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, at least 2, at least 3, at least 4, at least 5, at least 6, or at least 7 of the N biomarker proteins are selected from LKHA4, EIF1B, RAGP1, SCFD1, PLD3, Lectin, mannose-binding 2, ILK1, and RPL5, wherein the sample is a serum sample.

2. A method comprising:

a) measuring the level of each of N biomarker proteins in a serum sample from a subject, wherein N is at least 1, and wherein at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, or at least 7 of the N biomarker proteins are selected from LKHA4, EIF1B, RAGP1, SCFD1, PLD3, Lectin, mannose-binding 2, ILK1, and RPL5; 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 serum 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, at least 2, at least 3, at least 4, at least 5, at least 6, or at least 7 of the N biomarker proteins is selected from LKHA4, EIF1B, RAGP1, SCFD1, PLD3, Lectin, mannose-binding 2, ILK1, and RPL5; 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.

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

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

8. The method of claim 7, wherein the determining is based on comparing the detected levels of the N biomarker proteins to reference levels, wherein the reference levels are average levels of the N biomarker proteins present in samples having 1 freeze-thaw cycle or 2 freeze-thaw cycles, optionally wherein the determining is based on a panel of N biomarker proteins having an R^2 value of at least 0.65, at least 0.7, at least 0.75, at least 0.8, at least 0.85, at least 0.9, or at least 0.95.

9. The method of claims 1-8, wherein the detected levels of the N biomarker proteins compared to 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.

10. The method of any one of claims 7-9, comprising performing protein biomarker discovery analysis, protein expression level analysis, a diagnostic method, or a prognostic method on the sample.

11. The method of any one of claims 1-10, 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.

12. The method of claim 11, 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.

13. The method of claim 11, 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.

14. The method of any one of claims 1-13, comprising detecting the level of each of N biomarkers in a plurality of samples from a plurality of subjects.

15. A method for comparing a plurality of samples collected from a plurality of subjects comprising detecting the 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, at least 2, at least 3, at least 4, at least 5, at least 6, or at least 7 of the N biomarker proteins is selected from LKHA4, EIF1B, RAGP1, SCFD1, PLD3, Lectin, mannose-binding 2, ILK1, and RPL5, wherein the sample is a serum sample.

16. The method of claim 15, comprising a) determining the number of freeze-thaw cycles and b) comparing the determined number freeze-thaw cycles for each of the plurality of samples.

17. The method of claim 16, 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.

18. The method of claim 16 or 17, 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.

19. The method of any one of claims 15-18, 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.

20. The method of any one of claims 15-19, wherein the determining is based on a panel of N biomarker proteins having an R^2 value of at least 0.65, at least 0.7, at least 0.75, at least 0.8, at least 0.85, at least 0.9, or at least 0.95.

21. The method of any one of claims 15-20, comprising performing protein biomarker discovery analysis, protein expression level analysis, a diagnostic method, or a prognostic method on the plurality of samples.

22. The method of any one of claims 15-21, comprising modifying a panel of biomarker proteins in a protein biomarker discovery analysis, a protein expression level analysis, a diagnostic method, or a 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 panel of biomarker proteins used in a diagnostic, a prognostic, or a health assessment related test based on the predicted number of freeze-thaw cycles; removing the proteins used in a diagnostic, a prognostic, or a health assessment related test based on the predicted number of freeze-thaw cycles.

23. The method of claim 22, wherein the panel of biomarker proteins is reduced in number of biomarker proteins measured.

24. The method of any one of claims 15-23, wherein the determining measures compliance with a clinical trial sample collection and processing protocol.

25. The method of any one of claims 15-24, 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.

26. The method of any one of claims 15-25, wherein one or more of the plurality of samples may be removed based on the number of freeze-thaw cycles.

27. The method of any one of claims 1-3 or 15-26,

wherein 2 of the N biomarker proteins are LKHA4 and EIF1B; or

wherein 2 of the N biomarker proteins are LKHA4 and RAGP1; or

wherein 2 of the N biomarker proteins are LKHA4 and SCFD1; or

wherein 2 of the N biomarker proteins are LKHA4 and PLD3; or

wherein 2 of the N biomarker proteins are LKHA4 and Lectin, mannose-binding 2; or

wherein 2 of the N biomarker proteins are LKHA4 and ILK1; or

wherein 2 of the N biomarker proteins are LKHA4 and RPL5; or

wherein 2 of the N biomarker proteins are EIF1B and RAGP1; or

wherein 2 of the N biomarker proteins are EIF1B and SCFD1; or

wherein 2 of the N biomarker proteins are EIF1B and PLD3; or

wherein 2 of the N biomarker proteins are EIF1B and Lectin, mannose-binding 2; or

wherein 2 of the N biomarker proteins are EIF1B and ILK1; or

wherein 2 of the N biomarker proteins are EIF1B and RPL5; or

wherein 2 of the N biomarker proteins are RAGP1 and SCFD1; or

wherein 2 of the N biomarker proteins are RAGP1 and PLD3; or

wherein 2 of the N biomarker proteins are RAGP1 and Lectin, mannose-binding 2; or

wherein 2 of the N biomarker proteins are RAGP1 and ILK1; or

wherein 2 of the N biomarker proteins are RAGP1 and RPL5; or

wherein 2 of the N biomarker proteins are SCFD1 and PLD3; or

wherein 2 of the N biomarker proteins are SCFD1 and Lectin, mannose-binding 2; or

wherein 2 of the N biomarker proteins are SCFD1 and ILK1; or

wherein 2 of the N biomarker proteins are SCFD1 and RPL5; or

wherein 2 of the N biomarker proteins are PLD3 and Lectin, mannose-binding 2; or

wherein 2 of the N biomarker proteins are PLD3 and ILK1; or

wherein 2 of the N biomarker proteins are PLD3 and RPL5; or

wherein 2 of the N biomarker proteins are Lectin, mannose-binding 2 and ILK1; or

wherein 2 of the N biomarker proteins are Lectin, mannose-binding 2 and RPL5; or

wherein 2 of the N biomarker proteins are ILK1 and RPL5.

28. The method of any one of claims 1-3 or 15-27, wherein N is 3, N is 4, N is 5, N is 6, N is 7, N is 8, or wherein all of the N biomarker proteins are selected from LKHA4, EIF1B, RAGP1, SCFD1, PLD3, Lectin, mannose-binding 2, ILK1, and RPL5.

29. The method of any one of claims 15-28, wherein the sample was processed, frozen, and thawed after the sample collection and prior to the detecting.

30. The method of claim 29, wherein the sample processing steps comprised at least one freeze-thaw cycle.

31. The method of claim 29, wherein the sample processing steps comprised greater than one freeze-thaw cycle.

32. The method of any one of claims 1-31, wherein the detecting comprises performing mass spectrometry, an aptamer based assay, and/or an antibody based assay.

33. The method of any one of claims 1-31, 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.

34. The method of claim 33, wherein each capture reagent is an antibody or an aptamer.

35. The method of claim 34, wherein each capture reagent is an aptamer.

36. The method of claim 35, 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 $\geq$ 20 minutes, $\geq$ 30 minutes, $\geq$ 60 minutes, $\geq$ 90 minutes, $\geq$ 120 minutes, $\geq$ 150 minutes, $\geq$ 180 minutes, $\geq$ 210 minutes, or $\geq$ 240 minutes.

37. The method of claim 36, 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.

38. A kit comprising N biomarker protein capture reagents, wherein N is at least 1, and wherein at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, or at least 7 of the capture reagents bind to proteins selected from LKHA4, EIF1B, RAGP1, SCFD1, PLD3, Lectin, mannose-binding 2, ILK1, and RPL5.

39. The kit of claim 38, wherein N is at least 2, and wherein at least 2 of the capture reagents bind to proteins selected from LKHA4, EIF1B, RAGP1, SCFD1, PLD3, Lectin, mannose-binding 2, ILK1, and RPL5, optionally wherein each of the capture reagents binds to a different protein.

40. The kit of claim 38 or 39, wherein N is 2, N is 3, N is 4, N is 5, N is 6, N is 7, N is 8, or wherein each of the capture reagents binds to a protein selected from LKHA4, EIF1B, RAGP1, SCFD1, PLD3, Lectin, mannose-binding 2, ILK1, and RPL5.

41. The kit of any one of claims 38-40, wherein each of the capture reagents is an antibody or an aptamer.

42. The kit of claim 41, wherein each capture reagent is an aptamer.

43. The kit of claim 42, 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 $\geq$ 20 minutes, $\geq$ 30 minutes, $\geq$ 60 minutes, $\geq$ 90 minutes, $\geq$ 120 minutes, $\geq$ 150 minutes, $\geq$ 180 minutes, $\geq$ 210 minutes, or $\geq$ 240 minutes.

44. The kit of claim 43, 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.

45. The kit of claim 38-44, 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, optionally for use in determining the number of freeze-thaw cycles for the sample.

46. A method comprising detecting the level of each of at least 1, 2, 3, 4, 5, 6, 7, or 8 biomarker proteins in a sample, wherein the biomarker proteins are selected from LKHA4, EIF1B, RAGP1, SCFD1, PLD3, Lectin, mannose-binding 2, ILK1, and RPL5.

47. The method of claim 46, wherein the sample is a serum sample.

48. The method of claim 46 or 47, wherein a number of freeze-thaw cycles is determined with the level of each of the at least 1, 2, 3, 4, 5, 6, 7 or 8 biomarker proteins, optionally 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 48, wherein the determined number of freeze-thaw cycles 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 is derived from input of the level of at least 1, 2, 3, 4, 5, 6, 7, or 8 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 linear regression model.