

A method for detecting a genetic variant.**Field of the invention**

The present invention relates to methods of detecting genetic
5 variants in DNA samples.

Background to the invention

A genetic variant is one or more nucleotides which differ from a
reference DNA sequence for a given region. For example, a genetic
10 variant may comprise a deletion, substitution or insertion of one or
more nucleotides.

A DNA sample may be analysed for known genetic variants or to
discover previously unknown genetic variants in a region of interest
15 by determining the DNA sequence in the region of interest and
comparing the determined sequence to the reference sequence.

DNA sequencing can be performed using a variety of techniques, such
as the classic chain termination method, or one of several high-
20 throughput, next generation sequencing (NGS) methodologies, reviewed
by Metzker, M.L., Nat Rev Genet 2010 Jan;11(1): 31-46.

Illumina sequencing, 454 pyrosequencing, Heliscope single molecule
sequencing, single molecule real time (SMRT) sequencing and Ion
25 semiconductor sequencing platforms are examples of DNA sequencing
methods based on the "sequencing by synthesis" principle. In these
methods, the sequence of a template strand of DNA is determined
through the detection of signals emitted as nucleotide bases are
incorporated into a newly-synthesised complementary strand.

30 DNA sequencing platforms have error rates. For example, occasionally
the polymerase used in the amplification reaction will incorporate
the wrong nucleotide base in the complementary strand being
synthesised, leading to an incorrect determination of the nucleotide
35 at that position in the DNA template. The detection limit of NGS
methods is defined by errors at two stages: library preparation

(which usually involves amplification by PCR) and by sequencing itself.

This is problematic especially for the detection of genetic variants that will only be present in a DNA sample at low frequency, for example a frequency approaching or below the error rate of the sequencing method used. Under such circumstances, it is difficult or impossible to determine whether a genetic variant identified is real (i.e. actually present in the DNA template molecule) or an error.

For Illumina sequencing, the background error rate varies for different genetic variants and genomic locations and has a large variance. Therefore, detecting mutations which are present in a DNA sample at frequency of ~1% or lower is problematic.

Existing methods of DNA sequencing and genetic variant identification have limitations with regards to the detection of rare, novel variants in multiple regions, especially in samples having small amounts of DNA.

Methods are typically incapable of identifying mutations occurring at a frequency lower than or similar to the error rate of method used (i.e. background noise).

Digital PCR (dPCR; Vogelstein B., Kinzler K.W. Proc. Natl. Acad. Sci. U.S.A. 1999 96(16):9236-41; Sykes, P.J. et al., BioTechniques 1992 13(3): 444-9) is not useful for identification of novel (i.e. previously unidentified) genetic variants, as dPCR involves use of primers and assays designed to detect particular variants. Moreover, dPCR has a limited scope for analysing multiple regions of interest in parallel, especially where DNA sample is limited.

Other complex methods exist for tagging single DNA molecules from a single pool of DNA, such as Safe-SeqS and single-molecule molecular inversion probes (Kinde I, et al., Proc Natl Acad Sci U S A. 2011 108(23): 9530-5; Hiatt JB, et al., Genome Res. 2013 23(5):843-54.).

These methods are not suitable for simultaneous analysis of multiple genes (i.e. multiple regions of interest) and when DNA is limited.

Several studies have demonstrated non-invasive detection of cancer DNA (Dawson SJ, et al., N Engl J Med. 2013 368(13):1199-209; Forshew T, et al., Sci Transl Med. 2012 4(136):136ra68; Murtaza M, et al. Nature. 2013 497(7447):108-12). However, major challenges persist in this field, such as (a) screening sufficient bases of the genome to detect relevant cancer mutations (b) screening of small quantities of fragmented DNA for such mutations, and (c) detection of low frequency mutant tumour DNA molecules amongst many 'wild-type' molecules.

For example, Forshew T, et al., Sci Transl Med. 2012 4(136):136ra68 describes screening of large regions of the genome for cancer mutations in blood, but the detection limit for this method was ~1%-2% allele frequency (AF).

Summary of the invention

The present invention provides a solution to the above problems. Real genetic variants are identified by determining background frequencies for genetic variants at each position taking into account the error of the method (i.e. error rates of DNA amplification and sequencing platform).

In a first aspect, the present invention provides a method for detecting a genetic variant in a region of interest in a DNA sample comprising

(i) determining, for a given sequencing platform, sequencing process and sequencing depth, the distribution of the number of reads supporting a genetic variant or plurality of variants expected to be observed in the sequencing results of amplification reactions due to amplification and sequencing error (read count distribution);

(ii) based on read count distribution determined in step (i), establishing a threshold frequency at or above which the genetic variant must be observed in sequencing results of amplification

reactions to assign a positive determination for the presence of the genetic variant in a given amplification reaction;

(iii) partitioning the DNA sample into a plurality of replicate amplification reactions so that the mean number of amplifiable template molecules of the region of interest in a replicate amplification reaction is fewer than the reciprocal of the threshold frequency determined in step (ii);

(iv) performing the amplification reactions of step (iii) and sequencing the products of amplification reactions,

(v) based on step (ii) and the results of step (iv), determining the presence/absence of the genetic variant in each replicate amplification reaction; and

(vi) integrating the results of (v) to determine the presence/absence of the genetic variant in the region of interest in the DNA sample.

The present invention provides a method for detecting a genetic variant in a region of interest in a DNA sample comprising

(i) determining, for a given sequencing platform, the mean frequency and variance of the frequency at which a genetic variant or plurality of genetic variants is expected to be observed in the sequencing results of amplification reactions due to amplification and sequencing error;

(ii) based on the mean frequency and variance of the frequency determined in step (i), establishing a threshold frequency at or above which the genetic variant must be observed in sequencing results of amplification reactions to assign a positive determination for the presence of the genetic variant in a given amplification reaction;

(iii) partitioning the DNA sample into a plurality of replicate amplification reactions so that the mean number of amplifiable template molecules of the region of interest in a replicate amplification reaction is fewer than the reciprocal of the threshold frequency determined in step (ii);

(iv) performing the amplification reactions of step (iii) and sequencing the products of amplification reactions,

(v) based on step (ii) and the results of step (iv),
determining the presence/absence of the genetic variant in each
replicate amplification reaction; and

(vi) integrating the results of (v) to determine the
5 presence/absence of the genetic variant in the region of interest in
the DNA sample.

Advantageously, the method allows detection of genetic variants at
very low frequency within a DNA sample. Accordingly, the method
10 enables earlier identification (e.g. in the context of disease
pathology such as cancer-related mutations) of the presence of
genetic mutations (i.e. when the mutation is present at a lower
frequency) in comparison with previously known methods for mutation
detection. The method therefore finds use in a variety of
15 applications, such as screening for tumour reappearance, tumour
growth, development of drug resistance/tumour evolution and
identification of therapeutically actionable mutations. The method
also allows for the identification of the presence of genetic
mutations at low frequencies with improved statistical confidence.

20 A key feature of the method of the invention is the partitioning of
the DNA sample into a plurality of replicate amplification reactions
(e.g. by dilution and aliquoting into wells) so that, on average,
the number of amplifiable template molecules of the region of
25 interest present in a replicate amplification reaction is fewer than
the reciprocal of the threshold frequency for a positive
determination. In this way, for each amplification reaction having
an amplifiable template region in which the genetic variant is
present, there is a high probability that the variant will be
30 observed at a frequency greater than the threshold frequency for
determining the presence of the variant. The method thereby allows
detection of the presence of genetic variants in a DNA sample even
when present at very low frequency within the DNA sample. For
example, the method allows detection at a frequency of less than 1%.

35 Moreover, the present method is useful in discovery of genetic
variants. That is, for a region of interest, the background levels

for each of the three potential base changes from a reference DNA sequence can be readily determined, and frequencies for the genetic variant above background levels (in particular DNA samples) can subsequently be identified using the method. Thus, without screening
5 for any particular genetic variant, new genetic variants at any position within the region of interest can be identified. This feature is associated with clear advantages in a wide range of fields, including diagnostics, prognostics, mutation discovery, monitoring of response to treatment and drug resistance.

10 In some embodiments, for the genetic variant to be determined as being present in the region of interest in the DNA sample in step (vi), a positive determination for the presence of the genetic variant must be made in more than one replicate amplification
15 reaction in step (v). In some embodiments, a positive determination for the presence of the genetic variant must be made in at least 3 replicate amplification reactions.

In some embodiments, the genetic variant may be a single nucleotide
20 variant, that is a change from one nucleotide to a different nucleotide in the same position. In some embodiments, the genetic variant may be an insertion or deletion, that adds or removes nucleotides. In some embodiments, the genetic variant may be a combination of multiple events including single nucleotide variants
25 and insertions and/or deletions. In some embodiments, a genetic variant may be composed of multiple genetic variants present in different regions of interest.

Requiring a positive determination for the genetic variant in a
30 plurality of replicate amplification reactions reduces the probability of a false positive determination of the genetic variant being present in the DNA sample. The method requiring multiple positive determinations in replicate amplification reactions
35 therefore has higher specificity for the detection of genetic variants.

The mean frequency and coefficient of variation (CV) at which a given variant is observed (i.e. in sequencing results) as a result of error in the method used to sequence a DNA sample can be used to determine and/or model background levels (i.e. noise) for a genetic variant. These values can be used, for example, to determine cumulative distribution function (CDF) values and/or to calculate z-scores.

In turn, measurements and/or models of background noise for a genetic variant can then be used to establish threshold frequencies above which a genetic variant must be observed to be determined as being present in a given amplification reaction (a positive determination). For a positive determination, the frequency of the variant must be higher than the mean frequency at background levels.

In some embodiments of the method of the invention, the threshold frequency of step (ii) is determined using a binomial, over-dispersed binomial, Beta, Normal, Exponential or Gamma probability distribution model. In some embodiments, the threshold frequency at which a given genetic variant must be observed at or above to be determined as being present in a replicate amplification reaction is the frequency at which the cumulative distribution function (CDF) value of that genetic variant reaches a predefined threshold value (CDF_thresh) of 0.99, 0.995, 0.999, 0.9999, 0.99999 or greater.

In some embodiments of the method of the invention, the threshold frequency of step (ii) is determined using a z-score cut-off. Here, the background mean frequency and variance of the frequency for the genetic variant determined in step (i) are modelled with a Normal distribution, and the threshold frequency for calling a mutation is the frequency at the z-score which is a number of standard deviations above the background mean frequency. In some embodiments, the threshold frequency is the frequency at z-score of 20. In some embodiments, the threshold frequency is the frequency at z-score of 30.

In some embodiments, establishing a threshold frequency at or above which the genetic variant must be observed in sequencing results of amplification reactions to assign a positive determination for the presence of the genetic variant in a given amplification reaction

comprises

(a) based on the read count distribution determined for a plurality of genetic variants - which is optionally a normal distribution defined by the mean frequency and variance of the frequency determined for a plurality of genetic variants - in step (i), establishing a plurality of threshold frequencies at or above which the genetic variants should be observed in sequencing results of amplification reactions to assign a positive determination for the presence of the genetic variant in a given amplification reaction, and

(b) based on step (a), establishing an overall threshold frequency at or above which a genetic variant must be observed in sequencing results of a given amplification reaction to assign a positive determination for the presence of the genetic variant in that amplification reaction, which is the threshold frequency at which 90%, 95%, 97.5%, 99% or more of the threshold frequencies determined in step (a) are less than this value.

In this way, threshold frequencies need not be determined for each possible base at each position of the region of interest, and an overall threshold based on a plurality of genetic variants can be used in the method of the invention.

In some embodiments, the mean number of amplifiable template molecules of the region of interest to be present in a given replicate amplification reaction is determined such that when the genetic variant is present in a single amplifiable template molecule of a replicate amplification reaction, the probability that a positive determination will be made for that replicate is 0.9 or greater.

This minimises the probability that a given replicate amplification reaction will incorrectly be determined as being negative for a genetic variant when the variant is in fact present.

In some embodiments, the plurality of reactions all have the same amount of starting template material from the sample. In some embodiments, different reactions have different amounts of template material from the sample. These amounts can be considered when estimating the allele frequency of genetic variants in the sample.

In some embodiments, step (i) comprises sequencing a DNA sample multiple times, to determine the read count distribution for a genetic variant or plurality of genetic variants, which is optionally a normal distribution defined by the mean frequency and variance of the frequency for a genetic variant or plurality of genetic variants.

Advantageously, when background error rates are empirically determined for genetic variants in a region of interest in this way, the estimate of the background error rate will be more accurate, thereby allowing greater sensitivity for detecting the presence of a genetic variant in the DNA sample, and with a greater degree of confidence.

In some embodiments, the read count distribution at which a genetic variant or plurality of genetic variants is expected to be observed in the sequencing results of amplification reactions due to amplification and sequencing error (optionally a normal distribution defined by the mean frequency and variance of the frequency at which a genetic variant or plurality of genetic variants is expected to be observed in the sequencing results of amplification reactions due to amplification and sequencing error) is determined in step (i) based on sequencer and/or polymerase error rates. In some embodiments, this is determined taking sequence context into account.

In some embodiments, step (i) comprises 'looking-up' a reference value or plurality of reference values in a database, chart, table, list, catalogue, index, directory, or register. In some embodiments the reference values are determined by sequencing a reference DNA sample multiple times, to determine the read count distribution for

a genetic variant or plurality of genetic variants, which is optionally a Normal distribution defined by the mean frequency and variance of the frequency for a genetic variant or plurality of genetic variants. In some embodiments, the reference DNA sample is a
5 'matched normal' sample.

Advantageously, the method of the invention can be performed without having to determine background error rates empirically each time.

10 In some embodiments, following partitioning of the DNA sample in step (iii), each replicate amplification reaction has a mean of more than a single amplifiable template molecule for the region of interest per replicate amplification reaction. In some embodiments, the mean number of amplifiable template molecules per replicate
15 amplification reaction will be more than 1 and less than 1000, more than 2 and less than 1000, or more than 5 and less than 1000.

Advantageously, the DNA sample need not be partitioned more than necessary to achieve the efficiencies of the method associated with
20 partitioning of template molecules. This has advantages at least in terms of reducing running and materials costs.

In some embodiments, the method is capable of detecting genetic variants which are present within the population of amplifiable
25 template molecules of a DNA sample at a frequency of less than 2%, less than 1%, less than 0.5%, less than 0.1% or less than 0.05%.

In some embodiments, partitioning the DNA sample into a plurality of replicate amplification reactions comprises diluting the DNA sample
30 and aliquoting into replicate amplification reactions. For example, the amplification reactions may be carried out in separate wells. Alternatively, replicate amplification reactions can be partitioned by other means known to those skilled in the art.

35 In some embodiments of the method of the invention, replicate amplification reactions are performed in parallel, and sequencing of the products of amplification reactions is performed in parallel.

In some embodiments of the invention the method further comprises:

(vii) determining the frequency of the genetic variant in the DNA sample.

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Advantageously, this allows determination of changes in the frequencies of genetic variants over time (e.g. over the course of disease and/or during the course of treatment) and/or differences in frequencies of genetic variants between samples.

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Amplification reactions may be performed by one-step PCR or by two-step PCR.

In some embodiments, amplification reactions are performed using one or more primer pairs flanking the region of interest which integrate sample and/or amplification reaction replicate specific identifier sequences into the products of amplification. Identifier sequences may be defined as any series of DNA bases that is sufficiently different from another series of DNA bases such that when read along with an attached targeted region of interest, the identifier can be used to identify from which sample and/or amplification reaction replicate the targeted sequence originated. The terms "identifier sequences" and "barcodes" are used interchangeably herein.

25 In some embodiments, the primers integrate sequence adapters into the products of amplification. In some embodiments the primers flanking the region of interest comprise sample and/or amplification reaction replicate specific identifier sequences and sequence adapters allowing these identifier and adapter sequences to be added during a one-step PCR. In some embodiments universal "tagging" sequences are included within the primer pairs. A tagging sequence may be defined as any series of DNA bases that may be used as a target for subsequent rounds of PCR. Attachment of common tagging sequences to a plurality of primers will result, after
35 amplification, in a plurality of products with these common tagging sequences attached. An optimal tagging sequence will be sufficiently different from the genome of interest to prevent non-specific

amplification of the genomic sequence. In some embodiments the tagging sequence may comprise additional features such as a binding site for sequencing primers. In some embodiments a second round of PCR is performed, using primers that comprise the tagging sequences, sequence adapters and optionally additional barcodes, to attach sequencing adapters and optionally additional barcodes to the original PCR product. In some embodiments ligation is used to attach sequence adapters and optionally additional barcodes to the original PCR product. In some embodiments, a plurality of regions of interest are analysed in parallel.

In some cases the method may therefore be implemented as a high-throughput method, allowing screening of multiple regions of interest for genetic variants simultaneously. This has advantages in terms of the speed, efficiency and reducing running and materials costs.

In some embodiments of the method of the invention, the read count distribution may be defined as a normal distribution characterised by parameters which are the mean frequency and variance of the frequency at which a genetic variant or plurality of genetic variants is/are observed or expected to be observed in the sequencing results of amplification reactions due to amplification and sequencing error.

Read count distribution may be defined as the general set of probabilities to observe the non-reference allele at any count.

The read count distribution may be the distribution of the number of reads supporting a genetic variant or plurality of variants expected to be observed in the sequencing results of amplification reactions due to amplification and sequencing error. A read supporting a genetic variant is a positive read for a genetic variant.

For example, the read count distribution may be the general set of probabilities to observe the genetic variant or plurality of genetic

variants, for a given sequencing platform, sequencing process and sequencing depth, due to amplification and sequencing error.

Read depth, also termed sequencing depth, may be defined as the number of times a specific genomic position (e.g. a given nucleotide) is read during the sequencing process.

The method of the invention finds use in a wide variety of applications. In fact, the method is useful for detection of genetic variants in any region of interest in any DNA sample, for any purpose.

In another aspect, the present invention provides the method as described hereinabove to detect and/or quantify tumour DNA in a sample. In some embodiments, the method is for detecting and/or quantifying circulating tumour DNA in a sample.

In some cases in accordance with any aspect of the present invention, the sample is a biological sample obtained from a subject. In some embodiments the sample is a tissue sample, for example a surgical sample. In some embodiments the sample is a liquid biopsy, such as blood, plasma, urine, seminal fluid, stool, sputum, pleural fluid, ascetic fluid, synovial fluid, cerebrospinal fluid, lymph, nipple fluid, or bronchial lavage. In some embodiments the sample is a cytological sample or smear or a fluid containing cellular material, such as cervical smear, nasal brushing, or esophageal sampling by a sponge (cytosponge), Endoscopic / gastroscopic / colonoscopic biopsy or brushing, cervical mucus or brushing.

Many of the above samples can be obtained non-invasively, and can therefore be taken regularly without great risk or discomfort to the subject.

Accordingly, in one aspect the present invention provides the method as described hereinabove in an *in vitro* method of diagnosis or prognosis or monitoring a disease.

The method can be used to analyse DNA samples for genetic variation associated with or predictive of susceptibility, resistance or response to a given therapy.

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Accordingly, in another aspect the present invention provides a method of identifying a subject having an increased probability of developing a disease (i.e. having increased susceptibility to a disease), the method comprising: obtaining a DNA-containing sample
10 from the subject, and carrying out the method in accordance with the first aspect of the invention on the DNA-containing sample obtained from the subject. In some cases, in accordance with this aspect of the invention, the DNA-containing sample is determined to comprise a disease-associated genetic variant, thereby identifying a subject as
15 having an increased probability of developing a disease (as compared to a subject not having a disease-associated genetic variant detected in a DNA-containing sample).

In another aspect the present invention provides a method of
20 diagnosis, the method comprising: obtaining a DNA-containing sample from a subject, and carrying out the method in accordance with the first aspect of the invention on the DNA-containing sample obtained from the subject. In some cases, in accordance with this aspect of the invention, the DNA-containing sample is determined to comprise a
25 disease-associated genetic variant.

A subject or plurality of subjects who may have a particular susceptibility, resistance or response to a given therapy can be analysed for genetic variation predictive of such susceptibility,
30 resistance or response. Accordingly, in one aspect the present invention provides the method as described hereinabove in a method of identifying genetic variation predictive of susceptibility, resistance or response to a therapy.

35 Accordingly, the present invention provides a method of selecting a patient for therapy, the method comprising: obtaining a DNA-containing sample from the patient, and carrying out the method in

accordance with the first aspect of the invention on the DNA-containing sample obtained from the patient. In some cases, in accordance with this aspect of the invention, the DNA-containing sample is determined to comprise a disease-associated genetic variant (e.g. a risk allele) and/or a genetic variant predictive of resistance or response to a therapy. The method may further comprise selecting the patient for therapy based on the determination that the DNA-containing sample from the patient comprises a genetic variant. In some cases the method may further comprise a step of administering a therapy and/or recommending administration of a therapy based on the determination that the DNA-containing sample from the patient comprises a genetic variant.

The method of the invention can also be used to identify novel (i.e. previously unidentified) determinants and/or predictors of susceptibility to or prognosis of a disease, or of resistance or response to a therapy.

Accordingly, in another aspect the present invention provides a method of identifying a disease-associated genetic variant, the method comprising: obtaining a DNA-containing sample from a patient or plurality of patients having a disease, and carrying out the method in accordance with the first aspect of the invention on the DNA-containing sample obtained from the patient or plurality of patients. In some cases, in accordance with this aspect of the invention, the DNA-containing sample or samples is/are determined to comprise a genetic variant, which is thereby identified as being a disease-associated genetic variant. In accordance with this aspect, in some embodiments the patient or plurality of patients may have a particular clinical phenotype and/or disease prognosis.

Accordingly, in some embodiments the method identifies determinants or predictors of a particular clinical phenotype and/or disease prognosis.

In another aspect the present invention provides a method of identifying a genetic variant associated with resistance or response to a therapy, the method comprising: obtaining a DNA-containing

sample from a patient or plurality of patients having resistance to or a response to a therapy for a disease, and carrying out the method in accordance with the first aspect of the invention on the DNA-containing sample obtained from the patient or plurality of patients. In some cases, in accordance with this aspect of the invention, the DNA-containing sample or samples is/are determined to comprise a genetic variant, which is thereby identified as being a genetic variant associated with resistance or response to a therapy.

In another aspect, the present invention provides methods for monitoring or evaluating response to a therapy, wherein the method in accordance with the first aspect of the invention is performed on DNA samples obtained from a patient at different stages of therapy (for example, pre-intervention and during/post intervention).

Comparison of genetic variation in samples taken at different times may reveal changes in response to therapy. For example, genetic variation or the relative frequency of a genetic variant in samples obtained during or after therapy and absent from samples obtained before therapy may reflect e.g. tumour evolution and/or tumour burden, or other biologic responses to therapy.

In another aspect, the frequency of genetic variants, or the ratio of frequencies of different variants, can be used to predict, monitor, or evaluate response to therapy. In another aspect, the presence or the frequency of genetic variants, or the ratio of frequencies of different variants, can be used to predict the risk level or prognosis of a patient if the patient is not treated or if the patient is given one of a set of therapies.

Brief Description of the figures

Figure 1. Graphs showing Distributions of the background noise values of the amplicon sequencing process. (A) the mean, and (B) the coefficient of variation (CV, defined as standard deviation divided by the mean), for different single-nucleotide variants observed in an amplicon sequencing panel.

Figure 2. Graphs showing the cumulative distributions for several base changes, and the cumulative distribution functions for the Normal distribution, and the Beta distribution, fitted using the values for the mean and CV that were calculated for those base changes, compared against the empirical distributions of the data. (A) EGFR_D0016_006_R 55248959 C>G. (B) EGFR_D0016_009_F 55249159 G>T. (C) EGFR_D0016_003_R 55241757 C>A. (D) EGFR_D0016_012_R 55259573 G>C.

Figure 3. Graphs showing cumulative values of the Minimal Detectable Frequencies (MDFs) for different values of CDF_thresh. (B) Zoom in of (A). The vertical line indicates the 97.5 percentile point, for which 97.5% of the possible base changes have lower MDF values. For CDF_thresh = 0.9999, the 97.5 percentile is at allele frequency (AF)=0.0382, indicated by a horizontal line.

Figure 4. Tables 2 and 3, showing results for proof of principle application of the method in a dilution series of cell lines.

Figure 5. Graph showing the probability of a compound mutation detection in multiple reactions, showing the Poisson probability to find at least N number of molecules in the sample as a function of the expected number of molecules (based on the concentration and starting amount of material), the different lines show a different N such that a compound call is made with $\geq N$ positive reactions.

Figure 6. Summary of an exemplary library preparation strategy. TAm-Seq primers are generated with multiple different barcodes. Each barcode combination is dispensed into a separate PCR well. A) The first PCR amplifies the region of interest, and adds molecular identifier tags (barcodes) that identify the reaction from the other replicate amplification reactions that have the same target-specific primers, but different barcodes. B) All PCR products from one sample are pooled and a second round of PCR attaches sequencer specific adapters and sample specific barcodes.

Figure 7. Representation of combination target specific primer barcodes. Each target specific primer was synthesised 7 times with 7 different barcodes. The forward and reverse primers were then combined to produce 49 different well barcode combinations by mixing together each of 7 forward primers with each of 7 reverse primers.

Figure 8. Graph showing the relationship between the probability of a call and the mean number of molecules per reaction. For different values of a MDF (as indicated in the figure legend), the probability of $AF > MDF$ is plotted as a function of the average number of molecules per reaction based on the template dilution. The horizontal line shows probability = 0.90. For $MDF = 0.0382$, a probability of 0.90 that $AF > MDF$ is obtained at an extrapolated $N = 20.59$ (indicated by the vertical line).

Figure 9. Plots showing Mutations identified (true positives (TP)), false positive calls (FP), and mutations missed (false negatives (FN)) by performing the method on a dilution series of DNA from three cell lines. (A) CDF cut-off = 0.9999 on a Beta distribution with $N \geq 2$. (B) CDF cut-off = 0.9999 on a Beta distribution with $N \geq 3$.

Figure 10. Plot showing concordance between expected and measured AF. False negatives are shown as "Not Detected" (ND) on the vertical axis. Expected values are shown as crosses, connected by a dotted line as a guide to the eye.

Detailed description of the invention

The method of the invention uses partitioning of the DNA sample into replicates within which a given variant if present will be at a frequency higher than in the total DNA sample, combined with detection of the mutation in multiple wells/reactions, thereby allowing a variant to be 'called' over error rates inherent in the method used for sequence determination; i.e. the sequencing platform..

Sequencer and polymerase error rates can be determined in various ways well known to those of skill in the art (Tindall, K.R., Kunkel, T.A. Biochemistry 1988 27(16): 6008-13; Forshaw, T. et al. Sci. Transl. Med. 2012 4(136):136ra68). Often these are published, and/or
5 are available from manufacturers. The error rates can then be used to determine the expected frequency at which a genetic variant will be observed due to background noise.

Method error can also be introduced during e.g. library preparation,
10 in the case of NGS methods.

Often, the error differs depending on the position of the base in the molecule being sequenced (see e.g. Loman NJ et al., Nature Biotechnology 30: 434-439, 2012; Forshaw, T. et al. Sci. Transl. Med. 2012 4(136):136ra68). One way to address this is by modelling
15 the noise using parameters such as sequence context (Ross, MG et al., Genome Biology 2013 14:R51), however this is not able to give an accurate value for each possible change at each locus, and fails to account for changing properties of the sequencing system or
20 amplification process over time.

Background frequencies for genetic variants at a particular base can also be determined empirically, by sequencing the region of interest for a reference DNA sample multiple times. For example, the
25 reference DNA sample may be obtained from whole blood, or plasma from healthy subjects, or from a cell line. Results from sequencing the region of interest of the reference sample multiple times can then be used to establish background frequencies for each of four possible bases (A, G, T and C) at each position of the DNA sequence
30 of the region of interest. This allows the frequency at which genetic variants are identified due to the error of the method (i.e. error rates of the DNA sequencing platform used) to be determined for each position of the DNA sequence of the region of interest. In some embodiments, the reference DNA sample may be a 'matched normal'
35 sample. For example, the reference DNA sample may be obtained from the same tissue and/or sample type, from a healthy subject.

In some embodiments of the method of the invention, the mean and variance of the frequency of the genetic variant are determined for a specific panel of amplicons covering the region of interest.

5 'Region of interest' as used herein means the portion or portions of the genome being investigated. It may be a single sequence of DNA or a plurality of sequences of DNA. When the region of interest is a plurality of regions, these may be spread across the genome. That is, 'region of interest' encompasses a plurality of sequences of DNA
10 being investigated being interspersed with portions of the genome which are not being investigated. In some cases the region of interest will depend on, for example, any clinical question being investigated.

15 For example, in some embodiments the region of interest may be a plurality of regions which are known to be or candidates for harbouring disease-associated genetic variants, or genetic variants influencing response to therapy. For example, in some embodiments the region of interest may be a panel of cancer-associated genes.

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The frequency of a given nucleotide at a given position (allele frequency, AF) is determined as the proportion of reads for that position which identify that nucleotide at that position, out of the total number of determinations of the nucleotide at that position.

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The AF for each nucleotide, at each position of the region of interest determined from each sequencing reaction of the reference sample can then be used to calculate the mean AF, and the coefficient of variation (CV) of the AF. The CV of the AF is
30 calculated as the standard deviation of the AF divided by the mean AF.

The mean AF and CV of the AF can then be used to model background noise (i.e. sequencing error) for given genetic variant. For
35 example, a Normal, Beta, Exponential or Gamma distribution or other function can be used to model the background noise for a genetic variant, depending on which model best fits the empirical

distribution of the data. Similarly, the number of mutant reads and sequencing depths can be modelled with discrete functions.

5 Probability distributions and methods of modelling such to data are well known to those of skill in the art. Preferably several distributions will be modelled to AF data and the model with the best fit will be selected as the model for subsequent steps of the method of the invention. For example, different models may be analysed for Kolmogorov-Smirnov values for goodness of fit to the
10 empirical data.

In the Examples below, Beta and Normal probability distributions are used.

15 **Thresholds for determining presence of a genetic variant**

Probability distributions fitted to the empirically determined background error AF and CV values, or based on predicted background error based on the sequencer and polymerase error rates, region of interest and genetic variant, can then be used to establish the
20 threshold AF at or above which a genetic variant must be observed in the sequencing results of a replicate amplification reaction to be determined as being present in the DNA sample, herein referred to as the minimum detectable frequency (MDF).

25 For example, in Example 7 below the AF at z-scores of 20 and 30 were selected. That is, for a genetic variant to be determined as being present in the DNA sample in a given replicate amplification reaction, the frequency of that allele had to be 20 or more, or 30 or more standard deviations above the background mean AF for that
30 particular variant.

Depending on the particular genetic variant in question, the region of interest, the sequencing platform used, etc., various z-score cut-offs are useful with the method of the invention. For example,
35 the z-score threshold can be selected from one of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 19, 20, 22, 24, 26, 28, 30, 35, 40, 45, 50, 60, 70, 80, 90 and 100.

Using probability distributions, the cumulative probability of observing a particular genetic variant at a given AF, when the variant is actually present in a replicate amplification reaction, can be determined. This in turn can be used to establish a threshold frequency a genetic variant must be observed at or above in the products of a replicate amplification reaction to be determined as being present in the DNA sample.

The probability that putative mutations observed in sequencing data at a frequency at or above the MDF are 'real' rather than the result of sequencing error is very high. Such variants can therefore be determined as being present in a given amplification reaction with high confidence.

In some embodiments of the method of the invention, the threshold frequency of step (ii) is determined using a Beta probability distribution model of the background frequencies for genetic variants. Here, for each possible genetic variant at each position of the region of interest, the background mean frequency and variance of the frequency for the genetic variant determined in step (i) are used to define a Beta distribution. The threshold frequency at which a given genetic variant must be observed at or above to be determined as being present in a replicate amplification reaction is the frequency at which the cumulative distribution function (CDF) value of that genetic variant reaches a predefined threshold value (CDF_thresh). In some embodiments, CDF_thresh is 0.99, 0.995, 0.999, 0.9999, 0.99999 or greater.

For example, in Example 6 below, a cumulative probability (based on a Beta distribution) of observing a particular genetic variant a given AF of 0.9999 was used as the threshold AF for a positive determination (i.e. MDF). That is, the probability of observing a given genetic variant in sequencing results for a replicate amplification reaction, where the genetic variant is not present, is 0.01% or less. In some embodiments, the threshold frequency is the frequency at which the cumulative distribution function for the

probability of observing the genetic variant at that frequency (CDF_thresh) is 0.8, 0.85, 0.9, 0.95, 0.96, 0.97, 0.98, 0.99, 0.995, 0.999, 0.9995, 0.9999, 0.99995, 0.99999, 0.999995, 0.999999 or greater, corresponding to a probability of observing the genetic variant in sequencing results for an amplification reaction where the genetic variant is not present of 20%, 15%, 10%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1%, 0.05%, 0.01%, 0.005%, 0.001%, 0.0005%, 0.0001% or less.

In some embodiments, MDF values are determined for a plurality of possible genetic variants and subsequently used to establish an overall MDF for a given region of interest and/or panel of genetic variants of interest. Accordingly, in some embodiments, establishing a threshold frequency at or above which the genetic variant must be observed in sequencing results of amplification reactions to assign a positive determination for the presence of the genetic variant in a given amplification reaction comprises

(a) based on the mean frequency and variance of the frequency determined for the plurality of genetic variants in step (i), establishing a plurality of threshold frequencies at or above which the genetic variants should be observed in sequencing results of amplification reactions to assign a positive determination for the presence of the genetic variant in a given amplification reaction (that is, establishing MDFs for the plurality of genetic variants), and

(b) based on step (a), establishing an overall threshold frequency at or above which a genetic variant must be observed in the sequencing results of a given amplification reaction to assign a positive determination for the presence of the genetic variant in that amplification reaction (that is, establishing an overall MDF), which is the threshold frequency at which at least 90%, 95%, 97.5%, or 99% of the plurality of threshold frequencies determined in step (a) are less than this value.

In some embodiments, the overall MDF is the frequency at which 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 97.5%, 98%, 98.5%, 99%, or 99.5% or more of the MDF values determined for the plurality of

genetic variants are smaller (i.e. less) than the overall MDF.
In some embodiments the overall MDF is determined based on MDF
values established for a plurality of genetic variants distributed
across the region of interest. In some embodiments the plurality of
5 genetic variants will be 5, 10, 20, 25, 30 or more variants.

The threshold for determining the presence of a genetic variant is
selected - in conjunction with the number of copies of DNA template
of the region of interest in a given replicate amplification
10 reaction - to be such that if present, the frequency of the genetic
variant in a given replicate amplification reaction is significantly
higher than the background level for that genetic variation. In this
way presence/absence of the genetic variant in a given amplification
reaction can confidently be determined, minimising the possibility
15 of a false positive determination.

Similarly, the threshold for determining the presence of a genetic
variant is chosen such as to minimise the number of false negative
determinations.

Numbers of amplifiable template molecules per reaction

The lower limit at which a mutation can be identified is determined
by the background frequency of a genetic variant (i.e. observed
frequency due to method error). That is, for example, in a method
25 whereby incorrect determinations are made at a frequency of 5%, real
variants can only be distinguished from errors if their frequency is
substantially greater than 5%.

The present method overcomes this problem by placing an upper limit
30 on the mean number of amplifiable template molecules of the region
of interest in a given replicate amplification reaction.

In the method of the present invention, the mean number of
amplifiable template molecules of the region of interest (Mol_mean)
35 in a given replicate amplification reaction is determined using the
threshold for determining the presence of a genetic variant (MDF),
as follows:

$$\text{Mol_mean} < 1/\text{MDF}$$

Thus a genetic variant, if present in a given replicate
5 amplification reaction, will be expected to be represented (as a
fraction) within the mean total number of amplifiable template
copies of the region of interest within that replicate amplification
reaction at a frequency greater than the threshold frequency for
determining the presence of the genetic variant in a given
10 amplification reaction.

In this way, a single molecule having the variant will have a high
probability of being detected at a frequency which is equal to or
higher than the MDF determined in step (ii).

15 Here, the MDF can be the MDF calculated for a given genetic variant,
or the overall MDF, which is an umbrella value representative of a
plurality of MDFs, and which is described hereinabove.

20 For example, if a given genetic variant can only be confidently
determined as being present in a DNA sample when observed at a
frequency of, e.g. 5% or more (as defined by the MDF), the method
requires that on average, fewer than 20 molecules be present in a
given replicate amplification reaction. In this way, for any given
25 replicate where the genetic variant is present (and up to 19 non-
variant molecules are present), the variant will be observed at a
frequency equal to or greater than 5%.

In the Examples provided below, the distribution of molecules into
30 replicate amplification reactions is modelled with a Poisson
distribution. The probability of positive determination for an
amplifiable molecule having the genetic variant in a given
amplification reaction can be determined based on a Poisson
distribution. Alternatively, the distribution of molecules into
35 replicate amplification reactions could be modelled with a Negative
Binomial distribution.

Accordingly, in some embodiments, Mol_mean is determined using a Poisson distribution to model the number of amplifiable molecules that will be present in a given replicate amplification reaction and the expected mean number of amplifiable molecules. For different possible values of Mol_mean, the cumulative distribution function of the Poisson distribution is calculated. Mol_mean is then selected such that the cumulative distribution function value for the Poisson distribution will be greater than a threshold such as 0.8, 0.85, 0.9, 0.95 or 0.99.

In some embodiments of the method of the present invention the DNA sample is partitioned so that the mean number of amplifiable template molecules per reaction is such based on an expected Poisson distribution of molecules in reactions, a genetic variant if present will be detected more than 90% of the time. This threshold can be higher or lower, and plateaus as the mean number of molecules per reaction decreases to 1 (see e.g. Figure 8). In some embodiments, the mean number of amplifiable template molecules per replicate amplification reaction is selected so that a genetic variant if present will be detected one of more than 80%, more than 81%, more than 82%, more than 83%, more than 84%, more than 85%, more than 86%, more than 87%, more than 88%, more than 89%, more than 90%, more than 91%, more than 92%, more than 93%, more than 94%, more than 95%, more than 96%, more than 97%, more than 98% and more than 99% of the time.

In the interests of efficiency and cost effective use of time and resources, it is preferred that a DNA sample is not partitioned more than necessary to achieve the efficiencies of the method associated with partitioning of template molecules. This has advantages at least in terms of reducing running and materials costs. Of course, the minimum number of molecules per amplification reaction will depend on the genetic variant to be determined, the region of interest, the error of the method (i.e. error rates of the DNA sequencing platform) and calculated thresholds etc. In certain embodiments of the method of the invention, it is preferred that

more than one amplifiable template molecule of the region of interest is provided per replicate amplification reaction.

For example, in some embodiments the mean number of amplifiable template molecules per replicate amplification reaction will be more than 1 and fewer than Mol_mean.

In some embodiments, the mean number of amplifiable template molecules per replicate amplification reaction is more than 1 and less than 1000, more than 1 and less than 750, more than 1 and less than 500, more than 1 and less than 250, more than 1 and less than 200, more than 1 and less than 150, more than 1 and less than 100, more than 1 and less than 80, more than 1 and less than 60, more than 1 and less than 50, more than 1 and less than 40, more than 1 and less than 35, more than 1 and less than 30, more than 1 and less than 29, more than 1 and less than 28, more than 1 and less than 27, more than 1 and less than 26, more than 1 and less than 25, more than 1 and less than 24, more than 1 and less than 23, more than 1 and less than 22, more than 1 and less than 21, more than 1 and less than 20, more than 1 and less than 19, more than 1 and less than 18, more than 1 and less than 17, more than 1 and less than 16, more than 1 and less than 15, more than 1 and less than 14, more than 1 and less than 13, more than 1 and less than 12, more than 1 and less than 11, more than 1 and less than 10, more than 1 and less than 9, more than 1 and less than 8, more than 1 and less than 7, more than 1 and less than 6, more than 1 and less than 5, more than 1 and less than 4, more than 1 and less than 3, or more than 1 and less than 2.

In some embodiments, the mean number of amplifiable template molecules per replicate amplification reaction is more than 2 and less than 1000, more than 2 and less than 100, more than 2 and less than 75, more than 2 and less than 50, more than 2 and less than 40, more than 2 and less than 30, more than 2 and less than 29, more than 2 and less than 28, more than 2 and less than 27, more than 2 and less than 26, more than 2 and less than 25, more than 2 and less than 24, more than 2 and less than 23, more than 2 and less than 22, more than 2 and less than 21, more than 2 and less than 20, more

than 2 and less than 19, more than 2 and less than 18, more than 2 and less than 17, more than 2 and less than 16, more than 2 and less than 15, more than 2 and less than 14, more than 2 and less than 13, more than 2 and less than 12, more than 2 and less than 11, more than 2 and less than 10, more than 2 and less than 9, more than 2 and less than 8, more than 2 and less than 7, more than 2 and less than 6, more than 2 and less than 5, more than 2 and less than 4, or more than 2 and less than 3.

10 In some embodiments, the mean number of amplifiable template molecules per replicate amplification reaction is more than 5 and less than 1000, more than 5 and less than 100, more than 5 and less than 75, more than 5 and less than 50, more than 5 and less than 40, more than 5 and less than 30, more than 5 and less than 29, more than 5 and less than 28, more than 5 and less than 27, more than 5 and less than 26, more than 5 and less than 25, more than 5 and less than 24, more than 5 and less than 23, more than 5 and less than 22, more than 5 and less than 21, more than 5 and less than 20, more than 5 and less than 19, more than 5 and less than 18, more than 5 and less than 17, more than 5 and less than 16, more than 5 and less than 15, more than 5 and less than 14, more than 5 and less than 13, more than 5 and less than 12, more than 5 and less than 11, more than 5 and less than 10, more than 5 and less than 9, more than 5 and less than 8, more than 5 and less than 7, or more than 5 and less than 6.

In some embodiments, the mean number of amplifiable template molecules per replicate amplification reaction is in the range of 2-40, 3-30, 4-30, 5-30, 5-25, 10-25, 15-25, or 18-22.

30

'Partitioning' may be achieved by any means suitable to separate replicate amplification reactions. For example, partitioning can be achieved by aliquoting the (diluted) DNA sample into separate wells. A variety of other methods for compartmentalising into separate (i.e. discrete, individual or independent) replicate amplification reactions will be known to the skilled person.

35

Requiring plural positive replicates for a positive determination

To minimise the probability of a false positive determination of the presence of a genetic variant in a DNA sample, the method of the invention requires a genetic variant to be determined as being
 5 present in more than one replicate.

The mean number of molecules per reaction, and the number of replicate calls needed to minimised false positive calls, determine the number of reactions to be performed to obtain the required sensitivity.

10 The theoretical probability of a false positive occurring in N reactions out of total reactions T (P_{fpNT}) depends on the probability of a false positive in one reaction (P_{fp1T} , which is equal to $1 - CDF_thresh$) and the number of reactions, and is equal to

$$15 \quad P_{fpNT} = ((P_{fp1T})^N) * C_{NT} = ((1 - CDF_thresh)^N) * C_{NT}$$

where C_{NT} is the combinatorial coefficient depending on the total number of reactions T, as follows ("!" indicates the factorial function)

$$C_{NT} = T! / ((T - N)! * N!)$$

20 The total number of false positives expected from this process is equal to the probability of false positives (P_{fpNT}), multiplied by the number of variants examined in this process. For example, when single-nucleotide variants are investigated, this will be the number of positions multiplied by 3 (for the three possible non-reference
 25 alterations).

Requiring a positive determination for the genetic variant in a plurality of replicate amplification reactions reduces the probability of a false positive determination of the genetic variant
 30 being present in the DNA sample. This is clear from the experimental examples below.

The method requiring multiple positive determinations in replicate amplification reactions therefore has higher specificity for the detection of genetic variants.

5 However, requiring a plurality of replicates to be positive for a given genetic variant also increases the probability that a false negative determination will be made. Figure 5 shows the Poisson probability that at least N DNA template molecules will be present in the DNA sample as a function of the expected number of molecules
10 (based on the concentration and starting amount of material).

The number of reactions, and the number of variant molecules in these reactions, should be high enough that, given the random distribution of mutant molecules, the probability that at least the
15 required number of replicates contains one mutant is sufficiently high.

Therefore, the number of positive replicates required for a genetic variant to be determined as being present in a DNA sample in step
20 (vi) will be chosen such as to minimise false positive and false negatives. That is, the number of positive replicates required will be determined to achieve a desired sensitivity and specificity of the method. In some embodiments, the number of positive replicates will be the number which maximises sensitivity and specificity of
25 the method.

The number will always be greater than one. In some embodiments, the number will be 2, 3, 4, 5, 6, 7, 8, 9, or 10 replicates. In certain
30 embodiments, the number will be 2 or 3.

The number may vary depending on the number and size of regions being analysed, the amount of DNA available, the total number of replicate amplification reactions etc.

35 The number may also vary based on the particular type of variation from the reference nucleotide; for example, whether the variant is a transition or transversion from the reference allele.

The number of positive replicates to be required can be determined in part by the total number of replicate amplification reactions for the DNA sample. For example, in some embodiments, for a genetic variant to be determined as being present in a DNA sample in step (vi), a positive determination for the presence of the variant must be made in more than 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or 10% of replicates.

The optimal number of positive replicates to be required - that is to minimise false positives and false negatives - for a given variant and/or region of interest can be determined, for example, by performing the method of the invention on reference DNA samples.

The method of the invention requires integration of the results of presence/absence determinations for replicate amplification reactions for the ultimate determination of the presence/absence of the genetic variant in the region of interest in the DNA sample.

As used herein, 'integrating' means combining or consolidating the results of the presence/determinations for replicate amplification reactions.

Relationship between the variant calling threshold, numbers of amplifiable template DNA molecules and number of replicate amplification reactions

As described above and in the experimental examples below, it will be immediately apparent to the skilled person that the threshold AF for determining the presence of a genetic variant in a replicate amplification reaction, the number of amplifiable template DNA molecules to be present in a given replicate amplification reaction and the number of replicates required to be 'positive' for a genetic variant to be determined as being present in a DNA sample are interrelated.

Essentially, the overriding principle is that the threshold for determining the presence of a genetic variant and the number of

copies of DNA template of the region of interest should be selected such that if present, the frequency of the genetic variant in a given replicate amplification reaction is significantly higher than the background level for that genetic variation, and that the number of replicates to be positive should be selected to optimise sensitivity and specificity of the method.

In this way presence/absence of the genetic variant in a given amplification reaction can confidently be determined, minimising the possibility of a false positive determination.

The relative importance of sensitivity and specificity in establishing these parameters will also depend on the particular investigation. For example, in cases where the method of the invention is being used to identify novel mutations, the principal consideration may be sensitivity. Conversely, where a DNA sample is being analysed for a presence of a variant for informing therapeutic decisions the principal consideration may be specificity.

Tagged Amplicon Deep Sequencing

The method of the invention is suitable for use with high-throughput DNA sequencing methodologies. Advantageously, multiple regions of interest can be screened for mutations in parallel.

In the experimental examples below, the tagged amplicon deep sequencing (TAm-Seq) method is used. The method is described in detail in Forsheew et al. 2012 Sci Transl Med 4(136) 136ra68. TAm-Seq allows amplification and deep sequencing of genomic regions spanning thousands of bases from as little as individual copies of fragmented DNA.

Briefly, primers are designed to generate amplicons that tile regions of interest in segments of a size range selected based on the quality (e.g. average fragment length) of the template DNA, incorporating universal sequencing adapter sequences and to tag each replicates with identifier sequences or 'barcode' (see Figures 6 and

7). The products are then sequenced and identifier sequences are used to demultiplex reads and align them to the genome.

Uses of the method of the invention

5 The method is useful for a wide range of applications, which will be immediately evident to the skilled person. Essentially, the method is useful for the detection of any genetic variant in any sample of interest.

10 For example, the method of the invention is useful in diagnostic and/or prognostic methods, or in microbe or virus analysis.

In particular, the method is useful for the detection of rare genetic variants and/or rare mutations. The method allows detection
15 of variants present at a frequency of less than 1% in the DNA sample. Further, the method is suitable for detecting novel variants at such low frequency, as well as analysing samples for known variants.

20 Accordingly, the method enables earlier identification of the presence of genetic variants that may appear in the body such as in cancer or during pregnancy (i.e. when the genetic variant is present at a lower frequency).

25 In some cases in accordance with the method of any aspect of the present invention, the method comprises assaying a sample that has previously been obtained from a subject. The sample may in general be any suitable biological sample from which DNA can be isolated. In some cases, the sample is selected from the group consisting of:
30 urine, saliva, blood, serum, faeces, other biological fluids, hair, cells and tissues.

In some embodiments in accordance with any aspect of the present invention, the DNA may be treated with bisulphite prior to
35 performing the method. Bisulphite treatment of DNA converts unmethylated cytosine residues to uracil, but leaves methylated cytosine residues unaffected. In this way, the method is useful to

detect variation in DNA methylation.

The ability of the method to detect the presence of variants at low frequency allows analysis of samples obtained by non-invasive and/or minimally invasive means. For example, liquid biopsies, such as blood, plasma, urine, seminal fluid, stool, sputum, pleural fluid, ascetic fluid, synovial fluid, cerebrospinal fluid or bronchial lavage samples. This has the advantage that samples can be taken regularly without great risk or discomfort to the subject.

The sample may be fresh or have been previously stored (e.g. frozen), and/or may have been previously processed.

Moreover, the method is quantitative, allowing accurate measurement e.g. of circulating tumour DNA (ctDNA) mutant levels for clinical correlations or of other DNA, such as viral or microbial DNA.

Quantification can be performed, for example, by counting of the number of molecules determined as having the variant. This is suitable when the number of molecules having the variant is low.

Quantification can also be performed by Poisson correction of the count, or by modelling the observed allele frequencies.

Quantification can also be performed by taking into account the allele frequencies of the genetic variant in each of the plurality of reactions and the relative amounts of template in each reaction, for example by using an average or an average that is weighted by the amounts of material or by considering the fraction of reactions in which the variant was detected for different amounts of starting material.

For example, the method is useful for tumour load monitoring, wherein the method is used to monitor levels of ctDNA mutations, or to monitor reappearance of mutations, to inform as an early indicator of tumour regrowth. The method clearly has diagnostic and prognostic uses.

The method is also useful for monitoring drug resistance and/or tumour evolution in response to therapy. The method is particularly

well suited for assessment of large numbers of regions of interest in parallel, and can be used to detect mutations in likely resistance pathways that might be early indicators of drug resistance. Such uses may be beyond of the capabilities of prior methods.

Furthermore, the method is useful in the primary diagnosis of tumours. The method can be used to look for ctDNA mutations in healthy patients for early diagnosis. For example, key oncogenes and tumour suppressor genes can be monitored.

The method is also useful with samples obtained from healthy subjects, for routine screening of or testing (i.e. monitoring) for genetic variants. In some embodiments the healthy subject may have recovered from a disease, for example the subject may be in remission from a cancer. Alternatively, the healthy subject may be at increased risk of a disease, for example the healthy subject may have a family history of a disease. The method of the invention can be used to routinely screen for genetic variants, optionally for genetic variants known to be associated with a given disease. In this way samples obtained from healthy subjects can be used to detect disease-associated genetic variants before clinical symptoms manifest, thereby facilitating early therapeutic intervention.

The method of the invention is useful for informing therapeutic decisions. That is, identification of genetic variants predictive of susceptibility, resistance or response to therapy can be used to select an appropriate course of treatment for a subject.

By way of example, the T790M mutation in EGFR is known to be associated with resistance to treatment of cancers using the EGFR inhibitors gefitinib and erlotinib. Subjects in which this mutation is identified using the method of the invention would therefore be identified as being unsuitable candidates for treatment using these inhibitors.

Similarly, the V600E mutation in B-Raf is associated with increased sensitivity to B-Raf inhibitors. Subjects in which this mutation is identified using the method of the invention would therefore be identified as good candidates for treatment using these inhibitors.

5

The method can be performed on DNA samples obtained from a subject at different time points, for example at different stages of a disease or course of treatment.

- 10 The method can be used to analyse DNA samples for genetic variation associated with or predictive of susceptibility, progression (i.e. prognosis), resistance or response to a given therapy. For example, the method can be used to identify novel (i.e. previously unidentified) determinants and/or predictors of susceptibility to or
15 prognosis of a disease, or of resistance or response to a therapy.

Being quantitative, the method of the invention is useful for investigating the relative frequency of genetic variants at different stages of disease, in response to treatment and/or in
20 healthy subjects over time.

This information can in turn can be used to inform therapeutic decisions. For example, an increase or decrease in the frequency of a genetic variant known/and or predicted to be associated with e.g.
25 susceptibility or resistance to a particular therapy will guide the decision as to which therapy is most appropriate for the treatment of a given subject.

Examples

30 Example 1 - Determination of background noise

41 amplicons were designed, covering all of *TP53* and hotspot regions in *EGFR*, *KRAS*, *BRAF* and *PIK3CA*, and were read in forward and reverse directions, giving 82 read families in total (Table 1). The amplicons cover 5,038 bases including overlapping forward and
35 reverse reads (excluding primer sequences).

Table 1:

Chromosome	Left coordinate	Right coordinate	Amplicon name
chr7	140453098	140453187	BRAF_D0016_001_F
chr7	140453128	140453217	BRAF_D0016_001_R
chr7	55241589	55241678	EGFR_D0016_001_F
chr7	55241620	55241709	EGFR_D0016_001_R
chr7	55241658	55241745	EGFR_D0016_002_F
chr7	55241659	55241746	EGFR_D0016_002_R
chr7	55241705	55241792	EGFR_D0016_003_F
chr7	55241706	55241793	EGFR_D0016_003_R
chr7	55242385	55242474	EGFR_D0016_004_F
chr7	55242397	55242486	EGFR_D0016_004_R
chr7	55242427	55242516	EGFR_D0016_005_F
chr7	55242448	55242537	EGFR_D0016_005_R
chr7	55248931	55249020	EGFR_D0016_006_F
chr7	55248938	55249027	EGFR_D0016_006_R
chr7	55248989	55249078	EGFR_D0016_007_F
chr7	55249011	55249100	EGFR_D0016_007_R
chr7	55249062	55249151	EGFR_D0016_008_F
chr7	55249101	55249190	EGFR_D0016_008_R
chr7	55249144	55249233	EGFR_D0016_009_F
chr7	55249160	55249249	EGFR_D0016_009_R
chr7	55259388	55259477	EGFR_D0016_010_F
chr7	55259409	55259498	EGFR_D0016_010_R
chr7	55259456	55259545	EGFR_D0016_011_F
chr7	55259485	55259574	EGFR_D0016_011_R
chr7	55259526	55259615	EGFR_D0016_012_F
chr7	55259546	55259635	EGFR_D0016_012_R
chr12	25378518	25378607	KRAS_D0016_001_F
chr12	25378524	25378613	KRAS_D0016_001_R
chr12	25380216	25380305	KRAS_D0016_002_F
chr12	25380248	25380337	KRAS_D0016_002_R
chr12	25398246	25398335	KRAS_D0016_003_F
chr12	25398248	25398337	KRAS_D0016_003_R
chr3	178936028	178936117	PIK3CA_D0016_001_F
chr3	178936046	178936135	PIK3CA_D0016_001_R

Chromosome	Left coordinate	Right coordinate	Amplicon name
chr3	178952022	178952111	PIK3CA_D0016_002_F
chr3	178952056	178952145	PIK3CA_D0016_002_R
chr17	7572903	7572992	TP53_D0016_001_F
chr17	7572942	7573031	TP53_D0016_001_R
chr17	7573904	7573993	TP53_D0016_002_F
chr17	7573930	7574019	TP53_D0016_002_R
chr17	7573975	7574064	TP53_D0016_003_F
chr17	7573988	7574077	TP53_D0016_003_R
chr17	7576789	7576878	TP53_D0016_004_F
chr17	7576828	7576917	TP53_D0016_004_R
chr17	7576873	7576960	TP53_D0016_005_F
chr17	7576874	7576961	TP53_D0016_005_R
chr17	7576996	7577085	TP53_D0016_006_F
chr17	7577026	7577115	TP53_D0016_006_R
chr17	7577074	7577163	TP53_D0016_007_F
chr17	7577093	7577182	TP53_D0016_007_R
chr17	7577434	7577523	TP53_D0016_008_F
chr17	7577439	7577528	TP53_D0016_008_R
chr17	7577484	7577573	TP53_D0016_009_F
chr17	7577523	7577612	TP53_D0016_009_R
chr17	7577561	7577650	TP53_D0016_010_F
chr17	7577578	7577667	TP53_D0016_010_R
chr17	7578120	7578209	TP53_D0016_011_F
chr17	7578124	7578213	TP53_D0016_011_R
chr17	7578173	7578262	TP53_D0016_012_F
chr17	7578189	7578278	TP53_D0016_012_R
chr17	7578228	7578316	TP53_D0016_013_F
chr17	7578229	7578317	TP53_D0016_013_R
chr17	7578343	7578432	TP53_D0016_014_F
chr17	7578361	7578450	TP53_D0016_014_R
chr17	7578407	7578496	TP53_D0016_015_F
chr17	7578434	7578523	TP53_D0016_015_R
chr17	7578483	7578572	TP53_D0016_016_F
chr17	7578492	7578581	TP53_D0016_016_R

Chromosome	Left coordinate	Right coordinate	Amplicon name
chr17	7579284	7579373	TP53_D0016_017_F
chr17	7579319	7579408	TP53_D0016_017_R
chr17	7579364	7579452	TP53_D0016_018_F
chr17	7579365	7579453	TP53_D0016_018_R
chr17	7579405	7579494	TP53_D0016_019_F
chr17	7579444	7579533	TP53_D0016_019_R
chr17	7579488	7579577	TP53_D0016_020_F
chr17	7579527	7579616	TP53_D0016_020_R
chr17	7579677	7579765	TP53_D0016_021_F
chr17	7579678	7579766	TP53_D0016_021_R
chr17	7579816	7579905	TP53_D0016_022_F
chr17	7579839	7579928	TP53_D0016_022_R
chr17	7579887	7579976	TP53_D0016_023_F
chr17	7579892	7579981	TP53_D0016_023_R

Each locus can change to one of three possible non-reference alleles. Excluding known polymorphisms, polymorphisms identified in the cell-lines used, and loci that cannot be modelled, a total of 13,278 possible single-base changes were considered.

Sequencing data for this panel of amplicons was collected from 336 replicate amplifications of LNCaP cell line (a human prostate adenocarcinoma, androgen-sensitive cell line; ATCC CRL-1740) DNA samples.

For each base change in each read family (amplicon and read direction), other than the loci excluded above, the mean allele frequency (AF) and the coefficient of variation (CV) of the AF were calculated. For a given allele (i.e. genetic variant), the AF calculated as the proportion of reads containing this allele out of all the reads in that read family.

Figure 1A shows the number of occurrences of different values of the mean AF, binned by increasing values of the AF. The vertical line indicates mean = 0.00022, which is at the 95% percentile of the distribution.

Figure 1B shows the number of occurrences of different values of CV, binned by increasing values of CV. A vertical line indicates CV = 18.16, which is at the 95% percentile of the distribution.

5

Example 2 - Determining the AF required for a positive call for a base change in a given reaction

A reaction was defined as positive for a given sequence change if the observed AF was found to be greater than the minimal detectable frequency (MDF) for that allele. The MDF for an allele was
10 calculated as the AF at which the cumulative distribution function (CDF) for that particular base change crosses a predefined threshold (CDF_thresh).

15 Figure 2 shows cumulative distributions for several base changes of the panel of Example 1. Cumulative distribution functions for the Normal and Beta distributions are shown, fitted using the values for the mean AF and CV that were calculated for those base changes, compared against the empirical distributions of the data. The
20 Kolmogorov-Smirnov value for goodness of fit for the Normal (KS Normal) and Beta (KS Beta) distributions to the empirical distributions of the data are as follows:

Base change	KS Normal	KS Beta
EGFR_D0016_006_R 55248959 C>G	8.55	0.78
EGFR_D0016_009_F 55249159 G>T	9.26	2.89
EGFR_D0016_003_R 55241757 C>A	9.45	0.96
EGFR_D0016_012_R 55259573 G>C	8.83	0.45

The process described was used to scan 13,278 possible single-base changes in multiple samples. To maintain a low rate of false-positives, mutations were called if present at an AF such that $AF > MDF$ with a $CDF_thresh = 0.9999$.

The background noise was modelled as a Beta distribution, and for each of the 13,278 possible base changes, given the mean AF and CV measured for the base change in the control samples (Figure 1), $MDF(CDF_thresh)$ was calculated, which is the AF at which

$$F(AF|Mean,CV) = CDF_thresh$$

where "F" is the CDF of a Beta distribution.

Figure 3 shows $MDF(CDF_thresh)$ for different values of CDF_thresh (as indicated in the legend). The data in each case is sorted by the values of MDF obtained.

Figure 3B shows a zoom in. The vertical line indicates the 97.5 percentile point, for which 97.5% of the possible base changes have a lower AF value. For $CDF_thresh = 0.9999$, the 97.5 percentile is at $AF = 0.0382$, indicated by a horizontal line.

Thus it was determined that for the 13,278 possible single-base changes, an MDF at $CDF_thresh = 0.9999$ would be 0.0382 or lower for 97.5% of the possible single base changes (see Figure 3).

The probability of a false positive determination for a given base change in each reaction (P_{fp1}), according to this model, is one minus CDF_thresh , which is the value of the CDF at $AF = MDF$:

$$P_{fp1T} = 1 - F(AF = MDF | \text{Mean}, CV) = 1 - CDF_thresh$$

5 Example 3 - Determining the number of replicate amplification reactions to be positive for a given base change to determine presence of the base change in a sample

To minimise false positive determinations for the presence of a base change in a sample, multiple positive replicate amplification
 10 reactions (N) were required out of the total number of replicate amplification reactions for that sample (T).

The theoretical probability of a false positive appearing in N out of T reactions (P_{fpNT}) is

15

$$P_{fpNT} = (P_{fp1T})^N * C_{NT} = ((1 - CDF_thresh)^N) * C_{NT}$$

where " C_{NT} " is the number of possibilities of choosing N wells out of T without attention to order, and is

20

$$C_{NT} = T! / ((T-N)! * N!)$$

where "!" indicates the factorial function.

25 For example, for choosing 3 reactions out of 48 there are 17,296 possibilities. For choosing 2 reactions out of 48 there are 1,128 possibilities. The expected rate of false positives was calculated for each sample and is shown in Tables 2 and 3 (Figure 4).

30 The requirement to observe multiple positive reactions also increases probability of false negatives, and decreases the probability that a true positive will be observed in multiple reactions.

35 Figure 5 shows the Poisson probability of finding at least N number of molecules in the sample as a function of the expected number of molecules (based on the concentration and starting amount of

material). The different lines show a different N such that a compound call is made with $\geq N$ positive reactions.

The system was designed so that

- (i) the total number of replicate amplification reactions (T) for each sample would be much larger than N (here, $T \geq 48$), and
- (ii) the probability of a call in any reaction would be close to 1 if a mutant molecule was present.

Example 4 - Determining the number of amplifiable molecules to be present in each amplification reaction

For an intended dilution rate and the corresponding average number of molecules per reaction, the actual reactions are expected to have a random number of molecules that can be modelled with a Poisson distribution.

A single mutant molecule within each such pool would lead to an observed AF equal to the reciprocal of the number of molecules (assuming that the read fractions are representative of the mutant allele frequency, see Forsheew et al. 2012 Sci Transl Med 4(136) 136ra68, Figure 3B).

For different values of a MDF (as indicated in the figure legend), the probability of $AF > MDF$ was plotted as a function of the average number of molecules per reaction, based on the template dilution (Figure 8).

The horizontal line shows probability = 0.90. For $MDF = 0.0382$ (for which 97.5% of the base changes would pass a $CDF_thresh = 0.9999$, see Figure 3), a probability of 0.90 that $AF > MDF$ is obtained at an extrapolated $N = 20.59$ (indicated by the vertical line).

A dilution rate for the DNA sample was selected so that each amplification reaction would have an expected 20 amplifiable template molecules, such that for each reaction which has an amplifiable mutant molecule present the probability to have a mutant $AF > 0.0382$ would be > 0.9 .

The Poisson probability of observing $\geq N$ molecules in the samples was approximately equal to the probability of a compound call based on identification of the mutant sequence above the background rates in $\geq N$ reactions. The approximate probability of a false negative is calculated for each sample and is shown in Tables 2 and 3 (Figure 4).

Example 5 - PCR primers and design for proof of principle experiments

41 pairs of primers were designed for the panel of 41 amplicons. Each primer was produced with a tagging sequence at the 5' end and one of 7 different barcode sequences in the middle (Figure 6). The target specific primers were split into two optimised multiplex PCR pools, and the forward and reverse primers were pooled in such a way as to produce 49 different barcode combinations (Figure 7) 48 of the primer pools were dispensed into different PCR wells using the Fluidigm platform, to do this in high throughput.

DNA was digitally quantified and added so that an average of 20 molecules would enter each PCR. The Fluidigm Access Array has a 68.32% dead volume which was accounted for when adding the DNA (dead vol = $33\text{nl} \times 48 / 5\mu\text{l}$).

This allowed amplification of 48 separate pools of ~20 molecules per sample. For samples where a low frequency alleles was expected, multiple sets of 48 wells were run.

Following the harvest of this first PCR, a second round of PCR was then performed to attach sequencer adapters and sample barcodes. Libraries were then cleaned and sequenced on both the Illumina MiSeq and HiSeq 2000 sequencers.

Example 6 - Proof of principle in a dilution series of cell lines

A cell line DNA serial dilution was created where heterozygous mutations were expected to be present at an AF between 3-0.04%.

NCI-H1975 and VCAP cell lines have 5 known mutations/SNPs detectable using the primer/amplicon panel described in Example 5 and not present in the LNCaP cell line (Table 4). VCAP, NCI-H1975 and LNCaP DNA were digitally quantified and normalised, and then serially diluted into LNCaP DNA.

Table 5:

Cell line	Gene	cDNA change	Protein change	Genomic change (hg19)
NCI-H1975	EGFR	c.2369C>T	p.T790M	chr7:55249071 C>T
NCI-H1975	EGFR	c.2573T>G	p.L858R	chr7:55259515 T>G
NCI-H1975	TP53	c.818G>A	p.R273H	chr17:7577120 C>T
NCI-H1975	TP53	SNP	rs17880604	chr17:7577644C>G
VCAP	TP53	p.R248W	c.742C>T	chr17:7577539 G>A

The method was performed on a dilution series of two cell lines, on a total of 5 different samples, using different numbers of reactions for different samples (see Tables 2 and 3 (Figure 4)).

The two cell lines differed from LNCaP by 5 single-base polymorphisms in the regions of the genome covered, for a total of 25 positives (50 when calling forward and reverse independently).

To model the background rates, the mean AF and CV at each position in the region of interest were used to estimate parameters and fit a Beta distribution specific for each locus and each possible base change.

Based on the model above and calculations in Tables 2 and 3 (Figure 4), using CDF_thresh=0.9999 and a compound call requiring multiple (N) positive reactions, the following results were obtained.

$N \geq 2$

Overall sensitivity of 0.96, 36 false positive compound calls. Table 2 (Figure 4A) shows sensitivity at different dilution rates.

$N \geq 3$

Overall sensitivity of 0.90, 1 false positive compound call. Table 3 (Figure 4B) shows sensitivity at different dilution rates.

Mutations identified (true positives (TP)), false positive calls (FP), and mutations missed (false negatives (FN)) by performing the method on a dilution series of DNA from two cell lines are shown in Table 4 and Figure 9. Data points in Figure 9 are ordered by increasing measured AF, showing for each mutation the measured AF, except for FN mutations, which show the expected AF.

Figure 10 shows concordance between expected and measured AF Based on compound mutation calls using CDF_thresh=0.9999 and $N \geq 3$. False negatives are shown as "Not Detected" (ND) on the vertical axis. Expected values are shown as crosses, connected by a dotted line as a guide to the eye.

Example 7 - Proof of principle with alternative method of mutation calling

The method was performed on a dilution series as described in

Example 6.

VCAP and NCI-H1975 DNA was diluted serially into LNCaP DNA as shown in Table 6.

Table 6:

Name	% mutant	Mutant mols per reaction	Repeats	Total Mut mols
DIL 3%	3	28.8	1x48=48	28.8
DIL 1%	1	9.6	2x48=96	19.2
DIL 0.33%	0.33	3.20	2x48=96	6.4
DIL 0.11%	0.11	1.07	6x48=288	6.4
DIL 0.037%	0.04	0.36	12x48=576	4.266667

In the first experiment 7(x48) LNCaP, 1(x48) VCAP, 1(x48) NCI-H1975 then 1 or more of the dilutions were sequenced (Table 6, "Repeats").

Mutation calling

- 5 336 LNCaP PCR reactions were used to determine the background AF at each base. A Normal distribution was used to model background for all possible bases from the non-reference base at all positions of the region of interest.
- 10 Each reaction was then screened for changes at each base differing from the background by a specified z-score and depth. Base changes identified a specified number of times above this score were determined to have the mutation.

15 *Results*

Mutation calling was first performed using a z-score cut-off of 20 and 3 positive wells. Table 7 shows mutation detection results.

- All mutations/SNPs were detected down to 0.33%. Of an estimated
20 1,920 molecules screened in the 0.33% dilution (2 samples x 48 wells x 20 DNA molecules), between 4 and 12 positive wells/molecules were detected, corresponding to almost exactly to 0.33% (Table 7, Dil 0.33).

- 25 In the 0.11% dilution 4 of the 5 changes were detected. 1 was missed as only 2 wells were positive (Table 7, Dil 0.11).

- Finally in the 0.037% dilution 1 of 5 mutations was missed entirely; another (chr17:7577644 C>G) was missed in one of the two overlapping amplicons. These results fit with the random
30 distribution of these mutant molecules (Table 7, Dil 0.037).

The 2 false positive reactions were most likely due to polymerase error during early rounds of library amplification. Such errors should typically be at lower frequencies than normal changes.

- 35 By increasing our z-score cut-off to 30 all real changes were kept, and the 2 false positives were removed (Table 7).

Table 7: number of positive reactions determined by z-score greater than 30. For true positives, this number is averaged over the two overlapping amplicons (forward and reverse). False positive calls are shown if at least the minimum of 3 reactions was positive.

Expected changes	NCI-H1975	VCAP	DIL 3	DIL 1	DIL 0.33	DIL 0.11	DIL 0.037
chr17:7577120 C>T	48	0	26	27.5	4	6.5	3
chr17:7577539 G>A	0	48	19.5	18	5.5	2	0
chr17:7577644 C>G	46.5	0	29	22	11.5	3	2.5
chr7:55249071 C>T	47.5	0	21.5	15	6.5	8	4
chr7:55259515 T>G	41	0	17	9.5	8	7	3
False positives							
chr17:7576861 T>C	0	0	0	0	0	2*	0

*called at z-score = 20

Claims

1. A method for detecting a genetic variant in a region of interest in a DNA sample comprising:
 - (i) establishing, for a given sequencing platform, sequencing process and sequencing depth, a threshold frequency at or above which the genetic variant must be observed in sequencing results of amplification reactions to assign a positive determination for the presence of the genetic variant in a given amplification reaction, wherein the threshold frequency is based on the distribution of the number of reads supporting the genetic variant expected to be observed in the sequencing results of amplification reactions due to amplification and sequencing error (read count distribution);
 - (ii) partitioning the DNA sample into a plurality of replicate amplification reactions, so that, for the genetic variant, the mean number of amplifiable template molecules of the region of interest in a replicate amplification reaction is fewer than the reciprocal of the threshold frequency determined in step (i);
 - (iii) performing the amplification reactions of step (ii) and sequencing the products of amplification reactions;
 - (iv) based on step (i) and the results of step (iii), determining the presence/absence of the genetic variant in each replicate amplification reaction; and
 - (v) integrating the results of (iv) to determine the presence/absence of the genetic variant in the region of interest in the DNA sample.
2. The method according to claim 1, wherein for the genetic variant to be determined as being present in the region of interest in the DNA sample in step (v), a positive determination for the presence of the genetic variant must be made in more than one replicate amplification reaction in step (iv), optionally wherein a positive determination for the presence of the genetic variant must be made in at least 3 replicate amplification reactions in step (iv).
3. The method according to any one of the preceding claims, wherein the threshold frequency of step (i) is the frequency at which the cumulative distribution function value for the probability of observing the genetic variant at that frequency is 0.99 or greater, 0.995 or greater, 0.999 or greater, 0.9999 or greater, or 0.99999 or greater.
4. The method according to any one of the preceding claims, wherein threshold frequency of step (i) is determined using a binomial, over-dispersed binomial, Beta, Normal, Exponential or Gamma probability distribution model.
5. The method according to any one of the preceding claims, wherein step (i) comprises:
 - (a) based on the read count distribution for a plurality of genetic variants, establishing a plurality of threshold frequencies at or above which the genetic variants should be observed in sequencing results of amplification reactions to assign a positive determination for the presence of the genetic variant in a given amplification reaction; and
 - (b) based on step (a), establishing an overall threshold frequency at or above which a genetic variant must be observed in sequencing results of a given amplification reaction to assign a positive determination for the presence of the genetic variant in that amplification reaction, which is the threshold frequency at which at least 90%, 95%, 97.5%, 99% or more of the plurality of threshold frequencies determined in step (a) are less than this value.
6. The method according to any one of the preceding claims, wherein the mean number of amplifiable template molecules to be present in a replicate amplification reaction is the number at which when the genetic variant is present in a single amplifiable template molecule of a replicate amplification reaction, the probability that a positive determination will be made for that replicate is 0.9 or greater.

7. The method according to any one of the preceding claims, wherein the method comprises a step of determining, for a given sequencing platform, sequencing process and sequencing depth, the distribution of the number of reads supporting the genetic variant or a plurality of genetic variants expected to be observed in the sequencing results of amplification reactions due to amplification and sequencing error (read count distribution), optionally wherein the method of determining the read count distribution further comprises sequencing a DNA sample multiple times to determine the read count distribution for the genetic variant or a plurality of genetic variants.
8. The method according to any one of claims 1 to 6, wherein the read count distribution is based on sequencer and/or polymerase error rates, optionally taking sequence context into account.
9. The method according to any one of claims 1 to 5, wherein the method comprises 'looking-up' a reference value or plurality of reference values for the read count distribution for the genetic variant or a plurality of genetic variants in a database, chart, table, list, catalogue, index, directory, or register, optionally wherein the reference value or plurality of reference values were determined by sequencing a DNA sample multiple times, to determine the read count distribution for the genetic variant or a plurality of genetic variants.
10. The method according to any one of the preceding claims, wherein following partitioning of the DNA sample in step (ii), each replicate amplification reaction has more than a single amplifiable template molecule for the region of interest per replicate amplification reaction, optionally wherein the mean number of amplifiable template molecules per replicate amplification reaction is more than 1 and less than 1000, more than 2 and less than 1000, or more than 5 and less than 1000.
11. The method according to any of the preceding claims, which is capable of detecting a genetic variant which is present within the population of amplifiable template molecules of a DNA sample at a frequency of less than 2%, less than 1%, less than 0.5%, less than 0.2%, less than 0.1% or less than 0.05%.
12. The method according to any one of the preceding claims, wherein partitioning the DNA sample into a plurality of replicate amplification reactions comprises diluting the DNA sample and aliquoting into replicate amplification reactions.
13. The method according to any one of the preceding claims, wherein replicate amplification reactions are performed in parallel and sequencing of the products of amplification reactions is performed in parallel, optionally wherein amplification reactions are performed using one or more primers flanking the region of interest and which integrate sample and/or amplification reaction replicate specific identifier sequences into the products of amplification, and further optionally wherein the primers integrate sequence adapters into the products of amplification.
14. The method according to any one of the preceding claims, wherein a plurality of regions of interest are analysed in parallel.
15. The method according to any one of the preceding claims, wherein the method further comprises:
 - (vi) determining the frequency of the genetic variant in the DNA sample.
16. Use of the method according to any one of claims 1 to 15:
 - to detect and/or quantify circulating tumour DNA in a sample obtained from a subject;
 - in an in vitro method of diagnosis or prognosis or monitoring a disease;
 - in a method of selecting a patient for a therapy;
 - in a method of identifying genetic variation predictive of susceptibility, resistance or response to a therapy; or
 - to monitor or evaluate response to a therapy.