What is claimed is:

1. A method of assessing quality of a sample collected from a subject comprising detecting the level of each of N biomarker proteins in the sample, wherein N is at least 1, and wherein at least 1 of the N biomarker proteins is selected from Keratin-1, KRT5, PUR8, TEX29, RIC8A, LANC2, Glyoxalase I, PGP, FBXL4, SLAF1, and CASQ1, wherein the sample is a plasma sample.

2. A method comprising:

a) measuring the level of each of N biomarker proteins in a plasma sample from a subject, wherein N is at least 1, and wherein at least 1 of the N biomarker proteins is selected from Keratin-1, KRT5, PUR8, TEX29, RIC8A, LANC2, Glyoxalas I, PGP, FBXL4, SLAF1, and CASQ1; and

b) identifying the sample as an analysis sample or negative sample based on the level of the N biomarker proteins;

wherein the analysis sample is a sample that is suitable for use in one or more of the following: protein biomarker discovery analysis, protein expression level analysis, a diagnostic method, or a prognostic method, and the negative sample is a sample that is not suitable for use as an analysis sample.

3. A method comprising:

a) contacting a plasma sample from a subject with a set of capture reagents, wherein each capture reagent has affinity for a different biomarker protein of N biomarker proteins wherein N is at least 1, and wherein at least 1 of the N biomarker proteins is selected from Keratin-1, KRT5, PUR8, TEX29, RIC8A, LANC2, Glyoxalase I, PGP, FBXL4, SLAF1, and CASQ1; and

b) measuring the level of each N biomarker protein with the set of capture reagents.

4. The method of any one of claims 1-3, wherein the sample was processed, frozen, and thawed after the sample collection and prior to the detecting.

5. The method of claim 4, wherein the sample processing steps comprised at least one freeze-thaw cycle or wherein the sample processing steps comprised greater than one freeze-thaw cycle.

6. The method of any one of claims 4-5, comprising determining the number of freeze-thaw cycles for the sample.

7. The method of any one of claims 1-6, comprising identifying the sample as passing a quality assessment or failing a quality assessment, wherein the identifying is based, at least in part, on the detected levels of the N biomarker proteins.

8. The method of claim 7, wherein the sample is identified as passing if the number of freeze-thaw cycles is determined to be 1, less than 2, less than 3, less than 4, less than 5, or 5.

9. The method of claim 7, wherein the sample is identified as failing if the number of freeze-thaw cycles is determined to be greater than 5, greater than 6, greater than 7, greater than 8, greater than 9, or greater than 10.

10. The method of any one of claims 1-9, comprising detecting the level of each of N biomarkers in a plurality of samples from a plurality of subjects.

11. A method for comparing a plurality of samples collected from a plurality of subjects comprising detecting a level of each of N biomarker proteins in each of the plurality of samples, wherein N is at least 1, and wherein at least 1 of the N biomarker proteins is selected from Keratin-1, KRT5, PUR8, TEX29, RIC8A, LANC2, Glyoxalase I, PGP, FBXL4, SLAF1, and CASQ1, wherein the sample is a plasma sample.

12. The method of claim 11, comprising a) determining the number of freeze-thaw cycles and b) comparing the determined number of freeze-thaw cycles for each of the plurality of samples.

13. The method of claim 12, comprising identifying the plurality of samples as handled consistently or inconsistently, wherein samples handled consistently all have a determined number of freeze-thaw cycles within 1, 2, 3, 4, or 5 freeze-thaw cycles of each other.

14. The method of claim6 or 12, wherein the determining is based on comparing the detected levels of each of the N biomarker proteins to reference levels, wherein the reference levels are average levels of each of the N biomarker proteins present in samples having 1 freeze-thaw cycle or 2 freeze-thaw cycles.

15. The method of any one of claims 1-7 or 11-14, wherein the detected levels of each of the N biomarker proteins compared to the reference levels indicates that the number of freeze-thaw cycles was greater than 1, greater than 2, greater than 3, greater than 4, greater than 5, greater than 7, or greater than 10 freeze-thaw cycles; or wherein the levels of each of the N biomarker proteins used in a linear regression model predicts the number of freeze-thaw cycles

was greater than 1, greater than 2, greater than 3, greater than 4, greater than 5, greater than 7, or greater than 10 freeze-thaw cycles.

16. The method of any one of claims 11-15, wherein the determining is based on a panel of N biomarker proteins having an R^2 value of at least 0.600, at least 0.650, at least 0.700, at least 0.750, at least 0.800, at least 0.850, at least 0.900, or at least 0.950.

17. The method of any one of claims 11-16, comprising performing protein biomarker discovery analysis, protein expression level analysis, a diagnostic method, or a prognostic method on the sample or the plurality of samples.

18. The method of claim 17, comprising modifying a panel of proteins in the protein biomarker discovery analysis, the protein expression level analysis, the diagnostic method, or the prognostic method based on the determined number of freeze-thaw cycles for each of the plurality of samples; or identifying one or more proteins in the sample as being affected by the number of freeze-thaw cycles; or identifying the level of one or more proteins in the sample as being affected by the number of freeze-thaw cycles; or changing the proteins used in a diagnostic, a prognostic, or a health assessment related test based on the predicted number of freeze-thaw cycles; or removing the proteins used in a diagnostic, a prognostic, or a health assessment related test based on the predicted number of freeze-thaw cycles.

19. The method of claim 18, wherein the panel of biomarker proteins is reduced in number of biomarker proteins measured.

20. The method of any one of claims 11-19, wherein the determining measures compliance with a clinical trial sample collection and processing protocol.

21. The method of any one of claims 11-20, wherein the plurality of samples are collected at more than one sample collection site, optionally, wherein the plurality of samples from a first sample collection site are compared to a second plurality of samples from a second sample collection site.

22. The method of any one of claims 11-21, wherein one or more of the plurality of samples may be removed based on the number of freeze-thaw cycles.

23. The method of any one of claims 1-3 or 11-22, wherein 2 of the N biomarker proteins are Keratin-1 and KRT5; or

wherein 2 of the N biomarker proteins are Keratin -1 and PUR8; or

wherein 2 of the N biomarker proteins are Keratin-1 and TEX29; or

wherein 2 of the N biomarker proteins are Keratin-1 and RIC8A; or
wherein 2 of the N biomarker proteins are Keratin-1and LANC2; or
wherein 2 of the N biomarker proteins are Keratin-1 and Glyoxalase I; or
wherein 2 of the N biomarker proteins are Keratin-1 and PGP; or
wherein 2 of the N biomarker proteins are Keratin -1 and FBXL4; or
wherein 2 of the N biomarker proteins are Keratin-1 and SLAF1; or
wherein 2 of the N biomarker proteins are Keratin-1 and CASQ1; or
wherein 2 of the N biomarker proteins are K2C5 and PUR8; or
wherein 2 of the N biomarker proteins are K2C5 and TEX29; or
wherein 2 of the N biomarker proteins are K2C5 and RIC8A; or
wherein 2 of the N biomarker proteins are K2C5and LANC2; or
wherein 2 of the N biomarker proteins are K2C5 and Glyoxalase I; or
wherein 2 of the N biomarker proteins are K2C5 and PGP; or
wherein 2 of the N biomarker proteins are K2C5 and FBXL4; or
wherein 2 of the N biomarker proteins are K2C5 and SLAF1; or
wherein 2 of the N biomarker proteins are K2C5 and CASQ1; or
wherein 2 of the N biomarker proteins are PUR8 and TEX29; or
wherein 2 of the N biomarker proteins are PUR8 and RIC8A; or
wherein 2 of the N biomarker proteins are PUR8 and LANC2; or
wherein 2 of the N biomarker proteins are PUR8 and Glyoxalase I; or
wherein 2 of the N biomarker proteins are PUR8 and PGP; or
wherein 2 of the N biomarker proteins are PUR8 and FBXL4; or
wherein 2 of the N biomarker proteins are PUR8 and SLAF1; or
wherein 2 of the N biomarker proteins are PUR8 and CASQ1; or
wherein 2 of the N biomarker proteins are TEX29 and RIC8A; or
wherein 2 of the N biomarker proteins are TEX29 and LANC2; or
wherein 2 of the N biomarker proteins are TEX29 and Glyoxalase I; or
wherein 2 of the N biomarker proteins are TEX29 and PGP; or
wherein 2 of the N biomarker proteins are TEX29 and FBXL4; or
wherein 2 of the N biomarker proteins are TEX29 and SLAF1; or
wherein 2 of the N biomarker proteins are TEX29 and CASQ1; or

wherein 2 of the N biomarker proteins are RIC8A and LANC2; or

wherein 2 of the N biomarker proteins are RIC8A and Glyoxalase I; or

wherein 2 of the N biomarker proteins are RIC8A and PGP; or

wherein 2 of the N biomarker proteins are RIC8A and FBXL4; or

wherein 2 of the N biomarker proteins are RIC8A and SLAF1; or

wherein 2 of the N biomarker proteins are RIC8A and CASQ1; or

wherein 2 of the N biomarker proteins are LANC2 and Glyoxalase I; or

wherein 2 of the N biomarker proteins are LANC2 and PGP; or

wherein 2 of the N biomarker proteins are LANC2 and FBXL4; or

wherein 2 of the N biomarker proteins are LANC2 and SLAF1; or

wherein 2 of the N biomarker proteins are LANC2 and CASQ1; or

wherein 2 of the N biomarker proteins are Glyoxalase I and PGP; or

wherein 2 of the N biomarker proteins are Glyoxalase I and FBXL4; or

wherein 2 of the N biomarker proteins are Glyoxalase I and SLAF1; or

wherein 2 of the N biomarker proteins are Glyoxalase I and CASQ1; or

wherein 2 of the N biomarker proteins are PGP and FBXL4; or

wherein 2 of the N biomarker proteins are PGP and SLAF1; or

wherein 2 of the N biomarker proteins are PGP and CASQ1; or

wherein 2 of the N biomarker proteins are FBXL4 and SLAF1; or

wherein 2 of the N biomarker proteins are FBXL4 and CASQ1; or

wherein 2 of the N biomarker proteins are SLAF1 and CASQ1.

24. The method of any one of claims 1-3 or 11-23, wherein N is 3, N is 4, N is 5, N is 6, N is 7, N is 8, N is 9, N is 10, or N is 11.

25. The method of claim 24, wherein all of the N biomarker proteins are selected from Keratin-1, K2C5, PUR8, TEX29, RIC8A, LANC2, Glyoxalase I, PGP, FBXL4, SLAF1 and CASQ1.

26. The method of any one of claims 11-25, wherein the sample was processed, frozen, and thawed after the sample collection and prior to the detecting.

27. The method of claim 26, wherein the sample processing steps comprised at least one freeze-thaw cycle or wherein the sample processing steps comprised greater than one freeze-thaw cycle.

28. The method of any one of claims 1-27, wherein the detecting comprises performing mass spectrometry, an aptamer based assay, and/or an antibody based assay.

29. The method of any one of claims 1-28, wherein the method comprises contacting biomarker proteins of the sample from the subject with a set of capture reagents, wherein each capture reagent of the set of capture reagents specifically binds to one biomarker protein being detected, optionally, wherein each of the capture reagents specifically binds to a different biomarker protein being detected.

30. The method of claim 29, wherein each capture reagent is an antibody or an aptamer.

31. The method of claim 30, wherein each capture reagent is an aptamer.

32. The method of claim 31, wherein at least one aptamer is a slow off-rate aptamer, optionally, wherein each slow off-rate aptamer binds to its target protein with an off rate ($t_{½}$) of ≥ 30 minutes, ≥ 60 minutes, ≥ 90 minutes, ≥ 120 minutes, ≥ 150 minutes, ≥ 180 minutes, ≥ 210 minutes, or ≥ 240 minutes.

33. The method of claim 32, wherein at least one slow off-rate aptamer comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 nucleotides with modifications.

34. A kit comprising N biomarker protein capture reagents, wherein N is at least 1, and wherein at least 1 of the capture reagents bind to proteins selected from Keratin-1, KRT5, PUR8, TEX29, RIC8A, LANC2, Glyoxalase I, PGP, FBXL4, SLAF1, and CASQ1.

35. The kit of claim 34, wherein N is at least 2, and wherein at least 2 of the capture reagents binds to a protein selected from Keratin-1, KRT5, PUR8, TEX29, RIC8A, LANC2, Glyoxalase I, PGP, FBXL4, SLAF1, and CASQ1.

36. The kit of claim 34 or 35, wherein each of the capture reagents binds to a different protein.

37. The kit of any one of claims 34-36, wherein N is 2, N is 3, N is 4, N is 5, N is 6, N is 7, N is 8, N is 9, N is 10, or N is 11.

38. The kit of claim 37, wherein each of the capture reagents binds to a protein selected from Keratin-1, KRT5, PUR8, TEX29, RIC8A, LANC2, Glyoxalase I, PGP, FBXL4, SLAF1, and CASQ1.

39. The kit of any one of claims 34-38, wherein each of the capture reagents is an antibody or an aptamer.

40. The kit of claim 39, wherein each capture reagent is an aptamer.

41. The kit of claim 40, wherein at least one aptamer is a slow off-rate aptamer, optionally, wherein each slow off-rate aptamer binds to its target protein with an off rate ($t_{½}$) of ≥ 30 minutes, ≥ 60 minutes, ≥ 90 minutes, ≥ 120 minutes, ≥ 150 minutes, ≥ 180 minutes, ≥ 210 minutes, or ≥ 240 minutes.

42. The kit of claim 41, wherein at least one slow off-rate aptamer comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 nucleotides with modifications.

43. The kit of any one of claims 34-42, for use in detecting the N biomarker proteins in a sample from a subject.

44. The kit of claim 43, for use in assessing the quality of the sample based at least in part on the levels of the detected N biomarker proteins in the sample and/or for use in determining the number of freeze-thaw cycles for the sample based at least in part on the levels of the detected N biomarker proteins in the sample.

45. A method comprising detecting a level of each of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 biomarker proteins in a sample, wherein the biomarker proteins are selected from Keratin-1, KRT5, PUR8, TEX29, RIC8A, LANC2, Glyoxalase I, PGP, FBXL4, SLAF1, and CASQ1.

46. The method of claim 45, wherein the sample is a plasma sample.

47. The method of claim 45 or 46, wherein a number of freeze-thaw cycles is determined based on the level of each of the at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 biomarker proteins.

48. The method of claim 47, wherein the number of freeze-thaw cycles is determined to be greater than 1, greater than 2, greater than 3, greater than 4, greater than 5, greater than 7 or greater than 10 freeze-thaw cycles.

49. The method of claim 47 or 48, wherein the determined number of freeze-thaw cycles is derived from the input of the level of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 biomarker proteins in a statistical model optionally, wherein the statistical model is a linear regression model.

50. The method of claim 49, further comprising modifying a panel of proteins in a protein biomarker discovery analysis, a protein expression level analysis, a diagnostic method, or a prognostic method; identifying one or more proteins in the sample as being affected; identifying the level of one or more proteins in the sample as being affected; changing the proteins used in a diagnostic, a prognostic, or a health assessment related test; or removing one or more proteins used in a diagnostic, a prognostic, or a health assessment related test, each based on the outcome of the statistical model.