What is claimed is:

1. A method of predicting the cancer status of a subject comprising:
    a) determining a clinical risk score for the subject;
    b) determining a genomic risk score the subject;
    c) combining the clinical risk score with the genomic risk score, thereby predicting the cancer status of the subject.

2. The method of claim 1, wherein the clinical score comprises the age, sex and/or race of the subject.

3. The method of claim 1, wherein the genomic risk score comprises cell free DNA (cfDNA) fragment size density data from the subject.

4. The method of claim 3, wherein determining the cfDNA fragment size density data for the subject comprises:
    a) processing a sample that has been obtained from the subject comprising cfDNA fragments into libraries;
    b) subjecting the libraries to low-coverage whole genome sequencing to obtain sequenced fragments;
    c) mapping the sequenced fragments to a genome to obtain windows of mapped sequences;
    d) analyzing the windows of mapped sequences to determine cfDNA fragment lengths; and
    e) generating the cfDNA fragment size density data.

5. The method of claim 4, wherein the cfDNA fragment size density data comprises a curve.

6. The method of claim 5, wherein the cfDNA fragment size density curve from the subject is compared to a cfDNA fragment size density curve from a known healthy subject and/or a known cancer patient.

7. The method of claim 1, wherein combining the clinical risk score and the genomic risk score results in a greater number of positive cancer diagnoses per subject screenings, as compared to using clinical risk score or genomic risk score alone.

8. The method of claim 7, wherein the number of subject screenings needed to achieve one positive cancer diagnosis is reduced by at least an average of about 5%, 15%, 25%, 35%, 45%, 55%, 65%, 75% or more, compared to using clinical risk score alone.

9. The method of claim 7, wherein the number of subject screenings needed to achieve one positive cancer diagnosis is reduced by at least an average of about 5%, 10%, 15%, 20%, 25% or more, compared to using genetic risk score alone.

10. The method of claim 7, wherein the sensitivity of cancer prediction is at least about 50%, 60%, 70%, 80%, 90% or more.

11. The method of claim 10, wherein combining the clinical risk score and the genomic risk score results in a higher specificity of cancer prediction as compared to using clinical risk score alone or genomic risk score alone.

12. The method of claim 1, wherein combining the clinical risk score and the genomic risk score results in improved discrimination between subjects predicted to have a high risk for cancer and subjects precited to have a low risk for cancer.

13. The method of any of claims 1-12, wherein the cancer is lung cancer.

14. The method of claim 1, wherein the clinical risk score and the genomic risk score result in a combined score that increases as the subject's risk for cancer increases.

15. The method of claim 1, wherein the clinical risk score and the genomic risk score result in a combined score that decreases as the subject's risk for cancer decreases.

16. The method of claim 1, wherein a subject predicted to have cancer is to be administered a cancer treatment.