

CLAIMS

What is claimed is:

1. A method of monitoring treatment of a patient, comprising:
 - using a plurality of omics data to identify a patient-specific disease-associated protein;
 - determining at least one of presence and quantity of the patient-specific disease associated protein in a first exosome, wherein the first exosome is obtained from a biological fluid of the patient prior to a treatment;
 - wherein the treatment targets the patient-specific disease associated protein;
 - determining at least one of presence and quantity of the patient-specific disease associated protein in a second exosome, wherein the second exosome is obtained from the biological fluid of the patient during or after the treatment; and
 - updating a patient record based on the determination of the at least one of presence and quantity of the patient-specific disease associated protein in the second exosome.
2. The method of any of the preceding claims wherein the plurality of omics data include omics data from a diseased tissue and omics data from matched normal tissue.
3. The method of any of the preceding claims wherein the patient-specific disease associated protein is identified using a pathway analysis algorithm.
4. The method of any of the preceding claims wherein the patient-specific disease associated protein is an overexpressed protein or a mutated protein.
5. The method of any of the preceding claims wherein the patient-specific disease associated protein is a kinase, a receptor, a growth factor, a transcription factor, or a signal transduction-associated protein, and wherein the treatment comprises a chemotherapy targeting the kinase, the receptor, the growth factor, the transcription factor, or the signal transduction-associated protein.
6. The method of any of the preceding claims wherein the patient-specific disease associated protein is a patient and tumor-specific neoepitope, and wherein the treatment comprises an immune therapy targeting the patient and tumor-specific neoepitope.

7. The method of any of the preceding claims further comprising a step of analyzing a nucleic acid present in at least one of the first and second exosome, optionally wherein the nucleic acid is a double minute chromosome.
8. The method of any of the preceding claims wherein the presence and quantity of the patient-specific disease associated protein is determined using mass spectroscopic reaction monitoring.
9. The method of claim 8 wherein the mass spectroscopic reaction monitoring is selected from the group consisting of selected reaction monitoring, consecutive reaction monitoring, multiple reaction monitoring, and parallel reaction monitoring.
10. The method of any of the preceding claims wherein the exosome is isolated using at least one of non-specific entrapment and antibody-mediated capture.
11. The method of any of the preceding claims wherein the step of determining at least one of presence and quantity of the patient-specific disease associated protein in the second exosome is repeated at least once.
12. The method of any of the preceding claims wherein the step of updating the patient record comprises a recommendation to modify the treatment.
13. A method of selecting an exosomal marker for monitoring treatment, comprising:
 - using a plurality of omics data to identify a patient-specific disease associated protein, and identifying a treatment composition targeting the patient-specific disease associated protein;
 - determining at least one of presence and quantity of the patient-specific disease associated protein in an exosome, wherein the exosome is obtained from a biological fluid of the patient prior to a treatment;
 - selecting the patient-specific disease associated protein for monitoring treatment upon determination that the disease associated protein is present in an amount sufficient for quantification.
14. The method of claim 13 wherein the patient-specific disease associated protein is identified using a pathway analysis algorithm.

15. The method of any one of claims 13-14 wherein the plurality of omics data include omics data from a diseased tissue and omics data from matched normal tissue.
16. The method of any one of claims 13-15 wherein the patient-specific disease associated protein is an overexpressed protein or a mutated protein.
17. The method of any one of claims 13-16 wherein the patient-specific disease associated protein is a kinase, a receptor, a growth factor, a transcription factor, or a signal transduction-associated protein, and wherein the treatment comprises a chemotherapy targeting the kinase, the receptor, the growth factor, the transcription factor, or the signal transduction-associated protein.
18. The method of any one of claims 13-16 wherein the patient-specific disease associated protein is a patient and tumor-specific neoepitope, and wherein the treatment comprises an immune therapy targeting the patient and tumor-specific neoepitope.
19. The method of any one of claims 13-18 wherein the presence and quantity of the patient-specific disease associated protein is determined using mass spectroscopic reaction monitoring.
20. The method of any one of claims 13-19 wherein the amount sufficient for quantification is at least an attomol of the disease associated protein.