

Claims

What is claimed is:

1. A method for screening cancer, which detects the methylation status of target gene in the cells of a specimen, and methylation status is an indicator of the presence or absence of cancer, wherein the method comprises the following steps:

(a) providing the specimen in which the methylation status will be detected;

(b) detecting the methylation status of a CpG sequence the target gene POU4F3 in genomic DNA of the specimen, wherein the methylation status is detected by a primer pair having at least 80% sequence identity or complementary to each primer in the primer pair SEQ ID NO: 20 and 21, or at least 10 contiguous nucleotides identical to each primer in the primer pair having the nucleotide sequences as set forth in SEQ ID NO: 20-21; and

(c) determining whether cancer or precancerous lesions are indicated in the specimen according to the methylation status of the target gene.

2. The method for screening cancer according to Claim 1, wherein the specimen to be detected is Pap smear, ascites, blood, urine, feces, phlegm, oral mucosal cells, gastric fluid, bile, cervical epithelial cells, or an in vitro sample of cancer tissues after surgery.

3. The method for screening cancer according to Claim 1, wherein the method of detecting methylation is methylation specific polymerase chain reaction or quantitative methylation specific polymerase chain reaction.

4. A method for screening cervical cancer, which detects the methylation status of target gene in the cells of a specimen, and methylation status is an indicator of the presence or absence of cancer, wherein the method comprises the following steps:

(a) providing the specimen in which the methylation status will be detected;

(b) detecting the methylation status of a CpG sequence the target gene POU4F3 in genomic DNA of the specimen wherein the methylation status is detected by a primer pair having at least 80% sequence identity or complementary to each primer in the primer pair

SEQ ID NO: 20 and 21, or at least 10 contiguous nucleotides identical to each primer in the primer pair having the nucleotide sequences as set forth in SEQ ID NO: 20-21; and

(c) determining whether cervical cancer or precancerous lesions are indicated in the specimen according to the methylation status of the target gene.

5 5. The method for screening cervical cancer according to Claim 4, wherein the specimen to be detected is Pap smear, blood, cervical epithelial cells, or an in vitro sample of cancer tissues after surgery.

6. The method for screening cervical cancer according to Claim 4, wherein the specimen to be detected is abnormal Pap smear.

10 7. The method for screening cervical cancer according to Claim 4, wherein the specimen to be detected is cervical cell specimen which is positive in human papilloma virus testing.

8. The method for screening cervical cancer according to Claim 4, wherein the method of detecting methylation is methylation specific polymerase chain reaction or
15 quantitative methylation specific polymerase chain reaction.

9. A method for screening ovarian cancer, which detects the methylation status of target gene in the cells of a specimen, and methylation status is an indicator of the presence or absence of cancer, wherein the method comprises the following steps:

(a) providing the specimen in which the methylation status will be detected;

20 (b) detecting the methylation status of a CpG sequence the target gene POU4F3 in genomic DNA of the specimen, wherein the methylation status is detected by a primer pair having at least 80% sequence identity or complementary to each primer pair SEQ ID NO: 20 and 21, or at least 10 contiguous nucleotides identical to each primer in the primer pair having the nucleotide sequences as set forth in SEQ ID NO: 20-21; and

(c) determining whether ovarian cancer or precancerous lesions are indicated in the specimen according to the methylation status of the target gene.

10. The method for screening ovarian cancer according to Claim 9, wherein the specimen to be detected is ovarian cancer tissue, ascites, blood, or an in vitro sample of cancer tissues after surgery.

11. The method for screening ovarian cancer according to Claim 9, wherein the method of detecting methylation is methylation specific polymerase chain reaction or quantitative methylation specific polymerase chain reaction.

12. A method for screening colon cancer, which detects the methylation status of target gene in the cells of a specimen, and methylation status is an indicator of the presence or absence of cancer, wherein the method comprises the following steps:

(a) providing the specimen in which the methylation status will be detected;

(b) detecting the methylation status of a CpG sequence the target gene POU4F3 in genomic DNA of the specimen, wherein the methylation status is detected by a primer pair having at least 80% sequence identity or complementary to each primer in the primer pair SEQ ID NO: 20 and 21, or at least 10 contiguous nucleotides identical to each primer in the primer pair having the nucleotide sequences as set forth in SEQ ID NO: 20-21; and

(c) determining whether colon cancer or precancerous lesions are indicated in the specimen according to the methylation status of the target gene.

13. The method for screening colon cancer according to Claim 12, wherein the specimen to be detected is colon tissue, ascites, blood, feces, or an in vitro sample of cancer tissues after surgery.

14. The method for screening colon cancer according to Claim 12, wherein the method of detecting methylation is methylation specific polymerase chain reaction or quantitative methylation specific polymerase chain reaction.

15. A method for screening breast cancer, which detects the methylation status of target gene in the cells of a specimen, and methylation status is an indicator of the presence or absence of cancer, wherein the method comprises the following steps:

(a) providing the specimen in which the methylation status will be detected;

5 (b) detecting the methylation status of a CpG sequence the target gene POU4F3 in genomic DNA of the specimen, wherein the methylation status is detected by a primer pair having at least 80% sequence identity or complementary to each primer in the primer pair SEQ ID NO: 20 and 21, or at least 10 contiguous nucleotides identical ; and

10 (c) determining whether breast cancer or precancerous lesions are indicated in the specimen according to the methylation status of the target gene.

16. The method for screening breast cancer according to Claim 15, wherein the specimen to be detected is blood, milk, secretions of the breast, cyst, puncture and biopsy specimen, or an in vitro sample of cancer tissues after surgery.

15 17. The method for screening breast cancer according to Claim 15, wherein the method of detecting the methylation status is methylation specific polymerase chain reaction or quantitative methylation specific polymerase chain reaction.

18. A method for screening endometrial cancer, which detects the methylation status of target gene in the cells of a specimen, and methylation status is an indicator of the presence or absence of cancer, wherein the method comprises the following steps:

20 (a) providing the specimen in which the methylation status will be detected;

(b) detecting the methylation status of a CpG sequence the target gene POU4F3 in genomic DNA of the specimen, wherein the methylation status is detected by a primer pair having at least 80% sequence identity or complementary to each primer in the primer pair SEQ ID NO: 20 and 21, or at least 10 contiguous nucleotides identical to each primer in the primer pair having the nucleotide sequences as set forth in SEQ ID NO: 20-21; and

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(c) determining whether endometrial cancer or precancerous lesions are indicated in the specimen according to the methylation status of the target gene.

19. The method for screening endometrial cancer according to Claim 18, wherein the specimen to be detected is blood, vaginal-flushed substances, menses, tissues from dilatation
5 and curettage of uterine, or an in vitro sample of cancer tissues after surgery.

20. The method for screening endometrial cancer according to Claim 18, wherein the method of detecting methylation is methylation specific polymerase chain reaction or quantitative methylation specific polymerase chain reaction.

21. A method for screening sarcoma, which detects the methylation status of target
10 gene in the cells of a specimen, and methylation status is an indicator of the presence or absence of sarcoma, wherein the method comprises the following steps:

(a) providing the specimen in which the methylation status will be detected;

(b) detecting the methylation status of a CpG sequence the target gene POU4F3 in genomic DNA of the specimen, wherein the methylation status is detected by a primer pair
15 having at least 80% sequence identity or complementary to each primer in the primer pair SEQ ID NO: 20 and 21, or least 10 contiguous nucleotides identical to each primer in the primer pair having the nucleotide sequences as set forth in SEQ ID NO: 20-21; and

(c) determining whether sarcoma is indicated in the specimen according to the methylation status of the target gene.

22. The method for screening sarcoma according to Claim 21, the specimen to be
20 detected is blood, or an in vitro sample of cancer tissues after surgery.

23. The method for screening sarcoma according to Claim 21, wherein the method of detecting methylation is methylation specific polymerase chain reaction or quantitative methylation specific polymerase chain reaction.