We claim:

1. A method of testing a body sample of a human with a tumor, comprising:

amplifying tumor DNA of a body sample of the human with a set of amplification primers, wherein each primer consists of a sequence selected from:

sequences of SEQ ID NO: 3, 6, 9, 10, 13, and 14 that optionally further contain a tag sequence selected from SEQ ID NO: 28 and 29; and

sequences of SEQ ID NO: 1, 2, 4, 5, 7, 8, 11, and 12;

to generate amplification products comprising at least one TERT promoter sequence and amplification products comprising at least one IDH1 sequence and amplification products comprising at least one IDH2 sequence, wherein when said primers are used in amplification reactions, they are used in pairs that consist of:

a sequence of SEQ ID NO: 1 and a sequence of SEQ ID NO: 3 that optionally further contains a tag sequence selected from SEQ ID NO: 28 and 29;

a sequence of SEQ ID NO: 2 and a sequence of SEQ ID NO: 3 that optionally further contains a tag sequence selected from SEQ ID NO: 28 and 29;

a sequence of SEQ ID NO: 4 and a sequence of SEQ ID NO: 6 that optionally further contains a tag sequence selected from SEQ ID NO: 28 and 29;

a sequence of SEQ ID NO: 5 and a sequence of SEQ ID NO: 6 that optionally further contains a tag sequence selected from SEQ ID NO: 28 and 29;

a sequence of SEQ ID NO: 7 and a sequence of SEQ ID NO: 9 that optionally further contains a tag sequence selected from SEQ ID NO: 28 and 29;

a sequence of SEQ ID NO: 8 and a sequence of SEQ ID NO: 9 that optionally further contains a tag sequence selected from SEQ ID NO: 28 and 29;

a sequence of SEQ ID NO: 11 and a sequence of SEQ ID NO: 13 that optionally further contains a tag sequence selected from SEQ ID NO: 28 and 29;

a sequence of SEQ ID NO: 12 and a sequence of SEQ ID NO: 13 that optionally further contains a tag sequence selected from SEQ ID NO: 28 and 29;

a sequence of SEQ ID NO: 3 that optionally further contains a tag sequence selected from SEQ ID NO: 28 and 29 and a sequence of SEQ ID NO: 6 that optionally further contains a tag sequence selected from SEQ ID NO: 28 and 29;

a sequence of SEQ ID NO: 9 that optionally further contains a tag sequence selected from SEQ ID NO: 28 and 29 and a sequence of SEQ ID NO: 10 that optionally further contains a tag sequence selected from SEQ ID NO: 28 and 29; and

a sequence of SEQ ID NO: 13 that optionally further contains a tag sequence selected from SEQ ID NO: 28 and 29 and a sequence of SEQ ID NO: 14 that optionally further

contains a tag sequence selected from SEQ ID NO: 28 and 29;
wherein primers consisting of SEQ ID NO: 1, 2, 4, 5, 7, 8, 11, and 12 contain a modified LNA nucleotide at their 3' ends; and
detecting the amplification products.

2. The method of claim 1 further comprising amplifying tumor DNA in the body sample with a set of amplification primers comprising sequences of SEQ ID NO: 15-21.

3. The method of claim 1 wherein the tumor DNA is genomic DNA.

4. The method of claim 1 wherein the tumor DNA is genomic DNA that has been subjected to pre-amplification.

5. The method of claim 1 wherein at least a portion of cycles of the amplifying are conducted at $\geq 66^{\circ}$ C.

6. The method of claim 5 wherein a portion of the cycles of the amplifying are conducted at $\leq 60^{\circ}$C.

7. The method of claim 1 wherein separate aliquots of the tumor DNA of the body sample are amplified with sets of primers comprising sequences of: (a) SEQ ID NO: 1-3; (b) SEQ ID NO: 4-6; (c) SEQ ID NO: 3 and 6; (d) SEQ ID NO: 7-9; (e) SEQ ID NO: 9 and 10; (f) SEQ ID NO: 11-13; and (g) SEQ ID NO: 13-14.

8. The method of claim 1 wherein the amplification is performed as a quantitative PCR.

9. The method of claim 4 wherein the pre-amplification employs a high fidelity DNA polymerase.

10. The method of claim 4 wherein the pre-amplification employs an annealing temperature of $\geq 66^{\circ}$ C.

11. The method of claim 4 wherein the pre-amplification employs an annealing temperature of $\geq 68^{\circ}$ C.

12. The method of claim 4 wherein the pre-amplification is conducted as a multiplex

reaction.

13. The method of claim 1 wherein the body sample is selected from the group consisting of cerebral spinal fluid (CSF), blood, lymph, serum, plasma, urine, saliva, mucus, and tears.

14. The method of claim 1 wherein the body sample is a biopsy sample.

15. The method of claim 1 wherein the body sample is a needle aspirate.

16. The method of claim 2 wherein at least one of said primers comprising sequences of SEQ ID NOs: 15-21 comprise an LNA-modified nucleotide at its 3’ end.

17. The method of claim 2 wherein each of said primers comprising sequences of SEQ ID NOs: 15-21 comprise an LNA-modified nucleotide at its 3’ end.

18. The method of claim 1 wherein the tag sequence is located at the 5’ end of at least one of the primers.

19. The method of claim 2 wherein the tag sequence is located at the 5’ end of at least one of the primers.

20. The method of claim 1 wherein each of SEQ ID NO: 1-14 is represented in a primer in the set of amplification primers.