DESCRIPTION

METHOD FOR MEASURING DNA METHYLATION

TECHNICAL FIELD

The present invention relates to a method of measuring the content of methylated DNA in a DNA region of interest in a genomic DNA contained in a biological specimen, and so on.

BACKGROUND ART

As a method for evaluating the methylation state of DNA in an objective DNA region in a genomic DNA contained in a biological specimen, for example, there is known a method of measuring the content of methylated DNA in an objective DNA region in a genomic DNA (see, for example, Nucleic Acids Res., 1994, Aug 11; 22(15): 2990-7, and Proc. Natl. Acad. Sci. U.S.A., 1997, Mar 18; 94(6): 2284-9 for reference). In such a measuring method, first, it is necessary to extract DNA containing the objective DNA region from a DNA sample derived from a genomic DNA, and the extracting operation is complicated.

As a method of measuring the content of methylated DNA in an objective region of extracted DNA, for example, (1) a method of amplifying an objective region by subjecting the DNA to a chain reaction for DNA synthesis by DNA polymerase after modification of the DNA with a sulfite or the like (Polymerase Chain Reaction; hereinafter also referred to as PCR), and (2) a method of amplifying an objective region by subjecting the DNA to PCR after digestion of the DNA using a methylation

sensitive restriction enzyme are known. Both of these methods require time and labor for DNA modification for detection of methylation, subsequent purification of the product, preparation of a reaction system for PCR, and checking of DNA amplification.

DISCLOSURE OF THE INVENTION

It is an object of the present invention to provide a method of measuring the content of methylated DNA in an objective DNA region in a genomic DNA contained in a biological specimen in a simple and convenient manner.

That is, the present invention provides:

1. A method (hereinafter, also referred to as the present measuring method) of detecting or quantifying methylated DNA in a target DNA region possessed by genomic DNA contained in a biological specimen, comprising:

(1) First step of separating double-stranded DNA contained in a DNA sample derived from the genomic DNA contained in the biological specimen into single-stranded DNA,

(2) Second step of mixing (i) the single-stranded DNA separated in First step, (ii) a methylated DNA antibody, and (iii) an oligonucleotide (hereinafter, also referred to as the present oligonucleotide) capable of binding with the single-stranded DNA without inhibiting binding between the methylated DNA antibody and methylated DNA in a target DNA region, thereby forming a complex of the single-stranded DNA containing methylated DNA in the target DNA region, the methylated DNA antibody, and the oligonucleotide, and

separating the complex simultaneously or after the formation; and

(3) Third step of detecting or quantifying the methylated DNA antibody, or the oligonucleotide contained in the separated complex according to an identification function available for detection possessed by the methylated DNA antibody or the oligonucleotide, thereby detecting or quantifying methylated DNA in the target DNA region contained in the biological specimen;

2. The method according to the above 1., wherein as the oligonucleotide that is mixed in Second step, and does not inhibit binding between the methylated DNA antibody and a methylated base existing in single-stranded DNA containing the target DNA region, two or more kinds of oligonucleotides are used;

3. The method according to the above 1., wherein the complex formed in Second step, or a bound body of the single-stranded DNA separated in First step and the oligonucleotide not inhibiting binding between the methylated DNA antibody and a methylated base existing in single-stranded DNA containing the target DNA region arising during formation of the complex in Second step is formed in a reaction system containing a bivalent positive ion;

4. The method according to the above 3., wherein the bivalent positive ion is a magnesium ion;

5. The method according to any one of the above 1. to 4., comprising as a separating operation of the complex in Second step, a step of making the methylated DNA antibody contained

in the formed complex be bound to a support;

6. The method according to any one of the above 1. to 4., comprising as a separating operation of the complex in Second step, a step of making the oligonucleotide contained in the formed complex be bound to a support;

7. The method according to any one of the above 1. to 6., additionally comprising, between immediately after end of First step and immediately before start of Third step, a step of digesting the single-stranded DNA separated in First step by at least one kind of methylation sensitive restriction enzyme capable of digesting single-stranded DNA;

8. The method according to any one of the above 1. to 6., additionally comprising, between immediately after end of First step and immediately before start of Third step, (i) a step of mixing the single-stranded DNA separated in First step, and a masking oligonucleotide having a recognition sequence of at least one kind of methylation sensitive restriction enzyme as its part, and (ii) digesting a mixture obtained by the previous step (single-stranded DNA existing therein in which DNA is not methylated in the target DNA region) by the methylation sensitive restriction enzyme;

9. The method according to the above 7., wherein the at least one kind of methylation sensitive restriction enzyme capable of digesting single-stranded DNA is HhaI which is a methylation sensitive restriction enzyme capable of digesting single-stranded DNA;

10. The method according to the above 8., wherein the at least one kind of methylation sensitive restriction enzyme is HpaII

or HhaI which is a methylation sensitive restriction enzyme;

11. The method according to any one of the above 1. to 10., wherein the methylated DNA antibody is a methyl cytosine antibody;

12. The method according to any one of the above 1. to 11., wherein the biological specimen is serum or plasma of a mammal;

13. The method according to any one of the above 1. to 11., wherein the biological specimen is blood or a bodily fluid of a mammal;

14. The method according to any one of the above 1. to 11., wherein the biological specimen is a cell lysate or a tissue lysate;

15. The method according to any one of the above 1. to 14., wherein the DNA sample derived from the genomic DNA contained in the biological specimen is a DNA sample preliminarily subjected to a digestion treatment by a restriction enzyme whose recognition cleaving site excludes a target DNA region possessed by the genomic DNA;

16. The method according to any one of the above 1. to 15., wherein the DNA sample derived from the genomic DNA contained in the biological specimen is a DNA sample preliminarily subjected to a digestion treatment by at least one kind of methylation sensitive restriction enzyme;

17. The method according to any one of the above 1. to 15., wherein the DNA sample derived from the genomic DNA contained in the biological specimen is a DNA sample preliminarily subjected to a digestion treatment by at least one kind of

methylation sensitive restriction enzyme after addition of the masking oligonucleotide;

18. The method according to the above 16. or 17., wherein the at least one kind of methylation sensitive restriction enzyme is HpaII or HhaI which is a methylation sensitive restriction enzyme;

19. The method according to any one of the above 1. to 18., wherein the DNA sample derived from the genomic DNA contained in the biological specimen is a preliminarily purified DNA sample;

20. The method according to any one of the above 1. to 19., wherein the target DNA region possessed by the genomic DNA is a DNA region having a cleaving site recognized by at least one kind of methylation sensitive restriction enzyme;

21. The method according to any one of the above 1. to 20., wherein a counter oligonucleotide is added in separating double-stranded DNA contained in a DNA sample derived from the genomic DNA into single-stranded DNA in First step;

22. The method according to any one of the above 1. to 21., wherein separation of double-stranded DNA contained in a DNA sample derived from the genomic DNA into single-stranded DNA in First step is conducted in a reaction system containing a bivalent positive ion or a magnesium ion; and so on.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows results of Example 1 carried out using 1 μg/mL of a methylated cytosine antibody. For each of Solution A (2.5 pmol/100 μL solution in TE buffer), Solution B (0.25

pmol/100 μL solution in TE buffer), Solution C (0.025 pmol/100 μL solution in TE buffer), Solution D (0.0025 pmol/100 μL solution in TE buffer), Solution E (0.00025 pmol/100 μL solution in TE buffer), and Solution F (0 pmol/100 μL solution in TE buffer (negative control solution)), a residual amount of a methylated oligonucleotide, and a residual amount of an unmethylated oligonucleotide measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 2 shows results of Example 1 carried out using 10 μg/mL of a methylated cytosine antibody. For each of Solution A (2.5 pmol/100 μL solution in TE buffer), Solution B (0.25 pmol/100 μL solution in TE buffer), Solution C (0.025 pmol/100 μL solution in TE buffer), Solution D (0.0025 pmol/100 μL solution in TE buffer), Solution E (0.00025 pmol/100 μL solution in TE buffer), and Solution F (0 pmol/100 μL solution in TE buffer (negative control solution)), a residual amount of a methylated oligonucleotide, and a residual amount of an unmethylated oligonucleotide measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 3 shows results of Example 2. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a residual amount (formation amount of a complex) of a methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 25, and a residual amount (formation amount of a complex) of an unmethylated oligonucleotide UBC-UM8 having the

nucleotide sequence of SEQ ID NO: 26 measured by fluorescence (612 nm) are shown in this order from the left-hand.

Fig. 4 shows results of Group A (no treatment group) in Example 3. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a residual amount (complex formation amount) of a methylated oligonucleotide UBC-M having the nucleotide sequence of SEQ ID NO: 28, a residual amount (complex formation amount) of a partially methylated oligonucleotide UBC-HM having the nucleotide sequence of SEQ ID NO: 29, and a residual amount (complex formation amount) of an unmethylated oligonucleotide UBC-UM having the nucleotide sequence of SEQ ID NO: 30 measured by fluorescence (612 nm) are shown in this order from the left-hand.

Fig. 5 shows results of Group B (Hha treatment group) in Example 3. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a residual amount (complex formation amount) of a methylated oligonucleotide UBC-M having the nucleotide sequence of SEQ ID NO: 28, a residual amount (complex formation amount) of a partially methylated oligonucleotide UBC-HM having the nucleotide sequence of SEQ ID NO: 29, and a residual amount (complex formation amount) of an unmethylated oligonucleotide UBC-UM having the nucleotide

sequence of SEQ ID NO: 30 measured by fluorescence (612 nm) are shown in this order from the left-hand.

Fig. 6 shows results of Group A (no treatment group) in Example 4. For each of Solution A (0.1 pmol/100 µL solution in TE buffer), Solution B (0.01 pmol/100 µL solution in TE buffer), Solution C (0.001 pmol/100 µL solution in TE buffer), and Solution D (0 pmol/100 µL solution in TE buffer (negative control solution)), a residual amount (complex formation amount) of a methylated oligonucleotide UBC86-M having the nucleotide sequence of SEQ ID NO: 33, and a residual amount (complex formation amount) of a partially methylated oligonucleotide UBC118-HM having the nucleotide sequence of SEQ ID NO: 34 measured by fluorescence (612 nm) are shown in this order from the left-hand.

Fig. 7 shows results of Group B (Hha treatment group) in Example 4. For each of Solution A (0.1 pmol/100 µL solution in TE buffer), Solution B (0.01 pmol/100 µL solution in TE buffer), Solution C (0.001 pmol/100 µL solution in TE buffer), and Solution D (0 pmol/100 µL solution in TE buffer (negative control solution)), a residual amount (complex formation amount) of a methylated oligonucleotide UBC86-M having the nucleotide sequence of SEQ ID NO: 33, and a residual amount (complex formation amount) of a partially methylated oligonucleotide UBC118-HM having the nucleotide sequence of SEQ ID NO: 34 measured by fluorescence (612 nm) are shown in this order from the left-hand.

Fig. 8 shows results of experiments carried out by using a 5'-end biotin-labeled oligonucleotide UBC having the

nucleotide sequence of SEQ ID NO: 43 in Example 5. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a complex formation amount in a methylated oligonucleotide mixed solution, and a complex formation amount in an unmethylated oligonucleotide mixed solution measured by fluorescence (612 nm) are shown in this order from the left-hand.

Fig. 9 shows results of experiments carried out by using a 5'-end biotin-labeled oligonucleotide FBN having the nucleotide sequence of SEQ ID NO: 44 in Example 5. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a complex formation amount in a methylated oligonucleotide mixed solution, and a complex formation amount in an unmethylated oligonucleotide mixed solution measured by fluorescence (612 nm) are shown in this order from the left-hand.

Fig. 10 shows results of experiments carried out by using a 5'-end biotin-labeled oligonucleotide GPR having the nucleotide sequence of SEQ ID NO: 45 in Example 5. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0

pmol/100 μL solution in TE buffer (negative control solution)), a complex formation amount in a methylated oligonucleotide mixed solution, and a complex formation amount in an unmethylated oligonucleotide mixed solution measured by fluorescence (612 nm) are shown in this order from the left-hand.

Fig. 11 shows results of experiments using a mixed solution of a 5'-end biotin-labeled oligonucleotide UBC having the nucleotide sequence of SEQ ID NO: 43, a 5'-end biotin-labeled oligonucleotide FBN having the nucleotide sequence of SEQ ID NO: 44, and a 5'-end biotin-labeled oligonucleotide GPR having the nucleotide sequence of SEQ ID NO: 45 in Example 5. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a complex formation amount in a methylated oligonucleotide mixed solution, and a complex formation amount in an unmethylated oligonucleotide mixed solution measured by fluorescence (612 nm) are shown in this order from the left-hand.

Fig. 12 shows results of experiments using a methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 46, and an unmethylated oligonucleotide UBC-U8 having the nucleotide sequence of SEQ ID NO: 49 in Example 6. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0

pmol/100 μL solution in TE buffer (negative control solution)), a residual amount (complex formation amount) of a methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 46, and a residual amount (complex formation amount) of an unmethylated oligonucleotide UBC-U8 having the nucleotide sequence of SEQ ID NO: 49 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 13 shows results of experiments using a methylated oligonucleotide GPR-M8 having the nucleotide sequence of SEQ ID NO: 47, and an unmethylated oligonucleotide GPR-U8 having the nucleotide sequence of SEQ ID NO: 50 in Example 6. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a residual amount (complex formation amount) of a methylated oligonucleotide GPR-M8 having the nucleotide sequence of SEQ ID NO: 47, and a residual amount (complex formation amount) of an unmethylated oligonucleotide GPR-U8 having the nucleotide sequence of SEQ ID NO: 50 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 14 shows results of experiments using a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 48, and an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 51 in Example 6. For each of Solution A (0.1 pmol/100 μL solution in TE buffer),

Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a residual amount (complex formation amount) of a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 48, and a residual amount (complex formation amount) of an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 51 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 15 shows results of Group A (no treatment group) in Example 7. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a residual amount (complex formation amount) of a methylated oligonucleotide UBC-M having the nucleotide sequence of SEQ ID NO: 55, a residual amount (complex formation amount) of a partially methylated oligonucleotide UBC-HM having the nucleotide sequence of SEQ ID NO: 56, and a residual amount (complex formation amount) of an unmethylated oligonucleotide UBC-UM having the nucleotide sequence of SEQ ID NO: 57 measured by fluorescence (612 nm) are shown in this order from the left-hand.

Fig. 16 shows results of Group B (Hha treatment group) in Example 7. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE

buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a residual amount (complex formation amount) of a methylated oligonucleotide UBC-M having the nucleotide sequence of SEQ ID NO: 55, a residual amount (complex formation amount) of a partially methylated oligonucleotide UBC-HM having the nucleotide sequence of SEQ ID NO: 56, and a residual amount (complex formation amount) of an unmethylated oligonucleotide UBC-UM having the nucleotide sequence of SEQ ID NO: 57 measured by fluorescence (612 nm) are shown in this order from the left-hand.

Fig. 17 shows results of experiments using an oligonucleotide UBC labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 62 in Example 8. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a complex formation amount of a methylated oligonucleotide UBC/GPR/FBN-M having the nucleotide sequence of SEQ ID NO: 60, and a complex formation amount of an unmethylated oligonucleotide UBC/GPR/FBN-UM having the nucleotide sequence of SEQ ID NO: 61 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 18 shows results of experiments using an oligonucleotide GPR labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 63 in Example 8. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution

C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a complex formation amount of a methylated oligonucleotide UBC/GPR/FBN-M having the nucleotide sequence of SEQ ID NO: 60, and a complex formation amount of an unmethylated oligonucleotide UBC/GPR/FBN-UM having the nucleotide sequence of SEQ ID NO: 61 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 19 shows results of experiments using an oligonucleotide FBN labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 64 in Example 8. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a complex formation amount of a methylated oligonucleotide UBC/GPR/FBN-M having the nucleotide sequence of SEQ ID NO: 60, and a complex formation amount of an unmethylated oligonucleotide UBC/GPR/FBN-UM having the nucleotide sequence of SEQ ID NO: 61 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 20 shows results of experiments using a mixed solution of an oligonucleotide UBC labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 62, an oligonucleotide GPR labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 63, and an oligonucleotide FBN labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 64 in Example 8. For each of Solution A (0.1

pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a complex formation amount of a methylated oligonucleotide UBC/GPR/FBN-M having the nucleotide sequence of SEQ ID NO: 60, and a complex formation amount of an unmethylated oligonucleotide UBC/GPR/FBN-UM having the nucleotide sequence of SEQ ID NO: 61 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 21 shows results of experiments using an oligonucleotide UBC labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 71 in Example 9. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a complex formation amount in a methylated oligonucleotide mixed solution M0, and a complex formation amount in an unmethylated oligonucleotide mixed solution U0 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 22 shows results of experiments using an oligonucleotide FBN labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 73 in Example 9. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0

pmol/100 μL solution in TE buffer (negative control solution)), a complex formation amount in a methylated oligonucleotide mixed solution M0, and a complex formation amount in an unmethylated oligonucleotide mixed solution U0 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 23 shows results of experiments using an oligonucleotide GPR labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 72 in Example 9. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a complex formation amount in a methylated oligonucleotide mixed solution M0, and a complex formation amount in an unmethylated oligonucleotide mixed solution U0 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 24 shows results of experiments using a mixed solution of an oligonucleotide UBC labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 71, an oligonucleotide GPR labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 72, and an oligonucleotide FBN labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 73 in Example 9. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution

in TE buffer (negative control solution)), a complex formation amount in a methylated oligonucleotide mixed solution M0, and a complex formation amount in an unmethylated oligonucleotide mixed solution U0 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 25 shows results of Example 10. From the left-hand of the drawing, a chromatostrip (M) tested and developed using a solution of a methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 74, a chromatostrip (U) tested and developed using a solution of an unmethylated oligonucleotide UBC-U8 having the nucleotide sequence of SEQ ID NO: 75, and a chromatostrip (O) tested and developed using a TE buffer solution are shown.

Fig. 26 shows results obtained by using an oligonucleotide UBC labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 84 as a 5'-end FITC-labeled oligonucleotide in Example 11. From the left-hand of the drawing, a chromatostrip (M) tested and developed using a solution of a methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 78, a chromatostrip (U) tested and developed using a solution of an unmethylated oligonucleotide UBC-U8 having the nucleotide sequence of SEQ ID NO: 81, and a chromatostrip (O) tested and developed using a TE buffer solution are shown.

Fig. 27 shows results obtained by using an oligonucleotide FBN labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 85 as a 5'-end FITC-labeled oligonucleotide in Example 11. From the left-hand of the

drawing, a chromatostrip (M) tested and developed using a solution of a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 79, a chromatostrip (U) tested and developed using a solution of an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 82, and a chromatostrip (O) tested and developed using a TE buffer solution are shown.

Fig. 28 shows results obtained by using an oligonucleotide GPR labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 86 as a 5'-end FITC-labeled oligonucleotide in Example 11. From the left-hand of the drawing, a chromatostrip (M) tested and developed using a solution of a methylated oligonucleotide GPR-M8 having the nucleotide sequence of SEQ ID NO: 80, a chromatostrip (U) tested and developed using a solution of an unmethylated oligonucleotide GPR-U8 having the nucleotide sequence of SEQ ID NO: 83, and a chromatostrip (O) tested and developed using a TE buffer solution are shown.

Fig. 29 shows results obtained by using an oligonucleotide UBC labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 94 as a 5'-end FITC-labeled oligonucleotide in Example 12. From the left-hand of the drawing, a chromatostrip (M) tested and developed using a solution of a methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 88, a chromatostrip (U) tested and developed using a solution of an unmethylated oligonucleotide UBC-U8 having the nucleotide sequence of SEQ ID NO: 91, and a chromatostrip (O) tested and developed using

a TE buffer solution are shown.

Fig. 30 shows results obtained by using an oligonucleotide FBN labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 95 as a 5'-end FITC-labeled oligonucleotide in Example 12. From the left-hand of the drawing, a chromatostrip (M) tested and developed using a solution of a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 89, a chromatostrip (U) tested and developed using a solution of an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 92, and a chromatostrip (O) tested and developed using a TE buffer solution are shown.

Fig. 31 shows results obtained by using an oligonucleotide GPR labeled with FITC at 5'-end having the nucleotide sequence of SEQ ID NO: 96 as a 5'-end FITC-labeled oligonucleotide in Example 12. From the left-hand of the drawing, a chromatostrip (M) tested and developed using a solution of a methylated oligonucleotide GPR-M8 having the nucleotide sequence of SEQ ID NO: 90, a chromatostrip (U) tested and developed using a solution of an unmethylated oligonucleotide GPR-U8 having the nucleotide sequence of SEQ ID NO: 93, and a chromatostrip (O) tested and developed using a TE buffer solution are shown.

Fig. 32 shows results of experiments using Buffer 1 in Example 13. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative

control solution)), a residual amount (complex formation amount) of a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 98, and a residual amount (complex formation amount) of an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 99 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 33 shows results of experiments using Buffer 2 in Example 13. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a residual amount (complex formation amount) of a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 98, and a residual amount (complex formation amount) of an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 99 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 34 shows results of experiments using Buffer 3 in Example 13. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a residual amount (complex formation amount) of a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 98, and a residual amount (complex formation amount) of an unmethylated oligonucleotide

FBN-U8 having the nucleotide sequence of SEQ ID NO: 99 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 35 shows results of experiments using Buffer 4 in Example 13. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a residual amount (complex formation amount) of a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 98, and a residual amount (complex formation amount) of an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 99 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 36 shows results of experiments using Buffer 5 in Example 13. For each of Solution A (0.1 pmol/100 μL solution in TE buffer), Solution B (0.01 pmol/100 μL solution in TE buffer), Solution C (0.001 pmol/100 μL solution in TE buffer), and Solution D (0 pmol/100 μL solution in TE buffer (negative control solution)), a residual amount (complex formation amount) of a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 98, and a residual amount (complex formation amount) of an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 99 measured by absorbance (450 nm) are shown in this order from the left-hand.

Fig. 37 shows results of Example 14. For each of Metal

salt solution Mg (100 mM $MgCl_2$ aqueous solution), Metal salt solution Ba (100 mM $BaCl_2$ aqueous solution), and Metal salt solution H_2O (ultrapure water), a residual amount (complex formation amount) of a methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 102, and a residual amount (complex formation amount) of an unmethylated oligonucleotide UBC-U8 having the nucleotide sequence of SEQ ID NO: 103 measured by fluorescence (612 nm) are shown in this order from the left-hand.

Fig. 38 shows results of Example 15. For each of 10, 16, 22, 28, 34, 46, 58, 70 mM $MgCl_2$ solutions (final concentration), a residual amount (complex formation amount) of a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 105, and a residual amount (complex formation amount) of an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 106 measured by fluorescence (612 nm) are shown in this order from the left-hand.

Fig. 39 shows results of Example 16. For each of 10, 70, 130, 190, 250, 370, 490, 610 mM $MgCl_2$ solutions (final concentration), a residual amount (complex formation amount) of a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 108, and a residual amount (complex formation amount) of an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 109 measured by fluorescence (612 nm) are shown in this order from the left-hand.

Fig. 40 shows results of Example 17. From the left hand,

a formation amount of a complex measured by fluorescence (excitation 340 nm/detection 612 nm) is shown for each of Solution MA (10 ng/10 μL solution in TE buffer), Solution A (10 ng/10 μL solution in TE buffer), Solution MB (1 ng/10 μL solution in TE buffer), Solution B (1 ng/10 μL solution in TE buffer), Solution MC (0 ng/10 μL solution in TE buffer (negative control solution)), and Solution C (0 ng/10 μL solution in TE buffer (negative control solution)).

Fig. 41 shows results of Example 18. From the left hand, a formation amount of a complex measured by fluorescence (excitation 340 nm/detection 612 nm) is shown for each of Solution MA (10 ng/10 μL solution in TE buffer), Solution A (10 ng/10 μL solution in TE buffer), Solution MB (0 ng/0 μL solution in TE buffer (negative control solution)) and Solution B (0 ng/10 μL solution in TE buffer (negative control solution)).

Fig. 42 shows results of Example 19. From the left hand, a formation amount of a complex measured by fluorescence (excitation 340 nm/detection 612 nm) is shown for each of Solution MA (10 ng/10 μL solution in TE buffer), Solution A (10 ng/10 μL solution in TE buffer), Solution MB (1 ng/10 μL solution in TE buffer), Solution B (1 ng/10 μL solution in TE buffer), Solution MC (0.1 ng/10 μL solution in TE buffer), Solution C (0.1 ng/10 μL solution in TE buffer), Solution MD (0 ng/10 μL solution in TE buffer (negative control solution)), and Solution D (0 ng/10 μL solution in TE buffer (negative control solution)).

Fig. 43 shows results of Example 20. From the left hand,

a formation amount of a complex measured by fluorescence (excitation 340 nm/detection 612 nm) is shown for each of Solution MA (10 ng/10 μL solution in TE buffer), Solution A (10 ng/10 μL solution in TE buffer), Solution MB (1 ng/10 μL solution in TE buffer), Solution B (1 ng/10 μL solution in TE buffer), Solution MC (0.1 ng/10 μL solution in TE buffer), Solution C (0.1 ng/10 μL solution in TE buffer), Solution MD (0 ng/10 μL solution in TE buffer (negative control solution)), and Solution D (0 ng/10 μL solution in TE buffer (negative control solution)).

Fig. 44 shows results of Example 21. From the left hand, a formation amount of a complex measured by fluorescence (excitation 340 nm/detection 612 nm) is shown for each of Solution MA (10 ng/10 μL solution in TE buffer), Solution A (10 ng/10 μL solution in TE buffer), Solution MB (1 ng/10 μL solution in TE buffer), Solution B (1 ng/10 μL solution in TE buffer), Solution MC (0.1 ng/10 μL solution in TE buffer), Solution C (0.1 ng/10 μL solution in TE buffer), Solution MD (0 ng/10 μL solution in TE buffer (negative control solution)), and Solution D (0 ng/10 μL solution in TE buffer (negative control solution)).

Fig. 45 shows results of Example 22. From the left hand, a formation amount of a complex measured by fluorescence (excitation 340 nm/detection 612 nm) is shown for each of Solution MA (10 ng/10 μL solution in TE buffer), Solution A (10 ng/10 μL solution in TE buffer), Solution MB (1 ng/10 μL solution in TE buffer), Solution B (1 ng/10 μL solution in TE buffer), Solution MC (0.1 ng/10 μL solution in TE buffer),

Solution C (0.1 ng/10 μL solution in TE buffer), Solution MD (0 ng/10 μL solution in TE buffer (negative control solution)), and Solution D (0 ng/10 μL solution in TE buffer (negative control solution)).

Fig. 46 shows results of Example 23. From the left hand, a formation amount of a complex measured by fluorescence (excitation 340 nm/detection 612 nm) is shown for each of Solution MA (10 ng/10 μL solution in TE buffer), Solution A (10 ng/10 μL solution in TE buffer), Solution MB (1 ng/10 μL solution in TE buffer), Solution B (1 ng/10 μL solution in TE buffer), Solution MC (0.1 ng/10 μL solution in TE buffer), Solution C (0.1 ng/10 μL solution in TE buffer), Solution MD (0 ng/10 μL solution in TE buffer (negative control solution)), and Solution D (0 ng/10 μL solution in TE buffer (negative control solution)).

BEST MODE FOR CARRYING OUT THE INVENTION

It is known that DNA methylation abnormality occurs in various diseases (for example, cancer), and it is believed that the degree of various diseases can be measured by detecting this DNA methylation abnormality.

For example, when there is a region where methylation occurs at 100% in a specimen derived from a diseased organism, and the present measuring method is executed for the region, the amount of methylated DNA would increase. For example, when there is a region where methylation does not occur at 100% in a specimen derived from a diseased organism, and the present measuring method is executed for the region, the

amount of methylated DNA would be approximately 0. For example, when there is a region where the methylation rate is low in in a specimen derived from a healthy organism, and a region where the methylation rate is high in a specimen derived from a diseased organism, and the present measuring method is executed for the region, the amount of methylated DNA would be approximately 0 for a healthy subject, and a significantly higher value than that of a healthy subject would be exhibited by a disease subject, so that the "degree of disease" can be determined based on this difference in value. The "degree of disease" used herein has the same meaning as those commonly used in this field of art, and concretely means, for example, malignancy when the biological specimen is a cell, and means, for example, abundance of disease cells in the tissue when the biological specimen is a tissue. Further, when the biological specimen is plasma or serum, it means the probability that the individual has a disease. Therefore, the present measuring method makes it possible to diagnose various diseases by examining methylation abnormality.

As the "biological specimen" in the present invention, for example, a cell lysate, a tissue lysate (here the term "tissue" is used in a broad sense including blood, lymph node and so on) or biological samples including bodily sections such as plasma, serum and lymph, bodily secretions (urine, milk and so on) and the like and a genomic DNA obtained by extracting these biological samples, in mammals can be

recited. As a biological specimen, for example, samples derived from microorganisms, viruses and the like can be recited, and in such a case, "a genomic DNA" in the present measuring method also means genomic DNA of microorganisms, viruses and the like.

When the specimen derived from a mammal is blood, use of the present measuring method in a regular health check or a simple examination is expected.

For obtaining a genomic DNA from a specimen derived from a mammal, for example, DNA may be extracted using a commercially available DNA extraction kit.

When blood is used as a specimen, plasma or serum is prepared from blood in accordance with a commonly used method, and using the prepared plasma or serum as a specimen, free DNA (including DNA derived from cancer cells such as gastric cancer cells) contained in the specimen is analyzed. This enables analysis of DNA derived from cancer cells such as gastric cancer cells while avoiding DNA derived from hemocytes, and improves the sensitivity of detection of cancer cells such as gastric cancer cells and a tissue containing the same.

Usually, a gene (a genomic DNA) consists of four kinds of bases. In these bases, such a phenomenon is known that only cytosine is methylated, and such methylation modification of DNA is limited to cytosine in a nucleotide sequence represented by 5'-CG-3' (C represents cytosine, and G represents guanine. Hereinafter, the nucleotide sequence is also referred to as "CpG"). The site to be methylated in

cytosine is its position 5. In DNA replication prior to cell division, only cytosine in "CpG" of a template chain is methylated immediately after replication, however, cytosine in "CpG" of a newly-generated strand is immediately methylated by the action of methyltransferase. Therefore, the methylation state of DNA will be passed to new two sets of DNA even after DNA replication. The term "methylated DNA" in the present invention means DNA occurring by such methylation modification.

The term "CpG pair" in the present invention means double-stranded oligonucleotide in which a nucleotide sequence represented by CpG and a CpG that is complement with this are base-paired.

The term "objective DNA region" (hereinafter, also referred to as an "objective region") used in the present invention means a DNA region for which presence or absence of methylation of cytosine included in the region is to be examined, and has a recognition site of at least one kind of methylation sensitive restriction enzyme. A DNA region containing at least one cytosine in a nucleotide sequence represented by CpG which is present in a nucleotide sequence of a promoter region, an untranslated region, or a translated region (coding region) of a useful protein gene such as Lysyl oxidase, HRAS-like suppressor, bA305P22.2.1, Gamma filamin, HAND1, Homologue of RIKEN 2210016F16, FLJ32130, PPARG angiopoietin-related protein, Thrombomodulin, p53-responsive gene 2, Fibrillin2, Neurofilament3, disintegrin and metalloproteinase domain 23, G protein-coupled receptor 7, G-

protein coupled somatostatin and angiotensin-like peptide receptor, Solute carrier family 6 neurotransmitter transporter noradrenalin member 2 and so on can be recited.

To be more specific, when the useful protein gene is a Lysyl oxidase gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a Lysyl oxidase gene derived from human, and a promoter region located 5' upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 1 (corresponding to a nucleotide sequence represented by base No. 16001 to 18661 in the nucleotide sequence described in Genbank Accession No. AF270645) can be recited. In the nucleotide sequence of SEQ ID NO: 1, ATG codon encoding methionine at amino terminal of Lysyl oxidase protein derived from human is represented in base No. 2031 to 2033, and a nucleotide sequence of the above exon 1 is represented in base No. 1957 to 2661. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 1, in particular, cytosine in CpG which is present in a region where CpGs are densely present in the nucleotide sequence of SEQ ID NO: 1 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example, cancer cells such as gastric cancer cells. More concretely, as cytosine exhibiting high methylation frequency in gastric cancer cells, for example, cytosines represented by base Nos.

1539, 1560, 1574, 1600, 1623, 1635, 1644, 1654, 1661, 1682, 1686, 1696, 1717, 1767, 1774, 1783, 1785, 1787, 1795 and so on in the nucleotide sequence of SEQ ID NO: 1 can be recited.

To be more specific, when the useful protein gene is a HRAS-like suppressor gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a HRAS-like suppressor gene derived from human, and a promoter region located 5' upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 2 (corresponding to a nucleotide sequence represented by base No. 172001 to 173953 in the nucleotide sequence described in Genbank Accession No. AC068162) can be recited. In the nucleotide sequence of SEQ ID NO: 2, the nucleotide sequence of exon 1 of a HRAS-like suppressor gene derived from human is represented in base No. 1743 to 1953. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 2, in particular, cytosine in CpG which is present in a region where CpGs are densely present in the nucleotide sequence of SEQ ID NO: 2 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example, cancer cells such as gastric cancer cells. More concretely, as cytosine exhibiting high methylation frequency in gastric cancer cells, for example, cytosines represented by base Nos. 1316, 1341, 1357, 1359, 1362, 1374, 1390, 1399, 1405, 1409, 1414, 1416, 1422,

1428, 1434, 1449, 1451, 1454, 1463, 1469, 1477, 1479, 1483, 1488, 1492, 1494, 1496, 1498, 1504, 1510, 1513, 1518, 1520 and so on in the nucleotide sequence of SEQ ID NO: 2 can be recited.

To be more specific, when the useful protein gene is a bA305P22.2.1 gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a bA305P22.2.1 gene derived from human, and a promoter region located 5' upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 3 (corresponding to a nucleotide sequence represented by base No. 13001 to 13889 in the nucleotide sequence described in Genbank Accession No. AL121673) can be recited. In the nucleotide sequence of SEQ ID NO: 3, ATG codon encoding methionine at amino terminal of bA305P22.2.1 protein derived from human is represented in base No. 849 to 851, and a nucleotide sequence of the above exon 1 is represented in base No. 663 to 889. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 3, in particular, cytosine in CpG which is present in a region where CpGs are densely present in the nucleotide sequence of SEQ ID NO: 3 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example, cancer cells such as gastric cancer cells. More concretely, as cytosine exhibiting high methylation frequency in gastric cancer cells, for

example, cytosines represented by base Nos. 329, 335, 337, 351, 363, 373, 405, 424, 427, 446, 465, 472, 486 and so on in the nucleotide sequence of SEQ ID NO: 3 can be recited.

To be more specific, when the useful protein gene is a Gamma filamin gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a Gamma filamin gene derived from human, and a promoter region located 5' upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 4 (corresponding to a complementary sequence to a nucleotide sequence represented by base No. 63528 to 64390 in the nucleotide sequence described in Genbank Accession No. AC074373) can be recited. In the nucleotide sequence of SEQ ID NO: 4, ATG codon encoding methionine at amino terminal of Gamma filamin protein derived from human is represented in base No. 572 to 574, and a nucleotide sequence of the above exon 1 is represented in base No. 463 to 863. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 4, in particular, cytosine in CpG which is present in a region where CpGs are densely present in the nucleotide sequence of SEQ ID NO: 4 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example, cancer cells such as gastric cancer cells. More concretely, as cytosine exhibiting high methylation frequency in gastric cancer cells, for

example, cytosines represented by base Nos. 329, 333, 337, 350, 353, 360, 363, 370, 379, 382, 384, 409, 414, 419, 426, 432, 434, 445, 449, 459, 472, 474, 486, 490, 503, 505 and so on in the nucleotide sequence of SEQ ID NO: 4 can be recited.

To be more specific, when the useful protein gene is a HAND1 gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a HAND1 gene derived from human, and a promoter region located 5' upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 5 (corresponding to a complementary sequence to a nucleotide sequence represented by base No. 24303 to 26500 in the nucleotide sequence described in Genbank Accession No. AC026688) can be recited. In the nucleotide sequence of SEQ ID NO: 5, ATG codon encoding methionine at amino terminal of HAND1 protein derived from human is represented in base No. 1656 to 1658, and a nucleotide sequence of the above exon 1 is represented in base No. 1400 to 2198. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 5, in particular, cytosine in CpG which is present in a region where CpGs are densely present in the nucleotide sequence of SEQ ID NO: 5 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example, cancer cells such as gastric cancer cells. More concretely, as cytosine exhibiting

high methylation frequency in gastric cancer cells, for example, cytosines represented by base Nos. 1153, 1160, 1178, 1187, 1193, 1218, 1232, 1266, 1272, 1292, 1305, 1307, 1316, 1356, 1377, 1399, 1401, 1422, 1434 and so on in the nucleotide sequence of SEQ ID NO: 5 can be recited.

To be more specific, when the useful protein gene is a Homologue of RIKEN 2210016F16 gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a Homologue of RIKEN 2210016F16 gene derived from human, and a promoter region located 5′ upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 6 (corresponding to a complementary nucleotide sequence to a nucleotide sequence represented by base No. 157056 to 159000 in the nucleotide sequence described in Genbank Accession No. AL354733) can be recited. In the nucleotide sequence of SEQ ID NO: 6, a nucleotide sequence of exon 1 of a Homologue of a RIKEN 2210016F16 gene derived from human is represented in base No. 1392 to 1945. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 6, in particular, cytosine in CpG which is present in a region where CpGs are densely present in the nucleotide sequence of SEQ ID NO: 6 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example, cancer cells such as gastric cancer cells. More concretely, as cytosine exhibiting

high methylation frequency in gastric cancer cells, for example, cytosines represented by base Nos. 1172, 1175, 1180, 1183, 1189, 1204, 1209, 1267, 1271, 1278, 1281, 1313, 1319, 1332, 1334, 1338, 1346, 1352, 1358, 1366, 1378, 1392, 1402, 1433, 1436, 1438 and so on in the nucleotide sequence of SEQ ID NO: 6 can be recited.

To be more specific, when the useful protein gene is a FLJ32130 gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a FLJ32130 gene derived from human, and a promoter region located 5' upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 7 (corresponding to a complementary nucleotide sequence to a nucleotide sequence represented by base No. 1 to 2379 in the nucleotide sequence described in Genbank Accession No. AC002310) can be recited. In the nucleotide sequence of SEQ ID NO: 7, ATG codon encoding methionine at amino terminal of FLJ32130 protein derived from human is represented in base No. 2136 to 2138, and a nucleotide sequence assumed to be the above exon 1 is represented in base No. 2136 to 2379. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 7, in particular, cytosine in CpG which is present in a region where CpGs are densely present in the nucleotide sequence of SEQ ID NO: 7 exhibits high methylation frequency (namely, a high methylation state

(hypermethylation)) in, for example, cancer cells such as gastric cancer cells. More concretely, as cytosine exhibiting high methylation frequency in gastric cancer cells, for example, cytosines represented by base Nos. 1714, 1716, 1749, 1753, 1762, 1795, 1814, 1894, 1911, 1915, 1925, 1940, 1955, 1968 and so on in the nucleotide sequence of SEQ ID NO: 7 can be recited.

To be more specific, when the useful protein gene is a PPARG angiopoietin-related protein gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a PPARG angiopoietin-related protein gene derived from human, and a promoter region located 5′ upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 8 can be recited. In the nucleotide sequence of SEQ ID NO: 8, ATG codon encoding methionine at amino terminal of PPARG angiopoietin-related protein derived from human is represented in base No. 717 to 719, and a nucleotide sequence of the 5′ side part of the above exon 1 is represented in base No. 1957 to 2661. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 8, in particular, cytosine in CpG which is present in a region where CpGs are densely present in the nucleotide sequence of SEQ ID NO: 8 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example, cancer

cells such as gastric cancer cells. More concretely, as cytosine exhibiting high methylation frequency in gastric cancer cells, for example, cytosines represented by base Nos. 35, 43, 51, 54, 75, 85, 107, 127, 129, 143, 184, 194, 223, 227, 236, 251, 258 and so on in the nucleotide sequence of SEQ ID NO: 8 can be recited.

To be more specific, when the useful protein gene is a Thrombomodulin gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a Thrombomodulin gene derived from human, and a promoter region located 5′ upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 9 (corresponding to a nucleotide sequence represented by base No. 1 to 6096 in the nucleotide sequence described in Genbank Accession No. AF495471) can be recited. In the nucleotide sequence of SEQ ID NO: 9, ATG codon encoding methionine at amino terminal of Thrombomodulin protein derived from human is represented in base No. 2590 to 2592, and a nucleotide sequence of the above exon 1 is represented in base No. 2048 to 6096. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 9, in particular, cytosine in CpG which is present in a region where CpGs are densely present in the nucleotide sequence of SEQ ID NO: 9 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example,

cancer cells such as gastric cancer cells. More concretely, as cytosine exhibiting high methylation frequency in gastric cancer cells, for example, cytosines represented by base Nos. 1539, 1551, 1571, 1579, 1581, 1585, 1595, 1598, 1601, 1621, 1632, 1638, 1645, 1648, 1665, 1667, 1680, 1698, 1710, 1724, 1726, 1756 and so on in the nucleotide sequence of SEQ ID NO: 9 can be recited.

To be more specific, when the useful protein gene is a p53-responsive gene 2 gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a p53-responsive gene 2 gene derived from human, and a promoter region located 5' upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 10 (corresponding to a complementary sequence to a nucleotide sequence represented by base No. 113501 to 116000 in the nucleotide sequence described in Genbank Accession No. AC009471) can be recited. In the nucleotide sequence of SEQ ID NO: 10, a nucleotide sequence of exon 1 of a p53-responsive gene 2 gene derived from human is represented in base No. 1558 to 1808. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 10 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example, cancer cells such as pancreas cancer cells. More concretely, as cytosine exhibiting high methylation frequency in pancreas

cancer cells, for example, cytosines represented by base Nos. 1282, 1284, 1301, 1308, 1315, 1319, 1349, 1351, 1357, 1361, 1365, 1378, 1383 and so on in the nucleotide sequence of SEQ ID NO: 10 can be recited.

To be more specific, when the useful protein gene is a Fibrillin2 gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a Fibrillin2 gene derived from human, and a promoter region located 5' upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 11 (corresponding to a complementary sequence to a nucleotide sequence represented by base No. 118801 to 121000 in the nucleotide sequence described in Genbank Accession No. AC113387) can be recited. In the nucleotide sequence of SEQ ID NO: 11, a nucleotide sequence of exon 1 of a Fibrillin2 gene derived from human is represented in base No. 1091 to 1345. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 11 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example, cancer cells such as pancreas cancer cells. More concretely, as cytosine exhibiting high methylation frequency in pancreas cancer cells, for example, cytosines represented by base Nos. 679, 687, 690, 699, 746, 773, 777, 783, 795, 799, 812, 823, 830, 834, 843 and so on in the nucleotide sequence of SEQ ID NO: 11 can be recited.

To be more specific, when the useful protein gene is a Neurofilament3 gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a Neurofilament3 gene derived from human, and a promoter region located 5' upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 12 (corresponding to a complementary sequence to a nucleotide sequence represented by base No. 28001 to 30000 in the nucleotide sequence described in Genbank Accession No. AF106564) can be recited. In the nucleotide sequence of SEQ ID NO: 12, a nucleotide sequence of exon 1 of a Neurofilament3 gene derived from human is represented in base No. 614 to 1694. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 12 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example, cancer cells such as pancreas cancer cells. More concretely, as cytosine exhibiting high methylation frequency in pancreas cancer cells, for example, cytosines represented by base Nos. 428, 432, 443, 451, 471, 475, 482, 491, 499, 503, 506, 514, 519, 532, 541, 544, 546, 563, 566, 572, 580 and so on in the nucleotide sequence of SEQ ID NO: 12 can be recited.

To be more specific, when the useful protein gene is a disintegrin and metalloproteinase domain 23 gene, as a nucleotide sequence that includes at least one nucleotide

sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a disintegrin and metalloproteinase domain 23 gene derived from human, and a promoter region located 5' upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 13 (corresponding to a nucleotide sequence represented by base No. 21001 to 23300 in the nucleotide sequence described in Genbank Accession No. AC009225) can be recited. In the nucleotide sequence of SEQ ID NO: 13, a nucleotide sequence of exon 1 of a disintegrin and metalloproteinase domain 23 gene derived from human is represented in base No. 1194 to 1630. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 13 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example, cancer cells such as pancreas cancer cells. More concretely, as cytosine exhibiting high methylation frequency in pancreas cancer cells, for example, cytosines represented by base Nos. 998, 1003, 1007, 1011, 1016, 1018, 1020, 1026, 1028, 1031, 1035, 1041, 1043, 1045, 1051, 1053, 1056, 1060, 1066, 1068, 1070, 1073, 1093, 1096, 1106, 1112, 1120, 1124, 1126 and so on in the nucleotide sequence of SEQ ID NO: 13 can be recited.

To be more specific, when the useful protein gene is a G protein-coupled receptor 7 gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region,

untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a G protein-coupled receptor 7 gene derived from human, and a promoter region located 5' upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 14 (corresponding to a nucleotide sequence represented by base No. 75001 to 78000 in the nucleotide sequence described in Genbank Accession No. AC009800) can be recited. In the nucleotide sequence of SEQ ID NO: 14, a nucleotide sequence of exon 1 of a G protein-coupled receptor 7 gene derived from human is represented in base No. 1666 to 2652. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 14 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example, cancer cells such as pancreas cancer cells. More concretely, as cytosine exhibiting high methylation frequency in pancreas cancer cells, for example, cytosines represented by base Nos. 1480, 1482, 1485, 1496, 1513, 1526, 1542, 1560, 1564, 1568, 1570, 1580, 1590, 1603, 1613, 1620 and so on in the nucleotide sequence of SEQ ID NO: 14 can be recited.

To be more specific, when the useful protein gene is a G-protein coupled somatostatin and angiotensin-like peptide receptor gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a G-protein

coupled somatostatin and angiotensin-like peptide receptor gene derived from human, and a promoter region located 5' upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 15 (corresponding to a complementary sequence to a nucleotide sequence represented by base No. 57001 to 60000 in the nucleotide sequence described in Genbank Accession No. AC008971) can be recited. In the nucleotide sequence of SEQ ID NO: 15, a nucleotide sequence of exon 1 of a G-protein coupled somatostatin and angiotensin-like peptide receptor gene derived from human is represented in base No. 776 to 2632. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 15 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example, cancer cells such as pancreas cancer cells. More concretely, as cytosine exhibiting high methylation frequency in pancreas cancer cells, for example, cytosines represented by base Nos. 470, 472, 490, 497, 504, 506, 509, 514, 522, 540, 543, 552, 566, 582, 597, 610, 612 and so on in the nucleotide sequence of SEQ ID NO: 15 can be recited.

To be more specific, when the useful protein gene is a Solute carrier family 6 neurotransmitter transporter noradrenalin member 2 gene, as a nucleotide sequence that includes at least one nucleotide sequence represented by CpG present in a nucleotide sequence of its promoter region, untranslated region or translated region (coding region), a nucleotide sequence of a genomic DNA containing exon 1 of a Solute carrier family 6 neurotransmitter transporter

noradrenalin member 2 gene derived from human, and a promoter region located 5' upstream of the same can be recited, and more concretely, the nucleotide sequence of SEQ ID NO: 16 (corresponding to a complementary sequence to a nucleotide sequence represented by base No. 78801 to 81000 in the nucleotide sequence described in Genbank Accession No. AC026802) can be recited. In the nucleotide sequence of SEQ ID NO: 16, a nucleotide sequence of exon 1 of a Solute carrier family 6 neurotransmitter transporter noradrenalin member 2 gene derived from human is represented in base No. 1479 to 1804. Cytosine in the nucleotide sequence represented by CpG which is present in the nucleotide sequence of SEQ ID NO: 16 exhibits high methylation frequency (namely, a high methylation state (hypermethylation)) in, for example, cancer cells such as pancreas cancer cells. More concretely, as cytosine exhibiting high methylation frequency in pancreas cancer cells, for example, cytosines represented by base Nos. 1002, 1010, 1019, 1021, 1051, 1056, 1061, 1063, 1080, 1099, 1110, 1139, 1141, 1164, 1169, 1184 and so on in the nucleotide sequence of SEQ ID NO: 16 can be recited.

Detection in the phrase "detection or quantification of methylated DNA" in the present measuring method means that whether methylated DNA is present in a target DNA region can be determined according to whether a methylated DNA antibody or the present oligonucleotide is detected, and detecting a methylated DNA antibody or the present oligonucleotide indicates presence of methylated DNA in a target DNA region in

the specimen, and not detecting a methylated DNA antibody or the present oligonucleotide indicates that the abundance of methylated DNA in a target DNA region in the specimen is less than the detection limit.

Quantification in the phrase "detection or quantification of methylated DNA" in the present measuring method means an amount of methylated DNA in a target DNA region in a specimen estimated from the quantified amount of a methylated DNA antibody or the present oligonucleotide, and for example, an amount of methylated DNA in a target region contained in 1 mL of serum when the specimen is 1 mL of serum.

In First step of the present measuring method, double-stranded DNA contained in a DNA sample derived from genomic DNA contained in a biological specimen is separated to a single-stranded state. Concretely, for example, by adding an annealing buffer to double-stranded DNA, a mixture is obtained. Then, the obtained mixture is boiled at 95°C for about 30 seconds, and then rapidly cooled on ice-cooled water for several minutes. For example, free DNA contained in blood or the like can be single-stranded DNA. Therefore, when genomic DNA contained in a biological specimen is single-stranded DNA, this operation is not required.

The term "methylated DNA antibody" in Second step of the present measuring method means an antibody that binds to a methylated base in DNA as its antigen. For example, an antibody having a property of recognizing and binding to cytosine methylated at position 5 in single-stranded DNA can

be recited, and more concretely, a methyl cytosine antibody can be recited.

A methylated DNA antibody can be prepared by an usual immunological technique from a methylated base as an antigen. Concretely, it can be obtained by selecting from antibodies prepared against an antigen such as 5-methyl cytidine, 5-methyl cytosine or DNA containing 5-methyl cytosine based on specific binding to methyl cytosine in DNA as an index.

As an antibody obtainable by immunizing an animal against an antigen, an antibody of IgG fraction (polyclonal antibody), and an antibody produced by a single clone (monoclonal antibody) are recited. In the present measuring method, since an antibody capable of specifically recognizing a methylated base is desired, it is preferable to use a monoclonal antibody.

As a method of preparing a monoclonal antibody, a procedure based on a cell fusion method can be recited. For example, in the cell fusion method, a hybridoma is prepared by allowing cell fusion between a pancreatic cell (B cell) derived from an immunized mouse and a myeloma cell, and an antibody produced by the prepared hybridoma is selected for preparation of a methyl cytosine antibody (monoclonal antibody). When a monoclonal antibody is prepared by a cell fusion method, it is not necessary to purify an antigen, and for example, a mixture of 5-methyl cytidine, 5-methyl cytosine or DNA or the like containing 5-methyl cytosine may be administered as an antigen to an animal used for immunization. As an administration method, 5-methyl cytidine, 5-methyl

cytosine or DNA or the like containing 5-methyl cytosine is directly administered to a mouse for production of an antibody. When an antibody is difficult to be produced, an antigen bound to a support may be used for immunization. Also, by thoroughly mixing an adjuvant solution (prepared, for example, by mixing liquid paraffin and Aracel A, and mixing killed tubercle bacilli as an adjuvant) and an antigen, and immunizing via liposome incorporating the same, immunity of an antigen can be improved. Also a method involving adding equivalent amounts of a solution containing an antigen and an adjuvant solution, fully emulsifying them, and subcutaneously or intraperitoneally injecting the resultant mixture to a mouse, and a method of adding killed Bordetella pertussis as an adjuvant after mixing well with alum water are known. A mouse may be boosted intraperitoneally or intravenously after an appropriate term from initial immunization. When the amount of an antigen is small, a solution in which the antigen is suspended may be directly injected into a mouse spleen to effect immunization.

After exenterating a spleen and peeling an adipose tissue off after several days from the final immunization, a spleen cell suspension is prepared. The spleen cell is fused, for example, with an HGPRT-deficient myeloma cell to prepare a hybridoma. As a cell fusion agent, any means capable of efficiently fusing a spleen cell (B cell) and a myeloma cell is applicable, and for example, a method of using a hemagglutinating virus of Japan (HVJ), polyethyleneglycol (PEG) and the like are recited. Cell fusion may be conducted

by a method using a high voltage pulse.

After the cell fusion operation, cells are cultured in an HAT medium, a clone of a hybridoma in which a spleen cell and a myeloma cell are fused is selected, and the cell is allowed to grow until screening becomes possible. In a method of detecting an antibody for selecting a hybridoma that produces an intended antibody, or a method of measuring a titer of an antibody, an antigen-antibody reaction system may be used. Concretely, as a method of measuring an antibody against a soluble antigen, a radioisotope immune assay (RIA), an enzyme-linked immunosorbent assay (ELISA) and the like can be recited.

Considering the property of the methylated DNA antibody (one antibody binds to one methylated base (cytosine)), it is desired to select a region where a number of methylated bases (cytosine), namely CpG are present as a target DNA region, and thus an improvement in quantification accuracy and detection sensitivity is expected.

The term "the present oligonucleotide" in Second step of the present measuring method means an oligonucleotide that does not inhibit binding between a methylated DNA antibody and methylated DNA in a target DNA region, but is able to bind with the single-stranded DNA, and for example, an oligonucleotide having a nucleotide sequence capable of binding with single-stranded DNA containing a target DNA region, and not inhibiting binding to a methylated base (cytosine) in single-stranded DNA containing a target DNA

region of a methylated DNA antibody when it binds with single-stranded DNA containing a target DNA region.

The phrase "nucleotide sequence capable of binding with single-stranded DNA containing a target DNA region" means a nucleotide sequence required for forming a bound body (double-strand) with single-stranded DNA containing a target DNA region, namely, a nucleotide sequence containing a nucleotide sequence complementary to part of a nucleotide sequence of a target DNA region, or a nucleotide sequence containing a nucleotide sequence complementary to part of a nucleotide sequence of a DNA region which is located further 5'-end side from 5'-end of a target DNA region, or a nucleotide sequence containing a nucleotide sequence complementary to part of a nucleotide sequence of a DNA region which is located further 3'-end side from 3'-end of a target DNA region.

The wording "not inhibiting binding between a methylated DNA antibody and methylated DNA in a target DNA region" means that the present oligonucleotide has such a nucleotide sequence that complementary binding between the present oligonucleotide and the single-stranded DNA does not occur in an occupied space required for a methylated DNA antibody to bind with methylated single-stranded DNA. In other words, it appears that a methylated DNA antibody occupies not only a methylated base (cytosine) to which it directly binds, but also the space surrounding the methylated base (cytosine) to bind to a methylated base (cytosine). Therefore, the present oligonucleotide may be any one insofar as it does not

complementarily bind with the single-stranded DNA in a space occupied by a methylated DNA antibody to bind with methylated DNA. The present oligonucleotide to be bound to the single-stranded DNA is not necessarily one kind, but two or more kinds may be used insofar as binding of a methylated DNA antibody is not inhibited. Use of plural present oligonucleotides will improve quantification accuracy and detection sensitivity.

As a preferred embodiment of forming a complex formed in Second step of the present measuring method, or a bound body of single-stranded DNA separated in First step, a methylated DNA antibody and an oligonucleotide not inhibiting binding between a methylated DNA antibody and a methylated base present in single-stranded DNA containing a target DNA region arising in the course of forming a complex in Second step, formation in a reaction system containing a bivalent positive ion can be recited. More preferably, the bivalent positive ion is a magnesium ion. Here, the "reaction system containing a bivalent positive ion" means a reaction system containing a bivalent positive ion in an annealing buffer used for forming a complex formed in Second step of the present measuring method, or a bound body of single-stranded DNA separated in First step, a methylated DNA antibody and an oligonucleotide not inhibiting binding between a methylated DNA antibody and a methylated base present in single-stranded DNA containing a target DNA region arising in the course of forming a complex in Second step, and concretely, for example, it preferably contains a salt composed of a magnesium ion (for example,

$MgOAc_2$, $MgCl_2$ and so on) in a concentration ranging from 1 mM to 600 mM.

"Formation of a complex" in Second step of the present measuring method means formation of a mixture in the condition that single-stranded DNA separated in First step, the present oligonucleotide, and a methylated DNA antibody are bound.

"Separating a complex" in Second step of the present measuring method is enabled by binding and immobilizing the complex to a support. The material and form of the support are not particularly limited as far as a complex can bind thereto. For example, any form suited for use purpose may be employed, including the forms of tube, test plate, filter, disc, bead and so on. As the material, those used as supports for a usual immune measuring method, for example, synthetic resins such as polystyrene, polypropylene, polyacrylamide, polymethylmethacrylate, polysulfone, polyacrylonitrile and nylon, or the synthetic resins incorporating a reactive functional group such as a sulfonic group, or an amino group can be recited. Also, glass, polysaccharides or derivatives thereof (cellulose, nitrocellulose and so on), silica gel, porous ceramics, metal oxides and the like may be used.

As a method of binding and immobilizing a complex to a support for separating the complex, the following two approaches are recited: immobilizing a methylated DNA antibody to a support, and immobilizing the present oligonucleotide to a support. Therefore, the phrase "separate a complex at the same time or after formation of the complex" in Second step of the present measuring method concretely means "at the same

time or after formation of a complex, by allowing single-stranded DNA containing methylated DNA in a target DNA region, the present oligonucleotide, and a methylated DNA antibody immobilizable to a support to bind simultaneously or sequentially, the methylated DNA antibody immobilizable to a support contained in the complex is immobilized to a support, and the complex is separated", or "at the same time or after formation of a complex, by allowing single-stranded DNA containing methylated DNA in a target DNA region, the present oligonucleotide immobilizable to a support, and a methylated DNA antibody to bind simultaneously or sequentially, the present oligonucleotide immobilizable to a support contained in the complex is immobilized to a support, and the complex is separated". Here, when single-stranded DNA containing methylated DNA in a target DNA region is bound to a support via a methylated DNA antibody, the present oligonucleotide is detected or quantified according to its function (as will be described later), and when single-stranded DNA containing methylated DNA in a target DNA region is bound to a support via the present oligonucleotide, a methylated DNA antibody is detected or quantified according to its function (as will be described later).

When a methylated DNA antibody is used as an object immobilizable to a support, it suffices that a methylated DNA antibody is eventually immobilized to a support while it forms a complex with single-stranded DNA containing methylated DNA in a target DNA region and the present oligonucleotide, and

(1) a methylated DNA antibody may be immobilized to a support prior to binding between the single-stranded DNA and the methylated DNA antibody, or

(2) a methylated DNA antibody may be immobilized to a support after binding between the single-stranded DNA and the methylated DNA antibody.

One exemplary concrete method for immobilizing a methylated DNA antibody to a support involves immobilizing a biotinylated methylated DNA antibody obtained by biotinylating a methylated DNA antibody to a streptavidin-coated support (for example, a PCR tube coated with streptavidin, magnetic beads coated with streptavidin, a chromatostrip partially coated with streptavidin and so on).

Also there is a method of letting a molecule having an active functional group such as an amino group, a thiol group, or an aldehyde group covalently bind to a methylated DNA antibody, and letting the resultant bound body covalently bind to a support made of glass, a polysaccharide derivative, silica gel or the synthetic resin or thermostable plastic whose surface is activated by a silane coupling agent or the like. The above described covalent bonding may be achieved, for example, by covalently coupling the molecule having an active functional group to a methylated DNA antibody using a spacer formed by serially connecting five triglycerides, a cross linker or the like.

A methylated DNA antibody may be directly immobilized to a support, or an antibody against a methylated DNA antibody (secondary antibody) may be immobilized to a support, and a

methylated antibody may be bound to the secondary antibody to achieve immobilization to a support.

When the present oligonucleotide is used as an object immobilizable to a support, it suffices that the present oligonucleotide is eventually immobilized to a support while it forms a complex with single-stranded DNA containing methylated DNA in a target DNA region and a methylated DNA antibody, and

(1) the present oligonucleotide may be immobilized to a support prior to binding between the single-stranded DNA and the present oligonucleotide, or

(2) the present oligonucleotide may be immobilized to a support after binding between the single-stranded DNA and the present oligonucleotide.

One exemplary concrete method for immobilizing the present oligonucleotide to a support involves immobilizing a biotinylated oligonucleotide obtained by biotinylating 5'-end or 3'-end of the present oligonucleotide to a streptavidin-coated support (for example, a PCR tube coated with streptavidin, magnetic beads coated with streptavidin, a chromatostrip partially coated with streptavidin and so on).

Also there is a method of letting a molecule having an active functional group such as an amino group, a thiol group, or an aldehyde group covalently bind to 5'-end or 3'-end of the present oligonucleotide, and letting it be covalently bind to a support made of glass, a polysaccharide derivative, silica gel or the synthetic resin or thermostable plastic whose surface is activated by a silane coupling agent or the

like. The above described covalent bonding may be achieved, for example, by covalently coupling the molecule having an active functional group to a methylated DNA antibody using a spacer formed by serially connecting five triglycerides, a cross linker or the like. Furthermore, a direct chemical synthesis method on a support made of glass or silicone from an end side of the present oligonucleotide may be employed.

To "separate a complex at the same time or after formation of the complex" in Second step of the present measuring method, when "a methylated DNA antibody immobilizable to a support is immobilized to a support at the same time or after formation of a complex by binding of single-stranded DNA containing methylated DNA in a target DNA region, the present oligonucleotide, and a methylated DNA antibody immobilizable to a support", concretely, for example, it may be executed in the following manner using a "biotin-labeled biotinylated methylated DNA antibody" as a methylated DNA antibody immobilizable to a support.

(a) An appropriate amount of a biotinylated methylated DNA antibody is added (for example, a 4 μg/mL solution is added in an amount of 100 μL/well) to an avidin-coated plate, and then left still, for example, for about 2 hours at room temperature, to promote immobilization between the biotinylated methylated DNA antibody and streptavidin. Thereafter, the remaining solution is removed and washing is performed. A washing buffer (for example, a 0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154

mM NaCl, pH 7.4)) is added, for example, in a proportion of, for example, 300 μL/well, and the solution is removed. This washing operation is repeated several times, to leave the biotinylated methylated cytosine antibody immobilized on a support on wells.

(b) Single-stranded DNA obtained by separating double-stranded DNA contained in a DNA sample derived from genomic DNA contained in a biological specimen, the present oligonucleotide, and an annealing buffer (for example, 33 mM Tris-Acetate pH 7.9, 66 mM KOAc, 10 mM $MgOAc_2$, 0.5 mM Dithothreitol) are mixed, and heated at 95°C for several minutes, for example. Thereafter, in order to form a bound body of single-stranded DNA containing a target DNA region and the present oligonucleotide, the mixture is rapidly cooled to a temperature lower by about 10 to 20°C than the Tm value of the present oligonucleotide, and the reaction is kept at this temperature for several minutes, for example, and then the reaction is returned to room temperature (the bound body formed in this stage includes a bound body of single-stranded DNA containing methylated DNA in a target DNA region and the present oligonucleotide, as well as a bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide).

(c) The formed bound body of single-stranded DNA and the present oligonucleotide is added to an avidin-coated plate to which a biotinylated methylated DNA antibody is immobilized, and then left still at room temperature for about 3 hours, to promote formation of a complex of the biotinylated methylated

DNA antibody, single-stranded DNA containing methylated DNA in a target DNA region among the single-stranded DNA, and the present oligonucleotide (formation of a complex) (in this stage, the bound body of unmethylated single-stranded DNA containing a target DNA region and the present oligonucleotide does not form a complex). Thereafter, the remaining solution is removed and washing is performed. A washing buffer (for example, a 0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)) is added, for example, in a proportion of 300 μL/well, and the solution is removed. This washing operation is repeated several times, to leave the complex on wells (separation of a complex).

The annealing buffer used in (b) is not limited to the annealing buffer described above as far as it is suited for binding between the present oligonucleotide and single-stranded DNA containing a target DNA region. Use of a buffer in which a bivalent ion, preferably a magnesium ion is dissolved in a concentration of 1 to 600 mM will improve the binding stability.

The washing operation in (a) and (c) is important for removing an unimmobilized methylated DNA antibody suspended in the solution, unmethylated single-stranded DNA that does not bind with a methylated DNA antibody and hence is suspended in the solution, and single-stranded DNA in regions other than the target region that does not form a complex with the present oligonucleotide, or DNA digested by a restriction enzyme as will be described later and suspended in the solution, from the reaction solution. The washing buffer is

not limited to the washing buffer described above, insofar as it is suited for removing the free methylated DNA antibody, single-stranded DNA and so on suspended in the solution and the like, and a DELFIA buffer (available from Perkin Elmer, Tris-HCl pH 7.8 with Tween 80), a TE buffer and the like may be used.

As described above, in the above (a) to (c), after binding between the single-stranded DNA containing the target DNA region, and the present oligonucleotide, a complex is formed by causing a biotinylated methylated DNA antibody to bind with the resultant bound body, however, the order is not limited to this. In other words, after binding between the single-stranded DNA containing the target DNA region and a biotinylated methylated DNA antibody, the present oligonucleotide may be caused to bind with the resultant bound body to form a complex. For example, by adding single-stranded DNA obtained by separating double-stranded DNA contained in a DNA sample derived from genomic DNA contained in a biological specimen, to a biotinylated methylated DNA antibody immobilized to a streptavidin-coated support, a bound body of a biotinylated methylated DNA antibody immobilized to a support and the single-stranded DNA is formed (the bound body formed in this stage includes not only a bound body of single-stranded DNA containing methylated DNA in a target DNA region and a methylated antibody, but also a bound body of methylated single-stranded DNA other than in a target DNA region and a methylated antibody). Thereafter, the present oligonucleotide may be added to this, to form and separate a

complex with a bound body having single-stranded DNA containing methylated DNA in a target DNA region in the bound body (in this stage, the bound body of single-stranded DNA containing methylated DNA in regions other than the target DNA region and a methylated antibody does not form a complex).

The operations of (a) to (c) may be conducted using a chromatostrip. In that case, the operations are conducted in the following manner. For example, first, an appropriate amount of a biotinylated methylated DNA antibody is developed by a chromatostrip partially coated with streptavidin. By this operation, a biotinylated methylated DNA antibody is immobilized to the part coated with streptavidin. Then, a bound body of the single-stranded DNA and the present oligonucleotide obtained in (b) (the bound body formed in this stage includes not only a bound body of single-stranded DNA containing methylated DNA in a target DNA region and the present oligonucleotide, but also a bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide) is developed by the chromatostrip. By these operations, a complex of single-stranded DNA obtained by separating double-stranded DNA contained in a DNA sample derived from genomic DNA contained in a biological specimen, the present oligonucleotide, and a biotinylated methylated DNA antibody is immobilized to a part coated with streptavidin (formation and selection of a complex)(in this stage, the bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide does not form a complex). The order

of formation of a complex is not limited to the order of these operations. For example, after forming a complex of single-stranded DNA containing methylated DNA in a target DNA region, the present oligonucleotide, and a biotinylated methylated DNA antibody, the complex may be developed by a chromatostrip and immobilized to the part coated with streptavidin. In these operations, unnecessary components can be removed by developing the solution by a chromatostrip, and the washing operation can be omitted. Of course, the washing operation (development of a chromatostrip by a washing buffer (for example, a 0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)) may be conducted between operations without causing any problem.

Alternatively, to "separate a complex at the same time or after formation of the complex" in Second step of the present measuring method, when "a methylated DNA antibody immobilizable to a support is immobilized to a support at the same time or after formation of a complex by binding of single-stranded DNA containing methylated DNA in a target DNA region, the present oligonucleotide, and a methylated DNA antibody immobilizable to a support", concretely, for example, it may be executed in the following manner using a "biotin-labeled biotinylated methylated DNA antibody" as a methylated DNA antibody immobilizable to a support.

(a) By adding an annealing buffer (for example, 33 mM Tris-Acetate pH 7.9, 66 mM KOAc, 10 mM $MgOAc_2$, 0.5 mM Dithothreitol) and the biotinylated present oligonucleotide to

a DNA sample derived from genomic DNA contained in a biological specimen, a mixture is obtained. Then the obtained mixture is heated at 95°C, for example, for several minutes to separate double-stranded DNA contained in a DNA sample derived from genomic DNA contained in a biological specimen into single-stranded DNA. Then, in order to form a bound body of single-stranded DNA containing a target DNA region and the biotinylated present oligonucleotide, the mixture is rapidly cooled to a temperature lower by about 10 to 20°C than the Tm value of the biotinylated present oligonucleotide, and kept at this temperature, for example, for several minutes, and then returned to room temperature (the bound body formed in this stage includes a bound body of single-stranded DNA containing methylated DNA in a target DNA region and the present oligonucleotide, as well as a bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide).

(b) By adding the mixture obtained in the above (a) to a streptavidin-coated support and keeping the support at 37°C, for example, for several minutes, the bound body of single-stranded DNA containing a target DNA region and the biotinylated present oligonucleotide is immobilized to a streptavidin-coated support. Then the remaining solution is removed and washing is performed. A washing buffer (for example, a 0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)) is added, for example, in a proportion of 300 μL/well, and the solution is removed. This washing operation is repeated several times, to

leave the bound body of the biotinylated present oligonucleotide and single-stranded DNA containing a target DNA region immobilized on a support on wells (also in this stage, the bound body includes a bound body of single-stranded DNA containing methylated DNA in a target DNA region and the present oligonucleotide, as well as a bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide).

(c) An appropriate amount of a methylated DNA antibody (for example, a 4 μg/mL solution is added in an amount of 100 μL/well) is added to wells, and then left still at room temperature, for example, for about 3 hours, to promote formation of a complex of a methylated DNA antibody, single-stranded DNA containing methylated DNA in a target DNA region in the single-stranded DNA, and the biotinylated present oligonucleotide (formation of a complex)(in this stage, the bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide does not form a complex). Thereafter, the remaining solution is removed and washing is performed. A washing buffer (for example, a 0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)) is added, for example, in a proportion of 300 μL/well, and the solution is removed. This washing operation is repeated several times, to leave the complex on wells (separation of a complex).

The annealing buffer used in (a) is not limited to the annealing buffer described above as far as it is suited for binding between the present oligonucleotide and single-

stranded DNA containing a target DNA region. Use of a buffer in which a bivalent ion, preferably a magnesium ion is dissolved in a concentration of 1 to 600 mM will improve the binding stability.

The washing operation in (b) and (c) is important for removing an unimmobilized methylated DNA antibody suspended in the solution, unmethylated single-stranded DNA that does not bind with a methylated DNA antibody and hence is suspended in the solution, or DNA digested by a restriction enzyme as will be described later and suspended in the solution from the reaction solution. The washing buffer is not limited to the washing buffer described above, insofar as it is suited for removing the free methylated DNA antibody, single-stranded DNA and so on suspended in the solution and the like, and a DELFIA buffer (available from Perkin Elmer, Tris-HCl pH 7.8 with Tween 80), a TE buffer and the like may be used.

As described above, in the above (a) to (c), after binding between the single-stranded DNA containing the target DNA region and the biotinylated present oligonucleotide, the biotinylated present oligonucleotide contained in the resultant bound body is caused to bind with a streptavidin-coated support to form a complex, however, the order is not limited to this. In other words, after binding between the biotinylated present oligonucleotide and a streptavidin-coated support, the single-stranded DNA containing the target DNA region is caused to bind with the resultant bound body, to form a complex. For example, by adding double-stranded DNA contained in a DNA sample derived

from genomic DNA contained in a biological specimen to the biotinylated present oligonucleotide immobilized to a streptavidin-coated support, a mixture of the biotinylated present oligonucleotide immobilized to a support and the double-stranded DNA is obtained. For separating the double-stranded DNA contained in the obtained mixture to obtain single-stranded DNA, the mixture is heated at 95°C, for example, for several minutes. For forming a bound body of the obtained single-stranded DNA and the biotinylated present oligonucleotide, the mixture is rapidly cooled to a temperature lower by about 10 to 20°C than the Tm value of the biotinylated present oligonucleotide, and kept at this temperature, for example, for several minutes. Then the operation of (c) may be conducted to form and separate a complex (in this stage, the bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide does not form a complex).

The operations of (a) to (c) may be conducted using a chromatostrip. In that case, the operations are conducted in the following manner. For example, first, a solution containing a bound body of single-stranded DNA obtained by separating double-stranded DNA contained in a DNA sample derived from genomic DNA contained in a biological specimen and the biotinylated present oligonucleotide is developed by a chromatostrip partially coated with streptavidin. By this operation, the bound body of single-stranded DNA obtained by separating double-stranded DNA contained in a DNA sample derived from genomic DNA contained in a biological specimen

and the biotinylated present oligonucleotide is immobilized to the part coated with streptavidin (the bound body formed in this stage includes not only a bound body of single-stranded DNA containing methylated DNA in a target DNA region and a methylated antibody, but also a bound body of methylated single-stranded DNA other than in a target DNA region and a methylated antibody).

Then an appropriate amount of a methylated DNA antibody is developed by the chromatostrip. By this operation, a complex of single-stranded DNA obtained by separating double-stranded DNA contained in a DNA sample derived from genomic DNA contained in a biological specimen, the biotinylated present oligonucleotide, and a methylated DNA antibody is immobilized to part coated with streptavidin (formation and selection of a complex)(in this stage, the bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide does not form a complex). The order of formation of a complex is not limited to the order of these operations. For example, after forming a complex of single-stranded DNA containing methylated DNA in a target DNA region, the biotinylated present oligonucleotide, and a methylated DNA antibody, the complex may be developed by a chromatostrip and immobilized to the part coated with streptavidin. In these operations, unnecessary components can be removed by developing the solution by a chromatostrip, and a washing operation can be omitted. Of course, a washing operation (development of a chromatostrip by a washing buffer (for example, a 0.05% Tween 20-containing phosphate buffer (1

mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)) may be conducted between operations without causing any problem.

The "identification function" in Third step of the present measuring method is a function based on labeling used for detection or quantification, and concretely, in the case of a methylated DNA antibody, a fluorescent or a chromogenic property of a methylated DNA antibody labeled with europium, gold colloid, latex beads, a radioisotope, a fluorescent substance (FITC or the like), horseradish Peroxidase (HRP), alkaline phosphatase, biotin or the like can be recited, and the own property of an antibody (the property that the antibody itself binds to a secondary antibody) and the like are also recited as this function. On the other hand, in the case of the present oligonucleotide, a fluorescent or chromogenic property of the present oligonucleotide labeled at its 5'-end or 3'-end with europium, gold colloid, latex beads, a radioisotope, a fluorescent substance (FITC or the like), horseradish Peroxidase (HRP), alkaline phosphatase or the like can be recited. For detection or quantification based on such a function, for example, measurement by a radiation detector or a spectrophotometer, or visual check may be used.

In the case of a methylated DNA antibody, as described above, the own property of an antibody may be considered as a function, and even when the antibody itself is not labeled, a methylated DNA antibody can be indirectly detected or quantified by using a secondary antibody to which a detectable or quantifiable function is imparted.

When single-stranded DNA containing a target DNA region is bound to a support via a methylated DNA antibody, the present oligonucleotide is detected or quantified according to its function, whereas when single-stranded DNA containing a target DNA region is bound to a support via the present oligonucleotide, a methylated DNA antibody is detected or quantified according to its function.

When a methylated DNA antibody is detected or quantified according to its function, concretely when the own property of an antibody is used as a function, for example, the operation may be executed in the following manner. A secondary antibody against a methylated DNA antibody (for example, an Eu-N1-labeled mouse IgG antibody: available from Perkin Elmer) is added to a complex, and left still at room temperature for about an hour, to promote binding of the secondary antibody to the complex. Then, Enhancement Solution (available from Perkin Elmer) is added and mixed, and left still, for example, for about 45 minutes at room temperature. Thereafter, the fluorescence (excitation 340 nm/fluorescence 612 nm) is measured by a fluorescent detector to detect or quantify a methylated DNA antibody.

When an antibody to which FITC is bound is used as a secondary antibody, a methylated DNA antibody may be detected or quantified by measuring the fluorescence of FITC by a known method.

Also, for example, when biotin is not used for immobilization of the present oligonucleotide, a biotinylated

methylated DNA antibody may be used for detection or quantification. When a biotinylated methylated DNA antibody is detected or quantified, for example, a biotinylated methylated DNA antibody can be detected or quantified by adding and mixing HRP-labeled streptavidin to a biotinylated methylated DNA antibody, and measuring the activity of HRP by a known method after formation and separation of a bound body of the biotinylated methylated DNA antibody and HRP-labeled streptavidin.

When the present oligonucleotide is detected or quantified according to its function, concretely, for example, a complex is formed using FITC-labeled oligonucleotide labeled with FITC as the present oligonucleotide required for formation of a complex, according to the method as described above, and the complex is separated. For the obtained complex, the fluorescence of FITC is measured by a known method, to detect or quantify the present oligonucleotide. Also a secondary antibody against FITC (for example, an HRP-labeled anti-FITC antibody: available from Jackson ImmunoResearch Laboratories) is added, and left still for about 2 hours at room temperature, to promote binding of a secondary antibody to a complex. Thereafter, an appropriate substrate (for example, Substrate Reagent Pack #DY999: available from R&D SYSTEMS) is added and mixed, and left still, for example, for 5 to 20 minutes at room temperature. Then Stop Solution (1 N H_2SO_4) is added. In 30 minutes after addition, the absorbance at 450 nm is measured by an absorbance detector, and thus the present oligonucleotide may

be detected or quantified.

When biotin is not used for immobilization of a methylated DNA antibody, the biotinylated present oligonucleotide may be used for detection or quantification. When the biotinylated present oligonucleotide is detected or quantified, for example, HRP-labeled streptavidin is added or mixed to the biotinylated present oligonucleotide to form and separate a bound body of the biotinylated present oligonucleotide and HRP-labeled streptavidin, and then the activity of HRP is measured by a known method to detect or quantify a biotinylated methylated DNA antibody.

The present invention also provides a modified method additionally comprising a step of digesting the single-stranded DNA separated in First step by at least one kind of methylation sensitive restriction enzyme capable of digesting single-stranded DNA, between immediately after end of First step of the present measuring method and immediately before start of Third step (Modified method 1), or between immediately after end of First step of the present measuring method and immediately before start of Third step (Modified method 2).

The "methylation-sensitive restriction enzyme" in the modified methods (Modified method 1 and Modified method 2) present invention, for example, a restriction enzyme or the like that does not digest a recognition sequence containing methylated cytosine, but digests only a recognition sequence

containing unmethylated cytosine. In other words, in the case of DNA wherein cytosine contained in a recognition sequence inherently recognizable by the methylation sensitive restriction enzyme is methylated, the DNA will not be cleaved even when the methylation sensitive restriction enzyme is caused to act on the DNA. On the other hand, in the case of DNA wherein cytosine contained in a recognition sequence inherently recognizable by the methylation sensitive restriction enzyme is not methylated, the DNA will be cleaved when the methylation sensitive restriction enzyme is caused to act on the DNA. Concrete examples of such methylation sensitive restriction enzymes include HpaII, BstUI, NarI, SacII, and HhaI. The aforementioned methylation sensitive restriction enzyme will not cleave double-stranded DNA containing a CpG pair in a hemimethyl state (namely, double-stranded DNA wherein cytosine in one strand is methylated and cytosine in the other strand is not methylated in the above CpG pair) and this is already revealed by Gruenbaum et al. (Nucleic Acid Research, 9, 2509-2515). The wording "methylation sensitive restriction enzyme capable of digesting single-stranded DNA" means, for example, a restriction enzyme or the like capable of digesting only a recognition sequence containing unmethylated cytosine without digesting a recognition sequence containing methylated cytosine in single-stranded DNA. Specifically, some methylation sensitive restriction enzymes digest single-stranded DNA. For example, HhaI or the like is recited.

As a fear in a digestion treatment with a methylation

sensitive restriction enzyme, the possibility that the recognition sequence containing unmethylated cytosine may not be completely digested (so called "DNA remaining undigested") is recited. When such a possibility is problematic, the target DNA region has at least one recognition site of a methylation sensitive restriction enzyme, and as many as possible recognition sites would be preferred because it is possible to suppress the "DNA remaining undigested" as much as possible by presence of abundant recognition sites of a methylation sensitive restriction enzyme.

As described above, as to the target DNA region, from the view point of the property of a methylated DNA antibody (one antibody binds to one methylated base (cytosine)), a region where a number of methylated bases (cytosine, CpG) are present is desirably selected as a target DNA region, and from the view point of minimizing "DNA remaining undigested", a region where a number of recognition sites of a methylation sensitive restriction enzyme are present is desirably selected.

The term "masking oligonucleotide" in Modified method 2 means an oligonucleotide having a nucleotide sequence complementary to a nucleotide sequence of a recognition site of a methylation sensitive restriction enzyme, and is an oligonucleotide that forms a double strand by complementary binding with at least one site (even every site is possible, and one or more sites may be concurrently contained in the following 8 to 30 bases depending on the nucleotide sequence

of the target region) of several recognition sequences of a methylation sensitive restriction enzyme contained in a target DNA region in single-stranded DNA (namely, the site is made into a double-stranded state), thereby enabling a methylation sensitive restriction enzyme that uses only double-stranded DNA as a substrate to digest the site, and improving digestion efficiency at the site for a methylation sensitive restriction enzyme capable of digesting single-stranded DNA (a methylation sensitive restriction enzyme capable of digesting single-stranded DNA also digests double-stranded DNA, and digestion efficiency thereof is higher with respect to double-stranded DNA than with respect to single-stranded DNA), and is a nucleotide not inhibiting formation of a bound body between single-stranded DNA containing DNA of a target region and the present oligonucleotide.

As a masking oligonucleotide, more concretely, oligonucleotides having a nucleotide sequence complementary to a nucleotide sequence having a length of 8 to 30 bases containing one specific site (one or more sites may be concurrently contained in the following 8 to 30 bases depending on the nucleotide sequence of the target) among several recognition sequences of a methylation sensitive restriction enzyme contained in a target DNA region in single-stranded DNA, and not inhibiting formation of a bound body of single-stranded DNA containing DNA of a target region and the present oligonucleotide can be recited.

The masking oligonucleotide to be mixed with single-stranded DNA (plus strand) comprising a target DNA region

contained in a DNA sample derived from genomic DNA may be one kind or plural kinds. When plural kinds are used, many of recognition sites of a methylation sensitive restriction enzyme in single-stranded DNA comprising a target DNA region become a double-stranded DNA state, and "DNA remaining undigested" as described above by a methylation sensitive restriction enzyme can be minimized. However, since a methylated DNA antibody is no longer able to bind to the site where a masking oligonucleotide forms double-stranded DNA, it is not appropriate to use a masking oligonucleotide to too much recognition sites of a methylation sensitive restriction enzyme, and it is preferred to use appropriate kinds. If a masking oligonucleotide is used for every recognition site of a methylation sensitive restriction enzyme contained in a target DNA region, binding between a methylated base (cytosine) and a methylated DNA antibody in the recognition site is inhibited, and the probability of formation of a desired complex can be impaired (of course, a methylated DNA antibody binds to CpG other than the recognition site, however when a methylated DNA antibody is detected or quantified, the detection sensitivity and quantification accuracy are impaired). For example, it is particularly useful to use a masking oligonucleotide designed in accordance with a site intended not to be digested when it is methylated and intended to be digested when it is not methylated among several recognition sequences of a methylation sensitive restriction enzyme contained in a target DNA region (for example, the site that is methylated at 100% in a diseased patient specimen, but

is not methylated at 100% in a healthy specimen).

In these Modified methods (Modified method 1 and Modified method 2), by additionally conducting the step of digesting the single-stranded DNA separated in First step by at least one kind of methylation sensitive restriction enzyme capable of digesting single-stranded DNA between after First step and immediately before Third step, it is possible to minimize (exclude) formation of a complex having single-stranded DNA (plus strand) not containing methylated DNA in a target DNA region, so that the detection sensitivity and quantification accuracy of methylated DNA in a target DNA region are improved.

In Modified method 1, the step of digesting the single-stranded DNA separated in First step by at least one kind of methylation sensitive restriction enzyme capable of digesting single-stranded DNA executed between immediately after end of First step and immediately before start of Third step may be concretely executed in the following manner. To 10 μL of a solution containing single-stranded DNA separated in First step, 3 μL of an optimum 10 × buffer, 15 U of a methylation sensitive enzyme (HhaI) capable of digesting a single strand, and an appropriate amount of BSA or the like as necessary are added, and then the resultant mixture is added with sterile ultrapure water to a liquid volume of 30 μL, and then incubated at 37°C, for example, for an hour to overnight. As a result, an HhaI recognition site unmethylated in a target DNA region will be digested (a treatment solution). For example, when this step is executed before formation of a complex, the

treatment solution may be directly used for formation of a complex for executing formation of a complex and/or a washing operation at the time of separation. In executing this step after separation of a complex, since it is necessary to remove single-stranded DNA (digested and generated single-stranded DNA since a recognition site of the methylation sensitive restriction enzyme is not methylated) suspended in the treatment solution from the treatment solution, it is necessary to conduct a washing operation similar to that executed in formation of a complex and/or separation again after end of the step.

In Modified method 2, (i) a step of mixing single-stranded DNA separated in First step, a masking oligonucleotide having a recognition sequence of at least one kind of methylation sensitive restriction enzyme as its part, and (ii) digesting the mixture obtained by the previous step (single-stranded DNA in which DNA is not methylated in a target DNA region that is present therein) by the methylation sensitive restriction enzyme additionally executed between immediately after end of First step and immediately before start of Third step may be executed, for example, in the following manner. To 10 μL of a solution containing single-stranded DNA separated in First step, 3 μL of an optimum 10 × buffer, 15 U of a methylation sensitive enzyme (HhaI, HhaI or the like), about 10 pmol of a masking oligonucleotide for one specific site among recognition sequences of a methylation sensitive enzyme, and an appropriate amount of BSA or the like as necessary are added, and then the resultant mixture is

added with sterile ultrapure water to a liquid volume of 30 μL, and then incubated at 37°C, for example, for an hour to overnight. As a result, the site unmethylated in a target DNA region will be digested (a treatment solution). For example, when this operation is executed before formation of a complex, the treatment solution may be directly used for formation of a complex for executing formation of a complex and/or a washing operation at the time of separation. In executing this operation after separation of a complex, since it is necessary to remove single-stranded DNA (digested and generated single-stranded DNA since a recognition site of the methylation sensitive restriction enzyme is not methylated) suspended in the treatment solution from the treatment solution, it is necessary to conduct a washing operation similar to that executed in formation of a complex and/or separation again after end of the step.

In the present measuring method, in one preferred embodiment, "a DNA sample derived from genomic DNA contained in a biological specimen" is a DNA sample that is preliminarily digested with a restriction enzyme whose recognition cleaving site excludes the target DNA region possessed by the genomic DNA. In forming a bound body of single-stranded DNA separated in First step and the present oligonucleotide, it is expected that the shorter the single-stranded DNA is, the better the operability is as well as the more easily a complex is formed insofar as methylated DNA is contained in a target DNA region. To shorten the single-

stranded DNA, it is efficient to make it short when it is in former genomic DNA. Therefore, it is preferred to conduct a digestion treatment using a restriction enzyme whose recognition cleaving site excludes a target DNA region on a DNA sample derived from genomic DNA contained in a biological specimen as a pretreatment. As a method of the digestion treatment by a restriction enzyme whose recognition cleaving site excludes a target DNA region, a generally known restriction enzyme treatment method may be used. When the above DNA sample is a DNA sample preliminarily purified, a digestion treatment may be executed using a generally used amount of a restriction enzyme, whereas when a biological specimen is a tissue lysate, a cell lysate or the like, a digestion treatment may be conducted using an amount of 500 times or more the DNA amount of a restriction enzyme.

In one preferred embodiment, "a DNA sample derived from genomic DNA contained in a biological specimen" is a DNA sample that is digested with at least one kind of methylation sensitive restriction enzyme. By preliminarily digesting a biological specimen itself with a methylation sensitive restriction enzyme, it is possible to improve the accuracy of detection or quantification of methylated DNA in Third step. This method is useful for eliminating "DNA remaining undigested" as described above. As a method of digesting a biological specimen itself with a methylation sensitive restriction enzyme, when genomic DNA contained in a biological specimen exists in the condition of double-stranded DNA, a generally known restriction enzyme treatment may be conducted

using a methylation sensitive restriction enzyme. On the other hand, when genomic DNA contained in a biological specimen exists in the condition of single-stranded DNA or when genomic DNA contained in a biological specimen exists in the condition of combination of double-stranded DNA and single-stranded DNA, a digestion treatment may be conducted by the method according to Modified method 1 or Modified method 2. Concretely, for example, to 10 μL of a specimen solution, 5 μL of an optimum 10 × buffer, 15 U of a methylation sensitive enzyme (HhaI) capable of digesting single-stranded DNA, and an appropriate amount of BSA or the like as necessary are added, and then the resultant mixture is added with sterile ultrapure water to a liquid volume of 50 μL, and then incubated at 37°C, for example, for an hour to overnight. Alternatively, to 10 μL of a specimen solution, 5 μL of an optimum 10 × buffer, 15 U of a methylation sensitive restriction enzyme (HpaII, HhaI or the like), about 15 pmol of a masking oligonucleotide for one specific site among recognition sequences of the methylation sensitive enzyme, and then the resultant mixture is added with sterile ultrapure water to a liquid volume of 50 μL, and then incubated at 37°C, for example, for an hour to overnight. When the biological specimen is a specimen preliminarily purified, a digestion treatment may be executed using a generally used amount of a restriction enzyme, whereas when a biological specimen is a tissue lysate, or a cell lysate, a digestion treatment may be conducted using a large excess of a methylation sensitive restriction enzyme, for example, an amount of 500 times or

more DNA amount of a methylation sensitive restriction enzyme.

In a preferred embodiment in separating double-stranded DNA contained in a DNA sample derived from genomic DNA into single-stranded DNA in First step, a counter oligonucleotide may be added. The counter oligonucleotide is an oligonucleotide obtained by dividing a nucleotide sequence same as that of a target DNA region into shorter oligonucleotides. It is designed to have a length of usually 10 to 100 bases, and more preferably 20 to 50 bases. Preferably, a counter oligonucleotide is designed not to contain a nucleotide sequence that complementary binds to a nucleotide sequence on the aforementioned oligonucleotide required for complementary binding between the aforementioned methylated single-stranded DNA containing a target DNA region and the aforementioned oligonucleotide. The counter oligonucleotide is added in large excess relative to genomic DNA, and is added so as to prevent a complementary strand (minus strand) of a target DNA region and a single strand (plus strand) of a target DNA region from re-binding by complementation when binding with an immobilized methylated DNA antibody is caused after making a target DNA region into single strand (plus strand). Preferably, a counter oligonucleotide is added in an amount of at least 10 times, usually 100 times or more relative to a target DNA region.

"Adding a counter oligonucleotide in separating double-stranded DNA contained in a DNA sample derived from genomic DNA into single-stranded DNA in First step" is conducted, for

the purpose of mixing a DNA sample derived from genomic DNA contained in a biological specimen with a counter oligonucleotide, to form a double strand between a complementary strand of a target DNA region and a counter oligonucleotide, thereby making a target DNA region into a single strand. When a target DNA region is in a single strand state, it is intended to facilitate binding between (ii) a methylated DNA antibody, and (iii) an oligonucleotide capable of binding with the single-stranded DNA without inhibiting binding between the methylated DNA antibody and methylated DNA in a target DNA region in Second step. The counter oligonucleotide is not designed on a nucleotide sequence where (iii) an oligonucleotide capable of binding with the single-stranded DNA without inhibiting binding between the methylated DNA antibody and methylated DNA in a target DNA region complementarily binds with the methylated DNA.

That is, a counter oligonucleotide is mixed with (i) single-stranded DNA separated in First step, (ii) a methylated DNA antibody, and (iii) an oligonucleotide capable of binding with the single-stranded DNA without inhibiting binding between the methylated DNA antibody and methylated DNA in a target DNA region, to facilitate formation of a complex of methylated single-stranded DNA containing a target DNA region, a methylated DNA antibody, and the oligonucleotide, and may be added in separating single-stranded DNA in First step or added in forming the complex in Second step.

When a counter oligonucleotide is added, for example, in First step, it may be added in First step for separating

double-stranded DNA contained in a DNA sample derived from genomic DNA contained in a biological specimen into single-stranded DNA. Concretely, the DNA sample and the counter oligonucleotide are added to 5 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithiothreitol), 5 μL of a 100 mM $MgCl_2$ solution, and 5 μL of a 1 mg/mL BSA solution, and the resultant mixture is added with sterile ultrapure water to a liquid volume of 50 μL, and mixed, heated at 95°C for 10 minutes, rapidly cooled to 70°C, kept at this temperature for 10 minutes, then cooled to 50°C, kept at this temperature for 10 minutes, and then kept at 37°C for 10 minutes and returned to room temperature.

In a preferred embodiment in adding a counter oligonucleotide, the binding is caused in a reaction system containing a bivalent positive ion. More preferably, a bivalent positive ion is a magnesium ion. Here, the "reaction system containing a bivalent positive ion" means such a reaction system that contains a bivalent positive ion in an annealing buffer used for binding between the single-stranded DNA (plus strand) and the single-stranded immobilized oligonucleotide, and concretely, it is preferred to contain, for example, a salt composed of a magnesium ion (for example, $MgOAc_2$, $MgCl_2$ and so on) in a concentration of 1 mM to 600 mM.

As a method of detecting or quantifying minor substances contained in a biological sample such as blood or urine, immunological measuring methods are generally used. Among such immunological measuring methods, a so-called

immunochromatography using chromatography is widely used in various situations including, for example, clinical examinations in hospitals, assays in laboratories and so on because of its simple operation and short time required for assay. In recent years, a so-called hybrid chromatography has been utilized in which labeled DNA (gene) is developed on a chromatostrip, and target DNA (gene) is detected by hybridization using a probe capable of capturing the target DNA (gene). Also this method is now coming to be widely used in situations including, for example, clinical examinations in hospitals, assays in laboratories and so on because of its simple operation and short time required for assay. The present measuring method conceptually enables a combined method of the immunochromatography and the hybrid chromatography. In the present measuring method, since the order is not particularly limited in terms of formation of a complex and separation of a complex, various methods are possible. Concretely, the following methods may be executed.

Method 1: A sample immediately after end of First step is added with the biotinylated present oligonucleotide, to cause formation of a bound body of single-stranded DNA containing a target DNA region and the biotinylated present oligonucleotide (the bound body formed in this stage includes not only a bound body of single-stranded DNA containing methylated DNA in a target DNA region and the present oligonucleotide, but also a bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide), and added with a methylated antibody

having an identification function, to cause formation of a complex of single-stranded DNA containing methylated DNA in a target DNA region, the biotinylated present oligonucleotide, and a methylated DNA antibody having an identification function (in this stage, the bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide does not form a complex). Upon dropping (introduction) of the obtained sample into an introduction part of a chromatostrip, the complex migrates in a development part by a capillary phenomenon, and is trapped in the part preliminarily coated with streptavidin. Thereafter, by detecting or quantifying a methylated DNA antibody contained in the separated complex, according to its identification function, methylated DNA in a target DNA region can be detected or quantified.

Method 2: A sample immediately after end of First step is added with the biotinylated present oligonucleotide, to cause formation of a bound body of single-stranded DNA containing a target DNA region and the biotinylated present oligonucleotide (the bound body formed in this stage includes not only a bound body of single-stranded DNA containing methylated DNA in a target DNA region and the present oligonucleotide, but also a bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide). Upon dropping (introduction) of the obtained sample into an introduction part of a chromatostrip, the bound body migrates in a development part by a capillary phenomenon, and is trapped in the part preliminarily coated

with streptavidin (also in this stage, the bound body includes not only a bound body of single-stranded DNA containing methylated DNA in a target DNA region and the present oligonucleotide, but also a bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide). Then, upon dropping (introduction) of a methylated antibody having an identification function into an introduction part, it migrates in a development part and binds to methylated cytosine of the bound body, to form a complex of single-stranded DNA containing methylated DNA in a target DNA region, the biotinylated present oligonucleotide, and a methylated DNA antibody having an identification function (in this stage, the bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide does not form a complex). By detecting or quantifying a methylated DNA antibody contained in the obtained complex according to its identification function, methylated DNA in a target DNA region can be detected or quantified.

Method 3: Upon dropping (introduction) of the biotinylated present oligonucleotide into an introduction part of a chromatostrip, the oligonucleotide migrates in a development part by a capillary phenomenon, and is trapped in the part preliminarily coated with streptavidin. Then, upon dropping (introduction) of a sample immediately after end of First step into an introduction part, it migrates in a development part, and is trapped by the biotinylated present oligonucleotide that has been already trapped in the condition

that single-stranded DNA containing a target DNA region forms a bound body (the bound body formed in this stage includes not only a bound body of single-stranded DNA containing methylated DNA in a target DNA region and the present oligonucleotide, but also a bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide). Then, upon dropping (introduction) of a methylated antibody having an identification function into an introduction part, it migrates in a development part, and binds to methylated cytosine of the bound body, to form a complex of single-stranded DNA containing methylated DNA in a target DNA region, the biotinylated present oligonucleotide, and a methylated DNA antibody having an identification function (in this stage, the bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide does not form a complex). By detecting or quantifying a methylated DNA antibody contained in the obtained complex according to its identification function, methylated DNA in a target DNA region can be detected or quantified.

Method 4: Upon dropping (introduction) of the biotinylated present oligonucleotide into an introduction part of a chromatostrip, the oligonucleotide migrates in a development part by a capillary phenomenon, and is trapped in the part preliminarily coated with streptavidin. A sample immediately after end of First step is added with a methylated DNA antibody having an identification function, to form a bound body of single-stranded DNA having methylated cytosine

(in which single-stranded DNA containing a target DNA region and single-stranded DNA other than the target are present) and a methylated DNA antibody having an identification function (the bound body formed in this stage includes not only a bound body of single-stranded DNA containing methylated DNA in a target DNA region and a methylated antibody, but also a bound body of methylated single-stranded DNA other than in a target DNA region and a methylated antibody). Upon dropping (introduction) of the obtained bound body into an introduction part, it migrates in a development part, and single-stranded DNA containing methylated DNA in a target DNA region binds to the biotinylated present oligonucleotide that has been already trapped, to form a complex of single-stranded DNA containing methylated DNA in a target DNA region, the biotinylated present oligonucleotide, and a methylated DNA antibody having an identification function (in this stage, the bound body of methylated single-stranded DNA other than in a target DNA region and a methylated antibody does not form a complex). By detecting or quantifying a methylated DNA antibody contained in the obtained complex according to its identification function, methylated DNA in a target DNA region can be detected or quantified.

Method 5: A sample immediately after end of First step is added with the present oligonucleotide having an identification function, to form a bound body of single-stranded DNA containing a target DNA region and the present oligonucleotide having an identification function (the bound body formed in this stage includes not only a bound body of

single-stranded DNA containing methylated DNA in a target DNA region and the present oligonucleotide, but also a bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide), and then added with a biotinylated methylated antibody, to form a complex of single-stranded DNA containing methylated DNA in a target DNA region, the present oligonucleotide having an identification function, and a biotinylated methylated DNA antibody (in this stage, the bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide does not form a complex). Upon dropping (introduction) of the obtained sample into an introduction part of a chromatostrip, the complex migrates in a development part by a capillary phenomenon, and is trapped in the part preliminarily coated with streptavidin. Then by detecting or quantifying the present oligonucleotide contained in the obtained complex according to its identification function, methylated DNA in a target DNA region can be detected or quantified.

Method 6: A sample immediately after end of First step is added with a biotinylated methylated DNA antibody, to form a bound body of single-stranded DNA having methylated cytosine (in which single-stranded DNA containing a target DNA region and single-stranded DNA other than the target are present) and a biotinylated methylated DNA antibody (the bound body formed in this stage includes not only a bound body of single-stranded DNA containing methylated DNA in a target DNA region and a methylated antibody, but also a bound body of methylated

single-stranded DNA other than in a target DNA region and a methylated antibody). Upon dropping (introduction) of the obtained sample into an introduction part of a chromatostrip, the bound body migrates in a development part by a capillary phenomenon, and is trapped in the part preliminarily coated with streptavidin (also in this stage, the bound body includes not only a bound body of single-stranded DNA containing methylated DNA in a target DNA region and a methylated antibody, but also a bound body of methylated single-stranded DNA other than in a target DNA region and a methylated antibody). Then, upon dropping (introduction) of the present oligonucleotide having an identification function into an introduction part, it migrates in a development part, and binds only to methylated single-stranded DNA containing a target DNA region of a bound body, to form a complex of single-stranded DNA containing methylated DNA in a target DNA region, the present oligonucleotide having an identification function, and a biotinylated methylated DNA antibody (in this stage, the bound body of methylated single-stranded DNA other than in a target DNA region and a methylated antibody does not form a complex). By detecting or quantifying the present oligonucleotide contained in the obtained complex according to its identification function, methylated DNA in a target DNA region can be detected or quantified.

Method 7: Upon dropping (introduction) of a biotinylated methylated DNA antibody into an introduction part of a chromatostrip, the methylated DNA antibody migrates in a development part by a capillary phenomenon, and is trapped in

the part preliminarily coated with streptavidin. Then, upon dropping (introduction) of a sample immediately after end of First step into an introduction part, it migrates in a development part, and single-stranded DNA having methylated cytosine is trapped as a bound body by a methylated DNA antibody that has been already trapped (the bound body formed in this stage includes not only a bound body of single-stranded DNA containing methylated DNA in a target DNA region and a methylated antibody, but also a bound body of methylated single-stranded DNA other than in a target DNA region and a methylated antibody). Then, upon dropping (introduction) of the present oligonucleotide having an identification function, it migrates in a development part, and binds only to methylated single-stranded DNA containing a target DNA region of the bound body, to form a complex of single-stranded DNA containing methylated DNA in a target DNA region, the present oligonucleotide having an identification function, and a biotinylated methylated DNA antibody (in this stage, the bound body of methylated single-stranded DNA other than in a target DNA region and a methylated antibody does not form a complex). By detecting or quantifying the present oligonucleotide contained in the obtained complex according to its identification function, methylated DNA in a target DNA region can be detected or quantified.

Method 8: Upon dropping (introduction) of a biotinylated methylated DNA antibody into an introduction part of a chromatostrip, the methylated DNA antibody migrates in a development part by a capillary phenomenon, and is trapped in

the part preliminarily coated with streptavidin. A sample immediately after end of First step is added with the present oligonucleotide having an identification function, to form a bound body of single-stranded DNA containing a target DNA region and the present oligonucleotide having an identification function (the bound body formed in this stage includes not only a bound body of single-stranded DNA containing methylated DNA in a target DNA region and the present oligonucleotide, but also a bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide). Then, upon dropping (introduction) of the obtained bound body into an introduction part, it migrates in a development part, and only single-stranded DNA containing methylated DNA in a target DNA region of the bound body binds with a methylated DNA antibody that has been already trapped, to form a complex of single-stranded DNA containing methylated DNA in a target DNA region, the present oligonucleotide having an identification function, and a biotinylated methylated DNA antibody (in this stage, the bound body of single-stranded DNA not containing methylated DNA in a target DNA region and the present oligonucleotide does not form a complex). By detecting or quantifying the present oligonucleotide contained in the obtained complex according to its identification function, methylated DNA in a target DNA region can be detected or quantified.

Also a plurality of detection sites may be provided on a single chromatostrip (the present oligonucleotides capable of trapping different target DNA regions are immobilized to a

support), and each target DNA region may be sequentially detected or quantified, and by enabling one detection site to trap a plurality of target DNA regions, or by immobilizing a number of the present oligonucleotides capable of trapping a plurality of target DNA regions on one detection site, it is possible to dramatically improve the detection sensitivity. Also, using a number of the present oligonucleotides having an identification function capable of trapping a plurality of target DNA regions so as to allow formation of a complex with a plurality of target DNA regions will also improve the detection sensitivity dramatically. Further, designing a number of the present oligonucleotides in a single target region, and using these on the side of a support or on the side of detection will also improve the detection sensitivity dramatically.

The restriction enzyme, the present oligonucleotide, or the methylated DNA antibody which may be used in the present measuring method as described above is useful as a reagent in a detection kit. The present measuring method also provides a detection kit containing such a restriction enzyme, the present oligonucleotide, or a methylated DNA antibody and so on as a regent, and a detection chip including a support on which the present oligonucleotide, or a methylated DNA antibody and so on is immobilized, and the scope of the present measuring method implies use in the form of a detection kit or a detection chip as described above utilizing a substantial principle of the method.

Examples

In the following, the present invention will be explained in detail by way of examples, which are not intended to limit the present invention.

Example 1

Methylated oligonucleotides M1, M2, M3, and M4 having the nucleotide sequences of SEQ ID NOs: 17, 18, 19, and 20, and unmethylated oligonucleotides U1, U2, U3, and U4 having the nucleotide sequences of SEQ ID NOs: 21, 22, 23, and 24 labeled with biotin at 5'-end were synthesized, and the following solutions in TE buffer (10 mM Tris, 1 mM EDTA, pH 8.0) were prepared for each oligonucleotide.

Solution A: 2.5 pmol/100 µL solution in TE buffer

Solution B: 0.25 pmol/100 µL solution in TE buffer

Solution C: 0.025 pmol/100 µL solution in TE buffer

Solution D: 0.0025 pmol/100 µL solution in TE buffer

Solution E: 0.00025 pmol/100 µL solution in TE buffer

Solution F: 0 pmol/100 µL solution in TE buffer (negative control solution)

Then, for each solution (Solution A to Solution F), a methylated oligonucleotide mixed solution M0 in which equivalent amounts of respective solutions of the methylated oligonucleotides M1, M2, M3, and M4 are mixed, and a methylated oligonucleotide mixed solution U0 in which equivalent amounts of respective solutions of the unmethylated oligonucleotides U1, U2, U3, and U4 are mixed were prepared.

<5'-end biotin-labeled methylated oligonucleotides>

N represents methylated cytosine.

M1: 5'-ANGAANGTANGGANGC-3' (SEQ ID NO: 17)

M2: 5'-TNGATNGTTNGGTNGC-3' (SEQ ID NO: 18)

M3: 5'-GNGAGNGTGNGGGNGC-3' (SEQ ID NO: 19)

M4: 5'-CNGACNGTCNGGCNGC-3' (SEQ ID NO: 20)

<5'-end biotin-labeled unmethylated oligonucleotides>

U1: 5'-ACGAACGTACGGACGC-3' (SEQ ID NO: 21)

U2: 5'-TCGATCGTTCGGTCGC-3' (SEQ ID NO: 22)

U3: 5'-GCGAGCGTGCGGGCGC-3' (SEQ ID NO: 23)

U4: 5'-CCGACCGTCCGGCCGC-3' (SEQ ID NO: 24)

For each of the obtained solutions, the following treatment was executed (each solution was prepared in duplicate).

Each 100 µL of a 5'-end biotin-labeled oligonucleotide mixed solution (Solution A to Solution F of M0 and U0) prepared above was added to a 96-well plate coated with streptavidin, subjected to a plate shaker for about 10 seconds, and left still for about 30 minutes at room temperature, and thus the 5'-end biotin-labeled methylated oligonucleotide, or the 5'-end biotin-labeled unmethylated oligonucleotide was immobilized to the plate. After being left still, the solution in the plate was removed by decantation, and then each well in the plate was washed three times with 300 µL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154

mM NaCl, pH 7.4)].

After adding each of the wells with 100 µL of a methylated cytosine antibody [available from Aviva Systems Biology, a 1 or 10 µg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], the reaction was left still for 2 hours at room temperature. After being left still, each well was washed three times with 300 µL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Then, after adding each of the wells with 100 µL of an HRP-labeled mouse IgG antibody [available from Santa Cruz Biotechnology, 0.05 µg/100 µL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], the reaction was left still for 2 hours at room temperature. After being left still, each well was washed three times with 300 µL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and 100 µL of a substrate (available from R&D, #DY999) was added and mixed to each of the wells to start a reaction.

After being left still for about 20 minutes at room temperature, each well was added with 50 µL of a stop solution (1 N H_2SO_4 aqueous solution) to stop the reaction. The absorbance at 450 nm of the sample obtained within 30 minutes after stop of the reaction was measured.

The results are shown in Fig. 1 and Fig. 2. It was revealed that the immobilized 5'-end biotin-labeled methylated

oligonucleotide M0 is detected and quantified with very good sensitivity compared with the immobilized 5'-end biotin-labeled unmethylated oligonucleotide U0. It was also suggested that use of too much methylated antibody (10 µg/mL, Fig. 2) results in occurrence of non-specific binding in Solution A and Solution B containing a large amount of the immobilized 5'-end biotin-labeled unmethylated oligonucleotide.

These demonstrate that a methylated DNA fragment can be detected and quantified in the present measuring method using a methylated cytosine antibody.

Example 2

A methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 25, and an unmethylated oligonucleotide UBC-UM8 having the nucleotide sequence of SEQ ID NO: 26 were synthesized, and the following solutions in TE buffer were prepared for each oligonucleotide.

Solution A: 0.1 pmol/10 µL solution in TE buffer

Solution B: 0.01 pmol/10 µL solution in TE buffer

Solution C: 0.001 pmol/10 µL solution in TE buffer

Solution D: 0 pmol/10 µL solution in TE buffer (negative control solution)

<Methylated oligonucleotide> N represents methylated cytosine.

UBC-M8: 5'-ANGAANGTANGGANGCTNGATNGTTNGGTNGCCTGTCTGACTACAACATCCAGA-3' (SEQ ID NO: 25)

<Unmethylated oligonucleotide>

UBC-U8: 5′-ACGAACGTACGGACGCTCGATCGTTCGGTCGCCTGTCTGACTACAACATCCAGA-3′ (SEQ ID NO: 26)

Also, a 5′-end biotin-labeled oligonucleotide B1 having the nucleotide sequence of SEQ ID NO: 27 was synthesized, and a 0.002 μM solution in TE buffer was prepared.

<5′-end biotin-labeled oligonucleotide>

B1: 5′-TCTGGATGTTGTAGTCAGACAG-3′ (SEQ ID NO: 27)

For each solution of the obtained methylated oligonucleotide, or unmethylated oligonucleotide, the following treatment was executed (each solution was prepared singly).

To a PCR tube were added 10 μL of the oligonucleotide solution prepared above, 50 μL of the 5′-end biotin-labeled oligonucleotide solution, 10 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithiothreitol), and the mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed. Then the PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at that temperature for 10 minutes. Then the PCR tube was cooled to 50°C and kept at this temperature for 10 minutes, and then kept at 37°C for 10 minutes, and then returned to room temperature to promote formation of a bound body of a 5′-end biotin-labeled oligonucleotide and an

oligonucleotide.

Every obtained mixture was transferred to a 96-well plate coated with streptavidin, and left still for about 30 minutes at room temperature, to immobilize the bound body of a 5′-end biotin-labeled oligonucleotide and an oligonucleotide onto the plate. After being left still, the solution in the plate was removed by decantation, and then each well in the plate was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Each of the wells was added with 100 μL of a methylated cytosine antibody [available from Aviva Systems Biology, a 1 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and left still for an hour at room temperature. After being left still, each of the wells was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Then, each of the wells was added with 100 μL of an Eu-N1 labeled mouse IgG antibody [available from Perkin Elmer, a 0.25 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)] and left still for an hour at room temperature. After being left still, each of the wells was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

By adding and mixing 200 μL of Enhancement Solution (available from Perkin Elmer) into each of the wells, a

reaction was started. Then after being left still for about 3 minutes at room temperature, the fluorescence of the obtained sample was measured with excitation 340 nm/fluorescence 612 nm.

The result is shown in Fig. 3. It was revealed that the methylated oligonucleotide UBC-M8 is selected with higher accuracy and detected and quantified with higher sensitivity by an immobilized 5'-end biotin-labeled oligonucleotide B1 compared with the unmethylated oligonucleotide UBC-U8.

These demonstrate that it is possible to form and separate a complex of a methylated cytosine antibody, a methylated DNA fragment, and an immobilized 5'-end biotin-labeled oligonucleotide, and to detect and quantify a methylated cytosine antibody in the complex according to its identification function, and to detect and quantify a methylated DNA fragment by the present measuring method.

Example 3

A methylated oligonucleotide UBC-M having the nucleotide sequence of SEQ ID NO: 28, a partially methylated oligonucleotide UBC-HM having the nucleotide sequence of SEQ ID NO: 29, and an unmethylated oligonucleotide UBC-UM having the nucleotide sequence of SEQ ID NO: 30 were synthesized, and the following solutions in TE buffer were prepared for each oligonucleotide.

Solution A: 0.1 pmoL/10 μL solution in TE buffer

Solution B: 0.01 pmoL/10 μL solution in TE buffer

Solution C: 0.001 pmoL/10 μL solution in TE buffer

Solution D: TE buffer solution (negative control solution)

<Methylated oligonucleotide> N represents methylated cytosine.

UBC-M: 5′-
AGTGACACCATNGAGAATGTCAGATCNGGATCAGAGNGCCATCTAGATGGACATGTCACTGT
CTGACTACAACATCCAGA-3′ (SEQ ID NO: 28)

<Partially methylated oligonucleotide> N represents methylated cytosine.

UBC-HM: 5′-
AGTGACACCATNGAGAATGTCAGATCCGGATCAGAGCGCCATCTAGATGGACATGTCACTGT
CTGACTACAACATCCAGA-3′ (SEQ ID NO: 29)

<Unmethylated oligonucleotide>

UBC-UM: 5′-
AGTGACACCATCGAGAATGTCAGATCCGGATCAGAGCGCCATCTAGATGGACATGTCACTGT
CTGACTACAACATCCAGA-3′ (SEQ ID NO: 30)

For each obtained solution, the following treatment was executed (each solution was prepared singly).

Group A (no treatment group): After adding 10 μL of an oligonucleotide solution prepared as described above, 5 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithiothreitol), and 5 μL of BSA (Bovine serum albumin 1 mg/mL) to a PCR tube, 5 pmol of an oligonucleotide MA having the nucleotide sequence of SEQ ID NO: 31 was added as a masking oligonucleotide, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 50 μL, and mixed.

Group B (HhaI treatment group): After adding 10 μL of an oligonucleotide solution prepared as described above, 5 U of

HhaI, 5 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithiothreitol), and 5 μL of BSA (Bovine serum albumin 1 mg/mL) to a PCR tube, 5 pmol of an oligonucleotide MA having the nucleotide sequence of SEQ ID NO: 31 was added as a masking oligonucleotide, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 50 μL, and mixed.

<Masking oligonucleotide>

MA: 5'-GATGGCGCTCTG-3' (SEQ ID NO: 31)

After incubating each reaction solution at 37°C for 15 hours, 50 μL of a 0.002 μM solution of the 5'-end biotin-labeled oligonucleotide B1 having the nucleotide sequence of SEQ ID NO: 32 in TE buffer was added to this and mixed.

<5'-end biotin-labeled oligonucleotide>

B1: 5'-TCTGGATGTTGTAGTCAGACAG-3' (SEQ ID NO: 32)

Then the PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Then the tube was cooled to 50°C, kept at this temperature for 10 minutes, and then kept at 37°C for 10 minutes, and returned to room temperature, to promote formation of a bound body of a 5'-end biotin-labeled oligonucleotide and an oligonucleotide.

Every obtained mixture was transferred to a 96-well plate coated with streptavidin, and left still for about 30

minutes at room temperature, to immobilize the bound body of a 5'-end biotin-labeled oligonucleotide and an oligonucleotide onto the plate. After being left still, the solution in the plate was removed by decantation, and then each well in the plate was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Each of the wells was added with 100 μL of a methylated cytosine antibody [available from Aviva Systems Biology, a 1 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and left still for an hour at room temperature. After being left still, the solution was removed by decantation from each well, and each of the wells was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Then, each of the wells was added with 100 μL of an Eu-N1 labeled mouse IgG antibody [available from Perkin Elmer, a 0.25 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)] and left still for an hour at room temperature. After being left still, the solution was removed by decantation from each well, and each of the wells was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

By adding and mixing 200 μL of Enhancement Solution (available from Perkin Elmer) into each of the wells, a reaction was started. Then after being left still for about

45 minutes at room temperature, the fluorescence of the obtained sample was measured with excitation 340 nm/fluorescence 612 nm.

The results are shown in Fig. 4 and Fig. 5. In the case of Group A (no treatment group) (Fig. 4), it was revealed that in the methylated oligonucleotide UBC-M where all of three sites among three sites of CG sequences are methylated, it is possible to form and separate a complex of an immobilized 5'-end biotin-labeled oligonucleotide B1 and a methylated cytosine antibody, and to detect and quantify the complex with very high sensitivity by a biotin label in the complex. On the other hand, in a partially methylated oligonucleotide UBC-HM where only one site among three sites of CG sequences is methylated, it was revealed that a complex of an immobilized 5'-end biotin-labeled oligonucleotide B1 and a methylated cytosine antibody was formed and separated, and detected and quantified with a sensitivity of about 1/3 of that in the UBC-M. In the unmethylated oligonucleotide UBC-UM where no site among three sites of CG sequences is methylated, since a complex of an immobilized 5'-end biotin-labeled oligonucleotide B1 and a methylated cytosine antibody was not formed and separated, a value approximately equal to a background value (data of Solution D) was exhibited. In the case of Group B (HhaI treatment group) (Fig. 5), it was revealed that in the methylated oligonucleotide UBC-M where all of three sites among three sites of CG sequences are methylated, since it is not digested by a methylation sensitive restriction enzyme (HhaI), a complex of an

immobilized 5'-end biotin-labeled oligonucleotide B1 and a methylated cytosine antibody is formed and separated, and detected and quantified with excellent sensitivity by a biotin label in the complex as is the case with Group A (no treatment group). In a partially methylated oligonucleotide UBC-HM where only one site among three sites of CG sequences is methylated, a methylated CG sequence is lost by digestion by a methylation sensitive restriction enzyme (HhaI). Therefore, a complex is not formed and separated, and the value was approximately equal to the background value (data of Solution D). In the unmethylated oligonucleotide UBC-UM where no site among three sites of CG sequences is methylated, since a complex is not formed and separated, the value was approximately equal to the background value as is the case with A treatment group (no treatment group).

From the above, it was revealed that by a digesting treatment with a methylation sensitive restriction enzyme, a partially methylated DNA fragment can be digested, and by forming and separating a complex of a methylated cytosine antibody, a methylated DNA fragment, and an immobilized 5'-end biotin-labeled oligonucleotide, and detecting and quantifying the methylated cytosine antibody in the complex according to its identification function, it is possible to detect and quantify a methylated DNA fragment.

Example 4

A methylated oligonucleotide UBC86-M having the nucleotide sequence of SEQ ID NO: 33, and a partially

methylated oligonucleotide UBC118-HM having the nucleotide sequence of SEQ ID NO: 34 were synthesized, and the following solutions in TE buffer were prepared for each oligonucleotide.

Solution A: 0.1 pmoL/10 μL solution in TE buffer

Solution B: 0.01 pmoL/10 μL solution in TE buffer

Solution C: 0.001 pmoL/10 μL solution in TE buffer

Solution D: TE buffer solution (negative control solution)

<Methylated oligonucleotide> N represents methylated cytosine.

UBC86-M: 5'-
AGTGACACCATNGAGAATGTCAGATCNGGATCAGAGNGCCATCTACNGGATGGACATGNGCT
CACTGTCTGACTACAACATCCAGA-3' (SEQ ID NO: 33)

<Partially methylated oligonucleotide> N represents methylated cytosine.

UBC118-HM: 5'-
AGTGACACCATNGAGAATGTCAGANGATNGATNGTANGTANGGANGCTNGGTNGCATCNGGA
TCAGAGCGCCATCTACNGGATGGACATGNGCTCACTGTCTGACTACAACATCCAGA-3'
(SEQ ID NO: 34)

For each obtained solution, the following treatment was executed (each solution was prepared singly).

Group A (no treatment group): After adding 10 μL of an oligonucleotide solution prepared as described above, 5 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithiothreitol), and 5 μL of BSA (Bovine serum albumin 1 mg/mL) to a PCR tube, 5 pmol of an oligonucleotide MA having the nucleotide sequence of SEQ ID NO: 35 was added as a masking oligonucleotide, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 50

μL, and mixed.

Group B (HhaI treatment group): After adding 10 μL of an oligonucleotide solution prepared as described above, 5 U of HhaI, 5 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithiothreitol), and 5 μL of BSA (Bovine serum albumin 1 mg/mL) to a PCR tube, 5 pmol of an oligonucleotide MA having the nucleotide sequence of SEQ ID NO: 35 was added as a masking oligonucleotide, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 50 μL, and mixed.

<Masking oligonucleotide>

MA: 5'-GATGGCGCTCTG-3' (SEQ ID NO: 35)

After incubating each reaction solution at 37°C for 16 hours, 50 μL of a 0.002 μM solution of the 5'-end biotin-labeled oligonucleotide B1 having the nucleotide sequence of SEQ ID NO: 36 in TE buffer was added to this and mixed.

<5'-end biotin-labeled oligonucleotide>

B1: 5'-TCTGGATGTTGTAGTCAGACAG-3' (SEQ ID NO: 36)

Then the PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Then the tube was cooled to 50°C, kept at this temperature for 10 minutes, and then kept at 37°C for 10 minutes, and returned to room temperature, to promote formation of a bound body of a 5'-end biotin-labeled

oligonucleotide and an oligonucleotide.

Every obtained mixture was transferred to a 96-well plate coated with streptavidin, and left still for about 30 minutes at room temperature, to immobilize the bound body of a 5'-end biotin-labeled oligonucleotide and an oligonucleotide onto the plate. After being left still, the solution in the plate was removed by decantation, and then each well in the plate was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Each of the wells was added with 100 μL of a methylated cytosine antibody [available from Aviva Systems Biology, a 1 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and left still for an hour at room temperature. After being left still, the solution was removed by decantation from each well, and each of the wells was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Then, each of the wells was added with 100 μL of an Eu-N1 labeled mouse IgG antibody [available from Perkin Elmer, a 0.25 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)] and left still for an hour at room temperature. After being left still, the solution was removed by decantation from each well, and each of the wells was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

By adding and mixing 200 μL of Enhancement Solution (available from Perkin Elmer) into each of the wells, a reaction was started. Then after being left still for about 45 minutes at room temperature, the fluorescence of the obtained sample was measured with excitation 340 nm/fluorescence 612 nm.

The results are shown in Fig. 6 and Fig. 7. In the case of Group A (no treatment group) (Fig. 6), it was revealed that in the methylated oligonucleotide UBC86-M where all of five sites among five sites of CG sequences are methylated, a complex of an immobilized 5'-end biotin-labeled oligonucleotide and a methylated cytosine antibody can be formed and separated, and detected and quantified with high sensitivity by a biotin label in the complex. On the other hand, it was revealed that in the partially methylated oligonucleotide UBC118-HM where 12 sites among 13 sites of CG sequences are methylated, sensitivity of detection and quantification was about 1.4 times that in UBC86-M. In the case of Group B (HhaI treatment group) (Fig. 7), it was revealed that in the methylated oligonucleotide UBC86-M where all of five sites among five sites of CG sequences are methylated, since it is not digested by a methylation sensitive restriction enzyme (HhaI), a complex of an immobilized 5'-end biotin-labeled oligonucleotide and a methylated cytosine antibody is formed and separated, and detected and quantified with excellent sensitivity by a biotin label in the complex as is the case with Group A (no treatment group). On the other hand, in the partially methylated

oligonucleotide UBC118-HM where 12 sites among 13 sites of CG sequences are methylated, only two methylated sites are left as a result of digestion by a methylation sensitive restriction enzyme (HhaI). Therefore, the detection and quantification result of UBC118-HM was inferior to that of UBC86-M.

From the above, it was revealed that by a digesting treatment with a methylation sensitive restriction enzyme, a partially methylated DNA fragment can be digested, and by forming and separating a complex of a methylated cytosine antibody, a methylated DNA fragment, and an immobilized 5'-end biotin-labeled oligonucleotide, and detecting and quantifying the methylated cytosine antibody in the complex according to its identification function, it is possible to detect and quantify a methylated DNA fragment.

Example 5

A methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 37, a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 38, a methylated oligonucleotide GPR-M8 having the nucleotide sequence of SEQ ID NO: 39, an unmethylated oligonucleotide UBC-U8 having the nucleotide sequence of SEQ ID NO: 40, an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 41, and an unmethylated oligonucleotide GPR-U8 having the nucleotide sequence of SEQ ID NO: 42 were synthesized, and the following solutions in TE buffer were prepared for each of methylated oligonucleotides

and unmethylated oligonucleotides.

Solution A: 0.3 pmol/10 μL solution in TE buffer

Solution B: 0.03 pmol/10 μL solution in TE buffer

Solution C: 0.003 pmol/10 μL solution in TE buffer

Solution D: 0 pmol/10 μL solution in TE buffer (negative control solution)

Then, for each solution (Solution A to Solution D), a methylated oligonucleotide mixed solution M0 in which equivalent amounts of respective solutions of the methylated oligonucleotides UBC-M8, FBN-M8, and GPR-M8 are mixed, and a methylated oligonucleotide mixed solution U0 in which equivalent amounts of respective solutions of the unmethylated oligonucleotides UBC-U8, FBN-U8, and GPR-U8 are mixed were prepared.

<Methylated oligonucleotides> N represents methylated cytosine.

UBC-M8: 5′-
ANGAANGTANGGANGCTNGATNGTTNGGTNGCCTGTCTGACTACAACATCCAGA-3′ (SEQ ID NO: 37)

FBN-M8: 5′-
ANGAANGTANGGANGCTNGATNGTTNGGTNGCCAGCCGACGAAGGGCTTATTAG-3′ (SEQ ID NO: 38)

GPR-M8: 5′-
ANGAANGTANGGANGCTNGATNGTTNGGTNGCCTGCCGAGAACGAGGCGTTGTC-3′ (SEQ ID NO: 39)

<Unmethylated oligonucleotides>

UBC-U8: 5′-

ACGAACGTACGGACGCTCGATCGTTCGGTCGCCTGTCTGACTACAACATCCAGA-3' (SEQ ID NO: 40)

FBN-U8: 5'-ACGAACGTACGGACGCTCGATCGTTCGGTCGCCAGCCGACGAAGGGCTTATTAG-3' (SEQ ID NO: 41)

GPR-U8: 5'-ACGAACGTACGGACGCTCGATCGTTCGGTCGCCTGCCGAGAACGAGGCGTTGTC-3' (SEQ ID NO: 42)

0.1 pmol/50 μL solutions of 5'-end biotin-labeled oligonucleotides UBC, FBN, and GPR having the nucleotide sequences of SEQ ID NO: 43, SEQ ID NO: 44, and SEQ ID NO: 45 in TE buffer were prepared (a UBC-B solution, an FBN-B solution, and a GPR-B solution, respectively). Also, a biotin-labeled oligonucleotide solution (biotin-labeled oligonucleotide mixed solution) in TE buffer in which equivalent amounts of 5'-end biotin-labeled oligonucleotides UBC, FBN, and GPR having the nucleotide sequences of SEQ ID NO: 43, SEQ ID NO: 44, and SEQ ID NO: 45 (each 0.1 pmol/50 μL) are mixed were prepared.

<5'-end biotin-labeled oligonucleotides>

UBC: 5'-TCTGGATGTTGTAGTCAGACAG-3' (SEQ ID NO: 43)

FBN: 5'-CTAATAAGCCCTTCGTCGGCT-3' (SEQ ID NO: 44)

GPR: 5'-GACAACGCCTCGTTCTCGG-3' (SEQ ID NO: 45)

For each of solutions (Solution A to Solution D) of the methylated oligonucleotide mixed solution M0, and the unmethylated oligonucleotide mixed solution U0, the following

treatment was executed (each solution was prepared in quadruplicate).

After adding 10 μL of an oligonucleotide solution prepared as described above, and 10 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol) to a PCR tube, 50 μL of each solution of the 5'-end biotin-labeled oligonucleotide (UBC-B solution, FBN-B solution, GPR-B solution, and biotin-labeled oligonucleotide mixed solution) was added to each reaction solution, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed.

Then the PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Further, the tube was cooled to 50°C and kept at this temperature for 10 minutes, and then kept at 37°C for 10 minutes, and returned to room temperature, to promote formation of a bound body of a 5'-end biotin-labeled oligonucleotide and an oligonucleotide.

Every obtained mixture in solution was transferred to a 96-well plate coated with streptavidin, and left still for about 30 minutes at room temperature, to immobilize the bound body of a 5'-end biotin-labeled oligonucleotide and an oligonucleotide onto the plate. After being left still, the solution in the plate was removed by decantation, and then each well in the plate was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Each of the wells was added with 100 μL of a methylated

cytosine antibody [available from Aviva Systems Biology, a 1 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and left still for an hour at room temperature. Thereafter, each of the wells was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Then, each of the wells was added with 100 μL of an Eu-N1 labeled mouse IgG antibody [available from Perkin Elmer, a 0.25 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)] and left still for an hour at room temperature. After being left still, each of the wells was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

By adding and mixing 200 μL of Enhancement Solution (available from Perkin Elmer) into each of the wells, a reaction was started. Then after being left still for about 45 minutes at room temperature, the fluorescence of the obtained sample was measured with excitation 340 nm/fluorescence 612 nm.

The results are shown in Fig. 8 to Fig. 11. In the methylated oligonucleotide mixed solution M0, it was revealed that a complex is formed and separated between the immobilized 5′-end biotin-labeled oligonucleotide UBC (Fig. 8), FBN (Fig. 9), GPR (Fig. 10) and the oligonucleotides in which the foregoing three kinds are mixed (Fig. 11) and a methylated cytosine antibody, and detection and quantification with high

sensitivity are enabled by a biotin label in the complex. It was revealed that especially when three kinds of oligonucleotides are mixed (Fig. 11), detection and quantification with better sensitivity than that in detection by single oligonucleotide (Fig. 8 to Fig. 10) are realized. In the unmethylated oligonucleotide mixed solution U0, since a complex is not formed between the immobilized 5'-end biotin-labeled oligonucleotide UBC (Fig. 8), FBN (Fig. 9), GPR (Fig. 10), and the oligonucleotides in which the foregoing three kinds are mixed (Fig. 11) and a methylated cytosine antibody, the value approximately equal to the background value was exhibited in every case.

From the above, it was revealed that by forming and separating a complex of a methylated cytosine antibody, a methylated DNA fragment, and an immobilized 5'-end biotin-labeled oligonucleotide, and detecting and quantifying the methylated cytosine antibody in the complex according to its identification function, it is possible to detect and quantify a methylated DNA fragment. It was also revealed that by using a plurality of immobilized 5'-end biotin-labeled oligonucleotides, detection and quantification with high sensitivity are realized compared with the case where one kind of immobilized 5'-end biotin-labeled oligonucleotide is used (that is, by not only using one target DNA region, but also using a plurality of target DNA regions concurrently).

Example 6

A commercially available methylated cytosine antibody

(available from Aviva Systems Biology) was labeled with biotin using a commercially available biotinylating kit (Biotin Labeling Kit-NH_2, available from DOJINDO Laboratories) according to the method described in the catalogue. The obtained biotin-labeled methylated cytosine antibody was refrigerated as a solution [about 0.1 μg/100 μL solution of an antibody in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

The synthetically obtained biotin-labeled methylated cytosine antibody solution was added to a 96-well plate coated with streptavidin in an amount of 100 μL/well, and immobilized to wells by leaving the solution still for about an hour at room temperature. After being left still, the solution was removed from each well by decantation, and then each well was added with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and the buffer was removed from each well by decantation. This operation was repeated another two times.

A methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 46, a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 47, a methylated oligonucleotide GPR-M8 having the nucleotide sequence of SEQ ID NO: 48, an unmethylated oligonucleotide UBC-U8 having the nucleotide sequence of SEQ ID NO: 49, an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 50, and an unmethylated oligonucleotide GPR-U8 having the nucleotide sequence of SEQ

ID NO: 51 were synthesized, and the following solutions were prepared for each oligonucleotide.

Solution A: 0.1 pmoL/10 μL solution in TE buffer

Solution B: 0.01 pmoL/10 μL solution in TE buffer

Solution C: 0.001 pmoL/10 μL solution in TE buffer

Solution D: 0 pmoL/10 μL solution in TE buffer (negative control solution)

<Methylated oligonucleotides> N represents methylated cytosine.

UBC-M8: 5′-ANGAANGTANGGANGCTNGATNGTTNGGTNGCCTGTCTGACTACAACATCCAGA-3′ (SEQ ID NO: 46)

GPR-M8: 5′-ANGAANGTANGGANGCTNGATNGTTNGGTNGCCTGCCGAGAACGAGGCGTTGTC-3′ (SEQ ID NO: 47)

FBN-M8: 5′-ANGAANGTANGGANGCTNGATNGTTNGGTNGCCAGCCGACGAAGGGCTTATTAG-3′ (SEQ ID NO: 48)

<Unmethylated oligonucleotides>

UBC-UM8: 5′-ACGAACGTACGGACGCTCGATCGTTCGGTCGCCTGTCTGACTACAACATCCAGA-3′ (SEQ ID NO: 49)

GPR-UM8: 5′-ACGAACGTACGGACGCTCGATCGTTCGGTCGCCTGCCGAGAACGAGGCGTTGTC-3′ (SEQ ID NO: 50)

FBN-UM8: 5′-ACGAACGTACGGACGCTCGATCGTTCGGTCGCCAGCCGACGAAGGGCTTATTAG-3′ (SEQ

ID NO: 51)

Then an oligonucleotide UBC having the nucleotide sequence of SEQ ID NO: 52 labeled with FITC at 5'-end, an oligonucleotide GPR having the nucleotide sequence of SEQ ID NO: 53 labeled with FITC at 5'-end, and an oligonucleotide FBN having the nucleotide sequence of SEQ ID NO: 54 labeled with FITC at 5'-end were synthesized, and 1 pmol/50 μL solutions in TE buffer were prepared (UBC-FITC solution, FBN-FITC solution, and GPR-FITC solution, respectively).

<5'-end FITC-labeled oligonucleotides>
UBC: 5'-TCTGGATGTTGTAGTCAGACAG-3' (SEQ ID NO: 52)
GPR: 5'-GACAACGCCTCGTTCTCGG-3' (SEQ ID NO: 53)
FBN: 5'-CTAATAAGCCCTTCGTCGGCT-3' (SEQ ID NO: 54)

For each obtained solution, the following treatment was executed (each solution was prepared singly).

Preparation of UBC mixed solution: A PCR tube was added with 10 μL of an oligonucleotide solution prepared above (UBC-M8 or UBC-U8 solution), 50 μL of a 5'-end FITC-labeled oligonucleotide solution (UBC-FITC solution) prepared above, and 5 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed.

Preparation of FBN mixed solution: A PCR tube was added with 10 μL of an oligonucleotide solution prepared above (FBN-

M8 or FBN-U8 solution), 50 μL of a 5'-end FITC-labeled oligonucleotide solution (FBN-FITC solution) prepared above, and 5 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed.

Preparation of GPR mixed solution: A PCR tube was added with 10 μL of an oligonucleotide solution prepared above (GPR-M8 or GPR-U8 solution), 50 μL of a 5'-end FITC-labeled oligonucleotide solution (GPR-FITC solution) prepared above, and 5 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed.

Each PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Then the tube was cooled to 50°C and kept at this temperature for 10 minutes, and kept at 37°C for 10 minutes, and returned to room temperature, to promote formation of a bound body of a 5'-end FITC-labeled oligonucleotide and a methylated or unmethylated oligonucleotide.

The whole of the solution in the PCR tube containing a bound body of a 5'-end FITC-labeled oligonucleotide and a methylated or unmethylated oligonucleotide was transferred to a plate in which a biotin-labeled methylated cytosine antibody preliminarily prepared is immobilized, and left still for about an hour at room temperature. After being left still, the solution in the plate was removed by decantation, and then

200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)] was added to each well in the plate, and then the buffer was removed from each well by decantation. This operation was repeated another two times.

Then, after adding 100 μL of an HRP-labeled FITC antibody solution [available from Jackson ImmunoResearch Laboratories, a 0.01 μg/100 μL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)] to each of the wells, the plate was left still for an hour at room temperature. After being left still, each well was added with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and the buffer was removed from each well by decantation. This operation was repeated another two times.

Then, 100 μL of a substrate (available from R&D, #DY999) was added and mixed to each well to start a reaction.

Then after being left still for about 5 minutes at room temperature, each well was added and mixed with 50 μL of a stop solution (1 N H_2SO_4 aqueous solution) to stop the reaction. The absorbance at 450 nm of the sample obtained within 30 minutes after stop of the reaction was measured.

The results are shown in Fig. 12 to Fig. 14. It was revealed that in every case of UBC (Fig. 12), GPR (Fig. 13), and FBN (Fig. 14), in methylated fragments UBC-M8, GPR-M8 and FBN-M8, by forming and separating a complex of an immobilized methylated cytosine antibody and a 5'-end FITC-labeled

oligonucleotide, and detecting and quantifying the 5'-end FITC-labeled oligonucleotide in the complex according to its identification function, the methylated oligonucleotides UBC-M8, GPR-M8 and FBN-M8 can be detected and quantified with high sensitivity in any concentration. In the unmethylated fragments UBC-U8, GPR-U8 and FBN-MU, since a complex of an immobilized methylated cytosine antibody and a 5'-end FITC-labeled oligonucleotide is not formed and separated, a value approximately equal to the background value was exhibited in any case.

From the above, it was revealed that by forming and separating a complex of an immobilized methylated cytosine antibody, a methylated DNA fragment, and a 5'-end FITC-labeled oligonucleotide, and detecting and quantifying the 5'-end FITC-labeled oligonucleotide in the complex according to its identification function, it is possible to detect and quantify a methylated DNA fragment.

Example 7

A commercially available methylated cytosine antibody (available from Aviva Systems Biology) was labeled with biotin using a commercially available biotinylating kit (Biotin Labeling Kit-NH_2, available from DOJINDO Laboratories) according to the method described in the catalogue. The obtained biotin-labeled methylated cytosine antibody was refrigerated as a solution [about 0.1 μg/100 μL solution of an antibody in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

The synthetically obtained biotin-labeled methylated cytosine antibody solution was added to a 96-well plate coated with streptavidin in an amount of 100 μL/well, and immobilized to wells by leaving the solution still for about an hour at room temperature. After being left still, the solution was removed from each well by decantation, and then 300 μL of DELFIA Wash Concentrate (available from Perkin Elmer, Tris-HCl pH 7.8 with Tween 80) ×25 diluted with sterile ultrapure water was added, and the buffer was removed from each well by decantation. This operation was repeated another two times.

A methylated oligonucleotide UBC-M having the nucleotide sequence of SEQ ID NO: 55, a partially methylated oligonucleotide UBC-HM having the nucleotide sequence of SEQ ID NO: 56, and an unmethylated oligonucleotide UBC-UM having the nucleotide sequence of SEQ ID NO: 57 were synthesized, and the following solutions were prepared for each oligonucleotide.

Solution A: 0.1 pmoL/10 μL solution in TE buffer

Solution B: 0.01 pmoL/10 μL solution in TE buffer

Solution C: 0.001 pmoL/10 μL solution in TE buffer

Solution D: 0 pmoL/10 μL solution in TE buffer (negative control solution)

<Methylated oligonucleotide> N represents methylated cytosine.

UBC-M: 5′-
AGTGACACCATNGAGAATGTCAGATCNGGATCAGAGNGCCATCTAGATGGACATGTCACTGT
CTGACTACAACATCCAGA-3′ (SEQ ID NO: 55)

<Partially methylated oligonucleotide> N represents methylated

cytosine.

UBC-HM: 5′-

AGTGACACCATNGAGAATGTCAGATCCGGATCAGAGCGCCATCTAGATGGACATGTCACTGT

CTGACTACAACATCCAGA-3′ (SEQ ID NO: 56)

<Unmethylated oligonucleotide>

UBC-UM: 5′-

AGTGACACCATCGAGAATGTCAGATCCGGATCAGAGCGCCATCTAGATGGACATGTCACTGT

CTGACTACAACATCCAGA-3′ (SEQ ID NO: 57)

For each of the obtained solutions, the following treatment was executed (each solution was prepared in duplicate).

Group A (no treatment group): To 10 μL of the obtained solution, 5 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and 5 μL of BSA (Bovine serum albumin 1 mg/ml) were added, and then 10 pmol of an oligonucleotide CA1 having the nucleotide sequence of SEQ ID NO: 58 was added as a masking oligonucleotide, and the mixture was further added with sterile ultrapure water to a liquid volume of 50 μL, and mixed.

Group B (HhaI treatment group): To 10 μL of the obtained solution, 6 U of HhaI, 5 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and 5 μL of 10 × BSA (Bovine serum albumin 1 mg/ml) were added, and then 10 pmol of an oligonucleotide CA1 having the nucleotide sequence of SEQ ID NO: 58 was added as a masking oligonucleotide, and the mixture was further added with sterile ultrapure water to a liquid volume of 50 μL, and

mixed.

<Masking oligonucleotide>

CA1: 5'-GATGGCGCTCTG-3' (SEQ ID NO: 58)

After incubating each reaction solution at 37°C for 3 hours, 50 µL of a 1 pmol/50 µL solution in TE buffer of an oligonucleotide UBC having the nucleotide sequence of SEQ ID NO: 59 preliminarily synthesized and labeled with FITC at 5'-end was added to the PCR tube.

<5'-end FITC-labeled oligonucleotide>

UBC: 5'-TCTGGATGTTGTAGTCAGACAG-3' (SEQ ID NO: 59)

Then the PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Then the tube was cooled to 50°C and kept at this temperature for 10 minutes, and kept at 37°C for 10 minutes, and returned to room temperature, to promote formation of a bound body of a 5'-end FITC-labeled oligonucleotide and an oligonucleotide.

The whole of the solution in the PCR tube containing a bound body of a 5'-end FITC-labeled oligonucleotide and an oligonucleotide was transferred to a plate in which a biotin-labeled methylated cytosine antibody preliminarily prepared is immobilized, and left still for about an hour at room temperature. After being left still, the solution in the plate was removed by decantation, and then 300 µL of DELFIA Wash Concentrate (available from Perkin Elmer, Tris-HCl pH 7.8

with Tween 80) x25 diluted with sterile ultrapure water was added to each well in the plate, and then the buffer was removed from each well by decantation. This operation was repeated another two times.

Then, after adding 100 µL of an HRP-labeled FITC antibody solution [available from Jackson ImmunoResearch Laboratories, a 0.01 µg/100 µL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)] to each of the wells, the plate was left still for an hour at room temperature. After being left still, each well was added with 200 µL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and the buffer was removed from each well by decantation. This operation was repeated another two times.

Then, 100 µL of a substrate (available from R&D, #DY999) was added and mixed to each well to start a reaction.

Then after being left still for about 10 minutes at room temperature, each well was added and mixed with 50 µL of a stop solution (1 N H_2SO_4 aqueous solution) to stop the reaction. The absorbance at 450 nm of the sample obtained within 30 minutes after stop of the reaction was measured.

The results are shown in Fig. 15 and Fig. 16. In the case of Group A (no treatment group) (Fig. 15), it was revealed that in the methylated oligonucleotide UBC-M where all of three sites among three sites of CG sequences are methylated, a complex of a 5'-end FITC-labeled oligonucleotide UBC and an immobilized methylated cytosine antibody is formed

and separated, and detected and quantified with high sensitivity. On the other hand, in a partially methylated oligonucleotide UBC-HM where only one site among three sites of CG sequences is methylated, a complex of a 5'-end FITC-labeled oligonucleotide UBC and an immobilized methylated cytosine antibody is formed and separated, however, detection and quantification results were inferior to those of UBC-M possibly due to the lower complex forming rate than that of UBC-M because only one site is methylated. In the unmethylated oligonucleotide UBC-UM where no site among three sites of CG sequences is methylated, a complex is not formed and separated, so that a value approximately equal to the background value (data of Solution D) was exhibited. In the case of Group B (HhaI treatment group) (Fig. 16), in the methylated oligonucleotide UBC-M where all of three sites among three sites of CG sequences are methylated, it was revealed that a complex of a 5'-end FITC-labeled oligonucleotide UBC and an immobilized methylated cytosine antibody is formed and separated, and detected and quantified with sensitivity as good as the value in Group A (no treatment group) because it is not digested by a methylation sensitive restriction enzyme (HhaI). In a partially methylated oligonucleotide UBC-HM where only one site among three sites of CG sequences is methylated, methylated CG sequences are lost due to digestion by the methylation sensitive restriction enzyme (HhaI). Therefore, a complex is not formed and separated, so that a value approximately the same with the background value (data of Solution D) was exhibited. In the

unmethylated oligonucleotide UBC-UM where no site among three sites of CG sequences is methylated, a value approximately the same with the background value was exhibited as is the case with A treatment group (no treatment group) because a complex is not formed and separated.

From the above, it was revealed that a partially methylated DNA fragment can be digested by treatment using a methylation sensitive restriction enzyme, and a methylated DNA fragment can be detected and quantified by forming and separating a complex of an immobilized methylated cytosine antibody, a methylated DNA fragment, and a 5'-end FITC-labeled oligonucleotide, and detecting and quantifying the 5'-end FITC-labeled oligonucleotide in the complex according to its identification function.

Example 8

A commercially available methylated cytosine antibody (available from Aviva Systems Biology) was labeled with biotin using a commercially available biotinylating kit (Biotin Labeling Kit-NH_2, available from DOJINDO Laboratories) according to the method described in the catalogue. The obtained biotin-labeled methylated cytosine antibody was refrigerated as a solution [about 0.1 μg/100 μL solution of an antibody in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

The synthetically obtained biotin-labeled methylated cytosine antibody solution was added to a 96-well plate coated with streptavidin in an amount of 100 μL/well, and immobilized

to wells by leaving the solution still for about an hour at room temperature. After being left still, the solution was removed from each well by decantation, and then each well was added with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and the buffer was removed from each well by decantation. This operation was repeated another two times.

A methylated oligonucleotide UBC/GPR/FBN-M having the nucleotide sequence of SEQ ID NO: 60, and an unmethylated oligonucleotide UBC/GPR/FBN-UM having the nucleotide sequence of SEQ ID NO: 61 were synthesized, and the following solutions were prepared for each oligonucleotide.

Solution A: 0.1 pmoL/10 μL solution in TE buffer

Solution B: 0.01 pmoL/10 μL solution in TE buffer

Solution C: 0.001 pmoL/10 μL solution in TE buffer

Solution D: 0 pmoL/10 μL solution in TE buffer (negative control solution)

<Methylated oligonucleotide> N represents methylated cytosine.

UBC/GPR/FBN-M: 5'-CTGTCTGACTACAACATCCAGANGCCGAGAACGAGGCGTTGTCNGAGCCGACGAAGGGCTTATTAG-3' (SEQ ID NO: 60)

<Unmethylated oligonucleotide>

UBC/GPR/FBN-UM: 5'-CTGTCTGACTACAACATCCAGACGCCGAGAACGAGGCGTTGTCCGAGCCGACGAAGGGCTTATTAG-3' (SEQ ID NO: 61)

Then, 1 pmol/50 μL solutions of oligonucleotides UBC, FBN and GPR labeled with FITC at 5'-end having the nucleotide sequences of SEQ ID NO: 62, SEQ ID NO: 63 and SEQ ID NO: 64 in TE buffer (UBC-FITC solution, FBN-FITC solution and GPR-FITC solution) were prepared. Also an FITC-labeled oligonucleotide solution (FITC-labeled oligonucleotide mixed solution) in which solutions of 5'-end FITC-labeled oligonucleotides UBC, FBN and GPR having the nucleotide sequences of SEQ ID NO: 62, SEQ ID NO: 63 and SEQ ID NO: 64 in TE buffer are mixed (each 1 pmol/50 μL) was prepared.

<5'-end FITC-labeled oligonucleotides>
UBC: 5'-TCTGGATGTTGTAGTCAGACAG-3' (SEQ ID NO: 62)
GPR: 5'-GACAACGCCTCGTTCTCGG-3' (SEQ ID NO: 63)
FBN: 5'-CTAATAAGCCCTTCGTCGGCT-3' (SEQ ID NO: 64)

The following treatment was executed on each obtained solution.

To a new PCR tube, 10 μL of a methylated oligonucleotide solution or an unmethylated oligonucleotide solution prepared as described above (each solution was prepared in octuplicate), 10 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and 50 μL of a 5'-end FITC-labeled oligonucleotide solution prepared as described above (UBC-FITC solution, FBN-FITC solution, GPR-FITC solution, and FITC-labeled oligonucleotide mixed solution) were added, and the resultant mixture was added with

sterile ultrapure water to a liquid volume of 100 μL, and mixed.

Then the PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Then the tube was cooled to 50°C and kept at this temperature for 10 minutes, and kept at 37°C for 10 minutes, and returned to room temperature, to promote formation of a bound body of a 5'-end FITC-labeled oligonucleotide and an oligonucleotide.

The whole of the solution in the PCR tube containing a bound body of a 5'-end FITC-labeled oligonucleotide and an oligonucleotide was transferred to a plate in which a biotin-labeled methylated cytosine antibody preliminarily prepared is immobilized, and left still for about 2 hours at room temperature. After being left still, the solution in the plate was removed by decantation, and then each well was added with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and the buffer was removed from each well by decantation. This operation was repeated another two times.

Then, after adding 100 μL of an HRP-labeled FITC antibody solution [available from Jackson ImmunoResearch Laboratories, a 0.01 μg/100 μL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)] to each of the wells, the plate was left still for about an hour at room temperature. After being left still, each well was added with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM

$Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and the buffer was removed from each well by decantation. This operation was repeated another two times.

Then, 100 µL of a substrate (available from R&D, #DY999) was added and mixed to each well to start a reaction.

Then after being left still for about 5 minutes at room temperature, each well was added and mixed with 50 µL of a stop solution (1 N H_2SO_4 aqueous solution) to stop the reaction. The absorbance at 450 nm of the sample obtained within 30 minutes after stop of the reaction was measured.

The results are shown in Fig. 17 to Fig. 20. In the methylated oligonucleotide UBC/GPR/FBN-M, and the unmethylated oligonucleotide UBC/GPR/FBN-U, the 5'-end FITC-labeled oligonucleotides UBC, GPR and FBN are oligonucleotides capable of forming a double strand (respectively having a complementary nucleotide sequence in the oligonucleotide). In every case where the 5'-end FITC-labeled oligonucleotides UBC (Fig. 17), GPR (Fig. 18) and FBN (Fig. 19), and the mixture of the 5'-end FITC-labeled oligonucleotides (Fig. 20) were used, it was revealed that in the methylated fragment UBC/GPR/FBN-M, by forming and selecting a complex of an immobilized methylated cytosine antibody and a 5'-end FITC-labeled oligonucleotide and detecting and quantifying the 5'-end FITC-labeled oligonucleotide in the complex according to its identification function, it is possible to detect and quantify the methylated oligonucleotide/GPR/FBN-M with excellent sensitivity in any concentration. In an unmethylated fragment UBC/GPR/FBN-U, since a complex of an immobilized methylated

cytosine antibody and a 5'-end FITC-labeled oligonucleotide is not formed and separated, a value approximately equal to the background value was exhibited. Further, it was revealed that by using a plurality of 5'-end FITC-labeled oligonucleotides (Fig. 20), detection and quantification with higher sensitivity are realized compared with the case using only one kind of (single) immobilized 5'-end biotin-labeled oligonucleotide is used (Fig. 17 to Fig. 19).

From the above, it was revealed that by forming and separating a complex of an immobilized methylated cytosine antibody, a methylated DNA fragment, and a 5'-end FITC-labeled oligonucleotide, and detecting and quantifying the 5'-end FITC-labeled oligonucleotide in the complex according to its identification function, it is possible to detect and quantify a methylated DNA fragment. Further, by using a plurality of 5'-end FITC-labeled oligonucleotides for one target DNA region (in other words, by using a plurality of the present oligonucleotides concurrently for one target DNA region), detection and quantification with better sensitivity are realized compared with the case where only one kind of (single) 5'-end FITC-labeled oligonucleotide is used.

Example 9

A commercially available methylated cytosine antibody (available from Aviva Systems Biology) was labeled with biotin using a commercially available biotinylating kit (Biotin Labeling Kit-NH_2, available from DOJINDO Laboratories) according to the method described in the catalogue. The

obtained biotin-labeled methylated cytosine antibody was refrigerated as a solution [about 0.1 μg/100 μL solution of an antibody in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

The synthetically obtained biotin-labeled methylated cytosine antibody solution was added to a 96-well plate coated with streptavidin in an amount of 100 μL/well, and immobilized to wells by leaving the solution still for about an hour at room temperature. After being left still, the solution was removed from each well by decantation, and then each well was added with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and the buffer was removed from each well by decantation. This operation was repeated another two times.

A methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 65, a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 66, a methylated oligonucleotide GPR-M8 having the nucleotide sequence of SEQ ID NO: 67, an unmethylated oligonucleotide UBC-U8 having the nucleotide sequence of SEQ ID NO: 68, an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 69, and an unmethylated oligonucleotide GPR-U8 having the nucleotide sequence of SEQ ID NO: 70 were synthesized, and the following solutions were prepared for each of methylated oligonucleotides and unmethylated oligonucleotides.

Solution A: 0.3 pmol/10 μL solution in TE buffer

Solution B: 0.03 pmol/10 μL solution in TE buffer

Solution C: 0.003 pmol/10 μL solution in TE buffer

Solution D: TE buffer solution (negative control solution)

Then, for each solution (Solution A to Solution D), a methylated oligonucleotide mixed solution M0 in which equivalent amounts of respective solutions of the methylated oligonucleotides UBC-M8, FBN-M8, and GPR-M8 are mixed, and a methylated oligonucleotide mixed solution U0 in which equivalent amounts of respective solutions of the unmethylated oligonucleotides UBC-U8, FBN-U8, and GPR-U8 are mixed were prepared.

<Methylated oligonucleotides> N represents methylated cytosine.

UBC-M8: 5′-ANGAANGTANGGANGCTNGATNGTTNGGTNGCCTGTCTGACTACAACATCCAGA-3′ (SEQ ID NO: 65)

FBN-M8: 5′-ANGAANGTANGGANGCTNGATNGTTNGGTNGCCAGCCGACGAAGGGCTTATTAG-3′ (SEQ ID NO: 66)

GPR-M8: 5′-ANGAANGTANGGANGCTNGATNGTTNGGTNGCCTGCCGAGAACGAGGCGTTGTC-3′ (SEQ ID NO: 67)

<Unmethylated oligonucleotides>

UBC-U8: 5′-ACGAACGTACGGACGCTCGATCGTTCGGTCGCCTGTCTGACTACAACATCCAGA-3′ (SEQ ID NO: 68)

FBN-U8: 5′-

ACGAACGTACGGACGCTCGATCGTTCGGTCGCCAGCCGACGAAGGGCTTATTAG-3′ (SEQ ID NO: 69)

GPR-U8: 5′-ACGAACGTACGGACGCTCGATCGTTCGGTCGCCTGCCGAGAACGAGGCGTTGTC-3′ (SEQ ID NO: 70)

Then, 1 pmol/50 μL solutions of oligonucleotides UBC, FBN and GPR labeled with FITC at 5′-end having the nucleotide sequences of SEQ ID NO: 71, SEQ ID NO: 72 and SEQ ID NO: 73 in TE buffer (UBC-FITC solution, FBN-FITC solution and GPR-FITC solution) were prepared. Also an FITC-labeled oligonucleotide solution (FITC-labeled oligonucleotide mixed solution) in which solutions of 5′-end FITC-labeled oligonucleotides UBC, FBN and GPR having the nucleotide sequences of SEQ ID NO: 71, SEQ ID NO: 72 and SEQ ID NO: 73 in TE buffer are mixed (each 1 pmol/50 μL) was prepared.

<5′-end FITC-labeled oligonucleotides>

UBC: 5′-TCTGGATGTTGTAGTCAGACAG-3′ (SEQ ID NO: 71)

GPR: 5′-GACAACGCCTCGTTCTCGG-3′ (SEQ ID NO: 72)

FBN: 5′-CTAATAAGCCCTTCGTCGGCT-3′ (SEQ ID NO: 73)

The following treatment was executed on each obtained solution.

To a new PCR tube, 10 μL of oligonucleotide solutions prepared as described above (MA, MB, MC, MD, UA, UB, UC, UD), 10 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and 50 μL of a 5′-end

FITC-labeled oligonucleotide solution prepared as described above (UBC-FITC solution, FBN-FITC solution, GPR-FITC solution, and FITC-labeled oligonucleotide mixed solution) were added, and further the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed.

Then the PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Then the tube was cooled to 50°C and kept at this temperature for 10 minutes, and kept at 37°C for 10 minutes, and returned to room temperature, to promote formation of a bound body of a 5′-end FITC-labeled oligonucleotide and an oligonucleotide.

The whole of the solution in the PCR tube containing a bound body of a 5′-end FITC-labeled oligonucleotide and an oligonucleotide was transferred to a plate in which a biotin-labeled methylated cytosine antibody preliminarily prepared is immobilized, and left still for about an hour at room temperature. After being left still, the solution in the plate was removed by decantation, then each well was added with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and the buffer was removed from each well by decantation. This operation was repeated another two times.

Then, after adding 100 μL of an HRP-labeled FITC antibody solution [available from Jackson ImmunoResearch Laboratories, a 0.01 μg/100 μL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154

mM NaCl, pH 7.4)] to each well, the plate was left still for about an hour at room temperature. After being left still, the solution was removed from each well by decantation, and each well was added with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and the buffer was removed from each well by decantation. This operation was repeated another two times.

Then, 100 μL of a substrate (available from R&D, #DY999) was added and mixed to each well to start a reaction.

Then after being left still for about 5 minutes at room temperature, each well was added and mixed with 50 μL of a stop solution (1 N H_2SO_4 aqueous solution) to stop the reaction. The absorbance at 450 nm of the sample obtained within 30 minutes after stop of the reaction was measured.

The results are shown in Fig. 21 to Fig. 24. In the methylated oligonucleotide mixed solution M0, it was revealed that a complex is formed and separated between the 5'-end FITC-labeled oligonucleotide UBC (Fig. 21), FBN (Fig. 22), GPR (Fig. 23) and the oligonucleotides in which the foregoing three kinds are mixed (Fig. 24), and a methylated cytosine antibody, and detection and quantification with excellent sensitivity are realized. In particular, when three kinds of oligonucleotides are mixed (Fig. 24), it was revealed that detection and quantification with better sensitivity are realized compared with the case of detection by single oligonucleotide (Fig. 21 to Fig. 23). In the unmethylated oligonucleotide mixed solution U0, since a complex is not

formed between the immobilized 5′-end biotin-labeled oligonucleotide UBC (Fig. 21), FBN (Fig. 22), GPR (Fig. 23) and the oligonucleotide in which the foregoing three kinds are mixed (Fig. 24), and a methylated cytosine antibody, a value approximately equal to the background value was exhibited in every case.

From the above, it was revealed that by forming and separating a complex of an immobilized methylated cytosine antibody, a methylated DNA fragment, and a 5′-end FITC-labeled oligonucleotide, and detecting and quantifying the 5′-end FITC-labeled oligonucleotide in the complex according to its identification function, it is possible to detect and quantify a methylated DNA fragment. It was also revealed that by using a plurality of 5′-end FITC-labeled oligonucleotides (that is, by not only using one target DNA region, but also using a plurality of target DNA regions concurrently), detection and quantification with high sensitivity are realized compared with the case where one kind of 5′-end FITC-labeled oligonucleotide is used.

Example 10

The following experiment was conducted using a commercially available solution of a chromatostrip coated with streptavidin and a conjugate (an FITC antibody labeled with gold nano particles) in Bed-Side ICAN (TM) Legionella Detection Kit from TAKARA BIO INC.

A methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 74, and an unmethylated

oligonucleotide UBC-U8 having the nucleotide sequence of SEQ ID NO: 75 were synthesized, and a 0.1 pmol/μL solution in TE buffer was prepared for each oligonucleotide. Also, a TE buffer solution was prepared as a negative control.

<Methylated oligonucleotide> N represents methylated cytosine.

UBC-M8: 5′-ANGAANGTANGGANGCTNGATNGTTNGGTNGCCTGTCTGACTACAACATCCAGA-3′ (SEQ ID NO: 74)

<Unmethylated oligonucleotide>

UBC-U8: 5′-ACGAACGTACGGACGCTCGATCGTTCGGTCGCCTGTCTGACTACAACATCCAGA-3′ (SEQ ID NO: 75)

A 0.5 pmol/μL solution of a 5′-end biotin-labeled oligonucleotide UBC having the nucleotide sequence of SEQ ID NO: 76 in TE buffer was prepared (UBC solution).

<5′-end biotin-labeled oligonucleotide>

UBC: 5′-TCTGGATGTTGTAGTCAGACAG-3′ (SEQ ID NO: 76)

Using the methylated oligonucleotide solution, and the unmethylated oligonucleotide solution, the following treatment was conducted (each solution was prepared singly).

To a PCR tube, 2 μL of an oligonucleotide solution prepared as described above (UBC-M8, a UBC-U8 solution, a TE buffer solution), 2 μL of a 5′-end biotin-labeled oligonucleotide solution prepared as described above (UBC-B solution), 2 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and 2 μL of BSA (Bovine serum albumin 1 mg/mL) were added, followed by

addition of 5 pmol of an oligonucleotide CA1 having the nucleotide sequence of SEQ ID NO: 77 as carrier DNA, and the resultant mixture was further added with sterile ultrapure water to a liquid volume of 20 μL, and mixed.

<Carrier DNA>

CA1: 5'-GATGGCGCTCTG-3' (SEQ ID NO: 77)

Then, the PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Further, the tube was cooled to 50°C, and kept at this temperature for 10 minutes, and then kept at 37°C for 10 minutes, and returned to room temperature, to promote formation of a bound body of a 5'-end biotin-labeled oligonucleotide and an oligonucleotide.

The whole of the obtained reaction solution was transferred to a well of a flat-bottom plate, and a tip end of a streptavidin-coated chromatostrip was inserted to the bottom of each well, and developed (the entire solution was absorbed by the strip).

In another well of the flat-bottom plate charged with 20 μL of a methylated cytosine antibody [available from Aviva Systems Biology, 0.1 μg/20 μL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], a tip end of a streptavidin-coated chromatostrip obtained as described above was inserted to the bottom of each well, and further developed.

In still another well of the flat-bottom plate charged

with 20 μL of an FITC-labeled mouse IgG antibody (available from Medical & Biological Laboratories) solution [0.2 μg/20 μL in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], a tip end of a streptavidin-coated chromatostrip obtained as described above was inserted to the bottom of each well, and further developed.

Next, in another well of the flat-bottom plate charged with 20 μL of a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4) solution, a tip end of a streptavidin-coated chromatostrip obtained as described above was inserted to the bottom of each well, and further developed.

Thereafter, in another well of the flat-bottom plate charged with 20 μL of a conjugate solution (gold nano particle-labeled FITC antibody solution), a tip end of a streptavidin-coated chromatostrip obtained as described above was inserted to the bottom of each well, and further developed.

After completion of development, the streptavidin-coated chromatostrip was visually checked and presence or absence of a red-purple line was determined.

The results are shown in Fig. 25. In the case of the methylated oligonucleotide UBC-M8, a red-purple line was observed on the streptavidin-coated chromatostrip. This reveals that a complex of a methylated DNA antibody, an immobilized 5'-end biotin-labeled oligonucleotide, and a methylated DNA fragment is formed and separated. In the

unmethylated oligonucleotide UBC-U8, and the negative control (TE buffer solution), a red-purple line was not observed because a complex is not formed.

From the above, it was revealed that a methylated DNA fragment can be detected and quantified on a chromatostrip by forming and separating a complex of a methylated cytosine antibody, a methylated DNA fragment and an immobilized 5'-end biotin-labeled oligonucleotide, and detecting and quantifying the methylated cytosine antibody in the complex according to its identification function.

Example 11

The following experiment was conducted using a commercially available solution of a chromatostrip coated with streptavidin and a conjugate (an FITC antibody labeled with gold nano particles) in Bed-Side ICAN (TM) Legionella Detection Kit from TAKARA BIO INC.

A commercially available methylated cytosine antibody (available from Aviva Systems Biology) was labeled with biotin using a commercially available biotinylating kit (Biotin Labeling Kit-NH_2, available from DOJINDO Laboratories) according to the method described in the catalogue. The obtained biotin-labeled methylated cytosine antibody was refrigerated as a solution [about 0.1 μg/100 μL solution of an antibody in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

A methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 78, a methylated

oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 79, a methylated oligonucleotide GPR-M8 having the nucleotide sequence of SEQ ID NO: 80, an unmethylated oligonucleotide UBC-U8 having the nucleotide sequence of SEQ ID NO: 81, an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 82, and an unmethylated oligonucleotide GPR-U8 having the nucleotide sequence of SEQ ID NO: 83 were synthesized, and a 0.1 pmol/μL solution in TE buffer was prepared for each oligonucleotide. Also, a TE buffer solution was used as a negative control.

<Methylated oligonucleotides> N represents methylated cytosine.

UBC-M8: 5′-
ANGAANGTANGGANGCTNGATNGTTNGGTNGCCTGTCTGACTACAACATCCAGA-3′ (SEQ ID NO: 78)

FBN-M8: 5′-
ANGAANGTANGGANGCTNGATNGTTNGGTNGCCAGCCGACGAAGGGCTTATTAG-3′ (SEQ ID NO: 79)

GPR-M8: 5′-
ANGAANGTANGGANGCTNGATNGTTNGGTNGCCTGCCGAGAACGAGGCGTTGTC-3′ (SEQ ID NO: 80)

<Unmethylated oligonucleotides>

UBC-U8: 5′-
ACGAACGTACGGACGCTCGATCGTTCGGTCGCCTGTCTGACTACAACATCCAGA-3′ (SEQ ID NO: 81)

FBN-U8: 5′-
ACGAACGTACGGACGCTCGATCGTTCGGTCGCCAGCCGACGAAGGGCTTATTAG-3′ (SEQ

ID NO: 82)

GPR-U8: 5'-

ACGAACGTACGGACGCTCGATCGTTCGGTCGCCTGCCGAGAACGAGGCGTTGTC-3' (SEQ ID NO: 83)

0.5 pmol/μL solutions of oligonucleotides UBC, FBN and GPR labeled with FITC at 5'-end having the nucleotide sequences of SEQ ID NO: 84, SEQ ID NO: 85 and SEQ ID NO: 86 in TE buffer (UBC-FITC solution, FBN-FITC solution and GPR-FITC solution) were prepared.

<5'-end FITC-labeled oligonucleotides>

UBC: 5'-TCTGGATGTTGTAGTCAGACAG-3' (SEQ ID NO: 84)

FBN: 5'-CTAATAAGCCCTTCGTCGGCT-3' (SEQ ID NO: 85)

GPR: 5'-GACAACGCCTCGTTCTCGG-3' (SEQ ID NO: 86)

For each of the methylated oligonucleotide solutions, and the unmethylated oligonucleotide solutions, the following treatment was conducted (each solution was prepared singly).

Preparation of UBC mixed solution: To a PCR tube, 2 μL of an oligonucleotide solution prepared as described above (UBC-M8 or UBC-U8 solution), 2 μL of a 5'-end FITC-labeled oligonucleotide solution prepared as described above (UBC-FITC solution), 2 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and 2 μL of BSA (Bovine serum albumin 1 mg/mL) were added, followed by addition of 5 pmol of an oligonucleotide CA1 having the nucleotide sequence of SEQ ID NO: 87 as carrier DNA, and the

resultant mixture was added with sterile ultrapure water to a liquid volume of 20 μL, and mixed.

Preparation of FBN mixed solution: To a PCR tube, 2 μL of an oligonucleotide solution prepared as described above (FBN-M8 or FBN-U8 solution), 2 μL of a 5'-end FITC-labeled oligonucleotide solution prepared as described above (FBN-FITC solution), 2 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and 2 μL of BSA (Bovine serum albumin 1 mg/mL) were added, followed by addition of 5 pmol of an oligonucleotide CA1 having the nucleotide sequence of SEQ ID NO: 87 as carrier DNA, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 20 μL, and mixed.

Preparation of GPR mixed solution: To a PCR tube, 2 μL of an oligonucleotide solution prepared as described above (GPR-M8 or GPR-U8 solution), 2 μL of a 5'-end FITC-labeled oligonucleotide solution prepared as described above (GPR-FITC solution), 2 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and 2 μL of BSA (Bovine serum albumin 1 mg/mL) were added, followed by addition of 5 pmol of an oligonucleotide CA1 having the nucleotide sequence of SEQ ID NO: 87 as carrier DNA, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 20 μL, and mixed.

<Carrier DNA>

CA1: 5'-GATGGCGCTCTG-3' (SEQ ID NO: 87)

Then, the PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Further, the tube was cooled to 50°C, and kept at this temperature for 10 minutes, and then kept at 37°C for 10 minutes, and returned to room temperature, to promote formation of a bound body of a 5'-end FITC-labeled oligonucleotide and an oligonucleotide.

In another well of the flat-bottom plate charged with 20 μL of a biotin-labeled methylated cytosine antibody solution, a tip end of a streptavidin-coated chromatostrip was inserted to the bottom of each well, and developed (the entire solution was absorbed by the strip).

The whole of the reaction solution in which a bound body of a 5'-end FITC-labeled oligonucleotide and an oligonucleotide was formed was transferred to a well of a flat-bottom plate, and a tip end of a streptavidin-coated chromatostrip was inserted to the bottom of each well, and developed (the entire solution was absorbed by the strip).

In a still another well of the flat-bottom plate charged with 20 μL of a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4) solution, a tip end of a streptavidin-coated chromatostrip obtained as described above was inserted to the bottom of each well, and further developed.

In another well of the flat-bottom plate charged with 20 μL of a conjugate solution (gold nano particle-labeled FITC antibody solution), a tip end of a streptavidin-coated chromatostrip obtained as described above was inserted to the

bottom of each well, and further developed.

After completion of development, each streptavidin-coated chromatostrip was visually checked and presence or absence of a red-purple line was determined.

The results are shown in Fig. 26 to Fig. 28. In the case of the methylated oligonucleotides UBC-M8, FBN-M8 and GPR-M8, a red-purple line was observed on the streptavidin-coated chromatostrip. This reveals that a complex of an immobilized methylated DNA antibody, a 5'-end FITC biotin-labeled oligonucleotide, and a methylated DNA fragment is formed and separated. In the unmethylated oligonucleotides UBC-U8, FBN-M8 and GPR-M8, and the negative control (TE buffer solution), a red-purple line was not observed because a complex is not formed.

From the above, it was revealed that a methylated DNA fragment can be detected and quantified on a chromatostrip by forming and separating a complex of an immobilized methylated cytosine antibody, a methylated DNA fragment and a 5'-end FITC-labeled oligonucleotide, and detecting and quantifying the 5'-end FITC-labeled oligonucleotide in the complex according to its identification function.

Example 12

The following experiment was conducted using a commercially available solution of a chromatostrip coated with streptavidin and a conjugate (an FITC antibody labeled with gold nano particles) in Bed-Side ICAN (TM) Legionella Detection Kit from TAKARA BIO INC.

A commercially available methylated cytosine antibody (available from Aviva Systems Biology) was labeled with biotin using a commercially available biotinylating kit (Biotin Labeling Kit-NH_2, available from DOJINDO Laboratories) according to the method described in the catalogue. The obtained biotin-labeled methylated cytosine antibody was refrigerated as a solution [about 0.1 μg/100 μL solution of an antibody in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

A methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 88, a methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 89, a methylated oligonucleotide GPR-M8 having the nucleotide sequence of SEQ ID NO: 90, an unmethylated oligonucleotide UBC-U8 having the nucleotide sequence of SEQ ID NO: 91, an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 92, and an unmethylated oligonucleotide GPR-U8 having the nucleotide sequence of SEQ ID NO: 93 were synthesized, and a 0.2 pmol/μL solution in TE buffer was prepared for each oligonucleotide. Also, the TE buffer solution was used as a negative control.

<Methylated oligonucleotides> N represents methylated cytosine.

UBC-M8: 5'-
ANGAANGTANGGANGCTNGATNGTTNGGTNGCCTGTCTGACTACAACATCCAGA-3' (SEQ ID NO: 88)

FBN-M8: 5'-

ANGAANGTANGGANGCTNGATNGTTNGGTNGCCAGCCGACGAAGGGCTTATTAG-3' (SEQ ID NO: 89)

GPR-M8: 5'-

ANGAANGTANGGANGCTNGATNGTTNGGTNGCCTGCCGAGAACGAGGCGTTGTC-3' (SEQ ID NO: 90)

<Unmethylated oligonucleotides>

UBC-U8: 5'-

ACGAACGTACGGACGCTCGATCGTTCGGTCGCCTGTCTGACTACAACATCCAGA-3' (SEQ ID NO: 91)

FBN-U8: 5'-

ACGAACGTACGGACGCTCGATCGTTCGGTCGCCAGCCGACGAAGGGCTTATTAG-3' (SEQ ID NO: 92)

GPR-U8: 5'-

ACGAACGTACGGACGCTCGATCGTTCGGTCGCCTGCCGAGAACGAGGCGTTGTC-3' (SEQ ID NO: 93)

0.5 pmol/μL solutions of oligonucleotides UBC, FBN and GPR labeled with FITC at 5'-end having the nucleotide sequences of SEQ ID NO: 94, SEQ ID NO: 95 and SEQ ID NO: 96 in TE buffer (UBC-FITC solution, FBN-FITC solution and GPR-FITC solution) were prepared.

<5'-end FITC-labeled oligonucleotides>

UBC: 5'-TCTGGATGTTGTAGTCAGACAG-3' (SEQ ID NO: 94)

FBN: 5'-CTAATAAGCCCTTCGTCGGCT-3' (SEQ ID NO: 95)

GPR: 5'-GACAACGCCTCGTTCTCGG-3' (SEQ ID NO: 96)

For each of the methylated oligonucleotide solutions,

and the unmethylated oligonucleotide solutions, the following treatment was conducted (each solution was prepared singly).

Preparation of UBC mixed solution: To a PCR tube, 2 μL of an oligonucleotide solution prepared as described above (UBC-M8 or UBC-U8 solution), 2 μL of a 5'-end FITC-labeled oligonucleotide solution prepared as described above (UBC-FITC solution), 1 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and 1 μL of BSA (Bovine serum albumin 1 mg/mL) were added, followed by addition of 5 pmol of an oligonucleotide CA1 having the nucleotide sequence of SEQ ID NO: 97 as carrier DNA, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 10 μL, and mixed.

Preparation of FBN mixed solution: To a PCR tube, 2 μL of an oligonucleotide solution prepared as described above (FBN-M8 or FBN-U8 solution), 2 μL of a 5'-end FITC-labeled oligonucleotide solution prepared as described above (FBN-FITC solution), 1 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and 1 μL of BSA (Bovine serum albumin 1 mg/mL) were added, followed by addition of 5 pmol of an oligonucleotide CA1 having the nucleotide sequence of SEQ ID NO: 97 as carrier DNA, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 10 μL, and mixed.

Preparation of GPR mixed solution: To a PCR tube, 2 μL of an oligonucleotide solution prepared as described above (GPR-M8 or GPR-U8 solution), 2 μL of a 5'-end FITC-labeled oligonucleotide solution prepared as described above (GPR-FITC

solution), 1 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and 1 μL of BSA (Bovine serum albumin 1 mg/mL) were added, followed by addition of 5 pmol of an oligonucleotide CA1 having the nucleotide sequence of SEQ ID NO: 97 as carrier DNA, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 10 μL, and mixed.

<Carrier DNA>

CA1: 5'-GATGGCGCTCTG-3' (SEQ ID NO: 97)

Then, the PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Further, the tube was cooled to 50°C, and kept at this temperature for 10 minutes, and then kept at 37°C for 10 minutes, and returned to room temperature, to promote formation of a bound body of a 5'-end FITC-labeled oligonucleotide and an oligonucleotide.

The obtained solution was added with 10 μL of a biotin-labeled methylated cytosine antibody solution, and left still at room temperature for an hour.

The whole of the obtained reaction solution was transferred to a well of a flat-bottom plate, and a tip end of a streptavidin-coated chromatostrip was inserted to the bottom of each well, and developed (the entire solution was absorbed by the strip).

In another well of the flat-bottom plate charged with 20 μL of a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM

$Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4) solution, a tip end of a streptavidin-coated chromatostrip obtained as described above was inserted to the bottom of each well, and further developed.

In still another well of the flat-bottom plate charged with 20 μL of a conjugate solution (gold nano particle-labeled FITC antibody solution), a tip end of a streptavidin-coated chromatostrip obtained as described above was inserted to the bottom of each well, and further developed.

After completion of development, a streptavidin-coated chromatostrip was visually checked and presence or absence of a red-purple line was determined.

The results are shown in Fig. 29 to Fig. 31. In the case of the methylated oligonucleotides UBC-M8, FBN-M8 and GPR-M8, a red-purple line was observed on the streptavidin-coated chromatostrip. This reveals that a complex of an immobilized methylated DNA antibody, a 5'-end FITC biotin-labeled oligonucleotide, and a methylated DNA fragment is formed and separated. In the unmethylated oligonucleotides UBC-U8, FBN-M8 and GPR-M8, and the negative control (TE buffer solution), a red-purple line was not observed because a complex was not formed.

From the above, it was revealed that a methylated DNA fragment can be detected and quantified on a chromatostrip by forming and separating a complex of an immobilized methylated cytosine antibody, a methylated DNA fragment and a 5'-end FITC-labeled oligonucleotide, and detecting and quantifying the 5'-end FITC-labeled oligonucleotide in the complex

according to its identification function.

Example 13

A commercially available methylated cytosine antibody (available from Aviva Systems Biology) was labeled with biotin using a commercially available biotinylating kit (Biotin Labeling Kit-NH_2, available from DOJINDO Laboratories) according to the method described in the catalogue. The obtained biotin-labeled methylated cytosine antibody was refrigerated as a solution [about 0.1 μg/100 μL solution of an antibody in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

The synthetically obtained biotin-labeled methylated cytosine antibody solution was added to a 96-well plate coated with streptavidin in an amount of 100 μL/well, and immobilized to wells by leaving the solution still for about an hour at room temperature. After being left still, the solution was removed from each well by decantation, and then 300 μL of DELFIA Wash Concentrate (available from Perkin Elmer, Tris-HCl pH 7.8 with Tween 80) ×25 diluted with sterile ultrapure water was added to each well, and the buffer was removed from each well by decantation. This operation was repeated another two times.

A methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 98, and an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 99 were synthesized, and the following solutions in TE buffer were prepared for each oligonucleotide.

Solution A: 0.1 pmol/10 μL solution in TE buffer

Solution B: 0.01 pmol/10 μL solution in TE buffer

Solution C: 0.001 pmol/10 μL solution in TE buffer

Solution D: 0 pmol/10 μL solution in TE buffer (negative control solution)

<Methylated oligonucleotide> N represents methylated cytosine.

FBN-M8: 5′-ANGAANGTANGGANGCTNGATNGTTNGGTNGCCAGCCGACGAAGGGCTTATTAG-3′ (SEQ ID NO: 98)

<Unmethylated oligonucleotide>

FBN-U8: 5′-ACGAACGTACGGACGCTCGATCGTTCGGTCGCCAGCCGACGAAGGGCTTATTAG-3′ (SEQ ID NO: 99)

A 1 pmol/50 μL solution of a 5′-end FITC-labeled oligonucleotide FBN having the nucleotide sequence of SEQ ID NO: 100 in TE buffer was prepared (UBC-FITC solution).

<5′-end FITC-labeled oligonucleotide>

FBN: 5′-CTAATAAGCCCTTCGTCGGCT-3′ (SEQ ID NO: 100)

As a solution for promoting formation of a bound body of a 5′-end FITC-labeled oligonucleotide and an oligonucleotide, the following buffers were prepared.

Buffer 1: 100 mM Tris-HCl pH 7.5, 100 mM $MgCl_2$, 10 mM Dithothreitol

Buffer 2: 1 mM KH_2PO_4 pH 7.4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl

Buffer 3: 10 mM Tris-HCl pH 8.0, 1 mM EDTA

Buffer 4: 330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol

Buffer 5: ultrapure water

For each of the methylated oligonucleotide solutions and the unmethylated oligonucleotide solutions, the following treatment was executed (each solution was prepared singly).

To a PCR tube, 10 μL of an oligonucleotide solution prepared as described above (FBN-M8 or FBN-U8 solution), 50 μL of a 5'-end FITC-labeled oligonucleotide solution as described above (FBN-FITC solution), 5 μL of any one kind of a buffer selected from Buffers 1 to 5, and 5 μL of BSA (Bovine serum albumin 1 mg/mL) were added, followed by addition of 5 pmol of an oligonucleotide CA1 having the nucleotide sequence of SEQ ID NO: 101 as carrier DNA, and then the resultant mixture was added with sterile ultrapure water to a liquid volume of 50 μL, and mixed.

<Carrier DNA>

CA1: 5'-GATGGCGCTCTG-3' (SEQ ID NO: 101)

Then, the PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Further, the tube was cooled to 50°C, and kept at this temperature for 10 minutes, and then kept at 37°C for 10 minutes, and returned to room temperature, to promote formation of a bound body of a 5'-end FITC-labeled

oligonucleotide and an oligonucleotide.

The whole of the solution in the PCR tube containing a bound body of a 5'-end FITC-labeled oligonucleotide and an oligonucleotide was transferred to a plate in which a biotin-labeled methylated cytosine antibody preliminarily prepared is immobilized, and left still for about 2 hours at room temperature. After being left still, the solution in the plate was removed by decantation, and then 300 μL of DELFIA Wash Concentrate (available from Perkin Elmer, Tris-HCl pH 7.8 with Tween 80) ×25 diluted with sterile ultrapure water was added to each well in the plate, and then the buffer was removed from each well by decantation. This operation was repeated another two times.

Then, after adding 100 μL of an HRP-labeled FITC antibody solution [available from Jackson ImmunoResearch Laboratories, a 0.01 μg/100 μL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)] to each of the wells, the plate was left still for an hour at room temperature. After being left still, each well was added with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and the buffer was removed from each well by decantation. This operation was repeated another two times.

Then, 100 μL of a substrate (available from R&D, #DY999) was added and mixed to each well to start a reaction.

Then after being left still for about 10 minutes at room temperature, each well was added and mixed with 50 μL of a

stop solution (1 N H_2SO_4 aqueous solution) to stop the reaction. The absorbance at 450 nm of the sample obtained within 30 minutes after stop of the reaction was measured.

The results are shown in Figs. 32 to 36. In the buffers containing magnesium ions (Buffer 1 and Buffer 4, Fig. 32 and Fig. 35), the methylated oligonucleotide FBN-M is likely to form a complex with the 5'-end biotin-labeled oligonucleotide FBN, and it was revealed that in a specimen using such buffers, a complex of an immobilized methylated DNA antibody, a 5'-end FITC biotin-labeled oligonucleotide, and a methylated DNA fragment is formed and separated, and detected and quantified with high sensitivity.

From the above, it was demonstrated that in forming a bound body of single-stranded DNA containing a target DNA region and the present oligonucleotide, use of a reaction system containing a magnesium ion is preferred.

Example 14

A methylated oligonucleotide UBC-M8 having the nucleotide sequence of SEQ ID NO: 102, and an unmethylated oligonucleotide UBC-U8 having the nucleotide sequence of SEQ ID NO: 103 were synthesized, and a 0.01 pmol/10 μL solution in TE buffer was prepared for each oligonucleotide.

<Methylated oligonucleotide> N represents methylated cytosine.

UBC-M8: 5'-

ANGAANGTANGGANGCTNGATNGTTNGGTNGCCTGTCTGACTACAACATCCAGA-3' (SEQ ID NO: 102)

<Unmethylated oligonucleotide>

UBC-U8: 5'-ACGAACGTACGGACGCTCGATCGTTCGGTCGCCTGTCTGACTACAACATCCAGA-3' (SEQ ID NO: 103)

Also, a 5'-end biotin-labeled oligonucleotide B1 having the nucleotide sequence of SEQ ID NO: 104 was synthesized, and a 0.02 μM solution in TE buffer was prepared.

<5'-end biotin-labeled oligonucleotide>

B1: 5'-TCTGGATGTTGTAGTCAGACAG-3' (SEQ ID NO: 104)

Also, for preparation of a solution that promotes formation of a bound body of a 5'-end biotin-labeled oligonucleotide and an oligonucleotide, the following metal salt aqueous solutions were prepared.

Metal salt solution Mg: 100 mM $MgCl_2$ aqueous solution

Metal salt solution Ba: 100 mM $BaCl_2$ aqueous solution

Metal salt solution H_2O: ultrapure water

For each of the methylated oligonucleotide solutions and the unmethylated oligonucleotide solutions, the following treatment was executed (each solution was prepared singly).

To a PCR tube, 10 μL of an oligonucleotide solution prepared as described above, 5 μL of the aforementioned 5'-end biotin-labeled oligonucleotide solution, 10 μL of a phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4), and 60 μL of a metal salt solution (Metal salt solution Mg,

metal salt solution Ba, or Metal salt solution H_2O) were added, and then the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed. Then, the PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Further, the tube was cooled to 50°C, and kept at this temperature for 10 minutes, and then kept at 37°C for 10 minutes, and returned to room temperature, to promote formation of a bound body of a 5'-end biotin-labeled oligonucleotide and an oligonucleotide.

By transferring the entire obtained mixture to a 96-well plate coated with streptavidin, and leaving it still for about 30 minutes at room temperature, the bound body of a 5'-end biotin-labeled oligonucleotide and an oligonucleotide was immobilized to the plate. After being left still, the solution in the plate was removed by decantation, and then each well in the plate was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Each well was added with 100 μL of a methylated cytosine antibody [available from Aviva Systems Biology, a 1 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and left still for an hour at room temperature. Thereafter, each well was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Then, each well was added with 100 μL of an Eu-N1

labeled mouse IgG antibody [available from Perkin Elmer, a 0.25 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and left still for an hour at room temperature. After being left still, each well was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

By adding and mixing 200 μL of Enhancement Solution (available from Perkin Elmer) into each of the wells, a reaction was started. Then after being left still for about 3 minutes at room temperature, the fluorescence of the obtained sample was measured with excitation 340 nm/fluorescence 612 nm.

The result is shown in Fig. 37. In metal salt solutions containing a bivalent positive ion (Metal salt solution Mg and Metal salt solution Ba), the methylated oligonucleotide UBC-M is likely to form a bound body with a 5'-end biotin-labeled oligonucleotide UBC, and it was revealed that in a specimen using such a metal salt solution, a complex of an immobilized methylated DNA antibody, a 5'-end FITC biotin-labeled oligonucleotide and a methylated DNA fragment is formed and separated, and detection and quantification with excellent sensitivity are realized.

From the above, it was demonstrated that in forming a bound body of single-stranded DNA containing a target DNA region and the present oligonucleotide, use of a reaction system containing a bivalent positive ion is preferred.

Example 15

A methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 105, and an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 106 were synthesized, and a 0.01 pmol/10 μL solution in TE buffer was prepared for each oligonucleotide.

<Methylated oligonucleotide> N represents methylated cytosine.

FBN-M8: 5'-ANGAANGTANGGANGCTNGATNGTTNGGTNGCCAGCCGACGAAGGGCTTATTAG-3' (SEQ ID NO: 105)

<Unmethylated oligonucleotide>

FBN-U8: 5'-ACGAACGTACGGACGCTCGATCGTTCGGTCGCCAGCCGACGAAGGGCTTATTAG-3' (SEQ ID NO: 106)

Also, a 5'-end biotin-labeled oligonucleotide FBN having the nucleotide sequence of SEQ ID NO: 107 was synthesized, and a 0.02 μM solution in TE buffer was prepared (FBN-B solution).

<5'-end biotin-labeled oligonucleotide>

FBN: 5'-CTAATAAGCCCTTCGTCGGCT-3' (SEQ ID NO: 107)

Also for preparation of a solution that promotes formation of a bound body of a 5'-end biotin-labeled oligonucleotide and an oligonucleotide, the following 0, 10, 20, 30, 40, 60, 80, 100 mM $MgCl_2$ aqueous solutions were prepared.

For each of the methylated oligonucleotide solutions and

the unmethylated oligonucleotide solutions, the following treatment was executed (each solution was prepared singly).

To a PCR tube, 10 μL of an oligonucleotide solution prepared as described above, 5 μL of the aforementioned 5'-end biotin-labeled oligonucleotide solution, 10 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and 60 μL an $MgCl_2$ aqueous solution (0 to 1000 mM) were added, and then the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed.

Then, the PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Further, the tube was cooled to 50°C, and kept at this temperature for 10 minutes, and then kept at 37°C for 10 minutes, and returned to room temperature, to promote formation of a bound body of a 5'-end biotin-labeled oligonucleotide and an oligonucleotide.

By transferring the entire obtained mixture to a 96-well plate coated with streptavidin, and leaving it still for about 30 minutes at room temperature, the bound body of a 5'-end biotin-labeled oligonucleotide and an oligonucleotide was immobilized to the plate. After being left still, the solution in the plate was removed by decantation, and then each well in the plate was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Each well as added with 100 μL of a methylated cytosine antibody [available from Aviva Systems Biology, a 1 μg/mL

solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and left still for an hour at room temperature. Thereafter, each well was washed three times with 200 µL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Then, each well was added with 100 µL of an Eu-N1 labeled mouse IgG antibody [available from Perkin Elmer, a 0.25 µg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and left still for an hour at room temperature. After being left still, each well was washed three times with 200 µL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

By adding and mixing 200 µL of Enhancement Solution (available from Perkin Elmer) into each of the wells, a reaction was started. Then after being left still for about 3 minutes at room temperature, the fluorescence of the obtained sample was measured with excitation 340 nm/fluorescence 612 nm.

The result is shown in Fig. 38. It was revealed that in buffers containing a magnesium ion in a final concentration of 10 mM to 70 mM, the methylated oligonucleotide FBN-M is likely to form a bound body with a 5'-end biotin-labeled oligonucleotide FBN, and in a specimen using such buffers, a complex of an immobilized methylated DNA antibody, a 5'-end FITC biotin-labeled oligonucleotide and a methylated DNA fragment is formed and separated, and detected and quantified

with excellent sensitivity. In particular, it was expected that the methylated oligonucleotide FBN-M is more likely to form a bound body with the 5'-end biotin-labeled oligonucleotide FBN at a final concentration of a magnesium ion of 58 mM or more.

From the above, it was demonstrated that in forming a bound body of single-stranded DNA containing a target DNA region and the present oligonucleotide, use of a reaction system containing a magnesium ion is preferred.

Example 16

A methylated oligonucleotide FBN-M8 having the nucleotide sequence of SEQ ID NO: 108, and an unmethylated oligonucleotide FBN-U8 having the nucleotide sequence of SEQ ID NO: 109 were synthesized, and a 0.01 pmol/10 μL solution in TE buffer was prepared for each oligonucleotide.

<Methylated oligonucleotide> N represents methylated cytosine.

FBN-M8: 5'-

ANGAANGTANGGANGCTNGATNGTTNGGTNGCCAGCCGACGAAGGGCTTATTAG-3' (SEQ ID NO: 108)

<Unmethylated oligonucleotide>

FBN-U8: 5'-

ACGAACGTACGGACGCTCGATCGTTCGGTCGCCAGCCGACGAAGGGCTTATTAG-3' (SEQ ID NO: 109)

Also, a 5'-end biotin-labeled oligonucleotide FBN having the nucleotide sequence of SEQ ID NO: 110 was synthesized, and

a 0.02 μM solution in TE buffer was prepared (FBN-B solution).

<5′-end biotin-labeled oligonucleotide>

FBN: 5′-CTAATAAGCCCTTCGTCGGCT-3′ (SEQ ID NO: 110)

Also for preparation of a solution that promotes formation of a bound body of a 5′-end biotin-labeled oligonucleotide and an oligonucleotide, the following 0, 100, 200, 300, 400, 600, 800, 1000 mM $MgCl_2$ aqueous solutions were prepared.

For each of the methylated oligonucleotide solutions and the unmethylated oligonucleotide solutions, the following treatment was executed (each solution was prepared singly).

To a PCR tube, 10 μL of an oligonucleotide solution prepared as described above, 5 μL of the aforementioned 5′-end biotin-labeled oligonucleotide solution, 10 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithothreitol), and 60 μL of an $MgCl_2$ aqueous solution (0 to 1000 mM) were added, and then the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed.

Then, the PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Further, the tube was cooled to 50°C, and kept at this temperature for 10 minutes, and then kept at 37°C for 10 minutes, and returned to room temperature, to promote formation of a bound body of a 5′-end biotin-labeled oligonucleotide and an oligonucleotide.

By transferring the entire obtained mixture to a 96-well

plate coated with streptavidin, and leaving it still for about 30 minutes at room temperature, the bound body of a 5'-end biotin-labeled oligonucleotide and an oligonucleotide was immobilized to the plate. After being left still, the solution in the plate was removed by decantation, and then each well in the plate was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Each well as added with 100 μL of a methylated cytosine antibody [available from Aviva Systems Biology, a 1 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and left still for an hour at room temperature. Thereafter, each well was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Then, each well was added with 100 μL of an Eu-N1 labeled mouse IgG antibody [available from Perkin Elmer, a 0.25 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)], and left still for an hour at room temperature. After being left still, each well was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

By adding and mixing 200 μL of Enhancement Solution (available from Perkin Elmer) into each of the wells, a reaction was started. Then after being left still for about 3 minutes at room temperature, the fluorescence of the obtained

sample was measured with excitation 340 nm/fluorescence 612 nm.

The result is shown in Fig. 39. It was revealed that in buffers containing a magnesium ion in a final concentration of 10 mM to 610 mM, the methylated oligonucleotide FBN-M is likely to form a bound body with the 5'-end biotin-labeled oligonucleotide FBN, and in a specimen using such buffers, a complex of an immobilized methylated DNA antibody, a 5'-end FITC biotin-labeled oligonucleotide and a methylated DNA fragment is formed and separated, and detected and quantified with excellent sensitivity. In particular, it was expected that the methylated oligonucleotide FBN-M is more likely to form a bound body with the 5'-end biotin-labeled oligonucleotide FBN at a final concentration of a magnesium ion ranging from 70 mM to 610 mM.

Example 17

For genomic DNA derived from human blood purchased from Clontech, a DNA fragment (X, SEQ ID NO: 113, a region corresponding to the base numbers 25687390 to 25687775 shown in Genbank Accession No. NT_029419 and so on) to be used as a test sample was amplified by conducting PCR using oligonucleotide primers (PF1 and PR1) designed for PCR of SEQ ID NO: 111 and SEQ ID NO: 112 and the following reaction condition.

<Oligonucleotide primers designed for PCR>

PF1: 5'-CTCAGCACCCAGGCGGCC-3' (SEQ ID NO: 111)

PR1: 5'-CTGGCCAAACTGGAGATCGC-3' (SEQ ID NO: 112)

<DNA fragment>

X: 5'-

CTCAGCACCCAGGCGGCCGCGATCATGAGGCGCGAGCGGCGCGCGGGCTGTTGCAGAGTCTT

GAGCGGGTGGCACACCGCGATGTAGCGGTCGGCTGTCATGACTACCAGCATGTAGGCCGACG

CAAACATGCCGAACACCTGCAGGTGCTTCACCACGCGGCACAGCCAGTCGGGGCCGCGGAAG

CGGTAGGTGATGTCCCAGCACATTTGCGGCAGCACCTGGAAGAATGCCACGGCCAGGTCGGC

CAGGCTGAGGTGTCGGATGAAGAGGTGCATGCGGGACGTCTTGCGCGGCGTCCGGTGCAGAG

CCAGCAGTACGCTGCTGTTGCCCAGCACGGCCACCGCGAAAGTCACCGCCAGCACGGCGATC

TCCAGTTTGGCCAG (SEQ ID NO: 113)

As a reaction solution of PCR, 5 ng of genomic DNA which is a template, each 3 μL of oligonucleotide primer solutions prepared to 5 μM, each 5 μL of 2 mM dNTPs, 5 μL of a 10 × buffer (100 mM Tris-HCl pH 8.3, 500 mM KCl, 15 mM $MgCl_2$, 0.01% Gelatin), and 0.25 μL of a 5 U/μL thermostable DNA polymerase (AmpliTaq Gold, available from ABI) were mixed, and sterile ultrapure water was added to a liquid volume of 50 μL. The reaction solution was kept at 95°C for 10 minutes, and then subjected to PCR conducting 40 cycles of incubation each including 30 seconds at 95°C, 30 seconds at 61°C, and 45 seconds at 72°C.

After conducting PCR, amplification was checked by 1.5% agarose gel electrophoresis, and a DNA fragment X was purified with Wizard SV Gel/PCR Kit (PROMEGA).

For a part of the obtained DNA fragment solution, a reaction solution was prepared by mixing 1 μL of SssI methylase (available from NEB), 10 μL of 10 × NEBuffer 2

(available from NEB), and 1 μL of S-adenosyl methionine (3.2 mM, available from NEB), and adding sterile ultrapure water to a liquid volume of 100 μL. The reaction solution was incubated at 37°C for 15 to 30 minutes, and further added with 1 μL of S-adenosyl methionine (3.2 mM, available from NEB) and incubated at 37°C for 15 to 30 minutes. This was then purified with Wizard SV Gel/PCR Kit (PROMEGA). These operations were repeated another 5 times, to obtain a methylated DNA fragment (MX, SEQ ID NO: 114).

<DNA fragment> (N represents 5-methyl cytosine)

MX: 5'-

CTCAGCACCCAGGNGGCNGNGATCATGAGGNGNGAGNGGNGNGNGGGCTGTTGCAGAGTCTT

GAGNGGGTGGCACACNGNGATGTAGNGGTNGGCTGTCATGACTACCAGCATGTAGGCNGANG

CAAACATGCNGAACACCTGCAGGTGCTTCACCANGNGGCACAGCCAGTNGGGGCNGNGGAAG

NGGTAGGTGATGTCCCAGCACATTTGNGGCAGCACCTGGAAGAATGCCANGGCCAGGTNGGC

CAGGCTGAGGTGTNGGATGAAGAGGTGCATGNGGGANGTCTTGNGNGGNGTCNGGTGCAGAG

CCAGCAGTANGCTGCTGTTGCCCAGCANGGCCACNGNGAAAGTCACNGCCAGCANGGNGATC

TCCAGTTTGGCCAG-3' (SEQ ID NO: 114)

For the obtained DNA fragment X, the following solutions were prepared in duplicate.

Solution A: 10 ng/10 μL solution in TE

Solution B: 1 ng/10 μL solution in TE

Solution C: TE solution (negative control solution)

For the obtained DNA fragment MX, the following solutions were prepared in duplicate.

Solution MA: 10 ng/10 μL solution in TE

Solution MB: 1 ng/10 μL solution in TE

Solution MC: TE solution (negative control solution)

Also a 5′-end biotin-labeled oligonucleotide B1 having the nucleotide sequence of SEQ ID NO: 116 capable of complementarily binding to a target DNA region X′ having the nucleotide sequence of SEQ ID NO: 115 was synthesized, and a 0.02 μM solution thereof in TE buffer was prepared.

<Target DNA region> (5-methyl cytosine is also denoted by C)

X′: 5′-

CTCAGCACCCAGGCGGCCGCGATCATGAGGCGCGAGCGGCGCGCGGGCTGTTGCAGAGTCTT
GAGCGGGTGGCACACCGCGATGTAGCGGTCGGCTGTCATGACTACCAGCATGTAGGCCGACG
CAAACATGCCGAACACCTGCAGGTGCTTCACCACGCGGCACAGCCAGTCGGGGCCGCGGAAG
CGGTAGGTGATGTCCCAGCACATTTGCGGCAGCACCTGGAAGAATGCCACGGCCAGGTCGGC
CAGGCTGAGGTGTCGGATGAAGAGGTGCATGCGGGACGTCTTGCGCGGCGTCCGGTGCAGAG
CCAGCAGTACGCTGCTGTTGCCCAGCACGGCCACCGCGAAAGTCACCGCCAGCACGGCGATC
TCCAGTTTGGCCAG-3′ (SEQ ID NO: 115)

<5′-end biotin-labeled oligonucleotide>

B1: 5′Biotin-CTGGCCAAACTGGAGATCGC-3′ (SEQ ID NO: 116)

Counter oligonucleotides C1 to C12 having the nucleotide sequences of SEQ ID NO: 117 to SEQ ID NO: 128 capable of complementarily binding to a minus strand of the target DNA region X′ having the nucleotide sequence of SEQ ID NO: 115 were synthesized, and a solution in TE buffer wherein a

concentration of each oligonucleotide is 0.01 μM was prepared.

<Target DNA region> (5-methyl cytosine is also denoted by C)

X': 5'-

CTCAGCACCCAGGCGGCCGCGATCATGAGGCGCGAGCGGCGCGCGGGCTGTTGCAGAGTCTT
GAGCGGGTGGCACACCGCGATGTAGCGGTCGGCTGTCATGACTACCAGCATGTAGGCCGACG
CAAACATGCCGAACACCTGCAGGTGCTTCACCACGCGGCACAGCCAGTCGGGGCCGCGGAAG
CGGTAGGTGATGTCCCAGCACATTTGCGGCAGCACCTGGAAGAATGCCACGGCCAGGTCGGC
CAGGCTGAGGTGTCGGATGAAGAGGTGCATGCGGGACGTCTTGCGCGGCGTCCGGTGCAGAG
CCAGCAGTACGCTGCTGTTGCCCAGCACGGCCACCGCGAAAGTCACCGCCAGCACGGCGATC
TCCAGTTTGGCCAG-3' (SEQ ID NO: 115)

<Counter oligonucleotides>

C1: 5'-GCCACCGCGAAAGTCACCGCCAGCACGGCG-3' (SEQ ID NO: 117)

C2: 5'-GCCAGCAGTACGCTGCTGTTGCCCAGCACG-3' (SEQ ID NO: 118)

C3: 5'-CGGGACGTCTTGCGCGGCGTCCGGTGCAGA-3' (SEQ ID NO: 119)

C4: 5'-AGGCTGAGGTGTCGGATGAAGAGGTGCATG-3' (SEQ ID NO: 120)

C5: 5'-ACCTGGAAGAATGCCACGGCCAGGTCGGCC-3' (SEQ ID NO: 121)

C6: 5'-TAGGTGATGTCCCAGCACATTTGCGGCAGC-3' (SEQ ID NO: 122)

C7: 5'-CGGCACAGCCAGTCGGGGCCGCGGAAGCGG-3' (SEQ ID NO: 123)

C8: 5'-ATGCCGAACACCTGCAGGTGCTTCACCACG-3' (SEQ ID NO: 124)

C9: 5'-ATGACTACCAGCATGTAGGCCGACGCAAAC-3' (SEQ ID NO: 125)

C10: 5'-TGGCACACCGCGATGTAGCGGTCGGCTGTC-3' (SEQ ID NO: 126)

C11: 5'-CGCGCGGGCTGTTGCAGAGTCTTGAGCGGG-3' (SEQ ID NO: 127)

C12: 5'-CAGGCGGCCGCGATCATGAGGCGCGAGCGG-3' (SEQ ID NO: 128)

For each of the solutions of the DNA fragment X and the solutions of the methylated DNA fragment MX, the following treatment was executed.

To a PCR tube, 10 μL of a DNA fragment solution prepared as described above, 10 μL of a 5'-end biotin-labeled oligonucleotide solution prepared as described above, 10 μL of a counter oligonucleotide solution prepared as described above, 10 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithiothreitol), 10 μL of a 100 mM $MgCl_2$ solution, and 10 μL of a 1 mg/mL BSA solution were added, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed. Thereafter, this PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Then the tube was cooled to 50°C and kept at this temperature for 10 minutes, and further kept at 37°C for 10 minutes, and returned to room temperature (these correspond to First step of the present measuring method).

100 μL of a reaction solution of a DNA fragment prepared as described above was added to an 8-well strip coated with streptavidin (available from Perkin Elmer, a total of 12 wells), and immobilized to the well by leaving the solution still for 30 minutes at room temperature. Then the solution was removed by pipetting, and 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] was added, and the buffer was removed by decantation. This operation was repeated another two times (these correspond to Second step of the present measuring method).

A masking oligonucleotide M1 having the nucleotide sequence of SEQ ID NO: 129 capable of complementarily binding

to a 5'-end biotin-labeled oligonucleotide B1 having the nucleotide sequence of SEQ ID NO: 116 was synthesized, and a 0.1 μM solution thereof in TE buffer was prepared.

<5'-end biotin-labeled oligonucleotide>

B1: 5'Biotin-CTGGCCAAACTGGAGATCGC-3' (SEQ ID NO: 116)

<Masking oligonucleotide>

M1: 5'-ATCTCCAGTTTGGCCAG-3' (SEQ ID NO: 129)

Each well was added with 100 μL of a methylated cytosine antibody [available from Aviva Systems Biology, a 0.5 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] and 1 μL of the aforementioned masking oligonucleotide solution, and left still for an hour at room temperature. Thereafter, each well was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)].

Then each well was added with 100 μL of an Eu-N1 labeled mouse IgG antibody [available from Perkin Elmer, a 0.05 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)], and left still for an hour at room temperature. Then, the solution was removed by decantation, and each well was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)].

Each well was added with 150 μL of Enhancement Solution

(available from Perkin Elmer), stirred for 5 minutes, and left still for 15 minutes at room temperature. Thereafter, the fluorescence was measured at excitation 340 nm/fluorescence 612 nm (these correspond to Third step of the present measuring method).

The result is shown in Fig. 40. In Solutions MA and MB of the methylated DNA fragment MX, an increase in fluorescence intensity was observed, and the intensity was concentration-dependent. In the negative control solution MC, an increase in fluorescence intensity was not observed. In Solutions A, B and C of the unmethylated DNA fragment X, an increase in fluorescence intensity was not observed.

These demonstrate that DNA containing a methylated target DNA region can be selected and immobilized by a biotin-labeled oligonucleotide and a methyl cytosine antibody, and methylated DNA can be detected and quantified with high sensitivity.

Example 18

For genomic DNA derived from human blood purchased from Clontech, a DNA fragment (Y, SEQ ID NO: 132, a region corresponding to the base numbers 76606 to 76726 shown in Genbank Accession No. ac009800 and so on) to be used as a test sample was amplified by conducting PCR using oligonucleotide primers (PF2 and PR2) designed for PCR of SEQ ID NO: 130 and SEQ ID NO: 131 and the following reaction condition.

<Oligonucleotide primers designed for PCR>

PF2: 5'-TGAGCTCCGTAGGGCGTCC-3' (SEQ ID NO: 130)

PR2: 5'-GCGCCGGGTCCGGGCCC-3' (SEQ ID NO: 131)

<DNA fragment>

Y: 5'-

GCGCCGGGTCCGGGCCCGATGCGTTGGCGGGCCAGGGCTCCGAGAACGAGGCGTTGTCCATC
TCAACGAGGGCAGAGGAGCCGGCGACCTGGCGTCCCCCAAGGACGCCCTACGGAGCTCA-3'
(SEQ ID NO: 132)

As a reaction solution of PCR, 5 ng of genomic DNA which is a template, each 3 μL of oligonucleotide primer solutions prepared to 5 μM, each 5 μL of 2 mM dNTPs, 5 μL of a 10 × buffer (100 mM Tris-HCl pH 8.3, 500 mM KCl, 15 mM $MgCl_2$, 0.01% Gelatin), and 0.25 μL of a 5 U/μL thermostable DNA polymerase (AmpliTaq Gold, available from ABI) were mixed, and sterile ultrapure water was added to a liquid volume of 50 μL. The reaction solution was kept at 95°C for 10 minutes, and then subjected to PCR conducting 50 cycles of incubation each including 30 seconds at 95°C, 30 seconds at 60°C, and 45 seconds at 72°C.

After conducting PCR, amplification was checked by 1.5% agarose gel electrophoresis, and a DNA fragment Y was purified with Wizard SV Gel/PCR Kit (PROMEGA).

For a part of the obtained DNA fragment solution, a reaction solution was prepared by mixing 1 μL of SssI methylase (available from NEB), 10 μL of 10 × NEBuffer 2 (available from NEB), and 1 μL of S-adenosyl methionine (3.2 mM, available from NEB), and adding sterile ultrapure water to a liquid volume of 100 μL. The reaction solution was

incubated at 37°C for 15 to 30 minutes, and further added with 1 μL of S-adenosyl methionine (3.2 mM, available from NEB) and incubated at 37°C for 15 to 30 minutes. This was then purified with Wizard SV Gel/PCR Kit (PROMEGA). These operations were repeated another 5 times, to obtain a methylated DNA fragment (MY, SEQ ID NO: 133).

<Methylated DNA fragment> (N represents 5-methyl cytosine)

MY: 5'-

GNGCNGGGTCNGGGCCNGATGNGTTGGNGGGCCAGGGCTCNGAGAANGAGGNGTTGTCCATC TCAANGAGGGCAGAGGAGCNGGNGACCTGGNGTCCCCCAAGGANGCCCTANGGAGCTCA-3' (SEQ ID NO: 133)

For the obtained DNA fragment Y, the following solutions were prepared in duplicate.

Solution A: 10 ng/10 μL solution in TE

Solution B: TE solution (negative control solution)

For the obtained DNA fragment MY, the following solutions were prepared in duplicate.

Solution MA: 10 ng/10 μL solution in TE

Solution MB: TE solution (negative control solution)

Also a 5'-end biotin-labeled oligonucleotide B2 having the nucleotide sequence of SEQ ID NO: 135 capable of complementarily binding to a target DNA region Y' having the nucleotide sequence of SEQ ID NO: 134 was synthesized, and a

0.02 μM solution thereof in TE buffer was prepared.

<Target DNA region> (5-methyl cytosine is also denoted by C)

Y': 5'-

GCGCCGGGTCCGGGCCCGATGCGTTGGCGGGCCAGGGCTCCGAGAACGAGGCGTTGTCCATC

TCAACGAGGGCAGAGGAGCCGGCGACCTGGCGTCCCCCAAGGACGCCCTACGGAGCTCA-3'

(SEQ ID NO: 134)

<5'-end biotin-labeled oligonucleotide>

B2: 5'Biotin-GACAACGCCTCGTTCTCGG-3' (SEQ ID NO: 135)

Counter oligonucleotides C13, C14 and C15 having the nucleotide sequences of SEQ ID NO: 136, SEQ ID NO: 27 and SEQ ID NO: 138 capable of complementarily binding to the minus strand of a target DNA region Y' having the nucleotide sequence of SEQ ID NO: 134 were synthesized, and a solution in TE buffer wherein a concentration of each oligonucleotide is 0.01 μM was prepared.

<Target DNA region> (5-methyl cytosine is also denoted by C)

Y': 5'-

GCGCCGGGTCCGGGCCCGATGCGTTGGCGGGCCAGGGCTCCGAGAACGAGGCGTTGTCCATC

TCAACGAGGGCAGAGGAGCCGGCGACCTGGCGTCCCCCAAGGACGCCCTACGGAGCTCA-3'

(SEQ ID NO: 134)

<Counter oligonucleotides>

C13: 5'-GCGTCCCCCAAGGACGCCCTACGGAGCTCA-3' (SEQ ID NO: 136)

C14: 5'-CTCAACGAGGGCAGAGGAGCCGGCGACCTG-3' (SEQ ID NO: 137)

C15: 5'-CGCCGGGTCCGGGCCCGATGCGTTGGCGGG-3' (SEQ ID NO: 138)

For each of the solutions of the DNA fragment Y and the solutions of the methylated DNA fragment MY, the following treatment was executed.

To a PCR tube, 10 μL of a DNA fragment solution prepared as described above, 10 μL of a biotin-labeled oligonucleotide solution prepared as described above, 10 μL of a counter oligonucleotide solution prepared as described above, 10 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithiothreitol), 10 μL of a 100 mM $MgCl_2$ solution, and 10 μL of a 1 mg/mL BSA solution were added, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed. Thereafter, this PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Then the tube was cooled to 50°C and kept at this temperature for 10 minutes, and further kept at 37°C for 10 minutes, and returned to room temperature (these correspond to First step of the present measuring method).

100 μL of a reaction solution of a DNA fragment prepared as described above was added to an 8-well strip coated with streptavidin (available from Perkin Elmer, a total of 8 wells), and immobilized to the well by leaving the solution still for 30 minutes at room temperature. Then the solution was removed by pipetting, and 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] was added, and the buffer was removed by decantation. This operation was repeated another two times (these correspond to Second step of the

present measuring method).

A masking oligonucleotide M2 having the nucleotide sequence of SEQ ID NO: 139 capable of complementarily binding to a 5'-end biotin-labeled oligonucleotide B2 having the nucleotide sequence of SEQ ID NO: 135 was synthesized, and a 0.1 μM solution thereof in TE buffer was prepared.

<5'-end biotin-labeled oligonucleotide>
B2: 5'Biotin-GACAACGCCTCGTTCTCGG-3' (SEQ ID NO: 135)
<Masking oligonucleotide>
M2: 5'-CCGAGAACGAGGCGTTGTCT-3' (SEQ ID NO: 139)

Each well was added with 100 μL of a methylated cytosine antibody [available from Aviva Systems Biology, a 0.5 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] and 1 μL of the aforementioned masking oligonucleotide solution, and left still for an hour at room temperature. Thereafter, each well was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)].

Then each well was added with 100 μL of an Eu-N1 labeled mouse IgG antibody [available from Perkin Elmer, a 0.05 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)], and left still for an hour at room temperature. Then, the solution was removed by decantation, and each well was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing

phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Each well was added with 150 µL of Enhancement Solution (available from Perkin Elmer), stirred for 5 minutes, and left still for 15 minutes at room temperature. Thereafter, the fluorescence was measured at excitation 340 nm/fluorescence 612 nm (these correspond to Third step of the present measuring method).

The result is shown in Fig. 41. In Solution MA of the methylated DNA fragment MY, an increase in fluorescence intensity was observed. In the negative control solution MB, an increase in fluorescence intensity was not observed. In Solutions A and B of the unmethylated DNA fragment Y, an increase in fluorescence intensity was not observed.

These demonstrate that DNA containing a methylated target DNA region can be selected and immobilized by a biotin-labeled oligonucleotide and a methyl cytosine antibody, and methylated DNA can be detected with high sensitivity.

Example 19

Yeast strain X2180-1A of baker's yeast was cultured in a YPD medium (1% Yeast extract, 2% Peptone, 2% Glucose, pH 5.6 to 6.0) to a turbidity of OD_{600} 0.6 to 1.0, and centrifuged at 10,000 g for 10 minutes, to prepare 1×10^7 of yeast cells. From the prepared yeast cells, a yeast genome was acquired using a generally used preparation method of a yeast genome as described in Methods in Yeast Genetics (Cold Spring Harbor Laboratory).

The prepared yeast cells were suspended in Buffer A (1 M sorbitol, 0.1 M EDTA, pH 7.4), added with 2-mercaptoethanol (final concentration 14 mM) and 100 U zymolase (10 mg/ml), and incubated under stirring at 30°C for an hour until the solution became clear. After collecting a protoplast by centrifugation at 550 g for 10 minutes, it was suspended in Buffer B (50 mM Tris-HCl, pH 7.4, 20 mM EDTA), added with sodium dodecyl sulfate in 1% (w/v), and then incubated at 65°C for 30 minutes. Sequentially, 5 M CH_3COOK was added and mingled in a volume ratio of 2/5, and the mixture was cooled on ice for 30 minutes, and then centrifuged at 15,000 g for 30 minutes to collect the supernatant. The collected supernatant was added with 3 M CH_3COONa in a volume ratio of 1/10 and an equal amount of isopropanol and mingled well, and the precipitate obtained by centrifugation at 15,000 g at 4°C for 30 minutes was rinsed with 70% ethanol and collected. After drying, the precipitate was dissolved in 1 mL of TE buffer (10 mM Tris-HCl, pH 8.0, 1 mM EDTA), and added with RNase A (available from Sigma) in a concentration of 40 μg/ml, incubated at 37°C for an hour, and then the mixture was added with proteinase K (available from Sigma) and sodium dodecyl sulfate in a concentrations of 500 μg/mL and 1% (w/v), respectively, and shaken at 55°C for about 16 hours. After end of the shaking, the mixture was extracted with phenol [saturated with 1 M Tris-HCl (pH 8.0)]·chloroform. An aqueous layer was collected, added with NaCl in a concentration of 0.5 N, and allowed to precipitate from ethanol, and the generated precipitate was collected. The collected precipitate was

rinsed with 70% ethanol, to obtain genomic DNA.

From the obtained genomic DNA, a DNA fragment (S, SEQ ID NO: 142, a region corresponding to the base numbers 271743 to 272083 of yeast chromosome VII shown in Genbank Accession No. NC_001139 and so on) to be used as a test sample was amplified by conducting PCR using primers (PF3 and PR3) of SEQ ID NO: 140 and SEQ ID NO: 141 and the following reaction condition.

PF3: 5'-AGGTGAGCTACGTGTGTTTGG-3' (SEQ ID NO: 140)

PR3: 5'-AGACATGTGCTCACGTACGGT-3' (SEQ ID NO: 141)

<DNA fragment>

S: 5'-

AGGTGAGCTACGTGTGTTTGGGCGTCGTGCACTGGCTCACTTGTACGCGCAGAAATGGCAGC
TTGTACGATTGGTGACCCGCCTTTTCGACACTGGACCGCTATGGACGTGGCGGCGGTGTGGC
GGCGGCTCAATGACCTGTGGCGCCCGTTTGTGGCGTGCGATAGTCGAGCCGCCTGTCACGTG
CGCGGCCGCCCTGCTCCGTTTGACGCGATGCATAGCATGCGACCACCCAGTAATCATACTGC
TGACGCTATTGGTCACGTGGTTATGGCAGCTGCTGTTGACTGCGGTGGCGTCCCGTTTCCAC
ACCGTACGTGAGCACATGTCT-3' (SEQ ID NO: 142)

As a reaction solution of PCR, 10 ng of genomic DNA which is a template, each 3 μL of 5 μM of the aforementioned primer solutions, each 5 μL of 2 mM dNTPs, 5 μL of a 10 × buffer (100 mM Tris-HCl pH 8.3, 500 mM KCl, 15 mM $MgCl_2$, 0.01% Gelatin), and 0.25 μL of a 5 U/μL thermostable DNA polymerase (AmpliTaq Gold) were mixed, and sterile ultrapure water was added to a liquid volume of 50 μL. The reaction solution was kept at 95°C for 10 minutes, and then subjected to PCR conducting 40 cycles of incubation each including 20 seconds

at 95°C, 30 seconds at 58°C, and 30 seconds at 72°C.

After conducting PCR, amplification was checked by 2% agarose gel electrophoresis, and a DNA fragment S was purified with Wizard SV Gel/PCR Kit (PROMEGA).

For a part of the obtained DNA fragment solution, a reaction solution was prepared by mixing 1 μL of SssI methylase (available from NEB), 10 μL of 10 × NEBuffer 2 (available from NEB), and 1 μL of S-adenosyl methionine (3.2 mM, available from NEB), and adding sterile ultrapure water to a liquid volume of 100 μL. The reaction solution was incubated at 37°C for 15 to 30 minutes, and further added with 1 μL of S-adenosyl methionine (3.2 mM, available from NEB) and incubated at 37°C for 15 to 30 minutes. This was then purified with Wizard SV Gel/PCR Kit (PROMEGA). These operations were repeated another 5 times, to obtain a methylated DNA fragment (MS, SEQ ID NO: 143).

<Methylated DNA fragment> (N represents 5-methyl cytosine)

MS: 5'-

AGGTGAGCTANGTGTGTTTGGGNGTNGTGCACTGGCTCACTTGTANGNGCAGAAATGGCAGC
TTGTANGATTGGTGACCNGCCTTTTNGACACTGGACNGCTATGGANGTGGNGGNGGTGTGGN
GGNGGCTCAATGACCTGTGGNGCCNGTTTGTGGNGTGNGATAGTNGAGCNGCCTGTCANGTG
NGNGGCNGCCCTGCTCNGTTTGANGNGATGCATAGCATGNGACCACCCAGTAATCATACTGC
TGANGCTATTGGTCANGTGGTTATGGCAGCTGCTGTTGACTGNGGTGGNGTCCNGTTTCCAC
ACNGTAOGTGAGCACATGTCT-3' (SEQ ID NO: 143)

For the obtained DNA fragment S, the following solutions were prepared in duplicate.

Solution A: 10 ng/10 μL solution in TE

Solution B: 1 ng/10 μL solution in TE

Solution C: 0.1 ng/10 μL solution in TE

Solution D: TE solution (negative control solution)

For the obtained DNA fragment MS, the following solutions were prepared in duplicate.

Solution MA: 10 ng/10 μL solution in TE

Solution MB: 1 ng/10 μL solution in TE

Solution MC: 0.1 ng/10 μL solution in TE

Solution MD: TE solution (negative control solution)

Also a 5'-end biotin-labeled oligonucleotide B3 having the nucleotide sequence of SEQ ID NO: 145 capable of complementarily binding to a target DNA region S' having the nucleotide sequence of SEQ ID NO: 144 was synthesized, and a 0.02 μM solution thereof in TE buffer was prepared.

<Target DNA region> (5-methyl cytosine is also denoted by C)

S': 5'-
AGGTGAGCTACGTGTGTTTGGGCGTCGTGCACTGGCTCACTTGTACGCGCAGAAATGGCAGC
TTGTACGATTGGTGACCCGCCTTTTCGACACTGGACCGCTATGGACGTGGCGGCGGTGTGGC
GGCGGCTCAATGACCTGTGGCGCCCGTTTGTGGCGTGCGATAGTCGAGCCGCCTGTCACGTG
CGCGGCCGCCCTGCTCCGTTTGACGCGATGCATAGCATGCGACCACCCAGTAATCATACTGC
TGACGCTATTGGTCACGTGGTTATGGCAGCTGCTGTTGACTGCGGTGGCGTCCCGTTTCCAC
ACCGTACGTGAGCACATGTCT-3' (SEQ ID NO: 144)

<5'-end biotin-labeled oligonucleotide>

B3: 5'Biotin-AGACATGTGCTCACGTACGGT-3' (SEQ ID NO: 145)

Counter oligonucleotides C16 to C25 having the nucleotide sequences of SEQ ID NO: 146 to SEQ ID NO: 155 capable of complementarily binding to a minus strand of the target DNA region S' having the nucleotide sequence of SEQ ID NO: 144 were synthesized, and a solution in TE buffer wherein a concentration of each oligonucleotide is 0.01 μM was prepared.

<Target DNA region> (5-methyl cytosine is also denoted by C)

S': 5'-

AGGTGAGCTACGTGTGTTTGGGCGTCGTGCACTGGCTCACTTGTACGCGCAGAAATGGCAGC
TTGTACGATTGGTGACCCGCCTTTTCGACACTGGACCGCTATGGACGTGGCGGCGGTGTGGC
GGCGGCTCAATGACCTGTGGCGCCCGTTTGTGGCGTGCGATAGTCGAGCCGCCTGTCACGTG
CGCGGCCGCCCTGCTCCGTTTGACGCGATGCATAGCATGCGACCACCCAGTAATCATACTGC
TGACGCTATTGGTCACGTGGTTATGGCAGCTGCTGTTGACTGCGGTGGCGTCCCGTTTCCAC
ACCGTACGTGAGCACATGTCT-3' (SEQ ID NO: 144)

<Counter oligonucleotides>

C16: 5'-AGGTGAGCTACGTGTGTTTGG-3' (SEQ ID NO: 146)

C17: 5'-GCGTCGTGCACTGGCTCACTTGTACGCGCA-3' (SEQ ID NO: 147)

C18: 5'-CTTGTACGATTGGTGACCCGCCTTTTCGAC-3' (SEQ ID NO: 148)

C19: 5'-ACTGGACCGCTATGGACGTGGCGGCGGTGT-3' (SEQ ID NO: 149)

C20: 5'-GGCGGCGGCTCAATGACCTGTGGCGCCCGT-3' (SEQ ID NO: 150)

C21: 5'-TTGTGGCGTGCGATAGTCGAGCCGCCTGTC-3' (SEQ ID NO: 151)

C22: 5'-ACGTGCGCGGCCGCCCTGCTCCGTT-3' (SEQ ID NO: 152)

C23: 5'-TGACGCGATGCATAGCATGCGACCACCCAG-3' (SEQ ID NO: 153)

C24: 5'-ACTGCTGACGCTATTGGTCACGTGGTTATG-3' (SEQ ID NO: 154)

C25: 5'-CTGCTGTTGACTGCGGTGGCGTCCCGTTTC-3' (SEQ ID NO: 155)

For each of the solutions of the DNA fragment S and the solutions of the methylated DNA fragment MS, the following treatment was executed.

To a PCR tube, 10 μL of a DNA fragment solution prepared as described above, 10 μL of a biotin-labeled oligonucleotide solution prepared as described above, 10 μL of a counter oligonucleotide solution prepared as described above, 10 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithiothreitol), 10 μL of a 100 mM $MgCl_2$ solution, and 10 μL of a 1 mg/mL BSA solution were added, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed. Thereafter, this PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Then the tube was cooled to 50°C and kept at this temperature for 10 minutes, and further kept at 37°C for 10 minutes, and returned to room temperature (these correspond to First step of the present measuring method).

A masking oligonucleotide M3 having the nucleotide sequence of SEQ ID NO: 156 capable of complementarily binding to a 5'-end biotin-labeled oligonucleotide B3 having the nucleotide sequence of SEQ ID NO: 145 was synthesized, and a 0.02 μM solution thereof in TE buffer was prepared.

100 μL of a reaction solution of a DNA fragment prepared as described above was added to an 8-well strip coated with streptavidin (available from Perkin Elmer), and immobilized to the well by leaving the solution still for 30 minutes at room

temperature. Then the solution was removed by pipetting, and 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] was added, and the buffer was removed by decantation. This operation was repeated another two times (these correspond to Second step of the present measuring method).

<5'-end biotin-labeled oligonucleotide>

B3: 5'Biotin-AGACATGTGCTCACGTACGGT-3' (SEQ ID NO: 145)

<Masking oligonucleotide>

M3: 5'-ACCGTACGTGAGCACATGTCT-3' (SEQ ID NO: 156)

Each well was added with 100 μL of a methylated cytosine antibody [available from Aviva Systems Biology, a 0.5 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] and 1 μL of the aforementioned masking oligonucleotide solution, and left still for an hour at room temperature. Thereafter, each well was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)].

Then each well was added with 100 μL of an Eu-N1 labeled mouse IgG antibody [available from Perkin Elmer, a 0.05 μg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)], and left still for an hour at room temperature. Then, the solution was removed by decantation, and each well was washed three times with 200 μL of a washing buffer [0.05% Tween 20-containing

phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

Each well was added with 150 µL of Enhancement Solution (available from Perkin Elmer), mixed and left still for about 45 minutes at room temperature. Thereafter, the fluorescence was measured at excitation 340 nm/fluorescence 612 nm (these correspond to Third step of the present measuring method).

The result is shown in Fig. 42. In Solutions MA, MB and MC of the methylated DNA fragment MS, an increase in fluorescence intensity was observed and the intensity was concentration-dependent. In the negative control solution MD, an increase in fluorescence intensity was not observed. In Solutions A, B, C and D of the unmethylated DNA fragment S, an increase in fluorescence intensity was not observed.

These demonstrate that DNA containing a methylated target DNA region can be selected and immobilized by a biotin-labeled oligonucleotide and a methyl cytosine antibody, and methylated DNA can be detected and quantified with high sensitivity.

Example 20

Yeast strain X2180-1A of baker's yeast was cultured in a YPD medium (1% Yeast extract, 2% Peptone, 2% Glucose, pH 5.6 to 6.0) to a turbidity of OD_{600} 0.6 to 1.0, and centrifuged at 10,000 g for 10 minutes, to prepare 1×10^7 of yeast cells. From the prepared yeast cells, a yeast genome was acquired using a generally used preparation method of a yeast genome as described in Methods in Yeast Genetics (Cold Spring Harbor

Laboratory)..

The prepared yeast cells were suspended in Buffer A (1 M sorbitol, 0.1 M EDTA, pH 7.4), added with 2-mercaptoethanol (final concentration 14 mM) and 100 U zymolase (10 mg/ml), and incubated under stirring at 30°C for an hour until the solution became clear. After collecting a protoplast by centrifugation at 550 g for 10 minutes, it was suspended in Buffer B (50 mM Tris-HCl, pH 7.4, 20 mM EDTA), added with sodium dodecyl sulfate in 1% (w/v), and then incubated at 65°C for 30 minutes. Sequentially, 5 M CH_3COOK was added and mingled in a volume ratio of 2/5, and the mixture was cooled on ice for 30 minutes, and then centrifuged at 15,000 g for 30 minutes to collect the supernatant. The collected supernatant was added with 3 M CH_3COONa in a volume ratio of 1/10 and an equal amount of isopropanol and mingled well, and the precipitate obtained by centrifugation at 15,000 g at 4°C for 30 minutes was rinsed with 70% ethanol and collected. After drying, the precipitate was dissolved in 1 mL of TE buffer (10 mM Tris-HCl, pH 8.0, 1 mM EDTA), and added with RNase A (available from Sigma) in a concentration of 40 μg/ml, incubated at 37°C for an hour, and then the mixture was added with proteinase K (available from Sigma) and sodium dodecyl sulfate in a concentrations of 500 μg/mL and 1% (w/v), respectively, and shaken at 55°C for about 16 hours. After end of the shaking, the mixture was extracted with phenol [saturated with 1 M Tris-HCl (pH 8.0)]·chloroform. An aqueous layer was collected, added with NaCl in a concentration of 0.5 N, and allowed to precipitate from ethanol, and the generated

precipitate was collected. The collected precipitate was rinsed with 70% ethanol, to obtain genomic DNA.

From the obtained genomic DNA, a DNA fragment (T, SEQ ID NO: 159, a region corresponding to the base numbers 384569 to 384685 of yeast chromosome VII shown in Genbank Accession No. NC_001139 and so on) to be used as a test sample was amplified by conducting PCR using oligonucleotide primers (PF4 and PR4) designed for PCR of SEQ ID NO: 157 and SEQ ID NO: 158 and the following reaction condition.

<Oligonucleotide primers designed for PCR>

PF4: 5'-GGACCTGTGTTTGACGGGTAT-3' (SEQ ID NO: 157)

PR4: 5'-AGTACAGATCTGGCGTTCTCG-3' (SEQ ID NO: 158)

<DNA fragment>

T: 5'-

GGACCTGTGTTTGACGGGTATAACACTAAGTTGCGCAATTTGCTGTATTGCGAAATCCGCCC

GGACGATATCACTCTTGAGCGCATGTGCCGTTTCCGAGAACGCCAGATCTGTACT-3'

(SEQ ID NO: 159)

As a reaction solution of PCR, 10 ng of genomic DNA which is a template, each 3 μL of oligonucleotide primer solutions prepared to 5 μM, each 5 μL of 2 mM dNTPs, 5 μL of a 10 × buffer (100 mM Tris-HCl pH 8.3, 500 mM KCl, 15 mM $MgCl_2$, 0.01% Gelatin), and 0.25 μL of a 5 U/μL thermostable DNA polymerase (AmpliTaq Gold, available from ABI) were mixed, and sterile ultrapure water was added to a liquid volume of 50 μL. The reaction solution was kept at 95°C for 10 minutes, and then subjected to PCR conducting 40 cycles of incubation each

including 20 seconds at 95°C, 30 seconds at 58°C, and 30 seconds at 72°C.

After conducting PCR, amplification was checked by 1.5% agarose gel electrophoresis, and a DNA fragment T was purified with Wizard SV Gel/PCR Kit (PROMEGA).

For a part of the obtained DNA fragment solution, a reaction solution was prepared by mixing 1 μL of SssI methylase (available from NEB), 10 μL of 10 × NEBuffer 2 (available from NEB), and 1 μL of S-adenosyl methionine (3.2 mM, available from NEB), and adding sterile ultrapure water to a liquid volume of 100 μL. The reaction solution was incubated at 37°C for 15 to 30 minutes, and further added with 1 μL of S-adenosyl methionine (3.2 mM, available from NEB) and incubated at 37°C for 15 to 30 minutes. This was then purified with Wizard SV Gel/PCR Kit (PROMEGA). These operations were repeated another 5 times, to obtain a methylated DNA fragment (MT, SEQ ID NO: 160).

<Methylated DNA fragment> (N represents 5-methyl cytosine)

MT: 5'-
GGACCTGTGTTTGANGGGTATAACACTAAGTTGNGCAATTTGCTGTATTGNGAAATCNGCCN
GGANGATATCACTCTTGAGNGCATGTGCNGTTTCNGAGAANGCCAGATCTGTACT-3'
(SEQ ID NO: 160)

For the obtained DNA fragment T, the following solutions were prepared.

Solution A: 10 ng/10 μL solution in TE

Solution B: 1 ng/10 μL solution in TE

Solution C: 0.1 ng/10 μL solution in TE

Solution D: TE solution (negative control solution)

For the obtained DNA fragment MT, the following solutions were prepared.

Solution MA: 10 ng/10 μL solution in TE

Solution MB: 1 ng/10 μL solution in TE

Solution MC: 0.1 ng/10 μL solution in TE

Solution MD: TE solution (negative control solution)

Also a 5'-end biotin-labeled oligonucleotide B4 having the nucleotide sequence of SEQ ID NO: 162 capable of complementarily binding to a target DNA region T' having the nucleotide sequence of SEQ ID NO: 161 was synthesized, and a 0.02 μM solution thereof in TE buffer was prepared.

<Target DNA region> (5-methyl cytosine is also denoted by C)

T': 5'-

GGACCTGTGTTTGACGGGTATAACACTAAGTTGCGCAATTTGCTGTATTGCGAAATCCGCCC

GGACGATATCACTCTTGAGCGCATGTGCCGTTTCCGAGAACGCCAGATCTGTACT-3'

(SEQ ID NO: 161)

<5'-end biotin-labeled oligonucleotide>

B4: 5'Biotin-AGTACAGATCTGGCGTTCTCG-3' (SEQ ID NO: 162)

Counter oligonucleotides C26, C27, C28 and C29 having the nucleotide sequences of SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165 and SEQ ID NO: 166 capable of complementarily binding to a minus strand of the target DNA region T' having

the nucleotide sequence of SEQ ID NO: 161 were synthesized, and a solution in TE buffer wherein a concentration of each oligonucleotide is 0.01 μM was prepared.

<Target DNA region> (Methyl cytosine is also denoted by C)

T': 5'-

GGACCTGTGTTTGACGGGTATAACACTAAGTTGCGCAATTTGCTGTATTGCGAAATCCGCCC

GGACGATATCACTCTTGAGCGCATGTGCCGTTTCCGAGAACGCCAGATCTGTACT-3'

(SEQ ID NO: 161)

<Counter oligonucleotides>

C26: 5'-GGACCTGTGTTTGACGGGTAT-3' (SEQ ID NO: 163)

C27: 5'-AACACTAAGTTGCGCAATTTGCTGT-3' (SEQ ID NO: 164)

C28: 5'-ATTGCGAAATCCGCCCGGACGATAT-3' (SEQ ID NO: 165)

C29: 5'-CACTCTTGAGCGCATGTGCCGTTTC-3' (SEQ ID NO: 166)

For each of the solutions of the DNA fragment T and the solutions of the methylated DNA fragment MT, the following treatment was executed.

To a PCR tube, 10 μL of a DNA fragment solution prepared as described above, 10 μL of a biotin-labeled oligonucleotide solution prepared as described above, 10 μL of a counter oligonucleotide solution prepared as described above, 10 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithiothreitol), 10 μL of 100 mM $MgCl_2$ solution, and 10 μL of a 1 mg/mL BSA solution were added, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed. Thereafter, this PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and

kept at this temperature for 10 minutes. Then the tube was cooled to 50°C and kept at this temperature for 10 minutes, and further kept at 37°C for 10 minutes, and returned to room temperature (these correspond to First step of the present measuring method).

100 µL of a reaction solution of a DNA fragment prepared as described above was added to an 8-well strip coated with streptavidin (available from Perkin Elmer), and immobilized to the well by leaving the solution still for 30 minutes at room temperature. Then the solution was removed by pipetting, and 200 µL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] was added, and the buffer was removed by decantation. This operation was repeated another two times (these correspond to Second step of the present measuring method).

A masking oligonucleotide M4 having the nucleotide sequence of SEQ ID NO: 167 capable of complementarily binding to a 5'-end biotin-labeled oligonucleotide B4 having the nucleotide sequence of SEQ ID NO: 162 was synthesized, and a 0.02 µM solution thereof in TE buffer was prepared.

<5'-end biotin-labeled oligonucleotide>
B4: 5'Biotin-AGTACAGATCTGGCGTTCTCG-3' (SEQ ID NO: 162)
<Masking oligonucleotide>
M4: 5'-CGAGAACGCCAGATCTGTACT-3' (SEQ ID NO: 167)

Each well was added with 100 µL of a methylated cytosine antibody [available from Aviva Systems Biology, a 0.5 µg/mL

solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] and 1 µL of the aforementioned masking oligonucleotide solution, and left still for an hour at room temperature. Thereafter, each well was washed three times with 200 µL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)].

Then each well was added with 100 µL of an Eu-N1 labeled mouse IgG antibody [available from Perkin Elmer, a 0.05 µg/mL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)], and left still for an hour at room temperature. Then, the solution was removed by decantation, and each well was washed three times with 200 µL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)].

Each well was added with 150 µL of Enhancement Solution (available from Perkin Elmer), stirred for 5 minutes, and left still for 15 minutes at room temperature. Thereafter, the fluorescence was measured at excitation 340 nm/fluorescence 612 nm (these correspond to Third step of the present measuring method).

The result is shown in Fig. 43. In Solutions MA, MB and MC of the methylated DNA fragment MT, an increase in fluorescence intensity was observed and the intensity was concentration-dependent. In the negative control solution MD, an increase in fluorescence intensity was not observed. In Solutions A, B, C and D of the unmethylated DNA fragment T, an

increase in fluorescence intensity was not observed.

These demonstrate that DNA containing a methylated target DNA region T' can be selected and immobilized by a biotin-labeled oligonucleotide and a methyl cytosine antibody, and methylated DNA can be detected and quantified with high sensitivity.

Example 21

A commercially available methylated cytosine antibody (available from Aviva Systems Biology) was labeled with biotin using a commercially available biotinylating kit (Biotin Labeling Kit-NH_2, available from DOJINDO Laboratories) according to the method described in the catalogue. The obtained biotin-labeled methylated cytosine antibody was refrigerated as a solution [about 0.1 μg/100 μL solution of an antibody in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

A 0.5 μg/mL solution of the synthetically obtained biotin-labeled methylated cytosine antibody was prepared, and each 100 μL of this solution was added to an 8-well strip coated with streptavidin (available from Perkin Elmer), and immobilized to wells by leaving the solution still for about an hour at room temperature. Then the solution was removed by pipetting, and 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)] was added, and then the buffer was removed by decantation. This operation was repeated another two times (these correspond to preparation of an immobilized methylated

DNA antibody for use in the present measuring method).

For genomic DNA derived from human blood purchased from Clontech, a DNA fragment (X, SEQ ID NO: 113, a region corresponding to the base numbers 25687390 to 25687775 shown in Genbank Accession No. NT_029419 and so on) to be used as a test sample was amplified by conducting PCR using oligonucleotide primers (PF1 and PR1) designed for PCR of SEQ ID NO: 111 and SEQ ID NO: 112 and the following reaction condition.

<Oligonucleotide primers designed for PCR>

PF1: 5'-CTCAGCACCCAGGCGGCC-3' (SEQ ID NO: 111)

PR1: 5'-CTGGCCAAACTGGAGATCGC-3' (SEQ ID NO: 112)

<DNA fragment>

X: 5'-

CTCAGCACCCAGGCGGCCGCGATCATGAGGCGCGAGCGGCGCGCGGGCTGTTGCAGAGTCTT
GAGCGGGTGGCACACCGCGATGTAGCGGTCGGCTGTCATGACTACCAGCATGTAGGCCGACG
CAAACATGCCGAACACCTGCAGGTGCTTCACCACGCGGCACAGCCAGTCGGGGCCGCGGAAG
CGGTAGGTGATGTCCCAGCACATTTGCGGCAGCACCTGGAAGAATGCCACGGCCAGGTCGGC
CAGGCTGAGGTGTCGGATGAAGAGGTGCATGCGGGACGTCTTGCGCGGCGTCCGGTGCAGAG
CCAGCAGTACGCTGCTGTTGCCCAGCACGGCCACCGCGAAAGTCACCGCCAGCACGGCGATC
TCCAGTTTGGCCAG (SEQ ID NO: 113)

As a reaction solution of PCR, 5 ng of genomic DNA which is a template, each 3 μL of oligonucleotide primer solutions prepared to 5 μM, each 5 μL of 2 mM dNTPs, 5 μL of a 10 × buffer (100 mM Tris-HCl pH 8.3, 500 mM KCl, 15 mM $MgCl_2$, 0.01% Gelatin), and 0.25 μL of a 5 U/μL thermostable DNA polymerase

(AmpliTaq Gold, available from ABI) were mixed, and sterile ultrapure water was added to a liquid volume of 50 μL. The reaction solution was kept at 95°C for 10 minutes, and then subjected to PCR conducting 40 cycles of incubation each including 30 seconds at 95°C, 30 seconds at 61°C, and 45 seconds at 72°C.

After conducting PCR, amplification was checked by 1.5% agarose gel electrophoresis, and a DNA fragment X was purified with Wizard SV Gel/PCR Kit (PROMEGA).

For a part of the obtained DNA fragment solution, a reaction solution was prepared by mixing 1 μL of SssI methylase (available from NEB), 10 μL of 10 × NEBuffer 2 (available from NEB), and 1 μL of S-adenosyl methionine (3.2 mM, available from NEB), and adding sterile ultrapure water to a liquid volume of 100 μL. The reaction solution was incubated at 37°C for 15 to 30 minutes, and further added with 1 μL of S-adenosyl methionine (3.2 mM, available from NEB) and incubated at 37°C for 15 to 30 minutes. This was then purified with Wizard SV Gel/PCR Kit (PROMEGA). These operations were repeated another 5 times, to obtain a methylated DNA fragment (MX, SEQ ID NO: 114).

<DNA fragment> (N represents 5-methyl cytosine)

MX: 5'-

CTCAGCACCCAGGNGGCNGNGATCATGAGGNGNGAGNGGNGNGNGGGCTGTTGCAGAGTCTT
GAGNGGGTGGCACACNGNGATGTAGNGGTNGGCTGTCATGACTACCAGCATGTAGGCNGANG
CAAACATGCNGAACACCTGCAGGTGCTTCACCANGNGGCACAGCCAGTNGGGGCNGNGGAAG
NGGTAGGTGATGTCCCAGCACATTTGNGGCAGCACCTGGAAGAATGCCANGGCCAGGTNGGC

CAGGCTGAGGTGTNGGATGAAGAGGTGCATGNGGGANGTCTTGNGNGGNGTCNGGTGCAGAG
CCAGCAGTANGCTGCTGTTGCCCAGCANGGCCACNGNGAAAGTCACNGCCAGCANGGNGATC
TCCAGTTTGGCCAG-3′ (SEQ ID NO: 114)

For the obtained DNA fragment X, the following solutions were prepared.

Solution A: 10 ng/10 μL solution in TE

Solution B: 1 ng/10 μL solution in TE

Solution C: 0.1 ng/10 μL solution in TE

Solution D: TE solution (negative control solution)

For the obtained DNA fragment MX, the following solutions were prepared.

Solution MA: 10 ng/10 μL solution in TE

Solution MB: 1 ng/10 μL solution in TE

Solution MC: 0.1 ng/10 μL solution in TE

Solution MD: TE solution (negative control solution)

Also a 5′-end FITC-labeled oligonucleotide F1 having the nucleotide sequence of SEQ ID NO: 168 capable of complementarily binding to a target DNA region X′ having the nucleotide sequence of SEQ ID NO: 115 was synthesized, and a 0.02 μM solution thereof in a 10 mM Tris-HCl buffer was prepared.

<Target DNA region> (5-methyl cytosine is also denoted by C)

X′: 5′-

CTCAGCACCCAGGCGGCCGCGATCATGAGGCGCGAGCGGCGCGCGGGCTGTTGCAGAGTCTT

GAGCGGGTGGCACACCGCGATGTAGCGGTCGGCTGTCATGACTACCAGCATGTAGGCCGACG
CAAACATGCCGAACACCTGCAGGTGCTTCACCACGCGGCACAGCCAGTCGGGGCCGCGGAAG
CGGTAGGTGATGTCCCAGCACATTTGCGGCAGCACCTGGAAGAATGCCACGGCCAGGTCGGC
CAGGCTGAGGTGTCGGATGAAGAGGTGCATGCGGGACGTCTTGCGCGGCGTCCGGTGCAGAG
CCAGCAGTACGCTGCTGTTGCCCAGCACGGCCACCGCGAAAGTCACCGCCAGCACGGCGATC
TCCAGTTTGGCCAG-3' (SEQ ID NO: 115)

<5'-end FITC-labeled oligonucleotide>

F1: 5'FITC-CTGGCCAAACTGGAGATCGC-3' (SEQ ID NO: 168)

Counter oligonucleotides C1 to C12 having the nucleotide sequences of SEQ ID NO: 117 to SEQ ID NO: 128 capable of complementarily binding to a minus strand of the target DNA region X' having the nucleotide sequence of SEQ ID NO: 115 were synthesized, and a solution in TE buffer wherein a concentration of each oligonucleotide is 0.01 μM was prepared.

<Target DNA region> (5-methyl cytosine is also denoted by C)

X': 5'-
CTCAGCACCCAGGCGGCCGCGATCATGAGGCGCGAGCGGCGCGCGGGCTGTTGCAGAGTCTT
GAGCGGGTGGCACACCGCGATGTAGCGGTCGGCTGTCATGACTACCAGCATGTAGGCCGACG
CAAACATGCCGAACACCTGCAGGTGCTTCACCACGCGGCACAGCCAGTCGGGGCCGCGGAAG
CGGTAGGTGATGTCCCAGCACATTTGCGGCAGCACCTGGAAGAATGCCACGGCCAGGTCGGC
CAGGCTGAGGTGTCGGATGAAGAGGTGCATGCGGGACGTCTTGCGCGGCGTCCGGTGCAGAG
CCAGCAGTACGCTGCTGTTGCCCAGCACGGCCACCGCGAAAGTCACCGCCAGCACGGCGATC
TCCAGTTTGGCCAG-3' (SEQ ID NO: 115)

<Counter oligonucleotides>

C1: 5'-GCCACCGCGAAAGTCACCGCCAGCACGGCG-3' (SEQ ID NO: 117)

C2: 5'-GCCAGCAGTACGCTGCTGTTGCCCAGCACG-3' (SEQ ID NO: 118)

C3: 5'-CGGGACGTCTTGCGCGGCGTCCGGTGCAGA-3' (SEQ ID NO: 119)

C4: 5'-AGGCTGAGGTGTCGGATGAAGAGGTGCATG-3' (SEQ ID NO: 120)

C5: 5'-ACCTGGAAGAATGCCACGGCCAGGTCGGCC-3' (SEQ ID NO: 121)

C6: 5'-TAGGTGATGTCCCAGCACATTTGCGGCAGC-3' (SEQ ID NO: 122)

C7: 5'-CGGCACAGCCAGTCGGGGCCGCGGAAGCGG-3' (SEQ ID NO: 123)

C8: 5'-ATGCCGAACACCTGCAGGTGCTTCACCACG-3' (SEQ ID NO: 124)

C9: 5'-ATGACTACCAGCATGTAGGCCGACGCAAAC-3' (SEQ ID NO: 125)

C10: 5'-TGGCACACCGCGATGTAGCGGTCGGCTGTC-3' (SEQ ID NO: 126)

C11: 5'-CGCGCGGGCTGTTGCAGAGTCTTGAGCGGG-3' (SEQ ID NO: 127)

C12: 5'-CAGGCGGCCGCGATCATGAGGCGCGAGCGG-3' (SEQ ID NO: 128)

For each of the solutions of the DNA fragment X and the solutions of the methylated DNA fragment MX, the following treatment was executed.

To a PCR tube, 10 μL of a DNA fragment solution prepared as described above, 10 μL of a 5'-end FITC-labeled oligonucleotide solution prepared as described above, 10 μL of a counter oligonucleotide solution prepared as described above, 10 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithiothreitol), 10 μL of a 100 mM $MgCl_2$ solution, and 10 μL of a 1 mg/mL BSA solution were added, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed. Thereafter, this PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Then the tube was cooled to 50°C and kept at this temperature for 10 minutes, and further kept at 37°C for 10 minutes, and returned to room temperature (these correspond to

First step of the present measuring method).

To an 8-well strip coated with streptavidin onto which the aforementioned biotin-labeled methyl cytosine antibody is immobilized, 100 μL of a reaction solution of a DNA fragment prepared as described above was added, and left still at room temperature for an hour. Then, the solution was removed by pipetting, and 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] was added, and the buffer was removed by pipetting. This operation was repeated another two times (these correspond to Second step of the present measuring method).

Thereafter, 100 μL of an HRP-labeled FITC antibody solution [available from Jackson ImmunoResearch Laboratories, a 0.005 μg/100 μL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] was added to each well, and left still for an hour at room temperature. After being left still, each well was added with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)], and then the buffer was removed by decantation. This operation was repeated another two times.

Then, 100 μL of a substrate (available from R&D, #DY999) was added and mixed to each well to start a reaction.

Then after being left still for about 30 minutes at room temperature, each well was added and mixed with 50 μL of a stop solution (1 N H_2SO_4 aqueous solution) to stop the reaction. The absorbance at 450 nm within 30 minutes after

stop of the reaction was measured (these correspond to Third step of the present measuring method).

The result is shown in Fig. 44. In Solutions MA, MB and MC of the methylated DNA fragment MX, an increase in chromogenic intensity was observed, and the intensity was concentration-dependent. In the negative control solution MD, an increase in chromogenic intensity was not observed. In Solutions A, B, C and D of the unmethylated DNA fragment X, an increase in chromogenic intensity was not observed.

These demonstrate that DNA containing a methylated target DNA region can be selected by an immobilized methyl cytosine antibody, and methylated DNA can be detected and quantified with high sensitivity.

Example 22

A commercially available methylated cytosine antibody (available from Aviva Systems Biology) was labeled with biotin using a commercially available biotinylating kit (Biotin Labeling Kit-NH_2, available from DOJINDO Laboratories) according to the method described in the catalogue. The obtained biotin-labeled methylated cytosine antibody was refrigerated as a solution [about 0.1 μg/100 μL solution of an antibody in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

A 0.5 μg/mL solution of the synthetically obtained biotin-labeled methylated cytosine antibody was prepared, and each 100 μL of this solution was added to an 8-well strip coated with streptavidin (available from Perkin Elmer), and

immobilized to wells by leaving the solution still for about an hour at room temperature. Then the solution was removed by pipetting, and 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] was added, and then the buffer was removed by decantation. This operation was repeated another two times (these correspond to preparation of an immobilized methylated DNA antibody for use in the present measuring method).

Yeast strain X2180-1A of baker's yeast was cultured in a YPD medium (1% Yeast extract, 2% Peptone, 2% Glucose, pH 5.6 to 6.0) to a turbidity of OD_{600} 0.6 to 1.0, and centrifuged at 10,000 g for 10 minutes, to prepare 1×10^7 of yeast cells. From the prepared yeast cells, a yeast genome was acquired using a generally used preparation method of a yeast genome as described in Methods in Yeast Genetics (Cold Spring Harbor Laboratory).

The prepared yeast cells were suspended in Buffer A (1 M sorbitol, 0.1 M EDTA, pH 7.4), added with 2-mercaptoethanol (final concentration 14 mM) and 100 U zymolase (10 mg/ml), and incubated under stirring at 30°C for an hour until the solution became clear. After collecting a protoplast by centrifugation at 550 g for 10 minutes, it was suspended in Buffer B (50 mM Tris-HCl, pH 7.4, 20 mM EDTA), added with sodium dodecyl sulfate in 1% (w/v), and then incubated at 65°C for 30 minutes. Sequentially, 5 M CH_3COOK was added and mingled in a volume ratio of 2/5, and the mixture was cooled on ice for 30 minutes, and then centrifuged at 15,000 g for 30 minutes to collect the supernatant. The collected supernatant

was added with 3 M CH_3COONa in a volume ratio of 1/10 and an equal amount of isopropanol and mingled well, and the precipitate obtained by centrifugation at 15,000 g at 4°C for 30 minutes was rinsed with 70% ethanol and collected. After drying, the precipitate was dissolved in 1 mL of TE buffer (10 mM Tris-HCl, pH 8.0, 1 mM EDTA), and added with RNase A (available from Sigma) in a concentration of 40 μg/ml, incubated at 37°C for an hour, and then the mixture was added with proteinase K (available from Sigma) and sodium dodecyl sulfate in a concentrations of 500 μg/mL and 1% (w/v), respectively, and shaken at 55°C for about 16 hours. After end of the shaking, the mixture was extracted with phenol [saturated with 1 M Tris-HCl (pH 8.0)]·chloroform. An aqueous layer was collected, added with NaCl in a concentration of 0.5 N, and allowed to precipitate from ethanol, and the generated precipitate was collected. The collected precipitate was rinsed with 70% ethanol, to obtain genomic DNA.

From the obtained genomic DNA, a DNA fragment (S, SEQ ID NO: 142, a region corresponding to the base numbers 271743 to 272083 of yeast chromosome VII shown in Genbank Accession No. NC_001139 and so on) to be used as a test sample was amplified by conducting PCR using primers (PF3 and PR3) of SEQ ID NO: 140 and SEQ ID NO: 141 and the following reaction condition.

PF3: 5′-AGGTGAGCTACGTGTGTTTGG-3′ (SEQ ID NO: 140)

PR3: 5′-AGACATGTGCTCACGTACGGT-3′ (SEQ ID NO: 141)

<DNA fragment>

S: 5′-

AGGTGAGCTACGTGTGTTTGGGCGTCGTGCACTGGCTCACTTGTACGCGCAGAAATGGCAGC

TTGTACGATTGGTGACCCGCCTTTTCGACACTGGACCGCTATGGACGTGGCGGCGGTGTGGC

GGCGGCTCAATGACCTGTGGCGCCCGTTTGTGGCGTGCGATAGTCGAGCCGCCTGTCACGTG

CGCGGCCGCCCTGCTCCGTTTGACGCGATGCATAGCATGCGACCACCCAGTAATCATACTGC

TGACGCTATTGGTCACGTGGTTATGGCAGCTGCTGTTGACTGCGGTGGCGTCCCGTTTCCAC

ACCGTACGTGAGCACATGTCT-3′ (SEQ ID NO: 142)

As a reaction solution of PCR, 10 ng of genomic DNA which is a template, each 3 μL of 5 μM of the aforementioned primer solutions, each 5 μL of 2 mM dNTPs, 5 μL of a 10 × buffer (100 mM Tris-HCl pH 8.3, 500 mM KCl, 15 mM $MgCl_2$, 0.01% Gelatin), and 0.25 μL of a 5 U/μL thermostable DNA polymerase (AmpliTaq Gold) were mixed, and sterile ultrapure water was added to a liquid volume of 50 μL. The reaction solution was kept at 95°C for 10 minutes, and then subjected to PCR conducting 40 cycles of incubation each including 20 seconds at 95°C, 30 seconds at 58°C, and 30 seconds at 72°C.

After conducting PCR, amplification was checked by 2% agarose gel electrophoresis, and a DNA fragment S was purified with Wizard SV Gel/PCR Kit (PROMEGA).

For a part of the obtained DNA fragment solution, a reaction solution was prepared by mixing 1 μL of SssI methylase (available from NEB), 10 μL of 10 × NEBuffer 2 (available from NEB), and 1 μL of S-adenosyl methionine (3.2 mM, available from NEB), and adding sterile ultrapure water to a liquid volume of 100 μL. The reaction solution was incubated at 37°C for 15 to 30 minutes, and further added with

1 μL of S-adenosyl methionine (3.2 mM, available from NEB) and incubated at 37°C for 15 to 30 minutes. This was then purified with Wizard SV Gel/PCR Kit (PROMEGA). These operations were repeated another 5 times, to obtain a methylated DNA fragment (MS, SEQ ID NO: 143).

<DNA fragment> (N represents 5-methyl cytosine)

MS: 5′-

AGGTGAGCTANGTGTGTTTGGGNGTNGTGCACTGGCTCACTTGTANGNGCAGAAATGGCAGC

TTGTANGATTGGTGACCNGCCTTTTNGACACTGGACNGCTATGGANGTGGNGGNGGTGTGGN

GGNGGCTCAATGACCTGTGGNGCCNGTTTGTGGNGTGNGATAGTNGAGCNGCCTGTCANGTG

NGNGGCNGCCCTGCTCNGTTTGANGNGATGCATAGCATGNGACCACCCAGTAATCATACTGC

TGANGCTATTGGTCANGTGGTTATGGCAGCTGCTGTTGACTGNGGTGGNGTCCNGTTTCCAC

ACNGTANGTGAGCACATGTCT-3′ (SEQ ID NO: 143)

For the obtained DNA fragment S, the following solutions were prepared in duplicate.

Solution A: 10 ng/10 μL solution in TE

Solution B: 1 ng/10 μL solution in TE

Solution C: 0.1 ng/10 μL solution in TE

Solution D: TE solution (negative control solution)

For the obtained DNA fragment MS, the following solutions were prepared in duplicate.

Solution MA: 10 ng/10 μL solution in TE

Solution MB: 1 ng/10 μL solution in TE

Solution MC: 0.1 ng/10 μL solution in TE

Solution MD: TE solution (negative control solution)

Also, a 5′-end FITC-labeled oligonucleotide F2 having the nucleotide sequence of SEQ ID NO: 169 capable of complementarily binding to a target DNA region S′ having the nucleotide sequence of SEQ ID NO: 144 was synthesized, and a 0.02 μM solution thereof in a 10 mM Tris-HCl buffer was prepared.

<Target DNA region> (5-methyl cytosine is also denoted by C)

S′: 5′-
AGGTGAGCTACGTGTGTTTGGGCGTCGTGCACTGGCTCACTTGTACGCGCAGAAATGGCAGC
TTGTACGATTGGTGACCCGCCTTTTCGACACTGGACCGCTATGGACGTGGCGGCGGTGTGGC
GGCGGCTCAATGACCTGTGGCGCCCGTTTGTGGCGTGCGATAGTCGAGCCGCCTGTCACGTG
CGCGGCCGCCCTGCTCCGTTTGACGCGATGCATAGCATGCGACCACCCAGTAATCATACTGC
TGACGCTATTGGTCACGTGGTTATGGCAGCTGCTGTTGACTGCGGTGGCGTCCCGTTTCCAC
ACCGTACGTGAGCACATGTCT-3′ (SEQ ID NO: 144)

<5′-end FITC-labeled oligonucleotide>

F2: 5′FITC-AGACATGTGCTCACGTACGGT-3′ (SEQ ID NO: 169)

Also, counter oligonucleotides C16 to C25 having the nucleotide sequences of SEQ ID NO: 146 to SEQ ID NO: 155 capable of complementarily binding to a minus strand of the target DNA region S′ having the nucleotide sequence of SEQ ID NO: 144 were synthesized, and a solution in TE buffer wherein a concentration of each oligonucleotide is 0.01 μM was prepared.

<Target DNA region> (5-methyl cytosine is also denoted by C)

S': 5'-

AGGTGAGCTACGTGTGTTTGGGCGTCGTGCACTGGCTCACTTGTACGCGCAGAAATGGCAGC

TTGTACGATTGGTGACCCGCCTTTTCGACACTGGACCGCTATGGACGTGGCGGCGGTGTGGC

GGCGGCTCAATGACCTGTGGCGCCCGTTTGTGGCGTGCGATAGTCGAGCCGCCTGTCACGTG

CGCGGCCGCCCTGCTCCGTTTGACGCGATGCATAGCATGCGACCACCCAGTAATCATACTGC

TGACGCTATTGGTCACGTGGTTATGGCAGCTGCTGTTGACTGCGGTGGCGTCCCGTTTCCAC

ACCGTACGTGAGCACATGTCT-3' (SEQ ID NO: 144)

<Counter oligonucleotides>

C16: 5'-AGGTGAGCTACGTGTGTTTGG-3' (SEQ ID NO: 146)

C17: 5'-GCGTCGTGCACTGGCTCACTTGTACGCGCA-3' (SEQ ID NO: 147)

C18: 5'-CTTGTACGATTGGTGACCCGCCTTTTCGAC-3' (SEQ ID NO: 148)

C19: 5'-ACTGGACCGCTATGGACGTGGCGGCGGTGT-3' (SEQ ID NO: 149)

C20: 5'-GGCGGCGGCTCAATGACCTGTGGCGCCCGT-3' (SEQ ID NO: 150)

C21: 5'-TTGTGGCGTGCGATAGTCGAGCCGCCTGTC-3' (SEQ ID NO: 151)

C22: 5'-ACGTGCGCGGCCGCCCTGCTCCGTT-3' (SEQ ID NO: 152)

C23: 5'-TGACGCGATGCATAGCATGCGACCACCCAG-3' (SEQ ID NO: 153)

C24: 5'-ACTGCTGACGCTATTGGTCACGTGGTTATG-3' (SEQ ID NO: 154)

C25: 5'-CTGCTGTTGACTGCGGTGGCGTCCCGTTTC-3' (SEQ ID NO: 155)

For each of the solutions of the DNA fragment S and the solutions of the methylated DNA fragment MS, the following treatment was executed.

To a PCR tube, 10 μL of a DNA fragment solution prepared as described above, 10 μL of a 5'-end FITC-labeled oligonucleotide solution prepared as described above, 10 μL of a counter oligonucleotide solution prepared as described above, 10 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithiothreitol), 10 μL of a 100 mM

$MgCl_2$ solution, and 10 μL of a 1 mg/mL BSA solution were added, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed. Thereafter, this PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Then the tube was cooled to 50°C and kept at this temperature for 10 minutes, and further kept at 37°C for 10 minutes, and returned to room temperature (these correspond to First step of the present measuring method).

To an 8-well strip coated with streptavidin onto which the aforementioned biotin-labeled methyl cytosine antibody is immobilized, 100 μL of a reaction solution of a DNA fragment prepared as described above was added, and left still at room temperature for an hour. Then, the solution was removed by pipetting, and 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] was added, and the buffer was removed by pipetting. This operation was repeated another two times (these correspond to Second step of the present measuring method).

Thereafter, 100 μL of an HRP-labeled FITC antibody solution [available from Jackson ImmunoResearch Laboratories, a 0.005 μg/100 μL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] was added to each well, and left still for an hour at room temperature. After being left still, each well was added with 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH

7.4)], and then the buffer was removed by decantation. This operation was repeated another two times.

Then, 100 µL of a substrate (available from R&D, #DY999) was added and mixed to each well to start a reaction.

Then after being left still for about 15 minutes at room temperature, each well was added and mixed with 50 µL of a stop solution (1 N H_2SO_4 aqueous solution) to stop the reaction. The absorbance at 450 nm of the sample obtained within 30 minutes after stop of the reaction was measured (these correspond to Third step of the present measuring method).

The result is shown in Fig. 45. In Solutions MA, MB and MC of the methylated DNA fragment MS, an increase in chromogenic intensity was observed, and the intensity was concentration-dependent. In the negative control solution MD, an increase in chromogenic intensity was not observed. In Solutions A, B, C and D of the unmethylated DNA fragment S, an increase in chromogenic intensity was not observed.

These demonstrate that DNA containing a methylated target DNA region can be selected by an immobilized methyl cytosine antibody, and methylated DNA can be detected and quantified with high sensitivity.

Example 23

A commercially available methylated cytosine antibody (available from Aviva Systems Biology) was labeled with biotin using a commercially available biotinylating kit (Biotin Labeling Kit-NH_2, available from DOJINDO Laboratories)

according to the method described in the catalogue. The obtained biotin-labeled methylated cytosine antibody was refrigerated as a solution [about 0.1 μg/100 μL solution of an antibody in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)].

A 0.5 μg/mL solution of the synthetically obtained biotin-labeled methylated cytosine antibody was prepared, and each 100 μL of this solution was added to an 8-well strip coated with streptavidin (available from Perkin Elmer), and immobilized to wells by leaving the solution still for about an hour at room temperature. Then the solution was removed by pipetting, and 200 μL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO \cdot 7H_2O$, 154 mM NaCl, pH 7.4)] was added, and then the buffer was removed by decantation. This operation was repeated another two times (these correspond to preparation of an immobilized methylated DNA antibody for use in the present measuring method).

Yeast strain X2180-1A of baker's yeast was cultured in a YPD medium (1% Yeast extract, 2% Peptone, 2% Glucose, pH 5.6 to 6.0) to a turbidity of OD_{600} 0.6 to 1.0, and centrifuged at 10,000 g for 10 minutes, to prepare 1×10^7 of yeast cells. From the prepared yeast cells, a yeast genome was acquired using a generally used preparation method of a yeast genome as described in Methods in Yeast Genetics (Cold Spring Harbor Laboratory).

The prepared yeast cells were suspended in Buffer A (1 M sorbitol, 0.1 M EDTA, pH 7.4), added with 2-mercaptoethanol (final concentration 14 mM) and 100 U zymolase (10 mg/ml), and

incubated under stirring at 30°C for an hour until the solution became clear. After collecting a protoplast by centrifugation at 550 g for 10 minutes, it was suspended in Buffer B (50 mM Tris-HCl, pH 7.4, 20 mM EDTA), added with sodium dodecyl sulfate in 1% (w/v), and then incubated at 65°C for 30 minutes. Sequentially, 5 M CH_3COOK was added and mingled in a volume ratio of 2/5, and the mixture was cooled on ice for 30 minutes, and then centrifuged at 15,000 g for 30 minutes to collect the supernatant. The collected supernatant was added with 3 M CH_3COONa in a volume ratio of 1/10 and an equal amount of isopropanol and mingled well, and the precipitate obtained by centrifugation at 15,000 g at 4°C for 30 minutes was rinsed with 70% ethanol and collected. After drying, the precipitate was dissolved in 1 mL of TE buffer (10 mM Tris-HCl, pH 8.0, 1 mM EDTA), and added with RNase A (available from Sigma) in a concentration of 40 μg/ml, incubated at 37°C for an hour, and then the mixture was added with proteinase K (available from Sigma) and sodium dodecyl sulfate in a concentrations of 500 μg/mL and 1% (w/v), respectively, and shaken at 55°C for about 16 hours. After end of the shaking, the mixture was extracted with phenol [saturated with 1 M Tris-HCl (pH 8.0)]·chloroform. An aqueous layer was collected, added with NaCl in a concentration of 0.5 N, and allowed to precipitate from ethanol, and the generated precipitate was collected. The collected precipitate was rinsed with 70% ethanol, to obtain genomic DNA.

From the obtained genomic DNA, a DNA fragment (T, SEQ ID NO: 159, a region corresponding to the base numbers 384569 to

384685 of yeast chromosome VII shown in Genbank Accession No. NC_001139 and so on) to be used as a test sample was amplified by conducting PCR using oligonucleotide primers (PF4 and PR4) designed for PCR of SEQ ID NO: 157 and SEQ ID NO: 158 and the following reaction condition.

<Oligonucleotide primers designed for PCR>

PF4: 5'-GGACCTGTGTTTGACGGGTAT-3' (SEQ ID NO: 157)

PR4: 5'-AGTACAGATCTGGCGTTCTCG-3' (SEQ ID NO: 158)

<DNA fragment>

T: 5'-

GGACCTGTGTTTGACGGGTATAACACTAAGTTGCGCAATTTGCTGTATTGCGAAATCCGCCC

GGACGATATCACTCTTGAGCGCATGTGCCGTTTCCGAGAACGCCAGATCTGTACT-3'

(SEQ ID NO: 159)

As a reaction solution of PCR, 10 ng of genomic DNA which is a template, each 3 μL of oligonucleotide primer solutions prepared to 5 μM, each 5 μL of 2 mM dNTPs, 5 μL of a 10 × buffer (100 mM Tris-HCl pH 8.3, 500 mM KCl, 15 mM $MgCl_2$, 0.01% Gelatin), and 0.25 μL of a 5 U/μL thermostable DNA polymerase (AmpliTaq Gold, available from ABI) were mixed, and sterile ultrapure water was added to a liquid volume of 50 μL. The reaction solution was kept at 95°C for 10 minutes, and then subjected to PCR conducting 40 cycles of incubation each including 20 seconds at 95°C, 30 seconds at 58°C, and 30 seconds at 72°C.

After conducting PCR, amplification was checked by 1.5% agarose gel electrophoresis, and a DNA fragment T was purified

with Wizard SV Gel/PCR Kit (available from PROMEGA).

A part of the obtained DNA fragment solution was mixed with 1 μL of SssI methylase (available from NEB), 10 μL of 10 × NEBuffer 2 (available from NEB), and 1 μL of S-adenosyl methionine (3.2 mM, available from NEB), and added with sterile ultrapure water to a liquid volume of 100 μL. The reaction solution was incubated at 37°C for 15 to 30 minutes, and further added with 1 μL of S-adenosyl methionine (3.2 mM, available from NEB) and incubated at 37°C for 15 to 30 minutes. This was then purified with Wizard SV Gel/PCR Kit (PROMEGA). These operations were repeated another 5 times, to obtain a methylated DNA fragment (MT, SEQ ID NO: 160).

<DNA fragment> (N represents 5-methyl cytosine)

MT: 5'-
GGACCTGTGTTTGANGGGTATAACACTAAGTTGNGCAATTTGCTGTATTGNGAAATCNGCCN
GGANGATATCACTCTTGAGNGCATGTGCNGTTTCNGAGAANGCCAGATCTGTACT-3'
(SEQ ID NO: 160)

For the obtained DNA fragment T, the following solutions were prepared in duplicate.

Solution A: 10 ng/10 μL solution in TE

Solution B: 1 ng/10 μL solution in TE

Solution C: 0.1 ng/10 μL solution in TE

Solution D: TE solution (negative control solution)

For the obtained DNA fragment MT, the following solutions were prepared in duplicate.

Solution MA: 10 ng/10 μL solution in TE

Solution MB: 1 ng/10 μL solution in TE

Solution MC: 0.1 ng/10 μL solution in TE

Solution MD: TE solution (negative control solution)

Also, a 5'-end FITC-labeled oligonucleotide F3 having the nucleotide sequence of SEQ ID NO: 170 capable of complementarily binding to a target DNA region T' having the nucleotide sequence of SEQ ID NO: 161 was synthesized, and a 0.02 μM solution thereof in a 10 mM Tris-HCl buffer was prepared.

<Target DNA region> (5-methyl cytosine is also denoted by C)

T': 5'-

GGACCTGTGTTTGACGGGTATAACACTAAGTTGCGCAATTTGCTGTATTGCGAAATCCGCCC

GGACGATATCACTCTTGAGCGCATGTGCCGTTTCCGAGAACGCCAGATCTGTACT-3'

(SEQ ID NO: 161)

<5'-end FITC-labeled oligonucleotide>

F3: 5'FITC-AGTACAGATCTGGCGTTCTCG-3' (SEQ ID NO: 170)

Also, counter oligonucleotides C26, C27, C28 and C29 having the nucleotide sequences of SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165 and SEQ ID NO: 166 capable of complementarily binding to a minus strand of the target DNA region T' having the nucleotide sequence of SEQ ID NO: 161 were synthesized, and a solution in TE buffer wherein a concentration of each oligonucleotide is 0.01 μM was prepared.

<Target DNA region> (Methyl cytosine is also denoted by C)

T': 5'-

GGACCTGTGTTTGACGGGTATAACACTAAGTTGCGCAATTTGCTGTATTGCGAAATCCGCCC

GGACGATATCACTCTTGAGCGCATGTGCCGTTTCCGAGAACGCCAGATCTGTACT-3'

(SEQ ID NO: 161)

<Counter oligonucleotides>

C26: 5'-GGACCTGTGTTTGACGGGTAT-3' (SEQ ID NO: 163)

C27: 5'-AACACTAAGTTGCGCAATTTGCTGT-3' (SEQ ID NO: 164)

C28: 5'-ATTGCGAAATCCGCCCGGACGATAT-3' (SEQ ID NO: 165)

C29: 5'-CACTCTTGAGCGCATGTGCCGTTTC-3' (SEQ ID NO: 166)

For each of the solutions of the DNA fragment T and the solutions of the methylated DNA fragment MT, the following treatment was executed.

To a PCR tube, 10 μL of a DNA fragment solution prepared as described above, 10 μL of an FITC-labeled oligonucleotide solution prepared as described above, 10 μL of a counter oligonucleotide solution prepared as described above, 10 μL of a buffer (330 mM Tris-Acetate pH 7.9, 660 mM KOAc, 100 mM $MgOAc_2$, 5 mM Dithiothreitol), 10 μL of a 100 mM $MgCl_2$ solution, and 10 μL of a 1 mg/mL BSA solution were added, and the resultant mixture was added with sterile ultrapure water to a liquid volume of 100 μL, and mixed. Thereafter, this PCR tube was heated at 95°C for 10 minutes, rapidly cooled to 70°C, and kept at this temperature for 10 minutes. Then the tube was cooled to 50°C and kept at this temperature for 10 minutes, and further kept at 37°C for 10 minutes, and returned to room temperature (these correspond to First step of the present

measuring method).

To an 8-well strip coated with streptavidin onto which the aforementioned biotin-labeled methyl cytosine antibody is immobilized, 100 µL of a reaction solution of a DNA fragment prepared as described above was added, and left still at room temperature for an hour. Then, the solution was removed by pipetting, and 200 µL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] was added, and the buffer was removed by pipetting. This operation was repeated another two times (these correspond to Second step of the present measuring method).

Thereafter, 100 µL of an HRP-labeled FITC antibody solution [available from Jackson ImmunoResearch Laboratories, a 0.005 µg/100 µL solution in a 0.1% BSA-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)] was added to each well, and left still for an hour at room temperature. After being left still, each well was added with 200 µL of a washing buffer [0.05% Tween 20-containing phosphate buffer (1 mM KH_2PO_4, 3 mM $Na_2HPO{\cdot}7H_2O$, 154 mM NaCl, pH 7.4)], and then the buffer was removed by decantation. This operation was repeated another two times.

Then, 100 µL of a substrate (available from R&D, #DY999) was added and mixed to each well to start a reaction.

Then after being left still for about an hour at room temperature, each well was added and mixed with 50 µL of a stop solution (1 N H_2SO_4 aqueous solution) to stop the reaction. The absorbance at 450 nm within 30 minutes after

stop of the reaction was measured (these correspond to Third step of the present measuring method).

The result is shown in Fig. 46. In Solutions MA, MB and MC of the methylated DNA fragment MT, an increase in chromogenic intensity was observed, and the intensity was concentration-dependent. In the negative control solution MD, an increase in chromogenic intensity was not observed. In Solutions A, B, C and D of the unmethylated DNA fragment T, an increase in chromogenic intensity was not observed.

From the above, it was demonstrated that in forming a bound body of single-stranded DNA containing a target DNA region and the present oligonucleotide, a reaction system containing a magnesium ion is preferably used. Also from the above, it was confirmed that DNA containing a methylated target DNA region can be selected by an immobilized methyl cytosine antibody, and methylated DNA can be detected and quantified with high sensitivity.

INDUSTRIAL APPLICABILITY

Based on the present invention, it becomes possible to provide a method of detecting or quantifying methylated DNA in an objective DNA region in a genomic DNA contained in a biological specimen in a simple and convenient manner, and so on.

CLAIMS

1. A method of detecting or quantifying methylated DNA in a target DNA region possessed by genomic DNA contained in a biological specimen, comprising:

(1) First step of separating double-stranded DNA contained in a DNA sample derived from the genomic DNA contained in the biological specimen into single-stranded DNA,

(2) Second step of mixing (i) the single-stranded DNA separated in First step, (ii) a methylated DNA antibody, and (iii) an oligonucleotide (hereinafter, also referred to as the present oligonucleotide) capable of binding with the single-stranded DNA without inhibiting binding between the methylated DNA antibody and methylated DNA in a target DNA region, thereby forming a complex of the single-stranded DNA containing methylated DNA in the target DNA region, the methylated DNA antibody, and the oligonucleotide, and separating the complex simultaneously or after the formation; and

(3) Third step of detecting or quantifying the methylated DNA antibody, or the oligonucleotide contained in the separated complex according to an identification function available for detection possessed by the methylated DNA antibody or the oligonucleotide, thereby detecting or quantifying methylated DNA in the target DNA region contained in the biological specimen.

2. The method according to claim 1, wherein as the oligonucleotide that is mixed in Second step, and does not

inhibit binding between the methylated DNA antibody and a methylated base existing in single-stranded DNA containing the target DNA region, two or more kinds of oligonucleotides are used.

3. The method according to claim 1, wherein the complex formed in Second step, or a bound body of the single-stranded DNA separated in First step and the oligonucleotide not inhibiting binding between the methylated DNA antibody and a methylated base existing in single-stranded DNA containing the target DNA region arising during formation of the complex in Second step is formed in a reaction system containing a bivalent positive ion.

4. The method according to claim 3, wherein the bivalent positive ion is a magnesium ion.

5. The method according to any one of claims 1 to 4, comprising as a separating operation of the complex in Second step, a step of making the methylated DNA antibody contained in the formed complex be bound to a support.

6. The method according to any one of claims 1 to 4, comprising as a separating operation of the complex in Second step, a step of making the oligonucleotide contained in the formed complex be bound to a support.

7. The method according to any one of claims 1 to 6,

additionally comprising, between immediately after end of First step and immediately before start of Third step, a step of digesting the single-stranded DNA separated in First step by at least one kind of methylation sensitive restriction enzyme capable of digesting single-stranded DNA.

8. The method according to any one of claims 1 to 6, additionally comprising, between immediately after end of First step and immediately before start of Third step, (i) a step of mixing the single-stranded DNA separated in First step, and a masking oligonucleotide having a recognition sequence of at least one kind of methylation sensitive restriction enzyme as its part, and (ii) digesting a mixture obtained by the previous step (single-stranded DNA existing therein in which DNA is not methylated in the target DNA region) by the methylation sensitive restriction enzyme.

9. The method according to claim 7, wherein the at least one kind of methylation sensitive restriction enzyme capable of digesting single-stranded DNA is HhaI which is a methylation sensitive restriction enzyme capable of digesting single-stranded DNA.

10. The method according to claim 8, wherein the at least one kind of methylation sensitive restriction enzyme is HpaII or HhaI which is a methylation sensitive restriction enzyme.

11. The method according to any one of claims 1 to 10, wherein the methylated DNA antibody is a methyl cytosine antibody.

12. The method according to any one of claims 1 to 11, wherein the biological specimen is serum or plasma of a mammal.

13. The method according to any one of claims 1 to 11, wherein the biological specimen is blood or a bodily fluid of a mammal.

14. The method according to any one of claims 1 to 11, wherein the biological specimen is a cell lysate or a tissue lysate.

15. The method according to any one of claims 1 to 14, wherein the DNA sample derived from the genomic DNA contained in the biological specimen is a DNA sample preliminarily subjected to a digestion treatment by a restriction enzyme whose recognition cleaving site excludes a target DNA region possessed by the genomic DNA.

16. The method according to any one of claims 1 to 15, wherein the DNA sample derived from the genomic DNA contained in the biological specimen is a DNA sample preliminarily subjected to a digestion treatment by at least one kind of methylation sensitive restriction enzyme.

17. The method according to any one of claims 1 to 15, wherein the DNA sample derived from the genomic DNA contained in the biological specimen is a DNA sample preliminarily subjected to a digestion treatment by at least one kind of methylation sensitive restriction enzyme after addition of the masking oligonucleotide.

18. The method according to claim 16 or 17, wherein the at least one kind of methylation sensitive restriction enzyme is HpaII or HhaI which is a methylation sensitive restriction enzyme.

19. The method according to any one of claims 1 to 18, wherein the DNA sample derived from the genomic DNA contained in the biological specimen is a preliminarily purified DNA sample.

20. The method according to any one of claims 1 to 19, wherein the target DNA region possessed by the genomic DNA is a DNA region having a cleaving site recognized by at least one kind of methylation sensitive restriction enzyme.

21. The method according to any one of claims 1 to 20 wherein a counter oligonucleotide is added in separating double-stranded DNA contained in a DNA sample derived from the genomic DNA into single-stranded DNA in First step;

22. The method according to any one of claims 1 to 21, wherein

separation of double-stranded DNA contained in a DNA sample derived from the genomic DNA into single-stranded DNA in First step is conducted in a reaction system containing a bivalent positive ion or a magnesium ion.

SEQUENCE LISTING

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<210> 107

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed biotinated oligonucleotide for fixation

<400> 107

ctaataagcc cttcgtcggc t 21

<210> 108

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide

<220>

<223> n stands for m5c

<400> 108

angaangtan ggangctnga tngttnggtn gccagccgac gaagggctta ttag 54

<210> 109

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide

<400> 109

acgaacgtac ggacgctcga tcgttcggtc gccagccgac gaagggctta ttag 54

<210> 110

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed biotinated oligonucleotide for fixation

<400> 110

ctaataagcc cttcgtcggc t 21

<210> 111

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 111

ctcagcaccc aggcggcc 18

<210> 112

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 112

ctggccaaac tggagatcgc 20

<210> 113

<211> 386

<212> DNA

<213> Artificial Sequence

<220>

<223> Amplified oligonucleotide consist of objective DNA domain (Genbank Accession No. NT029419 25687390-25687775 Homo sapiens)

<400> 113

ctcagcaccc aggcggccgc gatcatgagg cgcgagcggc gcgcgggctg ttgcagagtc 60

ttgagcgggt ggcacaccgc gatgtagcgg tcggctgtca tgactaccag catgtaggcc 120

gacgcaaaca tgccgaacac ctgcaggtgc ttcaccacgc ggcacagcca gtcggggccg 180

cggaagcggt aggtgatgtc ccagcacatt tgcggcagca cctggaagaa tgccacggcc 240

aggtcggcca ggctgaggtg tcggatgaag aggtgcatgc gggacgtctt gcgcggcgtc 300

cggtgcagag ccagcagtac gctgctgttg cccagcacgg ccaccgcgaa agtcaccgcc 360

agcacggcga tctccagttt ggccag 386

<210> 114

<211> 386

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide consist of objective DNA domain (Genbank Accession No. NT029419 25687390-25687775 Homo sapiens) n=m5c

<400> 114

ctcagcaccc aggnggcngn gatcatgagg ngngagnggn gngngggctg ttgcagagtc 60

ttgagngggt ggcacacngn gatgtagngg tnggctgtca tgactaccag catgtaggcn 120

gangcaaaca tgcngaacac ctgcaggtgc ttcaccangn ggcacagcca gtnggggcng 180

nggaagnggt aggtgatgtc ccagcacatt tgnggcagca cctggaagaa tgccanggcc 240

aggtnggcca ggctgaggtg tnggatgaag aggtgcatgn gggangtctt gngnggngtc 300

nggtgcagag ccagcagtan gctgctgttg cccagcangg ccacngngaa agtcacngcc 360

agcanggnga tctccagttt ggccag 386

<210> 115

<211> 386

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide consist of objective DNA domain (Genbank Accession No. NT029419 25687390-25687775 Homo sapiens)

<400> 115

ctcagcaccc aggcggccgc gatcatgagg cgcgagcggc gcgcgggctg ttgcagagtc 60

ttgagcgggt ggcacaccgc gatgtagcgg tcggctgtca tgactaccag catgtaggcc 120

gacgcaaaca tgccgaacac ctgcaggtgc ttcaccacgc ggcacagcca gtcggggccg 180

cggaagcggt aggtgatgtc ccagcacatt tgcggcagca cctggaagaa tgccacggcc 240

aggtcggcca ggctgaggtg tcggatgaag aggtgcatgc gggacgtctt gcgcggcgtc 300

cggtgcagag ccagcagtac gctgctgttg cccagcacgg ccaccgcgaa agtcaccgcc 360

agcacggcga tctccagttt ggccag 386

<210> 116

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed biotinated oligonucleotide for fixation

<400> 116

ctggccaaac tggagatcgc 20

<210> 117

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 117

gccaccgcga aagtcaccgc cagcacggcg 30

<210> 118

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 118

gccagcagta cgctgctgtt gcccagcacg 30

<210> 119

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 119

cgggacgtct tgcgcggcgt ccggtgcaga 30

<210> 120

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 120

aggctgaggt gtcggatgaa gaggtgcatg 30

<210> 121

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 121

acctggaaga atgccacggc caggtcggcc 30

<210> 122

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a

single strand DNA

<400> 122

taggtgatgt cccagcacat ttgcggcagc 30

<210> 123

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 123

cggcacagcc agtcggggcc gcggaagcgg 30

<210> 124

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 124

atgccgaaca cctgcaggtg cttcaccacg 30

<210> 125

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 125

atgactacca gcatgtaggc cgacgcaaac 30

<210> 126

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 126

tggcacaccg cgatgtagcg gtcggctgtc 30

<210> 127

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 127

cgcgcgggct gttgcagagt cttgagcggg 30

<210> 128

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 128

caggcggccg cgatcatgag gcgcgagcgg 30

<210> 129

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide

<400> 129

atctccagtt tggccag 17

<210> 130

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 130

tgagctccgt agggcgtcc 19

<210> 131

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 131

gcgccgggtc cgggccc 17

<210> 132

<211> 121

<212> DNA

<213> Artificial Sequence

<220>

<223> Amplified oligonucleotide consist of objective DNA domain (Genbank Accession No. AC009800 76606-76726 Homo sapiens)

<400> 132

gcgccgggtc cgggccccgat gcgttggcgg gccagggctc cgagaacgag gcgttgtcca 60

tctcaacgag ggcagaggag ccggcgacct ggcgtccccc aaggacgccc tacggagctc 120

a 121

<210> 133

<211> 121

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide consist of objective DNA domain (Genbank Accession No. AC009800 76606-76726 Homo sapiens) n=m5c

<400> 133

gngcngggtc ngggccngat gngttggngg gccagggctc ngagaangag gngttgtcca 60

tctcaangag ggcagaggag cnggngacct ggngtccccc aaggangccc tanggagctc 120

a 121

<210> 134

<211> 121

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide consist of objective DNA domain (Genbank Accession No. AC009800 76606-76726 Homo sapiens)

<400> 134

gcgccgggtc cgggcccgat gcgttggcgg gccagggctc cgagaacgag gcgttgtcca 60

tctcaacgag ggcagaggag ccggcgacct ggcgtccccc aaggacgccc tacggagctc 120

a 121

<210> 135

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed biotinated oligonucleotide for fixation

<400> 135

gacaacgcct cgttctcgg 19

<210> 136

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 136

gcgtccccca aggacgccct acggagctca 30

<210> 137

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 137

ctcaacgagg gcagaggagc cggcgacctg 30

<210> 138

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 138

cgccgggtcc gggccccgatg cgttggcggg 30

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide

<400> 139

ccgagaacga ggcgttgtct 20

<210> 140

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 140

aggtgagcta cgtgtgtttg g 21

<210> 141

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 141

agacatgtgc tcacgtacgg t 21

<210> 142

<211> 331

<212> DNA

<213> Artificial Sequence

<220>

<223> Amplified oligonucleotide consist of objective DNA domain (Genbank Accession No. NC001139 271743-272083 Saccharomyces cereviciae chromosome VII)

<400> 142

aggtgagcta cgtgtgtttg ggcgtcgtgc actggctcac ttgtacgcgc agaaatggca 60

gcttgtacga ttggtgaccc gccttttcga cactggaccg ctatggacgt ggcggcggtg 120

tggcggcggc tcaatgacct gtggcgcccg tttgtggcgt gcgatagtcg agccgcctgt 180

cacgtgcgcg gccgccctgc tccgtttgac gcgatgcata gcatgcgacc acccagtaat 240

catactgctg acgctattgg tcacgtggtt atggcagctg ctgttgactg cggtggcgtc 300

ccgtttccac accgtacgtg agcacatgtc t 331

<210> 143

<211> 331

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide consist of objective DNA domain (Genbank Accession No. NC001139 271743-272083 Saccharomyces cereviciae chromosome VII) n=m5c

<400> 143

aggtgagcta ngtgtgtttg ggngtngtgc actggctcac ttgtangngc agaaatggca 60

gcttgtanga ttggtgaccn gccttttnga cactggacng ctatggangt ggnggnggtg 120

tggnggnggc tcaatgacct gtggngccng tttgtggngt gngatagtng agcngcctgt 180

cangtgngng gcngccctgc tcngtttgan gngatgcata gcatgngacc acccagtaat 240

catactgctg angctattgg tcangtggtt atggcagctg ctgttgactg nggtggngtc 300

cngtttccac acngtangtg agcacatgtc t 331

<210> 144

<211> 331

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide consist of objective DNA domain (Genbank Accession No. NC001139 271743-272083 Saccharomyces cereviciae chromosome VII)

<400> 144

aggtgagcta cgtgtgtttg ggcgtcgtgc actggctcac ttgtacgcgc agaaatggca 60

gcttgtacga ttggtgaccc gcctttcga cactggaccg ctatggacgt ggcggcggtg 120

tggcggcggc tcaatgacct gtggcgcccg tttgtggcgt gcgatagtcg agccgcctgt 180

cacgtgcgcg gccgccctgc tccgtttgac gcgatgcata gcatgcgacc acccagtaat 240

catactgctg acgctattgg tcacgtggtt atggcagctg ctgttgactg cggtggcgtc 300

ccgtttccac accgtacgtg agcacatgtc t 331

<210> 145

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed biotinated oligonucleotide for fixation

<400> 145

agacatgtgc tcacgtacgg t 21

<210> 146

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 146

aggtgagcta cgtgtgtttg g 21

<210> 147

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 147

gcgtcgtgca ctggctcact tgtacgcgca 30

<210> 148

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 148

cttgtacgat tggtgacccg ccttttcgac 30

<210> 149

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 149

actggaccgc tatggacgtg gcggcggtgt 30

<210> 150

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 150

ggcggcggct caatgacctg tggcgcccgt 30

<210> 151

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 151

ttgtggcgtg cgatagtcga gccgcctgtc 30

<210> 152

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 152

acgtgcgcgg ccgccctgct ccgtt 25

<210> 153

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 153

tgacgcgatg catagcatgc gaccacccag 30

<210> 154

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 154

actgctgacg ctattggtca cgtggttatg 30

<210> 155

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 155

ctgctgttga ctgcggtggc gtcccgtttc 30

<210> 156

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide

<400> 156

accgtacgtg agcacatgtc t 21

<210> 157

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 157

ggacctgtgt ttgacgggta t 21

<210> 158

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for PCR

<400> 158

agtacagatc tggcgttctc g 21

<210> 159

<211> 116

<212> DNA

<213> Artificial Sequence

<220>

<223> Amplified oligonucleotide consist of objective DNA domain (Genbank Accession No.NC001139 384569-384685 Saccharomyces cereviciae chromosome VII)

<400> 159

ggacctgtgt ttgacgggta taacactaag ttgcgcaatt tgctgtattg cgaaatccgc 60

ccggacgata tcactcttga gcgcatgtgc cgtttccgag aacgccagat ctgtact 116

<210> 160

<211> 116

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide consist of objective DNA domain (Genbank Accession No.NC001139 384569-384685 Saccharomyces cereviciae chromosome VII) n=m5c

<400> 160

ggacctgtgt ttgangggta taacactaag ttgngcaatt tgctgtattg ngaaatcngc 60

cnggangata tcactcttga gngcatgtgc ngtttcngag aangccagat ctgtact 116

<210> 161

<211> 116

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide consist of objective DNA domain (Genbank Accession No. NC001139 384569-384685 Saccharomyces cereviciae chromosome VII)

<400> 161

ggacctgtgt ttgacgggta taacactaag ttgcgcaatt tgctgtattg cgaaatccgc 60

ccggacgata tcactcttga gcgcatgtgc cgtttccgag aacgccagat ctgtact 116

<210> 162

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed biotinated oligonucleotide for fixation

<400> 162

agtacagatc tggcgttctc g 21

<210> 163

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 163

ggacctgtgt ttgacgggta t 21

<210> 164

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 164

aacactaagt tgcgcaattt gctgt 25

<210> 165

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 165

attgcgaaat ccgcccggac gatat 25

<210> 166

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed counter oligonucleotide for making a objective DNA domain a single strand DNA

<400> 166

cactcttgag cgcatgtgcc gtttc 25

<210> 167

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide

<400> 167

cgagaacgcc agatctgtac t 21

<210> 168

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed FITC labeled oligonucleotide

<400> 168

ctggccaaac tggagatcgc 20

<210> 169

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed FITC labeled oligonucleotide

<400> 169

agacatgtgc tcacgtacgg t 21

<210> 170

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed FITC labeled oligonucleotide

<400> 170

agtacagatc tggcgttctc g 21