Claims

1. A method for determining whether a biological sample originates from liver cancer tissue comprising;

(a) separating DNA from a biological sample isolated from a subject; and

(b) measuring a methylation level of the sequence represented by SEQ ID NO: 1 or 2 in the separated DNA.

2. The method for determining whether a biological sample originates from liver cancer tissue according to claim 1, wherein the methylation level is a methylation level of CpG site of the sequence represented by SEQ ID NO: 1 or 2.

3. The method for determining whether a biological sample originates from liver cancer tissue according to claim 1, wherein the biological sample is selected from the group consisting of tissue, tissue fragments, cells, cell fragments, blood, plasma, body fluids, feces and urine isolated from the subject.

4. The method for determining whether a biological sample originates from liver cancer tissue according to claim 1,

wherein the (b) is performed by a method selected from the group consisting of PCR, methylation specific PCR, real time methylation specific PCR, MethyLight PCR, MethyLight digital PCR, EpiTYPER, PCR using methylated DNA specific binding protein, quantitative PCR, DNA chip, molecular beacon, MS-HRM (Methylation-sensitive high resolution melting),

asymmetric PCR, asymmetric PCR MS-HRMA (asymmetric PCR Methylation-sensitive high resolution melting analysis), Recombinase Polymerase Amplification, LAMP (Loop-Mediated Isothermal Amplification), Eclipse probe, next generation sequencing panel (NGS panel), pyrosequencing and bisulfide sequencing.

5. A composition for determining whether a biological sample originates from liver cancer tissue comprising an agent capable of measuring a methylation level of the sequence represented by SEQ ID NO: 1 or 2.

6. The composition for determining whether a biological sample originates from liver cancer tissue according to claim 5, wherein the methylation level is a methylation level of CpG site of the sequence represented by SEQ ID NO: 1 or 2.

7. The composition for determining whether a biological sample originates from liver cancer tissue according to claim 5, wherein the agent capable of measuring the methylation level is a primer, probe or antisense nucleic acid binding to the sequence represented by SEQ ID NO: 1 or SEQ ID NO: 2.

8. A composition for diagnosing liver cancer comprising an agent capable of measuring a methylation level of the sequence represented by SEQ ID NO: 1 or 2.

9. The composition for diagnosing liver cancer according to claim 8, wherein the methylation level is a methylation level of CpG site of the sequence represented by SEQ ID NO:

1 or 2.

10. The composition for diagnosing liver cancer according to claim 8, wherein the agent is a primer, probe or antisense nucleic acid binding to the sequence represented by SEQ ID NO: 1 or 2.

11. Use of a composition comprising an agent capable of measuring a methylation level of the sequence represented by SEQ ID NO: 1 or 2 for diagnosing liver cancer.

12. Use of the composition for diagnosing liver cancer according to claim 11, wherein the agent is a primer, probe or antisense nucleic acid binding to the sequence represented by SEQ ID NO: 1 or 2.

13. Use of the composition for diagnosing liver cancer according to claim 11, wherein the methylation level is a methylation level of CpG site of the sequence represented by SEQ ID NO: 1 or 2.