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 C1GLC, ARL11, GFPT1, IF4A2, LONM, RBP56, RASN, RHG36, and FLII, wherein the sample is a serum 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 C1GLC, ARL11, GFPT1, IF4A2, LONM, RBP56, RASN, RHG36, and FLII; 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 C1GLC, ARL11, GFPT1, IF4A2, LONM, RBP56, RASN, RHG36, and FLII; 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, comprising determining the approximate duration of time that elapsed from the time that the sample was collected until the time of the start of sample centrifugation.

5. The method of claim 4, 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 from one hour or nearly one hour processing times up to three hours processing times.

6. The method of claim 4 or 5, 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.

7. The method of any one of claims 1-6, wherein the sample was processed, frozen, and thawed after the sample collection and prior to the detecting.

8. The method of claim any one of claims 4-7, 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 collection to centrifugation was greater than 0.5, greater than 0.67, greater than 1.0, greater than 1.33, greater than 1.5, greater than 3.0, greater than 9.0, 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 collection to centrifugation was greater than 0.5, greater than 0.67, greater than 1.0, greater than 1.33, greater than 1.5, greater than 3.0, greater than 9.0, 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 an approximate time that elapsed from sample collection to the start of sample centrifugation is determined to be 1 to 24 hours; 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24 hours; 1 to 20 hours; 1 to 18 hours; 1 to 15 hours; 1 to 12 hours; 1 to 10 hours; 1 to 8 hours; 1 to 6 hours; 1 to 4 hours; 1 to 3 hours; 2 to 24 hours; 3 to 24 hours; 3 or less hours; 5 or less hours; 6 or less hours; 8 or less hours; 10 or less hours; 12 or less hours; 14 or less hours; 16 or less hours; 18 or less hours; 20 or less hours; 22 or less hours; or 24 or less hours.

11. The method of claim 9, wherein the sample is identified as failing if an approximate time that elapsed from sample collection to the start of sample centrifugation is determined to be 1 to 24 hours; 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24 hours; 1 to 20 hours; 1 to 18 hours; 1 to 15 hours 1 to 12 hours; 1 to 10 hours; 1 to 8 hours; 1 to 6 hours; 1 to 4 hours; 1 to 3 hours; 2 to 24 hours; 3 to 24 hours; 3 or greater hours; 5 or greater hours; 6 or greater hours; 8 or greater hours; 10 or greater hours; 12 or greater hours; 14 or greater hours; 16 or greater hours; 18 or greater hours; 20 or greater hours; 22 or greater hours; or 24 or greater hours.

12. The method of any one of claims 4-11, 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 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 are selected from C1GLC, ARL11, GFPT1, IF4A2, LONM, RBP56, RASN, RHG36, and FLII, wherein the sample is a serum sample.

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

15. The method of claim 14, comprising identifying the plurality of samples as handled consistently or inconsistently, wherein samples handled consistently all have a determined approximate time between sample collection and centrifugation within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24 hours of each other.

16. The method of claim 14 or 15, wherein the determining is based on comparing each of 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 processing times of from one hour or nearly one hour up to three hours.

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 collection to sample centrifugation was greater than 0.5, greater than 0.67, greater than 1.0, greater than 1.33, greater than 1.5, greater than 3.0, greater than 9.0, or greater than 24 hours.

18. The method of any one of claims 4-8 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 4-8 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 claim 19, 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 approximate times for each of the plurality of samples; or identifying one or more proteins in the sample as being affected by the elapsed time from sample collection to sample centrifugation; or identifying the level of one or more proteins in the sample as being affected by the elapsed time from sample collection to sample centrifugation; or changing the proteins used in a diagnostic, a prognostic or a health assessment related test based on the predicted elapsed time from sample collection to sample centrifugation; or removing the proteins used in a diagnostic, a prognostic, or a health assessment related test based on the predicted elapsed time from sample collection to sample centrifugation.

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 from sample collection and sample centrifugation.

25. The method of any one of claims 1-3 or 13-24, wherein 2 of the N biomarker proteins are C1GLC are ARL11; or

wherein 2 of the N biomarker proteins are C1GLC and GFPT1; or

wherein 2 of the N biomarker proteins are C1GLC and IF4A2; or

wherein 2 of the N biomarker proteins are C1GLC and LONM; or

wherein 2 of the N biomarker proteins are C1GLC and RBP56; or

wherein 2 of the N biomarker proteins are C1GLC and RASN; or

wherein 2 of the N biomarker proteins are C1GLC and RHG36; or

wherein 2 of the N biomarker proteins are C1GLC and FLII; or

wherein 2 of the N biomarker proteins are ARL11 and GFPT1; or

wherein 2 of the N biomarker proteins are ARL11 and IF4A2; or

wherein 2 of the N biomarker proteins are ARL11 and LONM; or

wherein 2 of the N biomarker proteins are ARL11 and RBP56; or
wherein 2 of the N biomarker proteins are ARL11 and RASN; or
wherein 2 of the N biomarker proteins are ARL11 and RHG36; or
wherein 2 of the N biomarker proteins are ARL11 and FLII; or
wherein 2 of the N biomarker proteins are GFPT1 and IF4A2; or
wherein 2 of the N biomarker proteins are GFPT1 and LONM; or
wherein 2 of the N biomarker proteins are GFPT1 and RBP56; or
wherein 2 of the N biomarker proteins are GFPT1 and RASN; or
wherein 2 of the N biomarker proteins are GFPT1 and RHG36; or
wherein 2 of the N biomarker proteins are GFPT1 and FLII; or
wherein 2 of the N biomarker proteins are IF4A2 and LONM; or
wherein 2 of the N biomarker proteins are IF4A2 and RBP56; or
wherein 2 of the N biomarker proteins are IF4A2 and RASN; or
wherein 2 of the N biomarker proteins are IF4A2 and RHG36; or
wherein 2 of the N biomarker proteins are IF4A2 and FLII; or
wherein 2 of the N biomarker proteins are LONM and RBP56; or
wherein 2 of the N biomarker proteins are LONM and RASN; or
wherein 2 of the N biomarker proteins are LONM and RHG36; or
wherein 2 of the N biomarker proteins are LONM and FLII; or
wherein 2 of the N biomarker proteins are RBP56 and RASN; or
wherein 2 of the N biomarker proteins are RBP56 and RHG36; or
wherein 2 of the N biomarker proteins are RBP56 and FLII; or
wherein 2 of the N biomarker proteins are RASN and RHG36; or
wherein 2 of the N biomarker proteins are RASN and FLII; or
wherein 2 of the N biomarker proteins are RHG36 and FLII.

26. The method of any one of claims 1-3 or 13-25, wherein N is 3, N is 4, N is 5, N is 6, N is 7, N is 8, or N is 9.

27. The method of claim 26, wherein all of the N biomarker proteins are selected from C1GLC, ARL11, GFPT1, IF4A2, LONM, RBP56, RASN, RHG36, and FLII.

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 detecting comprises performing mass spectrometry, an aptamer based assay, and/or an antibody based assay.

30. The method of any one of claims 1-29, 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.

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

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

33. The method of claim 32, 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.

34. The method of claim 33, 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.

35. 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 C1GLC, ARL11, GFPT1, IF4A2, LONM, RBP56, RASN, RHG36, and FLII.

36. The kit of claim 35, wherein N is at least 2, and wherein at least 2 of the capture reagents bind to proteins selected from C1GLC, ARL11, GFPT1, IF4A2, LONM, RBP56, RASN, RHG36, and FLII.

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

38. The kit of any one of claims 35-37, wherein N is 3, N is 4, N is 5, N is 6, N is 7, N is 8, or N is 9.

39. The kit of claim 35, wherein each of the capture reagents binds to a protein selected from C1GLC, ARL11, GFPT1, IF4A2, LONM, RBP56, RASN, RHG36, and FLII.

40. The kit of any one of claims 35-39, 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 35-43, 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.

46. A method comprising detecting a level of each of at least 1, 2, 3, 4, 5, 6, 7, 8, or 9 biomarker proteins in a sample, wherein the biomarker proteins are selected from C1GLC, ARL11, GFPT1, IF4A2, LONM, RBP56, RASN, RHG36, and FLII, wherein the sample is a serum sample.

47. The method of claim 46, wherein the approximate time that elapsed from sample centrifugation to decanting or aspirating is determined based on the level of each of the at least 1, 2, 3, 4, 5, 6, 7, 8 or 9 biomarker proteins.

48. The method of claim 47, wherein the determined approximate time that elapsed from sample collection to sample centrifugation is greater than 0.5, greater than 0.67, greater than 1.0, greater than 1.33, greater than 1.5, greater than 3.0, greater than 9.0, 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 the at least 1, 2, 3, 4, 5, 6, 7, 8, or 9 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.