CLAIMS

WHAT IS CLAIMED IS:

1. A system for generating a report identifying a therapeutic agent for an individual with a cancer comprising:

   a. at least one nucleic acid sequencing device configured to assay a plurality of molecular targets in a biological sample from the individual to determine a nucleic acid sequence for the each of the plurality of molecular targets, wherein the plurality of molecular targets comprises AR, BRAF, CTNNB1, EGFR, ERRB2, ESR1, KIT, KRAS, MET, MLH1, PDGFRA, PDGFRB, PIK3CA (PI3K), PTEN, and TOP1;

   b. at least one computer database comprising:

      i. a reference sequence for each of the plurality of molecular targets; and

      ii. a listing of available therapeutic agents with efficacy linked to each of the plurality of molecular targets;

   c. a computer-readable program code comprising instructions to input the nucleic acid sequences for the each of the plurality of molecular targets and to compare each of the sequences with a corresponding reference sequence from the at least one computer database in (b)(i);

   d. a computer-readable program code comprising instructions to access the at least one computer database and to identify at least one therapeutic agent from the listing of available therapeutic agents in (b)(ii), wherein the comparison to the reference in (c) indicates a likely benefit of the at least one therapeutic agent for treating the cancer; and

   e. a computer-readable program comprising instructions to generate a report that comprises a listing of the molecular targets for which the comparison to the reference sequence indicated a likely benefit of the at least one therapeutic agent in (d) and the at least one therapeutic agent identified in (d).

2. The system of claim **1**, wherein the nucleic acid sequences are input into the system from a location that is remote from the at least one computer database.

3. The system of claim **1**, wherein the nucleic acid sequences are input into the system over an internet connection.

4. The system of claim **1**, wherein the report is in electronic or paper format.

5. The system of claim **1**, wherein the at least one computer database further comprises data corresponding to at least one clinical trial of a molecular target.

6. The system of claim **1**, wherein the reference sequence for each of the plurality of molecular targets comprises a wild type nucleic acid sequence for that molecular target.

7. The system of claim **1**, wherein the nucleic acid sequences are determined after the individual has received drug therapy for the cancer.

8. The system of claim **1**, wherein the nucleic acid sequences are determined by assessing nucleic acid collected from a cell, a tissue sample, a blood sample or any combination thereof.

9. The system of claim **1**, wherein each reference sequence is obtained from at least one individual without the cancer.

10. The system of claim **1**, wherein the plurality of molecular targets further comprises ATRX (RAD54), CDH1 (UVOMORULIN), CDKN1B (p27/kip1), CDKN2A (METASTASIN (MTS-1)), ERBB4, MYC (c-MYC), RAD51, and WISP3 (LOST IN INFLAMMATORY BREAST CANCER (LIBC)).

11. The system of claim **1**, wherein the report further comprises a listing of at least one additional molecular target for which the comparison to the reference in (c) indicates a likely lack of benefit of at least one therapeutic agent and the at least one additional therapeutic agent.

12. The system of claim **1**, further comprising a computer-readable program code comprising instructions to prioritize the list of the at least one therapeutic agent.

13. The system of claim **12**, wherein the report provides a prioritized list of the at least one therapeutic agent.

14. The system of claim **1**, wherein the individual has been treated by and failed to respond to at least one cancer therapeutic.

15. The system of claim **1**, wherein the at least one device configured to assay the plurality of molecular targets is configured to perform next generation (NextGen) sequencing.

16. The system of claim **1**, wherein the at least one device configured to assay the plurality of molecular targets is configured to perform at least one of polymerase chain reaction (PCR), pyrosequencing, real-time PCR, sequencing, NextGen sequencing, methylation specific PCR (MSPCR), restriction fragment length polymorphism (RFLP analysis), immunohistochemistry (IHC), immunoassay, an expression microarray, a comparative genomic hybridization (CGH) microarray, a single nucleotide polymorphism (SNP) microarray, in-situ hybridization (ISH), fluorescent in-situ hybridization (FISH), and a proteomic array.

17. The system of claim **1**, wherein the at least one nucleic acid sequencing device is configured to identify at least one of a mutation, polymorphism, deletion, insertion, substitution, translocation, fusion, break, duplication, amplification or repeat in a nucleic acid sequence corresponding to each of the plurality of molecular targets