Claims

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

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

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

(c) comparing the methylation level to a methylation level of a control group, wherein the control group is DNA isolated from a biological sample which originated from normal liver tissue, liver cancer tissue, or other tissue.

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

3. The method for determining whether a biological sample originates from liver 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.

4. A method for detecting liver tissue-derived DNA in a biological sample comprising

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

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

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

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

wherein the agent capable of measuring 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.