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(54) Titre : METHODE AMELIOREE ET KIT POUR LA GENERATION DE BIBLIOTHEQUE D'ADN POUR LE SEQUENCAGE MASSIVEMENT PARALLELE
(54) Title: IMPROVED METHOD AND KIT FOR THE GENERATION OF DNA LIBRARIES FOR MASSIVELY PARALLEL SEQUENCING

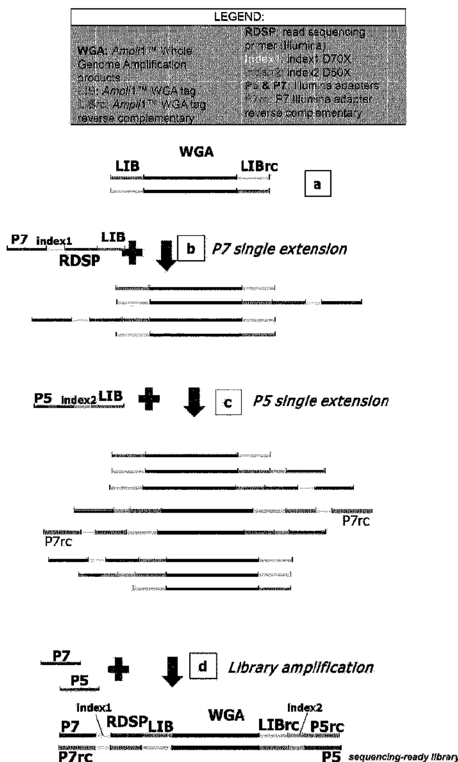

FIG. 2A

(57) Abrégé/Abstract:
There is disclosed a method of generating a massively parallel sequencing library comprising the steps of :a) providing a primary WGA DNA library (pWGAlib), including fragments comprising a WGA library universal sequence adapter; b) performing a single

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(57) **Abrégé(suite)/Abstract(continued):**
PCR cycle on the pWGAlib using a first primer (1PR) comprising from 5' to 3' a first sequencing adapter (1PR5SA) and a first primer 3' section (1PR3S) hybridizing to the reverse complementary of the WGA library universal sequence adapter; c) performing a single PCR cycle on the on the product of step b) using a second primer (2PR) comprising from 5' to 3' a second sequencing adapter (2PR5SA) different from the 1PR5SA, and a second primer 3' section (2PR3S) hybridizing to the WGA library universal sequence adapter reverse complementary; d) amplifying by PCR the product of step c) using a third primer comprising the 1PR5SA and a fourth primer comprising 2PR5SA.

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(54) Title: IMPROVED METHOD AND KIT FOR THE GENERATION OF DNA LIBRARIES FOR MASSIVELY PARALLEL SEQUENCING

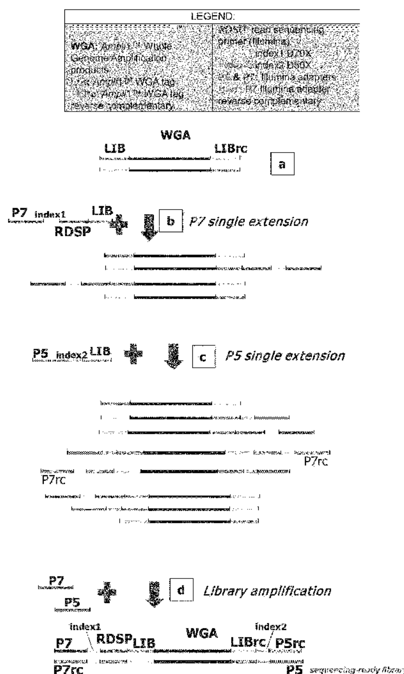
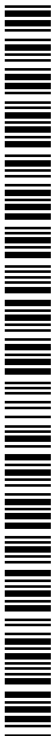


FIG. 2A

(57) Abstract: There is disclosed a method of generating a massively parallel sequencing library comprising the steps of :a) providing a primary WGA DNA library (pWGAlib), including fragments comprising a WGA library universal sequence adapter; b) performing a single PCR cycle on the pWGAlib using a first primer (1PR) comprising from 5' to 3' a first sequencing adapter (1PR5SA) and a first primer 3' section (1PR3S) hybridizing to the reverse complementary of the WGA library universal sequence adapter; c) performing a single PCR cycle on the on the product of step b) using a second primer (2PR) comprising from 5' to 3' a second sequencing adapter (2PR5SA) different from the 1PR5SA, and a second primer 3' section (2PR3S) hybridizing to the WGA library universal sequence adapter reverse complementary; d) amplifying by PCR the product of step c) using a third primer comprising the 1PR5SA and a fourth primer comprising 2PR5SA.



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IMPROVED METHOD AND KIT FOR THE GENERATION OF DNA LIBRARIES FOR MASSIVELY PARALLEL SEQUENCING

Cross-Reference to related Applications

5 This application claims priority from European Patent Application No. 17182693.6 filed on July 21, 2017, the disclosure of which is incorporated by reference.

Technical Field of the Invention

The present invention relates to a method and a kit to 10 generate a massively parallel sequencing library for Whole Genome Sequencing from Whole Genome Amplification products (WGA). In particular, the method can advantageously be applied to Deterministic Restriction-Site, Whole Genome Amplification (DRS-WGA) DNA products.

15 The library can advantageously be used for low-pass whole-genome sequencing and genome-wide copy-number profiling.

Prior Art

With single cells it is useful to carry out a Whole 20 Genome Amplification (WGA) for obtaining more DNA in order to simplify and/or make it possible to carry out different types of genetic analyses, including sequencing, SNP detection etc.

WGA with a LM-PCR based on a Deterministic Restriction 25 Site (as described in e.g. WO/2000/017390) is known from the

art (herein below referred to simply as DRS-WGA). A LM-PCR based, DRS-WGA commercial kit (*Ampli*1™ WGA kit, Menarini Silicon Biosystems) has been used in Hodgkinson C.L. et al., *Tumorigenicity and genetic profiling of circulating tumor* 5 *cells in small-cell lung cancer*, Nature Medicine 20, 897-903 (2014). In this work, a Copy-Number Analysis by low-pass whole genome sequencing on single-cell WGA material was performed. However, for the standard workflow used in this paper, the creation of Illumina libraries required several 10 steps, which included i) digestion of WGA adapters, ii) DNA fragmentation, and standard Illumina workflow steps such as iii) EndRepair iv) A-Tailing v) barcoded adapter ligation, plus the usual steps of vi) sample pooling of barcoded NGS libraries and vii) sequencing. As shown in the aforementioned 15 article (Fig 5b), WBC did present few presumably false-positive copy-number calls, although CTCs in general displayed many more aberrations.

*Ampli*1™ WGA is compatible with array Comparative Genomic Hybridization (aCGH); indeed several groups 20 (Moehlendick B, et al. (2013) *A Robust Method to Analyze Copy Number Alterations of Less than 100 kb in Single Cells Using Oligonucleotide Array CGH*. PLoS ONE 8(6): e67031; Czyz ZT, et al (2014) *Reliable Single Cell Array CGH for Clinical Samples*. PLoS ONE 9(1): e85907) showed that it is suitable 25 for high-resolution copy number analysis. However, aCGH

technique is expensive and labor intensive, so that different methods such as low-pass whole-genome sequencing (LPWGS) for detection of somatic Copy-Number Alterations (CNA) may be desirable.

5 Although the DRS-WGA provides best results in terms of uniform and balanced amplification, current protocols based on aCGH or metaphase CGH are laborious and/or expensive. Low-pass whole-genome sequencing has been proposed as a high-throughput method to analyze several samples with higher 10 processivity and lower cost than aCGH. However, known methods for the generation of a massively parallel sequencing library for WGA products (such as DRS-WGA) still require protocols including several enzymatic steps and reactions.

It would be desirable to have a more streamlined method, 15 combining the reproducibility and quality of DRS-WGA with the capability to analyze genome-wide Copy-Number Variants (CNVs). In addition, determining a whole-genome copy number profile also from minute amount of cells, FFPE or tissue biopsies would be desirable.

20 PCT/EP2017/059075 in the name of the present applicant discloses a method for generating a massively parallel sequencing library -also referred to as an NGS (next generation sequencing) library- starting from a WGA product in a streamlined way.

25 The method involves amplifying the primary WGA DNA

library with two primers, each of which includes a different sequencing adapter at the 5′ end that will allow sequencing on a specific sequencing platform. The sequencing platforms that can be used are e.g. the Ion-Torrent platform or the Illumina platform.

When using certain sequencing platforms, e.g. the Illumina platform, it is particularly advantageous to select library fragments including the two different sequencing adapters (in the case of Illumina: P5 and P7) on the opposite ends of the fragment. These fragments will be referred to as "heteroadapter fragments". In order to do this, one of the embodiments disclosed in the above mentioned application provides that one of the two primers for amplifying the primary WGA DNA library is biotinylated at the 5′ end. Figure 1 summarizes this embodiment. Once the primary WGA DNA library has been amplified with the two primers, the fragments are selected by streptavidin beads. Fragments harboring the same sequencing adapters on both ends (hereinafter referred to as "homoadapter fragments") are either eluted (if not biotinylated) or remain bound to the streptavidin beads (if biotinylated on both ends), whereas ssDNA heteroadapter fragments (harboring different sequencing adapters at the two ends) are denatured and eluted so as to be selected.

The selection by biotinylated primers has some

weaknesses. In particular, it leads to a single strand DNA library which is more difficult to quantify and less preferred for storage. In addition, for Illumina sequencing workflows the use of a double strand DNA library is preferable. This issue can be addressed by performing a double strand synthesis or further amplification cycles using P5 and P7 primers, but of course this renders the method somewhat more complicated and does not allow a single-tube reaction. The design of a kit is consequently more complex, as it requires e.g. the use of specific buffers designed for the purpose.

Summary of the Invention

It is therefore an object of the present invention to provide a method for generating a massively parallel sequencing library starting from a WGA product that overcomes the above mentioned issues.

Other objects of the present invention are to provide a method for low-pass whole genome sequencing and a method for genome-wide copy-number profiling starting from a WGA product, using the library preparation method according to the invention.

Further objects of the present invention are to provide a massively parallel sequencing library preparation kit and a low-pass whole genome sequencing kit for implementing the above mentioned methods.

Brief Description of the Drawings

Figure 1 shows a picture summarizing the steps of the method disclosed in PCT/EP2017/059075 by the applicant to select heteroadapter fragments.

5 Figure 2A shows a picture summarizing the steps of the method according to the present invention referring in particular to the situation in which the primary WGA DNA library is obtained by DRS-WGA. This is however not intended to limit the scope of the invention to this particular kind

10 of WGA.

Figure 2B shows the structure of the primary WGA DNA library and of the four primers used in the method according to the invention as shown in Figure 2A. The acronyms used in the claims and description for the different segments of the

15 primary WGA DNA library and of the four primers are also shown in parenthesis.

Figure 3A shows a picture of dual index sequencing on MiSeq, HiSeq 2000/2500 and 1000/1500 with one custom sequencing primer according to the invention.

20 Figure 3B shows a picture of dual index sequencing on MiniSeq, NextSeq, HiSeq 3000/4000 Illumina sequencing platforms, with two custom sequencing primers according to the invention.

Figures 4A and 4B show sequencing results of a Low-pass

25 Whole Genome Sequencing performed by the method according to

the present invention. The figure shows copy number alterations (CNA) profiles of two single cells belonging to NCI-H441 and SW-480 cell lines, sorted by DEPArray™ (Menarini Silicon Biosystems) (Figure 4A); and blood single cells (Circulating Tumor Cell [CTC] and White Blood Cell [WBC]), sorted by DEPArray™ (Menarini Silicon Biosystems) (Figure 4B).

Figure 5 shows sequencing results of a Low-pass Whole Genome Sequencing performed by the method according to the present invention. The figure shows copy number alterations (CNA) profiles of a tumor single cell and a population of 50 stromal cells, belonging to disaggregated FFPE section, digitally sorted by DEPArray™ (Menarini Silicon Biosystems) and whole-genome amplified using the *Ampli*1™ WGA kit.

Figures 6A and 6B show inter-method and inter-platform (IonTorrent and Illumina) comparison results. In particular, Figure 6A shows copy number alterations (CNA) profiles of a NCI-H23 single cell, obtained with a Low-pass Whole Genome Sequencing method for IonTorrent (presented in PCT/EP2017/059075) and with the method according to the present invention for Illumina platforms. Figure 6B shows NCI-H441 and WBC single-cells hierarchical clustering, based on CNAs profiles.

Definitions

Unless defined otherwise, all technical and scientific

terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. Although many methods and materials similar or equivalent to those described herein may be used in the practice or testing of the present invention, preferred methods and materials are described below. Unless mentioned otherwise, the techniques described herein for use with the invention are standard methodologies well known to persons of ordinary skill in the art.

By the term "Original DNA" there is intended the genomic DNA (gDNA) prior to amplification with the DRS-WGA.

By the term "Adapter" or "WGA Adapter" or "WGA PCR Primer" or "WGA library universal sequence adapter" there is intended the additional oligonucleotide ligated to each fragment generated by the action of the restriction enzyme, in case of DRS-WGA, or the known polynucleotide sequence present at 5' section of each molecule of the WGA DNA library as a result of extension and PCR process, in case of MALBAC.

By the term "Copy Number Alteration (CNA)" there is intended a somatic change in copy-numbers of a genomic region, defined in general with respect to the same individual genome.

By the term "Copy Number Variation (CNV)" there is intended a germline variant in copy-numbers of a genomic region, defined in general with respect to a reference

genome. Throughout the description CNA and CNV may be used interchangeably, as most of the reasoning can be applied to both situations. It should be intended that each of those terms refers to both situations, unless the contrary is specified.

By the term "massive-parallel sequencing" (MPS) or "next generation sequencing" (NGS) there is intended a method of sequencing DNA comprising the creation of a library of DNA molecules spatially and/or time separated, clonally sequenced (with or without prior clonal amplification). Examples include Illumina platform (Illumina Inc), Ion Torrent platform (ThermoFisher Scientific Inc), Pacific Biosciences platform, MinION (Oxford Nanopore Technologies Ltd).

By the term "Target sequence" there is intended a region of interest on the original DNA.

By the term "Primary WGA DNA library (pWGAlib)" there is indented a DNA library obtained from a WGA reaction.

By the term "Multiple Annealing and Looping Based Amplification Cycles (MALBAC)" there is intended a quasilinear whole genome amplification method (Zong et al., Genome-wide detection of single-nucleotide and copy-number variations of a single human cell, Science. 2012 Dec 21;338(6114):1622-6. doi: 10.1126/science.1229164.). MALBAC primers have a 8 nucleotides 3' random sequence, to hybridize

to the template, and a 27 nucleotides 5′ common sequence (GTG AGT GAT GGT TGA GGT AGT GTG GAG). After first extension, semiamplicons are used as templates for another extension yielding a full amplicon which has complementary 5′ and 3′ 5 ends. Following few cycles of quasi-linear amplification, full amplicon can be exponentially amplified with subsequent PCR cycles.

By the term "DNA library Purification" there is intended a process whereby the DNA library material is separated from 10 unwanted reaction components such as enzymes, dNTPs, salts and/or other molecules which are not part of the desired DNA library. Example of DNA library purification processes are purification with paramagnetic bead-based technology (in the scientific literature and hereinafter for simplicity often 15 referred to as "magnetic beads") such as Agencourt AMPure XP or solid-phase reversible immobilization (SPRI)-beads from Beckman Coulter or with spin column purification such as Amicon spin-columns from Merck Millipore. Another example of DNA library purification processes are purification with 20 magnetic beads conjugated to oligonucleotide baits either directly or through protein-protein interactions such as streptavidin coated magnetic beads interacting with biotinylated oligonucleotides.

By the term "DNA library Selection" there is intended 25 a process whereby either DNA library Purification or DNA

library Size selection or both are carried out.

By the term "sequencing adapter (SA)" there is intended one or more molecules which are instrumental for sequencing the DNA insert. Each molecule may comprise none, one or more of the following: a polynucleotide sequence, a functional group. In particular, there is intended a polynucleotide sequence which is required to be present in a massively parallel sequencing library in order for the sequencer to correctly generate an output sequence, but which does not carry information, (as non-limiting examples: a polynucleotide sequence to hybridize a ssDNA to a flow-cell, in case of Illumina sequencing, or to an ion-sphere, in case of Ion Torrent sequencing, or a polynucleotide sequence required to initiate a sequencing-by-synthesis reaction).

By the term "sequencing barcode" there is intended a polynucleotide sequence which, when sequenced within one sequencer read, allows that read to be assigned to a specific sample associated with that barcode.

By the term "low-pass whole genome sequencing" there is intended a whole genome sequencing at a mean sequencing depth lower than 1.

By the term "mean sequencing depth" there is intended here, on a per-sample basis, the total of number of bases sequenced, mapped to the reference genome divided by the total reference genome size. The total number of bases

sequenced and mapped can be approximated to the number of mapped reads times the average read length.

By "equalizing" there is intended the act of adjusting the concentration of one or more samples to make them equal.

5 By "normalizing" there is intended the act of adjusting the concentration of one or more samples to make them correspond to a desired proportion between them (equalizing being the special case where the proportion is 1). In the description, for the sake of simplicity, the terms 10 normalizing and equalizing will be used indifferently as they are obviously conceptually identical.

Detailed Description of the Invention

With reference to Figure 2A, which exemplifies the case in which the primary WGA DNA library is obtained by DRS-WGA 15 and the sequencing platform is the Illumina platform, the method of generating a massively parallel sequencing library according to the present invention comprises the following steps.

In step a, there is provided a primary WGA DNA library 20 (pWGAlib), which includes fragments comprising a known 5' sequence section (5SS), a middle sequence section (MSS), and a known 3' sequence section (3SS) reverse complementary to the known 5' sequence section. The known 5' sequence section (5SS) comprises a WGA library universal sequence adapter. 25 The middle sequence section (MSS) comprises at least an

insert section (IS), corresponding to a DNA sequence of the original unamplified DNA prior to WGA. The middle sequence section (MSS) optionally comprises, in addition to the insert section (IS), a flanking 5′ intermediate section (F5) and/or a flanking 3′ intermediate section (F3) (for example when the primary WGA DNA library is generated by MALBAC or by DRS-WGA according to the teachings of WO 2015/118077). In Figures 2A and 2B, the known 5′ sequence section (5SS) corresponds to the LIB sequence (SEQ ID NO:50) specific for the DRS-WGA, and the known 3′ sequence section (3SS) is the reverse complementary of the LIB sequence (LIBrc).

In step b, a single PCR cycle is performed on the primary WGA DNA library using at least one first primer (1PR), which comprises at least a first primer 5′ section (1PR5S) and a first primer 3′ section (1PR3S). The first primer 5′ section (1PR5S) comprises at least one first sequencing adapter (1PR5SA). The first primer 3′ section (1PR3S) hybridizes to the known 3′ sequence section (3SS). The result of the single PCR cycle of step b is a first primer extended WGA DNA library.

A single PCR cycle includes a double strand DNA denaturation step, a primer annealing step and an annealed primer extension step. A preferred embodiment includes a denaturation step of 30 seconds at 95°C, an annealing step of 30 seconds at 62°C, and an extension step of 3 minutes at

72°C.

The first primer (1PR) preferably further comprises at least one read sequencing primer sequence (1PRSEQ) in 3′ position of the first primer 5′ section (1PR5S) and in 5′
5 position of the first primer 3′ section (1PR3S).

The first primer (1PR) preferably has a sequence selected from the group consisting of SEQ ID NO:1 to SEQ ID NO:12.

After step b, it is necessary to prevent that the first
10 primer (1PR) polymerizes other primary WGA products or first primer extended WGA DNA library fragments. In a preferred embodiment the first primer extended WGA DNA library is purified after step b. This purification is preferably carried out with SPRIselect beads (Beckman Coulter).

15 In step c, a single PCR cycle is performed on the first primer extended WGA DNA library, using at least one second primer (2PR) comprising a second primer 5′ section (2PR5S) and a second primer 3′ section (2PR3S). The second primer 5′ section (2PR5S) comprises at least one second sequencing
20 adapter (2PR5SA) different from the at least one first sequencing adapter (1PR5SA). The second primer 3′ section (2PR3S) hybridizes to the known 3′ sequence section (3SS).

The result of the single PCR cycle of step c is a first and second primer extended WGA DNA library.

25 A single PCR cycle includes a double strand DNA

denaturation step, a primer annealing step and an annealed primer extension step. A preferred embodiment includes a denaturation step of 30 seconds at 95°C, an annealing step of 30 seconds at 60°C, and an extension step of 3 minutes at 5 72°C.

The second primer (2PR) preferably has a sequence selected from the group consisting of SEQ ID NO:13 to SEQ ID NO:20.

After step c, the first and second primer extended WGA 10 DNA library is purified, preferably with 2.5M NaCl PEG 20% solution.

In step d, the first and second primer extended WGA DNA library is amplified by using at least one third primer (3PR) comprising the first sequencing adapter (1PR5SA) and at least 15 one fourth primer (4PR) comprising the second sequencing adapter (2PR5SA). The result of the PCR amplification of step d is an amplified first and second primer extended WGA DNA library. The yield of this amplification step in terms of DNA library is sufficient to carry out sequencing thereon.

20 After step d, the amplified first and second primer extended WGA DNA library is purified, preferably with 2.5M NaCl PEG 20% solution.

The third primer (3PR) preferably has sequence SEQ ID NO:22 and the fourth primer (4PR) preferably has sequence 25 SEQ ID NO:21.

The first primer 5′ section (1PR5S) of the first primer (1PR) preferably further comprises at least one first sequencing barcode (1PR5BC) in 3′ position of the at least one first sequencing adapter (1PR5SA) and in 5′ position of
5 the first primer 3′ section (1PR3S). The second primer 5′ section (2PR5S) of the second primer (2PR) preferably further comprises at least one second sequencing barcode (2PR5BC), in 3′ position of the at least one second sequencing adapter (2PR5SA) and in 5′ position of the second primer 3′ section
10 (2PR3S). This allows for greater multiplexing. In particular, if SEQ ID NO:1 to SEQ ID NO:12 are used as first primer (1PR), each primer containing a different barcode, and SEQ ID NO:13 to SEQ ID NO:20 are used as second primer (2PR), each primer containing a different barcode, 96
15 combinations of barcodes can be obtained, leading to the analysis of 96 libraries.

The WGA library universal sequence adapter is preferably a DRS-WGA library universal sequence adapter or a MALBAC library universal sequence adapter, more preferably
20 a DRS-WGA library universal sequence adapter.

The DRS-WGA library universal sequence adapter preferably has SEQ ID NO:50 and the MALBAC library universal sequence adapter preferably has SEQ ID NO:51.

The method for low-pass whole genome sequencing
25 according to the present invention comprises the following

steps.

First, there is provided a plurality of barcoded, massively-parallel sequencing libraries obtained according to the above disclosed method of generating a massively parallel sequencing library and samples obtained using different sequencing barcodes (BC) are pooled. Then the pooled library is sequenced.

The step of pooling samples using different sequencing barcodes (BC) further comprises the steps of quantitating the DNA in each of the barcoded, massively-parallel sequencing libraries, and of normalizing the amount of barcoded, massively-parallel sequencing libraries.

A massively parallel sequencing library preparation kit according to the present invention comprises at least one first primer (1PR), one second primer (2PR), one third primer (3PR) and one fourth primer (4PR). The structure of these primers has already been disclosed above.

In one preferred embodiment, in which the primary WGA DNA library is a DRS-WGA, the massively parallel sequencing library preparation kit comprises one or more primers selected from the group consisting of SEQ ID NO:1 to SEQ ID NO:12, one or more primers selected from the group consisting of SEQ ID NO:13 to SEQ ID NO:20, and primers SEQ ID NO:21 and SEQ ID NO:22.

In an alternative preferred embodiment, in which the

primary WGA DNA library is a DRS-WGA, the massively parallel sequencing library preparation kit comprises one or more primers selected from the group consisting of SEQ ID NO:52 to SEQ ID NO:63, one or more primers selected from the group consisting of SEQ ID NO:13 to SEQ ID NO:20, and primers SEQ ID NO:21 and SEQ ID NO:22.

In an alternative preferred embodiment, in which the primary WGA DNA library is a MALBAC WGA, the massively parallel sequencing library preparation kit comprises one or more primers selected from the group consisting of SEQ ID NO:27 to SEQ ID NO:38, one or more primers selected from the group consisting of SEQ ID NO:39 to SEQ ID NO:46, and primers SEQ ID NO:21 and SEQ ID NO:22.

In an alternative preferred embodiment, in which the primary WGA DNA library is a MALBAC WGA, the massively parallel sequencing library preparation kit comprises one or more primers selected from the group consisting of SEQ ID NO:64 to SEQ ID NO:75, one or more primers selected from the group consisting of SEQ ID NO:39 to SEQ ID NO:46, and primers SEQ ID NO:21 and SEQ ID NO:22.

The low-pass whole genome sequencing kit according to one embodiment of the present invention comprises at least one primer selected from the group consisting of SEQ ID NO:1 to SEQ ID NO:12; at least one primer selected from the group consisting of SEQ ID NO:13 to SEQ ID NO:20; primers SEQ ID NO:21 and SEQ ID

NO:22; and a custom sequencing primer of SEQ ID NO:23. The kit preferably also comprises a primer selected from the group consisting of SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26. In particular one of the latter primers is used with MiniSeq, 5 NextSeq, HiSeq 3000/4000 Illumina sequencing platforms to read Index2. Additional explanation will be provided in the following. Among the three primers, SEQ ID NO:24 is particularly preferred.

In an alternative embodiment, the low-pass whole genome sequencing kit comprises at least one primer selected from the 10 group consisting of SEQ ID NO:52 to SEQ ID NO:63; at least one primer selected from the group consisting of SEQ ID NO:13 to SEQ ID NO:20; primers SEQ ID NO:21 and SEQ ID NO:22; a custom sequencing primer of SEQ ID NO:23 and a custom index 2 primer selected from the group consisting of SEQ ID NO:24, SEQ ID NO:25 15 and SEQ ID NO:26.

The low-pass whole genome sequencing kit according to another embodiment of the present invention comprises at least one primer selected from the group consisting of SEQ ID NO:27 to SEQ ID NO:38; at least one primer selected from the group 20 consisting of SEQ ID NO:39 to SEQ ID NO:46; primers SEQ ID NO:21 and SEQ ID NO:22; and primer of SEQ ID NO:47. The kit preferably also comprises SEQ ID NO:48. Even more preferably, the kit comprises a primer of SEQ ID NO:49.

In an alternative embodiment, the low-pass whole genome 25 sequencing kit comprises at least one primer selected from the

group consisting of SEQ ID NO:64 to SEQ ID NO:75; at least one primer selected from the group consisting of SEQ ID NO:39 to SEQ ID NO:46; primers SEQ ID NO:21 and SEQ ID NO:22; and primer of SEQ ID NO:47. The kit preferably also comprises SEQ ID NO:48. Even more preferably, the kit comprises a primer of SEQ ID NO:49.

The method for genome-wide copy number profiling according to the present invention comprises the steps of:

- sequencing a DNA library developed using one of the above said sequencing library preparation kits;
- analysing the sequencing read depth across different regions of the genome;
- determining a copy-number value for the regions of the genome by comparing the number of reads in that region with respect to the number of reads expected in the same for a reference genome.

Protocol 1 for Low Pass Whole Genome Sequencing on Illumina platforms

- Deterministic-Restriction Site Whole Genome Amplification (DRS-WGA)

Single cell DNA was amplified using the *Ampli*1™ WGA Kit (Menarini Silicon Biosystems) according to the manufacturer's instructions. 5 µL of WGA-amplified DNA were diluted by the addition of 5 µL of Nuclease-Free Water and purified using SPRIselect beads (Beckman Coulter) system (ratio 1.8x). The DNA was eluted in 12.5 µL and quantified by dsDNA HS Assay on the Qubit® 2.0 Fluorometer.

• P7 single extension

A single step of PCR extension was performed in a volume of 15 µl using *Ampli*1™ PCR Kit (Menarini Silicon Biosystems) and a LIB_IL_index D7xx (one of primers from SEQ ID NO:1 to
5 SEQ ID NO:12). Each PCR reaction contained: 1.5 µL *Ampli*1™ PCR Reaction Buffer (10X), 3 µL of one primer LIB_IL_index D7xx within the following range: from SEQ ID NO:1 to SEQ ID NO:12 [2.5 µM], 0.51 µL *Ampli*1™ PCR dNTPs (10 mM), 0.37 µL BSA, 0.12 µL *Ampli*1™ PCR Taq Polymerase, WGA-purified DNA
10 (from 10 to 75 ng) and *Ampli*1™ water to reach a final volume of 15 µL.

Applied Biosystems® 2720 Thermal Cycler was set as follows: 95°C for 4 minutes, 1 cycle of 95°C for 30 seconds, 62°C for 30 seconds, 72°C for 3 minutes.

15 • SPRIselect beads clean-up and P5 single extension

15 µL of *Ampli*1™ WGA-amplified from the previous step were purified using SPRIselect beads (Beckman Coulter) system (ratio 1.5x). The DNA was eluted in 15 µL of PCR reaction mix prepared as following: 1.5 µL *Ampli*1™ PCR
20 Reaction Buffer (10X), 3 µL of one primer LIB_IL_index D5xx (one of primers from SEQ ID NO:13 to SEQ ID NO:20) [2.5 µM], 0.51 µL Ampli1™ PCR dNTPs (10 mM), 0.37 µL BSA, 0.12 µL *Ampli*1™ PCR Taq Polymeras and 9.5 µL *Ampli*1™ water. The P5 single extension PCR reaction was performed in the presence
25 of beads.

Applied Biosystems® 2720 Thermal Cycler was set as follows: 95°C for 4 minutes, 1 cycle of 95°C for 30 seconds, 60°C for 30 seconds, 72°C for 3 minutes.

• 2.5M NaCl PEG 20% solution clean-up and library amplification

15 µL of *Ampli*1 ™ WGA-amplified from the previous step were purified using 2.5M NaCl PEG 20% solution (ratio 1.5x). The DNA was eluted in 15 µL of PCR reaction mix prepared as following: 1.5 µL *Ampli1*™ PCR Reaction Buffer (10X), 1 µL of one primer adapter P5 (SEQ ID NO:21) and 1 µL of one primer adapter P7 (SEQ ID NO:22) (7,5 µM each), 0.51 µL *Ampli*1™ PCR dNTPs (10 mM), 0.37 µL BSA, 0.12 µL *Ampli*1™ PCR Taq Polymerase and 10.5 µL *Ampli*1™ water.

The library amplification PCR reaction was performed in the presence of beads.

Applied Biosystems® 2720 Thermal Cycler was set as follows: 95°C for 4 minutes, 1 cycle of 95°C for 30 seconds, 60°C for 30 seconds, 72°C for 2 minutes, 10 cycles of 95°C for 30 seconds, 60°C for 30 seconds, 72°C for 2 minutes (extended by 20 seconds/cycle) and final extension at 72° C for 7 minutes.

In a preferred embodiment, the cycles of 95°C for 30 seconds, 60°C for 30 seconds, 72°C for 2 minutes can be extended to 12, to increase the library concentration of at least a 2(-4) factor by introducing 2 extra cycles during

library amplification, thus increasing the total number of cycles from 11 to 13.

- Final library clean-up

The amplified library (containing Illumina sequencing adapter sequences) was finally purified using 2.5M NaCl PEG 20% solution (ratio 1.5x) and eluted in 15 µL of *Ampli*1™ water. The purified libraries were qualified by Agilent DNA 7500, DNA 1000 or DNA HS Kits on the 2100 Bioanalyzer® and quantified by dsDNA HS Assay on Qubit® 2.0 Fluorometer, in order to obtain an equimolar pool. Based on library average size (usually an average length of 700bp is observed experimentally on DRS-WGA products obtained using Ampli1™ WGA kit -Menarini Silicon Biosystems), the library concentration generated by the quantification step can be converted to nM as known by those with ordinary skill in the art (for example 1 ng/µL=2.5 nM for 600bp library average size, 1 ng/µL=2 nM for 700bp library average size, 1 ng/µL=1.9 nM for 800bp library average size) -see Illumina Technical Note: DNA Sequencing "Nextera® Library Validation and Cluster Density Optimization" Pub No. 770-2013-003.

- As preferred alternative, the purified libraries were quantified by Quantitative real-time PCR (qPCR) methodology. The qPCR method accurately quantifies the functional libraries, in particular those fragments that have the correct adapter on each end (heteroadapter fragments), based

on a standard curve generated from a control template dilutions.Sequencing on MiSeq sequencing system

4 nM of the pool was denatured 5 minutes with 0.1N NaOH. Denatured sample was then diluted with HT1 buffer (Illumina)
5 to obtain a 20 pM denatured library. 600 µL of denatured library was loaded on MiSeq reagent cartridge (Illumina).

Single end reads of 150 bases or Paired end reads (75 PE) were generated using the v3 chemistry of the Illumina MiSeq.

10 Custom read1 sequencing primer (SEQ ID NO:23) was then diluted with HT1 to obtain a final concentration of 0,5 µM. 600 µL of diluted Custom read1 sequencing primer was loaded on MiSeq reagent cartridge (Illumina).

- Sequencing on HiSeq 1000/1500 and 2000/2500 systems

15 4 nM of the pool was denatured 5 minutes with 0.1N NaOH.

Single end reads of 100 bases or Paired end reads (100 PE) were generated using the v2 chemistry of the Illumina HiSeq, in Rapid run mode, or using the v4 chemistry of the Illumina HiSeq, in High Output run mode.

20 Custom read1 sequencing primer (SEQ ID NO:23) was then diluted with HT1 to obtain a final concentration of 0.5 µM.

- Sequencing on NextSeq, HiSeq 3000 and 4000, NovaSeq Series and HiSeq X Ten systems

4 nM of the pool was denatured 5 minutes with 0.1N NaOH.

25 Single end reads of 150 bases or Paired end reads (100

PE) were generated using specific chemistry for the Illumina platforms.

Custom read1 sequencing primer (SEQ ID NO:23) and Custom primer index 2A (i5) [LNA-5’] (SEQ ID NO:24) were then diluted with HT1 to obtain a final concentration of 0.5 µM.

The following table summarizes the sequences of the DRS-WGA compatible primers for all Illumina platforms (sequences in 5’ → 3’ direction, 5’ and 3’ omitted):

TABLE 1

SEQID	Name	Primer sequence
SEQID1	LIB_IL_index D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGGGATTCCTGCTGTCAGT
SEQID2	LIB_IL_index D702	CAAGCAGAAGACGGCATACGAGATTCTCCGGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGGGATTCCTGCTGTCAGT
SEQID3	LIB_IL_index D703	CAAGCAGAAGACGGCATACGAGATAATGAGCGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGGGATTCCTGCTGTCAGT
SEQID4	LIB_IL_index D704	CAAGCAGAAGACGGCATACGAGATGGAATCTCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGGGATTCCTGCTGTCAGT
SEQID5	LIB_IL_index D705	CAAGCAGAAGACGGCATACGAGATTTCTGAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGGGATTCCTGCTGTCAGT
SEQID6	LIB_IL_index D706	CAAGCAGAAGACGGCATACGAGATACGAATTCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGGGATTCCTGCTGTCAGT
SEQID7	LIB_IL_index D707	CAAGCAGAAGACGGCATACGAGATAGCTTCAGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGGGATTCCTGCTGTCAGT
SEQID8	LIB_IL_index D708	CAAGCAGAAGACGGCATACGAGATGCGCATTAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGGGATTCCTGCTGTCAGT
SEQID9	LIB_IL_index D709	CAAGCAGAAGACGGCATACGAGATCATAGCCGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGGGATTCCTGCTGTCAGT
SEQID10	LIB_IL_index D710	CAAGCAGAAGACGGCATACGAGATTTCGCGGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGGGATTCCTGCTGTCAGT
SEQID11	LIB_IL_index D711	CAAGCAGAAGACGGCATACGAGATGCGCGAGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGGGATTCCTGCTGTCAGT
SEQID12	LIB_IL_index D712	CAAGCAGAAGACGGCATACGAGATCTATCGCTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGGGATTCCTGCTGTCAGT
SEQID13	LIB_IL_index D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID14	LIB_IL_index D502	AATGATACGGCGACCACCGAGATCTACACATAGAGGCGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID15	LIB_IL_index D503	AATGATACGGCGACCACCGAGATCTACACCTATCCTGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID16	LIB_IL_index D504	AATGATACGGCGACCACCGAGATCTACACGGCTCTGAGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID17	LIB_IL_index D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID18	LIB_IL_index D506	AATGATACGGCGACCACCGAGATCTACACTAATCTTAGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID19	LIB_IL_index D507	AATGATACGGCGACCACCGAGATCTACACCAGGACGTGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID20	LIB_IL_index D508	AATGATACGGCGACCACCGAGATCTACACGTACTGACGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID21	Adapter P5	AATGATACGGCGACCACCGAGAT
SEQID22	Adapter P7	CAAGCAGAAGACGGCATACGA
SEQID23	Ampli1™ custom sequencing primer	GCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID24	Custom primer index 2 A (i5) [LNA-5’]	A+CAGC+AGGAA +TCCCACTTCGGTGAGC
SEQID25	Custom primer index 2 A (i5) [LNA-3’]	ACAGCAGGAATCCCACT+TCGG+TG+AGC
SEQID26	Custom primer index 2(i5)[RNA]	TTrAArCTrGrACArGrCAGrGArATCCrCrArCTArCGGrArGrAGC

The following table summarizes the sequences of the MALBAC-WGA primers compatible for all Illumina platforms (sequences in 5’ → 3’ direction, 5’ and 3’ omitted):

TABLE 2

SEQID	Name	Primer sequence
SEQID27	MAL_IL_index D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID28	MAL_IL_index D702	CAAGCAGAAGACGGCATACGAGATTCTCCGGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID29	MAL_IL_index D703	CAAGCAGAAGACGGCATACGAGATAATGAGCGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID30	MAL_IL_index D704	CAAGCAGAAGACGGCATACGAGATGGAATCTCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID31	MAL_IL_index D705	CAAGCAGAAGACGGCATACGAGATTTCTGAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID32	MAL_IL_index D706	CAAGCAGAAGACGGCATACGAGATACGAATTCGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID33	MAL_IL_index D707	CAAGCAGAAGACGGCATACGAGATAGCTTCAGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID34	MAL_IL_index D708	CAAGCAGAAGACGGCATACGAGATGCGCATTAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID35	MAL_IL_index D709	CAAGCAGAAGACGGCATACGAGATCATAGCCGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID36	MAL_IL_index D710	CAAGCAGAAGACGGCATACGAGATTTCGCGGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID37	MAL_IL_index D711	CAAGCAGAAGACGGCATACGAGATGCGCGAGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID38	MAL_IL_index D712	CAAGCAGAAGACGGCATACGAGATCTATCGCTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID39	MAL_IL_index D501	AATGATACGGCGACCACCGAGATCTACACTATAGCCTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID40	MAL_IL_index D502	AATGATACGGCGACCACCGAGATCTACACATAGAGGCGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID41	MAL_IL_index D503	AATGATACGGCGACCACCGAGATCTACACCCTATCCTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID42	MAL_IL_index D504	AATGATACGGCGACCACCGAGATCTACACGGCTCTGAGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID43	MAL_IL_index D505	AATGATACGGCGACCACCGAGATCTACACAGGCGAAGGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID44	MAL_IL_index D506	AATGATACGGCGACCACCGAGATCTACACTAATCTTAGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID45	MAL_IL_index D507	AATGATACGGCGACCACCGAGATCTACACCAGGACGTGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID46	MAL_IL_index D508	AATGATACGGCGACCACCGAGATCTACACGTACTGACGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID47	Custom Read 1 primer	GTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID48	Custom primer index 1 (i7)	CTCCACACTACCTCAACCATCACTCAC
SEQID49	Custom primer read 2 (optional)	GCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA

When DRS-WGA is used, the LIB reverse complementary is the target for the primers listed in TABLE 1, from SEQ ID NO:1 to SEQ ID NO:20, as shown in the figures 2A and 2B. Furthermore, a custom read1 sequencing primer (SEQ ID NO:23) has been designed, because the final library lacks the target sequence of Illumina read1 sequencing primer. The custom read1 sequencing primer (SEQ ID NO:23) contains the LIB sequence and is complementary to the LIB reverse complementary sequence.

Noteworthy, in the sequencing setup it is possible to avoid to use a PhiX spike-in control (Illumina), because this method enables the construction of high-complexity libraries from our *Ampli*1™ WGA product input.

Furthermore, the sequencing run are preferably performed using the custom read1 sequencing primer (SEQ ID

NO:23), the PhiX DNA library lacks the target sequence of custom read1 sequencing primer and for this reason the PhiX DNA will not be sequenced.

Moreover, the final library obtained by the method of the present invention does not have the canonical Illumina sequence-adapter used by MiniSeq, NextSeq, HiSeq 3000 and 4000 Illumina systems to read the index 2 (i5).

For this reason, with these platforms, a custom primer index 2 (SEQ ID NO:24 or SEQ ID NO:25 or SEQ ID NO:26) is used to allow the correct reading of index i5. Noteworthy is that the custom sequencing primer index 2 contains the LIB sequence. In detail, the custom primer index 2A (i5) [LNA-5′] (SEQ ID NO:24) and the custom primer index 2A (i5) [LNA-3′] (SEQ ID NO:25) have three LNA (Locked Nucleic Acid [LNA™] - Exiqon) modified nucleotides indicated in Table 1 with the "+" beside (e.g. "+A"). Furthermore, the custom primer index 2(i5)[RNA] (SEQ ID NO:26) is formed by fifteen RNA nucleotides indicated with the "r" beside (e.g. "rA").

The same considerations above apply mutatis mutandis when using the MALBAC compatible primers listed in Table 2 (SEQ ID NO:27 to SEQ ID NO:49).

As a further alternative embodiment, which allows the production of libraries suitable for all Illumina platforms (and in which the primary WGA library is a DRS-WGA library), the following combination of primers can be used:

- at least one primer selected from the group consisting of SEQ ID NO:52 to SEQ ID NO:63;

- at least one primer selected from the group consisting of SEQ ID NO:13 to SEQ ID NO:20;

5 - primers SEQ ID NO:21 and SEQ ID NO:22;

- a custom sequencing primer of SEQ ID NO:23 and a custom index 2 primer selected from the group consisting of SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26.

Primers from SEQ ID NO:52 to SEQ ID NO:63 include, instead 10 of the RDSP sequence, a sequence of 8 nucleotides, which are needed 5′ of the first primer 3′ section to increase the annealing temperature of custom sequencing primers. It should be noted that the second primer (SEQ ID NO:13 to SEQ ID NO:20) includes the same sequence of 8 nucleotides 5′ of the second primer 3′ section. 15 The custom sequencing primer of SEQ ID NO:23 is used for Illumina sequencing platforms to read the Read 1 and/or Read 2; the custom sequencing primer of SEQ ID NO:24 (or SEQ ID NO:25 or SEQ ID NO:26) is used for Illumina sequencing platforms to read the Index 1 and Index 2.

20 The following table summarizes the sequences of the DRS-WGA compatible primers for Illumina platforms according to this embodiment (sequences in 5′ → 3′ direction, 5′ and 3′ omitted)

TABLE 3

25

SEQID	Name	Primer sequence
SEQID52	LIB_IL_v2_index D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID53	LIB_IL_v2_index D702	CAAGCAGAAGACGGCATACGAGATTCTCCGGAGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID54	LIB_IL_v2_index D703	CAAGCAGAAGACGGCATACGAGATAATGAGCGGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID55	LIB_IL_v2_index D704	CAAGCAGAAGACGGCATACGAGATGGAATCTCGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID56	LIB_IL_v2_index D705	CAAGCAGAAGACGGCATACGAGATTTCTGAATGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID57	LIB_IL_v2_index D706	CAAGCAGAAGACGGCATACGAGATACGAATTCGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID58	LIB_IL_v2_index D707	CAAGCAGAAGACGGCATACGAGATAGCTTCAGGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID59	LIB_IL_v2_index D708	CAAGCAGAAGACGGCATACGAGATGCGCATTAGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID60	LIB_IL_v2_index D709	CAAGCAGAAGACGGCATACGAGATCATAGCCGGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID61	LIB_IL_v2_index D710	CAAGCAGAAGACGGCATACGAGATTTCGCGGAGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID62	LIB_IL_v2_index D711	CAAGCAGAAGACGGCATACGAGATGCGCGAGAGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA
SEQID63	LIB_IL_v2_index D712	CAAGCAGAAGACGGCATACGAGATCTATCGCTGCTCACCGAAGTGGGATTCCTGCTGTCAGTTAA

As a further alternative embodiment, which allows the production of libraries suitable for all Illumina platforms (and in which the primary WGA library is a MALBAC library), the
5 following combination of primers can be used:

- at least one primer selected from the group consisting of SEQ ID NO:64 to SEQ ID NO:75;

- at least one primer selected from the group consisting of SEQ ID NO:39 to SEQ ID NO:46;

10 - primers SEQ ID NO:21 and SEQ ID NO:22;

- a custom read primer of SEQ ID NO:47.

Preferably, also primer of SEQ ID NO:48 is used. Even more preferably, also primer of SEQ ID NO:49 is used.

The following table summarizes the sequences of the
15 DRS-WGA compatible primers for Illumina platforms according to this embodiment (sequences in 5′ → 3′ direction, 5′ and 3′ omitted)

TABLE 4

SEQID	Name	sequence
SEQID64	MAL_IL_v2_index D701	CAAGCAGAAGACGGCATACGAGATCGAGTAATGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID65	MAL_IL_v2_index D702	CAAGCAGAAGACGGCATACGAGATTCTCCGGAGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID66	MAL_IL_v2_index D703	CAAGCAGAAGACGGCATACGAGATAATGAGCGGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID67	MAL_IL_v2_index D704	CAAGCAGAAGACGGCATACGAGATGGAATCTCGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID68	MAL_IL_v2_index D705	CAAGCAGAAGACGGCATACGAGATTTCTGAATGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID69	MAL_IL_v2_index D706	CAAGCAGAAGACGGCATACGAGATACGAATTCGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID70	MAL_IL_v2_index D707	CAAGCAGAAGACGGCATACGAGATAGCTTCAGGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID71	MAL_IL_v2_index D708	CAAGCAGAAGACGGCATACGAGATGCGCATTAGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID72	MAL_IL_v2_index D709	CAAGCAGAAGACGGCATACGAGATCATAGCCGGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID73	MAL_IL_v2_index D710	CAAGCAGAAGACGGCATACGAGATTTCGCGGAGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID74	MAL_IL_v2_index D711	CAAGCAGAAGACGGCATACGAGATGCGCGAGAGTGAGTGATGGTTGAGGTAGTGTGGAG
SEQID75	MAL_IL_v2_index D712	CAAGCAGAAGACGGCATACGAGATCTATCGCTGTGAGTGATGGTTGAGGTAGTGTGGAG

Examples

Example 1

Sequenced reads were aligned to the hg19 human reference
5 genome using the BWA MEM algorithm (Li H. and Durbin R., 2010).

Control-FREEC (Boeva V. et al., 2011) algorithm was used to obtain copy-number calls without a control sample. Read counts were corrected by GC content and mappability (uniqMatch option) and window size were determined by software using
10 coefficientOfVariation = 0.06. Main ploidy parameter was set accordingly to ploidy of the genetic material tested and contamination adjustment was not used.

Plots for CNA profiles of two single cells belonging to NCI-441 and SW-480 cell lines, sorted by DEPArray™ (Menarini
15 Silicon Biosystems) and blood single cells, a circulating tumour cell (CTC) and a white blood cell (WBC) sorted by DEPArray™, were obtained using a custom python script, as shown in Figures 4A and 4B.

From the figures it can be noted that significant gains and

losses are depicted, along the 22 autosomes, expressed as absolute copy numbers in sorted tumor single cells.

The ploidy values are indicated in the y-axis; providing a better fit of profiles with segmented data (black lines) and improving CNA calling. Dots above the main ploidy assessed can be considered gains; dots below the main ploidy assessed can be considered losses.

On the other hand, there is the absence of gains and losses in WBC normal cell as expected.

Example 2

A tumor single cell and a population of 50 stromal cells, belonging to a disaggregated FFPE section, were digitally sorted by DEPArray™ (Menarini Silicon Biosystems) and whole-genome amplified using the *Ampli*1™ WGA kit. Figure 5 shows Low-pass Whole Genome Sequencing results performed by the method disclosed above. The figure shows copy number alterations (CNA) profiles, with gains and losses only for the tumor single cell. These high-quality CNA profiles demonstrate that the presented method is highly resilient to DNA degradation and proved to be a reliable and valuable method for the molecular characterization of tumour heterogeneity in FFPE tissues down to single level.

Example 3

Figures 6A and 6B show inter-method and inter-platform (IonTorrent and Illumina) comparison results.

In particular, Figure 6A shows copy number alterations (CNA) profiles of a NCI-H23 single cell, obtained with a Low-pass Whole Genome Sequencing method for IonTorrent (presented in PCT/EP2017/059075) and with the method 5 according to the present invention for Illumina platforms. The results obtained with the two platforms are highly consistent with one another.

Furthermore, NCI-H441 and WBC single-cells hierarchical clustering, based on CNAs profiles, shows that samples are 10 clustered by sample-types (tumor and normal) and not by methods or platforms (Figure 6B).

In conclusion, both *Ampli*1™ LowPass methods for IonTorrent and for Illumina sequencing platforms show high concordance of CNA profiles.

15 Although the present invention has been described with reference to the method for *Ampli*1™ WGA only, the technique described, as will be apparent for the skilled in the art, clearly applies *mutatis mutandis* also to any other kind of WGA (e.g. MALBAC) which comprises a library with self-complementary 5′ and 3′ 20 regions.

In an alternative embodiment of the present invention, the first or second primer (1PR and/or 2PR) could be modified so that they are bound at their 5′ end to a solid support during at least one step of the procedure.

25 As an example the first primer (1PR) may comprise a

Biotinylated 5′ end. After the first PCR cycle (step b), streptavidin coated beads are added to the reaction tube, capturing the first-primer extended DNA library fragments, whereas non-extended fragments which do not comprise the first primer are eluted away, along with primers dNTPs and polymerase. In step c, the second primer (2PR) is provided (along with other PCR reagents) and hybridizes to the first-primer extended DNA library fragments and polymerization occurs using the bead-bound DNA library fragments left in the tube as template, producing a heteroadapter DNA fragment. After washing the reaction mix of step c, the heteroadapter can be further amplified by PCR (step d) in the same tube using third (3PR) and fourth (4PR) primers (along with other PCR reagents). Alternatively the heteroadapter can be denatured and eluted from the tube for further PCR amplification (step d) using third (3PR) and fourth (4PR) primers in a separate tube.

As another example, the first primer (1PR) may be bound covalently to magnetic beads. After the first PCR cycle (step b), the first-primer extended DNA library fragments are bound to the beads and retained, whereas non-extended fragments which comprise the known 3′ sequence section (3SS) but do not comprise the first primer are eluted away. In step c, the second primer (2PR) hybridizes to the first-primer extended DNA library fragments known 3′ sequence section (3SS) and polymerization occurs using the bead-bound DNA library fragments left in the tube as template, producing a heteroadapter DNA fragment. After washing the reaction mix of

step c, the heteroadapter can be further amplified by PCR (step d) in the same tube using third (3PR) and fourth (4PR) primers. Alternatively the heteroadapter can be denatured and eluted from the tube for further PCR amplification (step d) using third (3PR) 5 and fourth (4PR) primers in a separate tube.

One advantage of these embodiments, is that no size-selective effect linked to the use of SPRIbeads is introduced in the process. This will allow fragments of lengths smaller and/or larger than what normally retained by SPRIbeads, to be represented in the final 10 sequenceable library. One disadvantage is the increased complexity of the kit reagents, inherent to conjugation of primers to beads or to Biotin. The presence of a broader range of fragments may be beneficial especially when pursuing whole genome sequencing at higher depth to achieve complete resquencing beyond the genome- 15 wide copy number profiling by low-pass WGS.

As yet another example of embodiment, after the first primer (1PR) is used in the first PCR cycle (step b), a SPRI purification is carried out to remove residual first primer, then said second primer (2PR) conjugated to magnetic beads (either directly, through 20 covalent bonds, or indirectly, through biotin modification of second primer and biotin-streptavidin interaction with streptavidin coated magnetic beads) is used in said single PCR cycle of step c, then the residual of reaction mix and mono-adapter fragments are eluted, magnetically retaining in the tube 25 exclusively the resulting heteroadapter fragments, before

proceeding to -step d- the PCR amplification with said third (3PR) and fourth (4PR) primer.

Advantages

The method of generating a massively parallel sequencing library according to the present invention allows to obtain a library including only heteroadapter fragments for those sequencing platforms which require so, in a rapid, efficient, reliable and cost-effective manner. Not least, it allows to generate double strand DNA and sequencing-ready libraries with a streamlined, single-day and single-tube workflow.

Finally, the advantages of low pass whole genome sequencing with respect to array CGH (aCGH) - the current leading technology for investigating CNV - should be highlighted. Array CGH (aCGH) is based on the use of differentially labeled test and reference genomic DNA samples that are simultaneously hybridized to DNA targets arrayed on a glass slide or other solid platform. However, limitations remain for certain applications as it has proved difficult to use low quality/quantity of DNA. Moreover, chromosomal copy number assessment based on a low-pass whole genome sequencing method may offer several advantages compared to aCGH including reduced DNA sequencing cost, enhanced detection of partial or segmental aneuploidies as a result of the potential increase in chromosomal analysis resolution, control-free calling of copy number alterations.

In addition, the potential automation of the sequencing library preparation allows to minimize human errors, reduce hands-on time, and enable higher throughput and consistency.

5

CLAIMS

1. A method of generating a massively parallel sequencing library comprising the steps of:

a. providing a primary WGA DNA library (pWGAlib) including
5 fragments comprising a known 5′ sequence section (5SS), a middle sequence section (MSS), and a known 3′ sequence section (3SS) reverse complementary to the known 5′ sequence section, the known 5′ sequence section (5SS) comprising a WGA library universal sequence adapter, and the middle
10 sequence section (MSS) comprising at least an insert section (IS), corresponding to a DNA sequence of the original unamplified DNA prior to WGA, the middle sequence section (MSS) optionally comprising, in addition, a flanking 5′ intermediate section (F5) and/or a flanking 3′ intermediate
15 section (F3);

b. performing a single PCR cycle on the primary WGA DNA library using at least one first primer (1PR) comprising at least a first primer 5′ section (1PR5S) and a first primer 3′ section (1PR3S), the first primer 5′ section (1PR5S)
20 comprising at least one first sequencing adapter (1PR5SA), and the first primer 3′ section (1PR3S) hybridizing to the known 3′ sequence section (3SS), so as to obtain a first primer extended WGA DNA library;

c. performing a single PCR cycle on the first primer extended
25 WGA DNA library using at least one second primer (2PR)

comprising a second primer 5′ section (2PR5S) and a second primer 3′ section (2PR3S), the second primer 5′ section (2PR5S) comprising at least one second sequencing adapter (2PR5SA) different from the at least one first sequencing adapter (1PR5SA), and the second primer 3′ section (2PR3S) hybridizing to the known 3′ sequence section (3SS), so as to obtain a first and second primer extended WGA DNA library;

d. amplifying by PCR the first and second primer extended WGA DNA library using at least one third primer (3PR) comprising the first sequencing adapter (1PR5SA) and at least one fourth primer (4PR) comprising the second sequencing adapter (2PR5SA), so as to obtain an amplified first and second primer extended WGA DNA library.

2. The method according to claim 1, wherein the at least one first primer (1PR) further comprises at least one read sequencing primer sequence (1PRSEQ) in 3′ position of the first primer 5′ section (1PR5S) and in 5′ position of the first primer 3′ section (1PR3S).

3. The method according to claim 1 or 2, wherein the first primer 5′ section (1PR5S) further comprises at least one first sequencing barcode (1PR5BC), in 3′ position of the at least one first sequencing adapter (1PR5SA) and in 5′ position of the first primer 3′ section (1PR3S) and/or the second primer 5′ section (2PR5S) further comprises at least one second sequencing barcode (2PR5BC), in 3′ position of

the at least one second sequencing adapter (2PR5SA) and in 5′ position of the second primer 3′ section (2PR3S).

4. The method according to any of claims 1 to 3, further comprising a step of purifying the first primer extended WGA DNA library after step b and/or further comprising a step of purifying the first and second primer extended WGA DNA library after step c and/or further comprising a step of purifying the amplified first and second primer extended WGA DNA library after step d.

5. The method according to any of claims 1 to 4, wherein the WGA library universal sequence adapter is a DRS-WGA library universal sequence adapter or a MALBAC library universal sequence adapter.

6. The method according to claim 5, wherein the WGA library universal sequence adapter is a DRS-WGA library universal sequence adapter.

7. The method according to claim 5 or 6, wherein the DRS-WGA library universal sequence adapter is SEQ ID NO:50 and the MALBAC library universal sequence adapter is SEQ ID NO:51.

8. A method for low-pass whole genome sequencing comprising the steps of:

- providing a plurality of barcoded, massively-parallel sequencing libraries obtained according to the method according to any of claims 3 to 7 and pooling samples

obtained using different sequencing barcodes (BC);
- sequencing the pooled library.

9. The method for low-pass whole genome sequencing according to claim 8, wherein the step of pooling samples using different sequencing barcodes (BC) further comprises the steps of:
- quantitating the DNA in each of the barcoded, massively-parallel sequencing libraries;
- normalizing the amount of barcoded, massively-parallel sequencing libraries.

10. A massively parallel sequencing library preparation kit comprising:
- at least one first primer (1PR) comprising at least a first primer 5′ section (1PR5S) and a first primer 3′ section (1PR3S), the first primer 5′ section (1PR5S) comprising at least one first sequencing adapter (1PR5SA), and the first primer 3′ section (1PR3S) hybridizing to a known 3′ sequence section (3SS) reverse complementary to a known 5′ sequence section (5SS) comprising a WGA library universal sequence adapter of fragments of a primary WGA DNA library (pWGAlib), the fragments further comprising a middle sequence section (MSS) 3′ of the known 5′ sequence section (5SS) and 5′ of the known 3′ sequence section (3SS);
- at least one second primer (2PR) comprising at least a second primer 5′ section (2PR5S) and a second 3′ section

(2PR3S), the second primer 5' section (2PR5S) comprising at least one second sequencing adapter (2PR5SA) different from the at least one first sequencing adapter (1PR5SA), the second 3' section hybridizing to the known 3' sequence 5 section (3SS) of the fragments;

- at least one third primer (3PR) comprising the first sequencing adapter (1PR5SA); and

- at least one fourth primer (4PR) comprising the second sequencing adapter (2PR5SA).

10 11. A massively parallel sequencing library preparation kit comprising:

a) one or more primers selected from the group consisting of SEQ ID NO:1 to SEQ ID NO:12, one or more primers selected from the group consisting of SEQ ID NO:13 to SEQ ID NO:20, 15 and primers SEQ ID NO:21 and SEQ ID NO:22;

or

b) one or more primers selected from the group consisting of SEQ ID NO:27 to SEQ ID NO:38, one or more primers selected from the group consisting of SEQ ID NO:39 to SEQ ID NO:46, 20 and primers SEQ ID NO:21 and SEQ ID NO:22;

c) one or more primers selected from the group consisting of SEQ ID NO:52 to SEQ ID NO:63, one or more primers selected from the group consisting of SEQ ID NO:13 to SEQ ID NO:20, and primers SEQ ID NO:21 and SEQ ID NO:22;

25 or

d) one or more primers selected from the group consisting of SEQ ID NO:64 to SEQ ID NO:75, one or more primers selected from the group consisting of SEQ ID NO:39 to SEQ ID NO:46, and primers SEQ ID NO:21 and SEQ ID NO:22.

5 12. A low-pass whole genome sequencing kit comprising:

a) at least one primer selected from the group consisting of SEQ ID NO:1 to SEQ ID NO:12; at least one primer selected from the group consisting of SEQ ID NO:13 to SEQ ID NO:20; primers SEQ ID NO:21 and SEQ ID NO:22; and a custom sequencing primer of 10 SEQ ID NO:23;

or

b) at least one primer selected from the group consisting of SEQ ID NO:27 to SEQ ID NO:38; at least one primer selected from the group consisting of SEQ ID NO:39 to SEQ ID NO:46; primers SEQ 15 ID NO:21 and SEQ ID NO:22; and primer of SEQ ID NO:47;

or

c) at least one primer selected from the group consisting of SEQ ID NO:52 to SEQ ID NO:63; at least one primer selected from the group consisting of SEQ ID NO:13 to SEQ ID NO:20; primers SEQ 20 ID NO:21 and SEQ ID NO:22; a custom sequencing primer of SEQ ID NO:23 and a custom index 2 primer selected from the group consisting of SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26;

or

d) at least one primer selected from the group consisting of SEQ 25 ID NO:64 to SEQ ID NO:75; at least one primer selected from the

group consisting of SEQ ID NO:39 to SEQ ID NO:46; primers SEQ ID NO:21 and SEQ ID NO:22; and primer of SEQ ID NO:47.

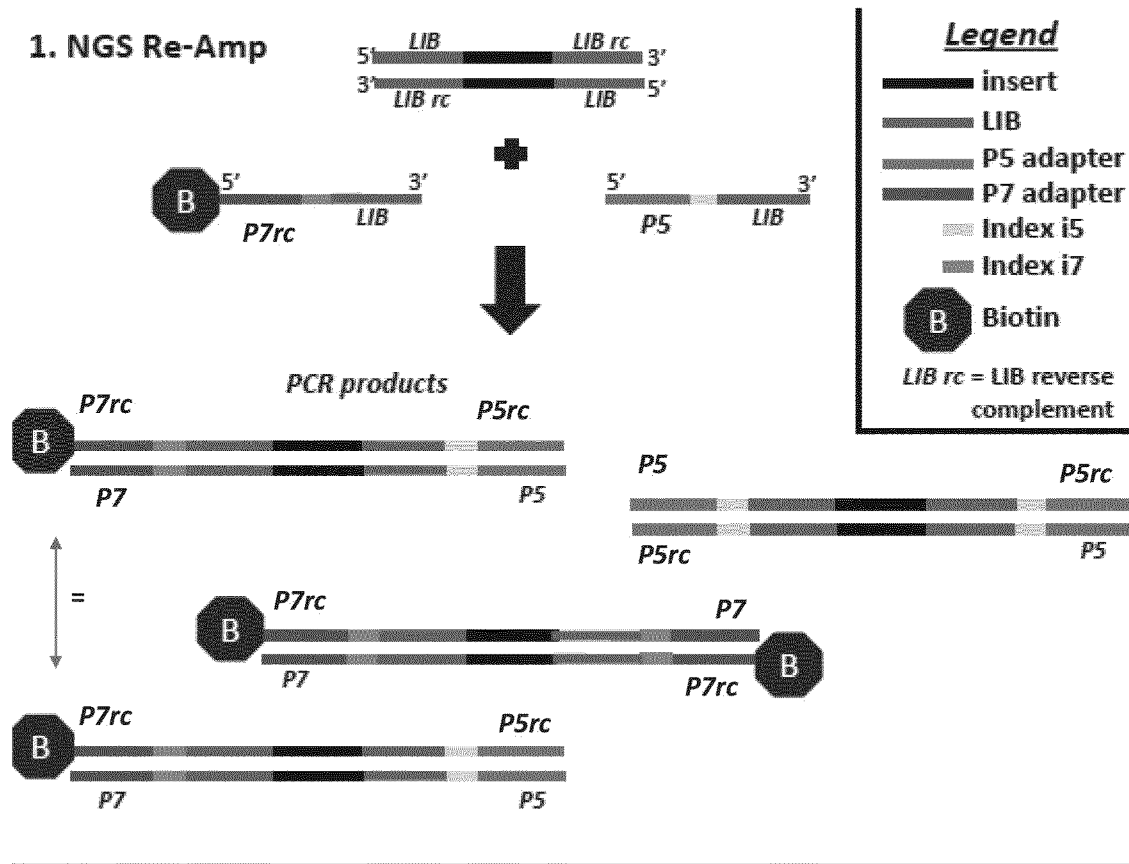
13. A low-pass whole genome sequencing kit according to claim 12, wherein alternative a) further comprises a primer
5 selected from the group consisting of SEQ ID NO:24, SEQ ID NO:25 and SEQ ID NO:26 and alternative b) or alternative d) further comprises SEQ ID NO:48.

14. A low-pass whole genome sequencing kit according to claim 13, wherein alternative b) or alternative d) further
10 comprises a primer of SEQ ID NO:49.

15. A method for genome-wide copy number profiling, comprising the steps of:

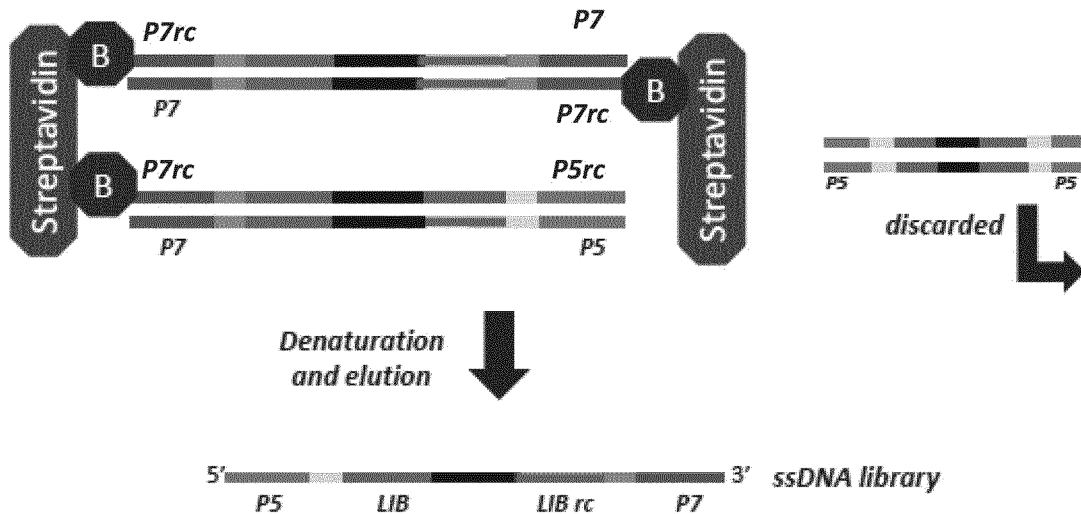
- sequencing a DNA library developed using the sequencing library preparation kit of claim 10 or 11;
15 - analysing the sequencing read depth across different regions of the genome;
- determining a copy-number value for the regions of the genome by comparing the number of reads in that region with respect to the number of reads expected in the same for a reference genome.

20



2. Size selection by SPRI beads

3. Fragment selection by Streptavidin beads



4. Check library quality and quantity

5. Sequencing by Illumina platforms

FIG. 1

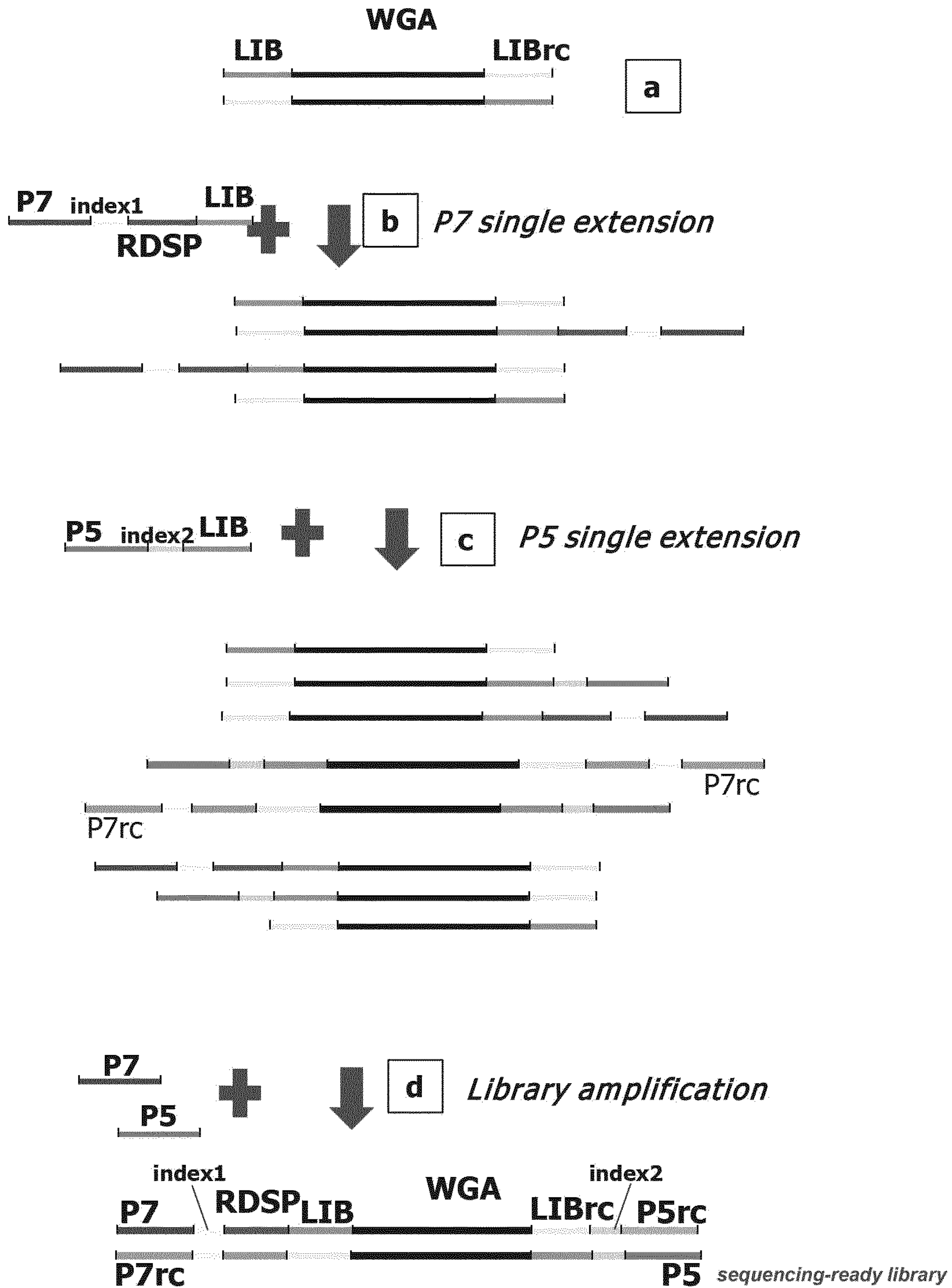


FIG. 2A

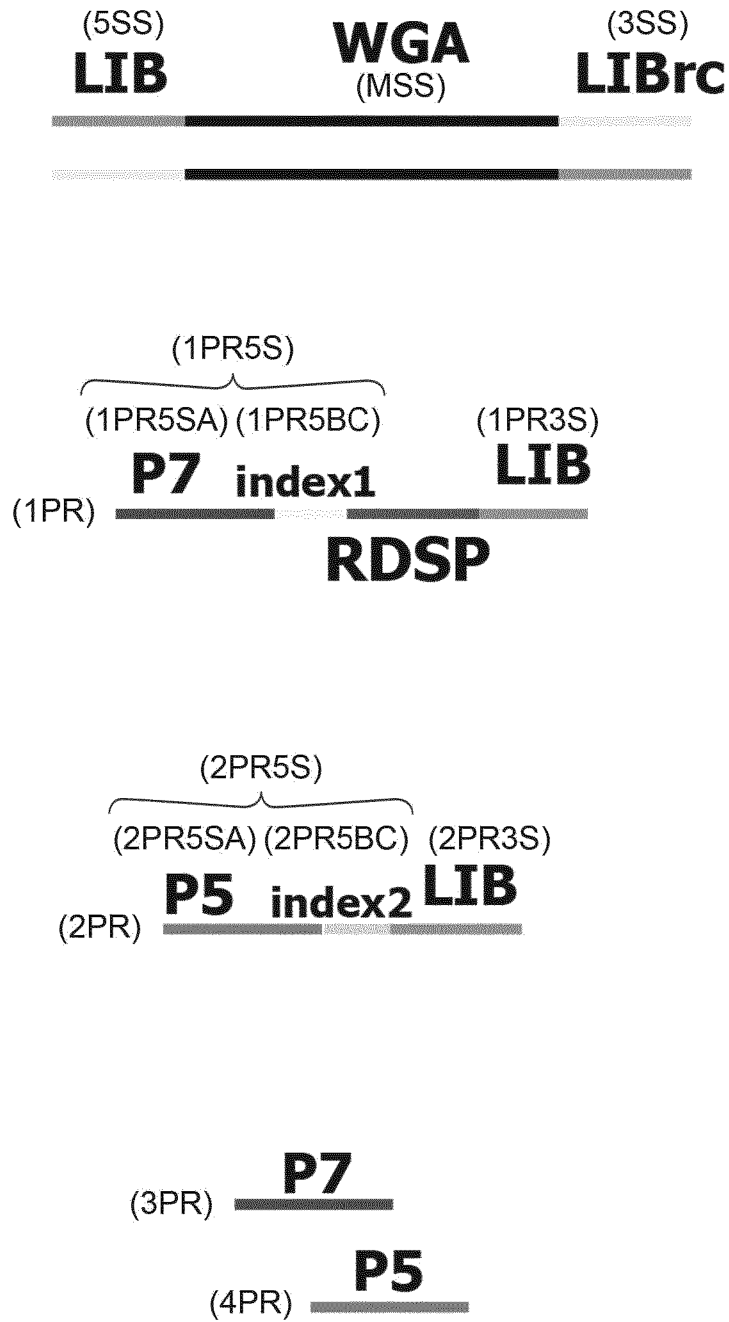


FIG. 2B

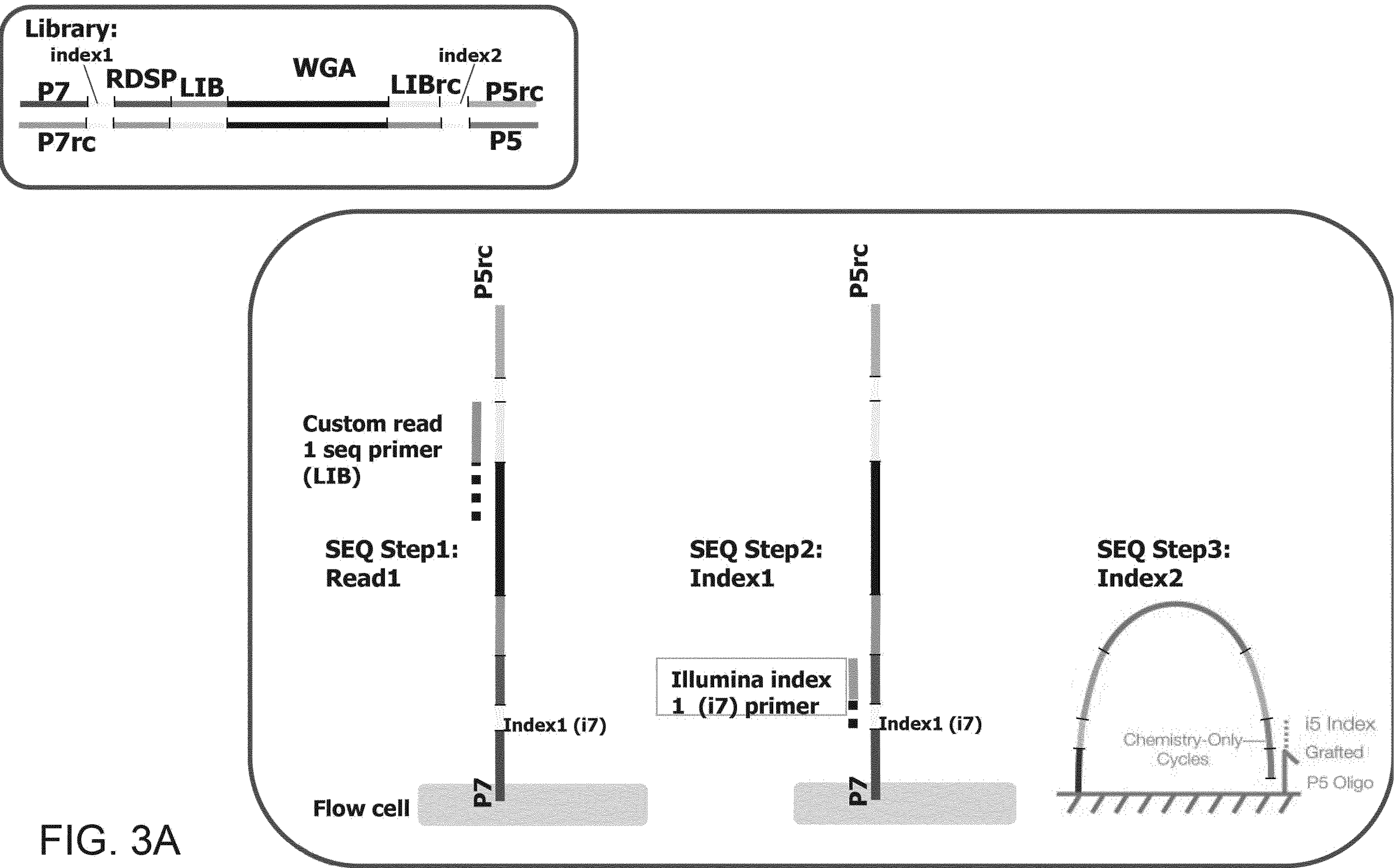


FIG. 3A

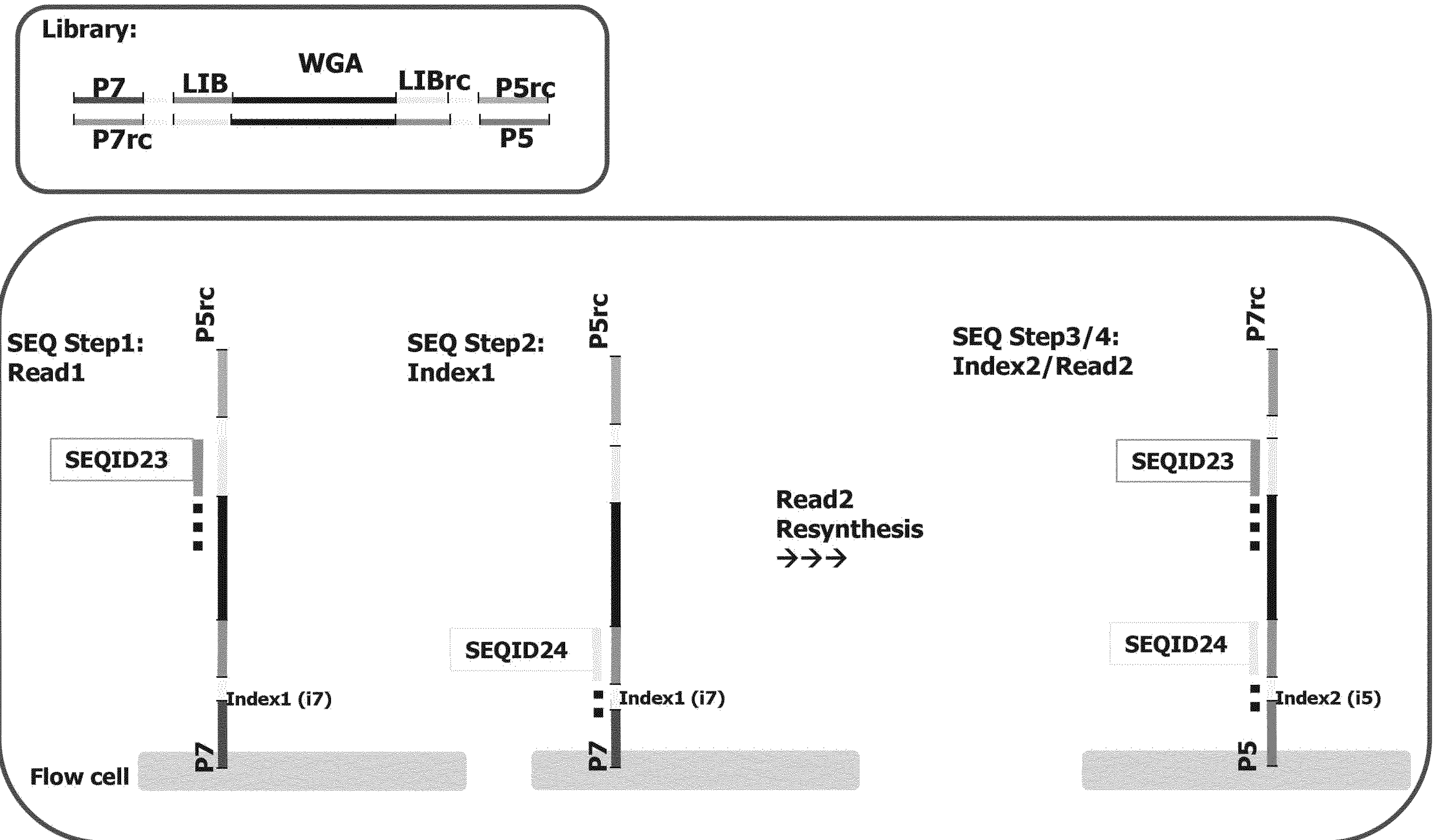


FIG. 3B

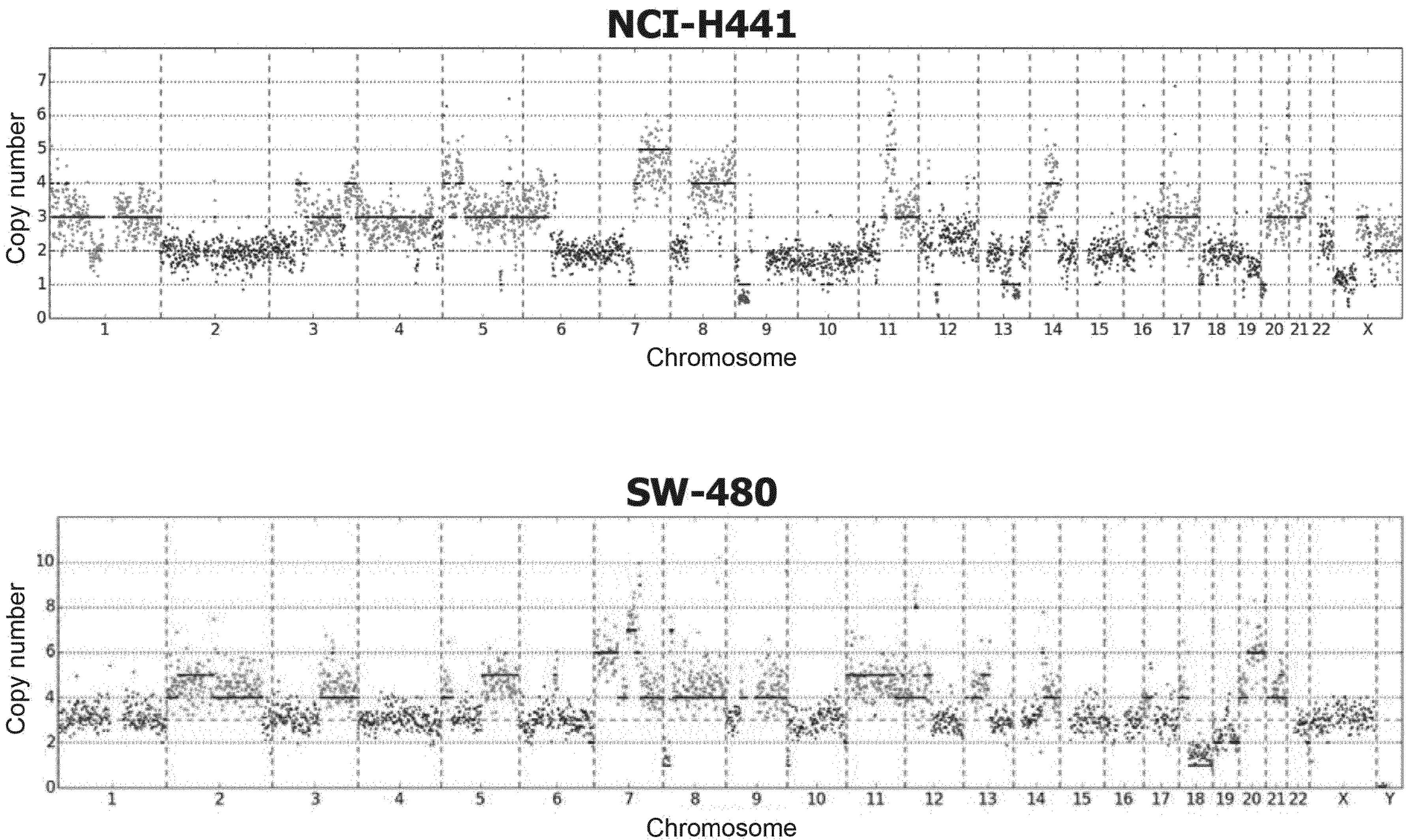
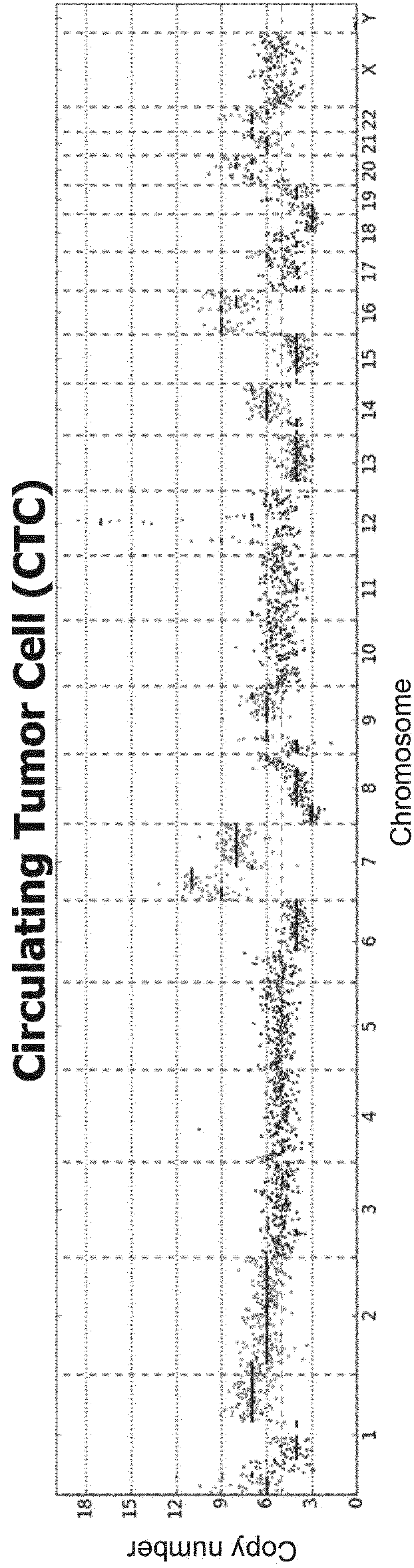


FIG. 4A



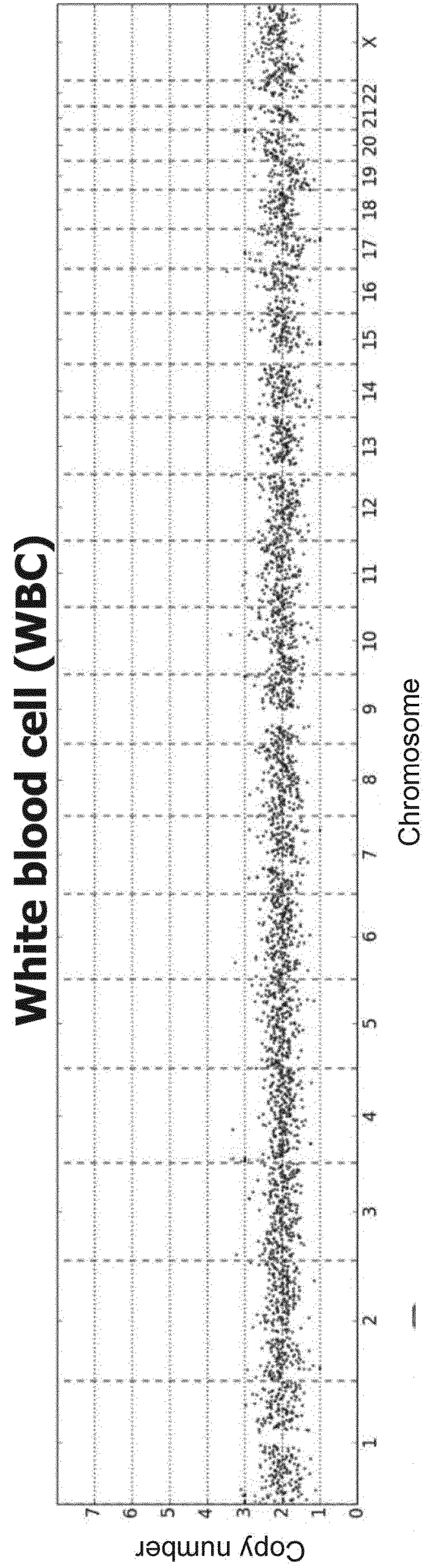


FIG. 4B

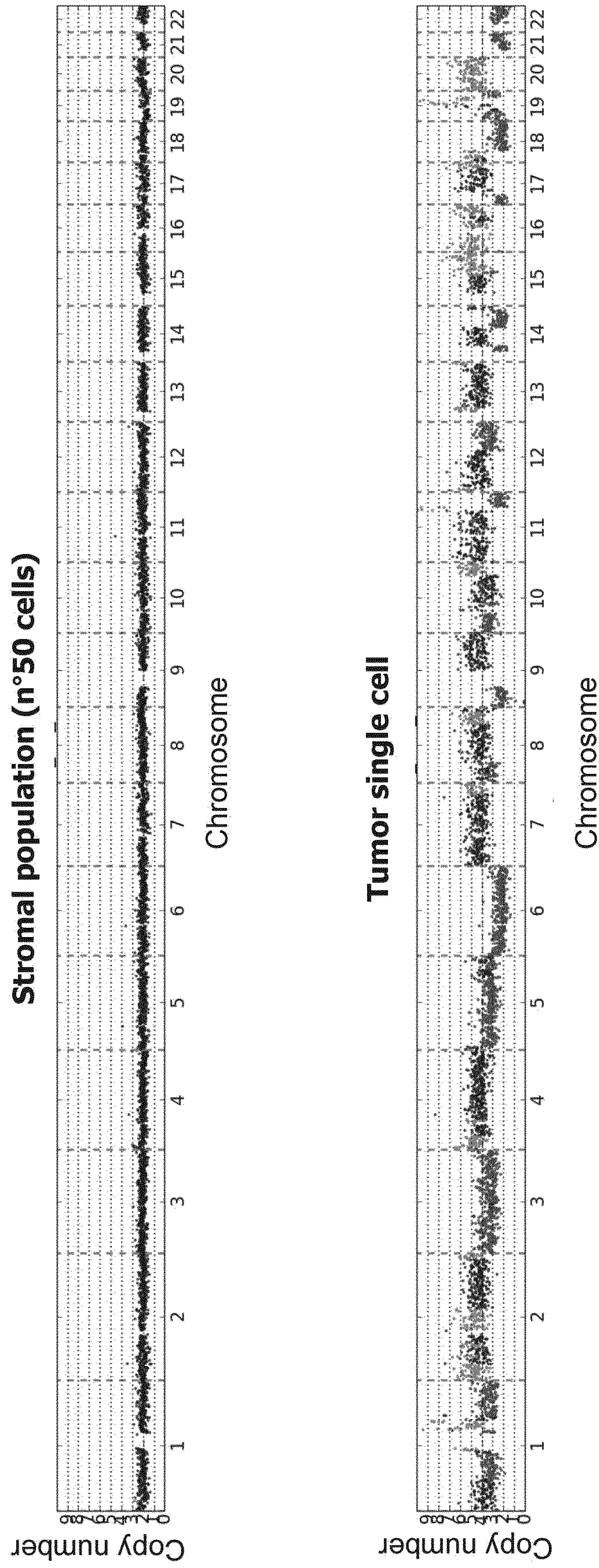
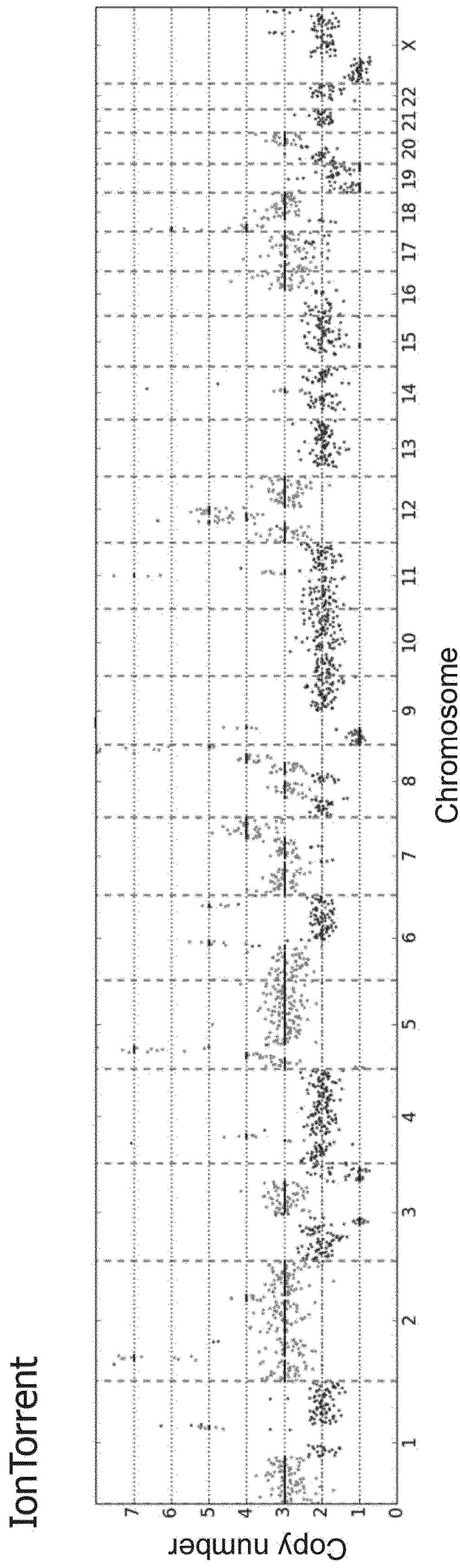


FIG. 5



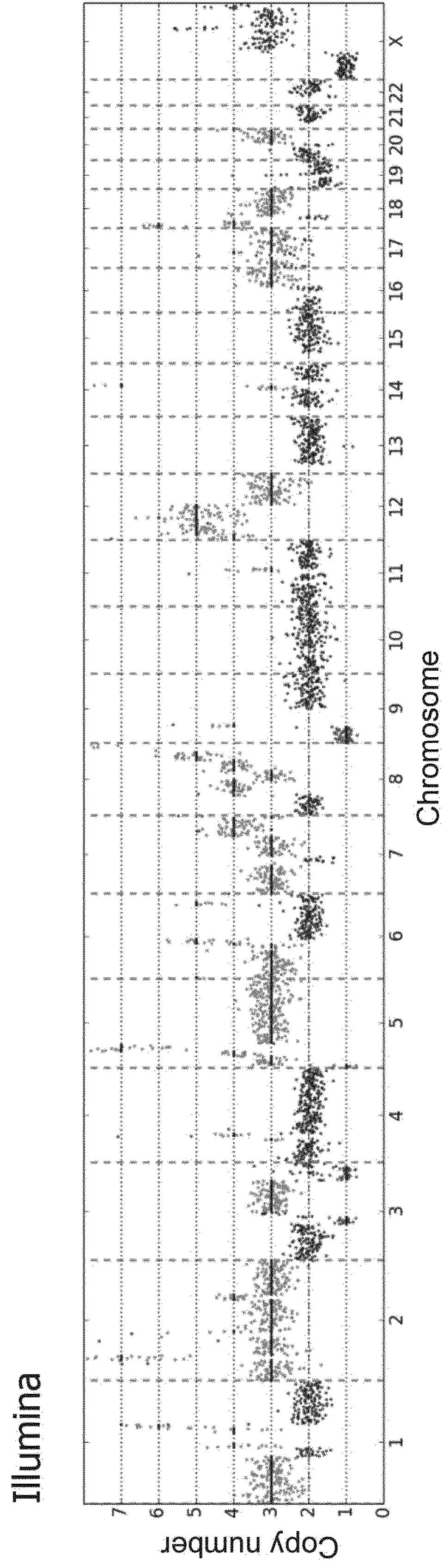


FIG. 6A

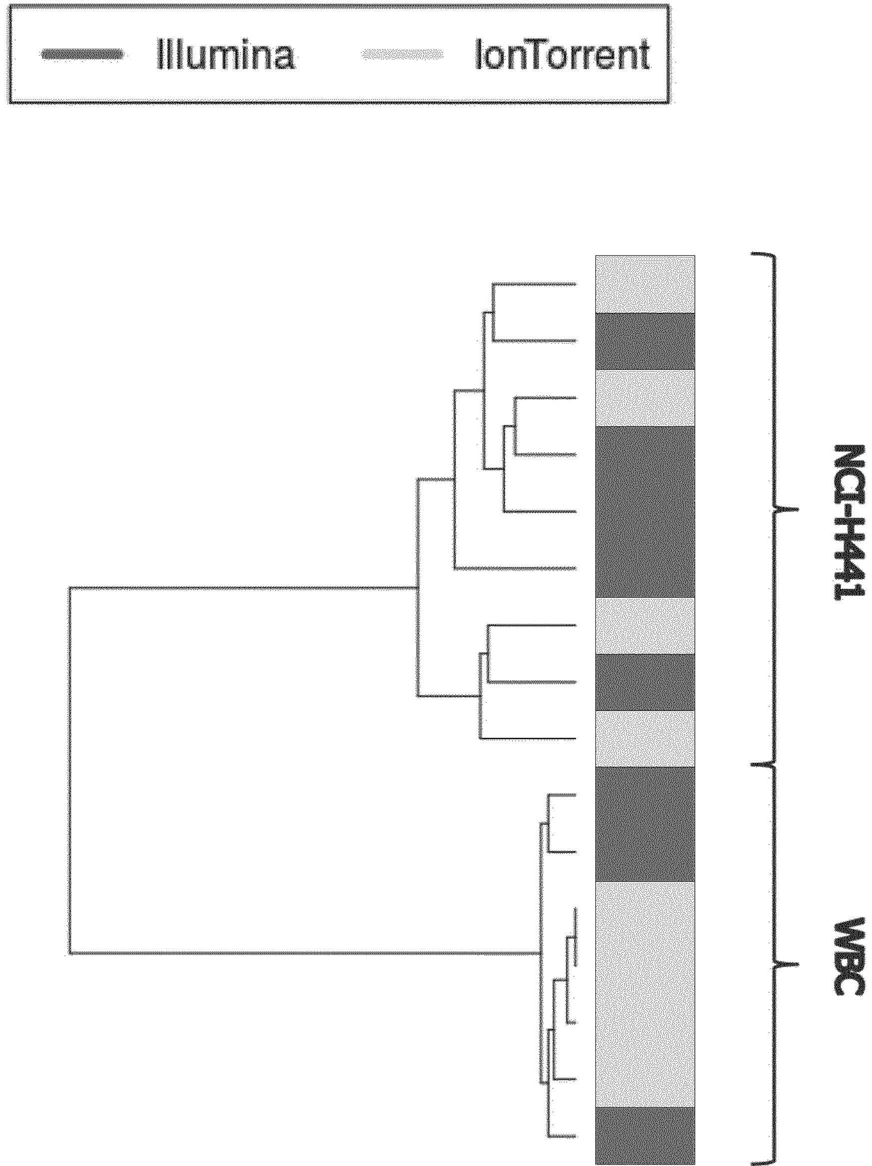


FIG. 6B

LEGEND:	
WGA: *Ampli*1™ Whole Genome Amplification products LIB: *Ampli*1™ WGA tag LIBrc: *Ampli*1™ WGA tag reverse complementary	RDSP: read sequencing primer (Illumina) Index1: index1 D70X Index2: index2 D50X **P5 & P7:** Illumina adapters P7rc: P7 Illumina adapter reverse complementary

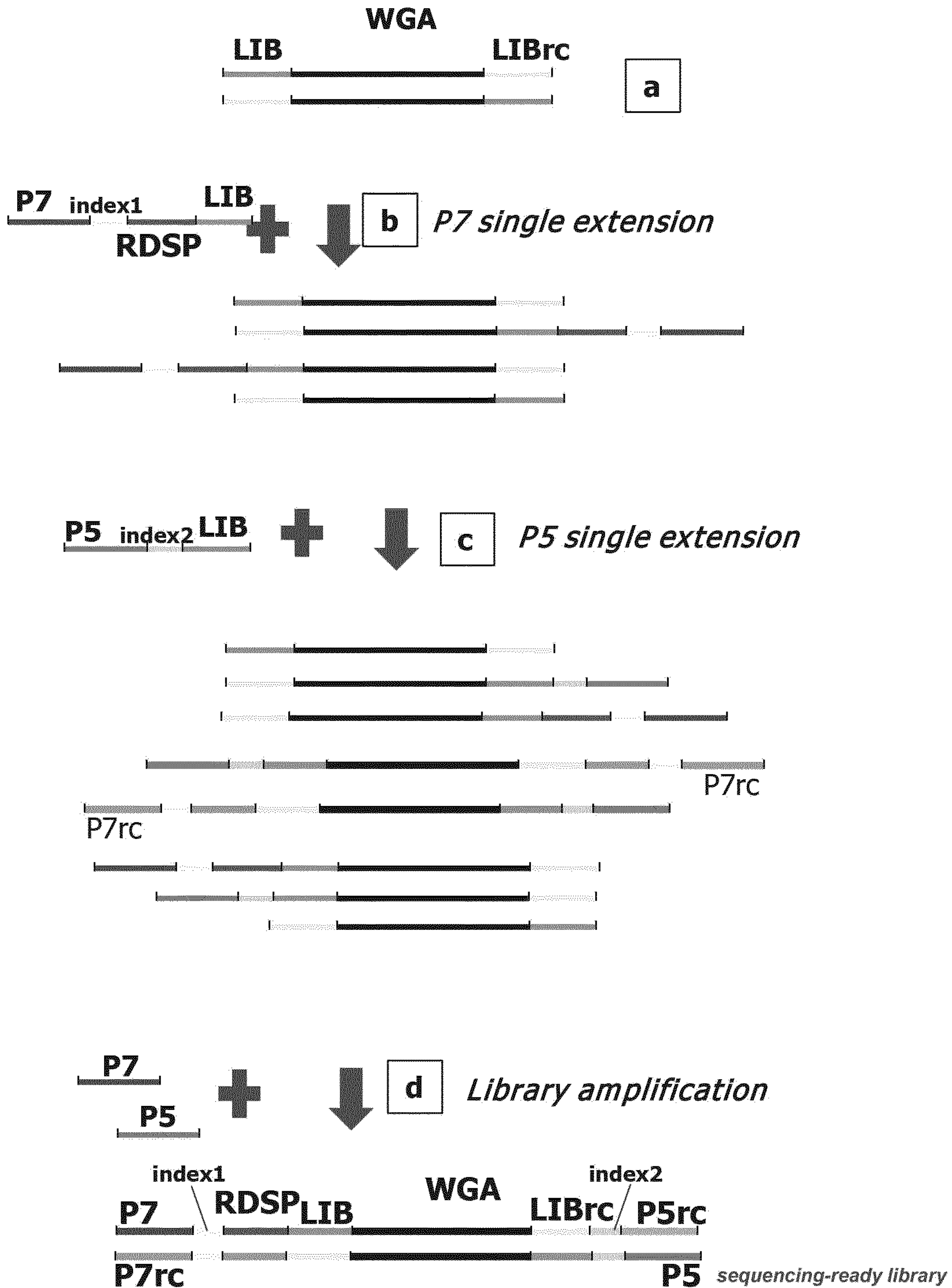


FIG. 2A