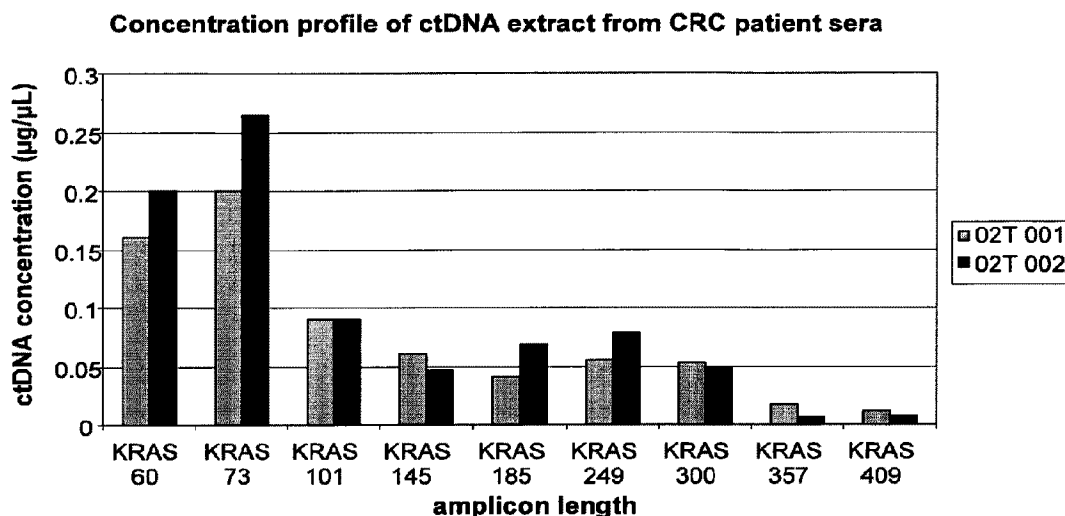




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(54) **Titre : PROCEDES ANALYTIQUES POUR ACIDES NUCLEIQUES ACELLULAIRES ET APPLICATIONS**
(54) **Title: ANALYTICAL METHODS FOR CELL FREE NUCLEIC ACIDS AND APPLICATIONS**



(57) **Abrégé/Abstract:**

The present invention is directed to an in vitro method of detecting cell free nucleic acids, preferably cell free DNA (cfDNA) in a body fluid sample from an individual or a patient, wherein the method comprises the step of accurately and sensitively determining the concentration of cell free nucleic acid in the sample and/or determining the concentration or amount of said cell free nucleic acid of a size range and/or the index of integrity or size fraction ratio (SFR) of said cell free nucleic acid and/or the determination of the presence of genetic polymorphisms (such as known Single Nucleotide Polymorphisms (SNPs) or mutations). The invention encompasses also a method to discriminate body fluid individuals where cfDNA are highly released by comparing the size profile obtained for at least one of three size ranges of cfDNA. The invention also encompasses a method for analysing cell free nucleic acids in individuals for the diagnosis, prognosis or for assessing the evolution of a physiological state, such as the progression of a tumor or metastatic cancer, for monitoring the efficacy of a cancer treatment in a patient or for theragnostic purposes implementing the analysis of these biomarkers.

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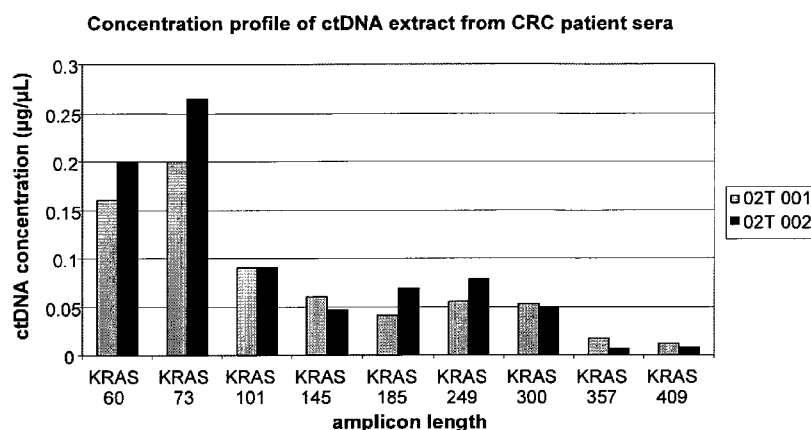
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(54) Title: ANALYTICAL METHODS FOR CELL FREE NUCLEIC ACIDS AND APPLICATIONS

**FIGURE 2A**

(57) **Abstract:** The present invention is directed to an in vitro method of detecting cell free nucleic acids, preferably cell free DNA (cfDNA) in a body fluid sample from an individual or a patient, wherein the method comprises the step of accurately and sensitively determining the concentration of cell free nucleic acid in the sample and/or determining the concentration or amount of said cell free nucleic acid of a size range and/or the index of integrity or size fraction ratio (SFR) of said cell free nucleic acid and/or the determination of the presence of genetic polymorphisms (such as known Single Nucleotide Polymorphisms (SNPs) or mutations). The invention encompasses also a method to discriminate body fluid individuals where cfDNA are highly released by comparing the size profile obtained for at least one of three size ranges of cfDNA. The invention also encompasses a method for analysing cell free nucleic acids in individuals for the diagnosis, prognosis or for assessing the evolution of a physiological state, such as the progression of a tumor or metastatic cancer, for monitoring the efficacy of a cancer treatment in a patient or for therapeutic purposes implementing the analysis of these biomarkers.

ANALYTICAL METHODS FOR CELL FREE NUCLEIC ACIDS AND APPLICATIONS

The present invention is directed to an *in vitro* method of detecting cell free nucleic acids, preferably cell free DNA (cfDNA) in a body fluid sample from an individual or a patient, wherein the method comprises the step of accurately and sensitively determining the concentration of cell free nucleic acid in the sample and/or
5 determining the concentration or amount of said cell free nucleic acid of a size range and/or the index of integrity or size fraction ratio (SFR) of said cell free nucleic acid and/or the determination of the presence of genetic polymorphisms (such as known Single Nucleotide Polymorphisms (SNPs) or mutations). The invention encompasses also a method to discriminate body fluid individuals where cfDNA are highly released
10 by comparing the size profile obtained for at least one of three size ranges of cfDNA. The invention also encompasses a method for analysing cell free nucleic acids in individuals for the diagnosis, prognosis or for assessing the evolution of a physiological state, such as the progression of a tumor or metastatic cancer, for monitoring the efficacy of a cancer treatment in a patient or for theragnostic purposes implementing the
15 analysis of these biomarkers.

In the coming years, the detection of cell free (cf) nucleic acid, such as circulating DNA (cirDNA or "ct DNA"), could become a non-invasive breakthrough technology that will allow the diagnosis of a specific pathological or physiological state,
20 the prognosis and the follow-up of cancer, the choice of therapeutic orientation for each individual patient and the mass screening as a complement to the existing tests. Cell free nucleic acids were proposed as biomarkers for various diseases (cancer, diabetes, Sickle Cell Disease, auto-immune diseases, myocardial infarction, Multiple Sclerosis, ...) and as well for particular physiological conditions such as (intense physical exercise,
25 hemodialysis, pregnancy), or some clinical conditions (trauma, sun burn, sepsis, ...).

They are previously two ways in the literature of using cf nucleic acids as biomarker: first by measuring their concentration and second by studying its nucleotidic sequence.

Cell free or extracellular nucleic acids (DNA or RNA) have been detected in
5 many biological fluids, such as blood, urine, faeces, milk, bronchial lavage and ascite. It is believed that cfDNA found in other body fluids may mainly originate from circulating nucleic acids. Most of the study on cell free nucleic acids were performed by detecting and quantifying circulating DNA (DNA in blood).

Circulating DNA (DNA in blood, cirDNA) was initially found in plasma
10 samples by Mandel and Metais (1) and a long time afterwards, was characterized in plasma samples of cancer patients by Stroun et al (2). The technical progress that has allowed the detection and quantification of specific RNAs or DNAs has made possible to diagnose and follow diseases. CirDNAs carry the genetic alterations associated with the development of some diseases (including cancer) and therefore for more than ten
15 years they have been considered as a potential non-invasive diagnostic marker of different physiological (prenatal test, ...) or pathological (cancer, ...) states.

The detection of genetic alterations in cirDNA seems to be a particularly attractive diagnostic approach (3-5) but at that time limited to costly and time consuming invasive approaches such as DNA sequencing from tumor section. As
20 mutant genes are not only markers of cancer but also the causes, at least partially, of tumour growth, they present advantages in comparison to conventional non invasive markers such as faecal blood or serum PSA. Particularly, conventional markers are not involved in a pathogenic way in the process of tumorigenesis and are less specific for the neoplasia than mutations. The genetic analysis of cirDNA in blood samples will be
25 easy to put in place and might potentially detect different cancers in an early and very sensitive way. Colorectal cancer remains a major problem of public health that has not been solved yet. Only an early screening of the patients at risk (age, heredity, way of life and chronic inflammatory diseases of the colon are the main quoted risk factors) remains one of the safest ways to prevent this disease (6, 7). Therefore, in France, like
30 in most of the industrialized countries, the search for the best mass screening strategy of colorectal cancer is a public health priority. Only one test is at the moment used for the

mass screening of colorectal cancer in subjects older than 50 years: the Hemoccult II[®] test. However, Hemoccult II[®] appears to be of low sensitivity and shows an important rate of false positives and false negatives. A second-line test is colonoscopy which shows a very high sensitivity and specificity and a low, but significant, rate of false
5 negatives. However, this test is invasive and can lead to severe complications (haemorrhage 1/300, perforation 1/800).

It is known that cell-free DNA levels in plasma of colorectal cancer (CRC) patients are significantly higher in patients with CRC compared to healthy patient, decrease progressively in the follow-up period in tumor-free patients, and increase in
10 patients with recurrence or metastasis (22). Thus CRC patient represent a useful model of physiological or pathological conditions resulting or leading to a large cell-free DNA release.

The mechanisms of release of cfDNA are very poorly known, but it has been suggested that necrosis, apoptosis, phagocytosis or active release might be implicated.
15 Tumour development is associated with necrosis of certain parts of the tumour but also of the adjacent, non-tumour tissues. On the other hand, the body defence mechanisms lead to the destruction of cancer cells by phagocytosis or apoptosis. Concerning cirDNA, it has been established that necrosis and phagocytosis lead to DNA degradation down to sizes rarely smaller than 1000 bp (5, 7, 9). In case of apoptosis the
20 region between nucleosomes can be degraded and this leads to the release in the circulation of DNA of the size of 180-200 bp (the size of one nucleosome plus linker) or multiples of that (7).

Many studies have been started in order to identify abnormal forms of DNA in plasma or serum (4, 7). At the moment, there are contradictory results although very
25 high rates of cancer detection have been reported in such a way. These studies, although promising, have led to many questions about the confidence (or: the reliability) of using abnormal cirDNA as a biomarker of cancer (4, 7). Particularly, it is imperative to develop technologies that can detect the number of mutant DNAs and the specific detection of mutation(s) in the same sample. In the case of colorectal cancer, many
30 mutations have been identified and it is now possible to define the sequence of appearance of such mutations; indeed, it seems that the APC gene, then *KRAS* (and

BRAF), then p53 are, among others, the targets of mutations that lead from normal epithelium to adenoma, then to dysplasia and finally to metastatic carcinoma (8-11). It is undeniable to think that this approach will be in the future an efficient diagnostic method. However, at the moment, the tests to detect gene mutation(s) are not sufficiently specific either for diagnostic, theragnostic or prognostic use. Currently, there is no specific test or developed analysis for the detection of free cell nucleic acid, such as cirDNAs. The technology of Quantitative Polymerase Chain Reaction (Q-PCR) is the method of choice for the detection and quantification of genetic variations or mutations. SNPs (Single Nucleotide Polymorphisms) are among the most frequent mutations; they might allow differentiating subjects and can be responsible of tumour progression in many cancers. They correspond to the modification of a single nucleotide thus making difficult the discrimination between the sequence carrying the point mutation and the non-mutated sequence. Consequently, their detection and even more their quantification by Q-PCR are of low specificity and sensitivity.

15

Current cancer therapies are focused on the patient's illness rather than targeted to individual patients. However, inter-individual differences in drug disposition or pharmacokinetics have led to heterogeneity in patient responses to traditional cancer chemotherapy. There remains a need for theragnostic methods capable of rendering cancer therapies that are more accurate, efficacious, and safe for individual patients. In addition, detection of mutations or specific genetic tag (such as polymorphisms) can help in evaluating individual response to numerous therapies such as antibody therapy, cytostatic therapy or antibody dependant cell-mediated cytotoxicity.

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Precise cirDNA size profiling was ascertained in only two publications:

- The team of D. Lo is one of the two top leading teams in the field and has analyzed the size distributions of maternal and fetal DNA in maternal plasma by using Q-PCR assay and primer set design for amplifying sequence from 105 to 798 bp (16). They suggested that "most of the cirDNA molecules were in the range of 145-201 bp" (which is approximately le nucleosome size). In regards to this invention authors did not study or neither discuss on the possibility of existing cirDNA of size below 105 bp.

30

- CirDNA size profile was very recently (January 2010) studied by using a highly performant method: the micro-fluidic single molecule spectroscopy (20). Although size profile shape of cirDNA extracted from stages I and IV lung cancer patient sera is somewhat similar to our results, they concluded that “the greatest distinguishing power occurred at a threshold of 800 bp”. In regards to this invention authors never mention or discuss about ctDNA of size below 320 arguing that “below 320bp the two curves appear similar”.

Before this invention it was not obvious at all that amplicon size <100 bp is better as compared what it was conventionally established. Since it was previously established that shortest cirDNA molecules lengths should theoretically be >180bp (size of a nucleosome) and since PCR efficiency is conventionally (with use of genomic DNA) optimal when amplifying sequence of 150-300 bp range, all the previously described reports showed the use of detection of amplicon of size circa 150 bp when analysing cfDNA. Q-PCR assay was often used as cell free nucleic acids study in the literature. Primer set design was mostly set upon their efficiency in amplifying a targeted nucleic acids region, and sometimes to match with the fact that some reports suggested the high proportion of mononucleosome in cell free nucleic acids (amplification of 100-180 bp nucleic acids region as compared to the 150-300 bp conventionally used range such as for genomic DNA analysis). Among the large literature only a couple of reports described the use of detecting amplified fragments <100 bp solely based on technical aspects linked to primer design and/or specific targeted gene region, but never on the assumption that higher proportion of cirDNA of size <100 bp were present in a particular physiological condition nor pathology.

For instance, Ellinger et al (BJU International, 2009, V.104, 5, 48-52) use a PCR primer system amplifying a 79 bp and a 230 bp region of mitochondrial ctDNA in purpose of determining an integrity index by comparing quantification using PCR system amplifying DNA region of a size shorter and greater size than the size of a mono-nucleosome (180-200 bp). They indicate that the 79 bp primer pair amplified a 79 bp fragment that corresponds to total mtDNA and includes DNA truncated by apoptosis.

Similarly, the same group (Ellinger et al., 2009, V.181, 1, 363-371) quantified a 106, a 193 and a 384 bp ATCB amplicon from ctDNA extracts and obtained similar DNA levels using the primer sets ACTB-106 and 193.

Board et al (Annals of the New York academy of Sciences, 2008, 98-107) quantified by Q-PCR a 77, a 272 and a 512 bp amplicon from ctDNA extracts in the same purpose than Ellinger et al. In.

Koide et al (Prenatal Diagnosis, 2005, V.25, 604-607) quantified a 63, a 107, a 137, a 193, a313, a 392 and a 524 bp amplicon of the SYR gene of cell free circulating fetal DNA in maternal plasma to study the degradation from storage and freezing by examining further fragmentation of said ctDNA.

DNA is a nucleotide chain and the modification or alteration of one or more nucleotides (genetic polymorphisms) in the sequence of a gene can change the message of that gene and lead to a modified or inactive protein. Genetic mutations are the cause or a risk factor in many pathologies and their detection seems to be more and more an efficient way to diagnose, follow and better orient the therapeutic choice for a patient. The technology of Quantitative Polymerase Chain Reaction (Q-PCR) is the method of choice for the detection and quantification of genetic mutations. Point mutations (Single Nucleotide Polymorphisms or SNPs) correspond to the modification of a single nucleotide on one of the two alleles and more rarely on both alleles. This, among other reasons (inherent non-specificity of the Q-PCR technology), leads to a low specificity of Q-PCR for discriminating between sequences with point mutations and the non-mutated sequences that are called «wild type» (WT). On the other hand, the detection of somatic point mutations (that do not interest the reproductive cells, the gametes, and thus are not heritable) should be very sensitive particularly in the case of circulating DNA because it has been established that only 0.1 to 10 % of circulating DNA of an individual with cancer carries the mutation (7). It is for this reason that many modifications of the Q-PCR technology have been described, such as ARMS-PCR, TaqMAMA and FLAG-PCR. These technologies require the use of modified bases, specific enzymes or additional procedures in addition to the reagents.

At the moment, there is no specific test or developed analysis for the detection of cell free nucleic acids, and particularly for detecting mutations such as mutations associated with cancer pathology or with resistance to cancer treatment.

In particular, there is a need to provide a method for the detection of gene mutations such as the ones in the *KRAS* gene using a blood sample. Indeed, colorectal cancer is one of the major cause of cancer and common cause of death from cancer in Europe. In this cancer, targeted therapy has appeared the last past few years with antibodies to epidermal growth factor receptor (EGFR) but numerous studies have shown the benefit of these antibodies limited to patients with wild-type *KRAS* gene only. These findings represent an important step forward in the field of personalized medicine by theragnostic method which can determinate the optimal treatment for each patient in order to avoid overtreatment with drugs that have potentially toxic adverse effects but little benefit.

The detection of cell free nucleic acids has been a frequent topic in the literature now for more than 10 years. However, partially due to the clinical origin of the analysed samples, the origin and form of cell free nucleic acids have been rarely studied systematically.

The authors demonstrated that nucleic fragment size is of crucial importance when analysing cell free nucleic acid and in particular when determining their concentration. They proved that specific detection of mutation by measuring cfDNA concentration is possible in one step by comparing concentration determined by targeting a short (<100 bp) mutated fragment and non-mutated fragment of similar size when both fragment size are <100 bp and of a similar size (+/- 10 %).

This way of identifying the presence or not of a gene mutation is very convenient because it is very fast and not very expensive. Moreover, it allows dispensing with sophisticated techniques like sequencing. On the other hand, sequencing leads to an answer without possible doubts (but for contamination or handling mistakes).

Cell free DNA in a cancer patient is constituted of DNA of tumour and non-tumour origin. Very little is known about the respective contribution of these two types

of cell free DNA during tumour progression. IntPlex should allow advancing on this issue and this information will bring valuable diagnostic and/or prognostic benefits. Indeed, the quantity of mutated, and thus of tumour DNA, can be linked by this method directly to the quantity of non-tumour DNA. The calculation of this percentage can be
5 correlated both with the total quantity of released cirDNA and with the progression or regression of the tumour.

The cirDNA integrity index has been linked to the concentration of mononucleosomes (180-200 bp), i.e., to the estimate of the apoptosis rate. Very few works have described how to calculate the integrity index and usually in a not very
10 rigorous way. This has led to contradictory results concerning the study of its changes during tumor progression (13-19). Moreover, the term integrity seems to be inappropriate if one takes into consideration the fact that very little or no genomic DNA circulates in the blood. If the data of the previously quoted works are contradictory and confusing on the clinical use of the integrity index it is because they did not take into
15 account the possibility that a big proportion of cirDNA is <100 bp.

The inventors, for the first time, have demonstrated the presence of a higher proportion of cirDNA of a size <100 bp that is directly correlated with the increase of the concentration of cirDNA, particularly in samples from cancer patients. The inventors have measured the integrity index by measuring cfDNA concentration with
20 detecting 2 amplified fragments: a short of <100 bp and a long ranging of 250-400 bp. They have demonstrated that it allowed a more specific and sensitive discrimination between cirDNAs of healthy individuals and cancer patients. Then identification of some pathologies (such as cancer) or a specific physiological state (such as intense effort) may be allowed by means here discovered. This was never observed or
25 anticipated before.

By focusing particularly on the study of the size of cell free nucleic acids in order to optimize their measurement and especially the specificity and sensitivity of their detection by Q-PCR, the inventors have developed by means of examples new optimal way(s) or method(s) first for quantifying cell free nucleic acids in body fluid
30 sample, secondly of analysis of genetic polymorphisms, such as mutation of the *KRAS* and *BRAF* genes, in cell free nucleic acids. Third, the inventors have developed an

integrated test which combines as well the estimation of the cell free nucleic acids fragmentation rate (also named “index of integrity” or “apoptosis rate” in the present description) as a third biomarker. Such a detection/quantification of cell free nucleic acids can be a breakthrough technology for the years to come as a non-invasive test that
5 allows the diagnosis, theragnostic, prognosis, follow-up of a disease, and the mass screening as a complement to currently available tests.

The Examples below strongly support the interest of measuring such cell free nucleic acids by the methods of the present invention as an innovative tool in various preclinical and clinical investigations.

10 The inventors propose here to use the technique of quantitative PCR in a one “step” analytical procedure that is specific for the analysis of cell free nucleic acids and leads to a simple, robust, highly sensitive and selective detection/quantification which is compatible with a standardized procedure which could be exploited industrially. It was earlier known that cell free nucleic acids are strongly fragmented down to sizes to
15 180 bp which correspond generally to the length of the sequences amplified by the primers that are usually chosen when optimally using PCR (between 100 and 300 bp). Thus, differently from the analysis of genomic DNA in which the concentration of quantified DNA is directly proportional to the number of amplified copies (of genome), the quantity of circulating DNA determined by Q-PCR is not proportional to the number
20 of copies. Our method takes into account the specificity of size and form of circulating DNA. This allows the precise and direct comparison of the concentration of two different sequences and also the calculation of the percentage of a sequence relative to another. By determining the size profile of cell free nucleic acids present in body fluid sample, the inventors have demonstrated that it is possible to discriminate healthy
25 individuals to individuals exhibiting high level of cfDNA.

Surprisingly, the inventors have demonstrated by using a single-step Q-PCR method, it is possible to determine simultaneously three important bio-markers for the follow up and treatment of cancer: (1) the specific quantity of cell free nucleic acids; (2) the presence of a genetic polymorphism (such as a SNP or a mutation); and (3) the
30 apoptosis rate (also named “integrity index” or “fragmentation rate”).

The method of the present invention presents particularly the following advantages:

- Decreases significantly the time needed for the analysis particularly in comparison to the analysis of a tumor biopsy (no need of the intervention of the anatomo-pathology service, ...).
- Makes easier the sampling and handling of the biological sample.
- Allows the non-invasive analysis of non-accessible tumors.
- Adds two non-negligible clinical parameters, i.e., the quantity of cell free nucleic acids and the apoptosis rate (fragmentation index or index of integrity), the value of which seems to be directly linked to the tumor growth.

The application field of the present invention concerns all utilizations of the detection of cell free nucleic acids such as, but non limited to:

- analysis of parental genes,
- clinical gene analysis (pathologies such as cancer, ...),
- theragnostics, a treatment strategy that allows to orient the therapy in function of a diagnostic marker (i.e. the mutational status of one or several genes),
- analysis of ethnic origins,
- determination of the sex in foetal cirDNA,
- evolution of a particular physiological state.

As discussed above, there are numerous discrepancies about ctDNA size pattern in the literature as formerly mentioned Ellinger et al. The few recent reports studying ctDNA and describing that ctDNA is mainly of low size always indicate that lower size is around the mononucleosome size. This is based on the various and numerous gel electrophoresis analysis which clearly showed an intense band of around 180 bp and a lower of around 360 bp and sometimes a smear at higher size while below 180 bp absolutely no band appears.

Our data on ctDNA size pattern as presented in this invention description clearly disagree with that conclusion. Being confident with our conclusion we demonstrate in

the example VIII that a significant amount of DNA is present in the gel at size below 180 bp.

As a consequence and as demonstrated by the examples below, ctDNA can mainly be of a size lower than 180 bp, and in particular lower than 100 bp.

5 According to the present invention, the inventors propose:

- to determine the quantity or concentration of ctDNA of size lower than 100 bp as an essential parameter of ctDNA analysis
- compare amount of ctDNA from the fraction comprising ctDNA of size lower than 100 bp to the fraction of size between 150 to 400 bp or to the fraction of size higher
10 than 300 or 400 bp.

Thus, in a first aspect, the present invention is directed to a method of quantifying cell free nucleic acids in a body fluid sample, comprising:

- a) identifying a subject of interest;
- 15 b) obtaining a body fluid from said subject;
- c) determining the concentration or amount of said cell free nucleic acid in said body fluid sample, wherein said nucleic acid is in a short size range nucleic acid and has a length inferior to 100 bp, preferably comprised between 40 and 99 bp.

20 By "circa" it is intended here to mean $\pm 10\%$ of the defined value.

In a preferred embodiment, the method of the invention is carried out to determine the concentration/amount of cf nucleic acid size inferior to 100 bp.

In a preferred embodiment, the step c) is carried out by a method implementing the PCR method and wherein the amount/concentration of cf nucleic acid of size <100
25 bp is determined by employing a primer set amplifying a DNA region <100 bp, preferably < 80 bp.

In a preferred embodiment, in step c) the amount/concentration of cf nucleic acid size fractions <100 bp is determined by calculating the difference of those determined by employing 2 sets of primer pairs detecting amplicons of different size, one of the two
30 or both being <100 bp.

In another aspect, the present invention is directed to a method for calculating a cf nucleic acid index of fragmentation by comparing the concentration/amount of size fractions obtained by a method of quantifying cell free nucleic acids in a body fluid according to the invention.

5

In a preferred embodiment, the present invention is directed to a method for determining the specific size profile of cell free nucleic acids in a body fluid sample, comprising:

- a) identifying a subject of interest;
 - 10 b) obtaining a body fluid from said subject;
 - c) determining the specific size profile of said cell free nucleic acid in said body fluid sample by:
 - determining at least the concentration or amount of short nucleic acids having a length inferior to 100 bp, preferably comprised between 40 and 99 bp, and
 - 15 - determining at least the concentration or amount of long nucleic acids having a length superior to 100 bp, preferably comprised between 145 bp and 450 bp,
- or a fraction (ratio) of cfDNA of a specific size range.

By “determining a fraction (ratio) of cfDNA of a specific size range”, it is intended to designate the determination of the ratio between the concentration or
20 amount of cell free nucleic acids having for example a length inferior to 100 bp, preferably comprised between 40 and 99 bp, and the concentration or amount of cell free nucleic acids having a length superior to 100 bp, preferably comprised between 145 bp and 450 bp, or the inverse ratio.

25 More preferably, said cell free nucleic acids which are desired to be quantified by the method of the present invention is a cf nucleic from autosome (or derived from autosome).

By cell free nucleic acids from autosome, it is intended to designate cf nucleic acid not coming or derived from sexual chromosomes.

30

In a preferred embodiment, the present invention is directed to a method of quantifying cell free nucleic acids in a body fluid sample, comprising:

- a) identifying a subject of interest;
- b) obtaining a body fluid from said subject;
- 5 c) determining the concentration or amount of said cell free nucleic acid in said body fluid sample by:
 - determining the concentration or amount of short nucleic acid having a length inferior to 100 bp, preferably comprised between 40 and 99 bp, and/or, preferably and,
 - determining the concentration or amount of a long nucleic acid having a length
 - 10 comprised between 145 bp and 450 bp.

The inventors have demonstrated that the cell free nucleic acid ("cf NA") size profile is specific when cf NA, particularly circulating DNA ("ct DNA") is released at level higher than the normal level being in higher proportion at length inferior to 100 bp and in much lower proportion at length range of 250-400 bp, these characteristics

15 forming part of the present invention.

In a preferred embodiment, said cell free nucleic acid is selected from the group consisting of cell free DNA (cfDNA), cell free RNA, cell free siRNA or cell free miRNA.

In the present invention, the wording "apoptosis rate", "DNA fragmentation index" and "index of integrity" have the same meaning; DNA fragmentation level being the inverse of the index of integrity level.

20

In a preferred embodiment of the method of the present invention, said cell free nucleic acids are circulating nucleic acids.

When the present invention is directed to a method of quantifying cell free nucleic acids in a body fluid sample according to the present invention and comprising the two steps of:

25

- c)i) determining the concentration or amount of short nucleic acid having a length inferior to 100 bp, preferably comprised between 40 and 99 bp; and
- c)ii)-determining the concentration or amount of long nucleic acid having a length
- 30 comprised between 145 bp and 450 bp,

it is preferred that said long cell free nucleic acid partially or fully comprises said short cell free nucleic acid.

In another aspect, the invention encompasses a method for determining the index of integrity of cell free nucleic acid a body fluid sample, said method comprising:

- a) identifying a subject of interest;
- b) obtaining a body fluid from said subject;
- c) determining the index of integrity of cell free nucleic acid in said body fluid sample,

wherein said index of integrity is calculated as the ratio of the concentration or the amount of cell free nucleic acid of a “long” size range and of a “short” size range, said concentrations being determined by the method of quantifying cell free nucleic acid in a body fluid sample according to the present invention,

wherein said nucleic acid short size range has a length inferior to 100 bp, and wherein said long size range being comprised between 180 bp and 450 bp.

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DNA Integrity index (DII)/ DNA Size Fraction Ratio (SFR)

According to the present invention, the inventors want to provide with a new DNA Integrity index calculation which takes account for the first time of the amount of ctDNA size lower than 100 bp. The inventors want also to provide for the first time with the calculation of a DNA Size Fraction Ratio (SFR) which further includes in its calculation the ratio of the amount of ctDNA having a specific size range, such as between 200 and 450 to the amount of ctDNA size between 60 bp and 100 bp or 43 and 100 bp. Integrity index (corresponding to the amount of cf nucleic acid higher than a long length to the amount of cf nucleic acid higher than a shorter length) and SFR (corresponding to the ratio of two size fractions) are both nucleic acid fragmentation indexes.

Thus calculation of integrity index can be done by determining a ratio of the amount of ctDNA size higher or lower than a specific size, or comprised in a specific range of sizes, to the amount of ctDNA size higher or lower than another specific size, or comprised in another specific range of sizes or to the total ctDNA. For instance by

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determining a ratio of the amount of ctDNA size higher than 180-200 bp to the amount of ctDNA size as much as possible lower than 100 bp.

By determining the ratio of quantities determined by using detection of an amplicon of 300 bp and of 60 bp may account of this notion as the value obtained
5 corresponds to the % of the amount of ctDNA higher than 300 bp from the amount of ctDNA higher than 60 bp.

In the present invention, by DNA Integrity index (DII), it is intended to designate the new DNA Integrity index calculation which takes account of the amount of ctDNA size lower than 100 bp.

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In examples XI to XV below, the inventors have determined this new DNA Integrity index calculation or DNA Size Fraction Ratio (SFR) by calculating the ratio of the amount of ctDNA size higher than 200 to the amount of ctDNA size between 60 bp and 100 bp or 43 and 100 bp. This new calculation determining the amount of ctDNA of
15 size as much as possible lower than 100 bp allow to more precisely estimate ctDNA fragmentation level, which is more accurate in particular for distinguishing cancer patient plasma to healthy individuals.

Such new DNA Integrity index calculation or DNA Size Fraction Ratio (SFR)
20 calculation can be carried out in the present invention by a method non-implementing the polymerase chain reaction (PCR) such as capillary zone electrophoresis, chip-based capillary electrophoresis or mass spectroscopy or by a method implementing the polymerase chain reaction (PCR) such as quantitative real-time polymerase chain reaction (Q-PCR) method.

25 When the PCR such as Q-PCR, is implemented, detecting an amplicon having X bp corresponds in fact to quantify all the ctDNA fragments having a size superior or equal to X bp.

In a similar way, when the PCR such as Q-PCR, is implemented, detecting an amplicon having X bp corresponds in fact to quantify all the ctDNA fragments having a
30 size superior or equal to X bp.

When the Q-PCR is implemented, detecting an amplicon having a size inferior to 100 bp corresponds in fact to quantify all the ctDNA fragments having a size superior or egal to this size. Consequently these amplicons having a size inferior to 100 bp have to be taken account in the total ctDNA quantification.

- 5 For instance, when the Q-PCR is implemented, detecting an amplicon having a size egal to 60 bp corresponds in fact to quantify all the ctDNA fragments having a size superior or egal to 60 bp, corresponding to the maximal concentration/quantification of ctDNA.

 In another aspect the present invention is directed to a method for determining
10 tsaid DNA Size Fraction Ratio (SFR) of cell free nucleic acid in a body fluid sample, said method comprising:

- a) identifying a subject of interest;
 - b) obtaining a body fluid from said subject;
 - c) determining the Size Fraction Ratio (SFR) of cell free nucleic acid,
- 15 wherein said SFR is calculated as the ratio of the amount of ctDNA having a specific size or range of specific sizes to the amount of ctDNA having another specific size or rang or specific sizes.

 In another aspect the present invention is directed to a method for determining
20 the said DNA integrity index (DII) new calculation or DNA Size Fraction Ratio (SFR) of cell free nucleic acid in a body fluid sample, said method comprising:

- a) identifying a subject of interest;
 - b) obtaining a body fluid from said subject;
 - c) determining the DII or Size Fraction Ratio (SFR) of cell free nucleic acid,
- 25 wherein said DII or SFR is calculated as the ratio of the amount of ctDNA size higher than 200 to the amount of ctDNA size between 60 bp and 100 bp or 43 and 100 bp or 60-145 bp.

 In a preferred embodiment of the method for determining the index of integrity of cell free nucleic acid or SFR in a body fluid sample of the present invention, said
30 long size range cell free nucleic acid partially or fully comprises said short size range cell free nucleic acid.

In a preferred embodiment of the method for determining the index of integrity or SFR of the present invention, said long size range being comprised between 250 bp and 350 bp and said short size range being comprised between 50 bp and 99 bp.

5 In a preferred embodiment of the method of the present invention, the concentration of cell free nucleic acid or the index of integrity or SFR of cell free nucleic acid is determined by a method non-implementing the polymerase chain reaction (PCR) such as capillary zone electrophoresis, chip-based capillary electrophoresis or mass spectroscopy.

10 Such methods are well known from the skilled person (see for example “Comparisons between capillary zone electrophoresis and real-time PCR for quantification of circulating DNA levels in human sera”, Fuming Sang et al., Journal of Chromatography B Volume 838, Issue 2, 11 July 2006, Pages 122-128; “Prenatal diagnosis of -thalassemia by chip-based capillary electrophoresis”, Hua Hu et al.,
15 Prenatal Diagnosis, Volume 28 Issue 3, Pages 222–229, 2008).

In a more preferred embodiment of the method of the present invention, the concentration of cell free nucleic acid or the index of integrity or SFR of cell free nucleic acid is determined by a method implementing the polymerase chain reaction (PCR).

20 In this more preferred embodiment, the PCR method is selected from the group consisting of the quantitative real-time polymerase chain reaction (Q-PCR) method.

PCR or Q-PCR methods are standard methods well known from the skilled person.

25 Among particular PCR or Q-PCR methods, the “allele specific PCR” method, the “allele specific Q-PCR” method or the “allele specific Q-PCR using blocker oligonucleotides” method can be particularly cited.

Thus, when the concentration of cell free nucleic acid is determined by a method implementing the polymerase chain reaction (PCR), the present invention is also directed to a method of quantifying cell free nucleic acids in a body fluid sample,
30 comprising:

a) identifying a subject of interest;

- b) obtaining a body fluid from said subject;
- c) - determining the concentration of amplified short fragment from cell free nucleic acid in said body fluid sample, wherein said nucleic acid short fragment has a length inferior to 100 bp, preferably comprised between 40 and 99 bp, and/or
- 5 - determining the concentration or amount of amplified long fragment from cell free nucleic acid in said body fluid sample, wherein said long fragment has a length superior or equal to 100 bp, preferably comprised between 145 bp and 450 bp.

In a preferred embodiment, said step c) is a step of:

- c) determining the amount of cell free nucleic acid in said body fluid sample, by
- 10 subtracting the value resulting from the amplification of a fragment >100 bp from that of a fragment <100 bp, preferably of a fragment of 100-145 bp range from that of a fragment of 60-99 bp range.

More preferably, said amplified short fragment from cell free nucleic acid has a length comprised between 55 and 65 bp, circa 60 bp ($60 \text{ bp} \pm 6 \text{ bp}$) being the most

15 preferred.

When the present invention is directed to a method of quantifying cell free nucleic acids in a body fluid sample according to the present invention by a method implementing the polymerase chain reaction (PCR), and comprising the two steps of:

- c)i) determining the concentration or amount of amplified short fragment; and
 - 20 c)ii)-determining the concentration or amount of amplified long fragment,
- it is preferred that said amplified long fragment partially or fully comprises the short fragment.

In a same aspect, when the index of integrity or SFR of cell free nucleic acid is

25 determined by a method implementing the polymerase chain reaction (PCR), the present invention is also directed to a method for determining the index of integrity of cell free nucleic acid a body fluid sample, said method comprising:

- a) identifying a subject of interest;
- b) obtaining a body fluid from said subject;
- 30 c) determining the index of integrity or SFR of cell free nucleic acid in said body fluid sample,

wherein said index of integrity or SFR is calculated as the ratio of the concentration of amplified long fragment and amplified short fragment from said cell free nucleic acid, wherein said short fragment has a length inferior to 100 bp, and wherein said amplified long fragment being comprised between 180 bp and 450 bp.

5 In a preferred embodiment of the method for determining the index of integrity or SFR of the present invention implementing the polymerase chain reaction PCR, said amplified long fragment being comprised between 250 bp and 350 bp and said amplified short fragment being comprised between 50 bp and 99 bp.

10 In a preferred embodiment of the method according to the present invention for determining the index of integrity or SFR of cell free nucleic acid in a body fluid sample, said amplified long fragment partially or fully comprises the short fragment.

 In a more preferred embodiment of the method for determining the index of integrity or SFR of the present invention, said amplified long fragment fully or partially comprises said short fragment.

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 In another aspect, the present invention encompasses a method for the detection of a genetic polymorphism, such as mutation or SNP, wherein said method comprises the steps of:

- a) identifying a subject of interest;
- 20 b) obtaining a body fluid from said subject;
- c) determining the concentration of amplified short fragment from cell free nucleic acid in said body fluid sample, wherein said cell free nucleic acid short fragment which is amplified contains said genetic polymorphism to be detected, and wherein said amplified acid short fragment has a length inferior to 100 bp, preferably comprised
- 25 between 40 and 99 bp. More preferably said amplified short fragment containing said genetic polymorphism to be detected has a length comprised between 55 and 65 bp, circa 60 bp being the most preferred.

 In a preferred embodiment, the present invention is directed to a method for the qualitative detection of the presence of a genetic polymorphism on a free cell nucleic

30 acid, said method comprising the steps of:

- a) determining the concentration or amount of cell free nucleic acids in a body fluid sample; b) determining the qualitative detection of the presence of genetic polymorphism by integrating the following parameters and the following step:
- A1A2 in one hand and B1B2 in another hand are the representation of two short sequences;
 - given the sequence length of A1A2 and B1B2 ranging between 50 to 100 bp, and being different in length from +/- 20%;
 - either A1A2 or B1B2 comprising the genetic polymorphism;
 - given CB1B2 and CA1A2 respectively the measured initial concentration of corresponding extracted nucleic acid by detecting the short fragment B1B2, and the short fragment A1A2, respectively,
- i) calculating the $\% \text{ CB1B2/CA1A2}$, where B1B2 is defined as the sequence containing the genetic polymorphism; or
 - ii) calculating the $\% \text{ CA1A2/CB1B2}$ where A1A2 is defined as the sequence containing the genetic polymorphism,
- optionally, the determination that $\% \text{ CB1B2/CA1A2}$ or $\% \text{ CA1A2/CB1B2}$ is higher than a specific threshold being significant of the qualitative detection of the presence of genetic polymorphism.
- Preferably, in step ii), and same %'s being the quantitative detection of mutated cf nucleic acid fragments.

- In a preferred embodiment, the present invention is directed to a method for the qualitative detection of the presence of a genetic polymorphism on a free cell nucleic acid, said method comprising the steps of:
- a) determining the concentration or amount of cell free nucleic acids in a body fluid sample by a method of quantifying cell free nucleic acids according to the present invention and wherein the concentration or amount of cell free nucleic acids is determined by a method implementing PCR;
 - b) determining the qualitative detection of the presence of genetic polymorphism by integrating the following parameters and the following step:

- A1A2 in one hand and B1B2 in another hand are the representation of two short amplified sequences;
 - given the sequence length of A1A2 and B1B2 ranging between 50 to 100 bp, and being different in length from +/- 20%;
 - 5 - either A1A2 or B1B2 comprising the genetic polymorphism;
 - given CB1B2 and CA1A2 respectively the measured initial concentration of corresponding extracted nucleic acid by detecting the amplified short fragment B1B2, and the amplified short fragment A1A2, respectively,
 - i) calculating the % CB1B2/CA1A2, where B1B2 is defined as the amplicon
 - 10 sequence containing the genetic polymorphism; or
 - ii) calculating the % CA1A2/CB1B2 where A1A2 is defined as the amplicon sequence containing the genetic polymorphism,
 - optionally, the determination that % CB1B2/CA1A2 or % CA1A2/CB1B2 is higher than a specific threshold being significant of the qualitative detection of the presence of
 - 15 genetic polymorphism.
- Preferably, in step ii), and same %'s being the quantitative detection of mutated cf nucleic acid fragments.

In a preferred embodiment, the positivity threshold is determined for each

20 mutation using a convenient number of known samples, more preferably the positivity threshold is at least 2 %, 5 %, 7 %, 8 %, 9 %, 10 %, 12,5 %, 15 %.

Also forms part of the present invention a method for the qualitative detection of the presence of a genetic polymorphism on a free cell nucleic acid according to the invention and wherein nucleic acid corresponding with the genetic polymorphism of

25 interest on the coding strand is located and the 3'-end extremity of the primer starting at position B1 or A2, and wherein the method implementing PCR is an allele specific PCR.

In a preferred embodiment, said genetic polymorphism to be detected is an inherited genetic polymorphism or a somatic genetic polymorphism.

30 By genetic polymorphisms, it is intended to designate particularly, but not to limit to:

- genetic polymorphisms able to discriminate individual or ethnic population,
- genetic polymorphisms in non coding region having an impact in a biological function,
- genetic polymorphisms due to post transcriptional modification such as RNA editing
- 5 or
- genetic polymorphisms in coding region such as a mutation implying modification of the protein sequence.

Among these genetic polymorphism, are preferred the genetic polymorphism of
10 a nucleic acid selected from the group consisting of genetic polymorphism associated with a pathology or a physiological state, or specific genetic polymorphisms in the nucleic acid, particularly in exonic, intronic or in non-coding regions of the nucleic acid sequence.

15 Is also encompassed by the present invention a method preferably implementing the PCR, particularly the Q-PCR, for the detection genetic polymorphism in said cell free nucleic acid in a body fluid sample and for determining the index of integrity or SFR of cell free nucleic acid, said method comprising the step of:

- implementing the method for the detection of a genetic polymorphism according
- 20 to the present invention in said cell free nucleic; and
- implementing the method according to the present invention for determining the index of integrity of said cell free nucleic acid.

In a preferred embodiment, said method comprises the step of implementing the
25 method of the invention for determining the index of integrity or SFR of cell free nucleic acid in a body fluid sample, wherein in said method:

- said amplified long fragment comprises a short non-mutated fragment and the short mutated fragment containing said genetic polymorphism (such as a SNP or a mutation)
- 30 to be detected; and

- said amplified long fragment being comprised between 250 bp and 350 bp and said amplified short fragments being inferior to 100 bp and preferentially comprised between 50 bp and 99 bp.

More preferably, said amplified mutated and non-mutated fragment have a
5 length comprised between 55 and 65 bp, circa 60 bp being the most preferred.

More preferably, in the method for determining the index of integrity or SFR of cell free nucleic acid in a body fluid sample, said amplified long fragment partially or fully comprises two short fragments, one of the short amplified fragment containing a genetic polymorphism.

10 By partially comprising a fragment, it is intended to designate herein that the long fragment contains at least 10 consecutive bp, more preferably 15, 20, 25, 30, 35 or 40 consecutive bp of the referenced short fragment.

In an also preferred embodiment of the method of the present invention, the concentration of said cf nucleic acid fragment of said cell free nucleic is calculated for
15 an mutated cf nucleic acid fragment and/or an non-mutated cf nucleic acid fragment.

By mutated fragment and non-mutated fragment, it is intended to designate herein a fragment exhibiting and not exhibiting respectively the genetic polymorphism which is desired to detect in the method of the present invention.

In a preferred embodiment of said above method of the invention, the ratio of the
20 concentration of long fragments and short fragments is calculated for the mutated short fragments and/or an non-mutated short fragments.

In a particular embodiment, the method of the present invention further comprising a step of determining the concentration of cell free nucleic acid fragments presenting a specific genetic polymorphism, said fragments exhibiting the genetic
25 polymorphism having a defined length and wherein said concentration is compared to the concentration of a non-mutated fragments, said non-mutated fragments having circa the same length of the mutated fragments, preferably the length mutated or non mutated amplified fragments can be similar in length + or - 20%.

In an also preferred embodiment of the method for the detection of a specific
30 genetic polymorphism of the present invention, said method further comprises:

- a step of determining the concentration in the cell free nucleic acid extract of non-mutated fragment and mutated fragment; and
 - calculating the percentage of the amount of short mutated fragments relative to the short non-mutated fragments obtained or not, the subject being considered as having
- 5 said genetic polymorphism (such as SNP or mutation) whether said calculated percentage is greater than a threshold value associated to said genetic polymorphism.

When the method implementing the PCR, particularly the Q-PCR, for the detection of genetic polymorphism in said cell free nucleic acid in a body fluid sample, in an also preferred embodiment of the method of the present invention, the

10 concentration of said amplified fragment of said cell free nucleic is calculated for an amplified mutated fragment and/or an amplified non-mutated fragment.

By mutated fragment and non-mutated fragment, it is intended to designate herein a fragment exhibiting and not exhibiting respectively the genetic polymorphism which is desired to detect in the method of the present invention.

15 In a preferred embodiment of said above method of the invention, the ratio of the concentration of amplified long fragment and amplified short fragment is calculated for the amplified mutated short fragment and/or an amplified non-mutated short fragment.

In a particular embodiment, the method of the present invention further comprising a step of determining the concentration of amplified fragment of cell free

20 nucleic acid presenting a specific genetic polymorphism, said amplified fragment exhibiting the genetic polymorphism having a defined length and wherein said concentration is compared to the concentration of a non-mutated amplified fragment of free cell nucleic acid, said non-mutated fragment having circa the same length of the mutated fragment, preferably the length mutated or non mutated amplified fragments

25 can be similar in length + or - 20%.

In an also preferred embodiment of the method for the detection of a specific genetic polymorphism of the present invention implementing the , said method further comprises:

- a step of determining the concentration in the cell free nucleic acid extract of amplified
- 30 non-mutated fragment and mutated fragment; and

- calculating the percentage of the amount of short amplified mutated fragment relative to the short amplified non-mutated fragment obtained or not, the subject being considered as having said genetic polymorphism (such as SNP or mutation) whether said calculated percentage is greater than a threshold value associated to said genetic polymorphism.

In another aspect particularly preferred, the present invention is directed to a method for the analysis of cell free nucleic acid, particularly circulating DNA, in an individual, said method comprising the steps of:

- a) the quantification of said free cell nucleic acid according to the invention by a method implementing the quantitative real-time polymerase chain reaction (Q-PCR); and
- b) the determination of the integrity index of said free cell nucleic acid according to the invention by a method implementing the Q-PCR; and
- c) the detection of the presence of a genetic polymorphism on said free cell nucleic acid according to the invention by a method implementing the Q-PCR.

In a preferred embodiment, said nucleic acid is nucleic acid carrying tumor-associated genetic alterations.

- More preferred are nucleic acids selected from the group consisting of:
- the *RAS* family gene, preferably *KRAS* or *NRAS*, carrying tumor-associated genetic alterations, preferably CRC-associated genetic alterations; and
 - the *BRAF* gene.

By body fluid sample, it is intended and preferred to designate the body fluids selected from the group consisting of whole blood, serum, plasma, urine, sputum, colonic effluent, bone marrow, lymph, cerebrospinal fluid, lacrymal fluid, sweat, milk, faeces, bronchial lavages and ascites.

In a preferred embodiment, the body fluid sample is blood sample selected from the group consisting of plasma and serum.

- In an also preferred embodiment of the method of the present invention, said cell free nucleic acid is selecting from the group of endogenous or exogenous cell free

nucleic acid, particularly exogenous cell free nucleic acid selected from the group consisting of cell free nucleic acids originating from viruses, bacteria, fungus, foetus and xenografts.

Among the endogenous cell free nucleic acid from a subject of interest, it is preferred that said subject of interest is a subject suffering from or at risk for developing a disease or exhibiting a physiological state or condition.

In a preferred embodiment, said disease is a cancer, more preferably but not limited to a cancer selected from the group of colorectal cancer, lungs cancer, breast cancer, prostate cancer, gynaecologic cancer, head and neck cancer, thyroid cancer, pancreatic cancer, liver cancer or hematopoietic cancers.

In an also preferred embodiment, said cancer is a metastatic cancer.

In another aspect, the present invention is directed to a method to identify or to analyse body fluid (preferably plasma) of cancer patient from body fluid (preferably plasma) from healthy individual wherein said method comprises the steps of:

- a) quantifying the cell free DNA (cfDNA) in the two body fluid samples by a method of the present invention, cfDNA of size within the 50-100 bp range and of size superior to 101 bp;
- b) comparing the ratio obtained between the level of these two fragment ranges for each of the two body fluid sample and wherein a ratio long/short size range <1 , and preferably <0.75 being indicative of presence of a tumor.

The present invention is directed to a method to identify whether a body fluid (preferably plasma) sample of an individual is from a cancer patient or from healthy individual wherein said method comprises the steps of:

- a) quantifying the cell free DNA (cfDNA) in the body fluid sample by a method of the present invention, cfDNA of size within the 50-100 bp range and of size superior to 101 bp;
- b) calculating the ratio obtained between the level of these two fragment ranges for said body fluid sample and wherein a ratio long/short size range <1 , and preferably <0.75 being indicative of presence of a tumor.

In a preferred embodiment, the present invention is directed to a method to identify or to analyse body fluid (preferably plasma or serum) of cancer patient from body fluid (preferably plasma or serum) from healthy individual wherein said method comprises the steps of:

- 5 a) quantifying the cell free DNA (cfDNA) in the two body fluid samples by a method of the present invention, cfDNA of size within the 50-100 bp range and of size within the range of 100 to 145 bp; preferably within the 73-99 bp range and of size within the range of 100-120 bp;
- b) comparing the ratio obtained between these two fragments for each of the two body
10 fluid sample and wherein a ratio long/short size range <1 , and preferably <0.5 being indicative of presence of a tumor.

In another aspect, the present invention is directed to a method to identify or to analyse body fluid (preferably plasma or serum) of cancer patient from body fluid
15 (preferably plasma or serum) from healthy individual wherein said method comprises the steps of:

- a) quantification of the cell free DNA (cfDNA) in the two body fluid samples by a method of the present invention, cfDNA of size <249 bp and of size >249 bp, preferably cfDNA of size <100 bp and of size within the range of 249-409 bp, and more preferably
20 within the 73-100 bp range and of size within the range of 300-357 bp;
- b) comparing the ratio obtained between these two fragments for each of the two body fluid sample and wherein a ratio long/short size range <0.5 , and preferably <0.1 being indicative of presence of a tumor.

25 In another aspect, the present invention is directed to a method to identify or to analyse body fluid (preferably plasma or serum) of cancer patient from body fluid (preferably plasma or serum) from healthy individual wherein said method comprises the steps of:

- a) quantification of the cell free DNA in the two body fluid samples by a method of the
30 present invention, wherein the cfDNA fragments whose concentration are determined

for each body fluid sample are long fragments superior to 180 bp in length and short fragments inferior to 100 bp in length;

- b) comparing the ratio obtained between these two fragments concentrations for each of the two body fluid sample and wherein a ratio long/short <0.4 , and preferably <0.1 being indicative of presence of a tumor.

In another aspect, when PCR, particularly the Q-PCR, is implemented, the present invention is directed to a method to identify or to analyse body fluid (preferably plasma or serum) of cancer patient from body fluid (preferably plasma or serum) from healthy individual wherein said method comprises the steps of:

- a) quantification of the cell free DNA in the two body fluid samples by a method of the present invention, wherein the amplified fragments whose concentration are determined for each body fluid sample are long fragments superior to 180 bp in length and short fragments inferior to 100 bp in length;
- b) comparing the ratio obtained between these two fragments concentrations for each of the two body fluid sample and wherein a ratio long/short <0.4 , and preferably <0.1 being indicative of presence of a tumor.

In another aspect, the present invention is directed to a method to identify or to analyse body fluid (preferably plasma) of cancer patient from body fluid (preferably plasma) from healthy individual wherein said method comprises the steps of:

- a) quantification of the cell free DNA (cfDNA) in the two body fluid samples by a method of the present invention, cfDNA of size >145 bp;
- b) calculating the percentage of cfDNA quantity obtained from the total cfDNA quantity wherein % is below 20 %, preferably % being indicative of presence of a tumor.

In another aspect, the present invention is directed to a method to identify or to analyse body fluid (preferably plasma) from individuals where cfDNA are highly released, such as cancer patients from body fluid (preferably plasma) from healthy individual wherein said method comprises the steps of:

- a) quantifying the cell free DNA (cfDNA) in the two body fluid samples by a method of the present invention, cfDNA of size range 60-80 bp, 100-145 bp and 180-400 bp;

b) directly comparing the three quantification levels obtained between healthy and non healthy individual.

The inventors discovered that there are three range of cfDNA size by which
5 concentration/amount can be determined, which can identify, analyse or discriminate
between cfDNA from healthy subject and cfDNA from individuals where cfDNA are
highly released, such as cancer patients. The size range being 60-80 bp, 100-145 bp and
180-400 bp. Diagnostic, prognostic, theragnostic, or evolution of a specific
physiological state might assessed by comparing cfDNA size profile; preferably by
10 combining at least three concentration values obtained when targeting circa 70bp, circa
100 bp and circa 300 bp fragments; and preferably by combining them in a logistic
(logarithmic) function.

Thus, in another aspect, the present invention is directed to a method to
discriminate body fluid (preferably plasma) from individuals where cfDNA are highly
15 released, such as cancer patients from body fluid (preferably plasma) from healthy
individual wherein said method comprises the steps of:

- a) quantifying the cell free DNA (cfDNA) in the two body fluid samples by a method
of the present invention, cfDNA of size range 60-80 bp, 100-145 bp and 180-400 bp;
- b) determining a size profile by using these three values as parameters in a logistic
20 function.

In a same aspect, the present invention is also directed to a method to
discriminate body fluid (preferably plasma) from individuals where cfDNA are highly
released, such as cancer patients from body fluid (preferably plasma) from healthy
individual wherein said method comprises the steps of:

- 25 a) quantifying the cell free DNA (cfDNA) in the two body fluid samples by a method of
the present invention, cfDNA at various size between 50-400 bp range;
- b) comparing the size profile obtained for these three ranges of size between the two
body fluid samples, preferably by combining at least three concentration values
obtained when targeting circa 70 bp, circa 100 bp and circa 300 bp fragments; and
30 preferably by combining them in a logistic function such as a logarithmic function.

In a same aspect, the present invention is also directed to a method to discriminate in a biological sample/fluid mutated cf nucleic acid fragment from non-mutated cf nucleic acid fragment, said method comprising the steps of:

determining and comparing the ratio of the concentration of long fragments and short fragments calculated for the mutated fragment and for the non-mutated fragment, and wherein in said method:

- said ratio being compared at various size between 50-450 bp range, preferably said long fragment being comprised between 200 bp and 450 bp, with preferably at least two concentrations values, such as circa 200 bp and circa 300 bp and said short fragments being inferior to 145 bp and preferentially comprised between 50 bp and 99 bp.

Preferably the ratio 80-145 bp/145-300 bp, or 100-145 bp/145 -350 is compared between the mutated and the non mutated cf nucleic acid fragment present in the biological fluid.

Also preferred is a method to discriminate body fluid (preferably plasma or serum) from individuals where cfDNA are highly released, such as cancer patients, from body fluid (preferably plasma or serum) from healthy individual wherein said method comprises the steps of:

a) quantifying the cell free DNA (cfDNA) in the two body fluid samples by a method of the present invention, cfDNA of size range 60-80 bp, 100-145 bp and 180-400 bp;
b) comparing the size profile obtained for these three ranges of size between the two body fluid samples, preferably by combining at least three concentration values obtained when targeting circa 70 bp, circa 100 bp and circa 300 bp fragments; and preferably by combining them in a logistic function such as a logarithmic function.

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In a preferred embodiment, the method to discriminate body fluid according to the present invention, is implemented for the diagnostic, prognostic, theragnostic or for monitoring the evolution of a specific physiological state of an individual, wherein the size profile comparison obtained in step b) is indicative of that specific physiological state.

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In another aspect, the present invention is directed to a method for the diagnostic, prognostic, theragnostic or for assessing the evolution of a specific physiological state of an individual, preferably in an individual where cfDNA are highly released, said method comprising the step of:

- 5 a) repeatedly calculating during an interval of time the index of integrity of a cell free nucleic acid in a body fluid sample obtained from said individual, the presence of said nucleic acid being associated to said specific physiological state, by a method for determining the index of integrity or SFR of cell free nucleic acid in a body fluid sample according to the present invention; and
- 10 b) comparing the indexes of integrity or SFR obtained and determining whether said index of integrity of cell free nucleic acid has been varied over this interval of time.

In a preferred embodiment, said specific physiological state is a physiological state resulting to the release of cfDNA or to cells apoptosis, preferably selected from the
15 group consisting of cancer, diabetes, sickle cell disease, tissue trauma, sunburn, hemodialysis or intense effort production.

In a particular aspect, the above method of the invention is directed to a method for diagnosis, prognosis or to a theragnostic method of tumor progression in a patient,
20 wherein in step a) said nucleic acid associated to the specific physiological state is associated to said tumor and wherein in step b), a decreased of index of integrity over this interval of time is indicative of the progression of the cancer.

In a preferred embodiment, a decreased of index of integrity or SFR to a value inferior to 0.5, preferably inferior to 0.1 is indicative of the progression of the cancer.

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In another aspect, the present invention is directed to a method for the diagnostic, prognostic, theragnostic or for assessing the evolution of a specific physiological state of an individual, preferably in an individual where cfDNA are highly released, said method comprising the step of:

- 30 a) repeatedly calculating during an interval of time the concentration of a short mutated or non-mutated cell free nucleic acid in a body fluid sample obtained from said

individual, the presence of said nucleic acid, mutated or non-mutated, being associated to said specific physiological state, by a method of quantifying cell free nucleic acid in a body fluid sample according to the present invention, and

- b) comparing the concentrations obtained and determining whether the concentration of said amplified mutated or non-mutated fragment of said cell free nucleic acid has been varied over this interval of time.

In a preferred embodiment, said specific physiological state is a physiological state resulting to the release of cfDNA, preferably selected from the group consisting of auto-immune lupus, sepsis, myocardial infarction, multiple sclerosis or intense effort production.

In an also preferred embodiment of the above method, said nucleic acid associated to the specific physiological state is associated to said tumor and wherein in step b), an increased of the concentration of said amplified mutated or non-mutated fragment of cell free nucleic acid over this interval of time is indicative of the progression of the cancer.

In another aspect, the present invention is directed to a method for monitoring the efficacy of a cancer treatment in a patient, comprising the step of:

- a) calculating during an interval of time the index of integrity of free nucleic acid in a body fluid sample obtained from said patient for at least one cancer marker nucleic acid by a method of quantifying cell free nucleic acid according to the present invention, and
b) comparing the index of integrity obtained and determining whether said index of integrity of said cell free nucleic acid has been increased or decreased over this interval of time, wherein an increase in said index of integrity is indicative of efficacy and a decrease in said index of integrity is indicative of a lack of efficacy of this cancer treatment.

In another aspect, the present invention is directed to a method for the analysis of cell free nucleic acid, particularly circulating DNA, in a individual such as in patient exhibiting a tumor or susceptible to exhibit a tumor, said method comprising the steps of:

- a) the qualitative detection of the presence of a genetic polymorphism, such as a SNP or a mutation, on said free cell nucleic acid according to the present invention;
- b) the quantification of said free cell nucleic acid according to the present invention; and
- c) the determination of the rate of apoptosis by implementing the determination of integrity index of said free cell nucleic acid according to the present invention,
- 5 said method integrating the following parameters and calculation:
- A1A2 in one hand and B1B2 in another hand are the representation of the short amplified sequences; and A1B2 the long amplified sequence,
 - either A1A2 or B1B2 comprising the genetic polymorphism,
 - 10 - given CB1B2, CA1A2 and CA1B2 respectively the measured initial concentration of corresponding extracted nucleic acid by detecting the amplified short fragment B1B2, the amplified short fragment A1A2 and the amplified long fragment, respectively;
 - the qualitative detection of the presence of a genetic polymorphism:
 - % CB1B2/CA1A2 higher than a specific threshold, where B1B2 is defined as the amplicon sequence containing the genetic polymorphism; or
 - 15 - % CA1A2/CB1B2 higher than a specific threshold, where A1A2 is defined as the amplicon sequence containing the genetic polymorphism,
 - the evaluation of the integrity index by determining the ratio CB1B2/CA1B2, or CA1A2/CA1B2,
 - 20 wherein, considering that X and Y is the distance on the nucleic acid between the 5' ends of the primers, or being the length of the amplified fragments (or amplicons):

$$\begin{cases} (A1A2) = (B1B2) = X \\ (A1B2) = Y \end{cases}$$
 - 25 with $X < 180$ and $Y > X$,
preferably $50 < X < 100$ and $200 < Y < 450$.

In a preferred embodiment, said nucleic acid corresponding with the genetic polymorphism of interest on the coding strand is located and the 3'-end extremity of the primer starting at position B1 or A2, and wherein the method implementing PCR is an allele specific PCR.

30

In a preferred embodiment, said amplified long fragment A1B2 partially or fully comprises the short non-mutated fragment and the mutated fragment containing said genetic polymorphism (such as SNP or mutation) to be detected (A1A2 and B1B2, or B1B2 and A1A2, respectively).

- 5 In a preferred embodiment, said amplified long fragment A1B2 is 300 bp +/- 20 % in length, and the short non-mutated fragment (A1A2 or B1B2) and the mutated fragment (B1B2 or A1A2) are 60 bp +/- 20 % in length.

10 In another aspect, the present invention is directed to a method for diagnosis or prognosis of tumor progression in a patient, or a theragnostic method comprising determining tumor progression in a patient, said method comprising the step of:

- a) determining the concentration of a cell free nucleic acid in a body fluid sample from said patient by a method of quantifying cell free nucleic acid according to the present invention, and
15 b) detecting a genetic polymorphism (such as SNP or mutation) in said amplified short fragment of said cell free nucleic acid by a method according to the present invention.

20 In another aspect, the present invention is directed to a method for diagnosis, prognosis a pathological or physiological state such as the presence of a tumor or tumor progression in a patient, or a theragnostic method comprising determining said pathological or physiological state in a patient, said pathological or physiological state being associated to a nucleic acid genetic polymorphism (such as SNP or mutation), said method comprising the steps of:

- a) studying at least two biomarkers selected from the group of:
25 - the determination of the concentration of cell free nucleic acid in a body fluid sample from said patient, by a method of quantifying cell free nucleic acid according to the present invention;
- the detection a said genetic polymorphism in said cell free nucleic acid by a method according to the present invention, wherein the classification of the patient as having or
30 not said genetic polymorphism, being obtained by determining whether the percentage of mutated versus non-mutated cell free nucleic acid found is higher than a threshold,

preferably said threshold being specific of a given genetic polymorphism and determined from a cohort of non-mutated and mutated patients; and

- the determination of the index of integrity of said cell free nucleic acid in the sample, by a method according to the present invention,

5 b) combining said at least two values through a logistic function including said at least two biomarkers, and

c) analyzing said end value of said logistic function in order to diagnosis or prognosis the pathological or physiological state, such as a tumor or tumor progression in said patient.

10 Such a threshold value associated to said SNP in the present method of the invention where it is necessary can be determined from a cohort of two groups of patients, patients exhibiting or not the specific genetic polymorphism (such as SNP or mutation) associated to said SNP. Said threshold represents the minimum value beyond which it is established without ambiguity that the gene is mutated.

15

The present invention is also directed to a kit comprising two set of nucleic acid primers, preferably for detecting or quantifying in a body fluid sample the presence of a cell free nucleic acid of a gene of interest, said gene of interest being susceptible to present a mutation, more preferably for its use in the Intplex system of the present invention, characterized in that said two set of primers comprising:

20

a) a first set of two primers, named A1 (forward primer) and A2 (reverse primer), said two primers A1 and A2:

- have a minimal size of 15 nucleotides and a maximal size of 30 nucleotides, and
- have a minimal spacing of at least 5 bp between the two primers, between the 3' extremities of both primer, and

25

- allows to obtain an amplicon having a size range comprised between 35 to 100 bp, said amplicon being in a region of said gene which does not exhibit the mutation of interest ; and

30

b) a second set of two primers, named B1 (forward primer) and B2 (reverse primer), said two primers B1 and B2:

- have a minimal size of 15 nucleotides and a maximal size of 30 nucleotides, and

- have a minimal spacing of at least 5 bp between the two primers, between the 3' extremities of both primer, and
 - allows to obtain an amplicon having a size range comprised between 35 to 100 bp, said amplicon being in a region of said gene which exhibit the mutation of interest ; and wherein
- 5 A1B2 being in the 250-450 bp size range.

The present invention is also directed to the kit according to the present invention, wherein:

- the targeted region of said gene of interest where the B2 primer is located from 5 to 85
- 10 nucleotides downstream from the position of said mutation of interest
- the region of said gene of interest where the primer pair A1 A2 is designed in the region which is located within the 430-100 nucleotides upstream from the position of said mutation of interest,
- preferably for its use in the conventional IntPlex system of the present invention.

15

The present invention is also directed to the kit according to the present invention, wherein:

- the region of said gene of interest where the A1 primer is located from 5 to 85 nucleotides upstream from the position of said mutation of interest.
- 20 the region of said gene of interest where the primer pair B1B2 is designed in the region located within the 100-430 nucleotides downstream from the position of said mutation of interest,
- preferably for its use in the inverse IntPlex system of the present invention.

- 25 The present invention is also directed to a method for the diagnosis, prognosis, or for assessing the evolution of a cancer in an individual, said method comprising calculating an index of integrity of cell free DNA in a body fluid sample obtained from said individual, wherein the index of integrity is calculated by a method comprising (i) performing an amplification by polymerase chain reaction (PCR) of a short size sequence from cell free

DNA in said body fluid sample, wherein said short size sequence has a length inferior to 100 bp, and determining a concentration or amount of said short size sequence from said PCR; (ii) performing an amplification by PCR of a long size sequence from cell free DNA in said body fluid sample, wherein said long size sequence has a length superior or equal to 100 bp, and determining a concentration or amount of said long size sequence from said PCR; and (iii) calculating a ratio of the concentration or the amount of said cell free DNA of long size and of short size, and wherein a ratio long/short size <1 is indicative of presence of the cancer.

The present invention is also directed to a method for the diagnosis, prognosis, or for assessing the evolution of a cancer in an individual, said method comprising calculating an index of integrity of cell free DNA in a body fluid sample obtained from said individual,

wherein the index of integrity is calculated by a method comprising (i) determining from an amplification by polymerase chain reaction (PCR) of a short size sequence from cell free DNA in said body fluid sample, the concentration or amount of a short amplicon, wherein said short size sequence has a length inferior to 100 bp; (ii) determining from an amplification by PCR of a long size sequence from cell free DNA in said body fluid sample, the concentration or amount of a long amplicon, wherein said long size sequence has a length superior or equal to 100 bp; and (iii) calculating the ratio of the concentration or the amount of said amplicons of long size and of short size, and

wherein the ratio long/short size is indicative of the presence of a cancer.

The present invention is also directed to a method for the diagnosis, prognosis, or for assessing the evolution of a cancer in an individual, said method comprising calculating an index of integrity of cell free DNA in a body fluid sample obtained from said individual,

wherein the index of integrity is calculated by a method comprising (i) determining from an amplification by polymerase chain reaction (PCR) of a short size sequence from cell free DNA in said body fluid sample, the concentration or amount of a short amplicon, wherein said short size sequence has a length between 50-100 bp; (ii) determining from an amplification by PCR of a long size sequence from cell free DNA in said body fluid sample, the concentration or amount of a long amplicon, wherein said long size sequence has a

length superior to 101 bp; and (iii) calculating the ratio of the concentration or the amount of said amplicons of long size and of short size, and

wherein the ratio long/short size is indicative of the presence of a cancer.

The present invention is also directed to a method for the diagnosis, prognosis, or for
5 assessing the evolution of a cancer in an individual, said method comprising: a) calculating a size fraction ratio (“SFR”) of cell free DNA in a body fluid sample obtained from said individual, and b) comparing the SFR obtained to that of a healthy individual, wherein a decreased SFR is indicative of the presence of a cancer, and wherein the SFR is calculated by a method comprising (i) performing amplifications by polymerase chain reaction (PCR)
10 from said body fluid sample and determining from said amplifications the concentration or amount of a range of short size cell free DNA in said body fluid sample; (ii) performing amplifications by PCR from said body fluid sample and determining from said amplifications the concentration or amount of a range of long size cell free DNA in said body fluid sample; and (iii) calculating the ratio of the concentration or the amount of said
15 cell free DNA of long size range and of short size range.

The present invention is also directed to a method for the diagnosis, prognosis, or for assessing the evolution of a cancer in an individual, said method comprising:

a) calculating a size fraction ratio (“SFR”) of cell free DNA in a body fluid sample obtained from said individual, and
20 b) comparing the SFR obtained to that of a healthy individual,

wherein a decreased SFR is indicative of the presence of a cancer, and

wherein the SFR is calculated by a method comprising (i) performing amplifications by polymerase chain reaction (PCR) from said body fluid sample and determining from said amplifications the concentration or amount of a range of short size cell free DNA in said
25 body fluid sample, wherein the range of short size cell free DNA is between 43bp and 100 pb or between 60 bp and 100 bp; (ii) performing amplifications by PCR from said body fluid sample and determining from said amplifications the concentration or amount of a range of

long size cell free DNA in said body fluid sample, wherein the range of long size cell free DNA is between 200 bp and 450 bp; and (iii) calculating the ratio of the concentration or the amount of said cell free DNA of long size range and of short size range.

5 The present invention is also directed to the kit comprising two set of nucleic acid primers according to the present invention, wherein the gene and/or the associated gene mutation of interest is selected from the group of:

A) Mutations in disorders in particular cancer:

(For each gene are presented the position number in the cDNA of the bp bearing the mutation upon NCBI 36 : Ensembl Contig).

- TP53: 394, 395, 451, 453, 455, 469, 517, 524, 527, 530, 586, 590, 637, 641, 724, 733, 734, 743, 744, 817, 818, 819, 820, 839, 844, 916
APC: 2626, 3340, 3907, 3934, 3964, 4012, 4099, 4132, 4133, 4285, 4286, 4348, 4729
MSH6: 1168
- 5 NF1: 3827, 3826
PIK3CA: 1530, 1624, 1633, 1634, 1636, 1656, 3140, 3140, 3140
SMAD4: 502, 931, 932, 988, 989, 1051, 1082, 1156, 1332, 1333, 1519, 1596, 1597, 1598, 1606
EGFR: 2155, 2155, 2156, 2303, 2369, 2573; deletions/loss: 2230 to 2244, from 2308 à
- 10 2328
CDKN2A: 172, 205, 238, 239, 298, 250, 322, 369, 427, 394
IDH1: 394; 395
PTEN: 125, 126, 182, 302, 314, 387, 388, 389, 1911, 577, 518, 519, 697, 698, 1003, 1004
- 15 SMARCB1: 118, 153, 154, 379, 380, 425, 471, 472, 473, 601, 618, 619, 777, 776, 778
CTNNB1: 7, 94, 95, 98, 100, 101, 110, 121, 122, 133, 134, 170
HNF1A: 82, 81, 83, 196, 378, 379, 493, 494, 495, 526, 527, 617, 618, 685, 710, 749, 787, 817
VHL: 194, 203, 241, 266, 340, 343, 388, 452, 473, 480, 478
- 20 ATM: 1229, 1810, 2571, 2572, 2573, 3925, 8774, 9023
EZH2: 1936, 1937
RET: 2753
NRAS: 181, 182, 183
PTCH1: 135, 338, 416, 417, 1242, 1243, 1244, 1280, 1281, 1284, 1301, 1302, 1315
- 25 KIT: 1668, 1669, 1670, 1679, 1680, 1681, 1682, 1727, 1728, 1924, 1925, 1961, 1962, 2467, Deletions from 1645 à 1727
NF2: 168, 169, 170, 459, 460, 586, 592, 634, 655, 656, 784, 1021, 1022, 1396
PDGFRA: 1680, 1681, 1682, 1975, 1976, 1977
MEN1: 124, 256, 291, 292, 293
- 30 PPP2R1A: 536, 767
STK11: 196, 910

MLL3: 1097, 4432, 6301, 6851, 8911, 10040, 10495, 12048, 12165

FOXL2: 402

GNAS: 601, 602, 680

HRAS: 34, 35, 36, 37, 39, 181, 182

5 FGFR3: 742, 743, 744, 746, 1108, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1949

PTCH1: 549, 550, 584, 1093, 1249, 1804, 2446, 3054, 3944, 3945, 3946

CDH1: 367, 368, 1000, 1057, 1108, 1204, 1436, 1437, 1742;

10 B) Mutation in disorders other than in cancer:

a) single gene disorders:

Autosomal dominant gene : Familial hypercholesterolemia, Huntington's disease, neurofibromatosis type 1, Marfan syndrome, hereditary nonpolyposis, colorectal cancer, hereditary multiple exostoses, Polycystic kidney disease, achondroplasia, Sickle-cell

15 anemia, achondroplasia, Sickle-cell anemia

b) Autosomal recessive allele : cystic fibrosis, sickle-cell disease, Tay-Sachs disease, Niemann-Pick disease, spinal muscular atrophy, Roberts syndrome, Phenylketonuria, Mucopolysaccharidoses, Glycogen storage diseases

20

c) X-linked dominant: Rett syndrome, incontinentia pigmenti, Aicardi syndrome, Klinefelter syndrome, incontinentia pigmenti, Duchenne muscular dystrophy, Hemophilia

25 d) Y linkage: male infertility and hypertrichosis pinnae

e) Mitochondrial disease: Leber's hereditary optic neuropathy

f) Multifactorial and polygenic (complex) disorders:

asthma, autoimmune diseases such as multiple sclerosis, cancers, ciliopathies, cleft palate, diabetes, heart disease, hypertension, inflammatory bowel disease, mental retardation, mood disorder, obesity, refractive error, infertility

5 The present invention is also directed to the kit comprising two set of nucleic acid primers according to the present invention, wherein the mutation of the gene of interest is selected from the group consisting of the mutations of *KRAS* and *BRAF* gene, particularly the BRAF V600E mutation.

10 The present invention is directed to a kit comprising one or two set of nucleic acid primers, preferably for detecting or quantifying in a body fluid sample the presence of a cell free nucleic acid of the gene *KRAS*, said gene *KRAS* being susceptible to present a mutation selected from the group of *KRAS* G12 mutation, preferably G12V, G12D, G12A, G12S and G12C mutation, and G13D mutation, more preferably for its
15 use in the Intplex system, characterized in that said set of primers or two sets of primers comprising:

 a) a first set of two primers, named A1 (forward primer) and A2 (reverse primer), said two primers A1 and A2 being selected from the group consisting of:

- for A1, SEQ ID NOs 163 to 196,

20 -for A2, SEQ ID NOs 250 to 256; or/and

 b) a second set of two primers, named B1 (forward primer) and B2 (reverse primer), said two primers B1 and B2 being selected from the group consisting of:

- for B1, SEQ ID NOs 244 to 249,

-for B2, SEQ ID NOs 83 to 120.

25

 The present invention is also directed to a kit comprising one or two set of nucleic acid primers, preferably for detecting or quantifying in a body fluid sample the presence of a cell free nucleic acid of the gene *BRAF*, said gene *BRAF* being susceptible to present the mutation V600E, more preferably for its use in the Intplex
30 system, characterized in that said one or two set of primers comprising:

a) a first set of two primers, named A1 (forward primer) and A2 (reverse primer), said two primers A1 and A2 being selected from the group consisting of:

- for A1, SEQ ID NOs 65 to 81,
- for A2, SEQ ID NO.19 ; or/and

5 b) a second set of two primers, named B1 (forward primer) and B2 (reverse primer), said two primers B1 and B2 being selected from the group consisting of:

- for B1, SEQ ID NO. 38 ,
- for B2, SEQ ID NOs 40 to 63.

10 In another aspect, the present invention is directed to a nucleic acid primer, preferably for detecting or quantifying in a body fluid sample the presence of a cell free *KRAS* DNA containing a sequence of a same *KRAS* intronic region, preferably for determining the size profile of such cell free nucleic acid in a body fluid sample from a patient, said nucleic acid being selecting from the group of the primers having the sequence SEQ ID NOs. 1 to 8 (see table 1).

15 The present invention is also directed to a set of nucleic acid primers, preferably for detecting or quantifying in a body fluid sample the presence of a cell free *KRAS* nucleic acid, more preferably *KRAS* DNA, said set of primers being selecting from the group of following set of primers:

- a) a set of primers comprising the primer having the sequence SEQ ID NO: 1 and at least two different primers, preferably three different primers selecting from the group of primers having the sequences SEQ ID NOs: 2 to 8;
- 20 b) a set of primers comprising the primer having the sequence SEQ ID NO: 1, the primer having the sequence SEQ ID NO: 8, and at least one or two primers selecting from the group of primers having the sequences SEQ ID NOs: 2 to 7;
- 25 c) a set of primers comprising the primer having the sequence SEQ ID NO: 1, the primer having the sequence SEQ ID NO: 7 and a primer selecting from the group of primers having the sequences SEQ ID NOs: 2 to 6; and
- d) a set of primers comprising the primers having the sequences SEQ ID NO: 1 to 8.

30 The present invention is also directed to a set of nucleic acid primers, preferably for its use in the Intplex system towards demonstrating the presence of the *KRAS* G12V

mutation in a body fluid sample, said set of nucleic acid primers comprising the primers having the sequences SEQ ID NOs: 9 to 14, preferably 9 to 15 (see table 2).

More preferably the present invention is directed to a set of nucleic acid primers, preferably for its use in the Intplex system towards demonstrating the presence of *KRAS* G12 mutation (G12V, G12D, G12A, G12S and G12C) and G13D mutation in a body fluid sample, said set of nucleic acid primers comprising the primers having the sequences SEQ ID NOs: 28 to 36, preferably 29 to 37 (see table 4).

The present invention is finally directed to a set of nucleic acid primers, preferably for its use in the Intplex system towards demonstrating the presence of the *BRAF* V600E mutation in a body fluid sample, said set of nucleic acid primers comprising the primers having the sequences SEQ ID NOs: 16 to 21, preferably 16 to 22 (see table 2).

More preferably the present invention is directed to a set of nucleic acid primers, preferably for its use in the Intplex system towards demonstrating the presence of the *BRAF* V600E mutation in a body fluid sample, said set of nucleic acid primers comprising the primers having the sequences SEQ ID NOs: 23 to 26, preferably 23 to 27 (see table 4).

Finally the present invention is directed to a kit for detecting or quantifying in a body fluid sample the presence of cell free *KRAS* or *BRAF* nucleic acid, more preferably cell free DNA, optionally cell free DNA exhibiting a genetic polymorphism, or to determine the size profile of said cell free *KRAS* nucleic acid in a biological sample, said kit comprising a set of primers as above indicated according to the present invention.

The following examples and also the figures and the legends hereinafter have been chosen to provide those skilled in the art with a complete description in order to be able to implement and use the present invention. These examples are not intended to limit the scope of what the inventor considers to be its invention, nor are they intended to show that only the experiments hereinafter were carried out.

Legend to the figures**Figure 1:**

Quantification by Q-PCR of genomic DNA isolated from CRC (colorectal cancer) HCT-116-s cells using primer pairs that lead to the amplification of amplicons of different sizes of the gene *KRAS*. The values are obtained by quantifying a sample at a dilution that corresponds to 45 pg/ μ L. The concentration of the genomic DNA sample was measured by optical density before use in Q-PCR. The histograms represent the mean values of three different experiments. The experiments were carried out in duplicate and the results are expressed in pg/ μ L of extract.

Figures 2A and 2B:

Quantification by Q-PCR of cirDNA isolated from 3 patients with metastatic CRC prior surgery and chemotherapy relative to the amplicon size. Figure 2A, serum samples (n=2 patients). Figure 2B, plasma sample of one patient. The determination of the concentrations of cirDNA of each patient was done in duplicate. Histogram corresponds to the mean of the duplicate. Results are expressed in ng/ μ L of cirDNA.

Figure 3:

Quantification by Q-PCR of cirDNA isolated from plasma samples of three healthy individuals aged between 20 and 25 years. The concentration of cirDNA was determined using a Q-PCR system that amplifies fragments of size ranging from 60 to 409 bp. The histograms show the mean values expressed in pg cirDNA/mL plasma. For instance, the maximum value obtained with the primer pair *KRAS* 101 corresponds to a concentration of 4.8 ng/ml plasma.

Figure 4:

Illustration of the advantage in amplifying short DNA sequence in regards to detection of mutated ctDNA. Use of 3 primer sets (A, B and C) producing amplicon of different sizes are represented when analyzing genomic DNA, poorly and highly fragmented DNA.

Figure 5:

Relative proportions of concentration values relative to the amplicon size.

Figure 6:

Concentrations of cirDNA obtained by amplifying a long fragment of 249 bp or a short fragment of 60 bp in plasma samples from one healthy subject with low level of cirDNA (23 ng/ml plasma), one mCRC patient with intermediate level of cirDNA (450
 5 ng/ml plasma) and one mCRC patient with high concentration of cirDNA (1860 ng/ml plasma). The cell line sample corresponds to the values obtained for genomic DNA isolated from HCT116-s cells (4.8 ng/ml, Figure 1). Values are expressed as fractions of the maximum value obtained with primer pairs for the amplification of DNA fragments of increasing size (60, 73, 101, 145, 185, 249, 300, 357 and 409 bp).

10 **Figures 7A and 7B:**

Specific tumoral ctDNA concentration size profile in xenografted mice. Two series of 7 primer sets generating amplicon of increasing length between 60 and 409 bp or 60 and 385 bp of human or mouse origin, respectively, were used. Each point corresponds to the mean of three pools of 4 different mouse plasmas.

15 **Figures 8A and 8B:**

Contribution of tumoral cirDNA amount in total cirDNA amount in xenografted mice plasma.

Figure 9:

20 Schematic representation of an example of the use of the IntPlex method for the analysis of SNPs.

Figure 10:

Application of the Intplex system to cancer.

Figures 11A and 11B:

25 Figure 11A) Schematic representation of the *KRAS* Conventional Intplex system in which the mutation is at the 3' end of the sense primer B1.

Figure 11B) Schematic representation of the *KRAS* Reverse Intplex system in which the mutation is at the 3' end of the antisense primer A2.

Figure 12:

30 Efficiency of the Kinv system for the quantification of cirDNA from mice xenografted with the human cancer cells SW620. Red numbers: size of the amplicons (in bp).

Figure 13:

Efficiency of the Kconv system for the quantification of cirDNA from mice xenografted with the human cancer cells SW620. Red numbers: size of the amplicons (in bp).

Figure 14:

- 5 Q-PCR quantification of theDNA from S4 HT29.

Figure 15:

S4 HT29DNA diluted (1/10) in human genomic DNA.

Figure 16:

Data presented as a percentage of the highest concentration in the series.

- 10 **Figure 17:**

Mutated fragments concentrations (in %) versus non-mutated fragments concentrations observed using the Intplex process from human plasma DNA.

Figure 18:

- 15 Discrimination of plasma from healthy to CRC individuals. CirDNA concentration values are presented in the table and expressed in ng/mL plasma. Histograms represent the % of cirDNA amount contained in the size fraction.

Figures 19A-19B:

Agarose gel electrophoresis of 20 µg of ctDNA extracted from two CRC patients (CRC021, Fig. 19A and CRC019, Fig. 19B).

- 20 **Figure 20:**

Comparison of the DII values (A) from genomic DNA, and ctDNA from human plasmas (healthy and CRC).

Figure 21:

- 25 Comparison of the DII values calculated with the primer design of the present invention with the value obtained with using primer pairs targeting distant DNA sequences.

Figures 22A-22E:

Determination of various parameters indicative of ctDNA fragment size pattern (data are plotted in histograms).

- 30 **Figure 23: Localisation of primers sequences for BRAF gene (conventional and reverse (or inverse) system)**

Example of DNA region to be targeted upon the IntPlex method when BRAF V600E point mutation is of interest. Figure 23 shows the regions where molecular entities such as primers could target upon our multiplex method applied to this mutation.

Yellow : conventional system; Green : reverse system; Red : blocker; Pink : SNP.

5 Figures 24A-24E: Localisation of the Exon 2 regions and primers sequences for the KRAS gene (conventional and reverse (or inverse) system)

Figure 24A: Example of DNA region to be targeted upon the IntPlex method when the hot spot point mutations of the 2nd and 3rd codon of the second exon of the KRAS gene is of interest.

10 Yellow: reverse primer for mutated amplicon: 6156 to 6236

Green: primer pair for non mutated amplicon: 5721 to 6051

Figure 24A shows the regions where molecular entities such as primers could target upon the multiplex method applied to this mutation.

15 Figure 24B: Localisation of primers sequences for KRAS conventional and reverse system.

Yellow: conventional system; Green : reverse system; Red : blocker; Pink : SNP.

Figure 24C: Selected DNA region target for B1B2 primer pair design for detecting exon 2 KRAS hot spot mutations upon the reverse configuration of the system of the present invention. A1: GCCTGCTGAAAATGACTG; A2: in yellow and in green.

20 Figure 24E: Selected DNA region target for A1 primer for detecting KRAS exon 2 hot spot mutations upon rev configuration:

A2: GTGGCGTAGGCAAGAGTGCCTT

A1: selected DNA region target in yellow and green.

25 Figure 24D: Selected DNA region target for B2 primer for detecting KRAS exon 2 hot spot mutations upon conv configuration:

B1: ACTTGTGGTAGTTGGAGCTGG

B2: selected DNA region target in yellow and green.

EXAMPLES**EXAMPLE I: Determination of the size range of cirDNAs**

In order to determine the optimal size of the amplicons for a more specific and sensitive analysis of cirDNAs by Q-PCR, we have designed and used 9 pairs of primers that allow the amplification of amplicons of 60, 73, 101, 145, 185, 249, 300, 357 and 409 bp within the same region. They have been designed in such a way that a smaller amplicon is always comprised within the sequence of a bigger amplicon, the antisense primer being the same for each pair of primers. This amplified region of 409 bp is located in intron 2 of *KRAS*. The sequence of the oligonucleotide primers are presented in Table1.

Table 1

	Kras rev	GGT CCT TTT CCG TGT GTA GG (20 bp)	(SEQ ID N0: 1)
	Kras 409	GCC TCC CTT TCC AGC ACT (18 bp)	(SEQ ID N0: 2)
	Kras 357	GGC ATC TCT AGG ACG AAG GT (20 bp)	(SEQ ID N0: 3)
15	Kras 300	GGT CCT TTT CCG TGT GTA GG (20 bp)	(SEQ ID N0: 4)
	Kras 249	TGG AAG AGC ATA GGA AAG TGC (21 bp)	(SEQ ID N0: 5)
	Kras 185	ATC TGC CTC CGA GTT CCT G (19 bp)	(SEQ ID N0: 6)
	Kras 101	CCC TAC ACG TAG AGC CTG TGA (21 bp)	(SEQ ID N0: 7)
20	Kras 73	GCC TGT GAC CTA CAG TGA AAA (21 bp)	(SEQ ID N0: 8)

Concentration obtained by using each primer pairs to analyse genomic DNA

Figure 1 describes the variation in the yield of the tested primer pairs. All results are from 3 experiments carried out in duplicate. The amplification reaction efficiency by Q-PCR of a given DNA sequence is linked to the thermodynamics properties of the primers and differs, among other things, in function of the amplicon size. As shown in Figure 1 the efficacy of detection of the primer pairs (with very similar hybridization properties) is relative to the size of the tested amplicons. As illustrated in Figure 1 the detection seems to be optimal for amplicons between 101 and 185 bp. In the literature, it has been conventionally chosen to amplify regions going from 150 to 250 bp.

The presence of monomers or multiples of nucleosomes that have a size close to 180-200 bp has been already reported and is indicative of a mechanism of apoptosis for the release of cirDNA.

Figure 2A summarizes the results obtained using two serum samples from two patients with metastatic colorectal cancer (mCRC). The cirDNA concentration curves of

these two serum samples shows comparable profiles that present approximately three phases. A first one in which the concentration for amplicons of sizes between 60 and 73 bp (up to values ranging between 0.2 and 0.3 ng/ μ l) is similar, a second one for amplicon of sizes between 101 and 145 bp in which the concentration decreases sharply
5 to values of about 0.05 ng/ μ l; and finally a third phase for amplicons of sizes between 145 and 409 bp in which the concentration of cirDNA is plateauing or very slowly decreasing up to 0.02 ng/ μ l.

Figure 2B shows the cirDNA concentration as determined by using the same amplification systems of increasing length amplicons in a CRC patient plasma. Data
10 show the same size profiling.

To note the two sera and the plasma used here originate from patients waiting for their first tumor resection surgery and not subjected to chemotherapy at the time of sampling.

Figure 3 summarizes the profiles of cirDNA concentrations in plasma samples of
15 healthy subjects relative to the amplicon sizes. These results indicate that higher concentrations of cirDNA are detected with amplicons of sizes between 101 and 145 bp. Differently from the results for mCRC patients, in healthy subjects the results do not indicate the presence of a very significant variation in the detection of amplicons bigger or smaller than 101-145 bp.

20 We can discriminate plasma of cancer patient plasma from healthy individual by comparing quantification of cfDNA when detecting a amplified sequence (amplicon) of 145-409 and another of range of 50-73 bp. A ratio long/short <0.5 , and preferably <0.1 being indicative of presence of a tumor.

25 The reason why amplicon size is crucial when analysing cirDNA vs genomic DNA

Thus, the size profile of cirDNA as determined by amplifying amplicon of increasing sequence length reveals that optimal detection is made when amplifying amplicon <100 bp and that a much higher proportion of cirDNA of size ranging from 150 to 350 bp is present in non tumoral cirDNA as compared with tumoral cirDNA. The
30 choice of the size of the amplified DNA region consequently appears crucial as illustrated by the scheme of the figure 4.

Thus, the choice of amplicon size is crucial for:

- the sensitivity of the analysis by Q-PCR (increase of more than ten folds and up to 50 folds according to the quantity of cirDNA in the sample),
- the specificity, because the analysis of the cirDNA concentration profile based on the amplicon size (or the determination of the optimal amplification) can distinguish the cirDNA of a patient with mCRC from the cirDNA of a healthy subject. The measure of the ratio between the quantification obtained for amplicons of sizes between 50 and 100 and the quantification obtained for amplicons bigger than 100 bp can be used to hypothesize the presence of cirDNA of tumour origin. In addition to the generally higher overall quantity of cirDNA in mCRC patients, the quality in terms of fragment size appears, for the first time, to be specific and informative about the presence of cancer cirDNA.

Moreover, it is possible to determine this specificity by measuring the integrity index that is calculated by comparing the concentrations of amplicons of specific sizes (Figure 5).

The 145/60 or 300/60 ratio is always lower than 1 in the case of the analysis of cirDNA from mCRC patients. Conversely, the 145/60 ratio is 2.07 for genomic DNA.

The integrity index for 300/60 is lower than that for 145/60 in cirDNA from mCRC patients. Indeed, it is <0.344 in mCRC patients; whereas it is >0.45 in cirDNA from healthy subjects. The 300/60 ratio is 0.38 in genomic DNA.

The initial study of the analysis of the 145/60 and 300/60 ratio in healthy subjects and mCRC patients shows a sensitivity of 100 % and a specificity of 100 %. The 145/60 ratio seems thus to discriminate better between healthy subjects and mCRC patients than the 300/60 ratio especially when the standard deviation of the mean is taken into account, but to differentiate less well when the specificity is considered. The 300/145 ratio is not optimal to discriminate healthy/cancer patients and in general gives results which are the opposite of those obtained with the 300/60 ratio, i.e., the mean of the values obtained for 300/145 is higher for cirDNA from mCRC patients; yet it is this type of ratio (short fragment >100 bp and <180) that has conventionally been used in the few studies previously carried out on the integrity index (13-19).

It is important to indicate that the choice of primer pairs used (and thus in particular the size of the amplified sequence) for the detection of cirDNA is based only on their amplification yield for fragments between 100 and 300 bp according to the targeted sequence. The calculation of these integrity indexes could be used to discriminate between the cirDNAs of healthy subjects and mCRC patients. It has to be stressed that other ratios or integrity indexes could be calculated in function of the tumour development or of the total concentration of cirDNA.

The histograms of figure 5 shows that the relative proportions of the values obtained by amplifying the fragments of 60 and 145 bp are the opposite in healthy subjects in comparison to mCRC patients.

We have found that the bigger the quantity of cirDNA is, the lower the integrity index is. For instance (figure 6), the amplification value of the long fragment of 249 bp decreases while the amplification of the short fragment of 60 bp increases in function of the total quantity of cirDNA.

In summary, the results of that example allow, for the first time, the determination of innovative features concerning the detection of cfDNA by Q-PCR:

1. The size of the amplified fragment (amplicon) influences greatly the quantification of cfDNAs.
2. The detection of amplicons smaller than 100 bp is optimal.
3. The determination of an integrity index can be used to discriminate between the cirDNA of a subject with mCRC, the cirDNA of a healthy individual and also genomic DNA.
4. The comparison of the results of the PCR amplification of extracts of cirDNA can be done accurately only by comparing the amplification of primer pairs that produce amplicons of identical size.

EXAMPLE II: Size distribution through Q-PCR analysis of cirDNA extracted from a CRC xenograft mouse model

Materials and Methods:

a) Cell lines and reagents

SW620 CRC cells were maintained in RPMI + 10% fetal bovine serum. SW620 cells have the homozygous *KRAS* G12V mutation (GGT to GTT)

b) Xenograft model

Female athymic nude mice (6-8 wk/old) were xenografted subcutaneously with 1x10⁶ cancer cells. Mice were euthanized with CO₂ three weeks post-graft, the tumors weight being within the 300-650 mg. Peripheral blood was drawn into EDTA tubes and was immediately (within one hour) used for plasma preparation.

c) Plasma and serum preparation

Following collection in 5 ml BD vacutainer KE35 tubes (Belliver Industrial), mouse blood samples were centrifuged at 2000 rpm at 4°C in a Heraeus Multifuge LR centrifuge with a CR 4j rotor for 10 minutes. Supernatants were collected in sterile 1.5 ml Eppendorf tubes and centrifuged at 14 000 rpm (16 000 g) at 4°C for 10 min. Then supernatants were either immediately handled for DNA extraction or stored at -80°C. No significant difference was found in Q-PCR assays when comparing freshly isolated or stored plasma. Serum was prepared using the same 2-step centrifugation process, but blood was drawn in tubes without EDTA which were then left at room temperature for one hour. Mouse and human plasma and sera were isolated within 3 hours following sampling.

d) DNA extraction

ctDNA and genomic DNA from the different cell lines were extracted following the same procedure. DNA was purified from 200 µl plasma with the QIAmp DNA mini Blood kit (Qiagen, CA) according to the "Blood and body fluid protocol" with an elution volume of 60 µl. Samples were kept at 4°C during plasma preparation. DNA samples were frozen at -20°C until use. No significant difference was found in Q-PCR assay when comparing freshly extracted or stored DNA.

e) ctDNA quantification by Q-PCR

DNA was quantified by Q-PCR assay. Real-time PCR amplifications were carried out in a reaction volume of 25µl on a My iCycler IQ 5IQ or a Chromo4 instrument using the IQ5 Optical system software 2.0 and the MJ Opticon Monitor 3 software (Bio-Rad). Each PCR reaction mixture consisted of 12.5 µl mix PCR (Bio-Rad Super mix SYBR Green = Taq polymerase, MgCl₂); 2.5 µl of each amplification primer

(100 pmol/ μ l); 2.5 μ l PCR-analyzed water and 5 μ l DNA extract. Thermal cycling started by a first denaturation step of 3 min at 95°C, followed by 40 cycles of 95°C for 10 sec and 60°C for 30 sec. Melting curves were obtained from 55°C to 90°C with reading every 0.2°C. As calibrators for quantification, serial dilutions of genomic DNA from HCT116-s and MC38 cells were used. Sample concentrations were extrapolated from the standard curve by the IQ 5 Optical system software 2.0 or MJ Opticon Monitor 3 software. The limit of detection as the concentration that can be detected with reasonable certainty (95% probability) as recommended in the MIQE guidelines was 3 copies/assay (21).

10 Plasma extract were assayed by amplifying the same 60 to 409 bp DNA sequences of human *KRAS* intron 2 as previously used for the analysis of CRC clinical sample. In addition non tumor cirDNA was assayed by the same approach by with amplifying 60-385 bp DNA sequences of mouse *KRAS* intron 1. Plasma extracts from non xenografted control nude mice were as well assayed with using that method.

15 Figures 7A and 7B demonstrate first that a significant discrimination between tumor and non tumor derived cirDNA when amplifying sequences ranging from 200 and 300 bp. Second, concentration was found maximal when amplifying region<100bp for tumoral cirDNA while maximum was reached when amplifying the 105 bp sequence for non tumor cirDNA and the 60 bp for tumor cirDNA.

20 Determination of the cirDNA integrity index (300/60) is therefore much lower for tumoral cirDNA than for non tumor cirDNA and for the non xenografted control mice cirDNA; being 0.05 as compared with 0.57 and 0.48, respectively.

Figures 8A and 8B present the contribution of tumor ctDNA amount in comparison with the total cirDNA amount (tumor + non tumor cirDNA amount) from data obtained in the same experiment. Data clearly show that the proportion of tumor cirDNA sharply decreased from 60-250 bp amplified region and then somewhat stabilized.

These observations confirm the results previously obtained with analysing human samples.

30 Moreover data highlight the difference between concentration profiles upon amplicon length between tumoral vs non-tumoral/control cirDNA.

EXAMPLE III: Intplex methodGeneral application of the IntPlex analysis

5 CirDNAs carry the genetic marks of healthy and pathological cells, or of infectious agents. Thus, genetic alterations are targets of choice due to their clinical repercussions. One of the technical challenges concerning cirDNAs is their use as a tool to detect genetic polymorphisms especially SNPs (Single Nucleotide Polymorphisms).

SNPs are the most abundant of the genetic variations in the human genome. They represent more than 90% of all the differences among individuals. It is a type of
10 DNA polymorphism in which two chromosomes differ on a given segment by one single base. In two human genomes at random, 99.9% of the DNA sequences are identical. The remaining 0.1% includes sequence variations of which the most common type is a single nucleotide polymorphism (SNP). SNPs are stable, very abundant and distributed uniformly in the entire genome. These variations are associated with the
15 diversity within a population or among individuals, with the differences in susceptibility to diseases and with the individual response to drugs. Some are responsible for the perturbations of the cell cycle that can result in cell proliferation and ultimately in cancer development.

The majority of the methods for the analysis of SNPs are based on the possibility
20 of denaturing DNA to single strands by heat and of renaturing it, by cooling down under precise conditions, with a strand of complementary sequence (PCR methods). Thus, PCR allows the identification and quantification of a DNA sequence through the analysis of its amplification thanks first to a particular polymerase and also to specific oligonucleotides that will « delimit » the sequence to be amplified.

25 PCR was previously adapted to detect SNP. One of the simplest PCR methods for the detection of known SNPs is the Allele-Specific Hybridization that is known also under the name of Allele-Specific Oligonucleotide hybridization (ASO). In this method, two short oligonucleotide probes, which differ only by one nucleotide, are used. The studied DNA is hybridized separately with these two labeled probes. The genomic DNA
30 will hybridize only with the probe with the perfectly complementary sequence. The technique of allele-specific PCR can be carried out by using a marker of double-

stranded DNA whose signal allows the quantification of the DNA amplification. The analysis by SYBR Green of a mutation has the considerable advantage of simplicity and rapidity.

Nevertheless, the simple analysis by SYBR Green generates, particularly for the
5 identification of point mutations, a non-negligible specific detection thus rendering this approach not very reliable when the objective is a clinical or industrial kit. Various methods were developed to circumvent this non-specificity effect but they consist of 2 or more steps rendering them more time consuming.

Therefore, we have designed and developed an analytical method that leads to a
10 qualitative conclusion about the presence or not of a genetic polymorphism. The determination of the positivity of the mutational status of a gene will be established by calculating the percentage of mutated cirDNA relative to the non-mutated cirDNA. For each given mutation, it will be possible to determine a percentage of non-specificity, called « threshold », beyond which it will be established without ambiguity that the gene
15 contains a polymorphism.

However, the use of a so-called «reference» amplification might be dangerous for the analysis of cirDNA because our results have demonstrated that the quantification of amplified DNA in this case varies very significantly in function of the length of the amplified fragment (the amplicon). Thus, keeping in mind our results, in the method
20 IntPlex we will compare the amplification of an amplicon smaller than 100 bp, which contains the mutation to be detected, and the amplification of an amplicon of identical size.

In order to limit as much as possible the potential disparity in the sequences included in the cirDNA, the control amplicon will be localized close to the amplified
25 sequence. The quantification of the reference amplicon will allow determining/confirming the specific total quantity of cirDNA as well.

Since mononucleosome has a size varying between 180 and 220 bp the ratio between the quantity of an amplicon bigger than 220 bp and the quantity of an amplicon smaller than 180 bp conventionally corresponds to a degree of integrity or of apoptosis.
30 We designed Intplex as such the ends of the mutated and control amplicons will be separated by a minimum distance of 220 bp.

The integrity index (amplification of a long fragment / amplification of a short fragment) can be optimized to discriminate more in general healthy subjects and individuals with a pathology (cancer, for instance) by decreasing the size of the long fragment to a size > short fragment, and > 180bp.

5 Figure 9 shows an example of the use of the IntPlex method for the analysis of SNPs. In this example, the primer B1 includes in its 3' end the base change relative to the « wild type » status. The amplification with the primers A1 and A2 produces a fragment of 60 bp. The mutated fragment is amplified by the primers B1 and B2. The amplification with using A1 and B2 primers will produce a fragment of 300 bp.

10

Consequently, the invention consists in a method for the analysis of cfDNA that will integrate, based on the schematic shown as an example:

- The qualitative detection of the presence of a genetic polymorphism (such as SNP or mutation),
- 15 • The specific quantification of cirDNA;
- The evaluation of the apoptosis rate;

By the following calculation upon the scheme in figure 9:

- The qualitative detection of the presence of a genetic polymorphism (such as SNP or mutation):
- 20 - % B1B2 / A1A2 higher than a specific threshold;
- with B1B2 defined as the sequence that contains the genetic polymorphism (such as SNP or mutation).

The specific quantification of the total cirDNA: A1A2 quantity.

The specific quantification of the tumoral cirDNA: B1B2 quantity.

- 25 The evaluation of the rate of apoptosis by determining cirDNA fragmentation in term of %: B1B2 or A1A2 / A1B2.

If we model the integrated system by considering that X and Y is the distance on the DNA between the 5' ends of the primers, the integrated system Intplex can be modelled as such:

30

$$(A1A2) = (B1B2) = X$$

$$(A1B2) = Y$$

With $X < 180$ and $Y > X$

Ideally: $50 < X < 100$ and $200 < Y < 350$.

5 This way of identifying the presence or not of a gene mutation is very convenient because it is very fast and not very expensive. Moreover, it allows dispensing with sophisticated techniques like sequencing. On the other hand, sequencing leads to an answer without possible doubts (but for contamination or handling mistakes).

10 CirDNA is constituted of DNA of tumour and non-tumour origin. Very little is known about the respective contribution of these two types of cirDNA during tumour progression. IntPlex should allow advancing on this issue and this information will bring valuable diagnostic and/or prognostic benefits. Indeed, the quantity of mutated, and thus of tumour DNA, can be linked by this method directly to the quantity of non-tumour DNA. The calculation of this percentage can be correlated both with the total
15 quantity of released cirDNA and with the progression or regression of the tumour.

EXAMPLE IV: Contribution of the combination “mutation identification /quantification/integrity index” to the diagnosis of cancer

20 These three diagnostic parameters can be studied separately, but more sensibly a multiplexed analysis (particularly with the aid of bioinformatics software) will enhance their diagnostic value for the follow-up of cancer patients and their theragnostic value for the individualized therapeutic choice (Figure 10).

The contribution of these three factors could be modeled using an algorithm that will allow evaluating the risk incurred by each single cancer patient.

25 As a simple example we can calculate a diagnostic factor as $= ([M_i + 1) \times (Q + A)$.

Where M, Q and A are risk factor determined by detecting a mutation, quantifying tumoral cirDNA and evaluating a apoptotic index, respectively.

EXAMPLE V: Examples of application of the IntPlex technology**1) Detection of *KRAS* mutations in human blood samples in the context of cancer diagnostic**

The gene *RAS* (*KRAS* and *NRAS*) is subject to somatic mutations in more than
5 50 % of colon tumours and in about 50 % of adenomas bigger than 1 cm in diameter.
Conversely, it is very rarely mutated in small adenomas (less than 10 %). The
mutations, generally SNPs, do not interest *HRAS*, but affect the codons 12 and 13 of
KRAS and 12, 13 and 61 of *NRAS*. The exact role of these mutations is not known.
They could transform a small adenoma into a big, dysplastic adenoma, or be present
10 from the beginning in very proliferative cells. The mutations of *KRAS* are present in 30
to 40 % of colorectal tumours.

Thus there is a strong need of a simple and fast test to detect the SNP mutations
of *KRAS* in order to individually orient the patients with CRC towards a targeted anti-
EGFR therapy (6). Indeed, the activity of the powerful specific inhibitors of EGFR is
15 blocked when tumour cells carry a mutated *KRAS* gene. A general consensus has been
reached during the annual ASCO meeting in 2008 in which it is advocated that all
patients eligible for therapies that target EGFR should first be tested for *KRAS*
mutations before starting a first line therapy (6).

Sequencing DNA obtained from tumour sections represents at the moment the
20 «gold standard» for the identification of SNPs. This method is carried out after exeresis,
requires the presence of an anatomopathology laboratory and of an analysis laboratory,
and it is time-consuming and expensive. CirDNA could be a non-invasive and powerful
diagnostic tool if a specific method of analysis could allow its quantification and the
detection of mutations in a simple and rigorous way, particularly of the *KRAS* SNPs in
25 the theragnostic context of the anti-EGFR treatments.

We have thus adapted the IntPlex methodology to the more specific detection of
the *KRAS* SNPs in the theragnostic context of the targeted treatment of CRC. It could
bring a response to the urgent clinical need concerning the use of powerful specific
inhibitors of EGFR and the mutational status of *KRAS*.

30 In this system the mutation is located at the 3' end, thus leading to two possible
designs: Conventional Intplex and Reverse Intplex. As described before, the Intplex

system includes two primer pairs (Figure 9) that amplify DNA fragments of a size smaller than 100 bp. This amplification gives fragments that are distant 300 bp from one end to the other. This design includes a primer pair for the amplification of the « wild type » sequence that constitutes the reference amplification or standard (A1A2) and
5 another primer pair to amplify the mutated sequence (B1B2) (Figure 4). It will be possible to determine, by using the “reference” amplicon of exactly the same size and with a sequence in proximity of the other, the percentage of mutated DNA by calculating the ratios: (A1G12Vrev16 / B1B2) and (G12Vconv19/A1A2; in the figures the name of the primers is different) (see Figure 11 and A), for instance, for the
10 “Reverse” *KRAS* (Krev) and “Conventional” *KRAS* (Kconv) systems, respectively. Our previous results have shown the huge importance of the size of the amplicons generated by Q-PCR using a cirDNA sample. Moreover, the Q-PCR analysis of the fragments obtained with the primers A1B2 (size = 300pb) will allows us to determine the integrity index (DNA Integrity Index (DII)) (ratio between long and short fragments). DII
15 indicates the fragmentation status of cirDNA. The integrity index corresponds to the inverse of the apoptosis rate (termed as well the ctDNA fragmentation index).

a) Design of the Q-PCR IntPlex systems

Conventional Intplex (Figure 11A) uses the primer G12V typically utilized in
20 the literature for the detection of the *KRAS* G12V mutation and this primer is a sense oligonucleotide with the mutation localized at its 3' end. Reverse Intplex (Figure 11B) uses the antisense primer with the mutation at its 3' end. All the primers of these two systems have been selected by software (Material and Methods). The systems Intplex Kconv and Krev have been applied to detect the *KRAS* mutation G12V. The primers
25 that specifically detect this mutation have been designed to cover the mutated area of the *KRAS* gene (Figures 11A-11B).

The sense primer is conventionally defined as containing a sequence enclosed in the coding DNA strand. The conventional and the reverse Intplex systems differentiate by the sense or the antisense orientation of the mutation targeting primer.

30

b) Illustration of the importance of the size parameter for the quantification of cirDNA

In this experiment we have tested the two Intplex systems Krev and Kconv using cirDNA isolated from plasma samples of xenografted mice. Sequences of oligonucleotide primers and of chemically modified blocker oligonucleotides specifically designed for the Intplex system towards demonstrating its efficacy and sensitivity or detecting presence of the *KRAS* G12V or *BRAF* V600E mutations are presented in Table 2. In this example AS or Q-PCR with using blocker (ASB Q-PCR) method was used. The *BRAF* and *KRAS* mutations were detected with using “conventional” and “Inverse” IntPlex systems.

Table 2

Kras B1 conv G12V	5'-ACTTGTGGTAGTTGGAGCTGT	SEQ ID NO: 9
Kras B2 conv	5'-GAATGGTCCTGCACCAAGTAA	SEQ ID NO: 10
Kras conv B1	5'-ACTTGTGGTAGTTGGAGCTGG	SEQ ID NO: 11
Kras Conv B2	5'-GATTCTGAATTAGCTGTATCGTCAAGG	SEQ ID NO: 12
Kras Conv A1	5'-TAAGCGTCGATGGAGGAGTT	SEQ ID NO: 13
Kras Conv A2	5'-CCAGTTGACTGCAGACGTGTA	SEQ ID NO: 14
Kras Inv MutG12V	5'-AACTCTTGCCTACGCCAC	SEQ ID NO: 15
Braf conv A1	5'-GGAGAGCAGGATACACAGC	SEQ ID NO: 16
Braf conv A2	5'-AGCAAGCAATCAAAAACCTCC	SEQ ID NO: 17
Braf inv A1	5'-TCATGAAGACCTCACAGTAAAAA	SEQ ID NO: 18
Braf inv A2 V600E	5'-CACTCCATCGAGATTTCT	SEQ ID NO: 19
Braf inv B1	5'-CTAGAAAGTCATTGAAGGTCTCAAC	SEQ ID NO: 20
Braf inv B2	5'-TGATTTTTGTGAATACTGGGAAC	SEQ ID NO: 21
Braf V600E blocker	5'-CCATCGAGATTTCACTGTAGCT-PHO	SEQ ID NO: 22

10

Our results gave identical profiles with both Krev and Kconv (Figures 12 and 13).

Figures 12 and 13 clearly show that the determination of the concentration of cirDNA is equivalent when the amplicon is of the same size independently from the targeted sequences. Moreover, the results indicate that the value obtained for the 67 bp amplicons (A1A2 and B1B2) is 2.2 times higher and 1.4 times higher than the value obtained for the 189 bp amplicon (KrasH2) and 7.9 times and 9.0 times higher when compared to the values for the 312 and 320 bp amplicons (A1B2) of Kconv and Krev, respectively. Thus, the cross-analysis of these results confirms the accuracy of the cirDNA quantification by Q-PCR with primer systems that generate amplicons of identical sizes and, as a consequence, validates the two systems of analysis Krev and Kconv.

20

Table 3: Apoptosis rate (inverse of index of integrity) of different types of DNA using Krev and Kconv

DNA	Apoptosis rate	
	Krev	Kconv
Placental genomic DNA	0.78	1.28
Genomic DNA from SW620 cells	2.00	1.92
CirDNA from xenografted mice	8.33	8.34

The integrity ratio (inversely relative to the apoptosis rate) corresponds to the ratio between the concentration of short DNA fragments (smaller than 180 bp) and the concentration of long DNA fragments (bigger than 220 bp), i.e. A1B2/B1B2 for Krev and A1B2/A1A2 for Kconv. The apoptosis rate allows an estimate of the proportion of DNA of apoptotic origin and of necrotic origin and thus the determination the origin of cirDNA. With the system Krev we have obtained an apoptosis rate of 0.78 for placental genomic DNA (a DNA which is not released and not mutated) and of 2.00 for mutated DNA of cultured SW620 CRC cells. With the system Kconv we have obtained a rate of 1.28 for placental DNA and 1.92 for DNA from SW620 cells (Table 3).

We have also calculated the apoptosis rate (equivalent to the inverse of the integrity index) of cirDNA isolated from plasma samples of xenografted mice (with SW620 cells that produce tumours) using the two systems Krev and Kconv. With Krev the obtained apoptosis rate was 8.33 and with Kconv 8.34. The apoptosis rate of cirDNA is higher (about 8 and 4 times) than that of genomic DNA (placental DNA and DNA from SW620 cells, respectively). The apoptosis rate might be different when comparing the rates of placental and cell DNA due to their tissue (placenta) and cell origins and thus of the different sampling methods.

Remarkably, the apoptosis rates for the same sample are very similar with the two systems Krev and Kconv, highlighting the robustness of this measure. In addition to the direct comparison of the amplification of two sequences of identical size, this robustness comes from the extreme proximity of such sequences. Although of the same

size, a « reference » sequence that is far away from the mutated sequence (localized on another chromosome, for instance) would not allow a similar level of accuracy.

2) Detection of *BRAF* mutations in blood samples

5 The gene *BRAF* is subject to somatic mutations in more than 14 % of CRC tumours. The mutation V600E represents more than 90 % of the *BRAF* mutations. Like for the *KRAS* mutations, the *BRAF* mutations lead to inefficacy of the anti-EGFR treatment. The assessment of the presence (or not) of this mutation is thus required at the moment of (or more precisely before) the treatment of a patient with metastatic
10 CRC. Therefore, we have designed and developed a Conventional IntPlex system (mutation at the 3' end of the primer B1) for the detection of *BRAF* mutations in cirDNA (Figure 14).

 Plasma samples of a mouse xenografted with human CRC HT29 cells that contain in their genome the *BRAF* mutation V600E have been analysed with this Intplex
15 system (Figure 15).

 The mean concentration of the short reference amplicon (A1A2) was 31.5 ng/ml and was thus about 8 times higher than that of the long amplicon (4.2 ng/ml) in the cirDNA of the sample S4 HT29 (figure14). Similarly, the concentration of the fragment obtained with the primer pair human WT *BRAF* was 15 ng/ml and was about 2 times
20 lower than that of the short *BRAF* amplicon. These results clearly confirm that targeting a short DNA sequence (≤ 100 bp) produces a more important amplification of cirDNA extracts than targeting longer sequences (149 and 288 bp). The percentage of mutated human DNA relative to the WT reference sequence (A1A2) was 77.5%. It should theoretically have been 50% when taking into account the heterozygosity of the *BRAF*
25 mutation in this HT29 cell line (only one of the two alleles of the chromosome pair has the mutation). In order to assess the sensitivity of the Intplex system the DNA sample S4 from the plasma of the xenografted mouse was diluted to 1/10 in a sample of placental genomic DNA (Figure 15). The results summarized in Figure 15 indicate that the mutated DNA corresponds to 6.95 % of the non-mutated DNA and this is
30 approximately 10 times lower than what obtained with the undiluted S4 sample. The

amplification of the long sequence is slightly but significantly lower than that of the reference sequence (82.5 %).

The results (presented as percentages of the concentrations obtained by
5 amplification of the reference sequence A1A2) of these two experiments show the
importance of taking into account accurately the size of the amplicons and the validity
of the IntPlex system (Figures 15 and 16). Indeed, the calculation of the percentage of
mutated cirDNA can be dramatically different in function of the system of amplification
used as a reference: 77.5 % when using a reference of the same size (101 bp) and
10 56.7 % when using a reference of 288 bp. The finding that when cirDNA is diluted in
genomic DNA (1/10) the percentage of cirDNA is 6.95 % with the reference of the
same size and 8.45 % with the reference of 288 bp shows that the size parameter is less
important when cirDNA is diluted in genomic DNA.

The apoptosis rate varies considerably in function of the quantity of cirDNA
15 because it corresponds to 7.41 in the case of undiluted cirDNA and to 1.21 in the case of
diluted cirDNA (i.e., more than 6 times higher). This difference is important in many
respects and is characteristic of cirDNAs.

3) Description of the use of the IntPlex method for the analysis of cirDNA in human 20 plasma samples

The SNP mutations of *KRAS* (G12V, G12D, G12C, G13D and G12A) and the
BRAF mutation V600E are the cause approximately of 82 % of the cases of sporadic
mutated CRCs (i.e., 75 % of all CRCs). These mutations are present in 94 % of patients
in whom the *KRAS* and *BRAF* mutations are associated with CRC and who do not
25 respond to anti-EGFR therapies (about 50 % of all CRCs).

We have adapted the IntPlex technology to the detection of these mutations in
cirDNA extracts. Sequences of oligonucleotide primers and of chemically modified
blocker oligonucleotides specifically designed for the Intplex system towards detecting
presence of the above mentioned mutations are presented in Table 4. In this example AS
30 Q-PCR with using blocker (ASB Q-PCR) method was used. *BRAF* mutation and the 6

KRAS mutations were detected with using “conventional” and “Inverse” IntPlex ASB Q-PCR systems, respectively.

Table 4

5

Braf conv A1v1	5'-TTATTGACTCTAAGAGGAAAGATGAA	SEQ ID NO: 23
Braf conv A2v2	5'-GAGCAAGCATTATGAAGAGTTTAGG	SEQ ID NO: 24
Braf conv B2	5'-TAGCCTCAATTCTTACCATCCACA	SEQ ID NO: 25
Braf conv B1 V600E	5'-GATTTTGGTCTAGCTACAGA	SEQ ID NO: 26
Braf conv V600E Blocker	5'-GCTACAGTGAAATCTCGATGG-PHO	SEQ ID NO: 27
Kras Inv A1 6126	5'-GCCTGCTGAAAATGACTGA	SEQ ID NO: 28
Kras Inv B1 6379	5'-CCTTGGGTTTCAAGTTATATG	SEQ ID NO: 29
Kras Inv B2 6445	5'-CCCTGACATACTCCCAAGGA	SEQ ID NO: 30
Kras Inv A2 MutG12V16	5'-CTCTTGCCTACGCCAA	SEQ ID NO: 31
Kras Inv A2 MutG13D64	5'-GCACTCTTGCCTACGT	SEQ ID NO: 32
Kras Inv A2 G12D low	5'-CTCTTGCCTACGCCAT	SEQ ID NO: 33
Kras Inv A2 G12A low	5'-CTCTTGCCTACGCCAG	SEQ ID NO: 34
Kras Inv A2 G12S low	5'-TCTTGCCTACGCCACT	SEQ ID NO: 35
Kras Inv A2 G12C low	5'-TCTTGCCTACGCCACA	SEQ ID NO: 36
Kras Inv mut Blocker	5'-GCCTACGCCACCAGCTC-PHO	SEQ ID NO: 37

As an example, Figure 17 shows the results obtained with plasma samples from a patient with CRC who apparently carried the *KRAS* mutation G12V (CRC1), a CRC patient who did not seem to have that mutation (CRC2) and a healthy individual (HHP1).

10

In CRC1, 68 % of the fragments of cirDNA carry the mutation *KRAS* G12V, whereas the percentage for the other *KRAS* mutations does not go above 1.2 % for this patient.

15

In CRC2, 0 to 6.6 % of the cirDNA fragments appear to carry *BRAF* or *KRAS* mutations.

In HHP1, 0 to 3.2 % of the cirDNA fragments appear to carry *BRAF* or *KRAS* mutations.

CRC2 data show significant % of apparently mutated cirDNA but the level appears the same for 4 mutations. Given the fact that, with the exception of very rare cases, these mutations are mutually exclusive the threshold of the % mutated cirDNA

20

for specifically defining the mutational status is not reached in the case of CRC2. Thus values obtained for quantifying mutated cirDNA in CRC2 plasma correspond to non-specific effect. The positivity threshold could be fixed at least at 7 % here, but a study using an important number of samples is needed in order to determine it for each mutation. Moreover, an algorithm could be used to integrate the threshold within a sample in order to estimate the discrimination of the percentage of a mutation relative to the percentage of the others. Nevertheless, this figure shows that only CRC1 carries a mutation (G12V).

Remarkably, these results and other on various clinical samples (not shown) show that the proportion of fragments of mutated cirDNA appears to be extremely high (between 17 % and 70 %) when compared to the results described in the literature (on average 1 % and never higher than 10 %) (5, 7). This illustrates the capacity of our method to produce a sensitive and specific analysis of tumour cirDNA and its innovative character.

As a consequence CRC1 patient in contrast to CRC2 patient can not unfortunately be treated with EGFR inhibitor.

Thus this adapted Intplex method which is part of the present invention appears to be a simple method for the analysis of cirDNAs based on the accurate knowledge of their size population. It relies on a precise choice of oligonucleotide primers that allow their direct analysis in one single step of Q-PCR. Three independent sets of data from the analysis of circulating nucleic acids (NA) (1. detection of mutation(s), 2. exact quantification of the tumoral and total cirDNA concentration and 3. estimate of a ratio concerning the apoptotic origin of the cirDNA) can be integrated in the same test.

25

EXAMPLE VI: CirDNA concentration profiles for HHP and CRC subjects

CirDNA concentrations were determined from plasma samples from three CRC patients and three healthy individuals by q-PCR with using the primer sets amplifying fragment of 60, 73, 101, 145, 185, 249, 300, 357, 409 bp, as previously described. Concentration profiles obtained are specific to either CRC or healthy subjects for all of them. Mean maximal value was 6.19 and 943.59 ng/ml plasma for HHP and CRC

subjects, respectively. The highest discrimination by calculating the ratio of HHP/CRC integrity index was obtained when using the 300/60 and 300/73 ratio (8.18 and 10.07, respectively), confirming the previous data. Ratio of 409/60 apparently is the highest but it was arbitrarily not considered since concentration obtained by amplifying the 409
5 fragment in CRC plasma is near the analysis sensitivity. By subtracting the concentration obtained by one fragment size amplification from the following, respective to increasing size, the % of the amount of the cirDNA within the 60-409 bp range between both successive amplicon sizes can be estimated (Given C_n the concentration of ctDNA when detecting an amplified fragment of a size n and C_{n+1} the
10 cirDNA concentration when detecting the amplified fragment of the proximate higher size in the increasing amplified fragment size serie, the concentration existing between both size is calculated as $C_n - C_{n+1}$).

Values expressed in % of ctDNA vs ctDNA length fraction (range) are presented
15 in histograms in Figure 18. Data suggest that CRC and HHP plasmas present same profile of cirDNA amount in the 60-73, 73-101 and 101-145 bp ranges with noticeably higher level for CRC plasma in the 73-101 range. In contrast to the absence of HHP cirDNA from 145-185 to 357-409 bp ranges, cirDNA level is significantly detected, decreasing from 9 to 2 %. High proportion (35 %) was found for cirDNA from HHP of
20 size higher than 409 bp, in contrast to the very low level determined for CRC cirDNA (2 %).

Clearly, these data show high discrimination between HHP and CRC plasmas which is not expected from man of the art for the time being.

25 **EXAMPLE VII: Parameters for logistic function proposed in a method for diagnosis or prognosis a pathological or physiological state, such as the presence of a tumor or tumor progression in a patient, said pathological or physiological state being associated to a SNP gene marker (i.e presence of a mutation associated to a cancer)**

Values which can be combined for through a logistic function including at least two biomarker in order to obtain a end value which is relevant of the nature of the diagnosis or the prognosis

(See Figure 9)

5 $(A1A2) = (B1B2) = X$

$(A1B2) = Y$

With $X < 180$ and $Y > X$

Ideally: $50 < X < 100$ and $200 < Y < 350$

Where:

10 - B1B2 is defined as the sequence that contains the genetic polymorphism (such as SNP or mutation)

- A1A2 is defined as the sequence that does not contain a genetic polymorphism (such as SNP or mutation) and is localized on the same DNA strand

15 - The numbers correspond to the number of nucleotides of the amplified sequence (amplicon)

- X and Y are the distance on the genomic DNA between the 5' ends of the primers used for amplifying the short and the longer amplicon, respectively.

These biomarkers allow:

1. The qualitative detection of the presence of a genetic polymorphism (such as SNP or mutation) by determining the % B1B2 / A1A2 at a higher level than a specific threshold for each genetic polymorphism primer sets.

20

With B1B2 defined as the sequence that contains the genetic polymorphism (such as SNP or mutation).

2. The specific quantification of total and tumoral cirDNA: A1A2 and B1B2 quantity, respectively.

25

3. The evaluation of the DNA fragmentation index (in the present invention, the wording "apoptosis rate", "DNA fragmentation index" and "integrity index" have the same meaning): % B1B2 or A1A2 / A1B2.

- The applicability to all circulating nucleic acids (DNA, RNA, siRNA, miRNA, ...).

30

- The use of nucleic acid of specific length, for instance <180 bp and ideally <100 bp, as nucleic acid standard for the Q-PCR calibration.

EXAMPLE VIII: Demonstration that ctDNA of size below 100 bp are of significant proportion and that the previously established hypothesis based on electrophoresis analysis is wrong.

Agarose gel electrophoresis of 20 µg of ctDNA extracted from two CRC patients (CRC021 and CRC019). Ladder are made of multiple of 100 bp DNA fragments. Portions of the gel were removed just after the end of the run. For CRC021 one portion of the gel corresponding to 10 to 440 bp were removed and subjected to Q-PCR. For CRC019 two portions of the gel corresponding to 30 to 130 and 130 to 500 bp were removed and subjected to Q-PCR. Conditions of Q-PCR analysis was performed as described earlier when quantifying ctDNA and detecting the 73 bp, 145 bp and 300 bp amplicon of the KRAS intron as previously described.

In CRC021 plasma, 47% of total ctDNA were found between 73 and 145 bp while 36% and 17% were found in the 145-300 and >300 bp ranges, respectively.

In CRC019 plasma, 61% of total ctDNA were found between 73 and 145 bp while 35% and 5% were found in the 145-300 and >300 bp ranges, respectively. In the gel portion between 30 and 130 bp 57% of total ctDNA was observed (see figures 19A and 19B).

These data prove that ctDNA of size lower than 180 bp and in particular lower than 100bp exist in a significant amount. Thus electrophoresis is not an appropriate analytical method to appreciate ctDNA size. This is the first demonstration that the previously established hypothesis based on electrophoresis analysis which apparently showed that ctDNA are of size higher than 180 bp, is wrong.

We postulate that ctDNA fragments of size below 180 bp are not visible following electrophoresis and labelling with fluorescent dye because they are below the signal threshold owing to:

1. ctDNA fragments below 180 bp might vary from one nucleotide from another leading to low local concentration at on precise size;

2. the fluorescent dye such as the Sybre green, have a maximal level of intercalation (i.e. one Sybre green molecule every 23 nucleotides) drastically limiting signal intensity of low size ctDNA. For instance, a 69 bp DNA fragment has 3-fold less signal than that of 207 bp fragment.

5

EXAMPLE IX: DII as determined from the ctDNA concentration of ctDNA of size below 100 bp, such as 60 bp, significantly discriminate healthy and CRC individuals

Comparison of the DII values (Table 5) from genomic DNA, and ctDNA from mice plasma (non-xenografted and xenografted) and (see figure 20) from human plasmas (healthy and CRC). The DII was estimated by the ratio of the concentration obtained by targeting a 300 bp sequence and a 60 bp sequence in a KRAS region. DII mean value of HHP (n=16) is significantly different from DII mean value of CRC (n=12) (mean, 0.565 and 0.122, respectively; $p < 0.001$). A similar difference was observed in the animal model where mean DII is 0.447 for healthy plasma ctDNA (n=9), 0.645 for non tumour-derived ctDNA (n=9) and 0.027 for tumour derived ctDNA (n=9).

This buttress the discovery of detecting amplicon of size lower than 100 bp in particular 60 bp as used here for determining a DII.

20

Table 5: Comparison of the DII values from genomic DNA, and ctDNA from mice plasma (non-xenografted and xenografted)

		mean DII
Genomic DNA		
	SW620 cells	1.120
	Human placental DNA	0.720
Circulating DNA		
<i>Animal model</i>	Healthy mice (n=9)	0.447
	Non tumor derived ctDNA from xenografted mice (n=9)	0.645
	Tumor derived ctDNA from xenografted mice (n=9)	0.027
<i>Human individuals</i>	Healthy (n=16)	0.565
	CRC (n=12)	0.122

EXAMPLE X: DII calculated with the primer design of the invention and in various gene regions show high accuracy and low variability

There are two configurations about the design of the primers used in the multiplex method according to the invention: conv and inv. Here we determined the DII from a CRC patient plasma with using the conv and the inv configuration in the KRAS and BRAF region (containing the 2th exon hot spot mutation and the V600E, respectively), the conv configuration in the 2th intron of the KRAS gene (BRAF conv). We have compared those DII with that calculated in distant region within the same gene (long KRASconv/ short KRAS int, representing the ratio of the concentration obtained with using the primer pair leading to the amplification of the long sequence as used in KRAS conv to that obtained with using the primer pair leading to the amplification of the short sequence as used in KRAS int) and with that calculated in distant region of two different genes (long KRASconv/ short BRAF inv, representing the ratio of the concentration obtained with using the primer pair leading to the amplification of the long sequence as used in KRAS conv to that obtained with using the primer pair leading to the amplification of the short sequence as used in BRAF inv).

First, data clearly demonstrate first the high accuracy and low variability of the DII value calculated upon our invention whatever the gene region, owing DII value vary from 0.077 to 0.094 (coefficient of correlation= 9.1%) (see figure 21).

Second, the value obtained with using primer pairs targeting distant DNA sequences either within the same gene or different genes are different and more precisely significantly lower (0.061 and 0.048, respectively) than those found according the primer designs of the invention.

Maximal coefficient of correlation of the value from the Q-PCR analysis and DNA extraction, under the previously described experimental conditions, is 23% (n=12).

EXAMPLE XI: Determination of various indexes involving the amount of the ctDNA size fraction below 100 bp

Various indexes were determined from data presented in Figure 18. Those indexes were calculated from different size fraction (see table 6).

5

Table 6:

	CRC	HHP	Fold difference
% < 100 bp	65%	46%	1.4
DII 300/60	0.025	0.355	14.2
SFR 409 / <100	0.038	0.770	20.3
SFR <100 / 145-409	3.3	460	139.0

% < 100 bp, percentage of ctDNA fragments of size below 100 bp (more precisely from the 60-100 bp fraction);

10

DII 300/60, ratio of the concentration of ctDNA fragments of size higher than 300bp to that of total ctDNA;

SFR 409 / <100, ratio of the concentration of ctDNA fragments of size higher than 409 bp to that of the concentration of 60-100 bp fraction;

15

SFR <100 / 145-409, ratio of the concentration of ctDNA fragments of the 60-100 bp fraction to that of ctDNA fragments of the 145-409 bp fraction.

Data clearly show that determining the concentration of ctDNA fraction below 100bp is of great interest and makes possible to largely discriminate between plasma of CRC patients and healthy subjects. Second, the use of ratio of ctDNA size fraction such as SFR greatly helps towards this goal.

20

EXAMPLE XII: Determination of various parameters, such as SFR, indicative of ctDNA fragment size pattern

We studied the size pattern of mutated ctDNA in comparison with that of non-mutated ctDNA. Towards this goal we used a set of primers amplifying increased target size within the same region. This set generates the amplification of sequences on the hot spot region of the KRAS gene (12 and 13th codon of the 2nd exon) where the forward primer for every primer pair is designed to specifically target a point mutation of this region or the wild type sequence (See Table 7 below and figures 22A-22E). These sets were cautiously selected to promote high sensibility and high specificity for quantifying either mutated or not mutated target sequences (see Table 8 below).

Table 7:

Samples	Q-PCR target	<138 %	138< >300 %	>300 %	DII	SFR
Healthy (n=9)	KRAS intron	66.20	0	37.90	0.45	20
CRC4	mut. KRAS 2th exon	70.11	23.60	6.41	0.06	2.97
CRC5	mut. KRAS 2th exon	74.10	17.90	8.00	0.08	4.14
CRC6	mut. KRAS 2th exon	89.20	6.00	4.80	0.05	14.87
CRC14	mut. KRAS 2th exon	52.11	30.21	17.60	0.18	1.73
CRC4	wt. KRAS 2th exon	10.62	77.76	11.69	0.12	0.14
CRC5	wt. KRAS 2th exon	0	89.00	11.10	0.11	0
CRC6	wt. KRAS 2th exon	0	77.10	30.10	0.30	0
CRC14	wt. KRAS 2th exon	18.36	49.77	32.04	0.32	0.37

Primers used to carry out this experiment are: (see Table 8):

Table 8:

				Sequence (SEQ.ID N°)	
Human	KRAS	Kras 60 Hf	sense	GCCTGTGACCTACAGTGAAAA (220)	60
		Kras 73 Hf	sense	CCCTACACGTAGAGCCTGTGA (221)	73
		Kras 101 Hf	sense	GAGATGGTGGAAGAACAGGTG (222)	101
		Kras 145 Hf	sense	TGGGCTGTGACATTGCTG (223)	145
		Kras 185 Hf	sense	ATCTGCCTCCGAGTTCCTG (224)	185
		Kras 249 Hf	sense	TGGAAGAGCATAGGAAAGTGC (225)	249
		Kras 300 Hf	sense	GGTCCTTTCCGTGTGTAGG (226)	300
		Kras 357 Hf	sense	GGCATCTCTAGGACGAAGGT (227)	357
		Kras 409 Hf	sense	GCCTCCCTTTCCAGCACT (228)	409
		Kras 145-300Hr	antisense	TGACCAAGCAAAACAGACCA (229)	-
Human	KRAS	Kras 46 Hr	antisense	GCTGTATCGTCAAGGCACTC (230)	46
		Kras 82 Hr	antisense	TTGGATCATATTCTGCCACAA (231)	82
		Kras 138 Hr	antisense	CAAAGAATGGTCCTGCACC (232)	138
		Kras 200 Hr	antisense	TGAAAATGGTCAGAGAAACCTT (233)	200
		Kras 250 Hr	antisense	TGAAACCCAAGGTACATTTTCAG (234)	250
		Kras 300 Hr	antisense	GAACATCATGGACCCTGACA (235)	300
		Kras 350 Hr	antisense	TTCTACCCTCTCACGAAACTCTG (236)	355
		Kras 400 Hr	antisense	AAAGATTGTCTTTTAGGTCCAGATAGG (237)	390
		KrasNonMutated Hf	sense	GTAGTTGGAGCTGGTGGC (238)	-
		Kras G13D Hf	sense	GTAGTTGGAGCTGGTGA (239)	-
		Kras G12V Hf	sense	TTGTGGTAGTTGGAGCTGT (240)	-
		Kras G12D Hf	sense	TGTGGTAGTTGGAGCTGA (241)	-
		Kras G12S Hf	sense	ACTTGTGGTAGTTGGAGCTA (242)	-
		Kras G12A Hf	sense	TGTGGTAGTTGGAGCTGC (243)	-

We then determined the % of mutated ctDNA by determining the concentration with using the primer set amplifying the shorter target (82bp) from the total ctDNA concentration (being the sum of the concentration of the mutated and the non mutated ctDNA).

Determination of various parameters indicative of ctDNA fragment size pattern. a, data are presented in a table (Table 7) or plotted in histograms (See Figure 22A-22E). Size fraction is expressed as % to the highest value obtained in each set. The proportion of ctDNA fragments <138 bp or 145 bp was determined by subtracting the concentration determined by using the primer set amplifying the 82 bp target to that of using the primer set amplifying the 138 bp target. When the value is negative data is arbitrarily expressed as 0. The proportion of ctDNA fragments >300 bp was determined by using the primer set amplifying the 300 bp target. The ctDNA integrity index (DII)

was determined by calculating the ratio of the concentration determined by using the primer set amplifying the 300 bp target to the concentration determined by using the primer set amplifying the 82 bp target. The size fraction ratio (SFR) was determined by calculating the ratio of the concentration of fragments <138 or 145 bp to the concentration of fragments between 138-145bp and 300 bp. Number under the histograms: 4,5,6,14, plasmas from CRC patients with positive mutational status for KRAS (CRC4-6 and CRC14). H, healthy individuals (n=9).

The proportion of various ctDNA size fractions, the integrity index and a size fraction ratio (we termed SFR) of the human plasmas from healthy individuals, and from four CRC patients with a KRAS point mutation are summarized in figure . Mutant ctDNA are mostly composed of fragments <138bp while non mutant ctDNA are mostly constituted of fragments in the 138-300 bp range and very poorly of fragments <138bp. alternatively, ctDNA of healthy individuals seem clearly constituted of fragment <138bp and >300bp with no apparent fragment between 138 and 300bp.

Data clearly show that ctDNA size fraction analysis especially by determining size fraction ratio, such as the SFR we calculated in this study, might help in distinguishing KRAS mutated vs. non mutated ctDNA. In addition, size fraction analysis could disclose indication about the nature of the ctDNA release mechanism. Nonetheless, data suggest that non tumour-derived ctDNA in CRC patient might mainly originate from apoptosis in contrast to ctDNA from healthy individuals and to a lesser extent tumour-derived ctDNA. Calculation of such indexes should facilitate size pattern analysis since amplification experiments with serial nested Q-PCR as performed here is time consuming.

EXAMPLE XIII: Comparison of the determination of the % mutated fragments from total ctDNA upon the use of the amplicon length

The quantification of ctDNA was determined by amplifying increasing size targets of 82, 138, 300 bp (see Table 9) from the plasma of patients with tumour cells bearing the KRAS G12D, KRAS G12D and KRAS G13D mutation in CRC40, CRC50 and CRC60, respectively. Mutated ctDNA quantification was performed with primer pairs constituted of the same reverse primer containing in 3' the mutation and of

primers targeting region distant to 82,138 and 300 bp from both 5' extremities. Non mutated ctDNA was quantified with using the same forward primers and the same reverse primer with wild type sequence (data from previous exemple...). Total ctDNA corresponds to the sum of the mutated fragments to the non mutated fragments.

5

Clearly data show that the determination of the % of mutant ctDNA fragments vary upon the size of the amplicon detected, and demonstrate that quantifying mutant ctDNA fragments is much higher when amplicon size is lower than 100 bp. This leads to a more accurate detection of the presence of a mutation from ctDNA by determining the percentage of mutants fragments; a positive detection being determined when this value is above the percentage of a threshold. There is for each CRC plasma about 2.5, 3.4 and 6.3 –fold increase of the % mutated when detecting the 82 bp amplicon as compared with detecting 138 bp amplicon while the proportion in % of ctDNA on which the value is calculated was 3.3, 3.9 and 9.3 fold higher, in CRC4, CRC5 and CRC6, respectively (see Table 9).

15

Table 9:

	% mutated from total ctDNA	proportion in % of ctDNA on which the value is calculated
	CRC4, G12D	
KRAS 82 bp	26.0	100.0
KRAS 138 bp	10.5	29.9
KRAS 300 bp	15.9	6.4
	CRC5, G12D	
Kras 82 pb	17.4	100.0
Kras 138 pb	5.1	25.9
	CRC6, G13D	
Kras 82 pb	52.7	100.0
Kras 138 pb	8.3	10.8

20

EXAMPLE XIV: Additional data showing the full agreement between KRAS mutational status determined by biopsy sequencing and by the method based on ctDNA according to the invention (see Table 10)

5 Table 10:

Sample	Clinical status	<i>KRAS</i> Status Sequencing	<i>KRAS</i> Status Intplex
CRC 1	metastatic ADK rectum; progression under chimio	WT	WT
CRC 2	metastatic ADK rectum; 3 meta foie	<i>KRAS</i> mutated	<i>KRAS</i> mutated
CRC 3	metastatic ADK rectum; progression under chimio	WT	WT
CRC 4	metastatic ADK colon; progression under chimio	<i>KRAS</i> mutated	<i>KRAS</i> mutated
CRC 5	metastatic ADK colon; progression meta	WT	WT
CRC 6	metastatic ADK rectum; progression meta	WT	WT
CRC 7	metastatic ADK colon; progression meta, Stage IV	WT	T
CRC 8	metastatic ADK rectum; progression under chimio	WT	WT
CRC 9	metastatic ADK rectum; progression under chimio	WT	WT
CRC 10	metastatic ADK colon; progression meta, Stage IV	G12D	G12D

EXAMPLE XV: DII calculated with ctDNA quantification from the detection of amplicons of various size

Table 11 and Table 12:

Xenografted mice										
DII	300/150	300/100	250/101	250/150	249/60	300/60	357/60			
tumor-derived	0,251	0,094	0,106	0,284	0,03	0,007	0,024			
non tumor-derived	0,959	0,404	0,441	1,046	0,429	0,645	0,517			
control	0,722	0,353	0,502	1,027	0,279	0,447	0,426			
DII ratio control/tumor-derived	2,87	3,75	4,73	3,62	9,3	63,86	17,75			

Clinical samples	300/101	300/145	300/185	249/73	249/101	249/145				
DII ratio HHP/CCR	5,84	5,44	3,84	6,12	4,88	4,18				
DII ratio HHP/CCR	73/60	101/60	145/60	185/60	300/60	357/60	409/60			
	0,99	1,37	1,47	2,56	8,18	7,8	13,88			
DII ratio HHP/CCR	101/73	145/73	185/73	249/73	300/73	357/73	409/73			
	1,49	1,52	2,7	7,34	10,07	7,95	20,64			

We determined DII with PCR amplification of various short and long sequences from the animal experiment (see Table 11 below and Examples above) and the size profiling of ctDNA of clinical samples (see Table 12 below and Examples above).

5 If we consider that the concentration determined by detecting the short amplicon such as 60 bp corresponds to the total ctDNA concentration, the DII corresponds to the % of the fraction of the ctDNA of size higher than the long amplicon.

Data show that the highest difference between healthy and CRC plasmas were observed when calculating the DII with detecting amplicon of size <100bp such as 60 or
10 73 bp and amplicon of size >249bp. The DII calculated from the mouse experiment confirm this observation.

When compared, more precisely, with DII which are calculated with using the Q-PCR detection of amplicon of size higher than 100 bp, such as 101 or 145 bp, DII calculated with 60 or 73 bp are about 1.5 fold lower in clinical samples and are about
15 17-fold lower in xenografted mice. Thus use of detection of amplicon size lower than 100 bp and in particular lower than 73 bp, allows a higher discrimination between healthy individuals and CRC patients.

To note the use of the fraction > 409 bp showed higher discrimination between CRC and healthy individuals than the use of the fraction > 300 bp.

20

EXAMPLE XVI: Description of the DNA regions located downstream or upstream of a mutation when using the method according to the present invention to detect a mutation (particularly the said IntPlex method)

25 Numerous reports described targeting the region located downstream or upstream of a mutation when proposing to detect a mutation. For instance, various primers (18 to 30 nucleotides) were designed to hybridize with the DNA sequence corresponding to that region. Here we claim to protect the use of molecular entities targeting other regions according to the description of the design of the primers used for
30 that method (Figure 11) in either the conv or rev configuration (respectively conventional and inverse (inv) configuration, named also conv and rev (or inv) design for the molecular entities associated respectively with these conv and inv

configurations). We can describe those regions from the mutation to be detected given the following parameters:

- primer minimal size= 15 nucleotides
- primer maximal size=30 nucleotides
- 5 • spacing between 2 primers (between the 3' extremities of both primer)= 5 bp
- amplicon size range for A1A2 or B1B2 = 35 to 100 bp
- A1B2 being in the 250-450 bp size range

In the case of the conv design, as presented in figure 11A, the molecular entities
10 to be protected are those which target:

- the region where the B2 primer should hybridize and which is located from 5 to 85 nucleotides downstream from the position of the mutation in the non sense DNA strand.
- the region where the primer pair A1A2 can be designed within the 430-100
15 nucleotides upstream from the position of the mutation to be detected.

In the case of the inv design, as presented in figure 11B, the molecular entities to be protected are those which target:

- the region where the A1 primer should hybridize and which is located from 5 to
20 85 nucleotides upstream from the position of the mutation in the non sense DNA strand.
- the region where the primer pair B1B2 can be designed within the 100-430 nucleotides downstream from the position of the mutation to be detected.

A) Example of DNA region to be targeted upon our method when BRAF V600E point
25 mutation is of interest

a) See Figure 23 which shows the regions where molecular entities such as primers could target upon our multiplex method applied to this mutation.

Selected oligonucleotides useful for that method applied to this mutation (see Tables 13
30 and 14).

b) Selected oligonucleotides for B2 primers for BRAF convention system (see Table 13)

Table 13:

Primer B1:

B1: GATTTTGGTCTAGCTACAG (SEQ ID NO. 38)

5 Or containing the mutation region:

Primer B2:

	Starting Region	Sequence	SEQ ID NO.
10	172098	ATTCTTACCATCCACAAAATGG	40
	172105	AGCCTCAATTCTTACCATCCA	41
	172104	GCCTCAATTCTTACCATCCA	42
	172104	GCCTCAATTCTTACCATCCAC	44
	172105	AGCCTCAATTCTTACCATCCAC	45
15	172103	CCTCAATTCTTACCATCCACAA	46
	172118	TCAGTGGAAAAATAGCCTCAA	47
	172117	CAGTGGAAAAATAGCCTCAATTC	48
	172117	CAGTGGAAAAATAGCCTCAATTCT	49
	172119	ATCAGTGGAAAAATAGCCTCAA	50
20	172118	TCAGTGGAAAAATAGCCTCAAT	51
	172497	TTCAACAGGGTACACAGAACA	52
	172491	CAGGGTACACAGAACATTTTGAA	53
	172489	GGGTACACAGAACATTTTGAACA	54
	172493	AACAGGGTACACAGAACATTTTGA	55
25	172010	GATTTTGGTCTAGCTACAG	56
	172496	TTCAACAGGGTACACAGAACATTT	57
	172537	TGTGGATCACACCTGCCTTA	58
	172535	TGGATCACACCTGCCTTAAA	59
	172010	GATTTTGGTCTAGCTACAG	60
30	172536	GTGGATCACACCTGCCTTAAA	61
	172598	GATTGCGAACAGCTTCTCTG	62
	172531	TCACACCTGCCTTAAATTGC	63

c) Selected oligonucleotide primers for A1 for BRAF reverse (inverse) system
(see Table 14)

Table 14

- 5 Primer A2 containing the mutation region:
CACTCCATCGAGATTTC (SEQ ID NO. 19)

Primer A1 (SEQ ID NOs. 65 to 81)

- TCATGAAGACCTCACAGTAAAAATA
10 TGTTTTCCTTTACTTACTACACCTCA
CTGTTTTCCTTTACTTACTACACCTCA
TGTTTTCCTTTACTTACTACACCTCAG
TTTTCCTTTACTTACTACACCTCAGA
GTTTTCCTTTACTTACTACACCTCAGA
15 TTATTGACTCTAAGAGGAAAGATGAA
GCCCCAAAAATCTTAAAAGCA
AAGCCCCAAAAATCTTAAAAGC
TTCAAGCCCCAAAAATCTTAAA
GCCCCAAAAATCTTAAAAGC
20 AGCCCCAAAAATCTTAAAAGC
ACACATTTCAGCCCCAAAA
AACACATTTCAGCCCCAAA
CACATTTCAGCCCCAAAA
TAACACATTTCAGCCCCAAA
25 CACATTTCAGCCCCAAA

B): Example of DNA region to be targeted upon our method when the hot spot point mutations of the 2nd and 3rd codon of the second exon of the KRAS gene is of interest

- a) See Figures 24A-24E which shows the regions and the primers where
30 molecular entities such as primers could target upon our multiplex method applied to this mutation.

KRAS region 2th exon

Upon: KRAS (ENSG00000133703) from the Ensembl data bank

v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog [Source:HGNC
Symbol;Acc:6407

Point mutation ; 6151

5 Design KRAS conventional and inverse: see figures 24A- 24E.

b) Selected DNA oligonucleotides for A1A2 primer pair for detecting KRAS
exon 2 hot spot mutations upon conv configuration (see Table 15)

10 Table 15:

Primer B1:

Mutation KrasG12V: TTGTGGTAGTTGGAGCTGT (SEQ ID NO. 244)

Mutation KrasG13D: GTAGTTGGAGCTGGTGA (245)

15 Mutation KrasG12D: TGTGGTAGTTGGAGCTGA (246)

Mutation KrasG12S: ACTTGTGGTAGTTGGAGCTA (247)

Mutation KrasG12A: TGTGGTAGTTGGAGCTGC (248)

Mutation KrasG12C: ACTTGTGGTAGTTGGAGCTT (249)

20

Primer B2: (SEQ ID NOs 83 to 120)

CTTAAGCGTCGATGGAGGAG

TGATTGAATTTTGTAAGGTATTTGAA

CATGATTGAATTTTGTAAGGTATTTG

25 TCATGATTGAATTTTGTAAGGTATTT

GATTGAATTTTGTAAGGTATTTGAA

ACGTCTGCAGTCAACTGGAAT

TGCAGTCAACTGGAATTTTCAT

TCTGCAGTCAACTGGAATTTT

30 GTATCGTCAAGGCACTCTTGC

CGATACACGTCTGCAGTCAAC

ACGATACACGTCTGCAGTCAAC

TACGATACACGTCTGCAGTCAA
CTTAAGCGTCGATGGAGGAG
TAAGCGTCGATGGAGGAGTT
CGTCGATGGAGGAGTTTGTA
5 AAGCGTCGATGGAGGAGTTT
TCTTAAGCGTCGATGGAGGA
TTTCTTAAGCGTCGATGGAG
TTTTTCTTAAGCGTCGATGG
TTTTTCTTAAGCGTCGATGG
10 GCATTTTTCTTAAGCGTCGAT
TGCTCTATGTAGCATTTATGCATTTTC
TGCTCTATGTAGCATTTATGCATTTT
CTGTCTATGTAGCATTTATGCATTTT
TGCTCTATGTAGCATTTATGCATTTT
15 CTGTCTATGTAGCATTTATGCATTTT
TCTGGCTATTTAGATAGAACAACCTTGA
CTGGCTATTTAGATAGAACAACCTTGA
GCAGAACAGCAGTCTGGCTA
CTTTAGCCGCCGCAGAAC
20 CAGAACAGCAGTCTGGCTATTTA
GAACAGCAGTCTGGCTATTTAGA
AGAACAGCAGTCTGGCTATTTAGA
TCCTTTGAGAGCCTTTAGCC
ATCCTTTGAGAGCCTTTAGC
25 TGATCCTTTGAGAGCCTTTAGC
GTATCGTCAAGGCACTCTTGC
ATGATCCTTTGAGAGCCTTTAGC

30 C) Selected DNA oligonucleotides for A1A2 primer pair for detecting KRAS
exon 2 hot spot mutations upon Inverse configuration (see Table 16)

Table 16:

Primer A2:

Sequence for A1for KRASinv:

5 A2: AAGGCACTCTTGCCTACGCCAC (SEQ ID NO. 250)

Or containing the mutation region:

	Mutation KrasG12V: AAGGCACTCTTGCCTACGCCAT	(251)
10	Mutation KrasG13D: AAGGCACTCTTGCCTACGCCAA	(252)
	Mutation KrasG12D: AAGGCACTCTTGCCTACGCCAA	(253)
	Mutation KrasG12S: AAGGCACTCTTGCCTACGCCAA	(254)
	Mutation KrasG12A: AAGGCACTCTTGCCTACGCCAC	(255)
	Mutation KrasG12C: AAGGCACTCTTGCCTACGCCAT	(256)

15

A1: SEQ ID NOs 163 to 196 (Amo 2 to Amo35, see figure 24D)

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CLAIMS

1. A method for the diagnosis, prognosis, or for assessing the evolution of a cancer in an individual, said method comprising calculating an index of integrity of cell free DNA in a body fluid sample obtained from said individual,

wherein the index of integrity is calculated by a method comprising (i) determining from an amplification by polymerase chain reaction (PCR) of a short size sequence from cell free DNA in said body fluid sample, the concentration or amount of a short amplicon, wherein said short size sequence has a length between 50-100 bp; (ii) determining from an amplification by PCR of a long size sequence from cell free DNA in said body fluid sample, the concentration or amount of a long amplicon, wherein said long size sequence has a length superior to 101 bp; and (iii) calculating the ratio of the concentration or the amount of said amplicons of long size and of short size, and

wherein the ratio long/short size is indicative of the presence of a cancer.

2. The method according to claim 1, wherein said long sequence in (ii) has a length comprised between 180bp and 450bp.

3. The method according to claim 1, wherein said short sequence in (i) has a length between 60-100bp, and said long sequence in (ii) has a length higher than 200bp.

4. The method according to claim 1, wherein said short sequence in (i) has a length between 50-100bp, and said long sequence in (ii) has a length higher than 180bp.

5. The method according to any one of claims 1 to 4, wherein the index of integrity is calculated repeatedly during an interval of time on body fluid samples from the individual,

wherein a decrease of the index of integrity during the interval is indicative of the progression of cancer in the individual.

6. The method according to any one of claims 1 to 5, wherein the body fluid sample is selected from the group consisting of whole blood, serum, plasma, urine, saliva, sputum,

colonic effluent, bone marrow, lymph, cerebrospinal fluid, lacrymal fluid, sweat, milk, faeces, bronchial lavages and ascites.

7. The method according to any one of claims 1 to 6, wherein said cell free DNA is circulating DNA.

8. The method according to any one of claims 1 to 7, wherein the long sequence partially or fully comprises the short sequence.

9. The method according to any one of claims 1 to 8, wherein the PCR is Q-PCR.

10. A method for the diagnosis, prognosis, or for assessing the evolution of a cancer in an individual, said method comprising:

a) calculating a size fraction ratio ("SFR") of cell free DNA in a body fluid sample obtained from said individual, and

b) comparing the SFR obtained to that of a healthy individual,

wherein a decreased SFR is indicative of the presence of a cancer, and

wherein the SFR is calculated by a method comprising (i) performing amplifications by polymerase chain reaction (PCR) from said body fluid sample and determining from said amplifications the concentration or amount of a range of short size cell free DNA in said body fluid sample, wherein the range of short size cell free DNA is between 43bp and 100 pb or between 60 bp and 100 bp; (ii) performing amplifications by PCR from said body fluid sample and determining from said amplifications the concentration or amount of a range of long size cell free DNA in said body fluid sample, wherein the range of long size cell free DNA is between 200 bp and 450 bp; and (iii) calculating the ratio of the concentration or the amount of said cell free DNA of long size range and of short size range.

11. The method according to claim 10, wherein the short size cell free DNA range is below 100bp, and the long size cell free DNA range is 249-409bp.

12. The method according to claim 11, wherein the short size cell free DNA range is 73-100bp, and the long size cell free DNA range is 300-357bp.

13. The method according to any one of claims 10 to 12, wherein the body fluid sample is selected from the group consisting of whole blood, serum, plasma, urine, saliva, sputum, colonic effluent, bone marrow, lymph, cerebrospinal fluid, lacrymal fluid, sweat, milk, faeces, bronchial lavages and ascites.

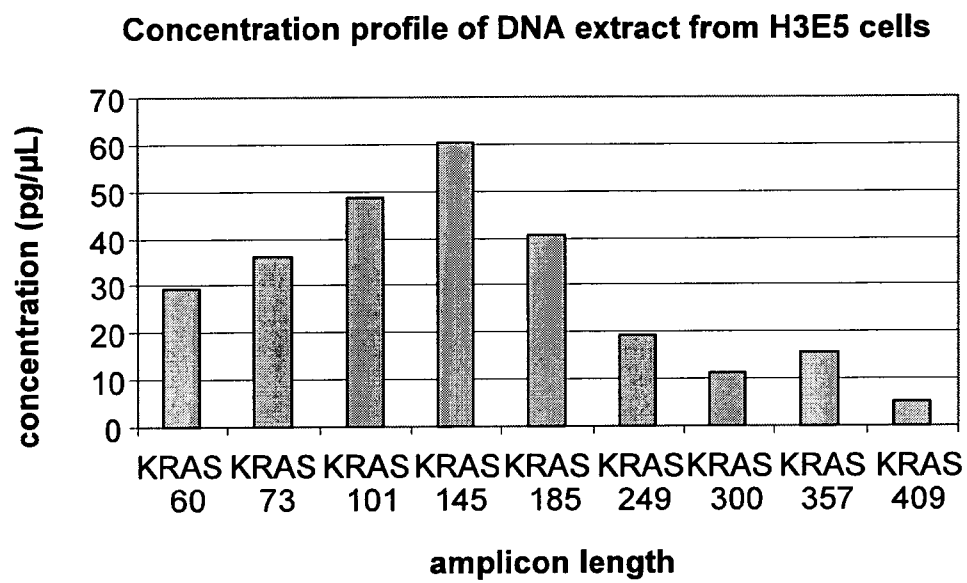
14. The method according to any one of claims 10 to 13, wherein said cell free DNA is circulating DNA.

15. The method according to any one of claims 10 to 14, wherein the long size cell free DNA partially or fully comprises the short size cell free DNA.

16. The method according to any one of claims 10 to 15, wherein the PCR is Q-PCR.

17. The method according to any one of claims 10 to 16, wherein the SFR is calculated repeatedly during an interval of time on body fluid samples from the individual, wherein a decrease of the SFR during the interval is indicative of the progression of the cancer in the individual.

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**FIGURE 1**

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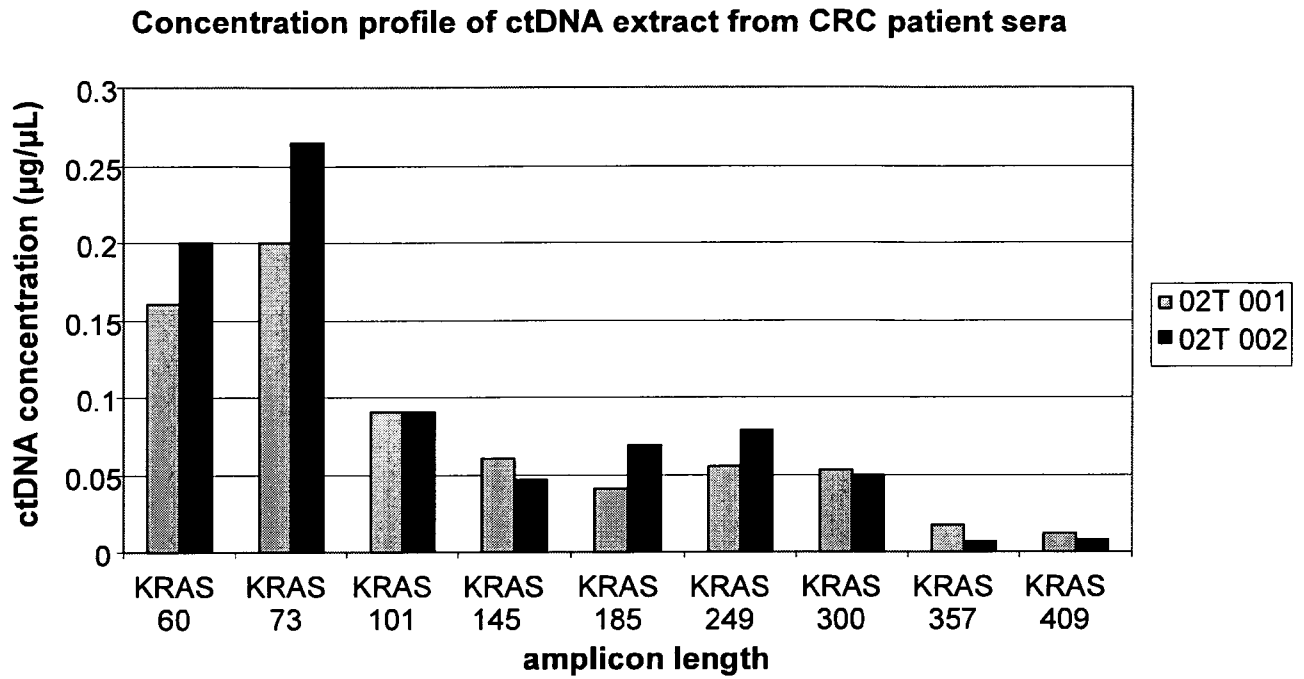


FIGURE 2A

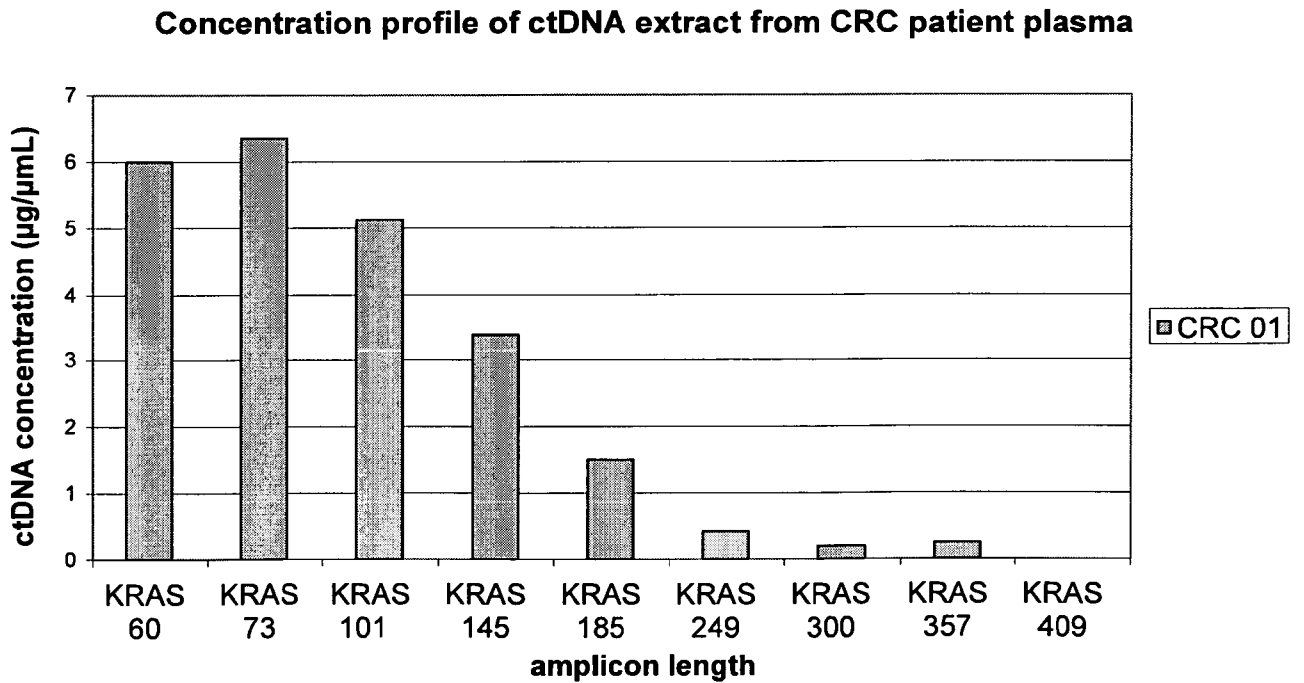


FIGURE 2B

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concentration profile of cirDNA from healthy individuals

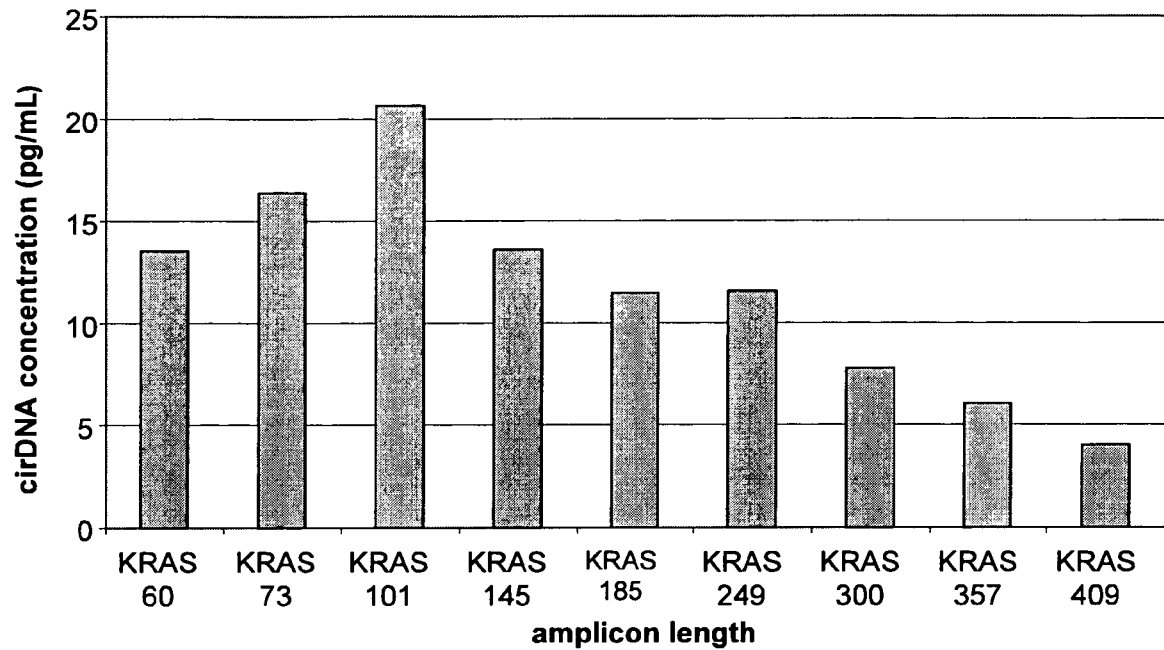


FIGURE 3

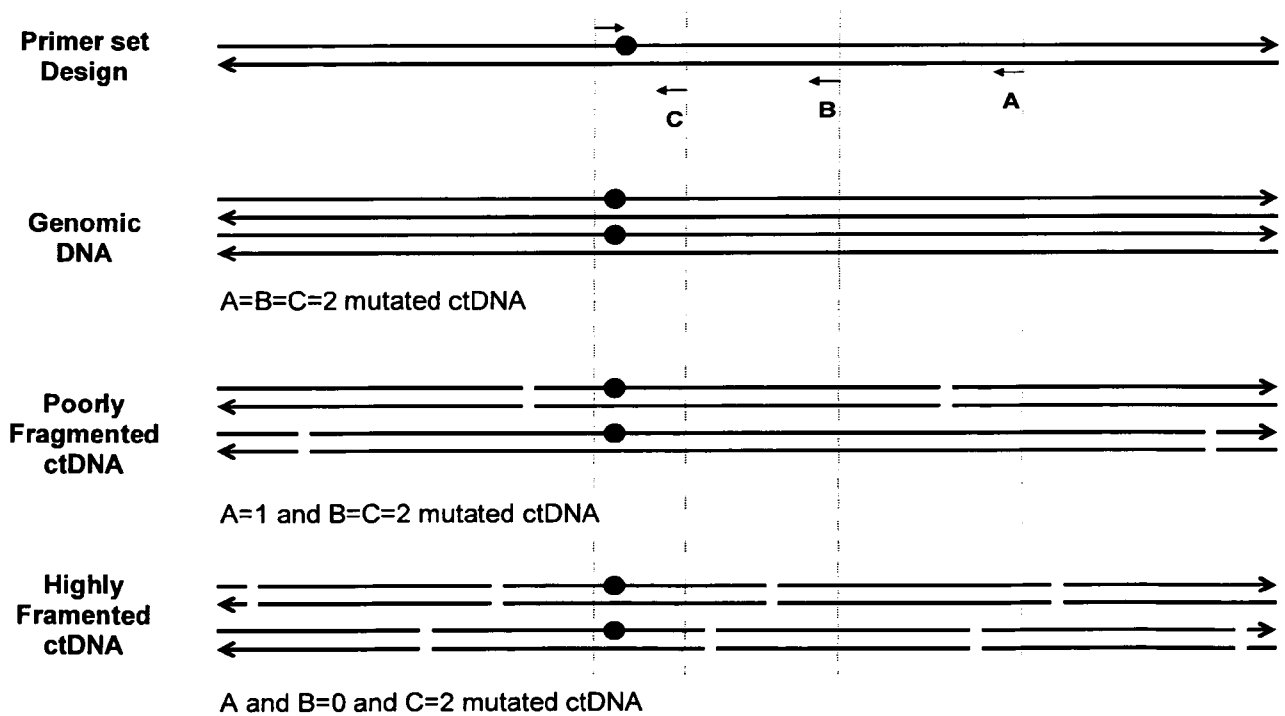


FIGURE 4

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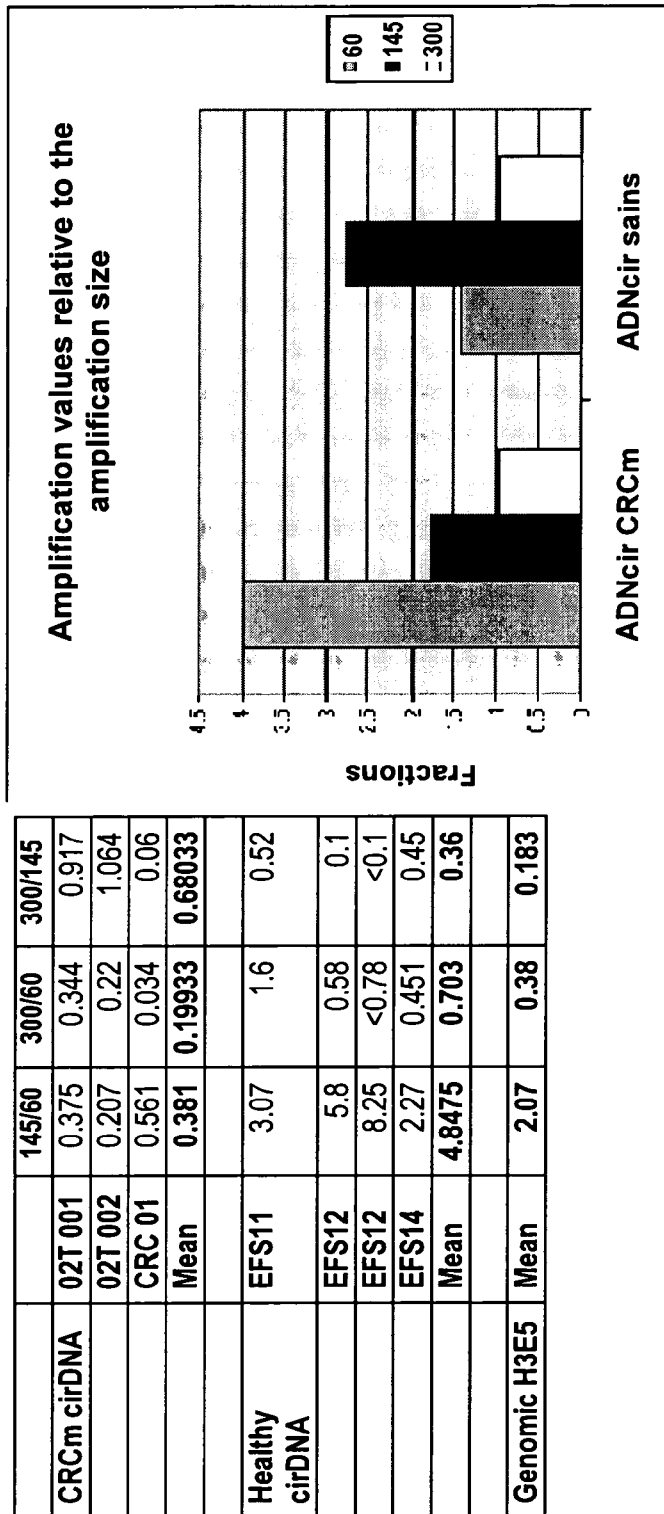


FIGURE 5

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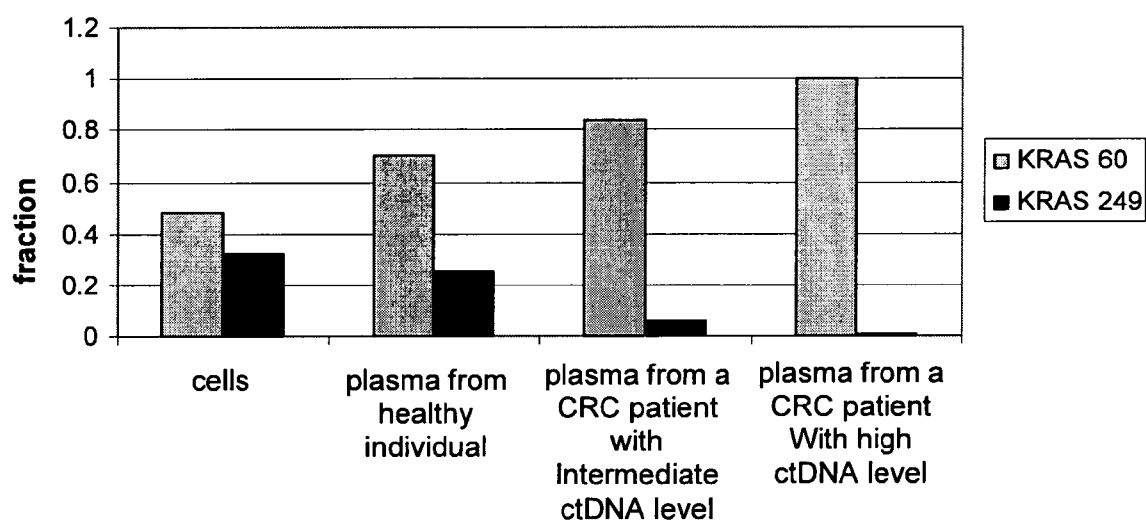


FIGURE 6

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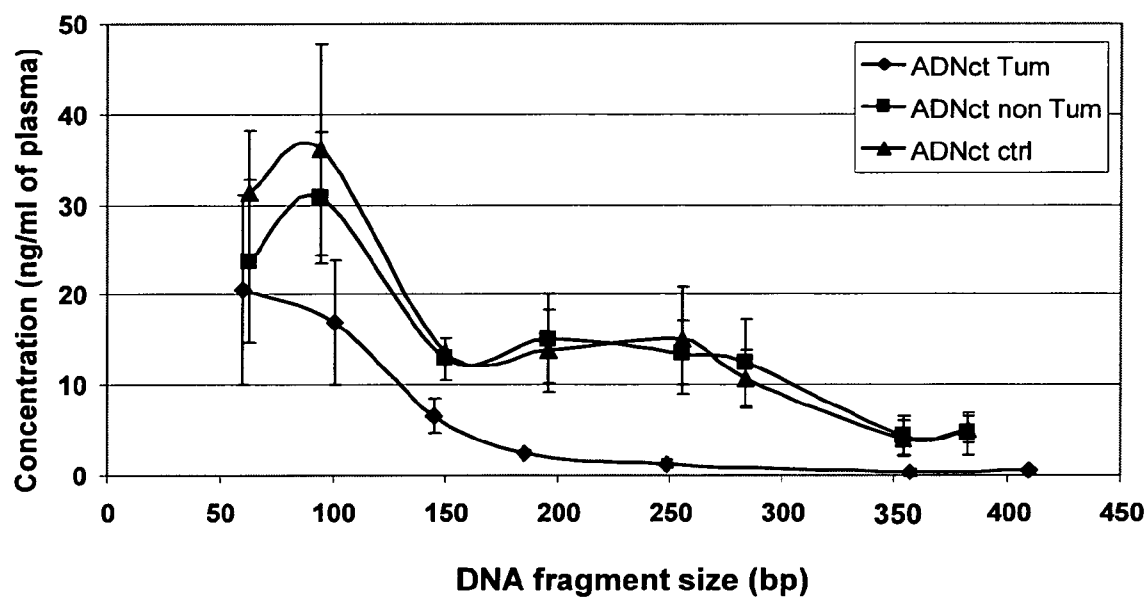


FIGURE 7A

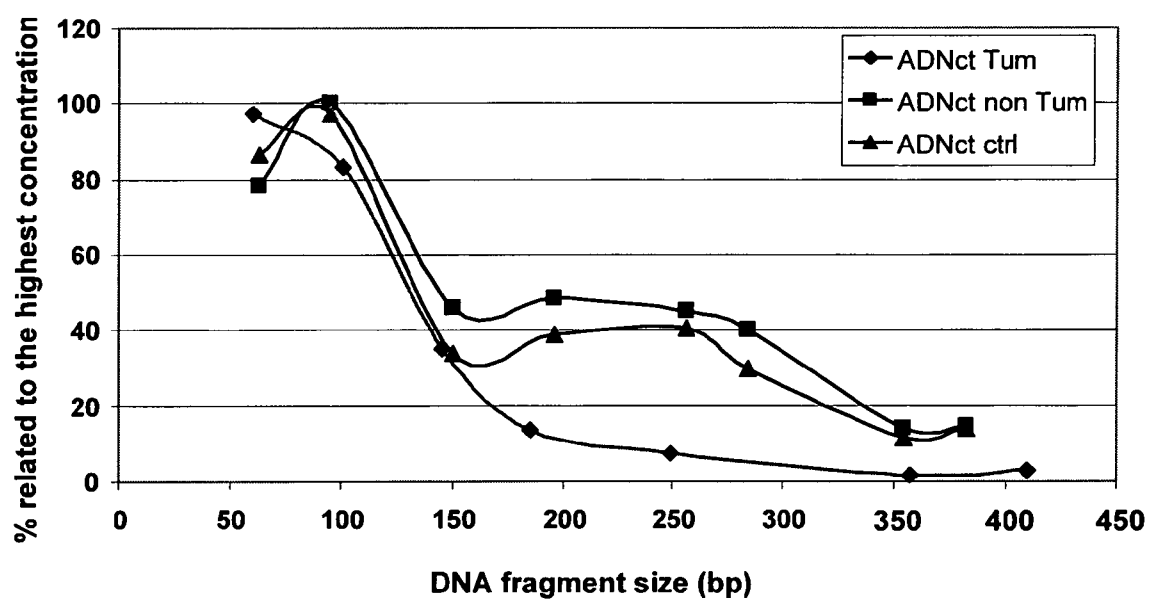
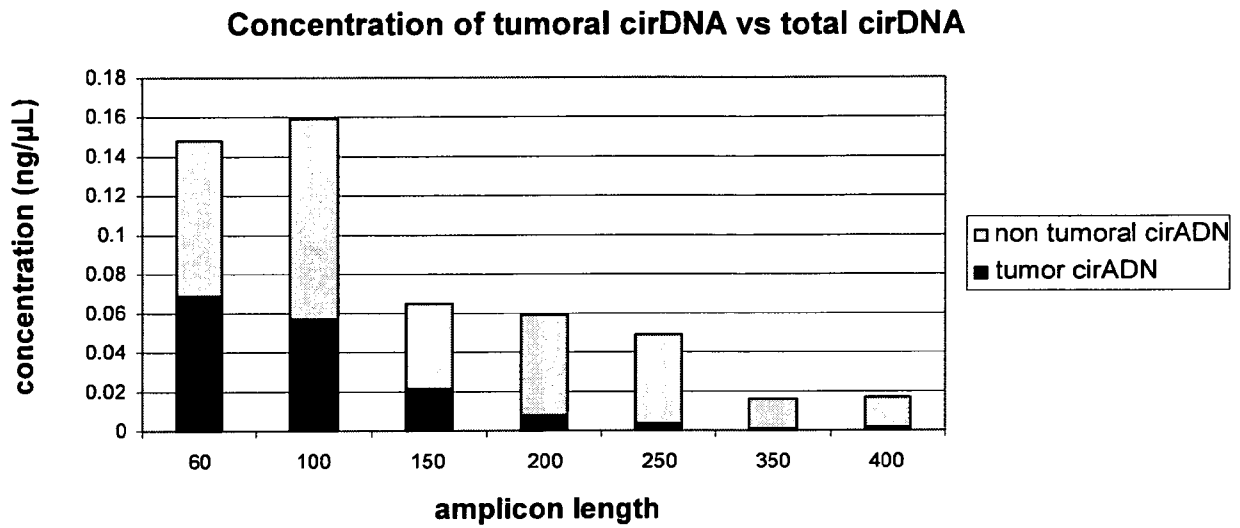
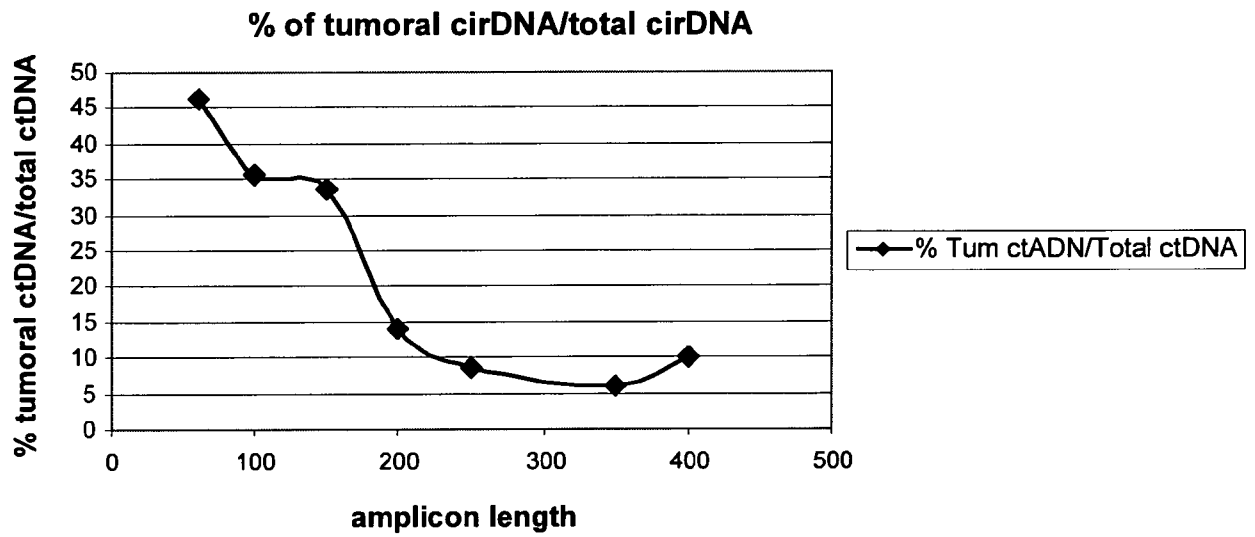


FIGURE 7B

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**FIGURE 8A****FIGURE 8B**

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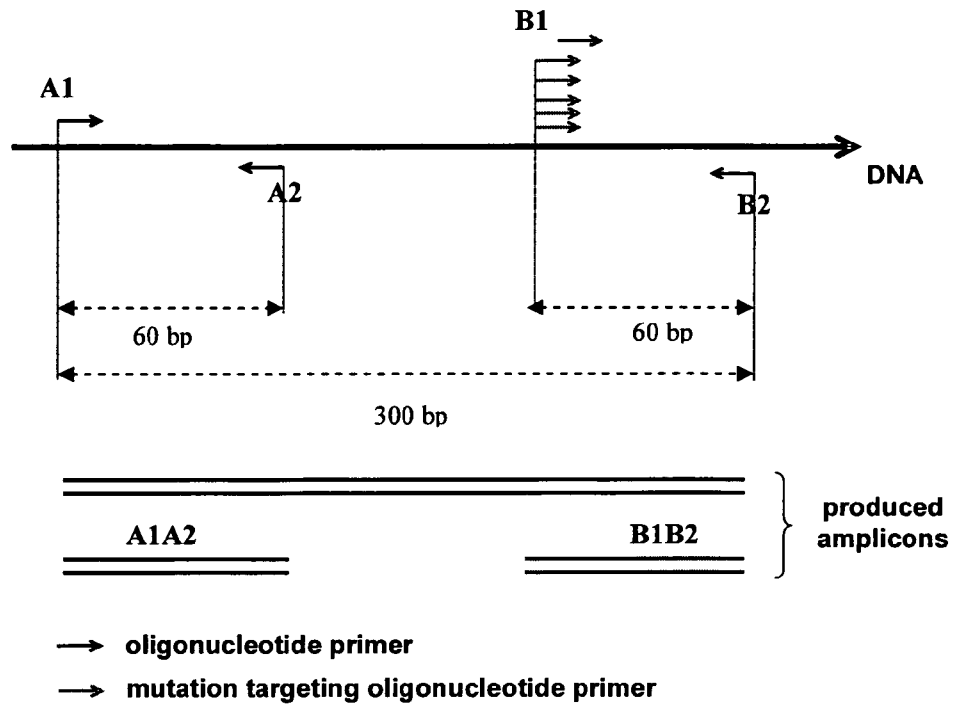


FIGURE 9

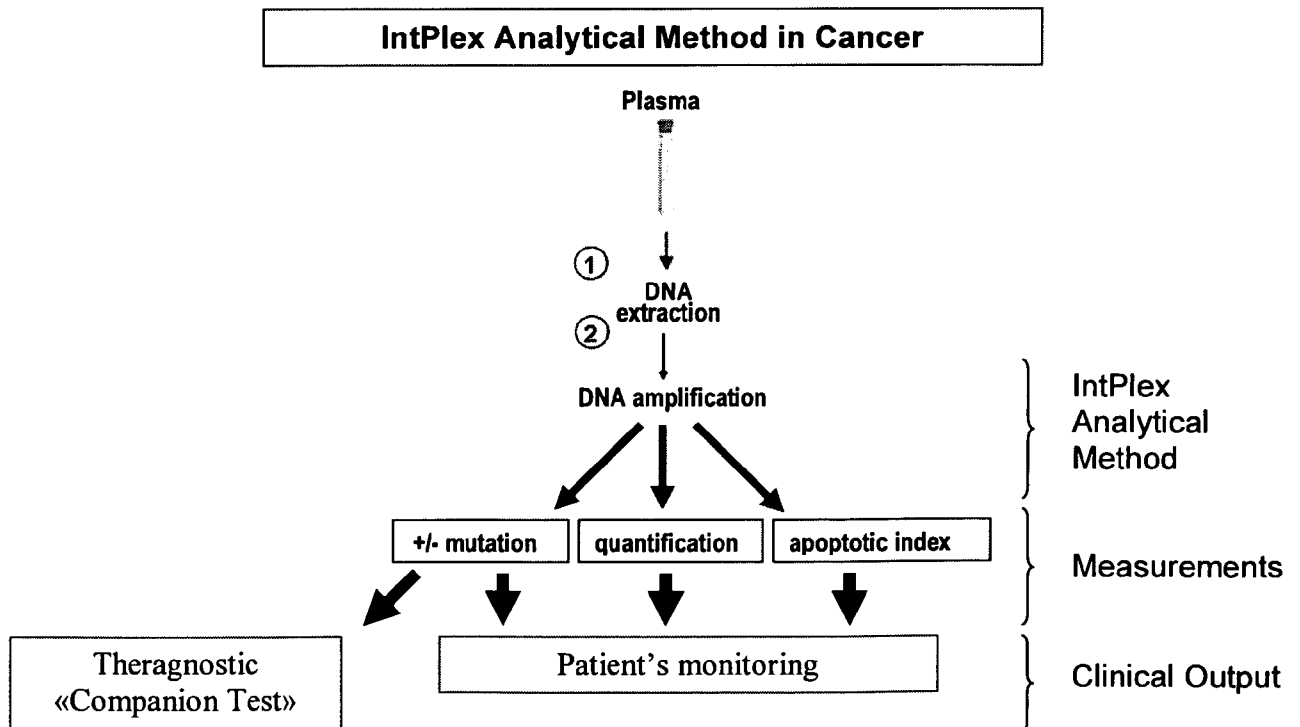


FIGURE 10

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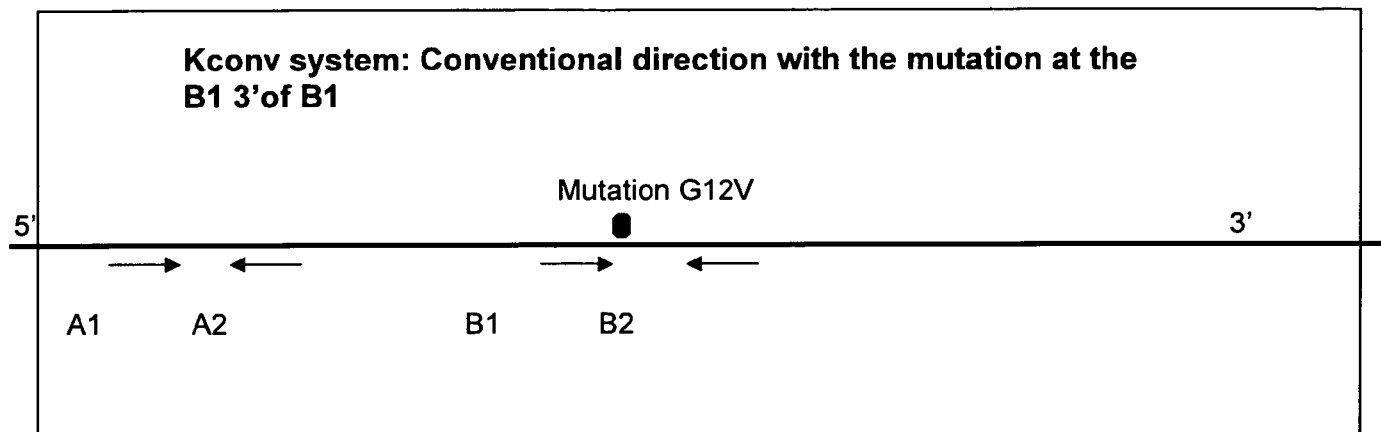


FIGURE 11A

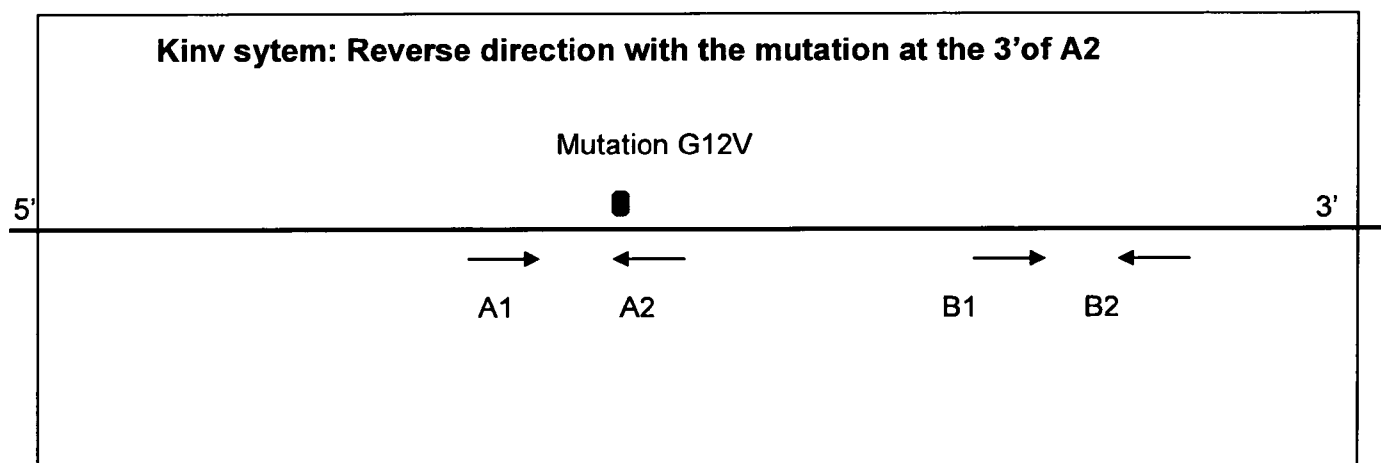


FIGURE 11B

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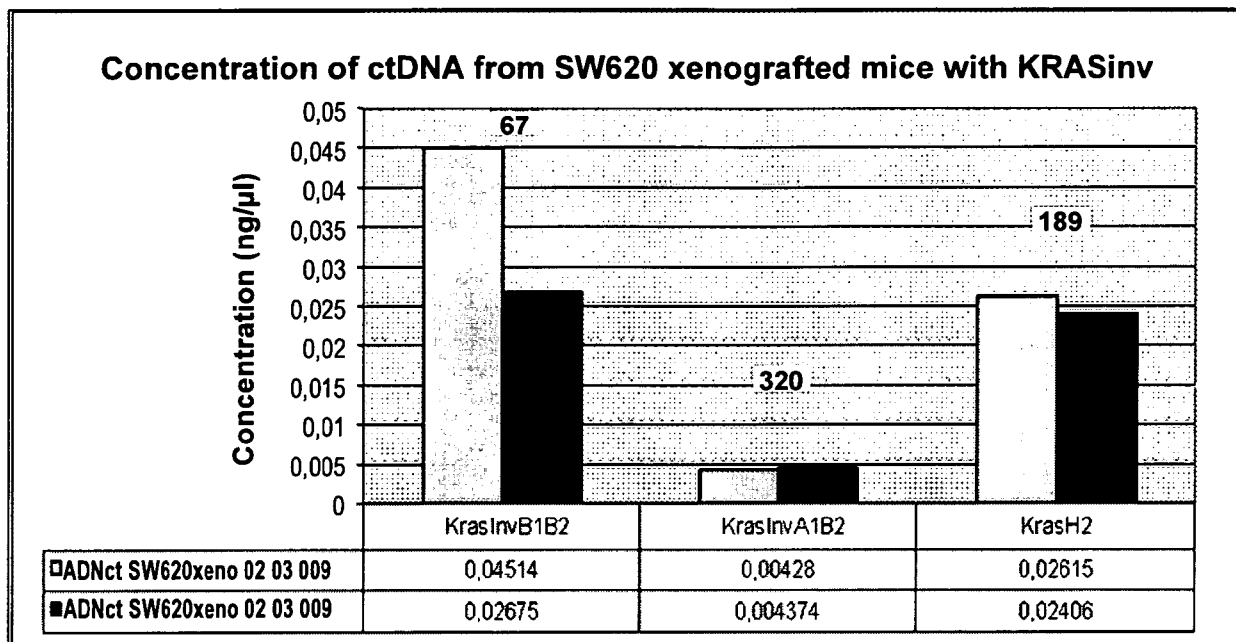


FIGURE 12

Concentration of ctDNA from SW620 xenografted with KRASconv Q-PCR

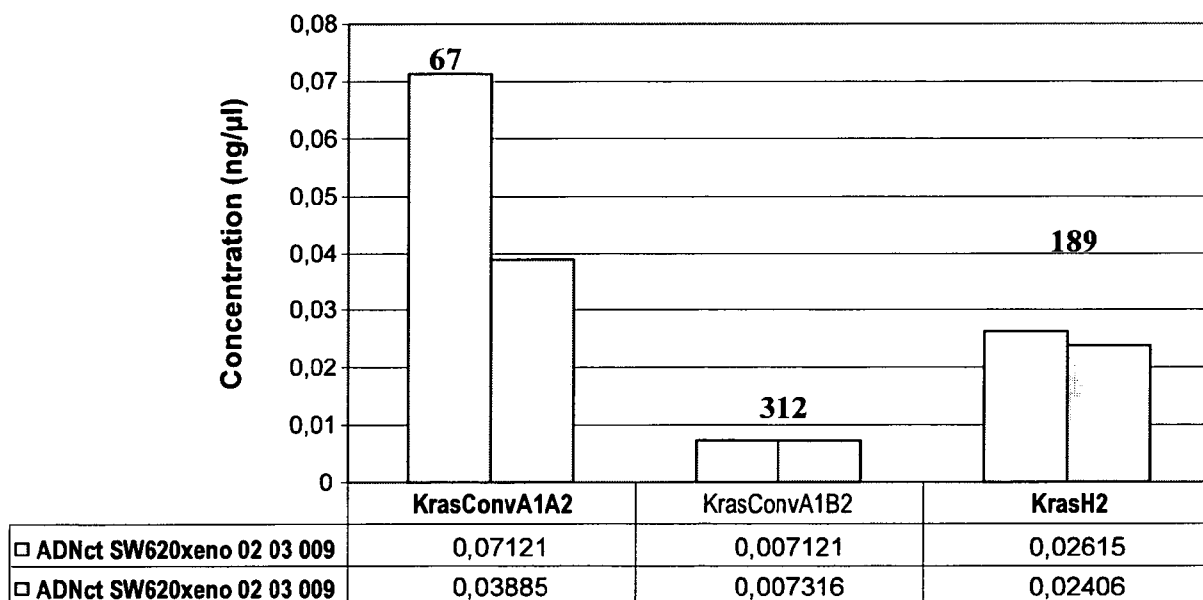
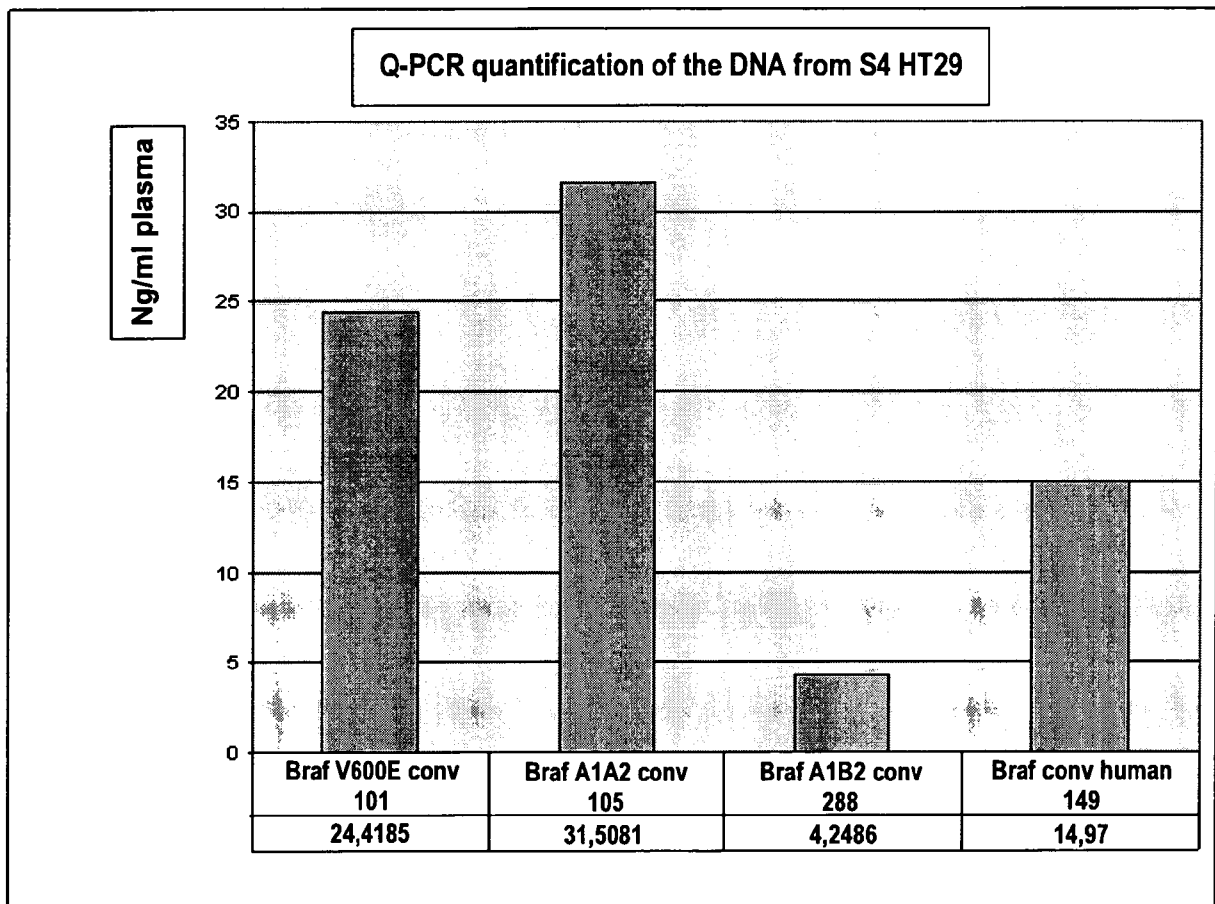
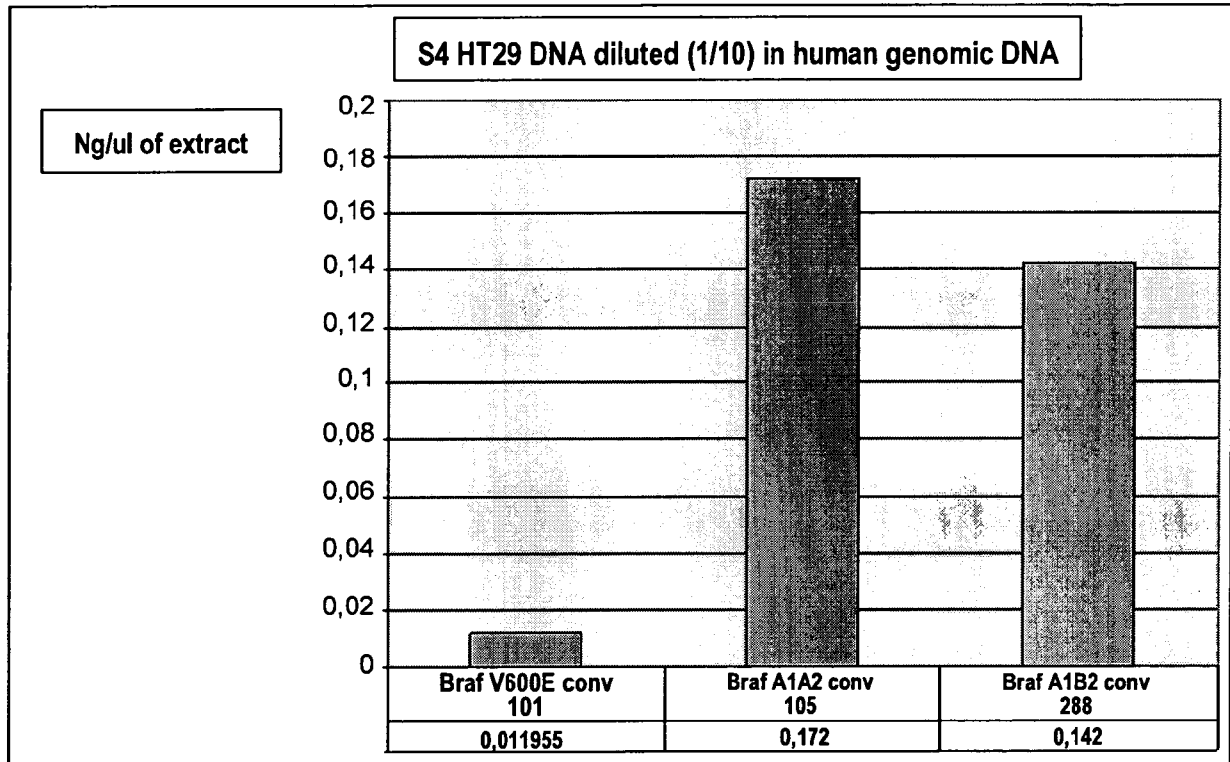


FIGURE 13

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**FIGURE 14**

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**FIGURE 15**

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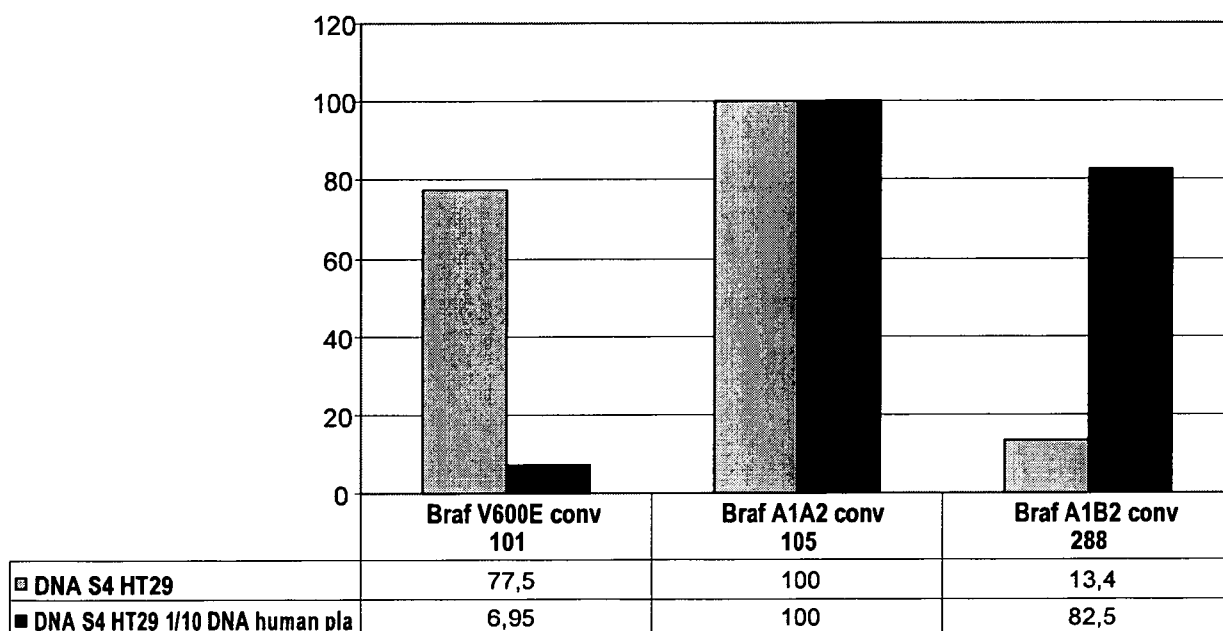
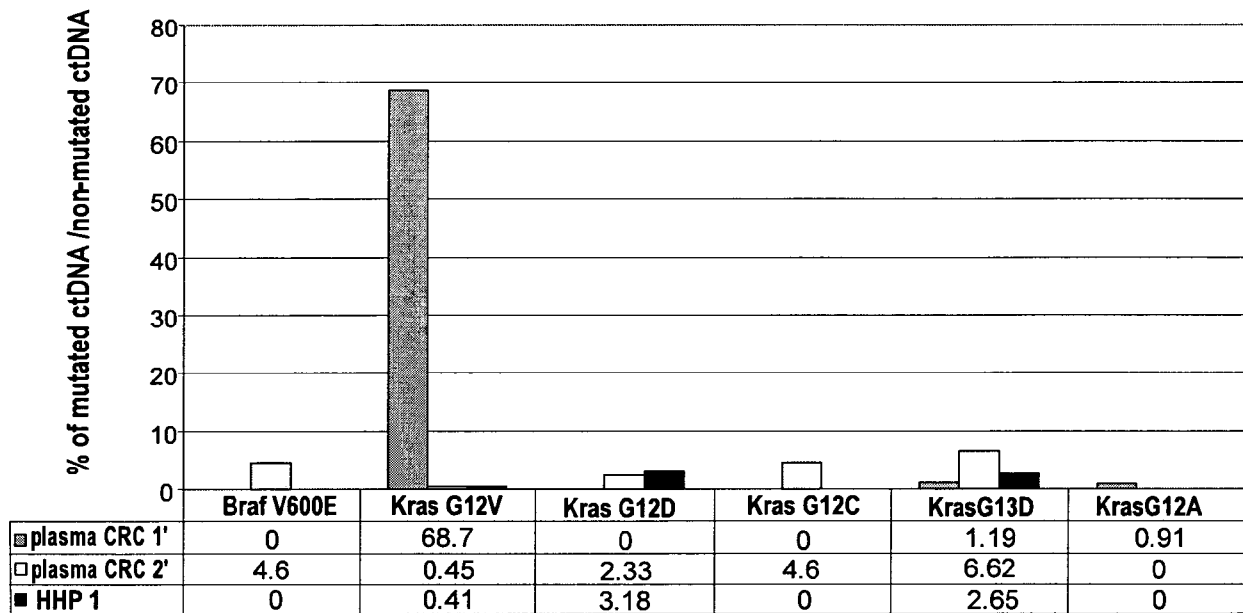


FIGURE 16

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Intplex analysis**FIGURE 17**

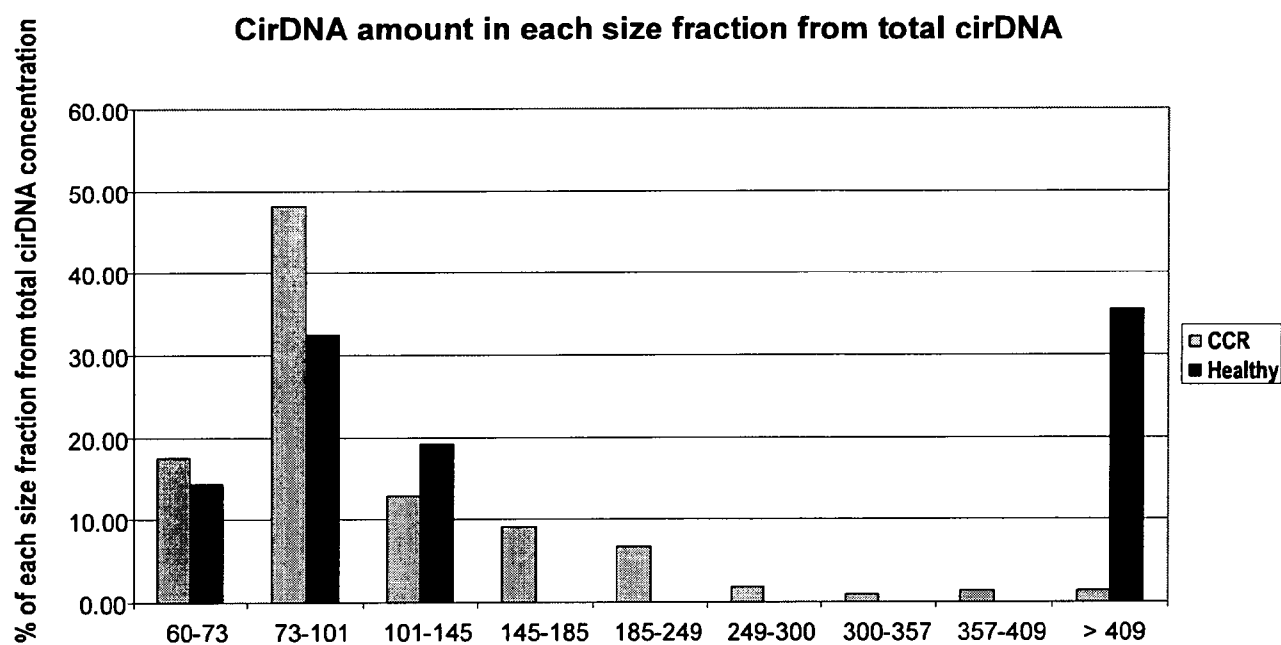
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Samples	Amplicons sizes (bp)										Integrity index									
	80	73	101	145	185	249	300	357	409		80	73	101	145	185	249	300	357	409	
CRC 1	1809.91	1905.15	1537.95	1015.81	453.61	128.49	80.91	74.82	1.81		1.000	1.053	0.850	0.561	0.251	0.070	0.034	0.014	0.001	
CRC 2	477.96	737.87	652.62	396.64	227.79	122.51	59.49	48.22	29.34		1.000	1.544	1.365	0.830	0.477	0.258	0.124	0.101	0.061	
CRC 3	138.44	187.85	186.15	124.94	51.83	21.16	12.74	9.33	2.34		1.000	1.355	1.345	0.902	0.374	0.153	0.092	0.067	0.017	
mean CCR	808.57	943.59	792.24	512.53	244.40	90.05	44.38	44.06	11.10	DII 300/60		1.317	1.187	0.765	0.367	0.160	0.083	0.070	0.028	
										DII 300/73	0.857		0.840	0.543	0.259	0.095	0.047	0.047	0.012	

HHP 1	5.55	5.22	6.28	3.94	3.91	2.77	1.24	1.11	0.72		1.000	0.941	1.128	0.710	0.705	0.499	0.223	0.200	0.130	
HHP 2	2.51	4.07	4.89	4.08	3.58	3.12	2.71	2.38	1.75		1.000	1.622	1.948	1.625	1.418	1.243	1.080	0.948	0.697	
HHP 3	4.12	5.49	7.42	4.26	2.89	4.48	3.06	2.00	2.12		1.000	1.333	1.801	1.034	0.701	1.087	0.743	0.485	0.272	
mean HHP	4.06	4.93	6.19	4.09	3.45	3.46	2.34	1.83	1.20	DII 300/60		1.298	1.626	1.123	0.941	0.943	0.682	0.545	0.366	
										DII 300/73	0.8235294		1.256	0.830	0.700	0.701	0.474	0.371	.243	
HHP/CCRDII 300/60												0.99	1.37	1.47	2.56	5.9	8.18	7.8	13.88	
HHP/CCRDII 300/73												0.96	1.49	1.82	2.7	7.34	10.07	7.95	20.64	

FIGURE 18

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**FIGURE 18 (continued)**

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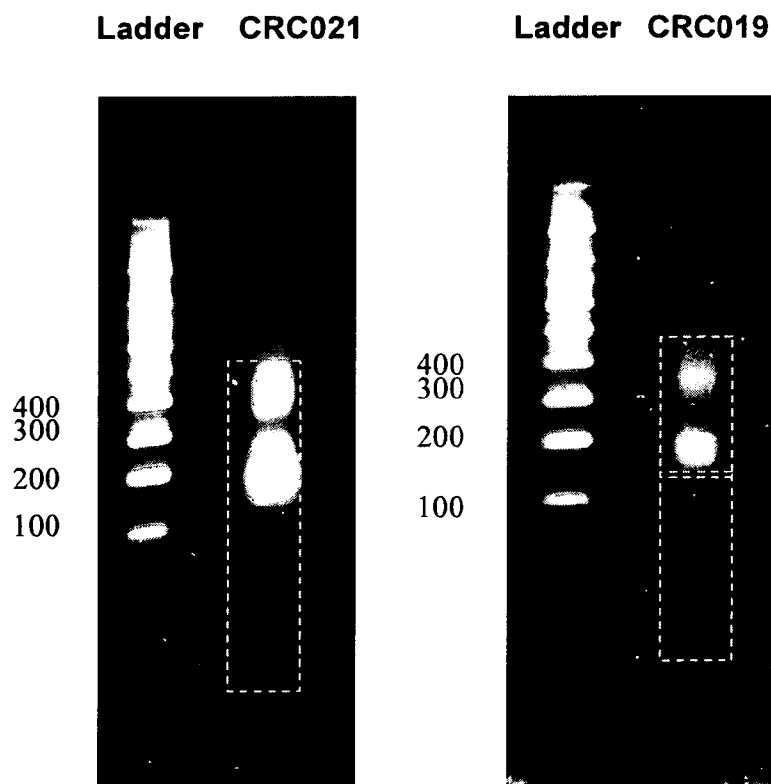


FIGURE 19A

FIGURE 19B

[]: Limit of the section of the gel which was removed, solubilised, extracted and subjected to Q-PCR.

FIGURES 19A-19B

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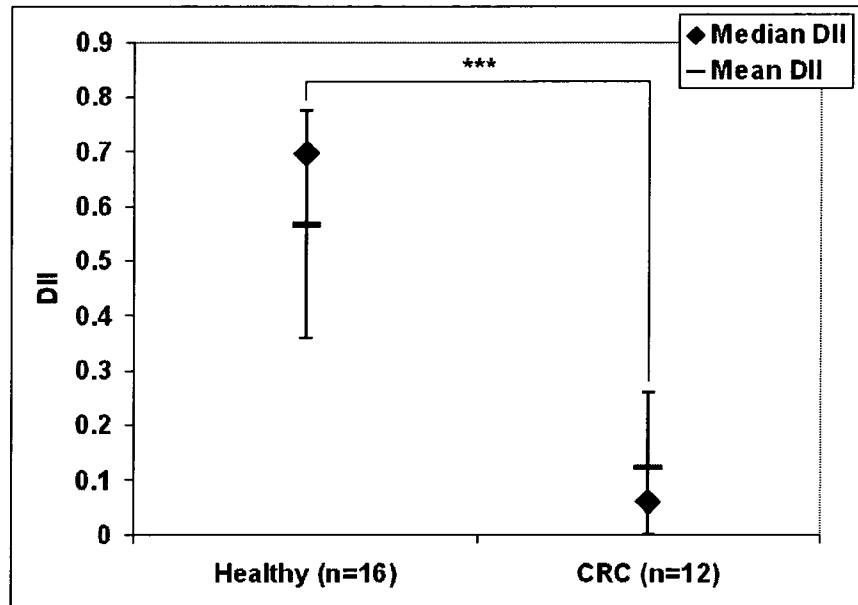


FIGURE 20

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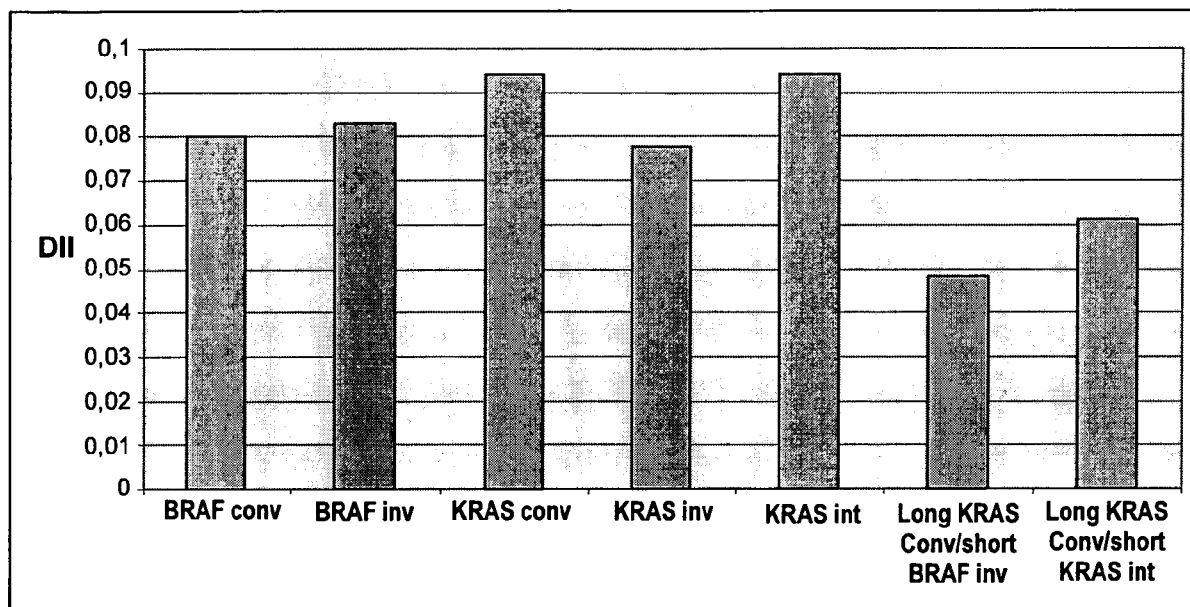


FIGURE 21

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Figure 22A

Figure 22B

Figure 22C

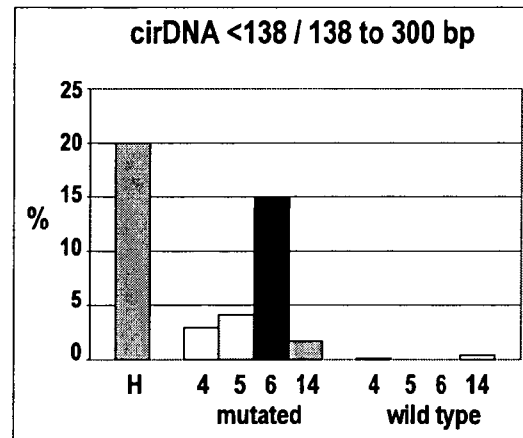
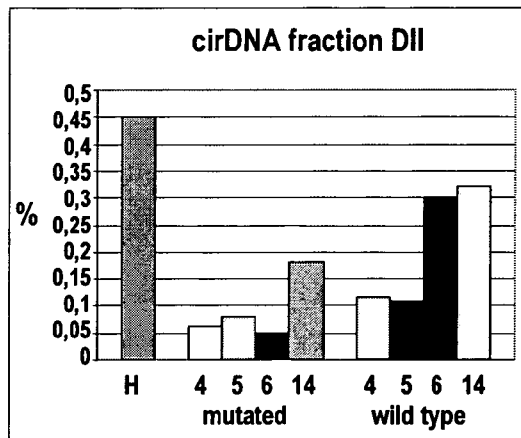
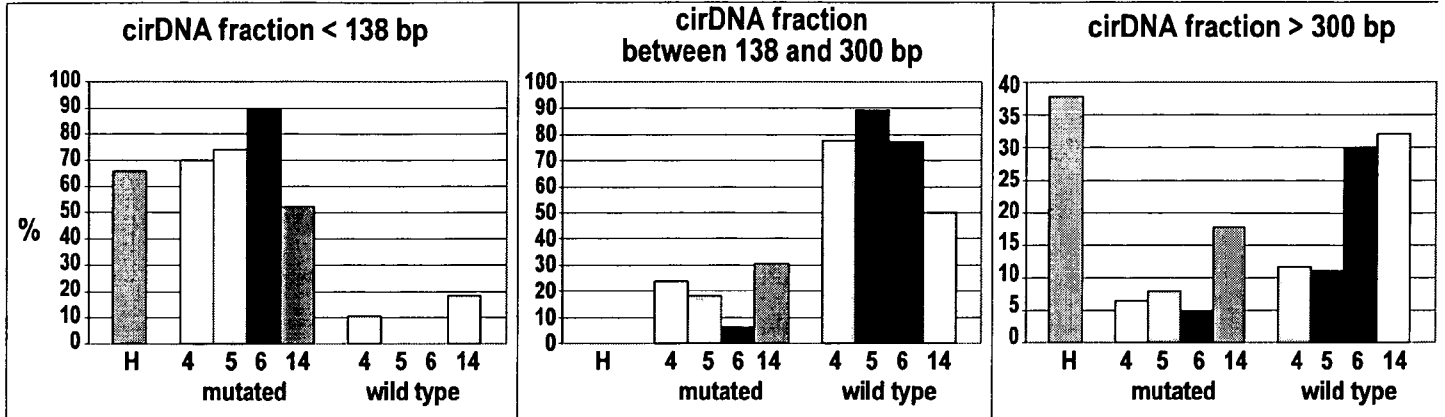


Figure 22D

Figure 22E

Figures 22A-22E

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Design KRAS conv:**XXXXX** : reverse primer for mutated amplicon: 6156 to 6236**XXXXX** : primer pair for non mutated amplicon: 5721 to 6051

```

5521 TTATTTCCCATGACACAATCCAGCTTTATTTGACACTCATTCTCTCAACTCTCATCTGA 5580
5581 TTCTTACTGTTAATATTTATCCAAGAGAACTACTGCCATGATGCTTTAAAAGTTTTTCTG 5640
5641 TAGCTGTTGCATATTGACTTCTAACACTTAGAGGTGGGGGTCCACTAGGAAAAGTGTAAAC 5700
5701 AATAAGAGTGGAGATAGCTGTCAGCAACTTTTGTGAGGGTGTGCTACAGGGTGTAGAGCA 5760
5761 CTGTGAAGTCTCTACATGAGTGAAGTCATGATATGATCCTTTGAGAGCCTTTAGCCGCCG 5820
5821 CAGAACAGCAGTCTGGCTATTTAGATAGAACAACCTTGATTTTAAGATAAAAGAACTGTCT 5880
5881 ATGTAGCATTTATGCATTTTCTTAAGCGTCGATGGAGGAGTTTGTAATGAAGTACAGT 5940
5941 TCATTACGATACACGTCTGCAGTCAACTGGAATTTTCATGATTGAATTTTGTAAAGGTATT 6000
6001 TTGAAATAATTTTTCATATAAAGGTGAGTTTGTATTAAAGGTACTGGTGGAGTATTTGA 6060
6061 TAGTGTATTAACCTTATGTGTGACATGTTCTAATATAGTCACATTTTCATTATTTTTATT 6120
6121 ATAAGGCCTGCTGAAAATGACTGAATATAAACTTGTGGTAGTTGGAGCTGGTGGCGTAGG 6180
6181 CAAGAGTGCCTTGACGATACAGCTAATTGAGAATCATTGTTGTGGACGAATATGATCCAAC 6240
6241 AATAGAGGTAAATCTTGTTTTAATATGCATATTACTGGTGCAGGACCATTCTTTGATACA 6300
6301 GATAAAGGTTTCTCTGACCATTTTCATGAGTACTTATTACAAGATAATTATGCTGAAAAGT 6360
6361 TAAGTTATCTGAAATGTACCTTGGGTTTCAAGTTATATGTAACCATTAAATATGGGAACTT 6420
6421 TACTTTCCTTGGGAGTATGTCAGGGTCCATGATGTTCACTCTCTGTGCATTTTGATTGGA 6480
6481 AGTGTATTTGAGAGTTTCGTGAGAGGGTAGAAATTTGTATCCTATCTGGACCTAAAAGAC 6540
6541 AATCTTTTTATTGTAACCTTTATTTTTATGGGTTTCTTGGTATTGTGACATCATATGTAA 6600
6601 AGGTTAGATTTAATTGTACTAGTGAATATAATTGTTTGTATGGTTGATTTTTTTAACTT 6660
6661 CATCAGCAGTATTTTCCTATCTTCTCTCAACATTAGAGAACCTACAACCTACCGGATAAA 6720
6721 TTTTACAAAATGAATTATTTGCCTAAGGTGTGGTTTATATAAAGGTACTATTACCAACTT 6780
6781 TACCTTTGCTTTGTTGTCAATTTTAAATTTACTCAAGGAAATACTAGGATTTAAAAAAA 6840

```

Design KRAS rev:**XXXXX** : reverse primer for mutated amplicon: 6066 to 6146**XXXXX** : primer pair for non mutated amplicon: 6251 to 6581

```

5521 TTATTTCCCATGACACAATCCAGCTTTATTTGACACTCATTCTCTCAACTCTCATCTGA 5580
5581 TTCTTACTGTTAATATTTATCCAAGAGAACTACTGCCATGATGCTTTAAAAGTTTTTCTG 5640
5641 TAGCTGTTGCATATTGACTTCTAACACTTAGAGGTGGGGGTCCACTAGGAAAAGTGTAAAC 5700
5701 AATAAGAGTGGAGATAGCTGTCAGCAACTTTTGTGAGGGTGTGCTACAGGGTGTAGAGCA 5760
5761 CTGTGAAGTCTCTACATGAGTGAAGTCATGATATGATCCTTTGAGAGCCTTTAGCCGCCG 5820
5821 CAGAACAGCAGTCTGGCTATTTAGATAGAACAACCTTGATTTTAAGATAAAAGAACTGTCT 5880
5881 ATGTAGCATTTATGCATTTTCTTAAGCGTCGATGGAGGAGTTTGTAATGAAGTACAGT 5940
5941 TCATTACGATACACGTCTGCAGTCAACTGGAATTTTCATGATTGAATTTTGTAAAGGTATT 6000
6001 TTGAAATAATTTTTCATATAAAGGTGAGTTTGTATTAAAGGTACTGGTGGAGTATTTGA 6060
6061 TAGTGTATTAACCTTATGTGTGACATGTTCTAATATAGTCACATTTTCATTATTTTTATT 6120
6121 ATAAGGCCTGCTGAAAATGACTGAATATAAACTTGTGGTAGTTGGAGCTGGTGGCGTAGG 6180
6181 CAAGAGTGCCTTGACGATACAGCTAATTGAGAATCATTGTTGTGGACGAATATGATCCAAC 6240
6241 AATAGAGGTAAATCTTGTTTTAATATGCATATTACTGGTGCAGGACCATTCTTTGATACA 6300
6301 GATAAAGGTTTCTCTGACCATTTTCATGAGTACTTATTACAAGATAATTATGCTGAAAAGT 6360
6361 TAAGTTATCTGAAATGTACCTTGGGTTTCAAGTTATATGTAACCATTAAATATGGGAACTT 6420
6421 TACTTTCCTTGGGAGTATGTCAGGGTCCATGATGTTCACTCTCTGTGCATTTTGATTGGA 6480
6481 AGTGTATTTGAGAGTTTCGTGAGAGGGTAGAAATTTGTATCCTATCTGGACCTAAAAGAC 6540
6541 AATCTTTTTATTGTAACCTTTATTTTTATGGGTTTCTTGGTATTGTGACATCATATGTAA 6600
6601 AGGTTAGATTTAATTGTACTAGTGAATATAATTGTTTGTATGGTTGATTTTTTTAACTT 6660
6661 CATCAGCAGTATTTTCCTATCTTCTCTCAACATTAGAGAACCTACAACCTACCGGATAAA 6720
6721 TTTTACAAAATGAATTATTTGCCTAAGGTGTGGTTTATATAAAGGTACTATTACCAACTT 6780
6781 TACCTTTGCTTTGTTGTCAATTTTAAATTTACTCAAGGAAATACTAGGATTTAAAAAAA 6840

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FIGURE 24A

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5881 ATGTAGCATTTATGCATTTTTCTTAAGCGTCGATGGAGGAGTTTGTAATGAAGTACAGT
 KRASconv A1 (ID : 13)

5941 TCATTACGATACACGTCTGCAGTCAACTGGAATTTTCATGATTGAATTTTGTAAGGTATT
 KRASconv A2 (ID : 14)

6001 TTGAAATAATTTTTCATATAAAGGTGAGTTTGTATTAAAAGGTACTGGTGGAGTATTTGA

6061 TAGTGTATTAACTTATGTGTGACATGTTCTAATATAGTCACATTTTCATTATTTTTATT

6121 ATAAGGCCTGCTGAAAATGACTGAATATAAACTTGTGGTAGTTGGAGCTGGTGGCGTAGG
 KRAS Inv A1 (ID : 28) KRAS conv B1 (ID : 11)
 Kras Inv mut Blocker (ID:37)

6151 -ACTTGTGGTAGTTGGAGCTGT
 Kras B1 conv G12V (ID : 9)

6186 - TGGCGTAGGCAAGAGTG
 Kras Inv MutG12V (ID : 15)

6186 - TGGCGTAGGCAAGAG
 Kras InvA2 MutG12V16 (ID : 31)

6186 - TGGCGTAGGCAAGAG
 Kras InvA2 G12D low (ID : 33)

6186 - TGGCGTAGGCAAGAG
 Kras InvA2 G12A low (ID : 34)

6185 - TGGCGTAGGCAAGAG
 Kras InvA2 G12S low (ID : 35)

6185 - TGGCGTAGGCAAGAG
 Kras InvA2 G12C low (ID : 36)

6189 - TCGTAGGCAAGAGTGC
 Kras InvA2 MutG13D64 (ID : 32)

6181 CAAGAGTGCTTGACGATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAAC
 KRAS conv B2 (ID : 12)

6241 AATAGAGGTAAATCTTGTTTTAATATGCATATTACTGGTGCAGGACCATTCTTTTGATACA
 KRAS B2 conv (ID : 10)

6301 GATAAAGGTTTCTCTGACCATTTTCATGAGTACTTATTACAAGATAATTATGCTGAAAGT

6361 TAAGTTATCTGAAATGTACCTTGGGTTTCAAGTTATATGTAACCATTAAATATGGGAACCTT
 KRAS Inv B1 (ID : 29)

6421 TACTTTCCTTGGGAGTATGTCAGGGTCCATGATGTTCACTCTCTGTGCATTTTGATTGGA
 KRAS Inv B2 (ID : 30)

6481 AGTGTATTTTCAGAGTTTCGTGAGAGGGTAGAAATTTGTATCCTATCTGGACCTAAAAGAC

FIGURE 24B

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6001 TTGAAATAATTTTTCATATAAAGGTGAGTTTGTATTAAAAGGTACTGGTGGAGTATTTGA
 6061 TAGTGTATTAACTTATGTGTGACATGTTCTAATATAGTCACATTTTCATTATTTTATT

6121 ATAAGGCCTGCTGAAAATGACTGAATATAAACTTGTGGTAGTTGGAGCTGGTGGCGTAGG
 Amo1

TGAATATAAACTTGTGGTAGTTGGA Amo10 51bp
 CTGAATATAAACTTGTGGTAGTTGGA Amo11
 TGAATATAAACTTGTGGTAGTTGGAG Amo12
 CTGAATATAAACTTGTGGTAGTTGGAG Amo13
 ACTGAATATAAACTTGTGGTAGTTGGA Amo14
 GAAAATGACTGAATATAAACTTGTGG Amo15
 GAAAATGACTGAATATAAACTTGTGGT Amo16
 TGAATATAAACTTGTGG Amo17
 AAAATGACTGAATATAAACTTGTGG Amo18
 AAAATGACTGAATATAAACTTGTGGT Amo19
 TGAAAATGACTGAATATAAACTTGTGG Amo20
 CTGCTGAAAATGACTGAATATAAA Amo21
 TGCTGAAAATGACTGAATATAAA Amo22
 GAAAATGACTGAATATAAACTTGTGG Amo23
 CTGCTGAAAATGACTGAATATAAAC Amo24
 GCCTGCTGAAAATGACTGAA Amo2
 AAGGCCTGCTGAAAATGACT Amo3
 GGCCTGCTGAAAATGACTGA Amo4
 GGCCTGCTGAAAATGACTG Amo5
 TAAGGCCTGCTGAAAATGACT Amo6
 TAAGGCCTGCTGAAAATGAC Amo7
 ATAAGGCCTGCTGAAAATGA Amo8
 ATAAGGCCTGCTGAAAATGAC Amo9
 ATTATAAGGCCTGCTGAAAATGA Amo25
 ATTATAAGGCCTGCTGAAAATGAC Amo26
 ATTATAAGGCCTGCTGAAAATG Amo27
 TATTATAAGGCCTGCTGAAAATGA Amo28
 ATTATAAGGCCTGCTGAAAA Amo29
 TTTTATTATAAGGCCTGCTG Amo30
 CATTATTTTATTATAAGGCCTGCTG Amo31
 ATTTTATTATAAGGCCTGCTG Amo32
 TTATTTTATTATAAGGCCTGCTG Amo33
 TATTTTATTATAAGGCCTGCTG Amo34
 TCATTATTTTATTATAAGGCCTGCTG Amo35 86 bp

6181 CAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAAC

6241 AATAGAGGTAAATCTTGTTTTAATATGCATATTACTGGTGCAGGACCATTCTTTGATACA

6301 GATAAAGGTTTCTCTGACCATTTTCATGAGTACTTATTACAAGATAATTATGCTGAAAGT

FIGURE 24D

[illegible]

ACGAAATATGATCCAACAATAGAGGTA Am088
Am088 ATGATCGCAACCAATAGACGCTATATCTT

Concentration profile of ctDNA extract from CRC patient sera

