick-specific ligase.

22. The method of any one of claims 1-20, wherein the ligase used in step (e) is selected from the list consisting of Taq DNA ligase, E. coli DNA ligase, and 9° North ligase.

23. The method of any one of claims 1-22, wherein the method does not comprise degradation or cleavage of the ligation strand oligonucleotide, the repair oligonucleotide, or the end-repaired DNA fragment.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high efficiency (he) ligation
A
adaptor
fragment
5'
3'
B
adaptor
fragment
5'
3'
C
fragment
fragment
D
adaptor
partner strand
ligation strand
fragment
5'
3'
E
adaptor
adapter
5'
3'
F
adapter
fragment
5'
3'

Figure 1

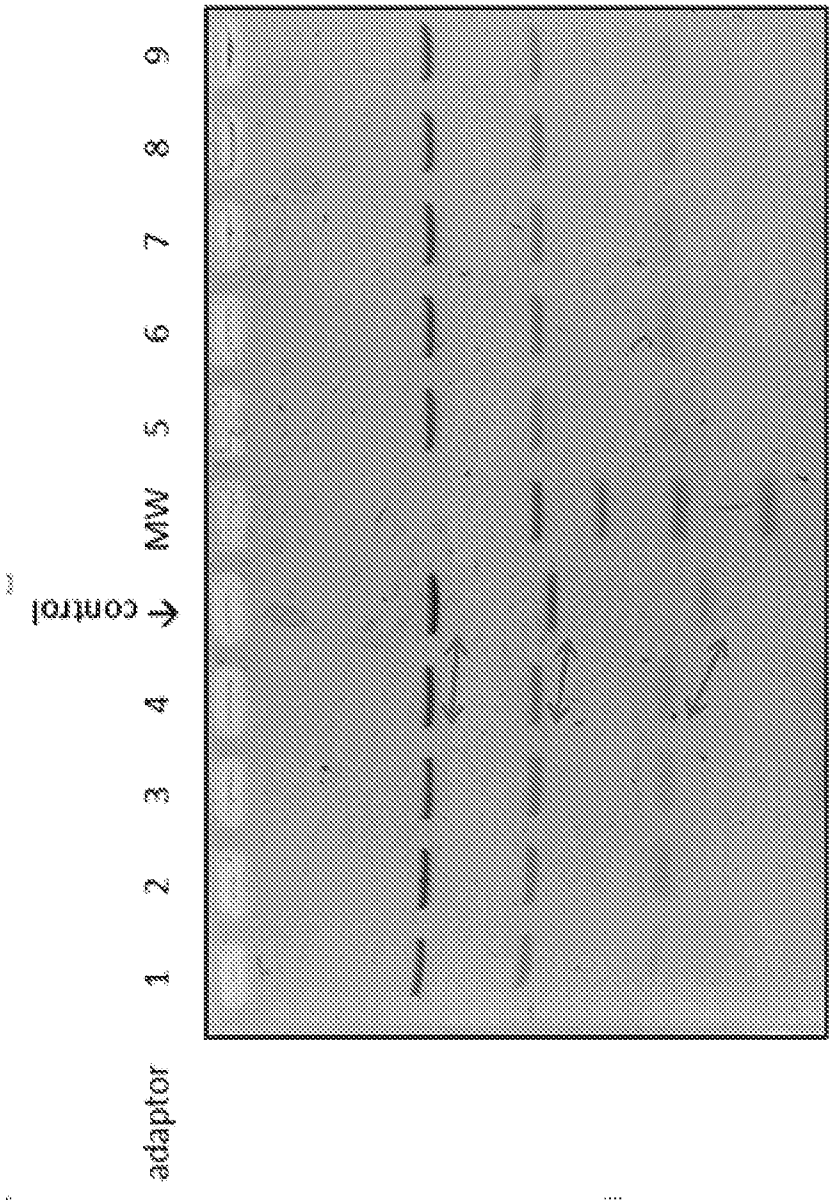


Figure 2

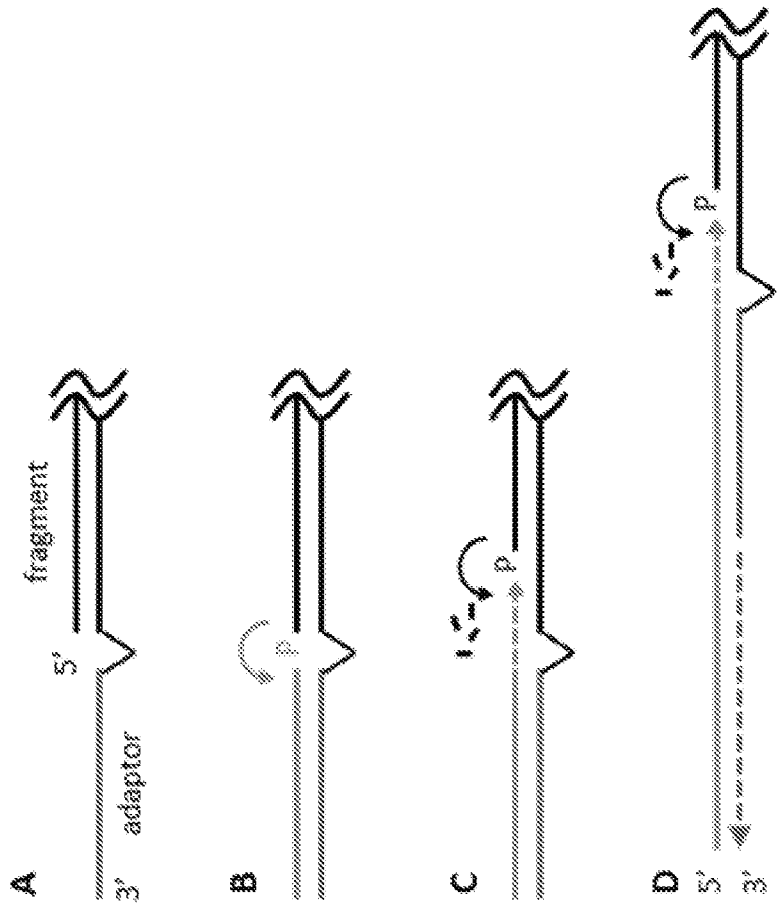
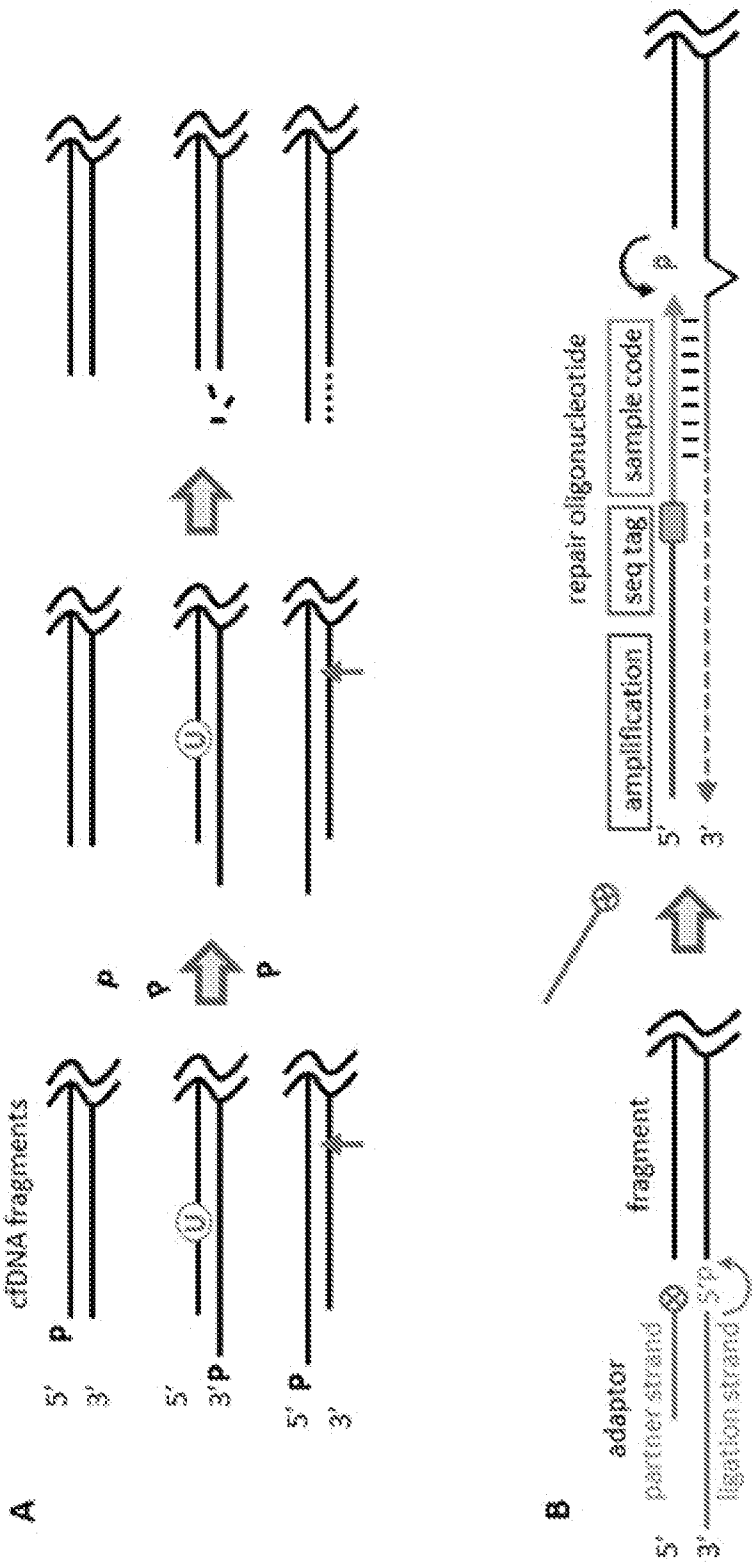
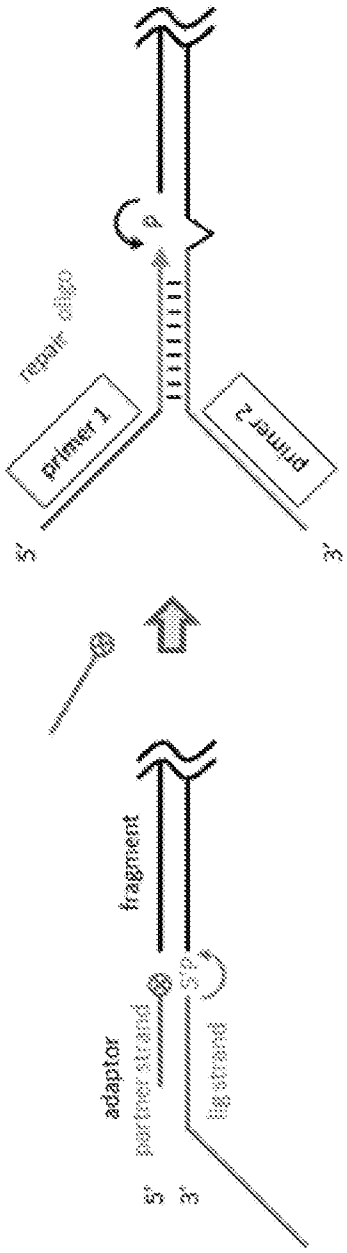


Figure 3

Figure 4


A
cfDNA fragments
5'
3'
P
U
B
adaptor
partner strand
ligation strand
fragment
repair oligonucleotide
amplification
seq tag
sample code


repair oligo
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primer 2
5'
3'
fragment
adaptor
partner strand
5'
3'
lig strand
5'
3'

Figure 5

SEQUENCE LISTING

<110> Resolution Bioscience, Inc.
Raymond, Christopher K
Lim, Lee P
Armour, Christopher D

<120> HIGH EFFICIENCY CONSTRUCTION OF DNA LIBRARIES

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<223> n is A, C, T or G, where the specific groups of bases from positions 26 to 30 are listed in Table 3

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