

METHODS FOR SAMPLE QUALITY ASSESSMENT

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application claims the benefit of priority of US Provisional Application No. 63/301,654, filed January 21, 2022, which is incorporated by reference herein in its entirety for any purpose.

FIELD OF THE INVENTION

[0002] The present application relates generally to the detection of biomarkers and a method of evaluating the quality or suitability of a sample or set of samples for use in biomarker discovery or in a medical evaluation of a subject, such as a diagnostic assay.

BACKGROUND

[0003] Blood contains various cellular and humoral systems for reacting to injury or foreign and infectious agents. Small challenges can induce the innate immune system (complement system and cells such as macrophages) to release signals and enzymes, lead to activation of the platelets and trigger the coagulation of the blood. These signals are of interest because they can be directly involved in defense and repair systems and serve as markers for disease. However, such process signals may also be responsive to the effects of blood sample preparation or processing. If cells in the samples lyse, if platelets degranulate, or if the complement system is activated, then changes in analyte concentration may occur in the sample after it has been taken, and a “high fidelity” measurement technique may detect them. Merely exposing blood to air can result in unintended activation of these mechanisms. Thus, altering the time of sample processing steps can alter the apparent composition of serum or plasma such that physiologic information is masked by the pre-analytic variability imparted on the sample during collection and processing. The susceptibility of these processes and proteins to subtle alterations in sample handling can compromise the use of them as biomarkers.

[0004] Currently, researchers in multivariate biology are concerned about pre-analytical sample variation (often called “batch effects”). The extent to which sample quality can be determined is largely limited to visually obvious changes, such as red color indicating red cell lysis and cloudiness indicating high lipid or other contaminants. These relatively crude methods limit the reliability of all but the hardiest and most robust protein

measurements. Ostroff, R. et al. (2010) J. Proteomics 73:649-666, documents some of the complex and nonlinear effects of variations in serum and plasma preparation.

[0005] Specific techniques to determine compliance with sample processing protocols are needed to monitor compliance, reject low quality samples, and/or make corrections in analytes of interest. Such techniques would improve evaluation of the quality of human or animal blood samples used in biomarker research, clinical diagnostic applications, bio-banks, and drug development.

SUMMARY OF THE INVENTION

[0006] The present application includes biomarkers, methods, reagents, devices, systems, and kits for assessing sample quality. The biomarkers of the present application were identified using linear regression of measurements of a specific set of proteins affected by variation in sample processing protocol. In some embodiments, the biomarker panels comprise proteins that are sensitive to sample handling.

[0007] In some embodiments, the methods comprise detecting the biomarkers using a multiplex slow off-rate aptamer-based assay described herein, for example, for assessing sample quality. In some embodiments, the sample is a blood sample, plasma sample, serum sample, or urine sample. In some embodiments, the sample is a plasma sample or a serum sample.

[0008] In some embodiments, the time, in hours, between one or more sample processing steps is predicted or estimated. In some embodiments, the sample processing steps include one or more of sample centrifugation, decanting or aspirating of the centrifuged supernatant, and freezing the decanted or aspirated sample.

[0009] In some embodiments, methods of assessing quality of a sample collected from a subject are provided, said method comprising detecting the level of each of N biomarker proteins in the sample, wherein N is at least 3, and wherein at least 3 of the N biomarker proteins are selected from LANC2, PKHM2, ENOA, the cytoplasmic domain of TMEM9, PMM2, PGAM2, EFHD1, and THIK, wherein the sample is a plasma sample. In some embodiments, a method comprises measuring the level of each of N biomarker proteins in a plasma sample from a subject, wherein N is at least 3, and wherein at least 3 of the N biomarker proteins are selected from LANC2, PKHM2, ENOA, the cytoplasmic domain of TMEM9, PMM2, PGAM2, EFHD1, and THIK, and 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. In some embodiments, the sample was frozen and thawed prior to the detecting. In some such embodiments, the methods comprise determining the approximate duration of time that elapsed from completion of sample collection and processing until the time that the sample was frozen.

[0010] In some embodiments, methods of assessing quality of a sample collected from a subject are provided, said method comprising detecting the level of each of N biomarker proteins in the sample, wherein N is at least 2, and wherein at least 2 of the N biomarker proteins are selected from LYAG, IL21R, C3b, IL36A, and GDF5, wherein the sample is a serum sample. In some embodiments, a method comprises measuring the level of each of N biomarker proteins in a serum sample from a subject, wherein N is at least 2, and wherein at least 2 of the N biomarker proteins are selected from LYAG, IL21R, C3b, IL36A, and GDF5, and 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. In some embodiments, the sample was frozen and thawed prior to the detecting. In some such embodiments, the methods comprise determining the approximate duration of time that elapsed from completion of sample collection and processing until the time that the sample was frozen.

[0011] In some embodiments, methods of assessing quality of a sample collected from a subject are provided, said method comprising detecting the level of each of N biomarker proteins in the sample, wherein N is at least 4, and wherein at least 4 of the N biomarker proteins are selected from IHH, SHH, PGAM1, and ROA2. In some embodiments, a method comprises measuring the level of each of N biomarker proteins in a sample from a subject, wherein N is at least 4, and wherein at least 4 of the N biomarker proteins are selected from IHH, SHH, PGAM1, and ROA2, and 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. In some embodiments, the sample was centrifuged prior to the detecting. In some such embodiments, the methods comprise determining the approximate duration of time

that elapsed from the time that the sample was collected until the time that the sample was centrifuged.

[0012] In some embodiments, methods of assessing quality of a sample collected from a subject are provided, said method detecting the level of each of N biomarker proteins in the sample, wherein N is at least 9, and wherein at least 9 of the N biomarker proteins are selected from APB, CFAD, PTN4, PGAM2, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, and TMEM9. In some embodiments, a method comprises measuring the level of each of N biomarker proteins in a sample from a subject, wherein N is at least 9, and wherein at least 9 of the N biomarker proteins are selected from APB, CFAD, PTN4, PGAM2, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, and TMEM9, and 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. In some embodiments, the sample was centrifuged and decanted or aspirated prior to the detecting. In some such embodiments, the methods comprise 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.

[0013] In some embodiments, methods of assessing quality of a sample collected from a subject comprise detecting N biomarker proteins, wherein one or more of the N biomarker proteins are associated with the time to centrifugation, one or more of the N biomarker proteins are associated with the time to decanting or aspirating, and one or more of the N biomarker proteins are associated with the time to freezing of the appropriate sample type. In some embodiments, methods of assessing quality of a sample collected from a subject comprise detecting N biomarker proteins, wherein one or more of the N biomarker proteins are associated with the time to centrifugation and one or more of the N biomarker proteins are associated with the time to decanting or aspirating. In some embodiments, methods of assessing quality of a sample collected from a subject comprise detecting N biomarker proteins, wherein one or more of the N biomarker proteins are associated with the time to centrifugation and one or more of the N biomarker proteins are associated with the time to freezing of the appropriate sample type. In some embodiments, methods of assessing quality of a sample collected from a subject comprise detecting N biomarker proteins, wherein one or more of the N biomarker proteins are associated with the time to decanting or

aspirating and one or more of the N biomarker proteins are associated with the time to freezing of the appropriate sample type.

[0014] In any of the foregoing amendments, N is 9, N is 10, N is 11, N is 12, N is 13, N is 14, N is 15, N is 16, N is 17, N is 18, N is 19, or N is 20. In some embodiments, N is 2, N is 3, N is 4, N is 5, N is 6, N is 7, or N is 8. In some embodiments, all of the N biomarker proteins are selected from the lists provided herein.

[0015] In some embodiments, the subject is a human subject, and the sample is a liquid sample. In some embodiments, the sample is a plasma or serum sample obtained from a whole blood sample. In some embodiments, the approximate duration of time between sample processing steps determined by a method herein is 0, 0.5, 1, 1.5, 3, 3.5, 6, 9, or 24, or greater than 24 hours. In some embodiments, the method is performed in vitro.

[0016] In some embodiments, the sample is identified as passing a quality assessment or failing a quality assessment. In some such embodiments, the identifying is based, at least in part, on the detected levels of the N biomarker proteins in the sample. In some embodiments, the identifying is based, at least in part, on the determined approximate duration or durations of time between two or more sample processing steps. In some embodiments, the sample undergoes further analysis if it is identified as passing quality assessment, or the sample is discarded if it is identified as failing the quality assessment.

[0017] In some embodiments, methods of assessing the quality of a plurality of samples are provided herein, comprising detecting the level of each of N biomarkers in a plurality of sample from a plurality of subjects. In some such embodiments, the approximate duration of time between two or more sample processing steps is determined and compared across the plurality of samples. In some such embodiments, the consistency of sample handling across the plurality of samples is determined.

[0018] In some embodiments, 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. In some embodiments, 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 a different biomarker protein being detected. In some embodiments, each capture reagent is an antibody or an aptamer. In some embodiments, each biomarker capture reagent is an aptamer. In some embodiments, at least one aptamer is a slow off-rate aptamer. In some embodiments, 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. In some embodiments, each slow off-rate aptamer binds to its target protein with an off rate ($t_{1/2}$) of ≥ 30 minutes, ≥ 60 minutes, ≥ 90 minutes, ≥ 120 minutes, ≥ 150 minutes, ≥ 180 minutes, ≥ 210 minutes, or ≥ 240 minutes.

[0019] In some embodiments, a kit is provided, the kit comprising N biomarker protein capture reagents, wherein N is at least 3 and at least 3 of the capture reagents bind to LANC2, PKHM2, ENOA, the cytoplasmic domain of TMEM9, PMM2, PGAM2, EFHD1, or THIK; or wherein N is at least 2 and at least 2 of the capture reagents bind to LYAG, IL21R, C3b, IL36A, or GDF5; or wherein N is at least 4 and at least 4 of the capture reagents bind to IHH, SHH, PGAM1, or ROA2; or wherein N is at least 9 and at least 9 of the capture reagents bind to APB, CFAD, PTN4, PGAM2, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, or TMEM9. In some embodiments, each capture reagent binds to a different biomarker protein. In some embodiments, 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, N is 11, N is 12, N is 13, N is 14, N is 15, N is 16, N is 17, N is 18, N is 19, or N is 20. In some embodiments, the kit comprises capture reagents from multiple sample processing panels.

[0020] In some embodiments, each of the N biomarker protein capture reagents specifically binds to a biomarker protein selected from Table 1, 2, 3, and/or 4. In some embodiments, each of the N biomarker capture reagents is an antibody or an aptamer. In some embodiments, each biomarker capture reagent is an aptamer. In some embodiments, at least one aptamer is a slow off-rate aptamer. In some embodiments, 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. In some embodiments, each slow off-rate aptamer binds to its target protein with an off rate ($t_{1/2}$) of ≥ 30 minutes, ≥ 60 minutes, ≥ 90 minutes, ≥ 120 minutes, ≥ 150 minutes, ≥ 180 minutes, ≥ 210 minutes, or ≥ 240 minutes. In some embodiments, the kit is for use in detecting the N biomarker proteins in a sample from a subject. In some embodiments, the kit is for use in assessing the quality of the sample or a plurality of samples.

BRIEF DESCRIPTION OF THE DRAWINGS

[0021] Fig. 1 illustrates a nonlimiting exemplary computer system for use with various computer-implemented methods described herein.

[0022] Fig. 2 illustrates a nonlimiting exemplary aptamer assay that can be used to detect one or more biomarkers in a biological sample.

[0023] Figs. 3-5 show certain exemplary modified pyrimidines that may be incorporated into aptamers, such as slow off-rate aptamers.

DETAILED DESCRIPTION

[0024] While the invention will be described in conjunction with certain representative embodiments, it will be understood that the invention is defined by the claims, and is not limited to those embodiments.

[0025] One skilled in the art will recognize many methods and materials similar or equivalent to those described herein may be used in the practice of the present invention. The present invention is in no way limited to the methods and materials described.

[0026] Unless defined otherwise, technical and scientific terms used herein have the meaning commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods, devices, and materials similar or equivalent to those described herein can be used in the practice of the invention, certain methods, devices, and materials are described herein.

[0027] All publications, published patent documents, and patent applications cited herein are hereby incorporated by reference to the same extent as though each individual publication, published patent document, or patent application was specifically and individually indicated as being incorporated by reference.

[0028] As used herein, the terms “comprises,” “comprising,” “includes,” “including,” “contains,” “containing,” and any variations thereof, are intended to cover a non-exclusive inclusion, such that a process, method, product-by-process, or composition of matter that comprises, includes, or contains an element or list of elements may include other elements not expressly listed.

[0029] “Biological sample”, “sample”, and “test sample” are used interchangeably herein to refer to any material, biological fluid, tissue, or cell obtained or otherwise derived from an individual. This includes blood (including whole blood, leukocytes, peripheral blood mononuclear cells, buffy coat, plasma, and serum), sputum, tears, mucus, nasal washes, nasal aspirate, urine, saliva, peritoneal washings, ascites, cystic fluid, glandular fluid, lymph fluid, bronchial aspirate, synovial fluid, joint aspirate, organ secretions, cells, a cellular extract, and cerebrospinal fluid. This also includes experimentally separated fractions of all of the preceding. For example, a blood sample can be fractionated into serum, plasma, or into fractions containing particular types of blood cells, such as red blood cells or white blood cells (leukocytes). In some embodiments, a sample is a plasma sample. As used herein, a

“plasma sample” comprises plasma and, optionally, one or more preservatives or additives. A plasma sample is isolated from whole blood and therefore does not comprise a substantial amount of any other blood component. In some embodiments, a sample is a serum sample. As used herein, a “serum sample” comprises serum and, optionally, one or more preservatives or additives. A serum sample is isolated from whole blood and therefore does not comprise a substantial amount of any other blood component. In some embodiments, a sample is a urine sample. As used herein, a “urine sample” comprises urine and, optionally, one or more preservatives or additives. In some embodiments, a blood sample is a dried blood spot. In some embodiments, a plasma sample is a dried plasma spot. In some embodiments, a sample can be a combination of samples from an individual, such as a combination of a tissue and fluid sample. The term “biological sample” also includes materials containing homogenized solid material, such as from a stool sample, a tissue sample, or a tissue biopsy, for example. The term “biological sample” also includes materials derived from a tissue culture or a cell culture. Any suitable methods for obtaining a biological sample can be employed; exemplary methods include, e.g., phlebotomy, swab (e.g., buccal swab), and a fine needle aspirate biopsy procedure. Exemplary tissues susceptible to fine needle aspiration include lymph node, lung, thyroid, breast, pancreas, and liver. Samples can also be collected, e.g., by micro dissection (e.g., laser capture micro dissection (LCM) or laser micro dissection (LMD)), bladder wash, smear (e.g., a PAP smear), or ductal lavage. A “biological sample” obtained or derived from an individual includes any such sample that has been processed in any suitable manner after being obtained from the individual.

[0030] Further, in some embodiments, a biological sample may be derived by taking biological samples from a number of individuals and pooling them, or pooling an aliquot of each individual’s biological sample. The pooled sample may be treated as described herein for a sample from a single individual, and, for example, if a poor sample quality is established in the pooled sample, then each individual biological sample can be re-tested to determine which must be discarded, or the entire group of samples may be discarded if known to have been handled or processed in the same way.

[0031] For purposes of this specification, the phrase “data attributed to a biological sample from an individual” is intended to mean that the data in some form derived from, or were generated using, the biological sample of the individual. The data may have been reformatted, revised, or mathematically altered to some degree after having been generated, such as by conversion from units in one measurement system to units in another measurement

system; but, the data are understood to have been derived from, or were generated using, the biological sample.

[0032] “Target”, “target molecule”, and “analyte” are used interchangeably herein to refer to any molecule of interest that may be present in a biological sample. A “molecule of interest” includes any minor variation of a particular molecule, such as, in the case of a protein, for example, minor variations in amino acid sequence, disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, or any other manipulation or modification, such as conjugation with a labeling component, which does not substantially alter the identity of the molecule. A “target molecule”, “target”, or “analyte” refers to a set of copies of one type or species of molecule or multi-molecular structure. Exemplary target molecules include proteins, polypeptides, nucleic acids, carbohydrates, lipids, polysaccharides, glycoproteins, hormones, receptors, antigens, antibodies, affybodies, antibody mimics, viruses, pathogens, toxic substances, substrates, metabolites, transition state analogs, cofactors, inhibitors, drugs, dyes, nutrients, growth factors, cells, tissues, and any fragment or portion of any of the foregoing. In some embodiments, a target molecule is a protein, in which case the target molecule may be referred to as a “target protein.”

[0033] As used herein, a “capture agent” or “capture reagent” refers to a molecule that is capable of binding specifically to a biomarker. A “target protein capture reagent” refers to a molecule that is capable of binding specifically to a target protein. Nonlimiting exemplary capture reagents include aptamers, antibodies, adnectins, ankyrins, other antibody mimetics and other protein scaffolds, autoantibodies, chimeras, small molecules, nucleic acids, lectins, ligand-binding receptors, imprinted polymers, avimers, peptidomimetics, hormone receptors, cytokine receptors, synthetic receptors, and modifications and fragments of any of the aforementioned capture reagents. In some embodiments, a capture reagent is selected from an aptamer and an antibody.

[0034] The term “antibody” refers to full-length antibodies of any species and fragments and derivatives of such antibodies, including Fab fragments, $F(ab')_2$ fragments, single chain antibodies, Fv fragments, and single chain Fv fragments. The term “antibody” also refers to synthetically-derived antibodies, such as phage display-derived antibodies and fragments, affybodies, nanobodies, etc.

[0035] As used herein, “marker” and “biomarker” are used interchangeably to refer to a target molecule that indicates or is a sign of a normal or abnormal process in an individual or of a high or low quality sample. More specifically, a “marker” or “biomarker” is an anatomic, physiologic, biochemical, or molecular parameter associated with the presence of a

specific state or process. Biomarkers are detectable and measurable by a variety of methods including laboratory assays and medical imaging.

[0036] As used herein, “biomarker level” and “level” refer to a measurement that is made using any analytical method for detecting the biomarker in a biological sample and that indicates the presence, absence, absolute amount or concentration, relative amount or concentration, titer, a level, an expression level, a ratio of measured levels, or the like, of, for, or corresponding to the biomarker in the biological sample. The exact nature of the “level” depends on the specific design and components of the particular analytical method employed to detect the biomarker.

[0037] When a biomarker indicates or is a sign of a poor quality sample, that biomarker is generally described as being either over-expressed or under-expressed as compared to an expression level or value of the biomarker that indicates or is a sign of a normal or quality sample. “Up-regulation”, “up-regulated”, “over-expression”, “over-expressed”, and any variations thereof are used interchangeably to refer to a value or level of a biomarker in a biological sample that is greater than a value or level (or range of values or levels) of the biomarker that is typically detected in similar, properly handled biological samples.

[0038] “Down-regulation”, “down-regulated”, “under-expression”, “under-expressed”, and any variations thereof are used interchangeably to refer to a value or level of a biomarker in a biological sample that is less than a value or level (or range of values or levels) of the biomarker that is typically detected in similar, properly handled biological samples.

[0039] Further, a biomarker that is either over-expressed or under-expressed can also be referred to as being “differentially expressed” or as having a “differential level” or “differential value” as compared to a “normal” expression level or value of the biomarker that indicates or is a sign of a normal process or proper sample handling. Thus, “differential expression” of a biomarker can also be referred to as a variation from a “normal” expression level of the biomarker.

[0040] A “control level” of a target molecule refers to the level of the target molecule in a properly handled sample of the same sample type. Control level may refer to the average level of the target molecule in properly handled samples from a population of individuals.

[0041] As used herein, “individual,” “subject,” and “patient” are used interchangeably to refer to a mammal. A mammalian individual can be a human or non-human. In various embodiments, the individual is a human. A healthy or normal individual is an individual in

which the disease or condition of interest (including, for example, chronic heart failure and cardiovascular events such as myocardial infarction, stroke and hospitalization for heart failure) is not detectable by conventional diagnostic methods.

[0042] As used herein, “detecting” or “determining” with respect to a biomarker value includes the use of both the instrument used to observe and record a signal corresponding to a biomarker level and the material/s required to generate that signal. In various embodiments, the biomarker level is detected using any suitable method, including fluorescence, chemiluminescence, surface plasmon resonance, surface acoustic waves, mass spectrometry, infrared spectroscopy, Raman spectroscopy, atomic force microscopy, scanning tunneling microscopy, electrochemical detection methods, nuclear magnetic resonance, quantum dots, and the like.

[0043] As used herein, “sample processing” and “sample handling” refer to steps or procedures performed on a sample, such as a blood sample, after sample collection in order to prepare it for storage or analysis. In some embodiments, sample processing steps include centrifugation of the sample and decanting or aspirating the supernatant. In some embodiments, sample quality is assessed by determining the approximate durations of time that elapsed between sample processing steps. A sample processing time of or near zero means that each sample processing step was performed immediately with minimal time elapsed in between sample processing steps.

[0044] As used herein, “time-to-centrifugation” means the time elapsed between the moment that a blood sample is collected from a subject into a tube to the moment that the tube begins spinning in a centrifuge. In some embodiments, time-to-centrifugation is measured in hours. In some embodiments, ideal time-to-centrifugation for optimal sample quality is two hours or less. In some embodiments, the time-to-centrifugation is rounded to the nearest hour. In some embodiments, the time-to-centrifugation is rounded to the nearest half hour. Thus, in some embodiments, a time-to-centrifugation of less than a half hour or less than a quarter of an hour is rounded to zero.

[0045] As used herein, “time-to-decant” means the time elapsed between the moment that centrifugation of a sample is complete to the moment that the supernatant of the centrifuged sample begins to be decanted or aspirated from the precipitate. In some embodiments, time-to-decant is measured in hours. In some embodiments, ideal time-to-decant for optimal sample quality is less than one hour or less than half an hour, or less than a quarter hour. In some embodiments, the time-to-decant is rounded to the nearest hour. In some embodiments, the time-to-decant is rounded to the nearest half hour. Thus, in some

embodiments, a time-to-decant of less than a half hour or less than a quarter of an hour is rounded to zero.

[0046] As used herein, “time-to-freeze” means the time elapsed between the moment that decanting or aspirating of a centrifuged sample is complete to the moment that the decanted or aspirated sample is placed in conditions at or under -20 °C. In some embodiments, time-to-freeze is measured in hours. In some embodiments, ideal time-to-decant for optimal sample quality is less than one hour or less than half an hour, or less than a quarter hour. In some embodiments, the time-to-freeze is rounded to the nearest hour. In some embodiments, the time-to-freeze is rounded to the nearest half hour. Thus, in some embodiments, a time-to-freeze of less than a half hour or less than a quarter of an hour is rounded to zero.

[0047] “Solid support” refers herein to any substrate having a surface to which molecules may be attached, directly or indirectly, through either covalent or non-covalent bonds. A “solid support” can have a variety of physical formats, which can include, for example, a membrane; a chip (e.g., a protein chip); a slide (e.g., a glass slide or coverslip); a column; a hollow, solid, semi-solid, pore- or cavity- containing particle, such as, for example, a bead; a gel; a fiber, including a fiber optic material; a matrix; and a sample receptacle. Exemplary sample receptacles include sample wells, tubes, capillaries, vials, and any other vessel, groove or indentation capable of holding a sample. A sample receptacle can be contained on a multi-sample platform, such as a microtiter plate, slide, microfluidics device, and the like. A support can be composed of a natural or synthetic material, an organic or inorganic material. The composition of the solid support on which capture reagents are attached generally depends on the method of attachment (e.g., covalent attachment). Other exemplary receptacles include microdroplets and microfluidic controlled or bulk oil/aqueous emulsions within which assays and related manipulations can occur. Suitable solid supports include, for example, plastics, resins, polysaccharides, silica or silica-based materials, functionalized glass, modified silicon, carbon, metals, inorganic glasses, membranes, nylon, natural fibers (such as, for example, silk, wool and cotton), polymers, and the like. The material composing the solid support can include reactive groups such as, for example, carboxy, amino, or hydroxyl groups, which are used for attachment of the capture reagents. Polymeric solid supports can include, e.g., polystyrene, polyethylene glycol tetraphthalate, polyvinyl acetate, polyvinyl chloride, polyvinyl pyrrolidone, polyacrylonitrile, polymethyl methacrylate, polytetrafluoroethylene, butyl rubber, styrenebutadiene rubber, natural rubber, polyethylene, polypropylene, (poly)tetrafluoroethylene, (poly)vinylidene fluoride,

polycarbonate, and polymethylpentene. Suitable solid support particles that can be used include, e.g., encoded particles, such as Luminex®-type encoded particles, magnetic particles, and glass particles.

Exemplary Uses of Biomarkers

[0048] In various exemplary embodiments, methods are provided for evaluating or assessing sample quality by detecting one or more biomarker values corresponding to one or more biomarkers present in a sample from an individual, such as a blood, serum, or plasma sample, by any number of analytical methods, including any of the analytical methods described herein. These biomarkers are, for example, present at different levels in samples with differing quality. In some embodiments, the differing sample quality is due to differences in sample processing. Detection of the different levels of a biomarker in a sample can be used, for example, to estimate the time that elapsed between sample processing steps, such as time-to-centrifugation, time-to-decant, and/or time-to-freeze.

[0049] In addition to detecting biomarkers to assess sample quality, biomarkers can be used in diagnostic applications or to determine if a disease or condition is present in the subject from whom the sample was taken. In some embodiments, only samples that pass the quality assessment are further analyzed for diagnostic applications.

Detection and Determination of Biomarkers and Biomarker Levels

[0050] Levels of the biomarkers described herein can be detected using any of a variety of known analytical methods. In one embodiment, a biomarker level is detected using a capture reagent. In various embodiments, the capture reagent can be exposed to the biomarker in solution or can be exposed to the biomarker while the capture reagent is immobilized on a solid support. In other embodiments, the capture reagent contains a feature that is reactive with a secondary feature on a solid support. In these embodiments, the capture reagent can be exposed to the biomarker in solution, and then the feature on the capture reagent can be used in conjunction with the secondary feature on the solid support to immobilize the biomarker on the solid support. The capture reagent is selected based on the type of analysis to be conducted. Capture reagents include but are not limited to aptamers, antibodies, adnectins, ankyrins, other antibody mimetics and other protein scaffolds, autoantibodies, chimeras, small molecules, F(ab')₂ fragments, single chain antibody fragments, Fv fragments, single chain Fv fragments, nucleic acids, lectins, ligand-binding receptors, affybodies, nanobodies, imprinted polymers, avimers, peptidomimetics, hormone

receptors, cytokine receptors, and synthetic receptors, and modifications and fragments of these.

[0051] In some embodiments, a biomarker level is detected using a biomarker/capture reagent complex.

[0052] In some embodiments, the biomarker level is derived from the biomarker/capture reagent complex and is detected indirectly, such as, for example, as a result of a reaction that is subsequent to the biomarker/capture reagent interaction, but is dependent on the formation of the biomarker/capture reagent complex.

[0053] In some embodiments, the biomarker level is detected directly from the biomarker in a biological sample.

[0054] In some embodiments, biomarkers are detected using a multiplexed format that allows for the simultaneous detection of two or more biomarkers in a biological sample. In some embodiments of the multiplexed format, capture reagents are immobilized, directly or indirectly, covalently or non-covalently, in discrete locations on a solid support. In some embodiments, a multiplexed format uses discrete solid supports where each solid support has a unique capture reagent associated with that solid support, such as, for example quantum dots. In some embodiments, an individual device is used for the detection of each one of multiple biomarkers to be detected in a biological sample. Individual devices can be configured to permit each biomarker in the biological sample to be processed simultaneously. For example, a microtiter plate can be used such that each well in the plate is used to uniquely analyze one or more biomarkers to be detected in a biological sample.

[0055] In one or more of the foregoing embodiments, a fluorescent tag can be used to label a component of the biomarker/capture reagent complex to enable the detection of the biomarker level. In various embodiments, the fluorescent label can be conjugated to a capture reagent specific to any of the biomarkers described herein using known techniques, and the fluorescent label can then be used to detect the corresponding biomarker level. Suitable fluorescent labels include rare earth chelates, fluorescein and its derivatives, rhodamine and its derivatives, dansyl, allophycocyanin, PBXL-3, Qdot 605, Lissamine, phycoerythrin, Texas Red, and other such compounds.

[0056] In some embodiments, the fluorescent label is a fluorescent dye molecule. In some embodiments, the fluorescent dye molecule includes at least one substituted indolium ring system in which the substituent on the 3-carbon of the indolium ring contains a chemically reactive group or a conjugated substance. In some embodiments, the dye molecule includes an AlexaFluor molecule, such as, for example, AlexaFluor 488, AlexaFluor 532,

AlexaFluor 647, AlexaFluor 680, or AlexaFluor 700. In other embodiments, the dye molecule includes a first type and a second type of dye molecule, such as, e.g., two different AlexaFluor molecules. In some embodiments, the dye molecule includes a first type and a second type of dye molecule, and the two dye molecules have different emission spectra.

[0057] Fluorescence can be measured with a variety of instrumentation compatible with a wide range of assay formats. For example, spectrofluorimeters have been designed to analyze microtiter plates, microscope slides, printed arrays, cuvettes, etc. See Principles of Fluorescence Spectroscopy, by J.R. Lakowicz, Springer Science + Business Media, Inc., 2004. See Bioluminescence & Chemiluminescence: Progress & Current Applications; Philip E. Stanley and Larry J. Kricka editors, World Scientific Publishing Company, January 2002.

[0058] In one or more embodiments, a chemiluminescence tag can optionally be used to label a component of the biomarker/capture complex to enable the detection of a biomarker level. Suitable chemiluminescent materials include any of oxalyl chloride, Rodamin 6G, $\text{Ru}(\text{bipy})_3^{2+}$, TMAE (tetrakis(dimethylamino)ethylene), Pyrogallol (1,2,3-trihydroxybenzene), Lucigenin, peroxyoxalates, Aryl oxalates, Acridinium esters, dioxetanes, and others.

[0059] In some embodiments, the detection method includes an enzyme/substrate combination that generates a detectable signal that corresponds to the biomarker level. Generally, the enzyme catalyzes a chemical alteration of the chromogenic substrate which can be measured using various techniques, including spectrophotometry, fluorescence, and chemiluminescence. Suitable enzymes include, for example, luciferases, luciferin, malate dehydrogenase, urease, horseradish peroxidase (HRPO), alkaline phosphatase, beta-galactosidase, glucoamylase, lysozyme, glucose oxidase, galactose oxidase, and glucose-6-phosphate dehydrogenase, uricase, xanthine oxidase, lactoperoxidase, microperoxidase, and the like.

[0060] In some embodiments, the detection method can be a combination of fluorescence, chemiluminescence, radionuclide or enzyme/substrate combinations that generate a measurable signal. In some embodiments, multimodal signaling could have unique and advantageous characteristics in biomarker assay formats.

[0061] In some embodiments, the biomarker levels for the biomarkers described herein can be detected using any analytical methods including, singleplex aptamer assays, multiplexed aptamer assays, singleplex or multiplexed immunoassays, mRNA expression profiling, miRNA expression profiling, mass spectrometric analysis, histological/cytological methods, etc. as discussed below.

Determination of Biomarker Levels using Aptamer-Based Assays

[0062] Assays directed to the detection and quantification of biomarker molecules in biological samples and other samples are important tools in scientific research and in the health care field. One class of such assays involves the use of a microarray that includes one or more aptamers immobilized on a solid support. The aptamers are each capable of binding to a target molecule in a highly specific manner and with very high affinity. See, e.g., U.S. Patent No. 5,475,096 entitled “Nucleic Acid Ligands”; see also, e.g., U.S. Patent No. 6,242,246, U.S. Patent No. 6,458,543, and U.S. Patent No. 6,503,715, each of which is entitled “Nucleic Acid Ligand Diagnostic Biochip”. Once the microarray is contacted with a sample, the aptamers bind to their respective target molecules present in the sample and thereby enable a determination of a biomarker level corresponding to a biomarker.

[0063] As used herein, an “aptamer” refers to a nucleic acid that has a specific binding affinity for a target molecule. It is recognized that affinity interactions are a matter of degree; however, in this context, the “specific binding affinity” of an aptamer for its target means that the aptamer binds to its target generally with a much higher degree of affinity than it binds to other components in a test sample. An “aptamer” is a set of copies of one type or species of nucleic acid molecule that comprises a particular nucleotide sequence. An aptamer can include any suitable number of nucleotides, including any number of chemically modified nucleotides. “Aptamers” refers to more than one such set of molecules. Different aptamers can have either the same or different numbers of nucleotides. Aptamers can be DNA or RNA or chemically modified nucleic acids and can be single-stranded, double-stranded, or contain double-stranded regions, and can include higher ordered structures. An aptamer can also be a photoaptamer, where a photoreactive or chemically reactive functional group is included in the aptamer to allow it to be covalently linked to its corresponding target. Any of the aptamer methods disclosed herein can include the use of two or more aptamers that specifically bind the same target molecule. As further described below, an aptamer may include a tag. If an aptamer includes a tag, all copies of the aptamer need not have the same tag. Moreover, if different aptamers each include a tag, these different aptamers can have either the same tag or a different tag.

[0064] An aptamer can be identified using any known method, including the SELEX process. Once identified, an aptamer can be prepared or synthesized in accordance with any known method, including chemical synthetic methods and enzymatic synthetic methods.

[0065] The terms “SELEX” and “SELEX process” are used interchangeably herein to refer generally to a combination of (1) the selection of aptamers that interact with a target molecule in a desirable manner, for example binding with high affinity to a protein, with (2) the amplification of those selected nucleic acids. The SELEX process can be used to identify aptamers with high affinity to a specific target or biomarker.

[0066] SELEX generally includes preparing a candidate mixture of nucleic acids, binding of the candidate mixture to the desired target molecule to form an affinity complex, separating the affinity complexes from the unbound candidate nucleic acids, separating and isolating the nucleic acid from the affinity complex, purifying the nucleic acid, and identifying a specific aptamer sequence. The process may include multiple rounds to further refine the affinity of the selected aptamer. The process can include amplification steps at one or more points in the process. See, e.g., U.S. Patent No. 5,475,096, entitled “Nucleic Acid Ligands”. The SELEX process can be used to generate an aptamer that covalently binds its target as well as an aptamer that non-covalently binds its target. See, e.g., U.S. Patent No. 5,705,337 entitled “Systematic Evolution of Nucleic Acid Ligands by Exponential Enrichment: Chemi-SELEX.”

[0067] The SELEX process can be used to identify high-affinity aptamers containing modified nucleotides that confer improved characteristics on the aptamer, such as, for example, improved *in vivo* stability or improved delivery characteristics. Examples of such modifications include chemical substitutions at the ribose and/or phosphate and/or base positions. SELEX process-identified aptamers containing modified nucleotides are described in U.S. Patent No. 5,660,985, entitled “High Affinity Nucleic Acid Ligands Containing Modified Nucleotides”, which describes oligonucleotides containing nucleotide derivatives chemically modified at the 5'- and 2'-positions of pyrimidines. U.S. Patent No. 5,580,737, see *supra*, describes highly specific aptamers containing one or more nucleotides modified with 2'-amino (2'-NH₂), 2'-fluoro (2'-F), and/or 2'-O-methyl (2'-Ome). See also, U.S. Patent Application Publication 20090098549, entitled “SELEX and PHOTOSELEX”, which describes nucleic acid libraries having expanded physical and chemical properties and their use in SELEX and photoSELEX.

[0068] SELEX can also be used to identify aptamers that have desirable off-rate characteristics. See U.S. Publication No. 20090004667, entitled “Method for Generating Aptamers with Improved Off-Rates”, which describes improved SELEX methods for generating aptamers that can bind to target molecules. Methods for producing aptamers and photoaptamers having slower rates of dissociation from their respective target molecules are

described. The methods involve contacting the candidate mixture with the target molecule, allowing the formation of nucleic acid-target complexes to occur, and performing a slow off-rate enrichment process wherein nucleic acid-target complexes with fast dissociation rates will dissociate and not reform, while complexes with slow dissociation rates will remain intact. Additionally, the methods include the use of modified nucleotides in the production of candidate nucleic acid mixtures to generate aptamers with improved off-rate performance. Nonlimiting exemplary modified nucleotides include, for example, the modified pyrimidines shown in Figs. 3-5. In some embodiments, an aptamer comprises at least one nucleotide with a modification, such as a base modification. In some embodiments, an aptamer comprises at least one nucleotide with a hydrophobic modification, such as a hydrophobic base modification, allowing for hydrophobic contacts with a target protein. Such hydrophobic contacts, in some embodiments, contribute to greater affinity and/or slower off-rate binding by the aptamer. Nonlimiting exemplary nucleotides with hydrophobic modifications are shown in Figure 3. In some embodiments, an aptamer comprises 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 hydrophobic modifications, where each hydrophobic modification may be the same or different from the others. In some embodiments, 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 hydrophobic modifications in an aptamer may be independently selected from the hydrophobic modifications shown in Figure 3.

[0069] In some embodiments, the aptamer is a slow off-rate aptamer. In some embodiments, a slow off-rate aptamer (including an aptamer comprising at least one nucleotide with a hydrophobic modification) has an off-rate ($t_{1/2}$) of ≥ 30 minutes, ≥ 60 minutes, ≥ 90 minutes, ≥ 120 minutes, ≥ 150 minutes, ≥ 180 minutes, ≥ 210 minutes, or ≥ 240 minutes.

[0070] In some embodiments, an assay employs aptamers that include photoreactive functional groups that enable the aptamers to covalently bind or “photocrosslink” their target molecules. See, e.g., U.S. Patent No. 6,544,776 entitled “Nucleic Acid Ligand Diagnostic Biochip”. These photoreactive aptamers are also referred to as photoaptamers. See, e.g., U.S. Patent No. 5,763,177, U.S. Patent No. 6,001,577, and U.S. Patent No. 6,291,184, each of which is entitled “Systematic Evolution of Nucleic Acid Ligands by Exponential Enrichment: Photoselection of Nucleic Acid Ligands and Solution SELEX”; see also, e.g., U.S. Patent No. 6,458,539, entitled “Photoselection of Nucleic Acid Ligands”. After the microarray is contacted with the sample and the photoaptamers have had an opportunity to bind to their

target molecules, the photoaptamers are photoactivated, and the solid support is washed to remove any non-specifically bound molecules. Harsh wash conditions may be used, since target molecules that are bound to the photoaptamers are generally not removed, due to the covalent bonds created by the photoactivated functional group(s) on the photoaptamers. In this manner, the assay enables the detection of a biomarker level corresponding to a biomarker in the test sample.

[0071] In some assay formats, the aptamers are immobilized on the solid support prior to being contacted with the sample. Under certain circumstances, however, immobilization of the aptamers prior to contact with the sample may not provide an optimal assay. For example, pre-immobilization of the aptamers may result in inefficient mixing of the aptamers with the target molecules on the surface of the solid support, perhaps leading to lengthy reaction times and, therefore, extended incubation periods to permit efficient binding of the aptamers to their target molecules. Further, when photoaptamers are employed in the assay and depending upon the material utilized as a solid support, the solid support may tend to scatter or absorb the light used to effect the formation of covalent bonds between the photoaptamers and their target molecules. Moreover, depending upon the method employed, detection of target molecules bound to their aptamers can be subject to imprecision, since the surface of the solid support may also be exposed to and affected by any labeling agents that are used. Finally, immobilization of the aptamers on the solid support generally involves an aptamer-preparation step (i.e., the immobilization) prior to exposure of the aptamers to the sample, and this preparation step may affect the activity or functionality of the aptamers.

[0072] Aptamer assays that permit an aptamer to capture its target in solution and then employ separation steps that are designed to remove specific components of the aptamer-target mixture prior to detection have also been described (see U.S. Publication No. 20090042206, entitled "Multiplexed Analyses of Test Samples"). The described aptamer assay methods enable the detection and quantification of a non-nucleic acid target (e.g., a protein target) in a test sample by detecting and quantifying a nucleic acid (i.e., an aptamer). The described methods create a nucleic acid surrogate (i.e., the aptamer) for detecting and quantifying a non-nucleic acid target, thus allowing the wide variety of nucleic acid technologies, including amplification, to be applied to a broader range of desired targets, including protein targets.

[0073] Aptamers can be constructed to facilitate the separation of the assay components from an aptamer biomarker complex (or photoaptamer biomarker covalent complex) and permit isolation of the aptamer for detection and/or quantification. In one

embodiment, these constructs can include a cleavable or releasable element within the aptamer sequence. In other embodiments, additional functionality can be introduced into the aptamer, for example, a labeled or detectable component, a spacer component, or a specific binding tag or immobilization element. For example, the aptamer can include a tag connected to the aptamer via a cleavable moiety, a label, a spacer component separating the label, and the cleavable moiety. In one embodiment, a cleavable element is a photocleavable linker. The photocleavable linker can be attached to a biotin moiety and a spacer section, can include an NHS group for derivatization of amines, and can be used to introduce a biotin group to an aptamer, thereby allowing for the release of the aptamer later in an assay method.

[0074] Homogenous assays, done with all assay components in solution, do not require separation of sample and reagents prior to the detection of signal. These methods are rapid and easy to use. These methods generate signal based on a molecular capture or binding reagent that reacts with its specific target. In some embodiments, the molecular capture reagents comprise one or more aptamers and/or antibodies or the like and the specific target of each of the one or more aptamers and/or antibodies or the like may be a biomarker shown in Table 1, Table 2, Table 3, or Table 4.

[0075] In some embodiments, a method for signal generation takes advantage of anisotropy signal change due to the interaction of a fluorophore-labeled capture reagent with its specific biomarker target. When the labeled capture reacts with its target, the increased molecular weight causes the rotational motion of the fluorophore attached to the complex to become much slower changing the anisotropy value. By monitoring the anisotropy change, binding events may be used to quantitatively measure the biomarkers in solutions. Other methods include fluorescence polarization assays, molecular beacon methods, time resolved fluorescence quenching, chemiluminescence, fluorescence resonance energy transfer, and the like.

[0076] An exemplary solution-based aptamer assay that can be used to detect a biomarker level in a biological sample includes the following: (a) preparing a mixture by contacting the biological sample with an aptamer that includes a first tag and has a specific affinity for the biomarker, wherein an aptamer affinity complex is formed when the biomarker is present in the sample; (b) exposing the mixture to a first solid support including a first capture element, and allowing the first tag to associate with the first capture element; (c) removing any components of the mixture not associated with the first solid support; (d) attaching a second tag to the biomarker component of the aptamer affinity complex; (e) releasing the aptamer affinity complex from the first solid support; (f) exposing the released

aptamer affinity complex to a second solid support that includes a second capture element and allowing the second tag to associate with the second capture element; (g) removing any non-complexed aptamer from the mixture by partitioning the non-complexed aptamer from the aptamer affinity complex; (h) eluting the aptamer from the solid support; and (i) detecting the biomarker by detecting the aptamer component of the aptamer affinity complex.

[0077] Any means known in the art can be used to detect a biomarker value by detecting the aptamer component of an aptamer affinity complex. A number of different detection methods can be used to detect the aptamer component of an affinity complex, such as, for example, hybridization assays, mass spectroscopy, or QPCR. In some embodiments, nucleic acid sequencing methods can be used to detect the aptamer component of an aptamer affinity complex and thereby detect a biomarker value. Briefly, a test sample can be subjected to any kind of nucleic acid sequencing method to identify and quantify the sequence or sequences of one or more aptamers present in the test sample. In some embodiments, the sequence includes the entire aptamer molecule or any portion of the molecule that may be used to uniquely identify the molecule. In other embodiments, the identifying sequencing is a specific sequence added to the aptamer; such sequences are often referred to as “tags,” “barcodes,” or “zipcodes.” In some embodiments, the sequencing method includes enzymatic steps to amplify the aptamer sequence or to convert any kind of nucleic acid, including RNA and DNA that contain chemical modifications to any position, to any other kind of nucleic acid appropriate for sequencing.

[0078] In some embodiments, the sequencing method includes one or more cloning steps. In other embodiments the sequencing method includes a direct sequencing method without cloning.

[0079] In some embodiments, the sequencing method includes a directed approach with specific primers that target one or more aptamers in the test sample. In other embodiments, the sequencing method includes a shotgun approach that targets all aptamers in the test sample.

[0080] In some embodiments, the sequencing method includes enzymatic steps to amplify the molecule targeted for sequencing. In other embodiments, the sequencing method directly sequences single molecules. An exemplary nucleic acid sequencing-based method that can be used to detect a biomarker value corresponding to a biomarker in a biological sample includes the following: (a) converting a mixture of aptamers that contain chemically modified nucleotides to unmodified nucleic acids with an enzymatic step; (b) shotgun sequencing the resulting unmodified nucleic acids with a massively parallel sequencing

platform such as, for example, the 454 Sequencing System (454 Life Sciences/Roche), the Illumina Sequencing System (Illumina), the ABI SOLiD Sequencing System (Applied Biosystems), the HeliScope Single Molecule Sequencer (Helicos Biosciences), or the Pacific Biosciences Real Time Single-Molecule Sequencing System (Pacific BioSciences) or the Polonator G Sequencing System (Dover Systems); and (c) identifying and quantifying the aptamers present in the mixture by specific sequence and sequence count.

[0081] A nonlimiting exemplary method of detecting biomarkers in a biological sample using aptamers is described in Example 1. *See also* Kraemer et al., 2011, *PloS One* 6(10): e26332.

Determination of Biomarker Levels using Immunoassays

[0082] Immunoassay methods are based on the reaction of an antibody to its corresponding target or analyte and can detect the analyte in a sample depending on the specific assay format. To improve specificity and sensitivity of an assay method based on antibody-reactivity, monoclonal antibodies and fragments thereof are often used because of their specific epitope recognition. Polyclonal antibodies have also been successfully used in various immunoassays because of their increased affinity for the target as compared to monoclonal antibodies. Immunoassays have been designed for use with a wide range of biological sample matrices. Immunoassay formats have been designed to provide qualitative, semi-quantitative, and quantitative results.

[0083] Quantitative results are generated through the use of a standard curve created with known concentrations of the specific analyte to be detected. The response or signal from an unknown sample is plotted onto the standard curve, and a quantity or level corresponding to the target in the unknown sample is established.

[0084] Numerous immunoassay formats have been designed. ELISA or EIA can be quantitative for the detection of an analyte. This method relies on attachment of a label to either the analyte or the antibody and the label component includes, either directly or indirectly, an enzyme. ELISA tests may be formatted for direct, indirect, competitive, or sandwich detection of the analyte. Other methods rely on labels such as, for example, radioisotopes (I^{125}) or fluorescence. Additional techniques include, for example, agglutination, nephelometry, turbidimetry, Western blot, immunoprecipitation, immunocytochemistry, immunohistochemistry, flow cytometry, Luminex assay, and others (see *ImmunoAssay: A Practical Guide*, edited by Brian Law, published by Taylor & Francis, Ltd., 2005 edition).

[0085] Exemplary assay formats include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay, fluorescent, chemiluminescence, and fluorescence resonance energy transfer (FRET) or time resolved-FRET (TR-FRET) immunoassays. Examples of procedures for detecting biomarkers include biomarker immunoprecipitation followed by quantitative methods that allow size and peptide level discrimination, such as gel electrophoresis, capillary electrophoresis, planar electrochromatography, and the like.

[0086] Methods of detecting and/or for quantifying a detectable label or signal generating material depend on the nature of the label. The products of reactions catalyzed by appropriate enzymes (where the detectable label is an enzyme; see above) can be, without limitation, fluorescent, luminescent, or radioactive or they may absorb visible or ultraviolet light. Examples of detectors suitable for detecting such detectable labels include, without limitation, x-ray film, radioactivity counters, scintillation counters, spectrophotometers, colorimeters, fluorometers, luminometers, and densitometers.

[0087] Any of the methods for detection can be performed in any format that allows for any suitable preparation, processing, and analysis of the reactions. This can be, for example, in multi-well assay plates (e.g., 96 wells or 386 wells) or using any suitable array or microarray. Stock solutions for various agents can be made manually or robotically, and all subsequent pipetting, diluting, mixing, distribution, washing, incubating, sample readout, data collection and analysis can be done robotically using commercially available analysis software, robotics, and detection instrumentation capable of detecting a detectable label.

Determination of Biomarker Levels using Gene Expression Profiling

[0088] Measuring mRNA in a biological sample may, in some embodiments, be used as a surrogate for detection of the level of the corresponding protein in the biological sample. Thus, in some embodiments, a biomarker or biomarker panel described herein can be detected by detecting the appropriate RNA.

[0089] In some embodiments, mRNA expression levels are measured by reverse transcription quantitative polymerase chain reaction (RT-PCR followed with qPCR). RT-PCR is used to create a cDNA from the mRNA. The cDNA may be used in a qPCR assay to produce fluorescence as the DNA amplification process progresses. By comparison to a standard curve, qPCR can produce an absolute measurement such as number of copies of mRNA per cell. Northern blots, microarrays, Invader assays, and RT-PCR combined with capillary electrophoresis have all been used to measure expression levels of mRNA in a

sample. See Gene Expression Profiling: Methods and Protocols, Richard A. Shimkets, editor, Humana Press, 2004.

Detection of Biomarkers Using *In Vivo* Molecular Imaging Technologies

[0090] In some embodiments, a biomarker described herein may be used in molecular imaging tests. For example, an imaging agent can be coupled to a capture reagent, which can be used to detect the biomarker *in vivo*.

[0091] *In vivo* imaging technologies provide non-invasive methods for determining the state of a particular disease in the body of an individual. For example, entire portions of the body, or even the entire body, may be viewed as a three dimensional image, thereby providing valuable information concerning morphology and structures in the body. Such technologies may be combined with the detection of the biomarkers described herein to provide information concerning the biomarker *in vivo*.

[0092] The use of *in vivo* molecular imaging technologies is expanding due to various advances in technology. These advances include the development of new contrast agents or labels, such as radiolabels and/or fluorescent labels, which can provide strong signals within the body; and the development of powerful new imaging technology, which can detect and analyze these signals from outside the body, with sufficient sensitivity and accuracy to provide useful information. The contrast agent can be visualized in an appropriate imaging system, thereby providing an image of the portion or portions of the body in which the contrast agent is located. The contrast agent may be bound to or associated with a capture reagent, such as an aptamer or an antibody, for example, and/or with a peptide or protein, or an oligonucleotide (for example, for the detection of gene expression), or a complex containing any of these with one or more macromolecules and/or other particulate forms.

[0093] The contrast agent may also feature a radioactive atom that is useful in imaging. Suitable radioactive atoms include technetium-99m or iodine-123 for scintigraphic studies. Other readily detectable moieties include, for example, spin labels for magnetic resonance imaging (MRI) such as, for example, iodine-123 again, iodine-131, indium-111, fluorine-19, carbon-13, nitrogen-15, oxygen-17, gadolinium, manganese or iron. Such labels are well known in the art and could easily be selected by one of ordinary skill in the art.

[0094] Standard imaging techniques include but are not limited to magnetic resonance imaging, computed tomography scanning, positron emission tomography (PET), single photon emission computed tomography (SPECT), and the like. For diagnostic *in vivo* imaging, the type of detection instrument available is a major factor in selecting a given

contrast agent, such as a given radionuclide and the particular biomarker that it is used to target (protein, mRNA, and the like). The radionuclide chosen typically has a type of decay that is detectable by a given type of instrument. Also, when selecting a radionuclide for *in vivo* diagnosis, its half-life should be long enough to enable detection at the time of maximum uptake by the target tissue but short enough that deleterious radiation of the host is minimized.

[0095] Exemplary imaging techniques include but are not limited to PET and SPECT, which are imaging techniques in which a radionuclide is synthetically or locally administered to an individual. The subsequent uptake of the radiotracer is measured over time and used to obtain information about the targeted tissue and the biomarker. Because of the high-energy (gamma-ray) emissions of the specific isotopes employed and the sensitivity and sophistication of the instruments used to detect them, the two-dimensional distribution of radioactivity may be inferred from outside of the body.

[0096] Commonly used positron-emitting nuclides in PET include, for example, carbon-11, nitrogen-13, oxygen-15, and fluorine-18. Isotopes that decay by electron capture and/or gamma-emission are used in SPECT and include, for example iodine-123 and technetium-99m. An exemplary method for labeling amino acids with technetium-99m is the reduction of pertechnetate ion in the presence of a chelating precursor to form the labile technetium-99m-precursor complex, which, in turn, reacts with the metal binding group of a bifunctionally modified chemotactic peptide to form a technetium-99m-chemotactic peptide conjugate.

[0097] Antibodies are frequently used for such *in vivo* imaging diagnostic methods. The preparation and use of antibodies for *in vivo* diagnosis is well known in the art. Similarly, aptamers may be used for such *in vivo* imaging diagnostic methods. For example, an aptamer that was used to identify a particular biomarker described herein may be appropriately labeled and injected into an individual to detect the biomarker *in vivo*. The label used will be selected in accordance with the imaging modality to be used, as previously described. Aptamer-directed imaging agents could have unique and advantageous characteristics relating to tissue penetration, tissue distribution, kinetics, elimination, potency, and selectivity as compared to other imaging agents.

[0098] Such techniques may also optionally be performed with labeled oligonucleotides, for example, for detection of gene expression through imaging with antisense oligonucleotides. These methods are used for *in situ* hybridization, for example,

with fluorescent molecules or radionuclides as the label. Other methods for detection of gene expression include, for example, detection of the activity of a reporter gene.

[0099] Another general type of imaging technology is optical imaging, in which fluorescent signals within the subject are detected by an optical device that is external to the subject. These signals may be due to actual fluorescence and/or to bioluminescence. Improvements in the sensitivity of optical detection devices have increased the usefulness of optical imaging for in vivo diagnostic assays.

[00100] For a review of other techniques, see N. Blow, *Nature Methods*, 6, 465-469, 2009.

Determination of Biomarker Levels using Mass Spectrometry Methods

[00101] A variety of configurations of mass spectrometers can be used to detect biomarker levels. Several types of mass spectrometers are available or can be produced with various configurations. In general, a mass spectrometer has the following major components: a sample inlet, an ion source, a mass analyzer, a detector, a vacuum system, and instrument-control system, and a data system. Difference in the sample inlet, ion source, and mass analyzer generally define the type of instrument and its capabilities. For example, an inlet can be a capillary-column liquid chromatography source or can be a direct probe or stage such as used in matrix-assisted laser desorption. Common ion sources are, for example, electrospray, including nanospray and microspray or matrix-assisted laser desorption. Common mass analyzers include a quadrupole mass filter, ion trap mass analyzer and time-of-flight mass analyzer. Additional mass spectrometry methods are well known in the art (see Burlingame et al. *Anal. Chem.* 70:647 R-716R (1998); Kinter and Sherman, New York (2000)).

[00102] Protein biomarkers and biomarker levels can be detected and measured by any of the following: electrospray ionization mass spectrometry (ESI-MS), ESI-MS/MS, ESI-MS/(MS)_n, matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF-MS), surface-enhanced laser desorption/ionization time-of-flight mass spectrometry (SELDI-TOF-MS), desorption/ionization on silicon (DIOS), secondary ion mass spectrometry (SIMS), quadrupole time-of-flight (Q-TOF), tandem time-of-flight (TOF/TOF) technology, called ultraflex III TOF/TOF, atmospheric pressure chemical ionization mass spectrometry (APCI-MS), APCI-MS/MS, APCI-(MS)_N, atmospheric pressure photoionization mass spectrometry (APPI-MS), APPI-MS/MS, and APPI-(MS)_N, quadrupole mass spectrometry, Fourier transform mass spectrometry (FTMS), quantitative mass spectrometry, and ion trap mass spectrometry.

[00103] Sample preparation and processing strategies are used to label and enrich samples before mass spectroscopic characterization of protein biomarkers and determination biomarker levels. Labeling methods include but are not limited to isobaric tag for relative and absolute quantitation (iTRAQ) and stable isotope labeling with amino acids in cell culture (SILAC). Capture reagents used to selectively enrich samples for candidate biomarker proteins prior to mass spectroscopic analysis include but are not limited to aptamers, antibodies, nucleic acid probes, chimeras, small molecules, an F(ab')₂ fragment, a single chain antibody fragment, an Fv fragment, a single chain Fv fragment, a nucleic acid, a lectin, a ligand-binding receptor, affibodies, nanobodies, ankyrins, domain antibodies, alternative antibody scaffolds (e.g. diabodies etc) imprinted polymers, avimers, peptidomimetics, peptoids, peptide nucleic acids, threose nucleic acid, a hormone receptor, a cytokine receptor, and synthetic receptors, and modifications and fragments of these.

Determination of Biomarker Levels using a Proximity Ligation Assay

[00104] A proximity ligation assay can be used to determine biomarker values. Briefly, a test sample is contacted with a pair of affinity probes that may be a pair of antibodies or a pair of aptamers, with each member of the pair extended with an oligonucleotide. The targets for the pair of affinity probes may be two distinct determinates on one protein or one determinate on each of two different proteins, which may exist as homo- or hetero-multimeric complexes. When probes bind to the target determinates, the free ends of the oligonucleotide extensions are brought into sufficiently close proximity to hybridize together. The hybridization of the oligonucleotide extensions is facilitated by a common connector oligonucleotide which serves to bridge together the oligonucleotide extensions when they are positioned in sufficient proximity. Once the oligonucleotide extensions of the probes are hybridized, the ends of the extensions are joined together by enzymatic DNA ligation.

[00105] Each oligonucleotide extension comprises a primer site for PCR amplification. Once the oligonucleotide extensions are ligated together, the oligonucleotides form a continuous DNA sequence which, through PCR amplification, reveals information regarding the identity and amount of the target protein, as well as, information regarding protein-protein interactions where the target determinates are on two different proteins. Proximity ligation can provide a highly sensitive and specific assay for real-time protein concentration and interaction information through use of real-time PCR. Probes that do not bind the determinates of interest do not have the corresponding oligonucleotide extensions brought

into proximity and no ligation or PCR amplification can proceed, resulting in no signal being produced.

[00106] The foregoing assays enable the detection of biomarker values that are useful in methods for assessing sample quality, wherein the methods comprise detecting, in a biological sample from an individual, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, , or all 8 biomarkers selected from the biomarkers in Table 1; or at least 2, at least 3, at least 4, or all 5 biomarkers selected from the biomarkers in Table 2; at least 2, at least 3, at or all 4 biomarkers selected from the biomarkers in Table 3; at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, or all 13 biomarkers selected from the biomarkers in Table 4; or a combination of biomarkers shown in Table 1 with biomarkers shown in Table 3 and/or Table 4; or a combination of biomarkers shown in Table 2 with biomarkers shown in Table 3 and/or Table 4. A classification, as described below, using the biomarker levels indicates whether the sample has acceptable quality for use in subsequent analysis. In accordance with any of the methods described herein, biomarker levels can be detected and classified individually or they can be detected and classified collectively, as for example in a multiplex assay format.

Classification of Biomarkers and Calculation of Sample Processing Times

[00107] In some embodiments, a biomarker “signature” for a given sample quality test contains a set of biomarkers, each biomarker having characteristic levels in samples of acceptable quality or in sample of poor quality. Characteristic levels, in some embodiments, may refer to the mean or average of the biomarker levels for the samples in a particular group. In some embodiments, a method described herein can be used to assign a sample into one of two groups, either passing quality assessment or failing quality assessment.

[00108] The assignment of a sample into one of two or more groups is known as classification, and the procedure used to accomplish this assignment is known as a classifier or a classification method. Classification methods may also be referred to as scoring methods. There are many classification methods that can be used to construct a classifier from a set of biomarker levels. In some instances, classification methods are performed using supervised learning techniques in which a data set is collected using samples from two (or more, for multiple classification states) distinct groups one wishes to distinguish. Since the class (group or population) to which each sample belongs is known in advance for each sample, the classification method can be trained to give the desired classification response. It is also possible to use unsupervised learning techniques to produce a quality classifier.

[00109] Common approaches for developing classifiers include decision trees; bagging + boosting + forests; rule inference based learning; Parzen Windows; linear models; logistic; neural network methods; unsupervised clustering; K-means; hierarchical ascending/descending; semi-supervised learning; prototype methods; nearest neighbor; kernel density estimation; support vector machines; hidden Markov models; Boltzmann Learning; and classifiers may be combined either simply or in ways which minimize particular objective functions. For a review, see, e.g., Pattern Classification, R.O. Duda, et al., editors, John Wiley & Sons, 2nd edition, 2001; see also, The Elements of Statistical Learning – Data Mining, Inference, and Prediction, T. Hastie, et al., editors, Springer Science+Business Media, LLC, 2nd edition, 2009.

[00110] To produce a classifier using supervised learning techniques, a set of samples called training data are obtained. In the context of quality tests, training data includes samples from the distinct groups (classes) to which unknown samples will later be assigned. For example, samples that underwent processing with differing, set times between processing steps can constitute training data to develop a classifier that can classify unknown samples as either passing or failing quality assessment based on the elapsed time between sample processing steps. The development of the classifier from the training data is known as training the classifier. Specific details on classifier training depend on the nature of the supervised learning technique. Training a naïve Bayesian classifier is an example of such a supervised learning technique (see, e.g., Pattern Classification, R.O. Duda, et al., editors, John Wiley & Sons, 2nd edition, 2001; see also, The Elements of Statistical Learning – Data Mining, Inference, and Prediction, T. Hastie, et al., editors, Springer Science+Business Media, LLC, 2nd edition, 2009). Training of a naïve Bayesian classifier is described, e.g., in U.S. Publication Nos: 2012/0101002 and 2012/0077695.

[00111] Since typically there are many more potential biomarker levels than samples in a training set, care must be used to avoid over-fitting. Over-fitting occurs when a statistical model describes random error or noise instead of the underlying relationship. Over-fitting can be avoided in a variety of way, including, for example, by limiting the number of biomarkers used in developing the classifier, by assuming that the biomarker responses are independent of one another, by limiting the complexity of the underlying statistical model employed, and by ensuring that the underlying statistical model conforms to the data.

[00112] An illustrative example of the development of a test using a set of biomarkers includes the application of a naïve Bayes classifier, a simple probabilistic classifier based on Bayes theorem with strict independent treatment of the biomarkers. Each biomarker is

described by a class-dependent probability density function (pdf) for the measured RFU values or log RFU (relative fluorescence units) values in each class. The joint pdfs for the set of biomarkers in one class is assumed to be the product of the individual class-dependent pdfs for each biomarker. Training a naïve Bayes classifier in this context amounts to assigning parameters (“parameterization”) to characterize the class dependent pdfs. Any underlying model for the class-dependent pdfs may be used, but the model should generally conform to the data observed in the training set.

[00113] The performance of the naïve Bayes classifier is dependent upon the number and quality of the biomarkers used to construct and train the classifier. A single biomarker will perform in accordance with its KS-distance (Kolmogorov-Smirnov). The addition of subsequent biomarkers with good KS distances (>0.3 , for example) will, in general, improve the classification performance if the subsequently added biomarkers are independent of the first biomarker. Using the sensitivity plus specificity as a classifier score, many high scoring classifiers can be generated with a variation of a greedy algorithm. (A greedy algorithm is any algorithm that follows the problem solving metaheuristic of making the locally optimal choice at each stage with the hope of finding the global optimum.)

[00114] Another way to depict classifier performance is through a receiver operating characteristic (ROC), or simply ROC curve or ROC plot. The ROC is a graphical plot of the sensitivity, or true positive rate, vs. false positive rate ($1 - \text{specificity}$ or $1 - \text{true negative rate}$), for a binary classifier system as its discrimination threshold is varied. The ROC can also be represented equivalently by plotting the fraction of true positives out of the positives (TPR = true positive rate) vs. the fraction of false positives out of the negatives (FPR = false positive rate). Also known as a Relative Operating Characteristic curve, because it is a comparison of two operating characteristics (TPR & FPR) as the criterion changes. The area under the ROC curve (AUC) is commonly used as a summary measure of diagnostic accuracy. It can take values from 0.0 to 1.0. The AUC has an important statistical property: the AUC of a classifier is equivalent to the probability that the classifier will rank a randomly chosen positive instance higher than a randomly chosen negative instance (Fawcett T, 2006. An introduction to ROC analysis. *Pattern Recognition Letters* .27: 861–874). This is equivalent to the Wilcoxon test of ranks (Hanley, J.A., McNeil, B.J., 1982. The meaning and use of the area under a receiver operating characteristic (ROC) curve. *Radiology* 143, 29–36.). Another way of describing performance of a diagnostic test in relation to a known reference standard is the net reclassification index: the ability of the new test to correctly upgrade or downgrade risk when compared with the reference standard test. See, e.g.,

Pencina et al., 2011, *Stat. Med.* 30: 11-21. While the AUC under the ROC curve is optimal for assessing performance of a 2-class classifier, stratified and personalized medicine relies upon the inference that the population contains more classes than 2. For such comparisons the hazard ratio of the upper vs. lower quartiles (or other stratifications such as deciles) can be used more appropriately.

Kits

[00115] Any combination of the biomarkers described herein can be detected using a suitable kit, such as for use in performing the methods disclosed herein. Furthermore, any kit can contain one or more detectable labels as described herein, such as a fluorescent moiety, etc.

[00116] In some embodiments, a kit includes (a) one or more capture reagents (such as, for example, at least one aptamer or antibody) for detecting one or more biomarkers in a biological sample, wherein the biomarkers include at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or all 8 biomarkers selected from the biomarkers in Table 1; or at least 2, at least 3, at least 4, at all 5 biomarkers selected from the biomarkers in Table 2; at least 2, at least 3, at or all 4 biomarkers selected from the biomarkers in Table 3; at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, or all 13 biomarkers selected from the biomarkers in Table 4; or a combination of biomarkers shown in Table 1 with biomarkers shown in Table 3 and/or Table 4; or a combination of biomarkers shown in Table 2 with biomarkers shown in Table 3 and/or Table 4; and optionally (b) one or more software or computer program products for classifying the sample was obtained as either passing or failing quality assessment or for determining the approximate time or times of sample processing steps, as further described herein. Alternatively, rather than one or more computer program products, one or more instructions for manually performing the above steps by a human can be provided.

[00117] In some embodiments, a kit comprises a solid support, at least one capture reagent, and a signal generating material. The kit can also include instructions for using the devices and reagents, handling the sample, and analyzing the data. Further the kit may be used with a computer system or software to analyze and report the result of the analysis of the biological sample.

[00118] The kit may further comprise reagents for diagnostic analysis of samples, particularly samples that pass quality assessment.

[00119] The kits can also contain one or more reagents (e.g., solubilization buffers, detergents, washes, or buffers) for processing a biological sample. Any of the kits described

herein can also include, e.g., buffers, blocking agents, mass spectrometry matrix materials, antibody capture agents, positive control samples, negative control samples, software and information such as protocols, guidance and reference data.

[00120] In some embodiments, the kits comprise PCR primers for one or more aptamers specific to biomarkers described herein. In some embodiments, a kit may further include instructions for use and correlation of the biomarkers with estimation of sample processing times and/or sample quality. In some embodiments, a kit may also include a DNA array containing the complement of one or more of the aptamers specific for the biomarkers described herein, reagents, and/or enzymes for amplifying or isolating sample DNA. In some embodiments, kits may include reagents for real-time PCR, for example, TaqMan probes and/or primers, and enzymes.

[00121] For example, a kit can comprise (a) reagents comprising at least one capture reagent for determining the level of one or more biomarkers in a test sample, and optionally (b) one or more algorithms or computer programs for performing the steps of comparing the amount of each biomarker quantified in the test sample to one or more predetermined cutoffs. In some embodiments, an algorithm or computer program assigns a score for each biomarker quantified based on said comparison and, in some embodiments, combines the assigned scores for each biomarker quantified to obtain a total score. Further, in some embodiments, an algorithm or computer program compares the total score with a predetermined score, and uses the comparison to determine whether a sample passes or fails quality assessment. Alternatively, rather than one or more algorithms or computer programs, one or more instructions for manually performing the above steps by a human can be provided.

Biomarker Panels

[00122] In some embodiments, one or more of the biomarkers listed in Table 1 are detected. In some embodiments, the one or more biomarkers listed in Table 1 are detected in a plasma sample from a subject. In some embodiments, all of the biomarkers listed in Table 1 are detected. In some embodiments, the level of each protein listed in Table 1 is detected. In some embodiments, the detecting of the one or more biomarkers or all of the biomarkers is performed in order to determine the length of time or approximate length of time between sample processing and sample freezing, i.e. the time-to-freeze. In some embodiments, the sample processing comprises or consists of sample centrifugation and removal of the sample supernatant by decanting or aspirating. In some such embodiments, sample processing was preformed immediately after sample collection from the subject.

Table 1: Panel for plasma samples

Protein	Gene	UniProt ID	Name
LANC2	LANCL2	Q9NS86	LanC-like protein 2
PKHM2	PLEKHM2	Q8IWE5	Pleckstrin homology domain-containing family M member 2
ENOA	ENO1	P06733	Alpha-enolase
TMEM9	TMEM9	Q9P0T7	Transmembrane protein 9, or Proton-transporting V-type ATPase complex assembly regulator TMEM9: Cytoplasmic domain
PMM2	PMM2	O15305	Phosphomannomutase 2
PGAM2	PGAM2	P15259	Phosphoglycerate mutase 2
EFHD1	EFHD1	Q9BUP0	EF-hand domain-containing protein D1
THIK	ACAA1	P09110	3-ketoacyl-CoA thiolase, peroxisomal

[00123] In some embodiments, one or more of the biomarkers listed in Table 2 are detected. In some embodiments, the one or more biomarkers listed in Table 2 are detected in a serum sample from a subject. In some embodiments, all of the biomarkers listed in Table 2 are detected. In some embodiments, the level of each protein listed in Table 2 is detected. In some embodiments, the detecting of the one or more biomarkers or all of the biomarkers is performed in order to determine the length of time or approximate length of time between sample processing and sample freezing, i.e., the time-to-freeze. In some embodiments, the sample processing comprises or consists of sample centrifugation and removal of the sample supernatant by decanting or aspirating. In some such embodiments, sample processing was performed immediately after sample collection from the subject.

Table 2: Panel for serum samples

Protein	Gene	UniProt ID	Name
LYAG	GAA	P10253	Lysosomal alpha-glucosidase
IL21R	IL21R	Q9HBE5	Interleukin-21 receptor
C3b	C3	P01024	Complement C3b (activated Complement C3)
IL36A	IL36A	Q9UHA7	Interleukin-36 alpha
GDF5	GDF5	P43026	Growth/differentiation factor 5

[00124] In some embodiments, one or more of the biomarkers listed in Table 3 are detected. In some embodiments, the one or more biomarkers listed in Table 3 are detected in a plasma sample from a subject. In some embodiments, all of the biomarkers listed in Table 3 are detected. In some embodiments, the level of each protein listed in Table 3 is detected. In some embodiments, the detecting of the one or more biomarkers or all of the biomarkers is

performed in order to determine the length of time or approximate length of time between sample collection and sample centrifugation, i.e., the time-to-centrifugation.

Table 3: Centrifugation Panel

Protein	Gene	UniProt ID	Name
IHH	IHH	Q14623	Indian hedgehog protein
SHH	SHH	Q15465	Sonic hedgehog protein
PGAM1	PGAM1	P18669	Phosphoglycerate mutase 1
ROA2	HNRNPA2B1	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1

[00125] In some embodiments, one or more of the biomarkers listed in Table 4 are detected. In some embodiments, the one or more biomarkers listed in Table 4 are detected in a plasma sample from a subject. In some embodiments, all of the biomarkers listed in Table 4 are detected. In some embodiments, the level of each protein listed in Table 4 is detected. In some embodiments, the detecting of the one or more biomarkers or all of the biomarkers is performed in order to determine or length of time or approximate length of time between sample centrifugation and removal of the supernatant by decanting or aspirating, i.e., the time-to-decant.

Table 4: Decanting or Aspirating Panel

Protein	Gene	UniProt ID	Name
APB	RNPEP	Q9H4A4	Aminopeptidase B
CFAD	CFD	P00746	Complement factor D
PTN4	PTPN4	P29074	Tyrosine-protein phosphatase non-receptor type 4
PGAM2	PGAM2	P15259	Phosphoglycerate mutase 2
HPPD	HPD	P32754	4-hydroxyphenylpyruvate dioxygenase
C4A	C4A	P0C0L4	C4a anaphylatoxin
IF4A2	EIF4A2	Q14240	Eukaryotic initiation factor 4A-II
IHH	IHH	Q14623	Indian hedgehog protein
SHH	SHH	Q15465	Sonic hedgehog protein
ADAM9	ADAM9	Q13443	Disintegrin and metalloproteinase domain-containing protein 9
PGAM1	PGAM1	P18669	Phosphoglycerate mutase 1
IL18	IL18	Q14116	Interleukin-18
TMEM9	TMEM9	Q9P0T7	Transmembrane protein 9

Computer Methods and Software

[00126] A method for assessing sample quality, such as the length of time between sample processing and freezing can comprise the following: 1) obtain a biological sample, such as a sample that has already undergone sample processing; 2) perform an analytical

method to detect and measure a biomarker or set of biomarkers in a panel in the biological sample; 3) optionally perform any data normalization or standardization; 4) determine each biomarker level; and 5) report the results. In some embodiments, the results are calibrated to the sample type. In some embodiments, the biomarker levels are combined in some way and a single value for the combined biomarker levels is reported. In this approach, in some embodiments, the score may be a single number or identity determined from the integration of all the biomarkers that is compared to a pre-set threshold value that is an indication of satisfactory (passing) or unsatisfactory (failing) quality. Or the predictive score may be a series of bars that each represent a biomarker value and the pattern of the responses may be compared to a pre-set pattern for determination of the satisfactory (passing) or unsatisfactory (failing) quality.

[00127] At least some embodiments of the methods described herein can be implemented with the use of a computer. An example of a computer system 100 is shown in Figure 1. With reference to Figure 1, system 100 is shown comprised of hardware elements that are electrically coupled via bus 108, including a processor 101, input device 102, output device 103, storage device 104, computer-readable storage media reader 105a, communications system 106, processing acceleration (e.g., DSP or special-purpose processors) 107 and memory 109. Computer-readable storage media reader 105a is further coupled to computer-readable storage media 105b, the combination comprehensively representing remote, local, fixed and/or removable storage devices plus storage media, memory, etc. for temporarily and/or more permanently containing computer-readable information, which can include storage device 104, memory 109 and/or any other such accessible system 100 resource. System 100 also comprises software elements (shown as being currently located within working memory 191) including an operating system 192 and other code 193, such as programs, data and the like.

[00128] With respect to Figure 1, system 100 has extensive flexibility and configurability. Thus, for example, a single architecture might be utilized to implement one or more servers that can be further configured in accordance with currently desirable protocols, protocol variations, extensions, etc. However, it will be apparent to those skilled in the art that embodiments may well be utilized in accordance with more specific application requirements. For example, one or more system elements might be implemented as sub-elements within a system 100 component (e.g., within communications system 106). Customized hardware might also be utilized and/or particular elements might be implemented in hardware, software or both. Further, while connection to other computing devices such as

network input/output devices (not shown) may be employed, it is to be understood that wired, wireless, modem, and/or other connection or connections to other computing devices might also be utilized.

[00129] In one aspect, the system can comprise a database containing features of biomarkers characteristic of sample quality. The biomarker data (or biomarker information) can be utilized as an input to the computer for use as part of a computer implemented method. The biomarker data can include the data as described herein.

[00130] In one aspect, the system further comprises one or more devices for providing input data to the one or more processors.

[00131] The system further comprises a memory for storing a data set of ranked data elements.

[00132] In another aspect, the device for providing input data comprises a detector for detecting the characteristic of the data element, e.g., such as a mass spectrometer or gene chip reader.

[00133] The system additionally may comprise a database management system. User requests or queries can be formatted in an appropriate language understood by the database management system that processes the query to extract the relevant information from the database of training sets.

[00134] The system may be connectable to a network to which a network server and one or more clients are connected. The network may be a local area network (LAN) or a wide area network (WAN), as is known in the art. Preferably, the server includes the hardware necessary for running computer program products (e.g., software) to access database data for processing user requests.

[00135] The system may include an operating system (e.g., UNIX or Linux) for executing instructions from a database management system. In one aspect, the operating system can operate on a global communications network, such as the internet, and utilize a global communications network server to connect to such a network.

[00136] The system may include one or more devices that comprise a graphical display interface comprising interface elements such as buttons, pull down menus, scroll bars, fields for entering text, and the like as are routinely found in graphical user interfaces known in the art. Requests entered on a user interface can be transmitted to an application program in the system for formatting to search for relevant information in one or more of the system databases. Requests or queries entered by a user may be constructed in any suitable database language.

[00137] The graphical user interface may be generated by a graphical user interface code as part of the operating system and can be used to input data and/or to display inputted data. The result of processed data can be displayed in the interface, printed on a printer in communication with the system, saved in a memory device, and/or transmitted over the network or can be provided in the form of the computer readable medium.

[00138] The system can be in communication with an input device for providing data regarding data elements to the system (e.g., expression values). In one aspect, the input device can include a gene expression profiling system including, e.g., a mass spectrometer, gene chip or array reader, and the like.

[00139] The methods and apparatus for analyzing sample quality biomarker information according to various embodiments may be implemented in any suitable manner, for example, using a computer program operating on a computer system. A conventional computer system comprising a processor and a random access memory, such as a remotely-accessible application server, network server, personal computer or workstation may be used. Additional computer system components may include memory devices or information storage systems, such as a mass storage system and a user interface, for example a conventional monitor, keyboard and tracking device. The computer system may be a stand-alone system or part of a network of computers including a server and one or more databases.

[00140] The sample quality biomarker analysis system can provide functions and operations to complete data analysis, such as data gathering, processing, analysis, reporting and/or sample quality identification. For example, in one embodiment, the computer system can execute the computer program that may receive, store, search, analyze, and report information relating to the sample quality assessment biomarkers. The computer program may comprise multiple modules performing various functions or operations, such as a processing module for processing raw data and generating supplemental data and an analysis module for analyzing raw data and supplemental data to generate a sample quality status and/or estimated sample processing time calculation. Calculation of sample processing time may optionally comprise generating or collecting additional information.

[00141] Some embodiments described herein can be implemented so as to include a computer program product. A computer program product may include a computer readable medium having computer readable program code embodied in the medium for causing an application program to execute on a computer with a database.

[00142] As used herein, a “computer program product” refers to an organized set of instructions in the form of natural or programming language statements that are contained on

a physical media of any nature (e.g., written, electronic, magnetic, optical or otherwise) and that may be used with a computer or other automated data processing system. Such programming language statements, when executed by a computer or data processing system, cause the computer or data processing system to act in accordance with the particular content of the statements. Computer program products include without limitation: programs in source and object code and/or test or data libraries embedded in a computer readable medium. Furthermore, the computer program product that enables a computer system or data processing equipment device to act in pre-selected ways may be provided in a number of forms, including, but not limited to, original source code, assembly code, object code, machine language, encrypted or compressed versions of the foregoing and any and all equivalents.

[00143] In one aspect, a computer program product is provided for evaluation of sample quality. The computer program product includes a computer readable medium embodying program code executable by a processor of a computing device or system, the program code comprising: code that retrieves data attributed to a biological sample from an individual, wherein the data comprises biomarker levels that each correspond to one of the biomarkers in Table 1 or Table 2, Table 3 and/or Table 4; and code that executes a classification method that indicates a sample quality status as a function of the biomarker levels.

[00144] In still another aspect, a computer program product is provided for determining sample processing time or times. The computer program product includes a computer readable medium embodying program code executable by a processor of a computing device or system, the program code comprising: code that retrieves data attributed to a biological sample from an individual, wherein the data comprises a biomarker value corresponding to at least one biomarker in the biological sample selected from the biomarkers provided in Table 1 or 2, Table 3 and/or Table 4; and code that executes a classification method that indicates a sample quality status as a function of the biomarker levels.

[00145] While various embodiments have been described as methods or apparatuses, it should be understood that embodiments can be implemented through code coupled with a computer, e.g., code resident on a computer or accessible by the computer. For example, software and databases could be utilized to implement many of the methods discussed above. Thus, in addition to embodiments accomplished by hardware, it is also noted that these embodiments can be accomplished through the use of an article of manufacture comprised of a computer usable medium having a computer readable program code embodied therein,

which causes the enablement of the functions disclosed in this description. Therefore, it is desired that embodiments also be considered protected by this patent in their program code means as well. Furthermore, the embodiments may be embodied as code stored in a computer-readable memory of virtually any kind including, without limitation, RAM, ROM, magnetic media, optical media, or magneto-optical media. Even more generally, the embodiments could be implemented in software, or in hardware, or any combination thereof including, but not limited to, software running on a general purpose processor, microcode, programmable logic arrays (PLAs), or application-specific integrated circuits (ASICs).

[00146] It is also envisioned that embodiments could be accomplished as computer signals embodied in a carrier wave, as well as signals (e.g., electrical and optical) propagated through a transmission medium. Thus, the various types of information discussed above could be formatted in a structure, such as a data structure, and transmitted as an electrical signal through a transmission medium or stored on a computer readable medium.

[00147] It is also noted that many of the structures, materials, and acts recited herein can be recited as means for performing a function or step for performing a function. Therefore, it should be understood that such language is entitled to cover all such structures, materials, or acts disclosed within this specification and their equivalents, including the matter incorporated by reference.

[00148] The utilization of the biomarkers disclosed herein, and the various methods for determining biomarker values are described in detail above with respect to evaluation of sample quality and suitability for further analysis, such as diagnostic analysis. In some embodiments, the biomarkers, methods, and kits described herein are used to assess the absolute sample quality of one or more samples or the relative consistency of sample quality across a plurality of samples. In some such embodiments, the methods comprise identifying samples that pass or fail a quality assessment. In some embodiments, samples that pass quality assessment are analyzed and samples that fail quality assessment are discarded. In some embodiments, information obtained using the biomarkers, methods, and kits herein can be used to determine whether a sample collection and processing method or facility is suitable.

EXAMPLES

[00149] The following examples are provided for illustrative purposes only and are not intended to limit the scope of the application as defined by the appended claims. Routine molecular biology techniques described in the following examples can be carried out as

described in standard laboratory manuals, such as Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 3rd. ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (2001).

Example 1: Exemplary Biomarker Detection Using Aptamers

[00150] An exemplary method of detecting one or more biomarker proteins in a sample is described, e.g., in Kraemer et al., *PLoS One* 6(10): e26332, and is described below. Three different methods of quantification: microarray-based hybridization, a Luminex bead-based method, and qPCR, are described.

Reagents

[00151] HEPES, NaCl, KCl, EDTA, EGTA, MgCl₂ and Tween-20 may be purchased, e.g., from Fisher Biosciences. Dextran sulfate sodium salt (DxSO₄), nominally 8000 molecular weight, may be purchased, e.g., from AIC and is dialyzed against deionized water for at least 20 hours with one exchange. KOD EX DNA polymerase may be purchased, e.g., from VWR. Tetramethylammonium chloride and CAPSO may be purchased, e.g., from Sigma-Aldrich and streptavidin-phycoerythrin (SAPE) may be purchased, e.g., from Moss Inc. 4-(2-Aminoethyl)-benzenesulfonylfluoride hydrochloride (AEBSF) may be purchased, e.g., from Gold Biotechnology. Streptavidin-coated 96-well plates may be purchased, e.g., from Thermo Scientific (Pierce Streptavidin Coated Plates HBC, clear, 96-well, product number 15500 or 15501). NHS-PEO4-biotin may be purchased, e.g., from Thermo Scientific (EZ-Link NHS-PEO4-Biotin, product number 21329), dissolved in anhydrous DMSO, and may be stored frozen in single-use aliquots. IL-8, MIP-4, Lipocalin-2, RANTES, MMP-7, and MMP-9 may be purchased, e.g., from R&D Systems. Resistin and MCP-1 may be purchased, e.g., from PeproTech, and tPA may be purchased, e.g., from VWR.

Nucleic acids

[00152] Conventional (including amine- and biotin-substituted) oligodeoxynucleotides may be purchased, e.g., from Integrated DNA Technologies (IDT). Z-Block is a single-stranded oligodeoxynucleotide of sequence 5'-(AC-BnBn)₇-AC-3', where Bn indicates a benzyl-substituted deoxyuridine residue. Z-block may be synthesized using conventional phosphoramidite chemistry. Aptamer capture reagents may also be synthesized by conventional phosphoramidite chemistry, and may be purified, for example, on a 21.5×75 mm PRP-3 column, operating at 80°C on a Waters Autopurification 2767 system (or Waters 600 series semi-automated system), using, for example, a timberline TL-600 or TL-150 heater and a gradient of triethylammonium bicarbonate (TEAB) / I to elute product. Detection

is performed at 260 nm and fractions are collected across the main peak prior to pooling best fractions.

Buffers

[00153] Buffer SB18 is composed of 40 mM HEPES, 101 mM NaCl, 5 mM KCl, 5 mM MgCl₂, and 0.05% (v/v) Tween 20 adjusted to pH 7.5 with NaOH. Buffer SB17 is SB18 supplemented with 1 mM trisodium EDTA. Buffer PB1 is composed of 10 mM HEPES, 101 mM NaCl, 5 mM KCl, 5 mM MgCl₂, 1 mM trisodium EDTA and 0.05% (v/v) Tween-20 adjusted to pH 7.5 with NaOH. CAPSO elution buffer consists of 100 mM CAPSO pH 10.0 and 1 M NaCl. Neutralization buffer contains of 500 mM HEPES, 500 mM HCl, and 0.05% (v/v) Tween-20. Agilent Hybridization Buffer is a proprietary formulation that is supplied as part of a kit (Oligo aCGH/ChIP-on-chip Hybridization Kit). Agilent Wash Buffer 1 is a proprietary formulation (Oligo aCGH/ChIP-on-chip Wash Buffer 1, Agilent). Agilent Wash Buffer 2 is a proprietary formulation (Oligo aCGH/ChIP-on-chip Wash Buffer 2, Agilent). TMAC hybridization solution consists of 4.5 M tetramethylammonium chloride, 6 mM trisodium EDTA, 75 mM Tris-HCl (pH 8.0), and 0.15% (v/v) Sarkosyl. KOD buffer (10-fold concentrated) consists of 1200 mM Tris-HCl, 15 mM MgSO₄, 100 mM KCl, 60 mM (NH₄)₂SO₄, 1% v/v Triton-X 100 and 1 mg/mL BSA.

Sample preparation

[00154] Serum (stored at -80°C in 100 µL aliquots) is thawed in a 25°C water bath for 10 minutes, then stored on ice prior to sample dilution. Samples are mixed by gentle vortexing for 8 seconds. A 6% serum sample solution is prepared by dilution into 0.94× SB17 supplemented with 0.6 mM MgCl₂, 1 mM trisodium EGTA, 0.8 mM AEBSF, and 2 µM Z-Block. A portion of the 6% serum stock solution is diluted 10-fold in SB17 to create a 0.6% serum stock. 6% and 0.6% stocks are used, in some embodiments, to detect high- and low-abundance analytes, respectively.

Capture reagent (aptamer) and streptavidin plate preparation

[00155] Aptamers are grouped into 2 mixes according to the relative abundance of their cognate analytes (or biomarkers). Stock concentrations are 4 nM for each aptamer, and the final concentration of each aptamer is 0.5 nM. Aptamer stock mixes are diluted 4-fold in SB17 buffer, heated to 95 °C for 5 min and cooled to 37 °C over a 15-minute period prior to use. This denaturation-renaturation cycle is intended to normalize aptamer conformer distributions and thus ensure reproducible aptamer activity in spite of variable histories. Streptavidin plates are washed twice with 150 µL buffer PB1 prior to use.

Incubation and plate capture

[00156] Heat-cooled 2× Aptamer mixes (55 µL) are combined with an equal volume of 6% or 0.6% serum dilutions, producing mixes containing 3% and 0.3% serum. The plates are sealed with a Silicone Sealing Mat (Axymat Silicone sealing mat, VWR) and incubated for 1.5 h at 37 °C. Mixes are then transferred to the wells of a washed 96-well streptavidin plate and further incubated on an Eppendorf Thermomixer set at 37 °C, with shaking at 800 rpm, for two hours.

Manual Assay

[00157] Unless otherwise specified, liquid is removed by dumping, followed by two taps onto layered paper towels. Wash volumes are 150 µL and all shaking incubations are done on an Eppendorf Thermomixer set at 25°C, 800 rpm. Mixes are removed by pipetting, and plates are washed twice for 1 minute with buffer PB1 supplemented with 1 mM dextran sulfate and 500 µM biotin, then 4 times for 15 seconds with buffer PB1. A freshly made solution of 1 mM NHS-PEO4-biotin in buffer PB1 (150 µL/well) is added, and plates are incubated for 5 minutes with shaking. The NHS-biotin solution is removed, and plates washed 3 times with buffer PB1 supplemented with 20 mM glycine, and 3 times with buffer PB1. Eighty-five µL of buffer PB1 supplemented with 1 mM D_xSO₄ is then added to each well, and plates are irradiated under a BlackRay UV lamp (nominal wavelength 365 nm) at a distance of 5 cm for 20 minutes with shaking. Samples are transferred to a fresh, washed streptavidin-coated plate, or an unused well of the existing washed streptavidin plate, combining high and low sample dilution mixtures into a single well. Samples are incubated at room temperature with shaking for 10 minutes. Unabsorbed material is removed and the plates washed 8 times for 15 seconds each with buffer PB1 supplemented with 30% glycerol. Plates are then washed once with buffer PB1. Aptamers are eluted for 5 minutes at room temperature with 100 µL CAPSO elution buffer. 90 µL of the eluate is transferred to a 96-well HybAid plate and 10 µL neutralization buffer is added.

Semi-Automated Assay

[00158] Streptavidin plates bearing adsorbed equilibration mixes are placed on the deck of a BioTek EL406 plate washer, which is programmed to perform the following steps: unadsorbed material is removed by aspiration, and wells are washed 4 times with 300 µL of buffer PB1 supplemented with 1 mM dextran sulfate and 500 µM biotin. Wells are then washed 3 times with 300 µL buffer PB1. One hundred fifty µL of a freshly prepared (from a 100 mM stock in DMSO) solution of 1 mM NHS-PEO4-biotin in buffer PB1 is added. Plates are incubated for 5 minutes with shaking. Liquid is aspirated, and wells are washed 8 times

with 300 μ L buffer PB1 supplemented with 10 mM glycine. One hundred μ L of buffer PB1 supplemented with 1 mM dextran sulfate are added. After these automated steps, plates are removed from the plate washer and placed on a thermoshaker mounted under a UV light source (BlackRay, nominal wavelength 365 nm) at a distance of 5 cm for 20 minutes. The thermoshaker is set at 800 rpm and 25 °C. After 20 minutes irradiation, samples are manually transferred to a fresh, washed streptavidin plate (or to an unused well of the existing washed plate). High-abundance (3% serum+3% aptamer mix) and low-abundance reaction mixes (0.3% serum+0.3% aptamer mix) are combined into a single well at this point. This “Catch-2” plate is placed on the deck of BioTek EL406 plate washer, which is programmed to perform the following steps: the plate is incubated for 10 minutes with shaking. Liquid is aspirated, and wells are washed 21 times with 300 μ L buffer PB1 supplemented with 30% glycerol. Wells are washed 5 times with 300 μ L buffer PB1, and the final wash is aspirated. One hundred μ L CAPSO elution buffer are added, and aptamers are eluted for 5 minutes with shaking. Following these automated steps, the plate is then removed from the deck of the plate washer, and 90 μ L aliquots of the samples are transferred manually to the wells of a HybAid 96-well plate that contains 10 μ L neutralization buffer.

Hybridization to custom Agilent 8×15k microarrays

[00159] 24 μ L of the neutralized eluate is transferred to a new 96-well plate and 6 μ L of 10× Agilent Block (Oligo aCGH/ChIP-on-chip Hybridization Kit, Large Volume, Agilent 5188–5380), containing a set of hybridization controls composed of 10 Cy3 aptamers is added to each well. Thirty μ L 2× Agilent Hybridization buffer is added to each sample and mixed. Forty μ L of the resulting hybridization solution is manually pipetted into each “well” of the hybridization gasket slide (Hybridization Gasket Slide, 8-microarray per slide format, Agilent). Custom Agilent microarray slides, bearing 10 probes per array complementary to 40 nucleotide random region of each aptamer with a 20× dT linker, are placed onto the gasket slides according to the manufacturers’ protocol. The assembly (Hybridization Chamber Kit – SureHyb-enabled, Agilent) is clamped and incubated for 19 hours at 60 °C while rotating at 20 rpm.

Post Hybridization Washing

[00160] Approximately 400 mL Agilent Wash Buffer 1 is placed into each of two separate glass staining dishes. Slides (no more than two at a time) are disassembled and separated while submerged in Wash Buffer 1, then transferred to a slide rack in a second staining dish also containing Wash Buffer 1. Slides are incubated for an additional 5 minutes in Wash Buffer 1 with stirring. Slides are transferred to Wash Buffer 2 pre-equilibrated to 37

°C and incubated for 5 minutes with stirring. Slides are transferred to a fourth staining dish containing acetonitrile, and incubated for 5 minutes with stirring.

Microarray Imaging

[00161] Microarray slides are imaged with an Agilent G2565CA Microarray Scanner System, using the Cy3-channel at 5 µm resolution at 100% PMT setting, and the XRD option enabled at 0.05. The resulting TIFF images are processed using Agilent feature extraction software version 10.5.1.1 with the GE1_105_Dec08 protocol.

Luminex probe design

[00162] Probes immobilized to beads have 40 deoxynucleotides complementary to the 3' end of the 40 nucleotide random region of the target aptamer. The aptamer complementary region is coupled to Luminex Microspheres through a hexaethyleneglycol (HEG) linker bearing a 5' amino terminus. Biotinylated detection deoxyoligonucleotides comprise 17–21 deoxynucleotides complementary to the 5' primer region of target aptamers. Biotin moieties are appended to the 3' ends of detection oligos.

Coupling of probes to Luminex Microspheres

[00163] Probes are coupled to Luminex Microplex Microspheres essentially per the manufacturer's instructions, but with the following modifications: amino-terminal oligonucleotide amounts are 0.08 nMol per 2.5×10^6 microspheres, and the second EDC addition is 5 µL at 10 mg/mL. Coupling reactions are performed in an Eppendorf ThermoShaker set at 25 °C and 600 rpm.

Microsphere hybridization

[00164] Microsphere stock solutions (about 40000 microspheres/µL) are vortexed and sonicated in a Health Sonics ultrasonic cleaner (Model: T1.9C) for 60 seconds to suspend the microspheres. Suspended microspheres are diluted to 2000 microspheres per reaction in $1.5 \times$ TMAC hybridization solutions and mixed by vortexing and sonication. Thirty-three µL per reaction of the bead mixture are transferred into a 96-well HybAid plate. Seven µL of 15 nM biotinylated detection oligonucleotide stock in $1 \times$ TE buffer are added to each reaction and mixed. Ten µL of neutralized assay sample are added and the plate is sealed with a silicon cap mat seal. The plate is first incubated at 96 °C for 5 minutes and incubated at 50°C without agitation overnight in a conventional hybridization oven. A filter plate (Dura pore, Millipore part number MSBVN1250, 1.2 µm pore size) is prewetted with 75 µL $1 \times$ TMAC hybridization solution supplemented with 0.5% (w/v) BSA. The entire sample volume from the hybridization reaction is transferred to the filter plate. The hybridization plate is rinsed with 75 µL $1 \times$ TMAC hybridization solution containing 0.5% BSA and any remaining

material is transferred to the filter plate. Samples are filtered under slow vacuum, with 150 μL buffer evacuated over about 8 seconds. The filter plate is washed once with 75 μL 1 $\times$ TMAC hybridization solution containing 0.5% BSA and the microspheres in the filter plate are resuspended in 75 μL 1 $\times$ TMAC hybridization solution containing 0.5% BSA. The filter plate is protected from light and incubated on an Eppendorf Thermalmixer R for 5 minutes at 1000 rpm. The filter plate is then washed once with 75 μL 1 $\times$ TMAC hybridization solution containing 0.5% BSA. 75 μL of 10 $\mu\text{g/mL}$ streptavidin phycoerythrin (SAPE-100, MOSS, Inc.) in 1 $\times$ TMAC hybridization solution is added to each reaction and incubated on Eppendorf Thermalmixer R at 25 $^{\circ}\text{C}$ at 1000 rpm for 60 minutes. The filter plate is washed twice with 75 μL 1 $\times$ TMAC hybridization solution containing 0.5% BSA and the microspheres in the filter plate are resuspended in 75 μL 1 $\times$ TMAC hybridization solution containing 0.5% BSA. The filter plate is then incubated protected from light on an Eppendorf Thermalmixer R for 5 minutes, 1000 rpm. The filter plate is then washed once with 75 μL 1 $\times$ TMAC hybridization solution containing 0.5% BSA. Microspheres are resuspended in 75 μL 1 $\times$ TMAC hybridization solution supplemented with 0.5% BSA, and analyzed on a Luminex 100 instrument running Xponent 3.0 software. At least 100 microspheres are counted per bead type, under high PMT calibration and a doublet discriminator setting of 7500 to 18000.

qPCR read-out

[00165] Standard curves for qPCR are prepared in water ranging from 108 to 102 copies with 10-fold dilutions and a no-template control. Neutralized assay samples are diluted 40-fold into diH₂O. The qPCR master mix is prepared at 2 $\times$ final concentration (2 $\times$ KOD buffer, 400 μM dNTP mix, 400 nM forward and reverse primer mix, 2 $\times$ SYBR Green I and 0.5 U KOD EX). Ten μL of 2 $\times$ qPCR master mix is added to 10 μL of diluted assay sample. qPCR is run on a BioRad MyIQ iCycler with 2 minutes at 96 $^{\circ}\text{C}$ followed by 40 cycles of 96 $^{\circ}\text{C}$ for 5 seconds and 72 $^{\circ}\text{C}$ for 30 seconds.

Example 2. Time-to-Freeze Plasma Model

[00166] Plasma samples obtained from a subject may be initially obtained as a whole blood sample, then centrifuged. The resulting plasma supernatant can then be collected by decanting or aspirating it from the precipitate. A plasma sample must be analyzed or frozen at or less than -20 $^{\circ}\text{C}$ immediately after centrifugation and decanting or aspirating in order to assure its quality, because the elapsed time from completion of these sample collection and processing steps at room temperature until the time that the sample is frozen can be a source of pre-analytic variability.

[00167] In order to assess the quality of a plasma sample, a linear regression elastic net model containing a panel of the 8 biomarker proteins listed in Table 1 was developed. The model provides a predicted value that is the time from the completion of sample centrifugation and decanting or aspirating to the time of freezing the sample, in hours. The training and verification datasets were obtained from analysis of samples from adult human volunteers, as described in Model Development below. Table 5 shows the performance metrics for the model. “CCC” is Concordance Correlation Coefficient.”R²” is the degree of linear correlation, or the goodness-of-fit. “CI” is confidence interval. CCC and R² are indicative of predictive performance of the model.

Table 5

Dataset	CCC (95% CI)	R² (95% CI)
Training	0.99 (0.99, 1.0)	0.99 (0.98, 0.99)
Verification	0.98 (0.97, 0.99)	0.95 (0.91, 0.99)

[00168] The time-to-freeze plasma model is an elastic net linear regression model. This model has 8 aptamers as its features, which bind the 8 different biomarker proteins listed in Table 1. The output of this model is the non-transformed prediction of time-to-freeze in hours, with values less than zero rounded up to zero. The time-to-freeze is the time, in hours, that plasma samples sat at room temperature after immediate centrifugation and decanting or aspiration of whole blood samples. Thus, the output is a number, 0 or higher, with 0 being immediate transfer of decanted or aspirated plasma samples to freezing conditions.

Model Development

[00169] Multiple K2-EDTA Plasma tubes (purple-topped, BD#367863) of blood were collected from each of ten adult human volunteers by applying a tourniquet and using a 21G butterfly needle set. The tubes were inverted 8x-10x after collection and immediately centrifuged at 2200xg for 15 or 30 minutes. The resulting plasma was carefully aspirated from each tube and pooled across a given donor.

[00170] Independent aliquots of plasma were made from each donor’s pool and incubated at room temperature for 0, 0.5, 1, 1.5, 3, 6, or 24 hours. After the appropriate incubation period, 90 µL matrix tube aliquots were made and stored frozen at -80 °C and 750µL aliquots were made and stored at -20 °C. Four to six days later, the aliquots stored at -20 °C were thawed, transferred to matrix tubes in 90 µL aliquots, and stored at -80 °C until thawed on the day that analysis with the aptamers was performed, for example, according to a protocol described in Example 1.

[00171] The data were split 80%/20% into training/verification datasets such that 2 samples were randomly selected from each of the 7 timepoints for the verification set (14 samples in the verification set) and the rest of the samples for the training set (56 samples in the training). For validation, a parallel time-to-freeze study where samples were stored at -20 °C instead of -80 °C was conducted. Due to low sample numbers, a hold-out test dataset was not used for model development. The model was developed on the training dataset and then assessed on the verification set, but it was not used as a holdout validation or test set. The sample numbers are shown in Table 6 below.

Table 6

Dataset	Number of Samples							
	Total	Time-to-Freeze (Hours)						
		0	0.5	1	1.5	3	6	24
Training	56	8	8	8	8	8	8	8
Verification	14	2	2	2	2	2	2	2
Validation	56	8	8	8	8	8	8	8

[00172] After the aptamer assay was performed, the data was normalized. Control samples were internally median normalized, plate scaled, calibrated, and samples normalized using adaptive normalization by maximum likelihood (ANML). All samples were within normalization scale factor pass/fail criteria and subsequently, no samples were removed from analysis. Normalization scale factors were not correlated with the endpoint.

POC Results

[00173] The POC results showed that a number of analytes were significant at different false-discovery rate (FDR) levels. Table 7 below shows those numbers and percentages (after removal of redlisted analytes) of analytes significant at different Type I error cut-offs for time-to-freeze plasma univariate results using the Student's t-test.

Table 7

FDR	# analytes (%) ≤ FDR level
0.10	609 (8.0%)
0.05	526 (6.9%)
0.01	399 (5.3%)

Refinement and Validation

[00174] For the models developed in refinement, the training and verification sets described above were used.

[00175] Feature selection was performed by starting with the 62 features in an initial elastic net model. The best subset selection was used to test various combinations of aptamers from 1 to 30 features. Results showed that model performance plateaus with 10 or more features and that 5 or more features are required to achieve an adjusted R^2 of 0.95. From here, a series of elastic net models were generated with the number of features ranging from 5 to 15 analytes with 5 repeats of 10-fold cross-validation. The final model chosen had high performance on the training set and low coefficient of variation (CV) with time-to-freeze predictions made on samples from the other sample handling studies to ensure time to freeze predictions are independent of other sample handling conditions. Model predictions were tested in the training and verification data sets, and Lin's correlation coefficient was calculated for the training and verification data (Table 8). No significant drop in model performance was observed between the training and verification data; however, sample sizes were limited to a few samples per condition in the verification data.

[00176] The model trained on the samples frozen at -80 °C was used to predict time to freeze in a parallel study where samples were processed in the same manner but frozen at -20 °C. The model performs well on the validation set with an R^2 of 0.934 and a root mean square error (RMSE) of 2.04 (Table 8).

Table 8

Dataset	CCC (95% CI)	R^2 (95% CI)	RMSE (95% CI)
Training	0.995 (0.991, 0.997)	0.990 (0.984, 0.995)	0.808 (0.556, 0.963)
Verification	0.978 (0.97, 0.99)	0.951 (0.91, 0.99)	1.749 (0.766, 2.225)
Validation	2.042 (1.905, 2.429)	0.934 (0.901, 0.949)	0.962 (0.946, 0.970)

[00177] The effect of winsorization and dropping features were evaluated to correct for outlier values in other datasets. For the original data the RMSE was 2.612, with winsorization it was 4.227 and for feature removal it was 3.037. Outlier values were therefore replaced with zero for this model. These results are shown in Tables 9 and 10 below.

Table 9: RMSE Values

Training Set RMSE	Winsorized	Replacement with Zero	Final Selection
1.168	4.371	1.942	Replace with zero

Table 10: Predictive variation due to assay noise

Bound	Error Bounds (95%)	Error Bounds (99%)
Upper Bound	2.62	2.84
Lower Bound	5.18	7.01

Example 3: Time-to-Freeze Serum Model

[00178] Serum samples obtained from a subject may be initially obtained as a whole blood sample, then clotted and centrifuged. The resulting serum supernatant can then be collected by decanting or aspirating it from the precipitate. A serum sample must be analyzed or frozen at or less than -20 °C immediately after centrifugation and decanting or aspirating in order to assure its quality, because the elapsed time from completion of these sample collection and processing steps at room temperature until the time that the sample is frozen can be a source of pre-analytic variability.

[00179] In order to assess the quality of a serum sample, a linear regression model containing a panel of the 5 biomarker proteins listed in Table 2 was developed. The model provides a predicted value that is the time from the completion of sample centrifugation and decanting or aspirating to the time of freezing the sample, in hours. The training and verification datasets were obtained from analysis of samples from adult human volunteers, as described in Model Development below. Table 11 shows the performance metrics for the model. “CCC” is Concordance Correlation Coefficient. “R²” is the degree of linear correlation, or the goodness-of-fit. “CI” is confidence interval. CCC and R² are indicative of predictive performance of the model.

Table 11

Dataset	CCC (95% CI)	R ² (95% CI)
Training	0.99 (0.97, 0.99)	0.97 (0.94, 0.98)
Verification	0.98 (0.95, 0.99)	0.96 (0.90, 0.97)

[00180] The time-to-freeze serum model is a linear regression model. This model has 5 aptamers as its features, which bind the 5 different biomarker proteins listed in Table 2. The output of this model is the non-transformed prediction of time-to-freeze in hours, with values

less than zero rounded up to zero. The time-to-freeze is the time, in hours, that serum samples sat at room temperature after immediate clotting, centrifugation, and decanting or aspiration of whole blood samples. Thus, the output is a number, 0 or higher, with 0 being immediate transfer of decanted or aspirated serum samples to freezing conditions.

Model Development

[00181] Multiple serum tubes (red-topped, BD#367814) of blood were collected from each of twelve adult human volunteers by applying a tourniquet and using a 21G butterfly needle set. The tubes were inverted 5x after collection and allowed to clot for 50-95 minutes at room temperature. Following clot formation, the blood tubes were centrifuged immediately at 2200xg for 15 minutes. The resulting serum was carefully aspirated from each tube and pooled across a given donor.

[00182] Independent aliquots of serum were made from each donor's pool and incubated at room temperature for 0, 0.5, 1, 1.5, 3, 3.5, 6, or 24 hours. After the appropriate incubation period, 90 μ L matrix tube aliquots were made and stored frozen at -80 °C and 550 μ L aliquots were made and stored at -20 °C. Four to six days later, the aliquots stored at -20 °C were thawed, transferred to matrix tubes in 90 μ L aliquots, and stored at -80 °C until thawed on the day that analysis with the aptamers was performed, for example, according to a protocol described in Example 1.

[00183] The data were split 80%/20% into training/verification. Individual donors were not assigned to training/verification, but each timepoint for each donor was assigned randomly. For validation, a parallel time-to-freeze study where samples were stored at -20 °C instead of -80 °C was conducted. The dataset was obtained from 12 donors, with 8 time-to-freeze points (8 unique points, but each donor was only measured at 7), but frozen at -20 °C instead of -80 °C. Sample numbers are shown in Table 12 below. The “*” indicates that one sample was removed from the analysis due to sample failure.

Table 12

Dataset	Number of Samples								
	Total	Time-to-Freeze (Hours)							
		0	0.5	1	1.5	3	3.5	6	24
Training	59	9	8*	9	9	3	9	3	9
Verification	24	3	3	3	3	3	3	3	3

Validation	84	12	12	12	6	12	6	12	12
------------	----	----	----	----	---	----	---	----	----

[00184] After the aptamer assay was performed, the data was normalized. Control samples were internally median normalized, plate scaled, calibrated, and samples normalized using adaptive normalization by maximum likelihood (ANML). One sample did not pass a check, leaving 83 total samples for training and verification.

POC Results

[00185] The POC results showed that a number of analytes were significant at different false-discovery rate (FDR) levels. Table 13 below shows those numbers and percentages (after removal of redlisted analytes) of analytes significant at different Type I error cut-offs for time-to-freeze serum univariate results using the Student's t-test.

Table 13

FDR	# analytes (%) $\leq$ FDR level
0.10	1175 (36.2%)
0.05	1004 (30.9%)
0.01	702 (21.6%)

Refinement and Validation

[00186] Feature selection was performed by starting with the top 200 features by rank identified in the POC univariate analysis. This list was pared down further through a series of elastic net regressions with alpha and lambda both set to 0.5, which were the optimal values identified in the POC analysis. After each round of elastic net regression, the features with the smallest coefficients were dropped from the feature list and a new model was trained. The performance of this new model was assessed on the verification set, and features continued to be dropped until performance on the verification set fell significantly. This process resulted in 7 features.

[00187] The final step in feature selection step was to use the log2 fold-change univariate analysis performed with the time-to-decant and time-to-clot data in version 4.0 and removed any analytes with a significant (defined as $FDR < 0.05$) fold-change over 24 hours for either of these endpoints. This filtering was performed because we desire a time-to-freeze model that is as independent as possible from the other sample handling time endpoints. This resulted in 2 features being dropped from the final feature list, for a total of 5 features. Lin's correlation coefficient was calculated for the training and verification data (Table 14).

Table 14

Dataset	CCC (95% CI)	R ² (95% CI)	RMSE (95% CI)
Training	0.985 (0.970, 0.987)	0.971 (0.938, 0.975)	1.374 (1.334, 1.694)
Verification	0.980 (0.949, 0.985)	0.963 (0.899, 0.972)	1.422 (1.154, 1.855)

[00188] The effect of winsorization and dropping features were evaluated to correct for outlier values in other datasets. For the original data the RMSE was 1.374, with winsorization it was 4.470 and for feature removal it was 2.245. Outlier values were therefore replaced with zero for this model. The results are shown in Tables 15 and 16 below.

Table 15: RMSE Values

Training Set RMSE	Winsorized	Replacement with Zero	Final Selection
1.374	4.47	2.245	Replace with zero

Table 16: Predictive variation due to assay noise

Bound	Error Bounds (95%)	Error Bounds (99%)
Upper Bound	4.17	5.93
Lower Bound	3.82	4.77

Example 4: Time-to-Centrifugation Model

[00189] Plasma and serum samples obtained from a subject may be initially obtained as a whole blood sample and subsequently centrifuged. The time between collection and centrifugation (time-to-centrifugation) ideally should be below two hours. Deviation from this processing time is known to activate platelets within a collection tube and shift overall analyte signal for an increasing proportion of the menu as time-to-centrifugation increases and can thereby be a source of pre-analytic variability.

[00190] In order to assess the quality of a plasma sample, an elastic net linear regression model containing a panel of the 4 biomarker proteins listed in Table 3 was developed. The model provides a predicted value that is the time from blood collection to the time that the sample is centrifuged, in hours. The training and verification datasets were obtained from analysis of samples from adult human volunteers, as described in Model Development below. Table 17 shows the performance metrics for the model. “CCC” is Concordance Correlation Coefficient. “R²” is the degree of linear correlation, or the goodness-of-fit. “CI” is confidence interval. CCC and R² are indicative of predictive performance of the model.

Table 17

Dataset	CCC (95% CI)	R² (95% CI)
Training	0.95 (0.93, 0.97)	0.93 (0.90, 0.96)
Verification	0.97 (0.94, 0.99)	0.96 (0.90, 0.98)

[00191] The time-to-centrifugation model is an elastic net linear regression model. This model has 4 aptamers as its features, which bind the 4 different biomarker proteins listed in Table 3. The output of this model is the estimated time-to-centrifugation in hours, with values less than zero rounded up to zero. Thus, the output is a number, 0 or higher, with 0 being immediate centrifugation of a collected sample.

Model Development

[00192] Multiple K2-EDTA Plasma tubes of blood were collected from each of eighteen adult human volunteers and centrifuged after 0, 0.5, 1.5, 3, 9, or 24 hours. Plasma was obtained from each sample and frozen at -80 °C prior to analysis with an aptamer assay, for example, according to a protocol described in Example 1.

[00193] The data were split 80%/20% into training/verification. Individual donors were not assigned to training/verification, but each timepoint for each donor was assigned randomly. Due to the low sample numbers, a separate validation hold-out set was not used. Sample numbers are shown in Table 18 below.

Table 18

Dataset	Number of Samples						
	Total	Time-to-Centrifugation (Hours)					
		0	0.5	1.5	3	9	24
Training	88	14	15	15	14	15	15
Verification	20	4	3	3	4	3	3

[00194] After the aptamer assay was performed, the data was normalized. Control samples were internally median normalized, plate scaled, calibrated, and samples normalized using adaptive normalization by maximum likelihood (ANML). All samples were within

normalization scale factor pass/fail criteria and subsequently, no samples were removed from analysis. Normalization scale factors were partially correlated with time-to-centrifugation, which was expected given the large proportion of the menu, particularly at 24 hours which showed significant change.

POC Results

[00195] The POC results showed that a number of analytes were significant at different false-discovery rate (FDR) levels. Table 19 below shows those numbers and percentages (after removal of redlisted analytes) of analytes significant at different Type I error cut-offs for time-to-centrifugation univariate results using the Kruskal-Wallis test.

Table 19

FDR	# analytes (%) $\leq$ FDR level
0.10	3087 (40%)
0.05	2721 (35%)
0.01	2048 (26%)

Refinement and Validation

[00196] Refinement was focused around reducing the number of features without observing significant performance loss in the model, the reproducibility of predictions from replicate samples, and the orthogonality to other sample handling studies. Further feature selection was performed using previous information, combined with hand-selection, in order to reduce the model complexity to obtain a set of analytes with a high degree of separation between time-points.

[00197] The final model contained four analytes in an elastic net regression model, which show good predictive performance in the training and verification set (Table 20). “MAE” is mean absolute error.

Table 20

Dataset	CCC (95% CI)	R² (95% CI)	MAE (95% CI)
Training	0.95 (0.93, 0.97)	0.93 (0.90, 0.96)	1.28 (0.91, 1.64)
Verification	0.97 (0.94, 0.99)	0.96 (0.90, 0.98)	1.18 (1.73, 1.69)

[00198] The effect of winsorization and dropping features was evaluated to correct for outlier values in other datasets. For the original data the RMSE was 1.619, with winsorization it was 1.619 and for feature removal it was 1.704. Outlier values were therefore winsorized. The results are shown in Tables 21 and 22 below.

Table 21: RMSE Values

Training Set RMSE	Winsorized	Replacement with Zero	Final Selection
1.619	1.619	1.704	Winsorize

Table 22: Predictive variation due to assay noise

Bound	Error Bounds (95%)	Error Bounds (99%)
Upper Bound	0.59	0.78
Lower Bound	0.62	0.82

Example 5: Time-to-Decant Model

[00199] Plasma and serum samples obtained from a subject may be initially obtained as a whole blood sample and subsequently centrifuged and decanted or aspirated. The time between centrifugation and decanting or aspirating to a fresh tube (time-to-decant) ideally should be below two hours. Deviation from this processing time is known to activate platelets within a collection tube and shift overall analyte signal for an increasing proportion of the menu as time-to-decant increases and can thereby be a source of pre-analytic variability.

[00200] In order to assess the quality of a plasma sample, an elastic net linear regression model containing a panel of the 13 biomarker proteins listed in Table 4 was developed. The model provides a predicted value that is the time from sample centrifugation to transfer (by, e.g., decanting or aspirating) to a fresh tube, in hours. The training and verification datasets were obtained from analysis of samples from adult human volunteers, as described in Model Development below. Table 23 shows the performance metrics for the model. “CCC” is Concordance Correlation Coefficient. “R²” is the degree of linear correlation, or the goodness-of-fit. “CI” is confidence interval. CCC and R² are indicative of predictive performance of the model.

Table 23

Dataset	CCC (95% CI)	R ² (95% CI)
Training	0.91 (0.93, 0.96)	0.90 (0.88, 0.93)
Verification	0.94 (0.91, 0.97)	0.90 (0.86, 0.95)

[00201] The time-to-decant model is an elastic net linear regression model. This model has 13 aptamers as its features, which bind the 13 different biomarker proteins listed in Table 4. The output of this model is the estimated time-to-decant in hours, with values less than zero rounded up to zero. Thus, the output is a number, 0 or higher, with 0 being immediate decanting of a centrifuged sample.

Model Development

[00202] Multiple K2-EDTA Plasma tubes of blood were collected from each of eighteen adult human volunteers and promptly centrifuged. Plasma was transferred to fresh tubes 0, 0.5, 1.5, 3, 9, or 24 hours after centrifugation. The plasma samples were frozen at -80 °C prior to analysis with an aptamer assay, for example, according to a protocol described in Example 1.

[00203] The data were split 80%/20% into training/verification. Individual donors were not assigned to training/verification, but each timepoint for each donor was assigned randomly. Due to the low sample numbers, a separate validation hold-out set was not used. Sample numbers are shown in Table 24 below.

Table 24

Dataset	Number of Samples						
	Total	Time-to-Centrifugation (Hours)					
		0	0.5	1.5	3	9	24
Training	81	13	14	15	12	13	14
Verification	27	5	4	3	6	5	4

[00204] After the aptamer assay was performed, the data was normalized. Control samples were internally median normalized, plate scaled, calibrated, and samples normalized using adaptive normalization by maximum likelihood (ANML). All samples were within normalization scale factor pass/fail criteria and subsequently, no samples were removed from analysis. Normalization scale factors were not significantly correlated with time-to-decant.

POC Results

[00205] The POC results showed that a number of analytes were significant at different false-discovery rate (FDR) levels. Table 25 below shows those numbers and percentages (after removal of redlisted analytes) of analytes significant at different Type I error cut-offs for time-to-decant univariate results using the Kruskal-Wallis test.

Table 25

FDR	# analytes (%) $\leq$ FDR level
0.10	436 (5.7%)
0.05	373 (4.9%)
0.01	266 (3.5%)

Refinement and Validation

[00206] Refinement was focused around reducing the number of features without observing significant performance loss in the model, the reproducibility of predictions from replicate samples, and the orthogonality to other sample handling studies. Further feature selection was performed using previous information, combined with hand-selection, in order to reduce the model complexity to obtain a set of analytes with a high degree of separation between time-points.

[00207] These 13 analytes were used in an elastic net regression against time-to-decant which show good predictive performance in the training and verification set. (Table 26). “MAE” is mean absolute error.

[00208] There was no loss associated with the verification set. Longer time-to-decant predictions were not as well captured; however, there is less concern with obtaining more accurate predictions in these long time-to-decant time-points as there is at the low time-to-decant.

Table 26

Dataset	CCC (95% CI)	R² (95% CI)	MAE (95% CI)
Training	0.91 (0.93, 0.96)	0.90 (0.88, 0.93)	1.28 (1.17, 2.06)
Verification	0.94 (0.91, 0.97)	0.90 (0.86, 0.95)	1.41 (0.66, 2.37)

[00209] The effect of winsorization and dropping features was evaluated to correct for outlier values in other datasets. For the original data the RMSE was 2.468, with winsorization it was 2.487 and for feature removal it was 3.653. Outlier values were therefore winsorized. Additional validation results are shown in Tables 27 and 28 below.

Table 27: RMSE Values

Training Set RMSE	Winsorized	Replacement with Zero	Final Selection
2.468	2.487	3.653	Winsorize

Table 28: Predictive variation due to assay noise

Bound	Error Bounds (95%)	Error Bounds (99%)
Upper Bound	1.32	1.75
Lower Bound	1.72	2.28

Example 6: Biomarker directionalities

[00210] The tables below show the directionality of each biomarker in each model. Negative log2 fold change values mean the level of the biomarker protein decreases with time, and positive log2 fold change values mean the level of the biomarker protein increases with time. In the tables below, “N/A” means that the biomarker did not meet the FDR significance threshold of 0.05.

Table 29: Time-to-Freeze (plasma) model directionalities

Protein	Log2 Fold Change
ENOA	-3.58
LANC2	-3.05
PMM2	-1.52
TMEM9	-1.15
EFHD1	-0.23
THIK	0.61
PKHM2	0.85
PGAM2	1.97

Table 30: Time-to-Freeze (serum) model directionalities

Protein	Log2 Fold Change
IL36A	-0.31
GDF5	-0.04
C3b	-0.11
IL21R	0.25
LYAG	NA

Table 31: Time-to-Centrifugation model directionalities

Protein	Log2 Fold Change
SHH	-2.1
IHH	-1.7
ROA2	2.9
PGAM1	6.7

Table 32: Time-to-Decant model directionalities

Protein	Log2 Fold Change
SHH	-1.95
CFAD	-1.4
IHH	-1.4
ADAM9	-1.2
PTN4	-1.15
TMEM9	-0.95

HPPD	0.65
IF4A2	1.05
APB	1.25
IL18	1.25
C4A	2.55
PGAM2	2.7

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 3, and wherein at least 3 of the N biomarker proteins are selected from LANC2, PKHM2, ENOA, the cytoplasmic domain of TMEM9, PMM2, PGAM2, EFHD1, and THIK, 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 3, and wherein at least 3 of the N biomarker proteins are selected from LANC2, PKHM2, ENOA, the cytoplasmic domain of TMEM9, PMM2, PGAM2, EFHD1, and THIK; 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. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are LANC2 and PKHM2.

4. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are LANC2 and ENOA.

5. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are LANC2 and the cytoplasmic domain of TMEM9.

6. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are LANC2 and PMM2.

7. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are LANC2 and PGAM2.

8. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are LANC2 and EFHD1.

9. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are LANC2 and THIK.

10. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are PKHM2 and ENOA.

11. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are PKHM2 and the cytoplasmic domain of TMEM9.
12. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are PKHM2 and PMM2.
13. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are PKHM2 and PGAM2.
14. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are PKHM2 and EFHD1.
15. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are PKHM2 and THIK.
16. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are ENOA and the cytoplasmic domain of TMEM9.
17. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are ENOA and PMM2.
18. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are ENOA and PGAM2.
19. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are ENOA and EFHD1.
20. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are ENOA and THIK.
21. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are the cytoplasmic domain of TMEM9 and PMM2.
22. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are the cytoplasmic domain of TMEM9 and PGAM2.
23. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are the cytoplasmic domain of TMEM9 and EFHD1.
24. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are the cytoplasmic domain of TMEM9 and THIK.
25. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are PMM2 and PGAM2.
26. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are PMM2 and EFHD1.
27. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are PMM2 and THIK.

28. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are PGAM2 and EFHD1.
29. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are PGAM2 and THIK.
30. The method of claim 1 or claim 2, wherein 2 of the N biomarker proteins are EFHD1 and THIK.
31. The method of any one of claims 1 to 30, wherein N is 3, N is 4, N is 5, N is 6, N is 7, or N is 8.
32. The method of claim 31, wherein all of the N biomarker proteins are selected from LANC2, PKHM2, ENOA, the cytoplasmic domain of TMEM9, PMM2, PGAM2, EFHD1, and THIK.
33. The method of any one of claims 1-32, wherein the subject is a human subject.
34. The methods of any one of claims 1-33, wherein the sample is a liquid sample.
35. The method of any one of claims 1-34, wherein the sample was processed, frozen, and thawed after the sample collection and prior to the detecting.
36. The method of claim 35, wherein the sample processing steps comprised centrifugation and decanting or aspirating.
37. The method of claim 36, comprising determining the approximate time that elapsed from sample decanting or aspirating until the time that the sample was frozen.
38. The method of claim 36 or 37, 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.
39. The method of claim 38, wherein a detected level greater than the reference level for one or more of THIK, PKHM2, and PGAM2, or a detected level less than the reference level for one or more of ENOA, LANC2, PMM2, TMEM9, and EFHD1 indicates that the approximate time that elapsed from sample decanting or aspirating to freezing was greater than 0, 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.
40. The method of any one of claims 1-39, comprising identifying the sample as passing a quality assessment or failing a quality assessment.
41. The method of claim 40, wherein the identifying is based, at least in part, on the detected levels of the N biomarker proteins.

42. The method of claim 40 or 41, wherein the sample is identified as passing if the approximate time that elapsed from sample decanting or aspirating to freezing is determined to be 0, less than 0.5, less than 1.0, less than 1.5, less than 3, less than 6, or less than 24 hours.

43. The method of claim 40 or 41, wherein the sample is identified as failing if the approximate time that elapsed from sample decanting or aspirating to freezing is determined to be greater than 1.0, greater than 1.5, greater than 3, greater than 6, or greater than 24 hours.

44. The method of any one of claims 40-44, comprising either a) performing further analysis of the sample if it is identified as passing the quality assessment; or b) discarding the sample if it is identified as failing the quality assessment.

45. The method of any one of claims 1-44, comprising detecting the level of each of N biomarkers in a plurality of samples from a plurality of subjects.

46. The method of claim 45, comprising a) determining the approximate time that elapsed between sample processing to sample freezing and b) comparing the determined approximate times for each of the plurality of samples.

47. The method of claim 46, comprising identifying the plurality of samples as handled consistently or inconsistently, wherein samples handled consistently all have a determined approximate times between sample processing to freezing within 1, 2, or 3 hours of each other.

48. 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 2, and wherein at least 2 of the N biomarker proteins are selected from LYAG, IL21R, C3b, IL36A, and GDF5, wherein the sample is a serum sample

49. 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 2, and wherein at least 2 of the N biomarker proteins are selected from LYAG, IL21R, C3b, IL36A, and GDF5; 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.

50. The method of claim 48 or claim 49, wherein 2 of the N biomarker proteins are LYAG and IL21R.
51. The method of claim 48 or claim 49, wherein 2 of the N biomarker proteins are LYAG and C3b.
52. The method of claim 48 or claim 49, wherein 2 of the N biomarker proteins are LYAG and IL36A.
53. The method of claim 48 or claim 49, wherein 2 of the N biomarker proteins are LYAG and GDF5.
54. The method of claim 48 or claim 49, wherein 2 of the N biomarker proteins are IL21R and C3b.
55. The method of claim 48 or claim 49, wherein 2 of the N biomarker proteins are IL21R and IL36A.
56. The method of claim 48 or claim 49, wherein 2 of the N biomarker proteins are IL21R and GDF5.
57. The method of claim 48 or claim 49, wherein 2 of the N biomarker proteins are C3b and IL36A.
58. The method of claim 48 or claim 49, wherein 2 of the N biomarker proteins are C3b and GDF5.
59. The method of claim 48 or claim 49, wherein 2 of the N biomarker proteins are IL36A and GDF5.
60. The method of any one of claims 48-59, wherein N is 2, N is 3, N is 4, or N is 5.
61. The method of claim 60, wherein all of the N biomarker proteins are selected from LYAG, IL21R, C3b, IL36A, and GDF5.
62. The method of any one of claims 48-61, wherein the subject is a human subject.
63. The methods of any one of claims 48-60, wherein the sample is a liquid sample.
64. The method of claim 63, wherein the sample was processed, frozen, and thawed after the sample collection and prior to the detecting.
65. The method of any one of claims 48-64, wherein the sample was processed, frozen, and thawed after the sample collection and prior to the detecting.
66. The method of claim 65, wherein the sample processing steps comprised centrifugation and decanting or aspirating.

67. The method of claim 66, comprising determining the approximate time that elapsed from sample deacnting or aspirating until the time that the sample was frozen.

68. The method of claim 66 or 67, wherein the determining the approximate time 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 zero or nearly zero processing times.

69. The method of claim 68, wherein a detected level greater than the reference level for IL21R, or a detected level less than the reference level for one or more of IL36A, GDF5, C3b indicates that the approximate time that elapsed from sample processing to freezing was greater than 0, 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.

70. The method of any one of claims 48-69, comprising identifying the sample as passing a quality assessment or failing a quality assessment.

71. The method of claim 70, wherein the identifying is based, at least in part, on the detected levels of the N biomarker proteins.

72. The method of claim 70 or 71, wherein the sample is identified as passing if the approximate time that elapsed from sample processing to freezing is determined to be 0, less than 0.5, less than 1.0, less than 1.5, less than 3, less than 6, or less than 24 hours.

73. The method of claim 70 or 71, wherein the sample is identified as failing if the approximate time that elapsed from sample processing to freezing is determined to be greater than 1.0, greater than 1.5, greater than 3, greater than 6, or greater than 24 hours.

74. The method of any one of claims 70-72, comprising either a) performing further analysis of the sample if it is identified as passing the quality assessment; or b) discarding the sample if it is identified as failing the quality assessment.

75. The method of any one of claims 48-74, comprising detecting the level of each of N biomarkers in a plurality of samples from a plurality of subjects.

76. The method of claim 75, comprising a) determining the approximate time that elapsed between sample processing to freezing and b) comparing the determined approximate times for each of the plurality of samples.

77. The method of claim 76, comprising identifying the plurality of samples as handled consistently or inconsistently, wherein samples handled consistently all have a determined approximate times between sample processing to freezing within 1, 2, or 3 hours of each other.

78. 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 4, and wherein 4 of the N biomarker proteins are IHH, SHH, PGAM1, and ROA2.

79. A method comprising:

- a) measuring the level of each of N biomarker proteins in a sample from a subject, wherein N is at least 4, and wherein at least 4 of the N biomarker proteins are selected from IHH, SHH, PGAM1, and ROA2; 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.

80. The method of claim 78 or claim 79, wherein N is 4.

81. The method of any one of claims 78-80, wherein the subject is a human subject.

82. The methods of any one of claims 78-81, wherein the sample is a plasma, serum, or urine sample.

83. The method of claim 82, wherein the sample is a plasma sample.

84. The method of any one of claims 78-83, 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.

85. The method of claim 84, comprising determining the approximate duration of time that elapsed from the time that the sample was collected until the time that the sample was centrifuged.

86. The method of claim 85, wherein the determining the approximate time 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 zero or nearly zero processing times.

87. The method of claim 86, wherein a detected level greater than the reference level for one or both of PGAM1 and ROA2, or a detected level less than the reference level for one or both of IHH and SHH indicates that the approximate time that elapsed from sample collection to the start of sample centrifugation was greater than 0, 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.

88. The method of any one of claims 78-87, comprising identifying the sample as passing a quality assessment or failing a quality assessment.

89. The method of claim 88, wherein the identifying is based, at least in part, on the detected levels of the N biomarker proteins.

90. The method of claim 88 or 89, wherein the sample is identified as passing if the approximate time that elapsed from sample collection to the start of sample centrifugation is determined to be 0, less than 0.5, less than 1.0, less than 1.5, less than 3, less than 6, or less than 24 hours.

91. The method of claim 88 or 89, wherein the sample is identified as failing if the approximate time that elapsed from sample collection to the start of sample centrifugation is determined to be greater than 1.0, greater than 1.5, greater than 3, greater than 6, or greater than 24 hours.

92. The method of any one of claims 88-91, comprising either a) performing further analysis of the sample if it is identified as passing the quality assessment; or b) discarding the sample if it is identified as failing the quality assessment.

93. The method of any one of claims 78-92, comprising detecting the level of each of N biomarkers in a plurality of samples from a plurality of subjects.

94. The method of claim 93, 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.

95. The method of claim 94, comprising identifying the plurality of samples as handled consistently or inconsistently, wherein samples handled consistently all have a determined approximate times between sample collection and centrifugation within 1, 2, or 3 hours of each other.

96. 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 9, and wherein at least 9 of the N biomarker proteins are selected from APB, CFAD, PTN4, PGAM2, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, and TMEM9 cytoplasmic domain.

97. A method comprising:

- a) measuring the level of each of N biomarker proteins in a sample from a subject, wherein N is at least 9, and wherein at least 9 of the N biomarker proteins are

selected from APB, CFAD, PTN4, PGAM2, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, and TMEM9 cytoplasmic domain; 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.

98. The method of claim 96 or claim 97, wherein N is 9, N is 10, N is 11, N is 12, or N is 13.

99. The method of claim 98, wherein all of the N biomarker proteins are selected from APB, CFAD, PTN4, PGAM2, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, and TMEM9.

100. The method of any one of claims 96-99, wherein the subject is a human subject.

101. The methods of any one of claims 96-100, wherein the sample is a plasma, serum, or urine sample.

102. The method of claim 101, wherein the sample is a plasma sample.

103. The method of any one of claims 96-102, 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.

104. The method of claim 103, 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.

105. The method of claim 104, wherein the determining the approximate time 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 zero or nearly zero processing times.

106. The method of claim 105, wherein a detected level greater than the reference level for one or more of HPPD, IF4A2, APB, IL18, C4A, PGAM1, and PGAM2, or a detected level less than the reference level for one or more of CFAD, ADAM9, PTN4, TMEM9, IHH, and SHH indicates that the approximate time that elapsed from sample collection to the start of sample centrifugation was greater than 0, 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.

107. The method of any one of claims 96-106, comprising identifying the sample as passing a quality assessment or failing a quality assessment.

108. The method of claim 107, wherein the identifying is based, at least in part, on the detected levels of the N biomarker proteins.

109. The method of claim 107 or 108, wherein the sample is identified as passing if the approximate time that elapsed from completion of sample centrifugation to the start of sample decanting or aspirating is determined to be 0, less than 0.5, less than 1.0, less than 1.5, less than 3, less than 6, or less than 24 hours.

110. The method of claim 107 or 109, wherein the sample is identified as failing if the approximate time that elapsed from sample collection to the completion of sample centrifugation to the start of sample decanting or aspirating is determined to be greater than 1.0, greater than 1.5, greater than 3, greater than 6, or greater than 24 hours.

111. The method of any one of claims 107-110, comprising either a) performing further analysis of the sample if it is identified as passing the quality assessment; or b) discarding the sample if it is identified as failing the quality assessment.

112. The method of any one of claims 96-111, comprising detecting the level of each of N biomarkers in a plurality of samples from a plurality of subjects.

113. The method of claim 112, comprising a) determining the approximate time that elapsed between sample centrifugation and sample decanting or aspirating for each sample and b) comparing the determined approximate times for each of the plurality of samples.

114. The method of claim 113, comprising identifying the plurality of samples as handled consistently or inconsistently, wherein samples handled consistently all have a determined approximate times between sample centrifugation and decanting or aspirating within 1, 2, or 3 hours of each other.

115. The method of any one of claims 1-30, 48-59, or 62-77, wherein N is at least 7, and wherein 4 of the N biomarker proteins are IHH, SHH, PGAM1, and ROA2.

116. The method of claim 115, wherein N is 7, N is 8, N is 9, N is 10, N is 11, or N is 12.

117. The method of claim 116, wherein all of the N biomarker proteins are selected from LANC2, PKHM2, ENOA, the cytoplasmic domain of TMEM9, PMM2, PGAM2, EFHD1, THIK, IHH, SHH, PGAM1, and ROA2.

118. The method of claim 116, wherein all of the N biomarker proteins are selected from LYAG, IL21R, C3b, IL36A, GDF5, IHH, SHH, PGAM1, and ROA2.

119. The method of any one of claims 115-118, 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.

120. The method of claim 119, comprising determining the approximate total time that elapsed from the time that the sample was collected until the time that the sample was centrifuged and from the time that decanting or aspirating was complete to the time of sample freezing.

121. The method of any one of claims 1-30, 48-59, 62-77, or 115, wherein N is at least 12, and wherein at least 9 of the N biomarker proteins are selected from APB, CFAD, PTN4, PGAM2, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, and TMEM9.

122. The method of claim 121, wherein N is 12, N is 13, N is 9, N is 10, N is 11, N is 12, N is 13, N is 14, N is 15, N is 16, N is 17, N is 18, N is 19, or N is 20.

123. The method of claim 122, wherein all of the N biomarker proteins are selected from LANC2, PKHM2, ENOA, the cytoplasmic domain of TMEM9, PMM2, PGAM2, EFHD1, THIK, APB, CFAD, PTN4, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, and ROA2.

124. The method of claim 122, wherein all of the N biomarker proteins are selected from LYAG, IL21R, C3b, IL36A, GDF5, APB, CFAD, PTN4, PGAM2, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, TMEM9, and ROA2.

125. The method of any one of claims 121-124, 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.

126. The method of claim 125, comprising determining the approximate total time that elapsed from sample collection to centrifugation and/or from centrifugation to decanting or aspirating, and from decanting or aspirating to freezing.

127. The method of any one of claims 1-126, wherein the detecting comprises performing mass spectrometry, an aptamer based assay, and/or an antibody based assay.

128. =The method of any one of claims 1-127, 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.

129. The method of claim 128, wherein each the capture reagents specifically binds to a different biomarker protein being detected.

130. The method of claim 128 or 129, wherein each capture reagent is an antibody or an aptamer.

131. The method of claim 130, wherein each capture reagent is an aptamer.

132. The method of claim 131, wherein at least one aptamer is a slow off-rate aptamer.

133. The method of claim 132, 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.

134. The method of claim 132 or 133, wherein each slow off-rate aptamer binds to its target protein with an off rate ($t_{1/2}$) of ≥ 30 minutes, ≥ 60 minutes, ≥ 90 minutes, ≥ 120 minutes, ≥ 150 minutes, ≥ 180 minutes, ≥ 210 minutes, or ≥ 240 minutes.

135. A kit comprising N biomarker protein capture reagents, wherein N is at least 3, and wherein at least 3 of the capture reagents bind to proteins selected from LANC2, PKHM2, ENOA, the cytoplasmic domain of TMEM9, PMM2, PGAM2, EFHD1, and THIK.

136. A kit comprising N biomarker protein capture reagents, wherein N is at least 2, and wherein at least 2 of the capture reagents bind to proteins selected from LYAG, IL21R, C3b, IL36A, and GDF5.

137. A kit comprising N biomarker protein capture reagents, wherein N is at least 4, and wherein 4 of the capture reagents bind to the proteins IHH, SHH, PGAM1, and ROA2.

138. A kit comprising N biomarker protein capture reagents, wherein N is at least 9, and wherein at least 9 of the capture reagents bind to proteins selected from APB, CFAD, PTN4, PGAM2, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, and TMEM9.

139. The kit of claim 135 or 136, wherein N is at least 4, and wherein at least 1 of the capture reagents binds to a protein selected from IHH, SHH, PGAM1, and ROA2.

140. The kit of claim 139, wherein N is at least 7, and wherein 4 of the capture reagents bind to proteins selected from IHH, SHH, PGAM1, and ROA2.

141. The kit of claim 135 or 136, wherein N is at least 4, and wherein at least 1 of the capture reagents binds to a protein selected from APB, CFAD, PTN4, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, and IL18.

142. The kit of claim 135 or 136, wherein N is at least 12, and wherein at least 9 of the capture reagents bind to proteins selected from APB, CFAD, PTN4, PGAM2, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, and TMEM9.

143. The kit of claim 142, wherein at least 9 of the capture reagents bind to proteins selected from APB, CFAD, PTN4, PGAM2, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, TMEM9, and ROA2.

144. The kit of any one of claims 135-143, wherein each of the capture reagents binds to a different protein.

145. The kit of claim 135, wherein N is 3, N is 4, N is 5, N is 6, N is 7, or N is 8.

146. The kit of claim 145, wherein each of the capture reagents binds to a protein selected from LANC2, PKHM2, ENOA, the cytoplasmic domain of TMEM9, PMM2, PGAM2, EFHD1, and THIK.

147. The kit of claim 136, wherein N is 2, N is 3, N is 4, or N is 5.

148. The kit of claim 147, wherein each of the capture reagents binds to a protein selected from LYAG, IL21R, C3b, IL36A, and GDF5.

149. The kit of claim 137, wherein N is 4.

150. The kit of claim 149, wherein each of the capture reagents binds to a protein selected from IHH, SHH, PGAM1, and ROA2.

151. The kit of claim 138, wherein N is 9, N is 10, N is 11, N is 12, or N is 13.

152. The kit of claim 151, wherein each of the capture reagents binds to a protein selected from APB, CFAD, PTN4, PGAM2, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, and TMEM9.

153. The kit of claim 139, wherein N is 4, N is 5, N is 6, N is 7, N is 8, N is 9, N is 10, N is 11, or N is 12.

154. The kit of claim 140, wherein N is 7, N is 8, N is 9, N is 10, N is 11, or N is 12.

155. The kit of claim 153 or 154, wherein each of the capture reagents binds to a protein selected from LANC2, PKHM2, ENOA, the cytoplasmic domain of TMEM9, PMM2, PGAM2, EFHD1, THIK, IHH, SHH, PGAM1, and ROA2.

156. The kit of claim 153 or 154, wherein each of the capture reagents binds to a protein selected from LYAG, IL21R, C3b, IL36A, GDF5, IHH, SHH, PGAM1, and ROA2.

157. The kit of claim 141, wherein N is 4, N is 5, N is 6, N is 7, N is 8, N is 9, N is 10, N is 11, N is 12, N is 13, N is 14, N is 15, N is 16, N is 17, N is 18, or N is 19.

158. The kit of claim 142, wherein N is 12, N is 13, N is 14, N is 15, N is 16, N is 17, N is 18, or N is 19.

159. The kit of claim 157 or 158, wherein each of the capture reagents binds to a protein selected from LANC2, PKHM2, ENOA, the cytoplasmic domain of TMEM9, PMM2,

PGAM2, EFHD1, THIK, APB, CFAD, PTN4, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, and IL18.

160. The kit of claim 157 or 158, wherein each of the capture reagents binds to a protein selected from LYAG, IL21R, C3b, IL36A, GDF5, APB, CFAD, PTN4, PGAM2, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, and TMEM9.

161. The kit of claim 143, wherein N is 12, N is 13, N is 14, N is 15, N is 16, N is 17, N is 18, N is 19, or N is 20.

162. The kit of claim 161, wherein each of the capture reagents binds to a protein selected from LANC2, PKHM2, ENOA, the cytoplasmic domain of TMEM9, PMM2, PGAM2, EFHD1, THIK, APB, CFAD, PTN4, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, and ROA2.

163. The kit of claim 161, wherein each of the capture reagents binds to a protein selected from LYAG, IL21R, C3b, IL36A, GDF5, APB, CFAD, PTN4, PGAM2, HPPD, C4A, IF4A2, IHH, SHH, ADAM9, PGAM1, IL18, TMEM9, and ROA2.

164. The kit of any one of claims 135-163, wherein each of the capture reagents is an antibody or an aptamer.

165. The kit of claim 164, wherein each capture reagent is an aptamer.

166. The kit of claim 165, wherein at least one aptamer is a slow off-rate aptamer.

167. The kit of claim 166, 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.

168. The kit of claim 166 or claim 167, wherein each slow off-rate aptamer binds to its target protein with an off rate ($t_{1/2}$) of ≥ 30 minutes, ≥ 60 minutes, ≥ 90 minutes, ≥ 120 minutes, ≥ 150 minutes, ≥ 180 minutes, ≥ 210 minutes, or ≥ 240 minutes.

169. The kit of any one of claims 135-168, for use in detecting the N biomarker proteins in a sample from a subject.

170. The kit of claim 169, 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.