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(54) Titre : BLOQUEUR D'AMPLIFICATION COMPRENANT DES ACIDES NUCLEIQUES INTERCALANTS (TNA)
CONTENANT DES PSEUDONUCLEOTIDES INTERCALANTS (IPN)
(54) Title: AMPLIFICATION BLOCKER COMPRISING INTERCALATING NUCLEIC ACIDS (INA) CONTAINING
INTERCALATING PSEUDONUCLEOTIDES (IPN)

(57) **Abrégé/Abstract:**

An amplification blocker comprising an intercalating nucleic acid (INA) containing two or more internal intercalating pseudonucleotides (IPNs) capable of blocking or reducing nucleic acid amplification. Use of the amplification blocker to block or reduce nucleic acid amplification.



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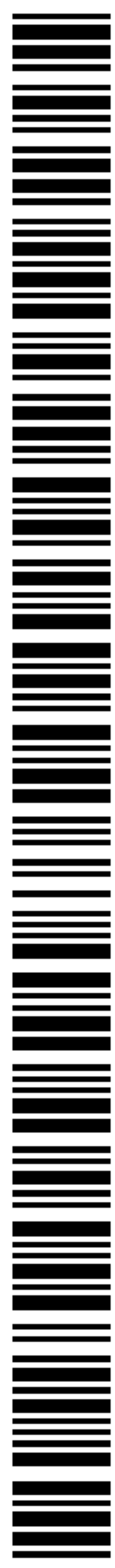
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(54) Title: AMPLIFICATION BLOCKER COMPRISING INTERCALATING NUCLEIC ACIDS (TNA) CONTAINING INTERCALATING PSEUDONUCLEOTIDES (IPN)

(57) Abstract: An amplification blocker comprising an intercalating nucleic acid (INA) containing two or more internal intercalating pseudonucleotides (IPNs) capable of blocking or reducing nucleic acid amplification. Use of the amplification blocker to block or reduce nucleic acid amplification.



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Amplification blocker comprising intercalating nucleic acids (INA) containing intercalating pseudonucleotides (IPN)Technical Field

The invention relates to nucleic acid detection assays and in particular to improved assays using blockers of DNA amplification. The invention also relates to
5 novel blockers of DNA amplification and methods suitable for the specific and sensitive detection of 5-methyl cytosine bases in nucleic acids.

Background Art

A number of procedures are presently available for the detection of specific
10 nucleic acid molecules. These procedures typically depend on sequence-dependent hybridisation between the target nucleic acid and nucleic acid probes which may range in length from short oligonucleotides (20 bases or less) to sequences of many kilobases (kb).

The most widely used method for amplification of specific sequences from within
15 a population of nucleic acid sequences is that of polymerase chain reaction (PCR) (Dieffenbach C and Dveksler G eds. PCR Primer: A Laboratory Manual. Cold Spring Harbor Press, Plainview NY). In this amplification method, oligonucleotides, generally 15 to 30 nucleotides in length of complementary strands and at either end of the region to be amplified, are used to prime DNA synthesis on denatured single-stranded DNA.
20 Successive cycles of denaturation, primer hybridisation and DNA strand synthesis using thermostable DNA polymerases allows exponential amplification of the sequences between the primers. RNA sequences can be amplified by first copying the RNA to DNA using reverse transcriptase to produce a cDNA copy. Amplified DNA fragments can be detected by a variety of means including gel electrophoresis, blotting, hybridisation with
25 labelled probes, use of tagged primers that allow subsequent identification (eg. by an enzyme linked assay), use of fluorescently-tagged primers that give rise to a signal upon hybridisation with the target DNA (eg. Beacon and TaqMan™ systems).

As well as PCR, a variety of other techniques have been developed for detection and amplification of specific nucleotide sequences. One example is the ligase chain
30 reaction (Barany F Genetic disease detection and DNA amplification using cloned thermostable ligase. Proc. Natl. Acad. Sci. USA 88:189-193 (1991)).

For direct detection, the target nucleic acid is most commonly separated on the basis of size by gel electrophoresis and transferred to a solid support prior to

hybridisation with a probe complementary to the target sequence (Southern and Northern blotting). The probe may be a natural nucleic acid or analogue such as peptide nucleic acid (PNA) or locked nucleic acid (LNA). The probe may be directly labelled (eg with ^{32}P) or an indirect detection procedure may be used. Indirect procedures
5 usually rely on incorporation into the probe of a "tag" such as biotin or digoxigenin and the probe is then detected by means such as enzyme-linked substrate conversion or chemiluminescence.

Another method for direct detection of nucleic acid that has been used widely is "sandwich" hybridisation. In this method, a capture probe is coupled to a solid support
10 and the target nucleic acid, in solution, is hybridised with the bound probe. Unbound target nucleic acid is washed away and the bound nucleic acid is detected using a second probe that hybridises to the target sequences. Detection may use direct or indirect methods as outlined above. The "branched DNA" signal detection system is an example that uses the sandwich hybridization principle (Urdea MS et al. Branched DNA
15 amplification multimers for the sensitive, direct detection of human hepatitis viruses. Nucleic Acids Symp Ser. 1991;(24):197-200).

A rapidly growing area that uses nucleic acid hybridisation for direct detection of nucleic acid sequences is that of DNA micro-arrays (Young RA Biomedical discovery with DNA arrays. Cell 102: 9-15 (2000); Watson A New tools. A new breed of high tech
20 detectives. Science 289:850-854 (2000)). In this process, individual nucleic acid species, that may range from oligonucleotides to longer sequences such as cDNA clones, are fixed to a solid support in a grid pattern. A tagged or labelled nucleic acid population is then hybridised with the array and the level of hybridisation with each spot in the array quantified. Most commonly, radioactively- or fluorescently-labelled nucleic
25 acids (eg. cDNAs) were used for hybridisation, though other detection systems can be employed.

Currently, the method of choice to detect methylation changes in DNA, such as were found in the GSTP1 gene promoter in prostate cancer, are dependent on PCR amplification of such sequences after bisulphite modification of DNA. In bisulphite-
30 treated DNA, cytosines are converted to uracils (and hence amplified as thymines during PCR) while methylated cytosines are non-reactive and remain as cytosines (Frommer M, McDonald LE, Millar DS, Collis CM, Watt F, Grigg GW, Molloy PL and Paul CL. A genomic sequencing protocol which yields a positive display of 5-methyl cytosine residues in individual DNA strands. PNAS 89: 1827-1831 (1992); Clark SJ, Harrison J,
35 Paul CL and Frommer M. High sensitivity mapping of methylated cytosines. Nucleic

Acids Res. 22: 2990-2997 (1994)). Thus, after bisulphite treatment, DNA containing 5-methyl cytosine bases will be different in sequence from the corresponding unmethylated DNA. Primers may be chosen to amplify non-selectively a region of the genome of interest to determine its methylation status, or may be designed to selectively amplify
5 sequences in which particular cytosines were methylated (Herman JG, Graff JR, Myohanen S, Nelkin BD and Baylin SB. Methylation-specific PCR: a novel PCR assay for methylation status of CpG islands. PNAS 93:9821-9826 (1996)).

Alternative methods for detection of cytosine methylation include digestion with restriction enzymes whose cutting is either blocked or not blocked by site-specific DNA
10 methylation, followed by Southern blotting and hybridisation probing for the region of interest. This approach is limited to circumstances where a significant proportion (generally >10%) of the DNA is methylated at the site and where there is sufficient DNA, about 1 to 5 µg, to allow for detection. Digestion with restriction enzymes whose cutting is blocked by site-specific DNA methylation is followed by PCR amplification using
15 primers that flank the restriction enzyme site(s). This method can utilise smaller amounts of DNA but any lack of complete enzyme digestion for reasons other than DNA methylation can lead to false positive signals.

The present inventor has now developed methods utilizing intercalating nucleic acids (INAs) suitable for the sensitive and specific detection of methylated nucleic acids
20 which can greatly reduce the problems associated with methylation specific PCR (MSP) reaction. An unexpected property of INAs is utilized to carry out the present invention.

Disclosure of Invention

In a first aspect, the present invention provides an amplification blocker
25 comprising an intercalating nucleic acid (INA) containing two or more internal intercalating pseudonucleotides (IPNs) capable of blocking or reducing nucleic acid amplification.

Preferably, the INA is about 15 to 50, more preferably about 18 to 35 nucleotides or nucleotide analogues in length having between 2 to 10, preferably between 2 to 6,
30 internally located IPNs. It will be appreciated, however, that even longer INAs with even greater than 10 IPNs could be used. It has been found by the present inventor that IPNs situated 2 or more bases from the 3' or 5' end of an oligonucleotide provide good blocking activity for DNA polymerases. Unlike other inhibiting strategies, such as the addition of 3 prime-dideoxy bases added to oligonucleotides to stop extension, blockers

according to the present invention do not require 3' or 5' positioning of chemical entities to function.

Preferably, the INA contains no IPNs at either the 3' or 5' end of the oligonucleotide.

5 The IPN is preferably selected from phosphoramidites of 1-(4,4'-dimethoxytriphenylmethoxy)-3-pyrenemethoxy-2-propanol. Preferably, the intercalator pseudonucleotide is selected from the phosphoramidite of (S)-1-(4,4'-dimethoxytriphenylmethoxy)-3-pyrenemethoxy-2-propanol or the phosphoramidite of (R)-1-(4,4'-dimethoxytriphenylmethoxy)-3-pyrenemethoxy-2-propanol. More
10 preferably, the IPN is the phosphoramidite of (S)-1-(4,4'-dimethoxytriphenylmethoxy)-3-pyrenemethoxy-2-propanol.

 An example of an IPN used for the examples in the present invention was the phosphoramidite of (S)-1-(4,4'-dimethoxytriphenylmethoxy)-3-pyrenemethoxy-2-propanol. It will be appreciated, however, that other chemical forms of IPNs can also be
15 used.

 The blockers according to the present invention are suitable for use in any form of amplification such as PCR and isothermal amplification methods. As PCR is the preferred method currently used by the health science industry, the present inventor has provided examples of the invention using PCR. It will be appreciated, however, that the
20 invention is not restricted to PCR or any other form of amplification.

 In a second aspect, the present invention provides use of a blocker according to the first aspect of the present invention to block or reduce nucleic acid amplification.

 In a third aspect, the present invention provides a method for detecting the methylation status of a target region of a nucleic acid molecule comprising:

25 treating the nucleic acid molecule with an agent which modifies cytosine bases but does not modify 5-methyl-cytosine bases under conditions to form a modified nucleic acid template;

 providing a first blocker according to the first aspect of the present invention to an amplification reaction, the first blocker being complementary to the unmethylated target
30 region on a first strand of the modified nucleic acid template;

 providing a second blocker according to the first aspect of the present invention to the amplification reaction, the second blocker being complementary to a region on the complementary second strand downstream of the first strand of the modified nucleic acid template;

providing a first primer complementary to nucleic acid region upstream from the target region on the first strand of the modified nucleic acid template;

providing a second primer complementary to nucleic acid region downstream from the second blocker region on the complementary second strand of the first strand of the modified nucleic acid template; and

carrying out a amplification reaction, wherein if the target region is methylated there will be an amplification product and if the target region is unmethylated there will be no amplification product.

In a fourth aspect, the present invention provides a method for detecting the methylation status of a target region of a nucleic acid molecule comprising:

treating the nucleic acid molecule with an agent which modifies cytosine bases but does not modify 5-methyl-cytosine bases under conditions to form a modified nucleic acid template;

providing a first blocker according to the first aspect of the present invention to an amplification reaction, the first blocker being complementary to the methylated target region on a first strand of the modified nucleic acid template;

providing a second blocker according to any according to the first aspect of the present invention to the amplification reaction, the second blocker being complementary to a region on the complementary second strand downstream of the first strand of the modified nucleic acid template;

providing a first primer complementary to nucleic acid region upstream from the target region on the first strand of the modified nucleic acid template;

providing a second primer complementary to nucleic acid region downstream from the second blocker region on the complementary second strand of the first strand of the modified nucleic acid template;

carrying out a polymerase amplification reaction, wherein if the target region is unmethylated there will be an amplification product and if the target region is methylated there will be no amplification product.

In a preferred from, the method further comprises:

providing third and fourth blockers according to the first aspect of the present invention to the amplification reaction, the third and fourth blockers being complementary to regions internal to the first and second blocker regions; and

providing third and fourth primers complementary to regions external to the third and fourth blocker regions and internal to the first and second primer regions.

In another preferred form, the method further comprises:

providing one or more additional blockers according to the first aspect of the present invention directed to one or more regions on the nucleic acid molecule.

Preferably, the regions on the nucleic acid molecule correspond to one or more regions on the modified nucleic acid template.

The method may further comprise:

providing three or more blockers according to the first aspect of the present invention directed to the first or second strands complementary to regions between the first and second primer regions.

In a fifth aspect, the present invention provides a method for detecting a conversion status of a target region of a nucleic acid molecule comprising:

treating the nucleic acid molecule with an agent which modifies cytosine bases but does not modify 5-methyl-cytosine bases under conditions to form a modified nucleic acid template;

providing a first blocker according to the first aspect of the present invention to an amplification reaction, the first blocker being complementary to the unconverted target region on a first strand of the nucleic acid molecule;

providing a second blocker according to the first aspect of the present invention to the amplification reaction, the second blocker being complementary to a region on the complementary second strand downstream of the first strand of the modified nucleic acid template;

providing a first primer complementary to nucleic acid region upstream from the target region on the first strand of the modified nucleic acid template;

providing a second primer complementary to nucleic acid region downstream from the second blocker region on the complementary second strand of the first strand of the modified nucleic acid template; and

carrying out an amplification reaction, wherein if the target region is converted there will be an amplification product and if the target region is unconverted there will be no amplification product.

In a sixth aspect, the present invention provides a method for detecting a conversion status of a target region of a nucleic acid molecule comprising:

treating the nucleic acid molecule with an agent which modifies cytosine bases but does not modify 5-methyl-cytosine bases under conditions to form a modified nucleic acid template;

providing a first blocker according to the first aspect of the present invention to an amplification reaction, the first blocker being complementary to the converted target region on a first strand of the nucleic acid molecule;

providing a second blocker according to the first aspect of the present invention to the amplification reaction, the second blocker being complementary to a region on the complementary second strand downstream of the first strand of the modified nucleic acid template;

providing a first primer complementary to nucleic acid region upstream from the target region on the first strand of the modified nucleic acid template;

providing a second primer complementary to nucleic acid region downstream from the second blocker region on the complementary second strand of the first strand of the modified nucleic acid template;

carrying out an amplification reaction, wherein if the target region is unconverted there will be an amplification product and if the target region is converted there will be no amplification product.

In a seventh aspect, the present invention provides a method for detecting a status of a target region of a nucleic acid molecule comprising:

treating the nucleic acid molecule with an agent which modifies cytosine bases but does not modify 5-methyl-cytosine bases under conditions to form a modified nucleic acid template;

providing a first blocker according to the first aspect of the present invention to an amplification reaction, the first blocker being complementary to a target region on a first strand of the modified nucleic acid template having an undesired status;

providing a second blocker according to the first aspect of the present invention to the amplification reaction, the second blocker being complementary to a region on the complementary second strand downstream of the first strand of the modified nucleic acid template;

providing a first primer complementary to nucleic acid region upstream from the target region on the first strand of the modified nucleic acid template;

providing a second primer complementary to nucleic acid region downstream from the second blocker region on the complementary second strand of the first strand of the modified nucleic acid template; and

carrying out a amplification reaction, wherein if the target region has a desired status there will be an amplification product and if the target region an undesired status there will be no amplification product.

In an eighth aspect, the present invention provides a method for detecting a status of a target region of a nucleic acid molecule comprising:

treating the nucleic acid molecule with an agent which modifies cytosine bases but does not modify 5-methyl-cytosine bases under conditions to form a modified nucleic acid template;

providing a first blocker according to the first aspect of the present invention to an amplification reaction, the first blocker being complementary to a target region on a first strand of the modified nucleic acid template having a desired status;

providing a second blocker according to the first aspect of the present invention to the amplification reaction, the second blocker being complementary to a region on the complementary second strand downstream of the first strand of the modified nucleic acid template;

providing a first primer complementary to nucleic acid region upstream from the target region on the first strand of the modified nucleic acid template;

providing a second primer complementary to nucleic acid region downstream from the second blocker region on the complementary second strand of the first strand of the modified nucleic acid template;

carrying out an amplification reaction, wherein if the target region has an undesired status there will be an amplification product and if the target region has a desired status there will be no amplification product.

Preferably, the status is methylation, mutation, or single nucleotide polymorphism.

In a ninth aspect, the present invention provides a method for blocking or reducing nucleic acid amplification comprising:

providing a blocker comprising an INA molecule containing two or more internal

IPNs to a nucleic acid amplification reaction, wherein the blocker being complementary to a nucleic acid sequence of interest; and

carrying out an amplification reaction such that the blocker binds to the nucleic acid sequence of interest and blocks or reduces amplification at or near the sequence of interest.

In a tenth aspect, the present invention provides a method for blocking or reducing nucleic acid amplification comprising:

providing a blocker according to the first aspect of the present invention to a nucleic acid amplification reaction, wherein the blocker being complementary to a nucleic acid sequence of interest; and

carrying out an amplification reaction such that the blocker binds to the nucleic acid sequence of interest and blocks or reduces amplification at or near the sequence of interest.

In a preferred form, the amplification assay is polymerase amplification in the form of PCR.

The nucleic acid molecule can be DNA or RNA. Preferably, the nucleic acid molecule is DNA.

In one preferred form, the methylation status is methylated.

In another preferred form, the methylation status is unmethylated.

Preferably, the potential methylation site is cytosine (C) flanked 3' by a guanine (G), termed in the art as CpG doublet.

The modifying agent is preferably selected from bisulfite, acetate or citrate. More preferably, the agent is sodium bisulfite, a reagent, which in the presence of water, modifies cytosine into uracil.

Sodium bisulfite (NaHSO_3) reacts readily with the 5,6-double bond of cytosine to form a sulfonated cytosine reaction intermediate which is susceptible to deamination, and in the presence of water gives rise to a uracil sulfite. If necessary, the sulfite group can be removed under mild alkaline conditions, resulting in the formation of uracil. Thus, potentially all cytosines will be converted to uracils. Any methylated cytosines, however, cannot be converted by the modifying reagent due to protection by methylation.

In one preferred form, one or more blockers are directed to one or more potential methylation sites on the nucleic acid molecule.

In another preferred form, the blockers do not bind to potential methylation sites on the nucleic acid molecule.

In a more general form, the present inventor has found that a polymerase can be blocked from moving along a stretch of DNA by hybridizing a probe/blocker to a region of the DNA. This causes suppression of amplification of certain sequences in PCR (Saiki et al, (1998) Primer-directed enzymatic amplification of DNA with a thermostable DNA polymerase. Science 239: 487-491. or other amplification processes such as, but not limited to, Ligase Chain Reaction (LCR, Barany F. (1991) Genetic disease detection and DNA amplification using cloned thermostable ligase. Proc. Natl. Acad. Sci. USA 88: 189-193 and isothermal methods of amplification including Strand Displacement amplification (SDA, Walker et al, (1992) Isothermal *in vitro* amplification of DNA by a restriction/DNA polymerase system. Proc. Natl. Acad. Sci. USA 89: 392-396, Nucleic Acid Sequence Based Amplification (NASBA, Kievit et al, (1991) NASBA™ isothermal enzymatic *in vitro* nucleic acid amplification optimised for the diagnosis of HIV-1. J. Virol. Methods 35: 273-286, Transcription Based Amplification (TAS) Kwoh et al (1989) Transcription-based amplification system and detection of amplified human immunodeficiency virus type 1 with a bead-based sandwich hybridization format. Proc Natl Acad Sci U S A. 4:1173-7, Helicase Chain Reaction (HCR, Vincent and Kong, (2004) Helicase-dependent isothermal DNA amplification. EMBO Reports 5(8): 1-6 Rolling Circle Amplification (RCA, Fire A. and Xu S.Q., (1995) Rolling replication of short DNA circles. Proc. Natl. Acad. Sci USA 92: 4641-4645 Self Sustained Sequence Replication (3SR, Guatelli et al, (1990) Isothermal, *in vitro* amplification of nucleic acids by a multienzyme reaction modelled after retroviral replication. Proc. Natl. Acad. Sci. USA 87: 1874-1878. Using modified 3' oligonucleotide sequences such as the addition of 3' dideoxy-nucleotides has been shown to stop polymerase extension. Unexpectedly, it has been found that the IPN molecules do not have to be placed at the terminal 3' end of the oligonucleotide but can in fact be internally placed in the INA and still block the extension of the polymerase.

It transpires that a DNA polymerase has great difficulty displacing / degrading an INA primer that has hybridized to a given genomic region, if that INA primer has multiple IPNs located within it. The IPNs in an INA effectively act as blockers to the progress of a polymerase. This unexpected property of INAs means that one can block unmethylated sequences in a region from being amplified and only amplify methylated sequences. In addition, unlike other methods to prevent polymerase extension such as the 3' terminal addition of a dideoxy-nucleotide, the present inventor has found that the IPN molecule can be placed internally and does not have to be 3' to produce the blocking effect. Thus

in a mixed population of methylated and unmethylated sequences, one can remove all the background.

The present invention is also applicable for 'real-time' detection assays.

5 In its simplest form, the present invention relates to the use of INA blockers to differentially amplify any desired region of the human or animal or plant or microbial genome that exists in a minimum of two states. These two states are alternatives at the same genomic locus, but at the level of human or animal or plant or microbial samples are usually embedded in a mixed population of cells in which there is a particular genomic state in one population and a different genomic state in another. By the 'needle
10 in a haystack' analogy, the invention allows for the amplification of the needle, and the blockage of amplification for all the hay that constitutes the haystack.

In practical molecular terms this means the following: if the needle is a particular methylated genomic sequence that occurs in a cancerous cell, whereas the normal cells have an unmethylated sequence at the same locus, then the invention allows for the
15 amplification and visualization of the methylated sequence by blocking amplification of the unwanted unmethylated sequence. The converse also applies. If the normal cells have a methylated genomic sequence, and the cancerous cells have an unmethylated sequence, then the invention also allows for the amplification and visualization of the unmethylated sequence by the blocking of the methylated sequence.

20 The beauty of the invention is that it allows for the detection of low level entities in a huge sea of unwanted entities. In the parlance of signal to noise ratios, in disease it is often the case of having a few cancerous cells (signal) amongst thousands of normal cells (the noise). The blocker technology according to the present invention does two things; it suppresses the noise and in addition amplifies the signal from the genomes of
25 these two types of cells.

Although the inventor has presented data for five genes shown in the examples below, the invention is general and applicable to any part of the human or animal or plant or microbial genome, be it coding or noncoding, when that part of the genome exists in one of two states. Although the invention can be used for any situation such as detection
30 of SNPs and genetic mutations, it has very useful application in looking for methylation status of genomic targets.

Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps,

but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

Any discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is solely for the purpose of providing a context for the present invention. It is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field relevant to the present invention as it existed in Australia before the priority date of each claim of this specification.

In order that the present invention may be more clearly understood, preferred embodiments will be described with reference to the following drawings and examples.

Brief Description of the Drawings

Figure 1 shows illustrative details of the INA blocker strategy providing an overview of the location of primers and blockers used in two rounds of DNA amplification.

Figure 2 shows illustrative details of how the INA blocker strategy works providing an overview of the location of primers and blockers used in two rounds of DNA amplification involving methylated or unmethylated DNA sequences. As this example this has been used for illustrative purposes, the blocker and primer sequences would not generally be used in a real assay. Genomic DNA sequence (SEQ ID NO 17); Bisulphite treated Methylated sequence (SEQ ID NO 18); Bisulphite treated Unmethylated sequence (SEQ ID NO 19); PCR Primer#2 (SEQ ID NO 20); PCR Primer#1 (SEQ ID NO 21); Methyl Blocker#2 (SEQ ID NO 22); Methyl Blocker#1 (SEQ ID NO 23); Unmethyl Blocker#2 (SEQ ID NO 24); Unmethyl Blocker#1 (SEQ ID NO 25).

Figure 3 is an illustration showing the hybridisation of PCR primers and methylated INA blockers to various bisulphite treated DNA types. **A.** Unconverted sequence (SEQ ID NO 26); **B.** Bisulphite treated Methylated sequence (SEQ ID NO 27); **C.** Bisulphite treated Unmethylated sequence (SEQ ID NO 28); **D.** Regional non-converted sequence (SEQ ID NO 29); PCR Primer#1 (SEQ ID NO 30); Methyl blocker#1 (SEQ ID NO 31).

Figure 4 is an illustration showing the hybridisation of PCR primers and unmethylated INA blockers to various bisulphite treated DNA types. **A.** Unconverted sequence (SEQ ID NO 26); **B.** Bisulphite treated Methylated sequence (SEQ ID NO 27); **C.** Bisulphite treated Unmethylated sequence (SEQ ID NO 28); **D.** Regional non-converted sequence (SEQ ID NO 29); PCR Primer#1 (SEQ ID NO 30); Unmethyl blocker#1 (SEQ ID NO 32).

Figure 5 is an illustration showing the hybridisation of PCR primers and non-converted INA blockers to various bisulphite treated DNA types. **A.** Unconverted sequence (SEQ ID NO 26); **B.** Bisulphite treated Methylated sequence (SEQ ID NO 27); **C.** Bisulphite treated Unmethylated sequence (SEQ ID NO 28); **D.** Regional non-converted sequence (SEQ ID NO 29); PCR Primer#1 (SEQ ID NO 30); non converted blocker#1 (SEQ ID NO 33).

Figure 6 shows the expected amplification products visualized on agarose gel electrophoresis using conventional PCR, MSP technology, or the INA blockers and primer combinations outlined in Figures 3, 4 and 5. The results are shown by illustration of the positions and sizes of the expected amplification products detected on gels using various amplification / detection methodologies relative to a defined set of known DNA markers.

Figure 7 shows data on the application of the INA blocker technology to bisulphite treated genomic DNA samples. INA blockers and PCR primers for the GSTP1 promoter region have been applied to nine genomic DNA samples (described in Table 3) to evaluate the methylation status of the promoter region.

Figure 8 shows amplification results and inferred methylation status of four genomic regions near to the CDKN2B, CXCL-2, GSN and HIC-1 genes using blockers and PCR primers applied to the eleven genomic DNA samples described in Table 2. The results are of the use of blockers and PCR primers applied to eleven genomic DNA samples described in Table 3, and reveals the amplification products from human genomic regions in the vicinity of the CDKN2B, CXCL-2, GSN and HIC-1 loci.

Mode(s) for Carrying Out the Invention

25 MATERIALS AND METHODS

INA / IPN Definition

Intercalating Nucleic Acids (INAs) are a unique class of DNA binding molecules. INAs are comprised of nucleotides and/or nucleotide analogues and intercalating pseudonucleotide (IPN) monomers. INAs have a very high affinity for complementary DNA with stabilisations of up to 10 degrees for internally placed IPNs and up to 11 degrees for end position IPNs. The INA itself is a selective molecule that prefers to hybridise with DNA over complementary RNA. It has been shown that INAs bind about 25 times less efficiently to RNA than oligonucleotide primers. Whereas, conventional oligonucleotides, oligonucleotide analogues and PNAs have an equal affinity for both

RNA and DNA. Thus INAs are the first truly selective DNA binding agents. In addition, INAs have a higher specificity and affinity for complementary DNA than other natural DNA molecules.

In addition, IPNs stabilise DNA best in AT-rich surroundings which make them especially useful in the field of epigenomics research. The IPNs are typically placed as bulge or end insertions into the INA molecule. The IPN is essentially a planar (hetero) polyaromatic compound that is capable of co-stacking with nucleobases in a nucleic acid duplex.

The INA molecule has also been shown to be resistant to exonuclease attack. This makes these molecules especially useful as primers for amplification using enzymes such as phi29. As phi29 has inherent exonuclease activity, primers used as templates for amplification must be specially modified at their 3' terminus to prevent enzyme degradation. INA molecules, however, can be added without further modification.

INAs can be used in conventional PCR amplification reactions and behave as conventional primers. INAs, however, have a higher specificity for the DNA template making them ideal for the use in situations where template is limiting and sensitivity of the reaction is critical. INAs stabilise DNA best in AT-rich surroundings which make them especially useful for amplification of bisulphite treated DNA sequences. This is due to the fact that after bisulphite conversion, all the cytosine residues are converted to uracil and subsequently thymine after PCR or other amplification. Bisulphite treated DNA is therefore very T rich. Increasing the number of IPN molecules in the INA results in increased stabilization of the INA/DNA duplex. The more IPNs in the INA, the greater the melting temperature of the DNA/INA duplex. Unexpectedly, when multiple IPNs were positioned in the nucleotide molecule, although the INA has a very high specificity for its complementary DNA, the inclusion of the IPNs resulted in the inhibition of PCR polymerase extension in the amplification reaction. Thus if INAs are designed with multiple IPNs, they act as blocking reagents in the PCR amplification reaction which does not occur using conventional oligonucleotides.

The present applicant has previously developed a class of intercalator pseudonucleotides which, when incorporated into an oligonucleotide or oligonucleotide analogue, form an intercalating nucleic acid (INA) (WO 03/051901, WO 03/052132, WO 03/052133 and WO 03/052134) which has novel and useful properties as a supplement to, or replacement of, oligonucleotides. It has now been found that oligonucleotides or oligonucleotide analogues can be modified to include

one or more intercalator pseudonucleotides (IPN) to form a blocker of nucleic acid amplification.

The intercalator pseudonucleotide is preferably selected from phosphoramidites of 1-(4,4'-dimethoxytriphenylmethoxy)-3-pyrenemethoxy-2-propanol. Preferably, the
 5 intercalator pseudonucleotide is selected from the phosphoramidite of (S)-1-(4,4'-dimethoxytriphenylmethoxy)-3-pyrenemethoxy-2-propanol or the phosphoramidite of (R)-1-(4,4'-dimethoxytriphenylmethoxy)-3-pyrenemethoxy-2-propanol.

The oligonucleotide or oligonucleotide analogue can be selected from DNA, RNA, locked nucleic acid (LNA), peptide nucleic acid (PNA), MNA, alritol nucleic acid (ANA),
 10 hexitol nucleic acid (HNA), intercalating nucleic acid (INA), cyclohexanyl nucleic acid (CNA) and mixtures thereof and hybrids thereof, as well as phosphorous atom modifications thereof, such as but not limited to phosphorothioates, methyl phospholates, phosphoramidites, phosphorodithiates, phosphoroselenoates, phosphotriesters and phosphoboranoates. Non-naturally occurring nucleotides include, but not limited to the
 15 nucleotides comprised within DNA, RNA, PNA, INA, HNA, MNA, ANA, LNA, CNA, CeNA, TNA, (2'-NH)-TNA, (3'-NH)-TNA, α -L-Ribo-LNA, α -L-Xylo-LNA, β -D-Xylo-LNA, α -D-Ribo-LNA, [3.2.1]-LNA, Bicyclo-DNA, 6-Amino-Bicyclo-DNA, 5-epi-Bicyclo-DNA, α -Bicyclo-DNA, Tricyclo-DNA, Bicyclo[4.3.0]-DNA, Bicyclo[3.2.1]-DNA, Bicyclo[4.3.0]amide-DNA, β -D-Ribopyranosyl-NA, α -L-Lyxopyranosyl-NA, 2'-R-RNA, α -L-RNA or α -D-RNA, β -D-
 20 RNA. In addition non-phosphorous containing compounds may be used for linking to nucleotides such as but not limited to methyliminomethyl, formacetate, thioformacetate and linking groups comprising amides. In particular nucleic acids and nucleic acid analogues may comprise one or more intercalator pseudonucleotides.

Preferably, the blockers are DNA oligonucleotides containing two or more internal
 25 IPNs forming blocking INAs.

When IPNs are placed in an INA molecule for the specific detection of methylated sites, the present inventor has found that it is useful to avoid placing an IPN between potential CpG sites. This is due to the fact that when a CpG site is split using an IPN the specificity of the resulting INA is reduced.

30

Genomic nucleic acid

Genomic nucleic acid can be DNA or RNA obtained from plants, animals, microorganisms such as bacteria, fungi, yeasts and viruses. Preferably, the nucleic acid

is DNA, more preferably genomic DNA from an animal or human, or nucleic acid of an infectious agent of animal or human cells.

Bisulphite treatment of DNA

5 An exemplary protocol for effective bisulphite treatment of nucleic acid is set out below. The protocol results in retaining substantially all DNA treated. This method is also referred to herein as the Human Genetic Signatures (HGS) method. It will be appreciated that the volumes or amounts of sample or reagents can be varied.

10 Preferred method for bisulphite treatment can be found in US 10/428310 or PCT/AU2004/000549.

15 To 2 µg of DNA, which can be pre-digested with suitable restriction enzymes if so desired, 2 µl (1/10 volume) of 3 M NaOH (6g in 50 ml water, freshly made) was added in a final volume of 20 µl. This step denatures the double stranded DNA molecules into a single stranded form, since the bisulphite reagent preferably reacts with single stranded molecules. The mixture was incubated at 37°C for 15 minutes. Incubation at temperatures above room temperature can be used to improve the efficiency of denaturation.

20 After the incubation, 208 µl 2 M Sodium Metabisulphite (7.6 g in 20 ml water with 416 ml 10 N NaOH; BDH AnalaR #10356.4D; freshly made) and 12 µl of 10 mM Quinol (0.055 g in 50 ml water, BDH AnalR #103122E; freshly made) were added in succession. Quinol is a reducing agent and helps to reduce oxidation of the reagents. Other reducing agents can also be used, for example, dithiothreitol (DTT), mercaptoethanol, quinone (hydroquinone), or other suitable reducing agents. The sample was overlaid with 200 µl of mineral oil. The overlaying of mineral oil prevents evaporation and oxidation of the reagents but is not essential. The sample was then incubated overnight at 55°C. Alternatively the samples can be cycled in a thermal cycler as follows: incubate for about 4 hours or overnight as follows: Step 1, 55°C / 2 hr cycled in PCR machine; Step 2, 95°C / 2 min. Step 1 can be performed at any temperature from about 37°C to about 90°C and can vary in length from 5 minutes to 8 hours. Step 2 can be performed at any temperature from about 70°C to about 99°C and can vary in length from about 1 second to 60 minutes, or longer.

30 After the treatment with Sodium Metabisulphite, the oil was removed, and 1 µl tRNA (20 mg/ml) or 2 µl glycogen were added if the DNA concentration was low. These additives are optional and can be used to improve the yield of DNA obtained by co-

precipitating with the target DNA especially when the DNA is present at low concentrations. The use of additives as carrier for more efficient precipitation of nucleic acids is generally desired when the amount nucleic acid is <0.5 µg.

5 An isopropanol cleanup treatment was performed as follows: 800 µl of water were added to the sample, mixed and then 1 ml isopropanol was added. The water or buffer reduces the concentration of the bisulphite salt in the reaction vessel to a level at which the salt will not precipitate along with the target nucleic acid of interest. The dilution is generally about 1/4 to 1/1000 so long as the salt concentration is diluted below a desired range, as disclosed herein.

10 The sample was mixed again and left at 4°C for a minimum of 5 minutes. The sample was spun in a microfuge for 10-15 minutes and the pellet was washed 2x with 70% ETOH, vortexing each time. This washing treatment removes any residual salts that precipitated with the nucleic acids.

The pellet was allowed to dry and then resuspended in a suitable volume of T/E (10 mM Tris/0.1 mM EDTA) pH 7.0-12.5 such as 50 µl. Buffer at pH 10.5 has been found to be particularly effective. The sample was incubated at 37°C to 95°C for 1 min to 96 hr, as needed to suspend the nucleic acids.

Blocker Production

20 A suitable method for the production of INA blockers can be found in Christensen UB, Pedersen EB. Intercalating nucleic acids containing insertions of 1-O-(1-pyrenylmethyl)glycerol: stabilisation of dsDNA and discrimination of DNA over RNA. Nucleic Acids Res. 2002 Nov 15;30(22):4918-25.

25 Blockers

As defined herein, a 'blocker' is an intercalating nucleic acid (INA) containing two or more internal intercalating pseudonucleotides (IPNs) capable of blocking or reducing nucleic acid amplification.

30 As defined herein, a 'methyl blocker' is blocker designed to target a region of converted nucleic acid that was originally methylated in its untreated genomic state.

As defined herein, an 'unmethyl blocker' is blocker designed to target a region of converted nucleic acid that was not methylated in its untreated genomic state.

As defined herein, a 'converted blocker' is blocker designed to target a region of converted nucleic acid.

As defined herein, an 'unconverted blocker' is blocker designed to target a region of genomic nucleic acid (ie unconverted by bisulfite or other treatment).

5 Examples of INA blockers used in the illustrative example for the GSTP1 gene are as follows:

MB-1 5' TYT TCG GTT AGY TTG CGC GGC GAY TTT CGG YGG A (SEQ ID NO 1)

UB-1 5' TYT TTG GTT AGY TTG TGT GGT GAY TTT TGG YGG A (SEQ ID NO 2)

NCB-1 5' CYC CCG GCC AGY CTG CGC GGC GAY CTC CGG YGG A (SEQ ID NO 3)

10 MB-2 5' TTA YTA ACG AAA YAC TYA CGA CGA CGA AAC YTC C (SEQ ID NO 4)

UB-2 5' TTA YTA ACA AAA YAC TYA CAA CAA CAA AAC YTC C (SEQ ID NO 5)

NCB-2 5' TGG YTG GCG AAG YAC TYG CGG CGG CGA AAC YTC C (SEQ ID NO 6)

MB-3 5' TTY AGG GCG TYT TTT TYT GCG GTC GAC GTY T (SEQ ID NO 7)

UB-3 5' TTY AGG GTG TYT TTT TYT GTG GTT GAT GTY T (SEQ ID NO 8)

15 NCB-3 5' CCY AGG GCG CYC CCT CYT GCG GCC GAC GCY C (SEQ ID NO 9)

MB-4 5' ATY AAT CCC GCC YCC GCT YCC GCC CCA YAT A (SEQ ID NO 10)

UB-4 5' ATY AAT CCC ACC YCC ACT YCC ACC CCA YAT A (SEQ ID NO 11)

NCB-4 5' GTY GGT CCC GCC YCC GCT YCC GCC CCA YGT G (SEQ ID NO 12)

20 wherein Y designates an IPN. Preferably, the IPN is in the form of the phosphoramidite of (S)-1-(4,4'-dimethoxytriphenylmethoxy)-3-pyrenemethoxy-2-propanol.

MB is a Methylated Blocker

UB is an Unmethylated blocker

NCB is an Non-converted blocker

25 The descriptor 'Y' denotes the placement of the IPN in the sequence, and is included in the base count of the sequence.

PCR Primers

Primers used for illustration were as follows:

30 GSTP1-1 TTT GTT GTT TGT TTA TTT TTT AGG TTT (SEQ ID NO 13)

GSTP1-2 AAC CTA ATA CTA CTA ATT AAC CCC AT (SEQ ID NO 14)

GSTP1-3 GGA TTT GGG AAA GAG GGA AAG GTT TT (SEQ ID NO 15)

GSTP1-4 ACT AAA AAC TCT AAA CCC CAT CCC (SEQ ID NO 16)

5 1st round INA blocking PCR

GSTP1-1/2 + appropriate Blocker 1/2

2nd round INA blocking PCR

GSTP1-3/4 + appropriate Blocker 3/4.

10 **Conventional bisulphite modification of DNA and visualization of a product for a given genomic region**

This involves treatment of a DNA sample with bisulphite followed by a PCR amplification step. The product of the PCR step, say the visualization of a band on a gel, does not tell the researcher if the DNA was methylated or not at this stage, only that

15 there was bisulphite treated DNA for that particular gene region present in the sample. After PCR and visualization, the product still needs to be either digested by restriction enzymes to see if a particular site is cut by the enzyme or not, (and hence whether it was methylated or not), or the DNA band or fragment needs to be sequenced to determine if

20 the gene region was methylated, or not, in that particular tissue sample. Sequencing a PCR band will reveal whether each C in a CpG doublet for example in that region was methylated or not. This method lacks sensitivity as methylation will only be confidently and routinely detected on a sequencing apparatus if greater than 10% of the sample was methylated. In a particular tissue sample, for example, if 90% of the cells in that sample had unmethylated DNA in the region under study and 10% had methylated DNA, the

25 conventional method described above would lack the sensitivity for the accurate determination of methylation profiling. Furthermore, this prior art method is very labour intensive and time consuming to perform.

Methylation Specific PCR (MSP)

30 Although MSP has been widely adopted by the methylation research community, MSP has a number of very serious limitations or drawbacks that are documented in the literature. These limitations or drawbacks include:

- I. The method is very prone to false positive signals especially if there are small numbers of cancerous cells with methylated DNA regions in a mixed population of normal and cancerous cells, as is the case with most cancerous tissues due to the heterogeneity of the tumour. For ease of illustration the normal cells have their equivalent regions in an unmethylated state. The false positive signals arise as a result of regional non-conversion of the DNA when treated with bisulphite. Thus PCR primers amplify non-converted regions (see Figure 3, 4 and 5 region D) of the DNA and so one obtains what one believes to be a methylated answer, but in fact it's a gene region that has simply failed to be converted by the bisulphite treatment. INA blockers do not suffer from this problem as it is possible to include non-converted INA blockers which will block the amplification of non-converted DNA regions. If a positive signal is obtained using INA blocker technology, the signal will be the result of fully converted DNA. Thus, false positive PCR signals are eliminated using the blockers according to the present invention.
- II. Unless the region has been previously sequenced after conventional bisulphite treatment (not a sensitive approach), the researcher does not know if the CpG site which is being targeted was methylated in the first place. Thus a certain CpG site may be unmethylated or under methylated and unless the region had been sequenced, a MSP primer designed against that particular CpG would either produce a false negative reaction or under estimate the degree of methylation of that particular gene. Again the INA blocker technology according to the present invention overcomes this limitation as the PCR primers can be designed to regions that do not contain CpG dinucleotides. Thus the PCR primers will bind whether the gene is methylated or not.
- III. If the sequence contains only a small area of methylation, for example in the 1st part of the sequence and this does not extend the full length of the sequence, then this would yield a false negative result with MSP. This is due to the fact that although the 1st MSP primer will bind to the complementary CpG site the second MSP primer will not bind as the second region was unmethylated. The blockers do not have this problem as already stated above as the PCR primers can be designed to regions that will amplify regardless of whether they were methylated or not.
- IV. MSP is very difficult to optimise as the reaction relies on the ability of the PCR enzyme to prime off the 3' terminal base which is either a methylated C or an unmethylated T base. Thus, different MSP reactions for different gene regions

may have very different hybridisation temperatures between the MSP primer and the converted target region (T_m optima). If one gene region contains a very dense CpG island and the other gene region has much fewer CpG's, then the gene region from the CpG island might have a T_m of 70°C while the other gene region might have a T_m of 50°C. Therefore, if an MSP reaction is performed at high stringency, the gene with T_m of 70°C will produce a PCR product, while the MSP reaction with the T_m of 50°C will produce no amplified product. Thus, it would be close to impossible to carry out multiple MSP reactions (each in a different well in the same plate 96 well or 384 well PCR plate) and get sensible results out the other end as each well will have different T_m optima and amplification or not will vary in an unpredictable manner. Again as the PCR primers in the blocker technology according to the present invention can be designed against regions of genes that are devoid of CpGs, the T_m optima of multiple different genes is much more easy to control as even in relatively dense CpG islands. It is usually possible to find a small region within that island that is devoid of CpG dinucleotides that will serve as a priming site for a PCR primer.

V. MSP only detects the presence of methylation at one specific CpG site per primer, so the MSP reaction only ever reports on two sites per gene region. This has always been a well documented criticism. It does not tell the researcher anything about the methylation state of the area between the PCR primers. The blocker INAs can contain on average 3-4 CpG sites thus using 4 blockers per gene the present invention can be used to interrogate on average from 12-16 CpG sites for methylation status.

25 RESULTS

Blocker Strategy

The present invention is first illustrated by the following an amplification assay.

In Figure 1, PCR primer#1 and blocker #1 hybridises to bisulphite treated DNA from the genomic region of interest. Taq polymerase then extends from PCR primer#1 until it reaches blocker#1 bound to the top DNA strand at which point the enzyme stops. If for some reason the enzyme does bypass blocker#1, the enzyme will copy the top strand of the DNA and produce the complementary strand creating the binding site for PCR primer#2. Therefore, a second blocker complementary to a sequence internal of PCR#2 is added. This then ensures that no amplification of genomic region.

Due to the nature of bisulphite treated DNA, amplification efficiency, particularly by PCR, is reduced as the DNA is now essentially composed of a 3 base genome. Therefore for maximum sensitivity, a second round of PCR can be performed. The second round PCR improves the sensitivity of the reaction at least five orders of magnitude, thus making the method ideal for the detection of DNA methylation changes that occur in a small subpopulation of cells, such as the very low numbers of cancer cells in a mixed population of cancerous and normal cells in a clinical sample. In this regard, a third and a fourth PCR primer (PCR primer#3 and PCR primer#4) internal to PCR primer#1 and primer#2 are added along with two further blockers (blocker#3 and blocker#4). Thus each PCR primer has a blocker sequence that is complementary to a sequence internal of that PCR primer.

Therefore, for each genomic region of interest, a total of four PCR primers are synthesised. If detection of the presence of methylated DNA sequences was required, four unmethylated blocking sequences would be used to block the amplification of unmethylated DNA. In addition, to ensure that the sequence had been fully converted by the bisulphite treatment (a potential problem associated with some bisulphite treatment reactions) a further four non-converted sequences could be used to block the amplification of regions of DNA that have undergone only partial conversion. In this regard, in each PCR (or other amplification) reaction there would be two PCR primers, 2 unmethylated blockers and 2 non-converted blockers.

Conversely, if detection of the presence of unmethylated DNA sequences was required, four methylated blocking sequences could be used to block the amplification of methylated DNA. In addition, to ensure that the sequence had been fully converted by the bisulphite treatment a further four non-converted sequences could be used to block the amplification of regions of DNA that have undergone only partial conversion. Again, in each PCR reaction there would be two PCR primers, 2 methylated blockers and 2 non-converted blockers.

It will be appreciated that the blockers can be used to block any amplification of nucleic acid.

Blocker specific amplification

Figure 2 shows normal and bisulphite treated artificial DNA sequences for demonstration purposes, PCR primer#1 and primer#2 targeting non-CpG containing regions and the sequences of the four blocker sequences (two methylated and two unmethylated) which hybridise to their appropriate target region.

Hybridisation of PCR primers and INA blockers to unconverted DNA (wild type)

In Figure 3, the PCR primer#1 will only hybridise to B, C and D, not the unconverted sequence A due to insufficient sequence similarity. The methyl-blocker will only bind to the bisulphite treated methylated sequence B, but not to the unconverted, unmethylated or regionally non-converted DNA sequences again due to insufficient sequence similarity. Taq polymerase will then begin extending the sequences shown in B, C and D. However, in case B the enzyme will come to the methyl blocker but will not be able to pass the methyl-blocker thus no product will be formed. In case C no blocker has bound due to mismatch bases at the TpG sites, so Taq will produce the desired PCR fragment. In case D again no blocker has bound due to insufficient sequence similarity therefore a PCR product will be obtained but this product will contain non-converted sequences.

Hybridisation of PCR primers and blockers to converted methylated DNA sequences

In Figure 4, the PCR primer#1 will only hybridise to B, C and D, not the unconverted sequence A due to insufficient sequence similarity. The unmethyl-blocker will only bind to the bisulphite treated unmethylated sequence C, not to the unconverted, methylated or regional unconverted DNA sequences again due to insufficient sequence similarity. Taq polymerase will then begin extending the sequences shown in B, C and D. In case C the enzyme will come to the unmethyl blocker but will not be able to pass the unmethyl-blocker thus no product will be formed. In case B no blocker has bound due to mismatched bases at the CpG, so Taq will produce the desired PCR fragment. In case D again no blocker has bound due to insufficient sequence similarity, therefore a PCR product will be obtained but this product will contain non-converted sequences.

Hybridisation of PCR primers and blockers to regionally non-converted DNA sequences

In Figure 5, the PCR primer#1 will only hybridise to B, C and D, not the unconverted sequence A due to insufficient sequence similarity. The non-converted blocker will bind to the non-converted sequence A and the regionally non-converted sequence D not to the methylated or unmethylated DNA sequences again due to insufficient sequence similarity. Taq polymerase will then begin extending of the sequences shown in B, C and D. In case D the enzyme will come to the non-converted blocker but will not be able to pass the non-converted blocker thus no product will be

formed. In case B and C no blocker has bound due to sequence mismatched bases at the CpG and TpG sites, so Taq will produce the desired PCR fragment.

Thus the non-converted blocker can be added to situations set out in Figures 3 and Figure 4 along with the appropriate blockers and primers to prevent the amplification
5 of regionally non-converted sequences, a major problem with conventional MSP.

Comparison of methodologies

Figure 6 shows a schematic representation of the banding patterns which would be observed on an agarose gel using conventional bisulphite PCR, Methylation Specific
10 PCR (MSP) and INA blocker technology.

With conventional bisulphite PCR a band would be seen whether or not the sample contained methylated sequences or not, normal tissue versus cancer tissue, (Lane 1 in both panels). This particular method only detects the presence of bisulphite treated DNA in the sample and has to be further processed to determine the methylation
15 status, usually by dideoxy sequencing.

Using MSP for the detection of methylated DNA sequences, no band would be seen in Lane 2 from the normal tissue sample as the normal tissue would be unmethylated. However, a band would be seen in Lane 2 of the cancer tissue sample. Using MSP primers directed against unmethylated sequences, a band would be
20 observed in the normal tissue sample (Lane 3) but not in the cancerous tissue sample (see Lane 3).

With INA blocker technology using methylated blockers, a band would be observed in the normal tissue (Lane 4) but not in the cancerous tissue (see Lane 4). Using unmethylated blockers a band would be observed in the cancerous tissue (Lane 5)
25 but not in the normal tissue (see Lane 5).

Blocker technology applied to bisulphite treated genomic DNA samples

Figure 7 shows that when unmethylated blockers were added to the PCR reaction mix, positive PCR signals were generated with the bisulphite converted DNA
30 HeLa cell line, T-cells from a clinical sample and the breast cancer cell line T47D2.

Table 1

Lane	Sample	Cell Type	Methylation [@]
1	HeLa	Cervical (cell line)	Yes
2	HuVec	Endothelial (cell line)	No
3	THP	Monocyte (cell line)	No
4	T-cell	Blood	No
5	B-cell	Blood	No
6	CD34+	Blood	No
7	T47D2	Breast (cell line)	Yes/No ^{\$}
8	500 ng placenta DNA	Placenta	No
9	100 ng placenta DNA	Placenta	No

[@] .Methylation measured by conventional bisulphite PCR, which will only detect methylation if greater than 10% of the sample contained methylated sequences.

- 5 ^{\$} When the T47D2 was sequenced by conventional bisulphite sequencing it was found that the first half of the sequence was methylated but the second half was not.

Purification of T-cells, B-cells and CD34+ cells from whole blood

10 Samples were obtained from a patient undergoing leukapheresis at the Royal North Shore Hospital, Sydney, Australia. Samples were obtained with prior Ethics Committee approval. White blood cells were concentrated using Ficoll Paque plus (Amersham Biosciences #17-1440-03; Piscataway NJ) according to the manufacturers instructions. T-cells, B-cells and CD34+ cells were isolated from the white cell population using CELLection CD2 Dynabeads (Dyna #116.03; Lake Success NY),
 15 Dynabeads CD19 (Pan B) Dynal#111.43 and Dynal CD34 Progenitor Cell selection system (Dyna #113.01) respectively according to the manufactures instructions.

Sequences and primers used are set out in Table 2.

PCR premixes were prepared as follows:

	Unmethylated mixes	Methylated mixes	Control reaction
	X2 Master mix (Promega)	12.5 µl	12.5 µl
	100 ng/µl PCR#1	1 µl	1 µl
5	100 ng/µl PCR#2	1 µl	1 µl
	100 ng/µl Blocker#1	3 µl (U)	3 µl (M)
	100 ng/µl Blocker#2	3 µl (U)	3 µl (M)
	Water	3.5 µl	9.5 µl

Table 2

NAME	SEQUENCE	SEQ ID NO	PCR PRIMER	SEQUENCE	SEQ ID NO
CDKN2B MB-1	GAT TYT TGC GYA CGC GYT TCG TAT YTT TG	34	CDKN2B -1	TTTTTGGTTTAGTTGAAAAAGGAATTT	35
CDKN2B MB-2	GTT YAA CGA YTC GGT CGT YTC GGT TYA TTG	36	CDKN2B -2	TTAGGAGTTTTTTTTTAGAAGTAATTTAGG	37
CDKN2B MB-3	CCY CGC GCC GCG YAC GCT YAA CCY AAA C	38	CDKN2B -3	ACTTCCAAAAACTATGTGACCTTCTCCACTAA	39
CDKN2B MB-4	AAC TCC GTT YAA AAY TCC GCG CCG YAC TTY C	40	CDKN2B -4	AAACCCCTAAAAACCCCAACTACCTAA	41
CDKN2B UB-1	GAT TYT TGT GYA TGT GYT TTG TAT YTT TG	42			
CDKN2B UB-2	GTT YAA TGA YTT GGT TGT YTT GGT TYA TTG	43			
CDKN2B UB-3	CCY CAC ACC ACA YAC ACT YAA CCY AAA C	44			
CDKN2B UB-4	AAC TCC ATT YAA AAY TCC ACA CCA YAC TTY C	45			
CDK2NB-NCB1	GAC TYC CGC GYA CGC GYT CCG CAC YCC TG	46			
CDK2NB-NCB2	GCT YAA CGA YCC GGC CGC YTC GGC CYA CTG	47			
CDK2NB-NCB3	CCY CGC GCC GCG YGC GCT YGG CCY AGA C	48			
CDK2NB-NCB4	GAC TCC GTT YGG GAY TCC GCG CCG YGC TTY C	49			
CYCL-2 MB-1	GGT TTY ACG AYA GCG TTT TYT TCG TAG YGC G	50	CYCL2-1	ATTGAAATGTTTTTTAGAGAAAGTAATTT	51
CYCL-2 MB-2	GAY GCG GCG GGT YTT TCG TYT TTC GTT TTY AG	52	CYCL2-2	GTGGGTTTAAGGGATTGATTT	53
CYCL-2 MB-3	YCC CGA AAC TCC AYA ATC GAT CYC CGA ATY TC	54	CYCL2-3	ACCCCTTTTATACATAAATTAAC	55
CYCL-2 MB-4	YCT AAA AYA ACC CGA AYA TCC CGA ACY C	56	CYCL2-4	AACTAACAAAAAACTACCTATAACC	57
CYCL-2 UB-1	GGT TTY ATG AYA GTG TTT TYT TTG TAG YGT G	58			
CYCL-2 UB-2	GAY GTG GTG GGT YTT TTG TYT TTT GTT TYT AG	59			
CYCL-2 UB-3	YCC CAA AAC TCY CAA ATC AAT CYC CAA ATY TC	60			
CYCL-2 UB-4	YCT AAA AYA ACC CAA AYA TCC CAA ACY C	61			
CYCL2-NCB1	GGT TCY ACG AYA GCG CCT CYC TCG CAG YGC G	62			

NAME	SEQUENCE	SEQ ID NO	PCR PRIMER	SEQUENCE	SEQ ID NO
CYCL2-NCB2	GAY GCG GCG GGC YTC TCG CYT CCC GCT CCY AG	63			
CYCL2-NCB3	YCC CGG AGC TCC AYG ATC GAT CYC CGA GTY TC	64			
CYCL2-NCB4	YCT GGA AYA GCC CGG AYG TCC CGG GYC C	65			
GSN MB-1	GTT YGG GTT CGT CGY TCG TTC GTY GTT TYG	66	GSN-1	TTGTAAATGGGTGGTAGTTGTATTT	67
GSN MB-2	GTT YAG CGT YTC GTC GTA TYG TTA YGG	68	GSN-2	TTGAAAAGGATGTGTTGATGTT	69
GSN MB-3	AYT CGA CCC GYA CAA AYA CGC GAC AYA C	70	GSN-3	AATCTTAAAAAACATCTAAATTC	71
GSN MB-4	YCC CGC CCA TCY CCG CCC AAY ACC GAA AYA C	72	GSN-4	ACAAAAAACCCCAATCTACAAC	73
GSN UB-1	GTT YGG GTT TGT TGY TTG TTT GTY GTT TYG	74			
GSN UB-2	GTT YAG TGT YTT GTT GTA TYG TTA YGG	75			
GSN UB-3	AYT CAA CCC AYA CAA AYA CAC AAC AYA C	76			
GSN UB-4	YCC CAC CCA TCY CCA CCC AAY ACC AAA AYA C	77			
GSN-NCB1	GCT YGG GCT CGC CGY CCG CTC GTY GCC TYG	78			
GSN-NCB2	GCT YAG CGC YCC GCC GTA TYG TCA YGG	79			
GSN-NCB3	AYT CGA CCC GYA CAG GYG CGC GGC AYG C	80			
GSN-NCB4	YCC CGC CCA TCY CCG CCC AAY GCC GGG GYA C	81			
HIC-1 MB-1	GYT TTT YGG GGC GTG TYA GGT CGT TTT YGG	82	HIC1-1	GGTAATTGTTTTTAAAGGGTTAT	83
HIC-1 MB-2	GYG TTA GGC GGT TYA GGG CGT CGT YAC GGY T	84	HIC1-2	GTTTTTATTTTAGAGGGTAGTTGG	85
HIC-1 MB-3	TAY ACC GAY ACG CCT CCY ATC GTA TCY C	- 86	HIC1-3	ATTAACTAATTATCATACACCACCAAAA	87
HIC-1 MB-4	CTT YAT ACG CGC GAY AAA AAY AAC GTY TC	88	HIC1-4	ATATAAATAAAATCCAACACCAAACTAAAC	89
HIC-1 UB-1	GYT TTT YGG GGT GTG TYA GGT TGT TTT YGG	90			
HIC-1 UB-2	GYG TTA GGT GGT TYA GGG TGT TGT YAT GGY T	91			
HIC-1 UB-3	TAY ACC AAY ACA CCT CCY ATC ATA TCY C	92			

NAME	SEQUENCE	SEQ ID NO	PCR PRIMER	SEQUENCE	SEQ ID NO
HIC-1 UB-4	CTT YAT ACA CAC AAY AAA AAY AAC ATY TC	93			
HIC1-NCB1	GYC CCT YGG GGC GTG CYA GGC CGC CCT YGG	94			
HIC1-NCB2	GYG CCA GGC GGC CYA GGG CGC CGC YAC GGY C	95			
HIC1-NCB3	TGY GCC GGY GCG CCT CCY ATC GTG TYC C	96			
HIC1-NCB4	CTT YGT GCG CGC GGY AAG AGY GGC GTY TC	97			

Two rounds of PCR amplification were performed in a Hybaid PX2 thermocycler according to the principles described in Figure 1. One μ l of bisulphite treated genomic DNA was added to each of the 1st round PCR reaction tubes. The PCR was carried out as follows.

5	95°C	3 minutes	1 cycle
	95°C	1 minute	
	55°C	2 minutes	30 cycles
	72°C	2 minutes	
10	72°C	10 minutes	1 cycle

After the 1st round PCR was complete, 1 μ l of the 1st round PCR reaction mixture was transferred to the second round amplification tubes and the above PCR program repeated.

15 Ten μ l of the PCR reaction mix was then resolved on a 2% agarose gel.

Conventional bisulphite genomic sequencing of these samples revealed that the HeLa cell DNA line was completely methylated for this particular genomic region. T-cell DNA showed a lack of methylation, however, the resolution of conventional bisulphite genomic sequencing is only 10%. Restriction digestion of the amplified product using the
20 restriction enzymes Taq 1 (cuts TCGA) and BstU1 (cuts CGCG) revealed methylation in the amplicon. This shows that the INA blocker technology is clearly superior to conventional bisulphite genomic sequencing at the detection of low level methylated sequences. In addition, when the T47D2 DNA was sequenced by conventional bisulphite sequencing, it was found that the first half of the sequence was methylated but
25 the second half was not. As can be seen in Figure 7A and 7B a band was detected using both the unmethylated blockers and the methylated blockers. If MSP had been used this particular sample would have produced a false positive band as the priming site for the second MSP PCR primer would be unmethylated hence the primer would not bind.

30 Using the methylated INA blockers all results agreed with the results obtained by conventional bisulphite sequencing.

Clinical testing results

Figure 8 and Table 3 show the results of blocker experiments on four genomic regions (CDKN2B, CXCL-2, GSN and HIC-1) from eleven different samples of cell lines or clinical samples. The blockers used and experimental protocol were as follows:

5

PCR premixes were prepared as follows for each gene region of interest:

		Unmethylated mixes	Methylated mixes
10	X2 Master mix (Promega)	12.5 µl	12.5 µl
	100 ng/µl PCR#1	1 µl	1 µl
	100 ng/µl PCR#2	1 µl	1 µl
	200 ng/µl Blocker#1	1.5 µl (U)	1.5 µl (M)
	200 ng/µl Blocker#2	1.5 µl (U)	1.5 µl (M)
15	200 ng/µl Blocker#3	1.5 µl (U)	1.5 µl (M)
	200 ng/µl Blocker#4	1.5 µl (U)	1.5 µl (M)
	Water	3.5 µl	3.5 µl

Two rounds of PCR amplification were performed in a Hybaid PX2 thermocycler according to the principles described in Figure 1. One µl of bisulphite treated genomic DNA was added to each of the 1st round PCR reaction tubes. The PCR was carried out as follows.

	95°C	3 minutes	1 cycle
25	95°C	1 minute	
	50°C	2 minutes	30 cycles
	72°C	2 minutes	
	72°C	10 minutes	1 cycle

After the 1st round PCR was complete, 1 µl of the 1st round PCR reaction mixture was transferred to the second round amplification tubes and the above PCR program repeated.

Ten µl of the PCR reaction mix was then resolved on a 2% agarose gel.

Table 3

Lane	Sample	Source	Methylation			
			CDKN2B	CXCL-2	GSN	HIC-1
1-CL	Du145	prostate cancer	ND	ND	ND	ND
2-CL	BL13	bladder cancer	no	No	mixed	yes
3-CL	MRC-5	fibroblast -normal	ND	ND	ND	ND
4-CL	T47D2	breast cancer	ND	ND	ND	ND
5-CL	HeLa	cervix cancer	No	No	ND	yes
6-CL	SMC	muscle - normal	ND	ND	ND	ND
7-CL	MCF-7	breast cancer	No	No	mixed	ND
8-CL	LNCaP	prostate cancer	No	No	mixed	yes
9-Pa	granulocytes	blood -Leukemia	No	No	No	No
10-Pa	T-cells	blood -Leukemia	No	No	mixed	No
11-CL	THP-1	blood -Leukemia	ND	ND	ND	ND

CL - Denotes the material was derived from a cell line.

Pa - Denotes cells were obtained from a patient

ND – Not Determined

5 No - No methylation detected by direct sequencing of the PCR product

mixed - Not all CpG sites methylated or methylation confined to one region within the amplicon

yes - Methylation detected by direct sequencing of the amplicon.

10 Genomic regions CDKN2B and CXCL-2 were found to be unmethylated in almost all samples except for a small amount of methylation revealed as a weak band in granulocytes. The results were confirmed by independent amplification on selected samples followed by direct sequencing of the PCR products. Direct DNA sequencing revealed no methylation in any of the CDKN2B or CXCL-2 PCR fragments. The sensitivity of direct sequencing is such that unless more than 10% of the amplified material are methylated the sequence will read as unmethylated. Thus the presence of the weak band for CXCL-2 in the granulocyte sample is indicative of a very low level of methylation in this sample (<10%) detected by the blocker assay.

In all samples sequenced for the GSN genomic region, mixed methylation patterns were observed agreeing with the results of the blocker assays. The methylation pattern of this genomic region varied throughout the length of the PCR amplicon and in many cases not all CpG dinucleotides were methylated or a mixture of unmethylated and
5 methylated sequences were observed at individual CpG sites.

Methylation of the Hypermethylated In Cancer (HIC-1) gene was observed for BL13, Hela and LNCaP cell lines with all CpG sites showing 100% methylation. Interestingly, the normal SMC (sample 6) cell line was the only cell line to show no methylation of the HIC-1 gene. The granulocytes and T-cells (samples 9 and 10) from a
10 patient in remission for leukemia showed mixed methylation by the blocker assay and although the PCR amplicons for the vast majority appeared unmethylated this again may be due to the lack of sensitivity of the direct sequencing approach.

It can be seen from the results that the blocker assay according to the present invention is a powerful tool to detect methylation patterns of various regions of the
15 human genome.

The scope of the claims should not be limited by the preferred embodiments set forth in the examples, but should be given the broadest interpretation consistent with the description as a whole.

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 2
CONTENANT LES PAGES 1 À 33

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JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE THAN ONE VOLUME

THIS IS VOLUME 1 OF 2
CONTAINING PAGES 1 TO 33

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NOM DU FICHER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

Claims:

1. A method for detecting the methylation status of a target region of a nucleic acid molecule comprising:

5 treating the nucleic acid molecule with an agent which modifies cytosine bases but does not modify 5-methyl-cytosine bases under conditions to form a modified nucleic acid template;

10 providing to an amplification reaction a first amplification blocker comprising an intercalating nucleic acid (INA) containing two or more internal intercalating pseudonucleotides, the first blocker being complementary to the unmethylated target region on a first strand of the modified nucleic acid template;

15 providing to the amplification reaction a second amplification blocker comprising an intercalating nucleic acid (INA) containing two or more internal intercalating pseudonucleotides, the second blocker being complementary to a second region on a second strand complementary to the first strand of the modified nucleic acid template, the second region being downstream of the target region of the first strand of the modified nucleic acid template;

 providing a first primer complementary to a nucleic acid region upstream from the target region on the first strand of the modified nucleic acid template;

20 providing a second primer complementary to a nucleic acid region upstream from the second blocker region on the second strand complementary to the first strand of the modified nucleic acid template; and

25 carrying out an amplification reaction on the modified nucleic acid template, wherein if the target region is methylated there will be an amplification product and if the target region is unmethylated there will be no amplification product;

30 wherein the internal intercalating pseudonucleotides are essentially planar polyaromatic or heteropolyaromatic compounds that are capable of co-stacking with nucleobases in a nucleic acid duplex and are not peptide nucleic acids, and wherein the internal intercalating pseudonucleotides prevent extension of at least one of the blockers by a polymerase when at least one of the blockers is bound to a nucleic acid template.

2. A method for detecting the methylation status of a target region of a nucleic acid molecule comprising:

35 treating the nucleic acid molecule with an agent which modifies cytosine bases but does not modify 5-methyl-cytosine bases under conditions to form a

modified nucleic acid template; providing to an amplification reaction a first amplification blocker comprising an intercalating nucleic acid (INA) containing two or more internal intercalating pseudonucleotides, the first blocker being complementary to the methylated target region on a first strand of the modified nucleic acid template;

providing to the amplification reaction a second amplification blocker comprising an intercalating nucleic acid (INA) containing two or more internal intercalating pseudonucleotides, the second blocker being complementary to a second region on a second strand complementary to the first strand of the modified nucleic acid template, the second region being downstream of the target region of the first strand of the modified nucleic acid template;

providing a first primer complementary to a nucleic acid region upstream from the target region on the first strand of the modified nucleic acid template;

providing a second primer complementary to a nucleic acid region upstream from the second blocker region on the second strand complementary to the first strand of the modified nucleic acid template; and

carrying out an amplification reaction on the modified nucleic acid template, wherein if the target region is unmethylated there will be an amplification product and if the target region is methylated there will be no amplification product;

wherein the internal intercalating pseudonucleotides are essentially planar polyaromatic or heteropolyaromatic compounds that are capable of co-stacking with nucleobases in a nucleic acid duplex and are not peptide nucleic acids, and wherein the internal intercalating pseudonucleotides prevent extension of at least one of the blockers by a polymerase when at least one of the blockers is bound to a nucleic acid template.

3. The method according to claim 1 or 2, further comprising:

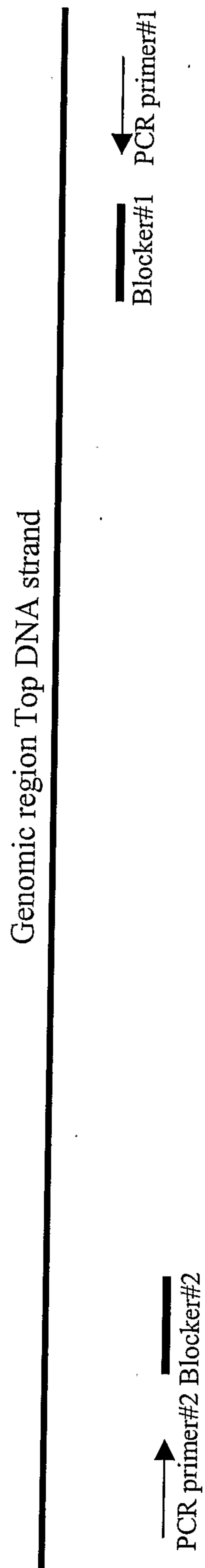
providing third and fourth amplification blockers comprising an intercalating nucleic acid (INA) containing two or more internal intercalating pseudonucleotides to the amplification reaction, the third and fourth blockers being complementary to regions internal to the first and second blocker regions; and providing third and fourth primers complementary to regions external to the third and fourth blocker regions and internal to the first and second primer regions.

4. The method according to any one of claims 1 to 3, further comprising:
providing one or more additional amplification blockers comprising an
intercalating nucleic acid (INA) containing two or more internal intercalating
pseudonucleotides directed to one or more additional regions on the nucleic acid
molecule.
5. The method according to claim 4, wherein the one or more additional regions on
the nucleic acid molecule correspond to one or more additional regions on the
modified nucleic acid template.
6. The method according to any one of claims 1 to 5, further comprising:
providing one or more additional amplification blockers comprising an
intercalating nucleic acid (INA) containing two or more internal intercalating
pseudonucleotides directed to the first strand of the modified nucleic acid
template or its complementary second strand complementary to regions between
the first and second primer regions.
7. The method according to any one of claims 1 to 6 wherein the target region
comprises cytosine (C) flanked 3' by a guanine (G).
8. The method according to any one of claims 1 to 7, wherein the agent is selected
from the group consisting of bisulfite, acetate and citrate.
9. The method according to claim 8 wherein the agent is sodium bisulfite.
10. The method according to any one of claims 1 to 9 wherein the nucleic acid
molecule is DNA.
11. The method according to any one of claims 1 to 10 wherein the INA is 15 to 50
nucleotides or nucleotide analogues in length having 2 to 6 internal intercalating
pseudonucleotides.
12. The method according to claim 11 wherein the INA is 18 to 35 nucleotides or
nucleotide analogues in length having 2 to 6 internal intercalating
pseudonucleotides.
13. The method according to any one of claims 1 to 12 wherein the internal
intercalating pseudonucleotides are situated two or more bases from the 3' or 5'
end of a blocker.
14. The method according to any one of claims 1 to 13 wherein the INA contains no
intercalating pseudonucleotides at either the 3' or 5' end of a blocker.

15. The method according to any one of claims 1 to 14 wherein the internal intercalating pseudonucleotide is selected from phosphoramidites of 1-(4,4'-dimethoxytriphenylmethyloxy)-3-pyrenemethyloxy-2-propanol.
- 5 16. The method according to claim 15 wherein the internal intercalating pseudonucleotide is selected from the phosphoramidite of (S)-1-(4,4'-dimethoxytriphenylmethyloxy)-3-pyrenemethyloxy -2-propanol or the phosphoramidite of (R)-1-(4,4'-dimethoxytriphenylmethyloxy) -3-pyrenemethyloxy-2-propanol.
- 10 17. The method according to claim 16 wherein the internal intercalating pseudonucleotide is the phosphoramidite of (S)-1-(4,4'-dimethoxytriphenylmethyloxy)-3-pyrenemethyloxy-2-propanol.
18. The method according to any one of claims 1 to 17 wherein the amplification reaction is polymerase chain reaction (PCR).

Figure 1

1st Round PCR amplification reaction



2nd Round PCR amplification reaction.

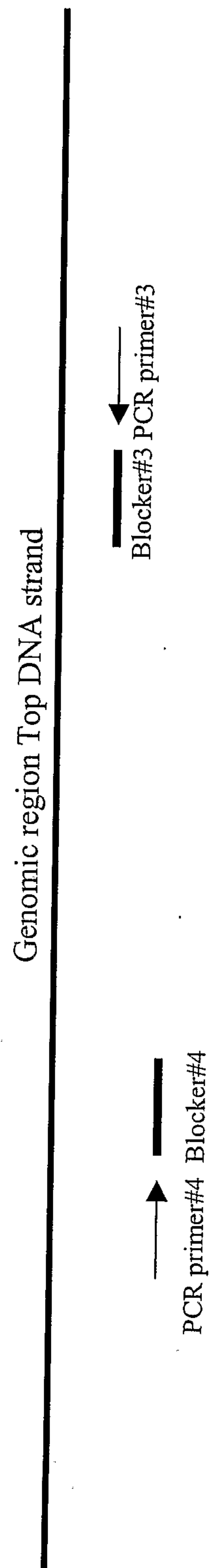


Figure 3**A. Unconverted sequence**

CGGGTGACCCCTCTCCCCTGCCCTGTGAAGCGCCTGCCCGCGCCCCCGA
| | | | |
C C A C T A A A A A A
PCR Primer#1
| | | | |
A A A C A G C A G C A A A A
Methyl blocker#1

B. Bisulphite treated Methylated sequence

CGGGTGATTTTTTTTTTTTTGTTTTGTGAAGCGCCTGTCGTCGTTTTCGA
| | | | |
C C A C T A A A A A A
PCR Primer#1
| | | | |
A A A C A G C A G C A A A A
Methyl blocker#1

C. Bisulphite treated Unmethylated sequence

TGGGTGATTTTTTTTTTTTTGTTTTGTGAAGTGTTTGTTGTTGTTTTTGA
| | | | |
C C A C T A A A A A A
PCR Primer#1
| | | | |
A A A C A G C A G C A A A A
Methyl blocker#1

D. Regional non-converted sequence

CGGGTGATTTTTTTTTTCCCCTGCCCTGTGAAGCGCCTGCCCGTCGCCCCCGA
| | | | |
C C A C T A A A A A A
PCR Primer#1
| | | | |
A A A C A G C A G C A A A A
Methyl blocker#1

Figure 4**A. Unconverted sequence**

CGGGTGACCCCTCTCCCCTGCCCTGTGAAGCGCCTGCCCGCGCCCCCGA
| | | | |
CCACTAAAAAA
PCR Primer#1
AAACAACAACAAAAA
Unmethyl blocker#1

B. Bisulphite treated Methylated sequence

CGGGTGATTTTTTTTTTTTGTGTTTGTGAAGCGCCTGTCGTCGTTTTCGA
| | | | |
CCACTAAAAAA
PCR Primer#1
AAACAACAACAAAAA
Unmethyl blocker#1

C. Bisulphite treated Unmethylated sequence

TGGGTGATTTTTTTTTTTTGTGTTTGTGAAGTGTTTGTTGTGTTTTGA
| | | | |
CCACTAAAAAA
PCR Primer#1
AAACAACAACAAAAA
Unmethyl blocker#1

D. Regional non-converted sequence

CGGGTGATTTTTTTTCCCCTGCCCTGTGAAGCGCCTGCCCGCGCCCCCGA
| | | | |
CCACTAAAAAA
PCR Primer#1
AAACAACAACAAAAA
Unmethyl blocker#1

Figure 5

A. Unconverted sequence

CGGGTGACCCCTCTCCCCTGCCCTGTGAAGCGCCTGCCCGCCGCCCCCGA
 |||||
 CCACTAAAAAA
 PCR Primer#1
 |||||
 GGACGGCGGCGGGG
 non converted blocker#1

B. Bisulphite treated Methylated sequence

CGGGTGATTTTTTTTTTTTGTTTTGTGAAGCGCCTGTCGTCGTTTTTCGA
 |||||
 CCACTAAAAAA
 PCR Primer#1

GGACGGCGGCGGGG
 non converted blocker#1

C. Bisulphite treated Unmethylated sequence

TGGGTGATTTTTTTTTTTTGTTTTGTGAAGTTGTTTGTTGTTTGTTTTTGA
 |||||
 CCACTAAAAAA
 PCR Primer#1

GGACGGCGGCGGGGG
 non converted blocker#1

D. Regional non-converted sequence

CGGGTGATTTTTTTTCCCCTGCCCTGTGAAGCGCCTGCCGCCGCCCCCGA

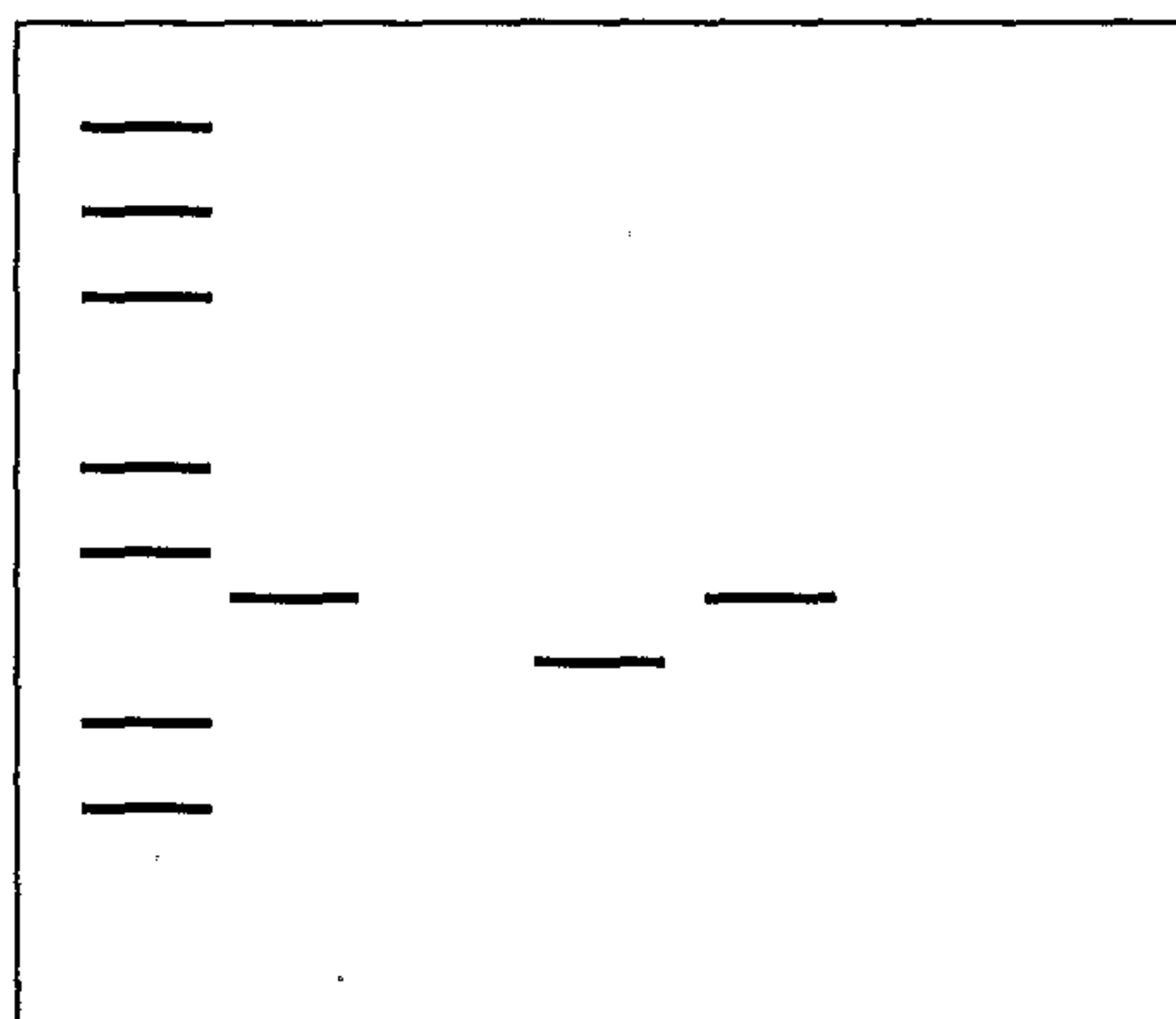
CCACTAAAAAA GGACGGCGGCGGGGG

PCR Primer#1 non converted blocker#1

Figure 6

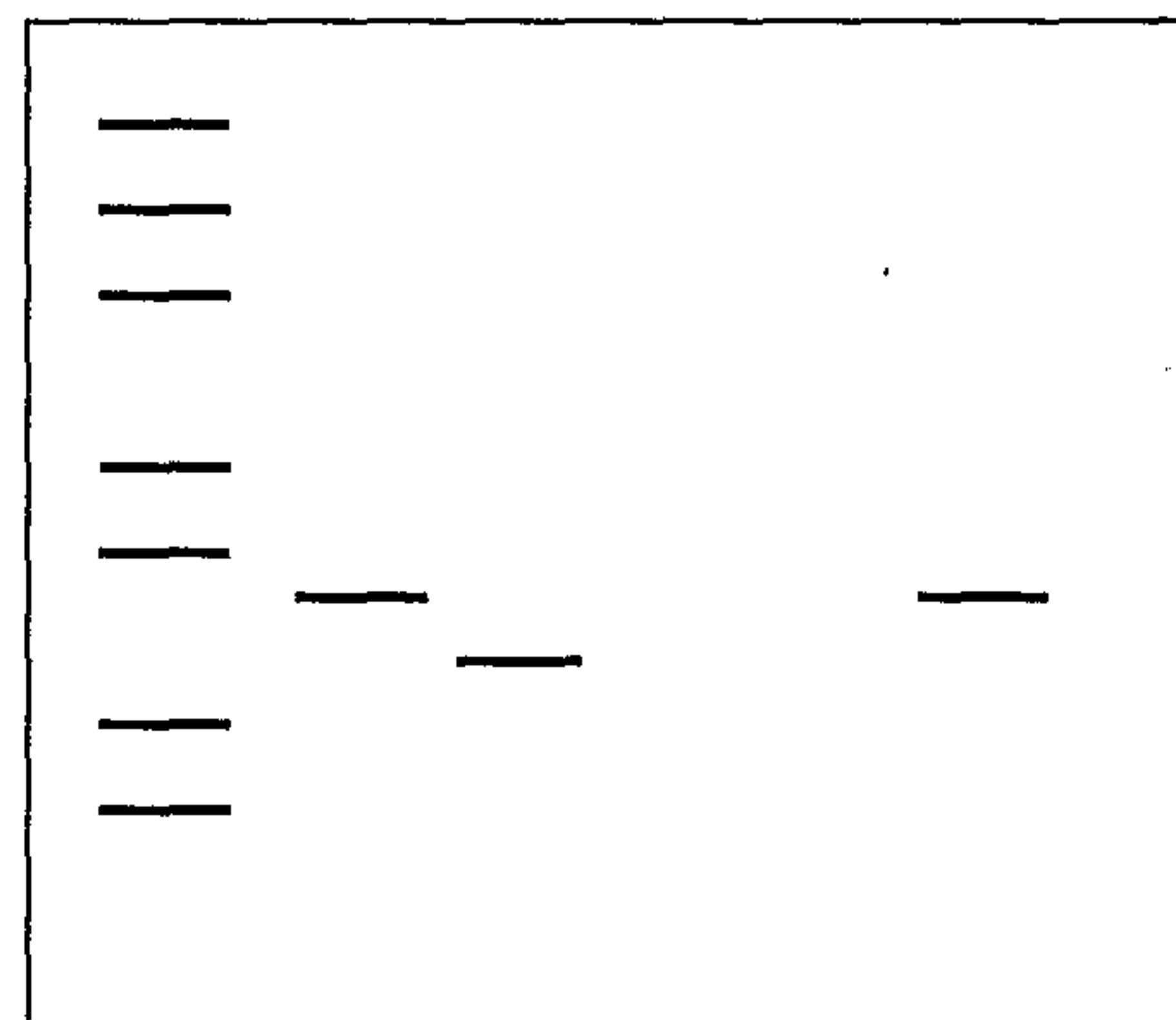
Normal Tissue (Unmethylated)

M 1 2 3 4 5



Cancer Tissue (Methylated)

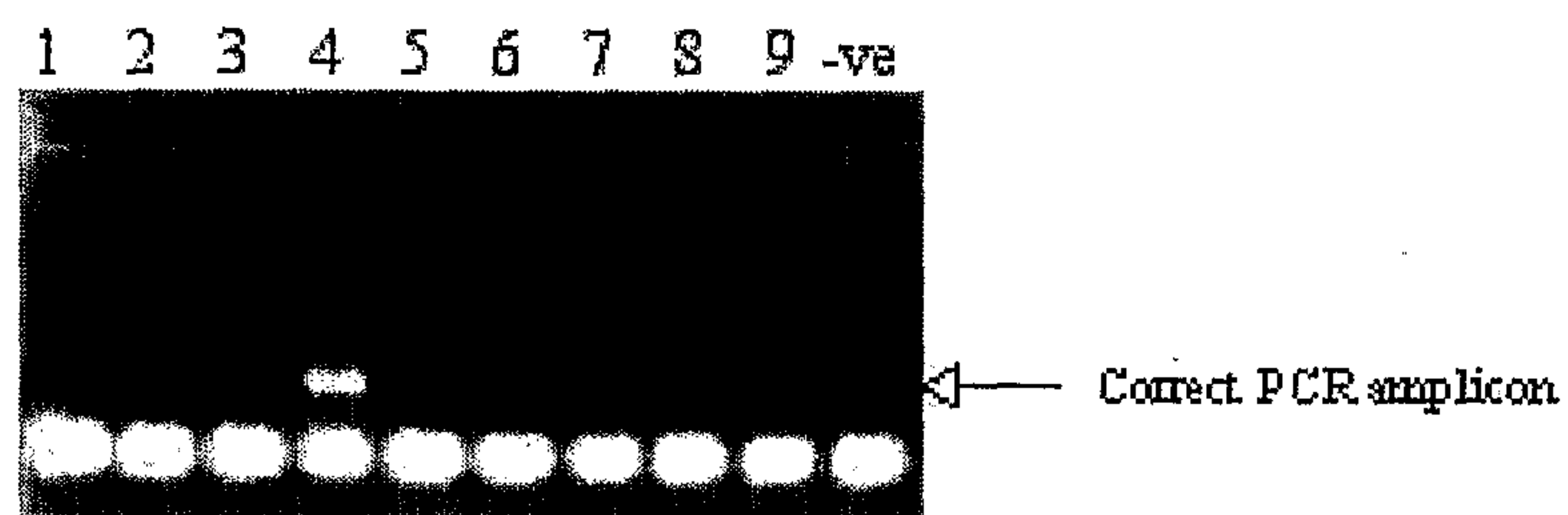
M 1 2 3 4 5



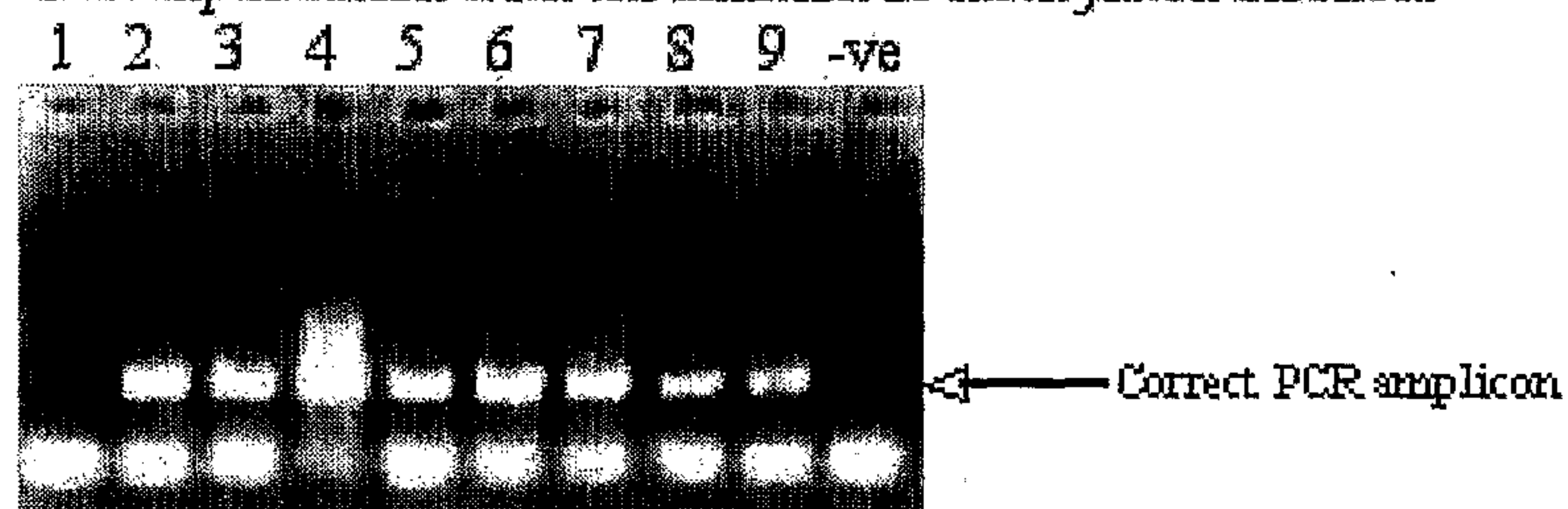
1. Conventional PCR
 2. MSP methylated detection
 3. MSP unmethylated detection
 4. INA blocker methylation block
 5. INA blocker unmethylation block
- M=DNA marker ladder

Figure 7
INA blockers applied to genomic DNA samples

7A. Results of PCR amplification with the addition of unmethylated blockers



7B Results of PCR amplification with the addition of methylated blockers



7C Control reaction no blockers added

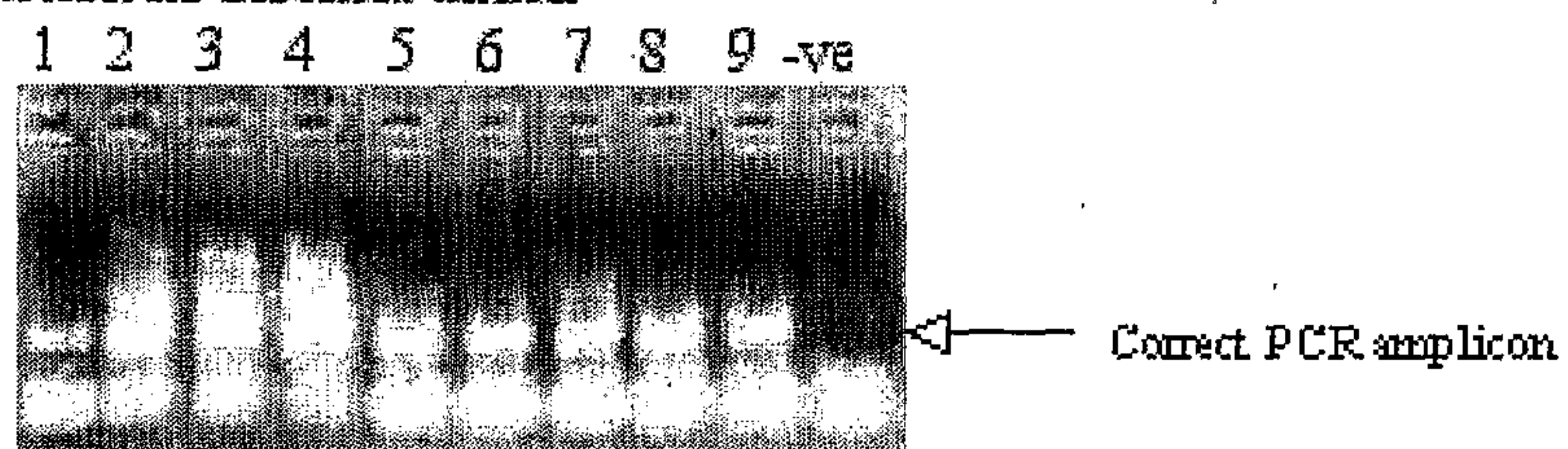


Figure 8