WHAT IS CLAIMED IS:

1. A method for analyzing a biological sample from a subject, comprising:

(a) assaying said biological sample from said subject to identify proteins in said biological sample to obtain proteomic information of said biological sample, wherein said proteomic information comprises signals assignable to a first plurality of proteins or protein fragments of said proteins in said biological sample;

(b) analyzing nucleic acid molecules from said biological sample to identify genotypic information of said biological sample, wherein said genotypic information comprises signals assignable to a second plurality of proteins or protein fragments associated with said nucleic acid molecules; and

(c) based on said proteomic information and said genotypic information, identifying a peptide variant or a genomic variant of said subject, wherein said peptide variant or said genomic variant is not otherwise identifiable in (a) or (b), respectively, wherein said identifying comprises identifying said peptide variant or said genomic variant based at least in part on a signal of said genotypic information which overlaps with a signal of said proteomic information.

2. The method of claim 1, wherein said signal of said proteomic information overlaps with another signal of said proteomic information, wherein said another signal is assignable to another protein or protein fragment.

3. The method of claim 1, wherein said signal of said genotypic information overlaps with another signal of said genotypic information, wherein said another signal of said genotypic information is assignable to another genomic variant or a nucleic acid sequence of a reference genome corresponding to said another genomic variant.

4. The method of claim 1, wherein (a) comprises subjecting said biological sample to an assay that identifies said proteins in said biological sample.

5. The method of claim 1, wherein (a) comprises contacting said biological sample with a particle under conditions sufficient for adsorption of said proteins from said biological sample to said particle.

6. The method of claim 5, wherein said proteins comprise a compressed dynamic range on said particle.

7. The method of claim 6, wherein said proteins comprise a concentration range of at least 6 orders of magnitude in said biological sample.

8. The method of claim 6, wherein said particle comprises a plurality of particles with different physicochemical properties.

9. The method of claim 8, wherein a first subset of proteins of said proteins adsorbed by a first particle of said plurality of particles comprises at most 80% of types of proteins in common with a second subset of proteins of said proteins adsorbed by a second particle of said plurality of particles.

10. The method of claim 5, wherein said proteins in said biological sample comprise about 250 to 25000 types of proteins or protein groups.

11. The method of claim 1, wherein said subject comprises one subject.

12. The method of claim 1, wherein said subject comprises a plurality of subjects.

13. The method of claim 9, wherein said proteins in said sample comprise from 0.2% to 2% of said types of proteins in said biological sample.

14. The method of claim 1, wherein (a) comprises identifying an abundance of said proteins in said biological sample.

15. The method of claim 1, wherein said nucleic acid molecules comprise a cell-free deoxyribonucleic acid (cfDNA), a cell-free ribonucleic acid (cfRNA), or any combination thereof.

16. The method of claim 15, wherein (b) comprises identifying said nucleic acid molecules as comprising genomic DNA, mitochondrial DNA (mtDNA), circulating tumor DNA (ctDNA), or any combination thereof.

17. The method of claim 16, wherein (b) comprises identifying a cell type, a cancer type, a cancer stage, or any combination thereof of said ctDNA.

18. The method of claim 1, wherein said nucleic acid molecules are derived from an exosome, an apoptotic body, a tumor cell, a healthy cell, a virtosome, an extracellular membrane vesicle, a neutrophil extracellular trap (NET), or any combination thereof.

19. The method of claim 1, further comprising obtaining sequences of said nucleic acid molecules to identify said genotypic information.

20. The method of claim 1, wherein (c) comprises identifying a splicing variant, a conformation, a post-translational modification, a cofactor association, or a substrate association of a protein of said proteins in said biological sample based on said proteomic information and said genotypic information.