CLAIMS

What is claimed:

1. A method of determining the presence or lack thereof cancer of a subject, the method comprising:
    (a) providing one or more sequencing reads of a biological sample obtained from a subject;
    (b) filtering the sequencing reads with a genome database to produce a set of filtered non-human sequencing reads;
    (c) decontaminating the filtered non-human sequencing reads to remove contaminant non-human sequencing reads from the filtered non-human sequencing reads;
    (d) translating the decontaminated non-human sequencing reads to non-human proteins;
    (e) mapping the non-human proteins to a protein database, thereby producing a set of protein database associations; and
    (f) processing the set of protein database associations with a trained model thereby determining the presence of cancer of the subject.
2. The method of claim 1, wherein the set of protein database associations comprises a set of functional genes, biochemical pathways, or any combination thereof.
3. The method of claim 1, wherein translating is completed *in silico*.
4. The method of claim 1, wherein the biological sample is a tissue, liquid biopsy, or any combination thereof.
5. The method of claim 1, wherein the subject is human or a non-human mammal.
6. The method of claim 1, wherein the biological sample comprises a nucleic acid composition, wherein the nucleic acid composition comprises DNA, RNA, cell-free DNA, cell-free RNA, exosomal DNA, exosomal RNA, or any combination thereof.
7. The method of claim 1, wherein the genome database is a human genome database.
8. The method of claim 1, wherein the trained model is trained with a set of functional gene and biochemical pathway abundances that are present or absent with a characteristic abundance for a cancer of interest.
9. The method of claim 1, wherein the non-human sequences originate from bacterial, archaeal, fungal, viral, or any combination thereof origins of life.
10. The method of claim 1, wherein the trained model is configured to determine a category or tissue-specific location of the cancer of the subject.

11. The method of claim 1, wherein the trained model is configured to determine one or more types of cancer of the subject.
12. The method of claim 1, wherein the trained model is configured to determine one or more subtypes of the cancer of the subject.
13. The method of claim 1, wherein the trained model is configured to determine a stage of cancer of the subject, cancer prognosis of the subject, or any combination thereof.
14. The method of claim 1, wherein the trained model is configured to determine the presence or lack thereof cancer at a low-stage (stage I or stage II) tumor.
15. The method of claim 1, wherein the trained model is configured to determine an immunotherapy response of the subject when the subject is provided the immunotherapy.
16. The method of claim 1, further comprising providing as an output of the trained model a therapy for the subject to treat the subject's cancer, wherein the subject will respond with positive therapeutic efficacy when administered the therapeutic.
17. The method of claim 1, wherein the cancer of the subject comprises: acute myeloid leukemia, adrenocortical carcinoma, bladder urothelial carcinoma, brain lower grade glioma, breast invasive carcinoma, cervical squamous cell carcinoma and endocervical adenocarcinoma, cholangiocarcinoma, colon adenocarcinoma, esophageal carcinoma, glioblastoma multiforme, head and neck squamous cell carcinoma, kidney chromophobe, kidney renal clear cell carcinoma, kidney renal papillary cell carcinoma, liver hepatocellular carcinoma, lung adenocarcinoma, lung squamous cell carcinoma, lymphoid neoplasm diffuse large B-cell lymphoma, mesothelioma, ovarian serous cystadenocarcinoma, pancreatic adenocarcinoma, pheochromocytoma and paraganglioma, prostate adenocarcinoma, rectum adenocarcinoma, sarcoma, skin cutaneous melanoma, stomach adenocarcinoma, testicular germ cell tumors, thymoma, thyroid carcinoma, uterine carcinosarcoma, uterine corpus endometrial carcinoma, uveal melanoma, or any combination thereof.
18. The method of claim 4, wherein the liquid biopsy comprises: plasma, serum, whole blood, urine, cerebral spinal fluid, saliva, sweat, tears, exhaled breath condensate, or any combination thereof.
19. The method of claim 1, wherein filtering comprises computationally filtering of the sequencing reads by bowtie2, Kraken, or any combination thereof programs.
20. The method of claim 1, wherein the trained model comprises one or more machine learning algorithms.