CLAIMS

What is claimed is:

1. A composition for detecting colorectal cancer, comprising reagents for detecting methylation status of *ADHFE1* gene, *PPP2R5C* gene, and *SDC2* gene, wherein:

the reagent for detecting the *ADHFE1* gene comprises sequences as set forth in SEQ ID NO: 7, SEQ ID NO: 8, and SEQ ID NO: 127;

the reagent for detecting the *PPP2R5C* gene comprises sequences as set forth in SEQ ID NO: 53, SEQ ID NO: 54, and SEQ ID NO: 139; and

the reagent for detecting the *SDC2* gene comprises sequences as set forth in SEQ ID NO: 89, SEQ ID NO: 90, and SEQ ID NO: 101.

2. The composition according to claim 1, wherein:

the composition further comprises a reagent for detecting a *GAPDH* gene, the reagent for detecting the *GAPDH* gene comprising sequences as set forth in SEQ ID NO: 1, SEQ ID NO: 2, and SEQ ID NO: 99.

3. The composition according to claim 1, further comprising at least one selected from PCR buffer, salt ion, dNTP, DNA polymerase, or target nucleic acid.

4. A kit for diagnosing colorectal cancer, the kit comprising the composition according to any one of claims 1 to 3.

5. The kit according to claim 4, further comprising at least one of the following reagents:

a DNA extraction reagent, a DNA methylation conversion reagent, and a nucleic acid purification reagent.

6. A method for determining methylation status of genes in a sample, wherein the genes are *ADHFE1* gene, *PPP2R5C* gene, and *SDC2* gene,

the method comprising:

(1) extracting genomic DNA from a biological sample;

(2) obtaining the conversion product by treating the genomic DNA wherein a methylated site exhibits a difference from non-methylated site through the methylation

treatment of the genomic DNA; and

(3) performing, by using reagents, fluorescent quantitative PCR detection on the conversion product to determine the methylation status the genes in the sample, wherein:

the reagent for detecting the *ADHFE1* gene comprises sequences as set forth in SEQ ID NO: 7, SEQ ID NO: 8, and SEQ ID NO: 127;

the reagent for detecting the *PPP2R5C* gene comprises sequences as set forth in SEQ ID NO: 53, SEQ ID NO: 54, and SEQ ID NO: 139; and

the reagent for detecting the *SDC2* gene comprises sequences as set forth in SEQ ID NO: 89, SEQ ID NO: 90, and SEQ ID NO: 101.

7. The method according to claim 6, wherein the sample comprises at least one selected from a tissue sample, a blood sample, secreta, or excreta.

8. The method according to claim 7, wherein the excreta comprises fecal sample.

9. The method according to claim 6, wherein the fluorescent quantitative PCR detection is performed at 95°C for 10 minutes, at 95°C for 15 seconds, at 55°C for 30 seconds, and at 72°C for 30 seconds, for 45 cycles in total.

10. A method for diagnosis of colorectal cancer by assessing a diseased state of colorectal cancer in a subject, the method comprising:

a) providing a sample of the subject, the sample comprising target nucleic acids of the subject, and the target nucleic acids are nucleic acids from *ADHFE1* gene, *PPP2R5C* gene, and *SDC2* gene;

b) assessing a methylation status of the target nucleic acids; and

c) assessing the diseased state of colorectal cancer in the subject based on the methylation status of the target nucleic acids;

the method further comprising: assessing the diseased state of colorectal cancer in the subject by means of a fluorescent quantitative PCR method using *GAPDH* as an internal reference gene; determining, when the Ct value of *GAPDH* is greater than 37, a failure of quality control; determining, when the Ct values of the *ADHFE1*, *PPP2R5C*, and *SDC2* genes, the diseased state of colorectal cancer in the subject as negative; and calculating, when the Ct values of the *ADHFE1*, *PPP2R5C*, and *SDC2* genes are ≤ 37,

the difference △Ct between the amplified Ct values of *ADHFE1*, *PPP2R5C*, and *SDC2* genes and the amplified Ct value of internal reference *GAPDH* gene, and evaluating a disease state of colorectal cancer in the subject based on the ROC curve results and AUC results of △Ct of the *ADHFE1*, *PPP2R5C*, and *SDC2* genes; when △Ct(*ADHFE1*) ≤ 8, △Ct(*PPP2R5C*) ≤ 5, and △Ct(*SDC2*) ≤ 12, the diseased state of colorectal cancer in the subject as positive;

wherein the methylation status of the target nucleic acids is assessed in step b) by using reagents, wherein:

the reagent for detecting the *ADHFE1* gene comprises sequences as set forth in SEQ ID NO: 7, SEQ ID NO: 8, and SEQ ID NO: 127;

the reagent for detecting the *PPP2R5C* gene comprises sequences as set forth in SEQ ID NO: 53, SEQ ID NO: 54, and SEQ ID NO: 139; and

the reagent for detecting the *SDC2* gene comprises sequences as set forth in SEQ ID NO: 89, SEQ ID NO: 90, and SEQ ID NO: 101.

11. The method according to claim 10, wherein the subject is a mammal.

12. The method according to claim 10, further comprising:

isolating the target nucleic acids from the sample.

13. The method according to claim 10, further comprising:

amplifying the target nucleic acids.