

WHAT IS CLAIMED IS:

1. A method of identifying an amount of viral-host junctions in ctDNAs from a subject infected with hepatitis B virus comprising:

obtaining the ctDNAs in a serum of the subject;

ligating each ctDNA with at least one adaptor;

amplifying all the ctDNAs ligating the at least one adaptor in a similar proportion by using a plurality of primers, wherein each of the primers is complementary to a sequence of the corresponding adaptor;

hybridizing polynucleotide probes with the ctDNAs ligated with the adaptors;

capturing and isolating target ctDNAs hybridized with the polynucleotide probes;

sequencing the target ctDNAs, wherein the target ctDNAs having one or more viral-host junction sequences, wherein each viral-host junction sequence comprises a viral genome sequence and a host genome sequence; and

accumulating a read number related to the viral-host junctions in the target ctDNAs to identify the amount of the viral-host junctions, wherein the amount of the viral-host junctions are defines as the accumulated read number, the read number is defined as the times the viral-host junction sequence appearing in the target ctDNAs, wherein the detected viral-host junctions sequences comprises same sequences, different sequences, or a combination thereof,

and each viral-host junction sequence is counted to give the read number; and wherein the amount of the viral-host junctions are configured to indicate the hepatitis B virus-related tumor status.

2. The method of claim 1, further comprising comparing the detected amount of the viral-host junctions of the subject at the different time points, to identify changes in size of the tumor.

3. The method of claim 1, wherein the target ctDNAs are enriched by the polynucleotide probes complementary to at least one sequence derived from hepatitis B viral genome.

4. The method of claim 1, wherein the polynucleotide probes cover the whole hepatitis B viral genome sequence.

5. The method of claim 1, wherein the ctDNAs ligating with the corresponding adaptor comprise one end of each ctDNA ligates with the corresponding adaptor, both ends of each ctDNA ligates with the corresponding adaptor, and a combination thereof.

6. A method of monitoring tumor status in a subject caused by infection of hepatitis B virus, comprising:

obtaining the ctDNAs in a serum of the subject;

ligating each ctDNA with at least one adaptor;

amplifying all the ctDNAs ligating the at least one adaptor in a similar proportion by using a plurality of primers, wherein each of the primers is complementary to a sequence of the corresponding adaptor;

hybridizing polynucleotide probes with the ctDNAs ligated with the adaptors;

capturing and isolating target ctDNAs hybridized with the polynucleotide probes;

sequencing the target ctDNAs, wherein the target ctDNAs having one or more viral-host junction sequences, wherein each viral-host junction sequence comprises a viral genome sequence and a host genome sequence;

accumulating a read number related to the viral-host junctions in the target ctDNAs to identify the amount of the viral-host junctions, wherein the amount of the viral-host junctions are defines as the accumulated read number, the read number is defined as the times the viral-host junction sequence appearing in the target ctDNAs, and wherein the detected viral-host junctions sequences comprises same sequences, different sequences, or a combination thereof, and each viral-host junction sequence is counted to give the read number; and

monitoring the tumor status based on the amount of the viral-host junctions in the target ctDNAs.

7. The method of claim 6, wherein the polynucleotide probes cover the whole hepatitis B viral genome sequence.

8. The method of claim 6, wherein the ctDNAs ligating with the corresponding adaptor comprise one end of each ctDNA ligates with the corresponding adaptor, both ends of each ctDNA ligates with the corresponding adaptor, and a combination thereof.

9. The method of claim 6, wherein the tumor is a hepatocellular carcinoma induced by hepatitis B virus.

10. The method of claim 6, wherein the ctDNAs obtained at different time points, and wherein the different time points are selected from a cancerous condition, a pre-treatment condition, a post-treatment condition, a recurrence condition of the subject, and any combination thereof.

11. The method of claim 10, further comprising monitoring the tumor development of the subject by comparing the detected the amount of the viral-host junctions of the subject at the different time points.

12. The method of claim 10, wherein increases in the amount of the at least one viral-host junction in the ctDNAs of the subject are indicative of the tumor development from the post-treatment condition to a recurrence condition and decreases in the amount of the at least one viral-host junction in the circulating cell-free DNA of the subject are indicative of the tumor development from the pre-treatment condition to a post-treatment condition of the subject.

13. The method of claim 10, wherein increases in the amount of the at least one viral-host junction in the ctDNAs of the subject in the cancerous condition are indicative of growth of

a tumor and decreases in the amount of the at least one viral-host junction in the circulating ctDNAs of the subject in the cancerous condition are indicative of shrinkage of the tumor.