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 MCP-3, iC3b, Clusterin, DHI1, and RIC8A, 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 of the N biomarker proteins is selected from MCP-3, iC3b, Clusterin, DHI1, and RIC8A; 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 of the N biomarker proteins is selected from MCP-3, iC3b, Clusterin, DHI1, and RIC8A; 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 prior to the detecting, wherein the processing comprised centrifugation and decanting or aspirating the resulting supernatant, and the detecting is performed in the supernatant.

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

6. The method of claim 4 or 5, comprising determining the approximate duration of time that elapsed from the time that centrifugation was complete until the time that the sample was decanted or aspirated.

7. The method of claim 6, 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 processing times that round to zero or that are nearly zero.

8. The method of claim 7, wherein the detected levels of the N biomarker proteins compared to the reference levels indicates that the approximate time that elapsed from sample centrifugation to decanting or aspirating was greater than 0.1, greater than 0.5, greater than 1.0, greater than 1.5, greater than 3, greater than 6, greater than 9, or greater than 24 hours.

9. The method of any one of claims 1-8, 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.

10. The method of claim 9, wherein the sample is identified as passing if the approximate time that elapsed from sample centrifugation to decanting or aspirating is determined to be 0, less than 0.5, less than 1, less than 1.5, less than 3, less than 6, or less than 24 hours, preferably, wherein the sample is identified as passing if the approximate time that elapsed from sample centrifugation to decanting or aspirating is determined to be 0, less than 0.5 hour, or less than 1 hour.

11. The method of claim 10, wherein the sample is identified as failing if the approximate time that elapsed from sample centrifugation to decanting or aspirating is determined to be greater than 0.5, greater than 1, greater than 1.5, greater than 3, greater than 6, or greater than 24 hours.

12. The method of any one of claims 1-11, comprising detecting the level of each of N biomarkers in a plurality of samples from a plurality of subjects.

13. 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, wherein at least 1 of the N biomarker proteins is selected from MCP-3, iC3b, Clusterin, DHI1, and RIC8A, and wherein the sample is a serum sample.

14. The method of claim 13, comprising a) determining the approximate time that elapsed between sample centrifugation to decanting or aspirating and b) comparing the determined approximate times for each of the plurality of samples.

15. The method of claim 13 or 14, comprising identifying the plurality of samples as handled consistently or inconsistently, wherein samples handled consistently all have a determined approximate time between sample centrifugation to decanting or aspirating within 0, 0.5, 1, 2, or 3 hours of each other.

16. The method of any one of claims 13-15, 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 the N biomarker proteins present in samples having processing times that round to zero or that are nearly zero.

17. The method of any one of claims 13-16, wherein the detected levels of each of the N biomarker proteins compared to the reference levels indicates that the approximate time that elapsed from sample centrifugation to decanting or aspirating was greater than 0.1, greater than 0.5, greater than 1.0, greater than 1.5, greater than 3, greater than 6, greater than 9, or greater than 24 hours; or wherein the levels of each of the N biomarker proteins used in a linear regression model predicts the approximate time that elapsed from sample centrifugation to decanting or aspirating was greater than 0.1, greater than 0.5, greater than 1.0, greater than 1.5, greater than 3, greater than 6, greater than 9, or greater than 24 hours.

18. The method of any one of claims 1-8 or 13-17, 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.

19. The method of any one of claims 1-8 or 13-18, comprising performing protein biomarker discovery analysis, protein expression level analysis, a diagnostic method or a prognostic method on the plurality of samples.

20. The method of any one of claims 13-19, 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 approximate time for each of the plurality of samples; or identifying one or more proteins in the sample as being affected by an elapsed time from sample centrifugation to decanting or aspirating; or identifying the level of one or more proteins in the sample as being affected by the elapsed time from sample centrifugation to decanting or aspirating; or changing the proteins used in a diagnostic, a prognostic, or a health assessment related test based on the predicted elapsed time from sample centrifugation to decanting or aspirating; removing the proteins used in a diagnostic, a prognostic, or a health assessment related test based on the predicted elapsed time from sample centrifugation to decanting or aspirating.

21. The method of claim 20, wherein the panel of biomarker proteins is reduced in number of biomarker proteins measured.

22. The method of any one of claims 13-21, wherein the determining measures compliance with a clinical trial sample collection and processing protocol.

23. The method of any one of claims 13-22, 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.

24. The method of any one of claims 13-23, wherein one or more of the plurality of samples may be removed based on the approximate time that elapsed between sample centrifugation to decanting or aspirating.

25. The method of any one of claims 1-3 or 13-24, wherein 2 of the N biomarker proteins are MCP-3 and Clusterin; or

wherein 2 of the N biomarker proteins are MCP-3 and DHI1; or

wherein 2 of the N biomarker proteins are MCP-3 and RIC8A; or

wherein 2 of the N biomarker proteins are iC3b and Clusterin; or

wherein 2 of the N biomarker proteins are iC3b and DHI1; or

wherein 2 of the N biomarker proteins are iC3b and RIC8A; or

wherein 2 of the N biomarker proteins are Clusterin and DHI1; or

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

wherein 2 of the N biomarker proteins are DHI1 and RIC8A; or

wherein 3 of the N biomarker proteins are MCP-3, iC3b, and Clusterin; or

wherein 3 of the N biomarker proteins are MCP-3, iC3b, and DHI1; or

wherein 3 of the N biomarker proteins are MCP-3, iC3b, and RIC8A; or

wherein 3 of the N biomarker proteins are MCP-3, Clusterin, and DHI1; or

wherein 3 of the N biomarker proteins are MCP-3, Clusterin, and RIC8A; or

wherein 3 of the N biomarker proteins are MCP-3, DHI1, and RIC8A; or

wherein 3 of the N biomarker proteins are iC3b, Clusterin, and DHI1; or

wherein 3 of the N biomarker proteins are iC3b, Clusterin, and RIC8A; or

wherein 3 of the N biomarker proteins are iC3b, DHI1, and RIC8A; or

wherein 3 of the N biomarker proteins are Clusterin, DHI1, and RIC8A.

26. The method of any one of claims 1-3 and 13-35, wherein N is 4 or N is 5.

27. The method of claim 26, wherein all of the N biomarker proteins are selected from MCP-3, iC3b, Clusterin, DHI1, and RIC8A.

28. The method of any one of claims 13-27, wherein the sample was processed prior to the detecting, wherein the processing comprised centrifugation and decanting or aspirating the resulting supernatant, and the detecting is performed in the supernatant.

29. The method of any one of claims 13-28, wherein the sample was processed, frozen, and thawed after the sample collection and prior to the detecting.

30. The method of any one of claims 1-29, wherein the detecting comprises performing mass spectrometry, an aptamer based assay, and/or an antibody based assay.

31. The method of any one of claims 1-30, 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.

32. The method of claim 31, wherein each capture reagent is an antibody or an aptamer.

33. The method of claim 32, wherein each capture reagent is an aptamer.

34. The method of claim 33, 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.

35. The method of claim 34, 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.

36. 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 MCP-3, iC3b, Clusterin, DHI1, and RIC8A.

37. The kit of claim 36, wherein N is at least 2, and wherein at least 2 of the capture reagents binds to a protein selected from MCP-3, iC3b, Clusterin, DHI1, and RIC8A.

38. The kit of claim 36 or claim 37, wherein each of the capture reagents binds to a different protein.

39. The kit of claim 38, wherein N is 2, N is 3, N is 4, or N is 5.

40. The kit of any one of claims 36-39, wherein each of the capture reagents is an antibody or an aptamer.

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

42. The kit of claim 41, 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.

43. The kit of claim 42, 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.

44. The kit of any one of claims 36-43, for use in detecting the N biomarker proteins in a sample from a subject, optionally wherein the kit comprises capture reagents from multiple sample processing panels.

45. The kit of claim 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 and/or for use in determining the approximate time that elapsed between sample centrifugation to decanting or aspirating.

46. A method comprising detecting a level of each of at least 1, 2, 3, 4, or 5 proteins in a sample, wherein the proteins are selected from MCP-3, iC3b, Clusterin, DHI1, and RIC8A, wherein the sample is a serum sample.

47. The method of claim 46, wherein an approximate time that elapsed from sample centrifugation to decanting or aspirating is determined with the level of each of the at least 1, 2, 3, 4, or 5 proteins.

48. The method of claim 47, wherein the determined approximate time that elapsed from sample centrifugation to decanting or aspirating is greater than 0.1, greater than 0.5, greater than 1.0, greater than 1.5, greater than 3, greater than 6, greater than 9, or greater than 24 hours.

49. The method of claim 47 or 48, wherein the determined approximate time is derived from the input of the level of each of at least 1, 2, 3, 4, or 5 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.