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(54) **METHODS TO SPECIFICALLY PROFILE
PROTEASE ACTIVITY AT LYMPH NODES**

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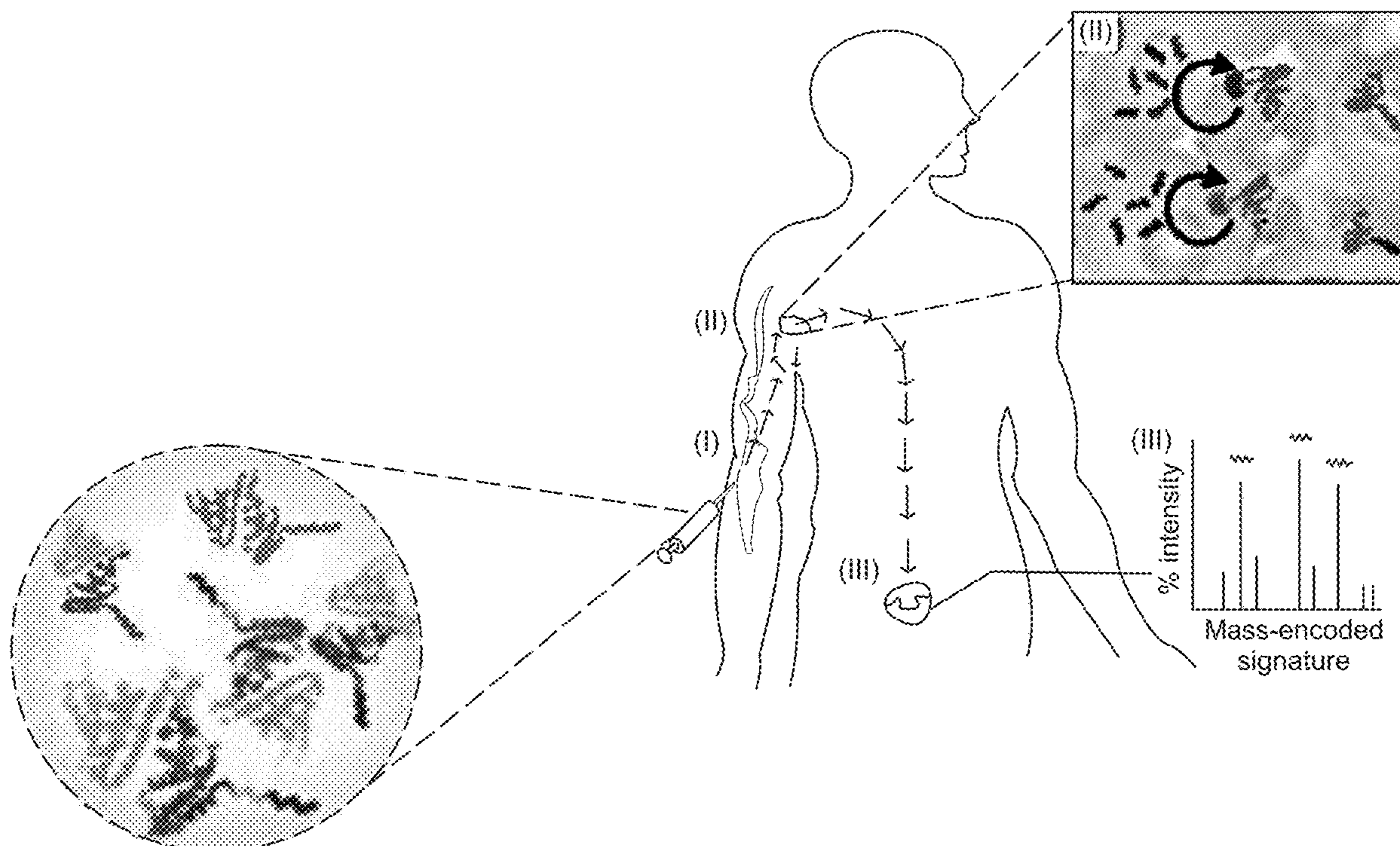
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7/00 (2013.01); **C12Q 1/37** (2013.01); **C07K**
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ABSTRACT

In some aspects, the disclosure provides compositions and methods for detecting and monitoring the activity of proteases in vivo using affinity assays. The disclosure relates, in part, to the discovery that biomarker nanoparticles targeted to the lymph nodes of a subject are useful for the diagnosis and monitoring of certain medical conditions (e.g., metastatic cancer, infection with certain pathogenic agents).

Specification includes a Sequence Listing.



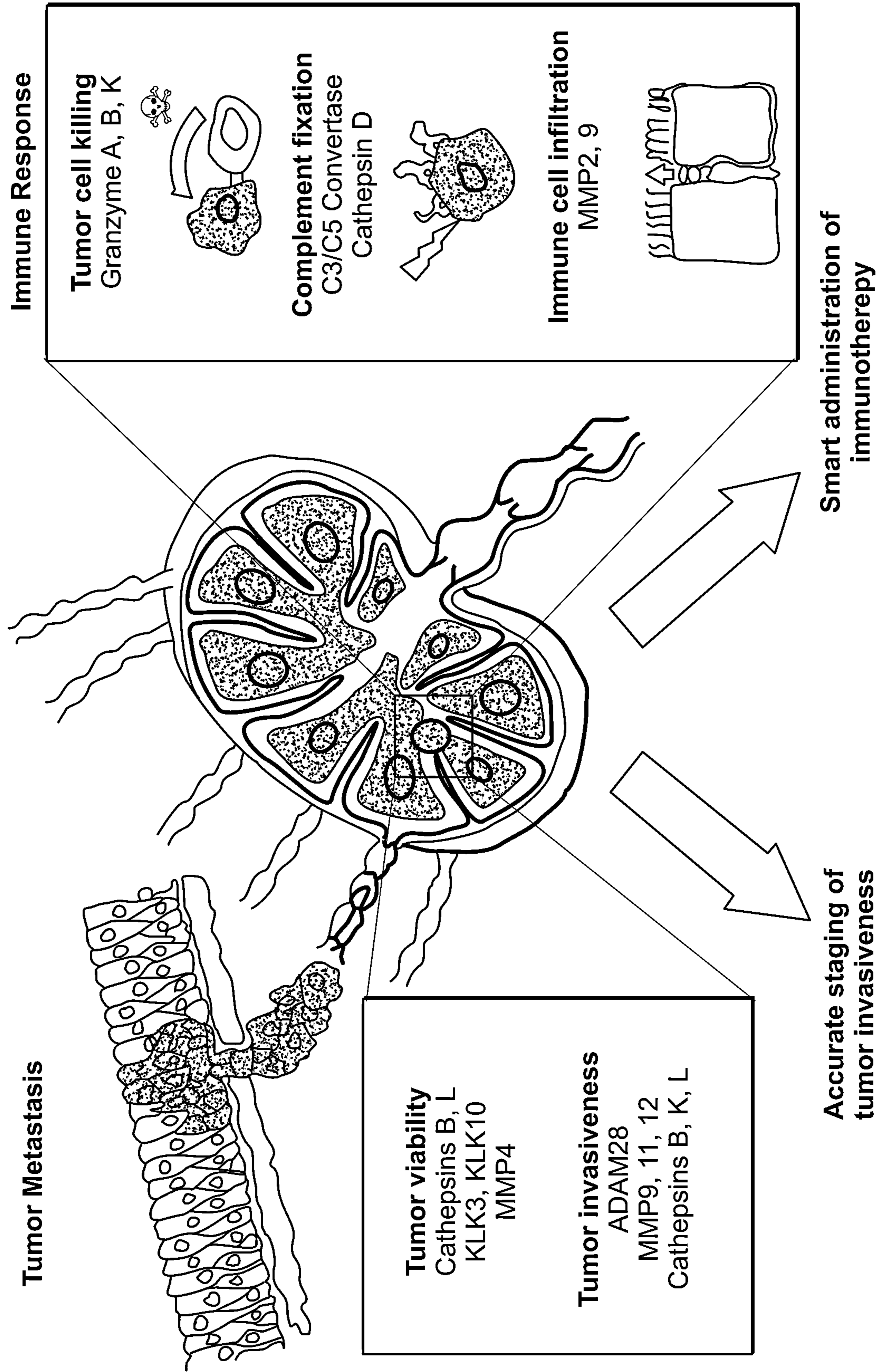


Figure 1

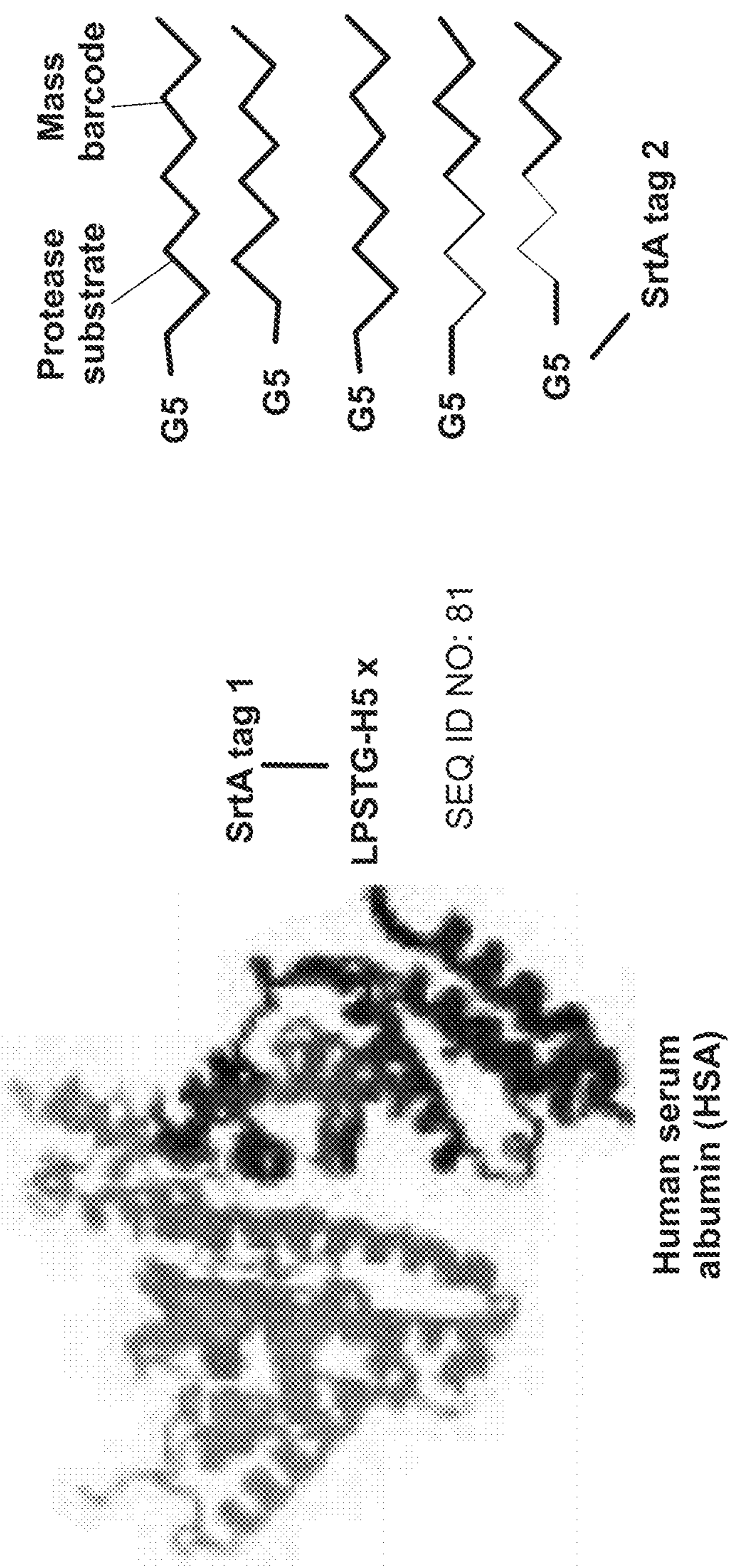


Figure 2A

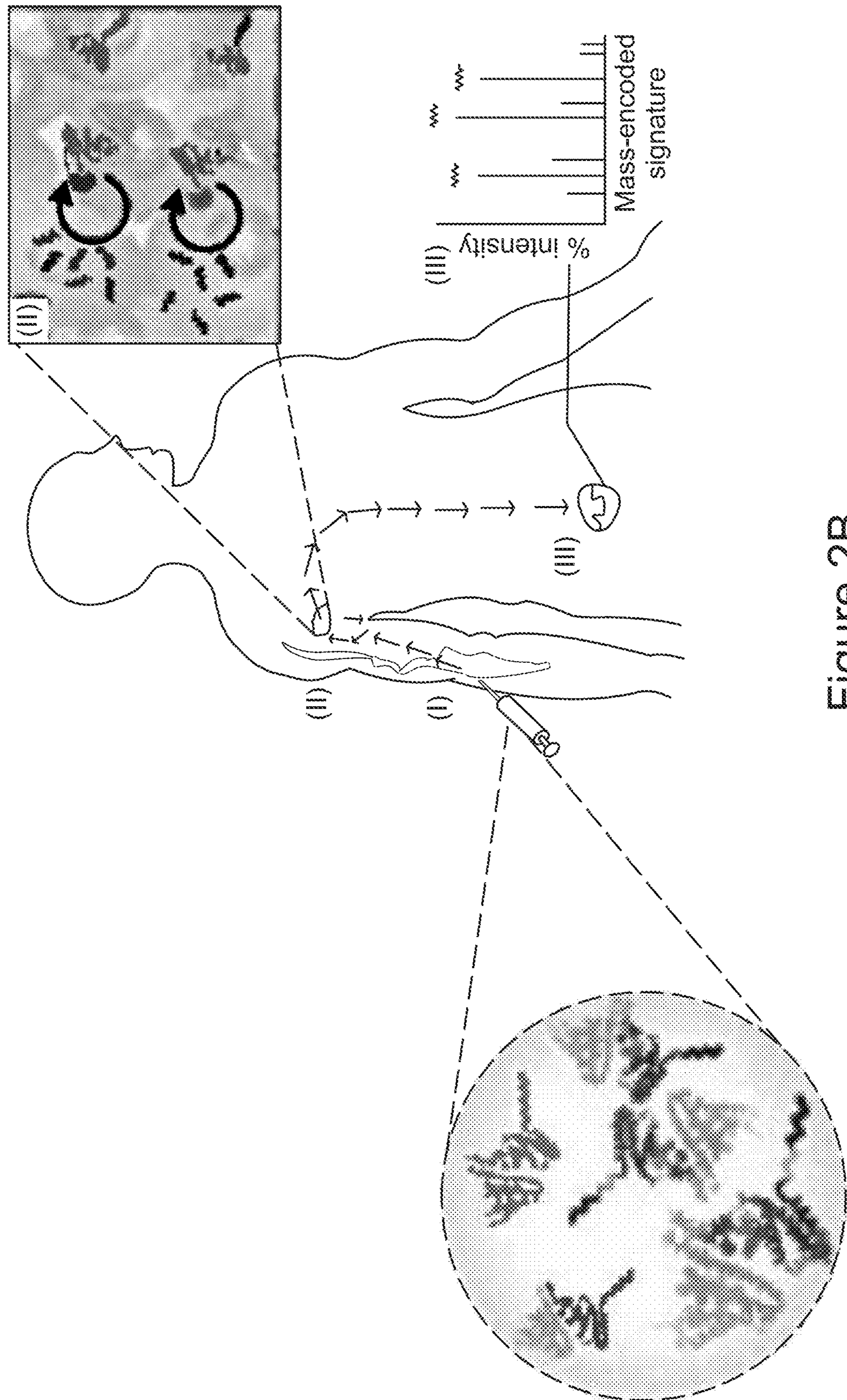


Figure 2B

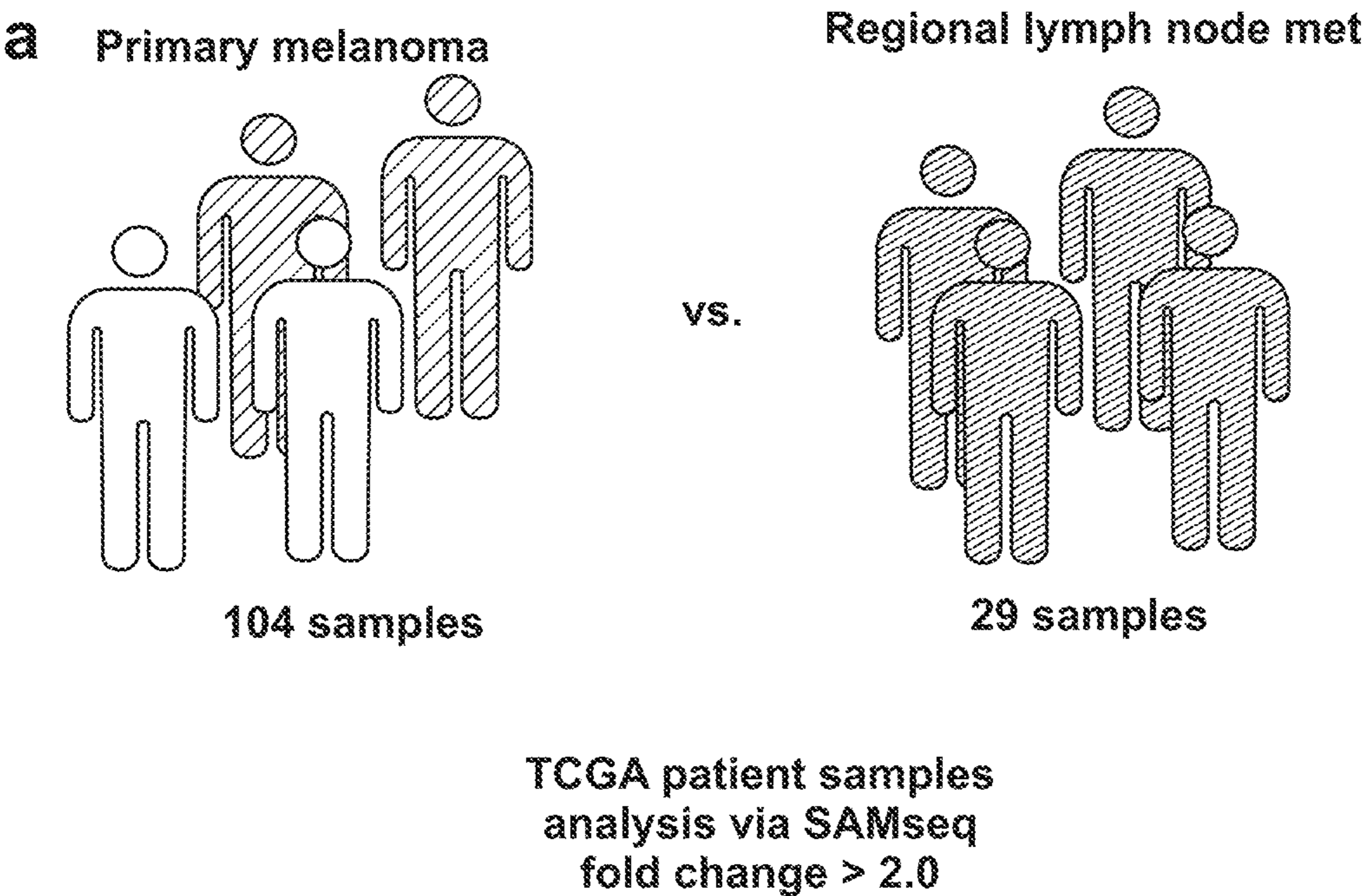


Figure 3A

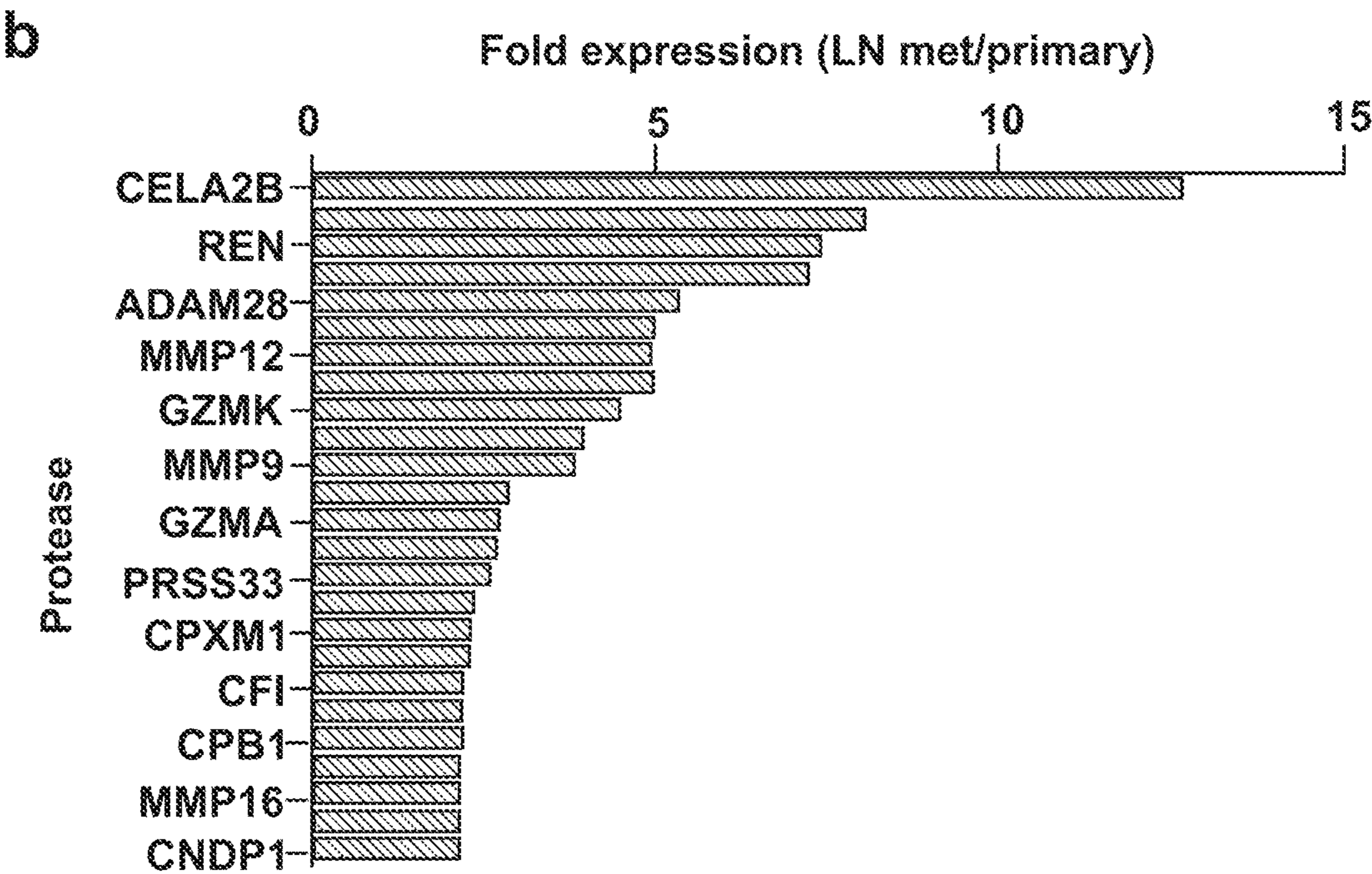


Figure 3B

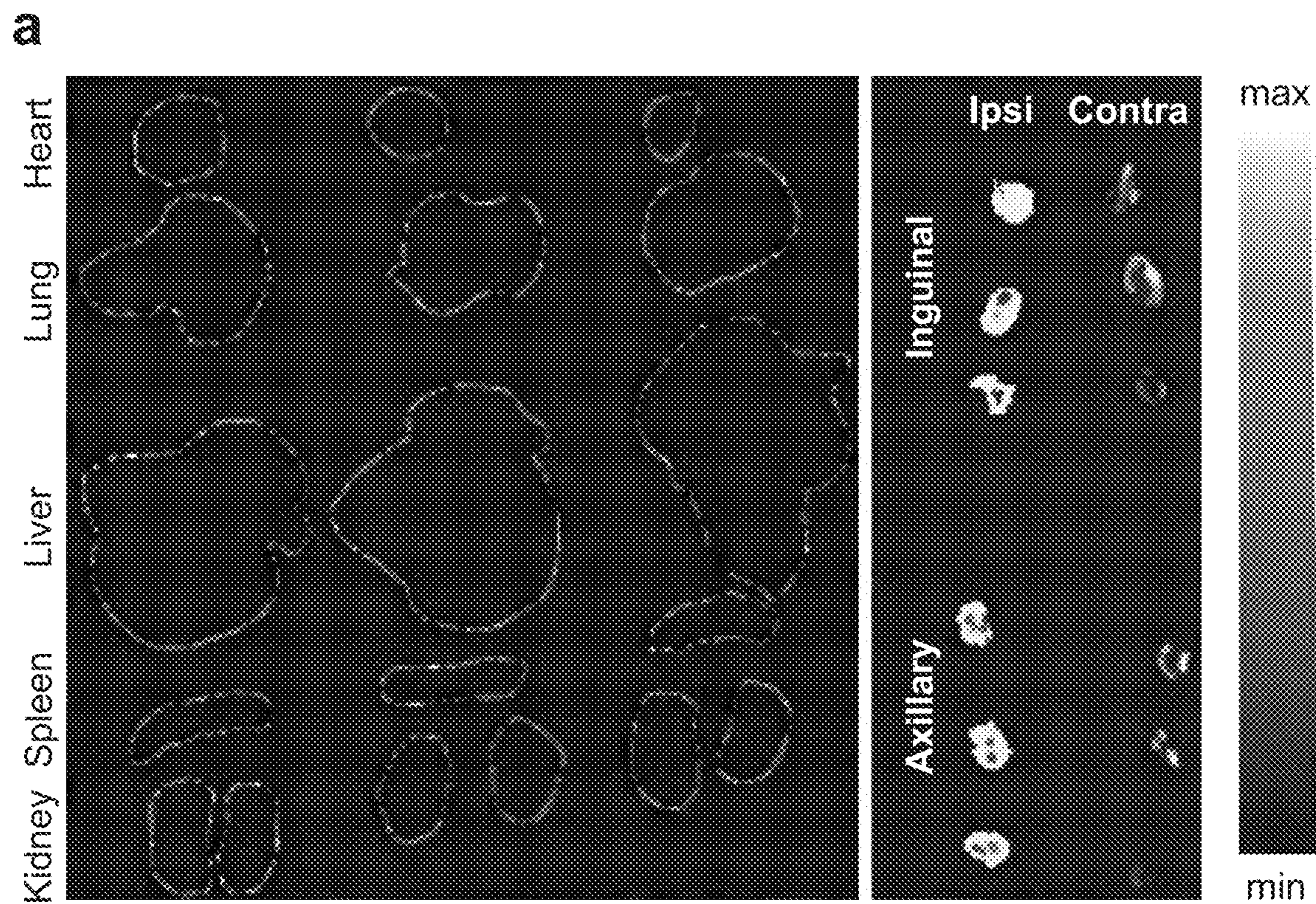


Figure 4A

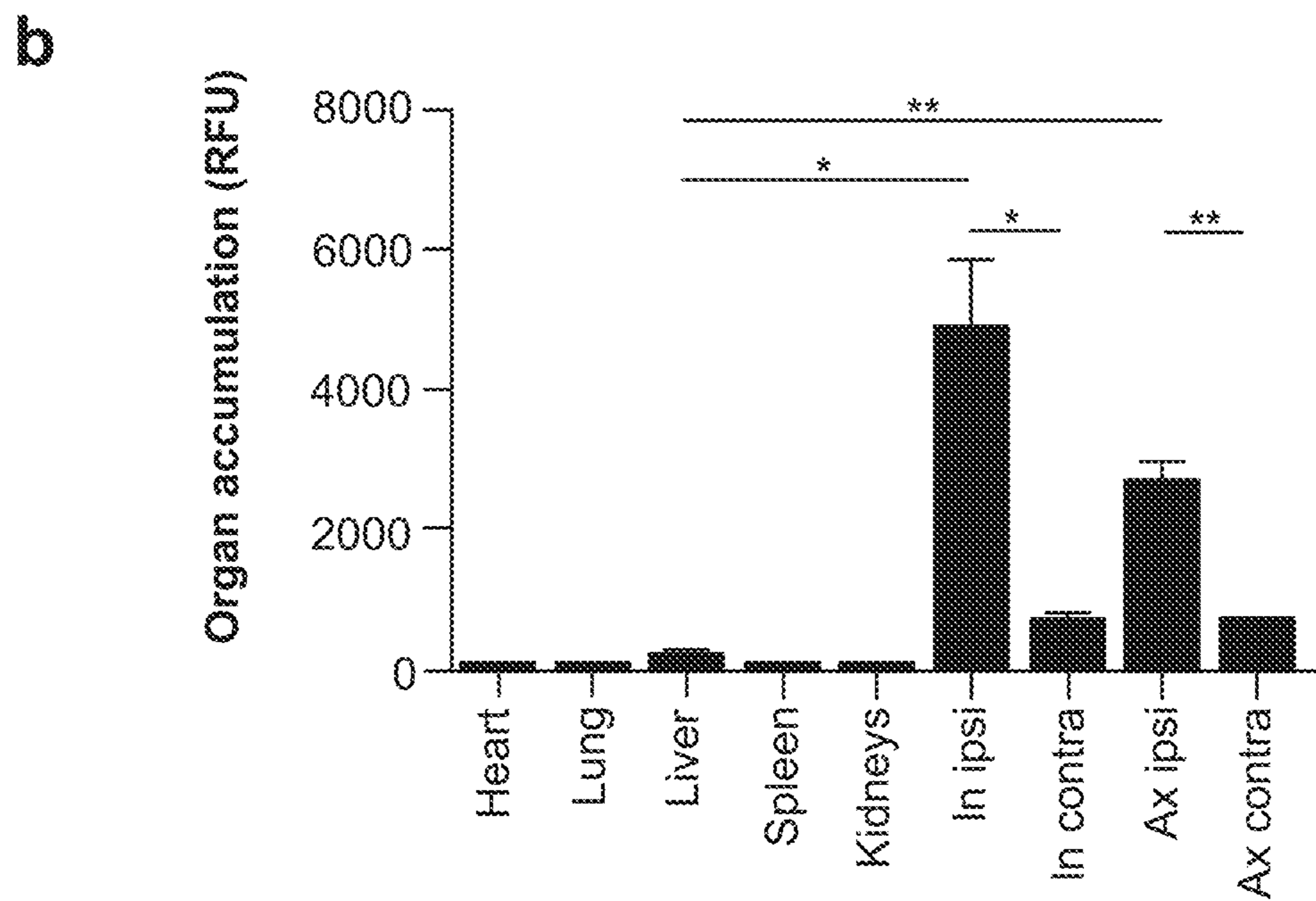


Figure 4B

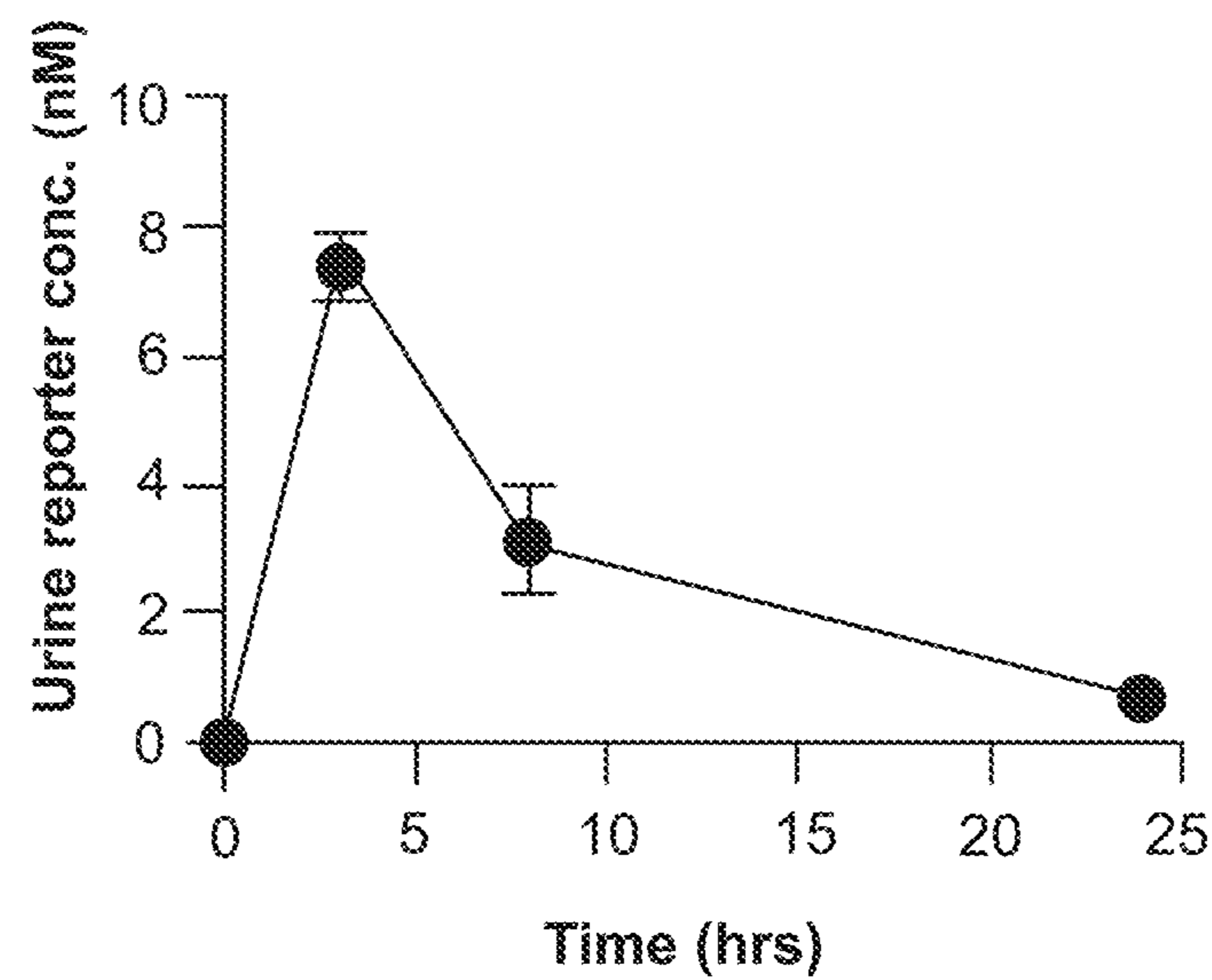


Figure 5

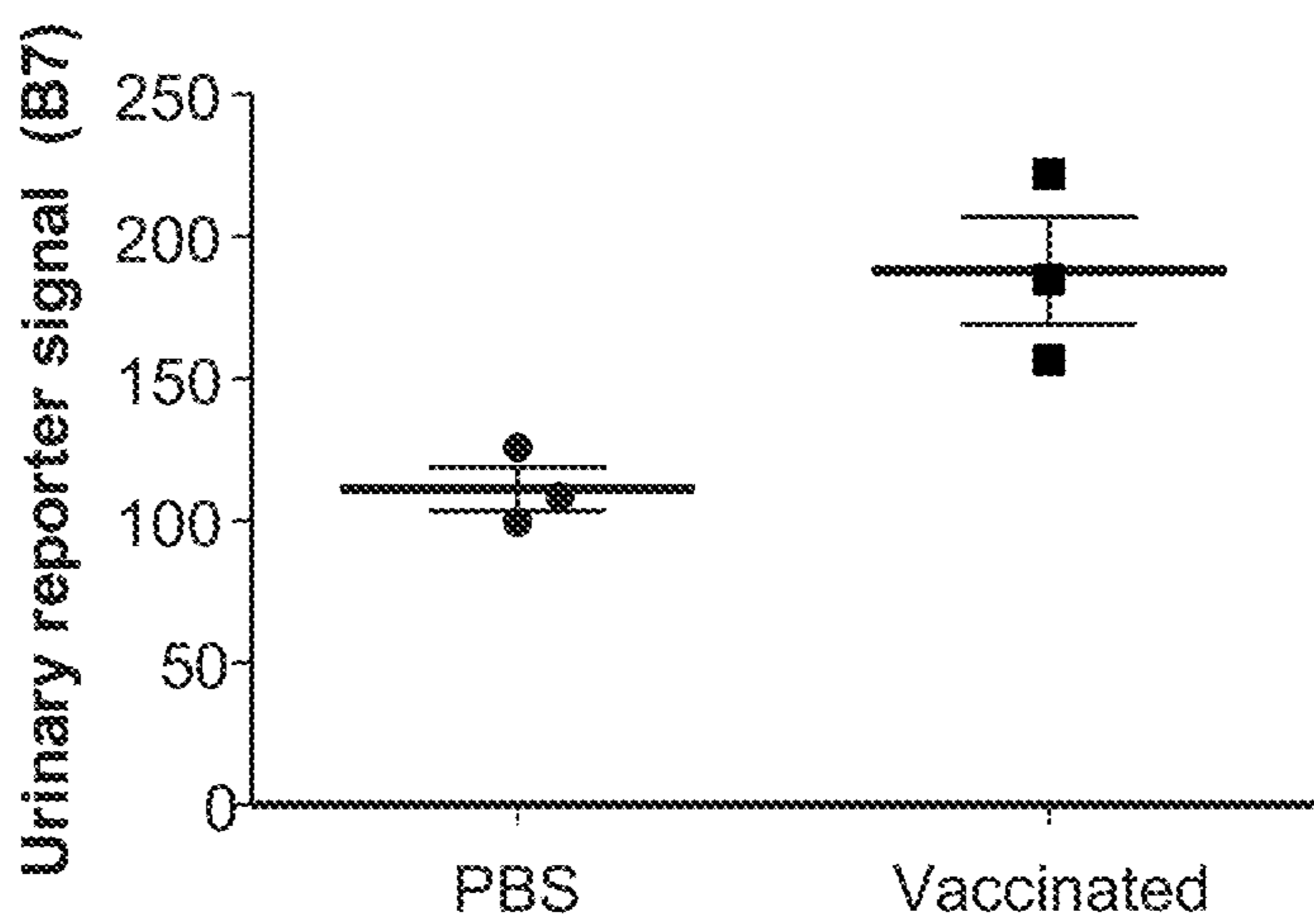


Figure 6

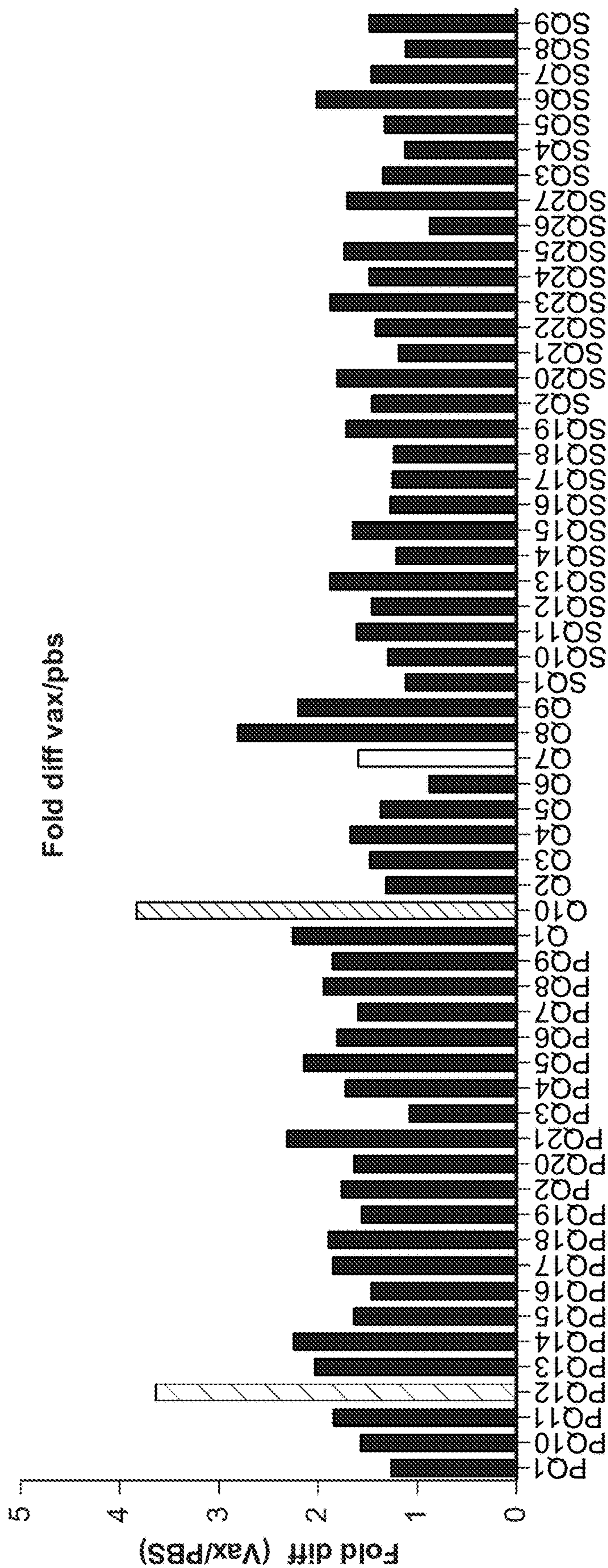


Figure 7

METHODS TO SPECIFICALLY PROFILE PROTEASE ACTIVITY AT LYMPH NODES

RELATED APPLICATIONS

[0001] This application is a divisional of U.S. application Ser. No. 16/091,145, filed on Oct. 4, 2018, which is a national stage filing under 35 U.S.C. § 371 of International Application No. PCT/US2017/026564, filed Apr. 7, 2017, which claims the benefit under 35 U.S.C. § 119(e) of U.S. provisional Application Ser. No. 62/319,820, filed on Apr. 8, 2016, entitled “METHODS TO SPECIFICALLY PROFILE PROTEASE ACTIVITY AT LYMPH NODES”, the entire contents of each of which are incorporated herein by reference.

GOVERNMENT SUPPORT

[0002] This invention was made with Government support under R01 CA174795 awarded by the National Institutes of Health. The Government has certain rights in the invention.

REFERENCE TO AN ELECTRONIC SEQUENCE LISTING

[0003] The contents of the electronic sequence listing (M0656.70383US02-SEQ-FL.xml; Size: 163,288 bytes; and Date of Creation: Aug. 2, 2022) is herein incorporated by reference in its entirety.

FIELD

[0004] The present invention relates to methods and products associated with detecting and monitoring the activity of proteases in vivo using affinity assays. These methods and products form the basis of and may be used as an ultrasensitive diagnostic platform. The invention also relates to products, kits, and databases for use in the methods of the invention.

BACKGROUND

[0005] Detection of nascent, clinically occult metastases may significantly benefit patient outcomes, as approximately nine out of ten deaths from cancer are due to metastases. Generally, it remains the prognostic rule of thumb that local tumors are curable, while disseminated tumors are often not and require more stringent therapeutic interventions. An early step in metastatic progression often involves invasive growth of the primary tumor to proximal lymph nodes (LN). **[0006]** Typically, lymph nodes (LN) are functionally probed via invasive surgical removal, which is associated with significant morbidity to patients. For example, patients and clinicians are often forced to proceed with aggressive LN extraction procedures without any information about the invasive nature of tumor cells, leading to unnecessary morbidity associated with surgeries. Currently, LN status is assessed via a combination of sentinel lymph node biopsy (whereby a dye is injected intratumorally and stained draining lymph nodes are presumed to be viable sites for metastasis) and imaging (including CT, PET and MRI). While these techniques can determine whether tumor cells are present, they fail to provide information regarding their metastatic potential. Furthermore, currently available diagnostic tools can also miss early metastatic events, which may lead to high relapse rates after surgeries for the primary tumor.

SUMMARY

[0007] In some aspects, the disclosure provides compositions and methods for detecting and monitoring the activity of proteases in vivo using affinity assays. The disclosure relates, in part, to the discovery that biomarker nanoparticles targeted to the lymph nodes of a subject are useful for the diagnosis and monitoring of certain medical conditions (e.g., metastatic cancer, infection with certain pathogenic agents). In some aspects, methods and compositions described by the disclosure are useful for monitoring of endogenous immune activity and efficacy of immunotherapies in causing an immune response.

[0008] Accordingly, in some aspects, the disclosure provides a composition comprising a lymph node biomarker nanoparticle, wherein the lymph node biomarker nanoparticle comprises a modular structure having a carrier domain linked to a lymph node specific enzyme susceptible detectable marker, wherein the enzyme susceptible detectable marker is comprised of a lymph node specific enzyme susceptible domain linked to a detectable marker whereby the detectable marker is capable of being released from the biomarker nanoparticle when exposed to an enzyme present in a lymph node.

[0009] In some aspects, the disclosure provides a method comprising administering to a subject a lymph node biomarker nanoparticle as described by the disclosure; analyzing a biological sample from the subject, wherein the biological sample is not a lymph node, and determining whether the detectable marker is in the biological sample, wherein the presence of the detectable marker in the biological sample is indicative of the enzyme being present in an active form within the lymph node of the subject. In some embodiments, the biological sample is urine.

[0010] In some aspects, the disclosure provides method comprising administering to the lymph node of a subject a lymph node biomarker nanoparticle, wherein the lymph node biomarker nanoparticle comprises a modular structure having a carrier domain linked to a lymph node specific enzyme susceptible detectable marker, wherein the lymph node specific enzyme susceptible detectable marker is comprised of an enzyme susceptible domain linked to a detectable marker whereby the detectable marker is capable of being released from the biomarker nanoparticle when exposed to an enzyme present in a lymph node; obtaining a urine sample from the subject for detection of the detectable marker; and, analyzing the urine sample using a capture assay in order to detect the presence of the detectable marker, wherein the presence of the detectable marker in the urine sample is indicative of the enzyme being present in an active form within a lymph node of the subject.

[0011] In some aspects, the disclosure provides a method for determining metastatic stage of a tumor comprising administering to the lymph node of a subject having a tumor a lymph node biomarker nanoparticle, wherein the lymph node biomarker nanoparticle comprises a modular structure having a carrier domain linked to a lymph node specific enzyme susceptible detectable marker, wherein the lymph node specific enzyme susceptible detectable marker is comprised of an enzyme susceptible domain linked to a detectable marker whereby the detectable marker is capable of being released from the biomarker nanoparticle when exposed to a metastatic tumor-associated enzyme in a lymph node; obtaining a urine sample from the subject for detection of the detectable marker; and, analyzing the urine sample

using a capture assay in order to detect the presence of the detectable marker, wherein the presence of the detectable marker in the urine sample is indicative of the subject having a metastatic tumor.

[0012] In some aspects, the disclosure provides a method for identifying a pathogenic agent comprising administering to the lymph node of a subject infected or suspected of being infected with a pathogenic agent a lymph node biomarker nanoparticle, wherein the lymph node biomarker nanoparticle comprises a modular structure having a carrier domain linked to a lymph node specific enzyme susceptible detectable marker, wherein the lymph node specific enzyme susceptible detectable marker is comprised of an enzyme susceptible domain linked to a detectable marker whereby the detectable marker is capable of being released from the biomarker nanoparticle when exposed to an enzyme associated with a pathogenic agent; obtaining a urine sample from the subject for detection of the marker; and, analyzing the urine sample using a capture assay in order to detect the presence of the detectable marker, wherein the presence of the detectable marker in the urine sample is indicative of the subject being infected with the pathogenic agent.

[0013] In some embodiments, a lymph node biomarker nanoparticle is administered to a subject by systemic administration. In some embodiments, systemic administration of a lymph node biomarker nanoparticle results in delivery of the lymph node biomarker nanoparticle to the lymph node of a subject. In some embodiments, a lymph node biomarker nanoparticle is administered to a subject by injection. In some embodiments, the injection is subcutaneous injection.

[0014] In some embodiments, a carrier domain comprises a lymph node trafficking carrier. In some embodiments, the lymph node trafficking carrier is albumin, an albumin-binding peptide (e.g., sso7d), or a molecular amphiphile having high affinity to albumin. In some embodiments, the lymph node trafficking carrier is human serum albumin (HSA). In some embodiments, the HSA is recombinant HSA. In some embodiments, the lymph node trafficking carrier is an antibody. In some embodiments, the antibody is an antibody targeting DEC-205, mannose receptor, mannose binding lectin, ficolins, DC-SIGN, DCAR, DCIR, dectins, DLEC, scavenger receptors, F4/80, Fc receptor, or DC-STAMP.

[0015] In some embodiments, the lymph node trafficking carrier is a polymeric scaffold that is greater than 40 kDa. In some embodiments, the lymph node trafficking carrier is a nanoparticle that is between about 10 nm and about 50 nm in diameter. In some embodiments, the lymph node trafficking carrier is a high molecular weight protein. In some embodiments, a high molecular weight protein is greater than 40 kDa.

[0016] In some embodiments, a lymph node specific enzyme susceptible domain comprises a cancer substrate. In some embodiments, the lymph node specific enzyme susceptible domain comprises a metastatic cancer substrate. In some embodiments, the cancer substrate is a substrate for a protease selected from ADAM28, MMP9, and MMP12.

[0017] In some embodiments, a lymph node specific enzyme susceptible domain comprises an immune-associated substrate. In some embodiments, the immune-associated substrate is a substrate for a protease selected from granzymes A, B, K and Cathepsin D. In some embodiments, the lymph node specific enzyme susceptible domain comprises a sequence selected from SEQ ID NO: 2-59.

[0018] In some embodiments, a lymph node biomarker nanoparticle is a multiplexed library of lymph node specific enzyme susceptible detectable markers. In some embodiments, the multiplexed library of lymph node specific enzyme susceptible detectable markers comprise 2, 5, 10, or more enzyme susceptible detectable markers.

[0019] In some embodiments, lymph node specific enzyme susceptible detectable markers are mass encoded protease substrates or ligand encoded protease substrates.

[0020] In some embodiments of methods described by the disclosure, the step of analyzing the biological sample (e.g., urine sample) detectable markers comprises identifying mass-encoded protease substrates using LC-MS/MS. In some embodiments, the step of analyzing the biological sample detectable markers comprises measuring fluorescence of the detectable markers, for example using spectrophotometry.

[0021] In some embodiments, an enzyme present in an active form within a lymph node (e.g., a lymph node specific enzyme that releases a detectable agent from a biomarker nanoparticle) is indicative of a metastatic cancer. In some embodiments, the enzyme present in an active form within the lymph node is indicative of an immune status indicating sensitivity to immune therapy.

[0022] Each of the embodiments of the invention can encompass various recitations made herein. It is, therefore, anticipated that each of the recitations of the invention involving any one element or combinations of elements can, optionally, be included in each aspect of the invention.

BRIEF DESCRIPTION OF DRAWINGS

[0023] FIG. 1 demonstrate how lymph nodes are critical sites in the body for both tumor metastasis and immune response. Cancer cells from the primary tumor invade the lymph node and have different proteolytic landscapes than the primary tumor. Immune cells also utilize proteases to engage with target cells and also infiltrate into the lymph node. Profiling both axes of lymph node proteases will enable accurate tumor staging and inform immunotherapy regimens.

[0024] FIGS. 2A-2B describe one embodiment of an approach for lymph node monitoring. FIG. 2A depicts one embodiment of multiplexed, mass-encoded substrate-reporter tandems ('synthetic biomarkers') conjugated to serum albumin (e.g., human serum albumin; HSA) as a protein chaperone to the lymph node. FIG. 2B depicts subcutaneous injection (I) of a protein-chaperoned synthetic biomarker library results specifically in lymph node accumulation (arrows), where substrates are cleaved by their cognate proteases (II); reporter fragments (e.g., mass barcode(s)) enter the blood stream and are concentrated in the urine by filtering through the kidney, and disease signatures are quantified by LC-MS/MS (III).

[0025] FIGS. 3A-3B show TCGA (the Cancer Genome Atlas) analysis reveals lymph node metastases specific protease profiles. FIG. 3A depicts patient data for primary melanoma (n=104) and regional lymph node metastatic (n=29) samples used to produce the fold expression data depicted in FIG. 3B. FIG. 3B shows fold expression data for a candidate protease "hit list", which includes proteases known to be involved in immune function (GZMK=Granzyme K; GZMA=Granzyme A) and cancer cell invasiveness (MMP9).

[0026] FIGS. 4A-4B show that albumin-conjugated synthetic biomarkers efficiently and selectively target lymph nodes. FIG. 4A shows accumulation of albumin-conjugated synthetic biomarkers is highly selective for ipsilateral lymph node delivery (e.g., tumor-draining lymph nodes). FIG. 4B shows organ accumulation of albumin-conjugated synthetic biomarkers in various tissues (e.g., heart, lung, liver, spleen, kidney, and lymph nodes).

[0027] FIG. 5 shows urine concentration of reporters after subcutaneous injection of Albumin-B7 in healthy mice shows peak urine signal at 3 hours post-injection with detectable signal 24 hours post-injection.

[0028] FIG. 6 shows quantification of urinary reporter signal (B7) in mice vaccinated with a cancer-specific peptide vaccine and adjuvant to stimulate immune response in the lymph nodes. Mice were injected subcutaneously and urine for analysis was collected 3 h post-administration.

[0029] FIG. 7 shows an ex vivo peptide screen of lymph nodes from vaccinated mice versus control mice. Substrate cleavage of 58 peptides was measured. Signal reported is the fold difference in cleavage between vaccinated mice and PBS-injected mice.

DETAILED DESCRIPTION

[0030] Aspects of the disclosure relate to methods and compositions for detecting and monitoring protease activity of lymph nodes as an indicator of certain disease states (e.g., metastatic cancers, infection with pathogenic agents, etc.). The disclosure relates, in some aspects, to the discovery that delivery of biomarker nanoparticles to the lymph nodes of a subject provides a minimally invasive snapshot of the state of immunity (e.g., tumor immunity) of the lymph node. Without wishing to be bound by any particular theory, synthetic biomarkers described herein can detect enzymatic activity in vivo and noninvasively quantify physiological processes by harnessing the capacity of the biomarker nanoparticles to circulate and sense the local microenvironment (e.g., lymph node environment) while providing a read-out (e.g., detection of a detectable marker) at a site that is remote (e.g., a urine sample) from the target tissue (e.g., lymph node).

[0031] For instance, as shown in the Example section described herein, lymph node specific protease activity can be assessed in order to determine the metastatic state of a tumor. In another example, lymph node specific protease activity can be assessed in order to determine whether a subject is infected with a pathogenic agent. Unlike other nanoparticle sensors that function by producing a localized signal, the compositions of the invention sense protease activity by releasing reporters locally at the sites of interest, i.e., in the lymph nodes, but then are filtered and detected remotely from the urine. By using distinct ligands and their cognate binding molecules, a panel of heterobifunctionalized reporters were also developed that can be detected using assays such as standardized 96-well plate assays, removing the need for mass spectrometry. This system is readily extensible by incorporating additional ligand-capture agent pairs and is amenable for detection by other methods including paper-based test strips (lateral flow assays) at the point of care, assays including bead-based assays (e.g., immunoprecipitation), surface plasmon resonance, nano-electronics (e.g., nanowires) etc.

[0032] The compositions and methods of the disclosure have a number of advantages over the prior art methods. For

example, current methods functionally probe lymph nodes (LN) via invasive surgical removal, which is associated with significant morbidity to patients. Less invasive imaging modalities can help determine whether tumor cells are present in the lymph node, but they fail to provide information regarding invasiveness or immune activity. In some aspects, the disclosure provides compositions and methods that addresses these issues. In some embodiments, the disclosure provides probes (e.g., biomarker nanoparticles) sensitive to proteases in the lymph node (LN) to accomplish this.

[0033] Aberrantly expressed proteases are candidate enzymes for cancer detection and analysis as they play critical roles in many cancers. Additionally, proteases are involved in many immune processes, including immune cell trafficking to and from the lymph node and target cell killing (FIG. 1). Accordingly, in some embodiments the disclosure relates to the delivery of a set of protease-sensitive substrates to the lymph node using lymph node specific trafficking carriers. Upon encountering their cognate proteases, peptide substrates are cleaved and reporter fragments are excreted into urine, providing a non-invasive diagnostic readout. In some embodiments, the delivered substrates are responsive to proteases enriched in different stages of tumor invasiveness (e.g., metastasis) and provide a high resolution, functionality driven snapshot of LN microenvironment (e.g., LN metastases).

[0034] Accordingly, in some aspects the disclosure provides a composition comprising a lymph node biomarker nanoparticle, wherein the lymph node biomarker nanoparticle comprises a modular structure having a carrier domain linked to a lymph node specific enzyme susceptible detectable marker, wherein the enzyme susceptible detectable marker is comprised of a lymph node specific enzyme susceptible domain linked to a detectable marker whereby the detectable marker is capable of being released from the biomarker nanoparticle when exposed to an enzyme present in a lymph node.

Carrier Domain

[0035] The biomarker nanoparticle comprises a modular structure having a carrier domain linked to an enzyme susceptible detectable marker. A modular structure, as used herein, refers to a molecule having multiple domains.

[0036] The carrier domain may include a single type of enzyme susceptible detectable marker, such as, a single type of enzyme susceptible domain and or detectable marker or it may include multiple type of enzyme susceptible detectable markers, such as, different enzyme susceptible domains and detectable markers. For instance each carrier may include 1 type of enzyme susceptible detectable marker or it may include 2-1,000 different enzyme susceptible detectable markers or any integer therebetween. Alternatively each carrier may include greater than 1,000 enzyme susceptible detectable markers. Multiple copies of the biomarker nanoparticle are administered to the subject. Some mixtures of biomarker nanoparticles may include enzyme susceptible detectable markers that are enzymes, others may be enzymatic susceptible domains, and other may be mixtures of the two. Additionally a plurality of different biomarker nanoparticles may be administered to the subject to determine whether multiple enzymes and/or substrates are present. In that instance, the plurality of different biomarker nanoparticles includes a plurality of detectable markers, such that

each enzyme susceptible domain is associated with a particular detectable marker or molecules.

[0037] In some embodiments, the carrier domain comprises a lymph node trafficking carrier. As used herein, a “lymph node trafficking carrier” refers to a carrier (e.g., a protein, nucleic acid, or other molecule, such as a biological molecule or a nanoparticle) that enters the reticuloendothelial system (RES) and preferentially directs a biomarker nanoparticle to a lymph node of a subject. Examples of lymph node trafficking carriers include but are not limited to albumin, albumin-binding peptides (e.g., peptides having the core sequence DICLPRWGCLW (SEQ ID NO: 60), as disclosed by Dennis et al., *J. Biol. Chem.* 277, 35035-35043, (2002)), a molecular amphiphile having high affinity to albumin, or peptides based on an Sso7d scaffold (for example as disclosed by Traxlmayr et al. *J. Biol. Chem.* 291, 22496-22508, (2016)). In some embodiments, a lymph node trafficking carrier is injected into a subject and self-assembles with albumin in interstitial space of the subject, resulting in trafficking to the lymph nodes.

[0038] In some embodiments, a lymph node trafficking carrier is an antibody. For example, in some embodiments, a lymph node trafficking carrier comprises a HIV neutralizing antibody. Examples of HIV neutralizing antibodies include antibodies targeting MPER of gp41, V1V2-glycan, V3-glycan, and HIV CD4 binding site. In some embodiments, a lymph node trafficking carrier comprises a cancer-targeted antibody (e.g., monoclonal antibody). Examples of cancer-targeted antibodies include but are not limited to bevacizumab, cetuximab, ipilimumab, and brentuximab.

[0039] In some embodiments, a lymph node trafficking carrier is a protein having a molecular weight greater than 40 kDa, for example as disclosed by McLennan, Danielle N., Christopher J. H. Porter, and Susan A. Charman. “Subcutaneous Drug Delivery and the Role of the Lymphatics.” *Drug Discovery Today: Technologies* 2, no. 1 (March 2005): 89-96. doi:10.1016/j.ddtec.2005.05.006. In some embodiments, a lymph node trafficking carrier is a non-protein-based (e.g., polymeric scaffold) that is greater than 40 kDa, or a nanoparticle that is between 10 nm and 50 nm in diameter. In some embodiments, the lymph node trafficking carrier is a high molecular weight protein or polymer, for example an Fc domain of an antibody, transthyretin, or a poly(ethylene glycol) polymer of a sufficient molecular weight (e.g., greater than 40 kDa).

[0040] The carrier domain may serve as the core of the nanoparticle. A purpose of the carrier domain is to serve as a platform for the enzyme susceptible detectable marker. As such, the carrier can be any material or size as long as it can serve as a carrier or platform. Preferably the material is non-immunogenic, i.e. does not provoke an immune response in the body of the subject to which it will be administered. Another purpose is that it may function as a targeting means to target the modular structure to a tissue, cell or molecule. In some embodiments the carrier domain is a particle. A particle, for example, a nanoparticle, may, for instance, result in passive targeting to tumors by circulation. Other types of carriers, include, for instance, compounds that cause active targeting to tissue, cells or molecules. Examples of carriers include, but are not limited to, microparticles, nanoparticles, aptamers, peptides (RGD, iRGD, LyP-1, CREKA, etc.), proteins, nucleic acids, polysaccharides, polymers, antibodies or antibody fragments

(e.g., herceptin, cetuximab, panitumumab, etc.) and small molecules (e.g., erlotinib, gefitinib, sorafenib, etc.).

[0041] As used herein the term “particle” includes nanoparticles as well as microparticles. Nanoparticles are defined as particles of less than 1.0 μm in diameter. A preparation of nanoparticles includes particles having an average particle size of less than 1.0 μm in diameter. Microparticles are particles of greater than 1.0 μm in diameter but less than 1 mm. A preparation of microparticles includes particles having an average particle size of greater than 1.0 μm in diameter. The microparticles may therefore have a diameter of at least 5, at least 10, at least 25, at least 50, or at least 75 microns, including sizes in ranges of 5-10 microns, 5-15 microns, 5-20 microns, 5-30 microns, 5-40 microns, or 5-50 microns. A composition of particles may have heterogeneous size distributions ranging from 10 nm to mm sizes. In some embodiments the diameter is about 5 nm to about 500 nm. In other embodiments, the diameter is about 100 nm to about 200 nm. In other embodiment, the diameter is about 10 nm to about 100 nm.

[0042] The particles may be composed of a variety of materials including iron, ceramic, metallic, natural polymer materials (including lipids, sugars, chitosan, hyaluronic acid, etc.), synthetic polymer materials (including polylactide-coglycolide, poly-glycerol sebacate, etc.), and non-polymer materials, or combinations thereof.

[0043] The particles may be composed in whole or in part of polymers or non-polymer materials. Non-polymer materials, for example, may be employed in the preparation of the particles. Exemplary materials include alumina, calcium carbonate, calcium sulfate, calcium phosphosilicate, sodium phosphate, calcium aluminate, calcium phosphate, hydroxyapatite, tricalcium phosphate, dicalcium phosphate, tricalcium phosphate, tetracalcium phosphate, amorphous calcium phosphate, octacalcium phosphate, and silicates. In certain embodiments the particles may comprise a calcium salt such as calcium carbonate, a zirconium salt such as zirconium dioxide, a zinc salt such as zinc oxide, a magnesium salt such as magnesium silicate, a silicon salt such as silicon dioxide or a titanium salt such as titanium oxide or titanium dioxide.

[0044] A number of biodegradable and non-biodegradable biocompatible polymers are known in the field of polymeric biomaterials, controlled drug release and tissue engineering (see, for example, U.S. Pat. Nos. 6,123,727; 5,804,178; 5,770,417; 5,736,372; 5,716,404 to Vacanti; U.S. Pat. Nos. 6,095,148; 5,837,752 to Shastri; U.S. Pat. No. 5,902,599 to Anseth; U.S. Pat. Nos. 5,696,175; 5,514,378; 5,512,600 to Mikos; U.S. Pat. No. 5,399,665 to Barrera; U.S. Pat. No. 5,019,379 to Domb; U.S. Pat. No. 5,010,167 to Ron; U.S. Pat. No. 4,946,929 to d'Amore; and U.S. Pat. Nos. 4,806,621; 4,638,045 to Kohn; see also Langer, *Acc. Chem. Res.* 33:94, 2000; Langer, *J. Control Release* 62:7, 1999; and Uhrich et al., *Chem. Rev.* 99:3181, 1999; all of which are incorporated herein by reference).

[0045] Polymers include, but are not limited to: polyamides, polycarbonates, polyalkylenes, polyalkylene glycols, polyalkylene oxides, polyalkylene terephthalates, polyvinyl alcohols, polyvinyl ethers, polyvinyl esters, polyvinyl halides, polyglycolides, polysiloxanes, polyurethanes and copolymers thereof, alkyl cellulose, hydroxyalkyl celluloses, cellulose ethers, cellulose esters, nitro celluloses, polymers of acrylic and methacrylic esters, methyl cellulose, ethyl cellulose, hydroxypropyl cellulose, hydroxy-propyl

methyl cellulose, hydroxybutyl methyl cellulose, cellulose acetate, cellulose propionate, cellulose acetate butyrate, cellulose acetate phthalate, carboxylethyl cellulose, cellulose triacetate, cellulose sulphate sodium salt, poly(methyl methacrylate), poly(ethylmethacrylate), poly(butylmethacrylate), poly(isobutylmethacrylate), poly(hexylmethacrylate), poly(isodecylmethacrylate), poly(lauryl methacrylate), poly(phenyl methacrylate), poly(methyl acrylate), poly(isopropyl acrylate), poly(isobutyl acrylate), poly(octadecyl acrylate), polyethylene, polypropylene poly(ethylene glycol), poly(ethylene oxide), poly(ethylene terephthalate), poly(vinyl alcohols), poly(vinyl acetate), poly(vinyl chloride) and polystyrene.

[0046] Examples of non-biodegradable polymers include ethylene vinyl acetate, poly(meth) acrylic acid, polyamides, copolymers and mixtures thereof.

[0047] Examples of biodegradable polymers include synthetic polymers such as polymers of lactic acid and glycolic acid, polyanhydrides, poly(ortho)esters, polyurethanes, poly(butic acid), poly(valeric acid), poly(caprolactone), poly(hydroxybutyrate), poly(lactide-co-glycolide) and poly(lactide-co-caprolactone), and natural polymers such as alginate and other polysaccharides including dextran and cellulose, collagen, chemical derivatives thereof (substitutions, additions of chemical groups, for example, alkyl, alkylene, hydroxylations, oxidations, and other modifications routinely made by those skilled in the art), albumin and other hydrophilic proteins, zein and other prolamines and hydrophobic proteins, copolymers and mixtures thereof. In general, these materials degrade either by enzymatic hydrolysis or exposure to water in vivo, by surface or bulk erosion. The foregoing materials may be used alone, as physical mixtures (blends), or as co-polymers. In some embodiments the polymers are polyesters, polyanhydrides, polystyrenes, polylactic acid, polyglycolic acid, and copolymers of lactic acid and glycolic acid and blends thereof.

[0048] PVP is a non-ionogenic, hydrophilic polymer having a mean molecular weight ranging from approximately 10,000 to 700,000 and the chemical formula $(C_6H_9NO)_n$. PVP is also known as poly[1-(2-oxo-1-pyrrolidinyl)ethylene], PovidoneTM, PolyvidoneTM, RP 143TM, KollidonTM, Pregel STTM, PeristonTM, PlasdoneTM, PlasmosanTM, ProtagentTM, SubtosanTM, and VinisilTM. PVP is non-toxic, highly hygroscopic and readily dissolves in water or organic solvents.

[0049] Polyethylene glycol (PEG), also known as poly(oxyethylene) glycol, is a condensation polymer of ethylene oxide and water having the general chemical formula $HO(CH_2CH_2O)_nH$.

[0050] Polyvinyl alcohol (PVA) is a polymer prepared from polyvinyl acetates by replacement of the acetate groups with hydroxyl groups and has the formula $(CH_2CHOH)_n$. Most polyvinyl alcohols are soluble in water.

[0051] PEG, PVA and PVP are commercially available from chemical suppliers such as the Sigma Chemical Company (St. Louis, Mo.).

[0052] In certain embodiments the particles may comprise poly(lactic-co-glycolic acid) (PLGA). The carrier may be composed of inorganic materials. Inorganic materials include, for instance, magnetic materials, conductive materials, and semiconductor materials.

[0053] In addition to particles the carrier may be composed of any organic carrier, including biological and living carriers such as cells, viruses, bacteria, as well as any

non-living organic carriers, or any composition enabling exposure of enzyme substrates to enzymes in disease (including extracellular, membrane-bound, and intracellular enzymes).

[0054] In some embodiments, the particles are porous. A porous particle can be a particle having one or more channels that extend from its outer surface into the core of the particle. In some embodiments, the channel may extend through the particle such that its ends are both located at the surface of the particle. These channels are typically formed during synthesis of the particle by inclusion followed by removal of a channel forming reagent in the particle. The size of the pores may depend upon the size of the particle. In certain embodiments, the pores have a diameter of less than 15 microns, less than 10 microns, less than 7.5 microns, less than 5 microns, less than 2.5 microns, less than 1 micron, less than 0.5 microns, or less than 0.1 microns. The degree of porosity in porous particles may range from greater than 0 to less than 100% of the particle volume. The degree of porosity may be less than 1%, less than 5%, less than 10%, less than 15%, less than 20%, less than 25%, less than 30%, less than 35%, less than 40%, less than 45%, or less than 50%. The degree of porosity can be determined in a number of ways. For example, the degree of porosity can be determined based on the synthesis protocol of the carriers (e.g., based on the volume of the aqueous solution or other channel-forming reagent) or by microscopic inspection of the carriers post-synthesis.

[0055] The plurality of particles may be homogeneous for one or more parameters or characteristics. A plurality that is homogeneous for a given parameter, in some instances, means that particles within the plurality deviate from each other no more than about $\pm 10\%$, preferably no more than about $\pm 5\%$, and most preferably no more than about $\pm 1\%$ of a given quantitative measure of the parameter. As an example, the particles may be homogeneously porous. This means that the degree of porosity within the particles of the plurality differs by not more than $\pm 10\%$ of the average porosity. In other instances, a plurality that is homogeneous means that all the particles in the plurality were treated or processed in the same manner, including for example exposure to the same agent regardless of whether every particle ultimately has all the same properties. In still other embodiments, a plurality that is homogeneous means that at least 80%, preferably at least 90%, and more preferably at least 95% of particles are identical for a given parameter.

[0056] The plurality of particles may be heterogeneous for one or more parameters or characteristics. A plurality that is heterogeneous for a given parameter, in some instances, means that particles within the plurality deviate from the average by more than about $\pm 10\%$, including more than about $\pm 20\%$. Heterogeneous particles may differ with respect to a number of parameters including their size or diameter, their shape, their composition, their surface charge, their degradation profile, whether and what type of agent is comprised by the particle, the location of such agent (e.g., on the surface or internally), the number of agents comprised by the particle, etc. The invention contemplates separate synthesis of various types of particles which are then combined in any one of a number of pre-determined ratios prior to contact with the sample. As an example, in one embodiment, the particles may be homogeneous with respect to shape (e.g., at least 95% are spherical in shape) but

may be heterogeneous with respect to size, degradation profile and/or agent comprised therein.

[0057] Particle size, shape and release kinetics can also be controlled by adjusting the particle formation conditions. For example, particle formation conditions can be optimized to produce smaller or larger particles, or the overall incubation time or incubation temperature can be increased, resulting in particles which have prolonged release kinetics.

[0058] The particles may also be coated with one or more stabilizing substances, which may be particularly useful for long term depoting with parenteral administration or for oral delivery by allowing passage of the particles through the stomach or gut without dissolution. For example, particles intended for oral delivery may be stabilized with a coating of a substance such as mucin, a secretion containing mucopolysaccharides produced by the goblet cells of the intestine, the submaxillary glands, and other mucous glandular cells.

[0059] To enhance delivery the particles may be incorporated, for instance, into liposomes, virosomes, cationic lipids or other lipid based structures. The term “cationic lipid” refers to lipids which carry a net positive charge at physiological pH. Such lipids include, but are not limited to, DODAC, DOTMA, DDAB, DOTAP, DC-Chol and DMRIE. Additionally, a number of commercial preparations of cationic lipids are available. These include, for example, LIPOFECTIN® (commercially available cationic liposomes comprising DOTMA and DOPE, from GIBCO/BRL, Grand Island, N.Y., USA); LIPOFECTAMINE® (commercially available cationic liposomes comprising DOSPA and DOPE, from GIBCO/BRL); and TRANSFECTAM® (commercially available cationic lipids comprising DOGS in ethanol from Promega Corp., Madison, Wis., USA). A variety of methods are available for preparing liposomes e.g., U.S. Pat. Nos. 4,186,183, 4,217,344, 4,235,871, 4,261,975, 4,485,054, 4,501,728, 4,774,085, 4,837,028, 4,946,787; and PCT Publication No. WO 91/17424. The particles may also be composed in whole or in part of GRAS components. i.e., ingredients are those that are Generally Regarded As Safe (GRAS) by the US FDA. GRAS components useful as particle material include non-degradable food based particles such as cellulose.

[0060] The carrier domain can serve several functions. As discussed above, it may be useful for targeting the product to a specific region, such as a tissue. In that instance it could include a targeting agent such as a glycoprotein, an antibody, or a binding protein.

[0061] Further, the size of the carrier domain may be adjusted based on the particular use of the biomarker nanoparticle. For instance, the carrier domain may be designed to have a size greater than 5 nm. Particles, for instance, of greater than 5 nm are not capable of entering the urine, but rather, are cleared through the reticuloendothelial system (RES; liver, spleen, and lymph nodes). By being excluded from the removal through the kidneys any uncleaved biomarker nanoparticle will not be detected in the urine during the analysis step. Additionally, larger particles can be useful for maintaining the particle in the blood or in a tumor site where large particles are more easily shuttled through the vasculature. In some embodiments the carrier domain is 500 microns-5 nm, 250 microns-5 nm, 100 microns-5 nm, 10 microns-5 nm, 1 micron-5 nm, 100 nm-5 nm, 100 nm-10 nm, 50 nm-10 nm or any integer size range therebetween. In other instances the carrier domain is smaller than 5 nm in size. In such instance the biomarker nanoparticle will be

cleared into the urine. However, the presence of free detectable marker can still be detected for instance using mass spectrometry. In some embodiments the carrier domain is 1-5 nm, 2-5 nm, 3-5 nm, or 4-5 nm.

[0062] Optionally the carrier domain may include a biological agent. In one embodiment a biological agent could be incorporated in the carrier domain or it may make up the carrier domain. For instance, it may form the scaffold or platform that the proteolytic domain is attached to. Thus the compositions of the invention can achieve two purposes at the same time, the diagnostic methods and delivery of a therapeutic agent. In some embodiments the biological agent may be an enzyme inhibitor. In that instance the biological agent can inhibit proteolytic activity at a local site and the detectable marker can be used to test the activity of that particular therapeutic at the site of action. HIV is an example of the disease in which active proteases can be monitored. In this embodiment the composition may include a micro-particle or other delivery device carrying a protease inhibitor. The protease susceptible site may be sensitive to the HIV proteases such that feedback can be provided regarding the activity of the particular protease inhibitor.

Enzyme Susceptible Detectable Markers

[0063] The enzyme susceptible detectable marker is a portion of the modular structure that is connected to the carrier. An enzyme susceptible detectable marker, as used herein, is the portion of the modular structure that promotes the enzymatic reaction in the subject, causing the release of a detectable marker. The enzyme susceptible detectable marker is an enzyme susceptible domain linked to a detectable marker.

[0064] The enzyme susceptible site is dependent on enzymes that are active in a specific disease state. For instance, tumors are associated with a specific set of enzymes. If the disease state being analyzed is a tumor then the product is designed with an enzyme susceptible site that matches that of the enzyme expressed by the tumor or other diseased tissue. Alternatively, the enzyme specific site may be associated with enzymes that are ordinarily present but are absent in a particular disease state. In this example, a disease state would be associated with a lack or signal associated with the enzyme, or reduced levels of signal compared to a normal reference.

[0065] An enzyme, as used herein refers to any of numerous proteins produced in living cells that accelerate or catalyze the metabolic processes of an organism. Enzymes act on substrates. The substrate binds to the enzyme at a location called the active site just before the reaction catalyzed by the enzyme takes place. Enzymes include but are not limited to proteases, glycosidases, lipases, heparinases, phosphatases.

[0066] In some embodiments, an enzyme susceptible detectable marker comprises a substrate for a protease (e.g., an amino acid sequence that is cleaved by a protease). In some embodiments, the protease substrate is a substrate of a serine protease, cysteine protease, threonine protease, aspartic protease, glutamic protease, or a metalloprotease. Examples of serine protease substrates include but are not limited to SLKRYGGG (SEQ ID NO: 61; plasma kallikrein) and AAFRSRGA (SEQ ID NO: 62; kallikrein 1). Examples of cysteine protease substrates include but are not limited to xxFRFFxx (SEQ ID NO: 63; cathepsin B), QSVGFA (SEQ ID NO: 64; cathepsin B), and LGLEGAD (SEQ ID NO: 65;

cathepsin K). A non-limiting example of a threonine protease substrate is GPLD (SEQ ID NO: 66; subunit beta 1c). Examples of aspartic protease substrates include but are not limited to LGVLIV (SEQ ID NO: 67; cathepsin D) and GLVLVA (SEQ ID NO: 68; cathepsin E. Examples of metalloprotease substrates include but are not limited to PAALVG (SEQ ID NO: 69; MMP2) and GPAGLAG (SEQ ID NO: 70; MMP9).

[0067] The enzyme susceptible site may be optimized to provide both high catalytic activity (or other enzymatic activity) for specified target enzymes but to also release optimized detectable markers for detection. Patient outcome depends on the phenotype of individual diseases at the molecular level, and this is often reflected in expression of enzymes. The recent explosion of bioinformatics has facilitated exploration of complex patterns of gene expression in human tissues (Fodor, S. A. Massively parallel genomics. Science 277, 393-395 (1997)). Sophisticated computer algo-

rithms have been recently developed capable of molecular diagnosis of tumors using the immense data sets generated by expression profiling (Khan J, Wei J S, Ringner M, Saal L H, Ladanyi M, Westermann F, et al. Classification and diagnostic prediction of cancers using gene expression profiling and artificial neural networks. Nat Med 2001; 7:673-679.). This information can be accessed in order to identify enzymes and substrates associated with specific diseases. Based on this information the skilled artisan can identify appropriate enzyme or substrates to incorporate into the biomarker nanoparticle.

[0068] Table 1 provides a non-limiting list of enzymes associated with (either increased or decreased with respect to normal) disease and in some instances, the specific substrate. Table 2 provides a non-limiting list of substrates associated with disease or other conditions. Numerous other enzyme/substrate combinations associated with specific diseases or conditions are known to the skilled artisan and are useful according to the invention.

TABLE 1

Disease	Enzyme	Substrate
Cancer	MMP	collagens, gelatin, various ECM proteins
Cancer	MMP-2	type IV collagen and gelatin
Cancer	MMP-9	type IV and V collagens and gelatin
Cancer	kallikreins	kininogens, plasminogen
Cancer	cathepsins	broad spectrum of substrates
Cancer	plasminogen activator, tPA	Plasminogen
Cancer	ADAM (A Disintegrin And Metalloprotease, also MDC, Adamalysin)	various extracellular domains of transmembrane proteins
Pancreatic carcinoma	MMP-7	various, e.g. collagen 18, FasL, HLE, DCN, IGFBP-3, MAG, plasminogen, other MMPs
Pancreatic Cancer	ADAM9, ADAM15	various extracellular domains of transmembrane proteins
Prostate adenocarcinoma	Matriptase, a type II transmembrane serine protease	unspecific, cleaves after Lys or Arg residues
Prostate cancer	Kallikrein 3	kininogens, plasminogen
Prostate cancer	ADAM15	various extracellular domains of transmembrane proteins
Ovarian carcinoma	Kallikrein 6	kininogens, plasminogen
Epithelial-derived tumors (breast, prostate, ovarian, colon, oral)	Matriptase, a type II transmembrane serine protease	unspecific, cleaves after Lys or Arg residues
Ovarian Cancer	MMP-2, MMP-9, kallikrein-10 (hk-10)	type IV and V collagens and gelatin, kininogens, plasminogen
Breast, gastric, prostate cancer	cathepsins B, L and D	broad spectrum of substrates
Endometrial cancer	cathepsin B	unspecific cleavage of a broad spectrum of substrates without clear sequence specificity
esophageal adenocarcinoma	cathepsin B	unspecific cleavage of a broad spectrum of substrates without clear sequence specificity
Invasive cancers, metastases	type II integral serine proteases (dipeptidyl peptidase IV (DPP4/CD26), seprase/fibroblast activation protein alpha (FAPalpha) and related type II transmembrane prolyl serine peptidases))	
Invasive cancers, metastases	Seprase	various ECM proteins

TABLE 1-continued

Disease	Enzyme	Substrate
Viral Infections		
All Retroviruses	viral protease	precursor GagPol fusion
HIV	HIV protease (HIV PR, an aspartic protease)	precursor Gag and GagPol proteins
Hepatitis C	NS3 serine protease	viral precursor polyprotein
Dengue	Dengue protease	auocleavage (NS2B/NS3), NS3/NS4A and NS4B/NS5 cleavage
West Nile	NS2B/NS3pro	viral precursor polyprotein
Bacterial Infections		
<i>Legionella</i> spp.	zinc metalloprotease	Me-Arg-Pro-Tyr
Meningencephalitis	histolytic cysteine protease	
<i>Streptococcus pyogenes</i> (Group A <i>Streptococcus</i>)	streptococcal pyrogenic exotoxin B (SpeB)	extracellular matrix, immunoglobulins, complement components
<i>Clostridium difficile</i>	Cwp84	fibronectin, laminin, vitronectin and other ECM proteins
Alzheimer's disease	BACE-1,2 (Alzheimer secretase)	β -amyloid precursor protein
Stroke and recovery	MMP, tPA	
cardiovascular disease	Angiotensin Converting Enzyme (ACE)	angiotensin I, bradykinin
Atherosclerosis	cathepsin K, L, S	broad spectrum of substrates
arthritis	MMP-1	triple-helical fibrillar collagens
rheumatoid arthritis	thrombin	Osteopontin
osteoarthritis	thrombin	Osteopontin
osteoporosis/osteoarthritis	cathepsin K, S	broad spectrum of substrates
Arthritis, inflammatory joint disease	Aggrecanase (ADAMTS4, ADAMTS11)	aggrecans (proteoglycans)
thrombosis	factor Xa (thrombokinase)	Prothrombin
thrombosis	ADAMTS13	von Willebrand factor (vWF)
thrombosis	plasminogen activator, tPA	Plasminogen
Stress-induced Renal pressure natriuresis	Prostasin	epithelial Na channel subunits

TABLE 2

DISEASE	TARGET SUBSTRATE	ENZYME
Inflammation	Interleukin 1 beta	MMP-2, MMP-3, MMP-9, Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Pituitary gland dysfunction, abnormal bone density, growth disorders	IGFBP-3	MMP-1, MMP-3, MMP-9, Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer	TGF-beta	MMP-9, Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer, autoimmune disease	TNF	MMP-7, Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer, autoimmune disease	FASL	MMP-7, Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Wound healing, cardiac disease	HB-EGF	MMP-3, Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Pfeiffer syndrome	FGFR1	MMP-2, Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer	Decorin	MMP-2, MMP-3, MMP-7, Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer	Tumor associated carbohydrate antigens	Endoglycosidases

TABLE 2-continued

DISEASE	TARGET SUBSTRATE	ENZYME
Cancer	Sialyl Lewis ^a	O-glycanase
Cancer	Sialyl Lewis ^X	O-glycanase
Cancer/Rheumatoid Arthritis, pulmonary hypertension	VEGF	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer	EGF	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer	IL2	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer	IL6	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
inflammation/angiogenesis	IFN-γ	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer	TNF-α	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer	TGF-β	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
inflammation/angiogenesis, Rheumatoid Arthritis	PDGF	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer, Pulmonary fibrosis, Asthma	Fibroblast growth factor (FGF)	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer, Pulmonary hypertension	Brain-derived neurotrophic factor (BDNF)	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer, pulmonary cystadenoma	Interferon regulatory factors (IRF-1, IRF-2)	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer	MIF	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Inhibitor of tumor suppressors	GM-CSF	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Lymphomas/carcinomas, alveolar proteinosis	M-CSF	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cancer invasion	IL-12	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Chemical carcinogenesis, multiple sclerosis, rheumatoid arthritis, Crohn's disease	IL-15	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Natural Killer T cell leukemias, inflammatory bowel disease, rheumatoid arthritis	Tissue inhibitor of MMPs (TIMPs)	Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cirrhosis	Collagen I, III	MMP-1, MMP-8, Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C
Cirrhosis	Collagen IV, V	MMP-2, Trypsin, chymotrypsin, pepsin, Lys-C, Glu-C, Asp-N, Arg-C

[0069] In some embodiments, the enzyme susceptible domain is a lymph node specific enzyme susceptible domain. As used herein, “lymph node specific enzyme susceptible domain” refers to an enzyme susceptible domain that is capable of being cleaved by a protease that is present (or upregulated) in a lymph node of a subject having a disease (e.g., cancer, metastatic cancer, an infection with a pathogenic agent, etc.). For example, certain cancers (e.g. metastatic cancers) are associated with upregulation of specific enzymes (e.g. ADAM28, MMP9, MMP12, ACE, C2, ADAMTS5, HTRA4, MMP16, etc.) in lymph nodes. In some embodiments, the lymph node specific enzyme susceptible domain comprises a cancer substrate, such as a metastatic cancer substrate. Examples of cancer substrates include but are not limited to substrates targeted by ADAM28, MMP9, MMP12, ACE, C2, ADAMTS5, HTRA4, or MMP16.

[0070] In some embodiments the enzyme susceptible detectable marker is a peptide that is susceptible to cleavage by an enzyme or causes cleavage of a substrate associated with a disease or condition. In some embodiments, the lymph node specific enzyme susceptible domain comprises

an immune-associated substrate. Examples of immune-associated substrates include substrates for proteases such as granzymes A (e.g., ASPRAGGK; SEQ ID NO: 71), B (e.g., YEADSLLEE; SEQ ID NO: 72), K (e.g., YQYRAL; SEQ ID NO: 73), and Cathepsin D (LGVLLIV; SEQ ID NO: 67).

[0071] An enzyme susceptible detectable marker may be attached directly to the carrier. For instance it may be coated directly on the surface of microparticles using known techniques. Alternatively if the carrier is a protein material it may be directly connected through a peptide bond. Additionally, the enzyme susceptible detectable marker may be connected to the carrier domain through the use of a linker. As used herein “linked” or “linkage” means two entities are bound to one another by any physicochemical means. Any linkage known to those of ordinary skill in the art, covalent or non-covalent, is embraced. Thus, in some embodiments the carrier has a linker attached to an external surface, which can be used to link the enzyme susceptible detectable marker. Another molecule can also be attached to the linker. In some embodiments, two molecules are linked using a transpeptidase, for example Sortase A.

[0072] The enzyme susceptible detectable marker is preferably a polymer made up of a plurality of chemical units. A “chemical unit” as used herein is a building block or monomer which may be linked directly or indirectly to other building blocks or monomers to form a polymer.

Detectable Markers

[0073] The detectable marker is capable of being released from the biomarker nanoparticle when exposed to an enzyme in vivo. The detectable marker once released is free to travel to a remote site for detection. A remote site is used herein to refer to a site in the body that is distinct from the bodily tissue housing the enzyme where the enzymatic reaction occurs. In some embodiments, the bodily tissue housing the enzyme where the enzymatic reaction occurs is a lymph node.

[0074] Modification of the enzyme susceptible domain by an enzyme in vivo, results in the production of a detectable marker. Alternatively, when the enzyme susceptible detectable marker is an enzyme the enzyme cleaves an endogenous substrate producing a detectable marker from the endogenous substrate. The detectable marker is a detectable molecule. It can be part of the enzyme susceptible domain, e.g. the piece that is released or added upon cleavage or it can be a separate entity. Preferably the detectable marker is composed of two ligands joined by a linker, as described above. The detectable marker may be comprised of, for instance one or more of a peptide, nucleic acid, small molecule, fluorophore/quencher, carbohydrate, particle, radiolabel, MRI-active compound, inorganic material, organic material, with encoded characteristics to facilitate optimal detection.

[0075] In some embodiments, a lymph node specific enzyme susceptible detectable marker comprises a capture ligand is a molecule that is capable of being captured by a binding partner. The detection ligand is a molecule that is capable of being detected by any of a variety of methods. While the capture ligand and the detection ligand will be distinct from one another in a particular detectable marker, the class of molecules that make up capture and detection ligands overlap significantly. For instance, many molecules are capable of being captured and detected. In some instances these molecules may be detected by being captured or capturing a probe. The capture and detection ligand each independently may be one or more of the following: a protein, a peptide, a polysaccharide, a nucleic acid, a fluorescent molecule, or a small molecule, for example. In some embodiments the detection ligand or the capture ligand may be, but is not limited to, one of the following: Alexa488, TAMRA, DNP, fluorescein, Oregon Green, Texas Red, Dansyl, BODIPY, Alexa405, Cascade Blue, Lucifer Yellow, Nitrotyrosine, HA-tag, FLAG-tag, His-tag, Myc-tag, V5-tag, S-tag, biotin or streptavidin. In some embodiments, the capture ligand and a detection ligand are connected by a linker. The purpose of the linker is prevent steric hindrance between the two ligands. Thus, the linker may be any type of molecule that achieves this. The linker may be, for instance, a polymer such as PEG, a protein, a peptide, a polysaccharide, a nucleic acid, or a small molecule. In some embodiments the linker is a protein of 10-100 amino acids in length. In other embodiments the linker is GluFib (SEQ ID NO: 1). Optionally, the linker may be 8 nm-100 nm, 6 nm-100 nm, 8 nm-80 nm, 10 nm-100 nm, 13 nm-100 nm, 15 nm-50 nm, or 10 nm-50 nm in length.

[0076] In some embodiments, the detectable marker is a ligand encoded reporter. Without wishing to be bound by any particular theory, a ligand encoded reporter binds to a target molecule (e.g., a target molecule present in a lymph node), allowing for detection of the target molecule at a site remote from where the ligand encoded reporter bound to the target (e.g., at a site remote from a lymph node). In some embodiments, a ligand encoded reporter binds to a target molecule associated with a pathogenic agent. As used herein, “pathogenic agent” refers to a molecule that is indicative of the presence of a particular infectious agent (e.g., a virus, bacterium, parasite, etc.). Examples of pathogenic agents include viral proteins, bacterial proteins, biological toxins, and parasite-specific proteins (e.g., *S. mansoni* OVA protein). In some embodiments, a detectable marker is a mass encoded reporter, for example an iCORE as described in WO2012/125808, filed Mar. 3, 2012, the entire contents of which are incorporated herein by reference. Upon arrival in the diseased microenvironment, the iCORE agents interface with aberrantly active proteases to direct the cleavage and release of surface-conjugated, mass-encoded peptide substrates into host urine for detection by mass spectrometry (MS) as synthetic biomarkers of disease.

[0077] The detectable marker may be detected by any known detection methods to achieve the capture/detection step. A variety of methods may be used, depending on the nature of the detectable marker. Detectable markers may be directly detected, following capture, through optical density, radioactive emissions, nonradiative energy transfers, or detectable markers may be indirectly detected with antibody conjugates, affinity columns, streptavidin-biotin conjugates, PCR analysis, DNA microarray, and fluorescence analysis.

[0078] The capture assay in some embodiments involves a detection step selected from the group consisting of an ELISA, including fluorescent, colorimetric, bioluminescent and chemiluminescent ELISAs, a paper test strip or LFA, bead-based fluorescent assay, and label-free detection, such as surface plasmon resonance (SPR). The capture assay may involve, for instance, binding of the capture ligand to an affinity agent.

[0079] The analysis step may be performed directly on the biological sample or the signature component may be purified to some degree first. For instance, a purification step may involve isolating the detectable marker from other components in the biological sample. Purification steps include methods such as affinity chromatography. As used herein an “isolated molecule” or “purified molecule” is a detectable marker that is isolated to some extent from its natural environment. The isolated or purified molecule need not be 100% pure or even substantially pure prior to analysis.

[0080] The methods for analysing detectable markers by identifying the presence of a detectable marker may be used to provide a qualitative assessment of the molecule (e.g., whether the detectable marker is present or absent) or a quantitative assessment (e.g., the amount of detectable marker present to indicate a comparative activity level of the enzymes. The quantitative value may be calculated by any means, such as, by determining the percent relative amount of each fraction present in the sample. Methods for making these types of calculations are known in the art.

[0081] The detectable marker may be labeled. For example, a label may be added directly to a nucleic acid when the isolated detectable marker is subjected to PCR. For

instance, a PCR reaction performed using labeled primers or labeled nucleotides will produce a labeled product. Labeled nucleotides (e.g., fluorescein-labeled CTP) are commercially available. Methods for attaching labels to nucleic acids are well known to those of ordinary skill in the art and, in addition to the PCR method, include, for example, nick translation and end-labeling.

[0082] Labels suitable for use in the methods of the present invention include any type of label detectable by standard means, including spectroscopic, photochemical, biochemical, electrical, optical, or chemical methods. Preferred types of labels include fluorescent labels such as fluorescein. A fluorescent label is a compound comprising at least one fluorophore. Commercially available fluorescent labels include, for example, fluorescein phosphoramidides such as fluoreprime (Pharmacia, Piscataway, N.J.), fluoredit (Millipore, Bedford, Mass.), FAM (ABI, Foster City, Calif.), rhodamine, polymethadine dye derivative, phosphores, Texas red, green fluorescent protein, CY3, and CY5. Polynucleotides can be labeled with one or more spectrally distinct fluorescent labels. "Spectrally distinct" fluorescent labels are labels which can be distinguished from one another based on one or more of their characteristic absorption spectra, emission spectra, fluorescent lifetimes, or the like. Spectrally distinct fluorescent labels have the advantage that they may be used in combination ("multiplexed"). Radionuclides such as ^3H , ^{125}I , ^{35}S , ^{14}C , or ^{32}P are also useful labels according to the methods of the invention. A plurality of radioactively distinguishable radionuclides can be used. Such radionuclides can be distinguished, for example, based on the type of radiation (e.g. α , β , or δ radiation) emitted by the radionuclides. The ^{32}P signal can be detected using a phosphorimager, which currently has a resolution of approximately 50 microns. Other known techniques, such as chemiluminescence or colorimetric (enzymatic color reaction), can also be used.

[0083] Quencher compositions in which a "donor" fluorophore is joined to an "acceptor" chromophore by a short bridge that is the binding site for the enzyme may also be used. The signal of the donor fluorophore is quenched by the acceptor chromophore through a process believed to involve resonance energy transfer (RET). Cleavage of the peptide results in separation of the chromophore and fluorophore, removal of the quench, and generation of a subsequent signal measured from the donor fluorophore.

[0084] The disease or condition assessed according to the methods of the invention is any disease or condition that is associated with an enzyme. For instance, cancer, cardiovascular disease, arthritis, viral, bacterial, parasitic or fungal infection, Alzheimer's disease emphysema, thrombosis, hemophilia, stroke, organ dysfunction, any inflammatory condition, vascular disease, parenchymal disease, or a pharmacologically-induced state are all known to be associated with enzymes. A pharmacologically induced state is a condition in which enzyme inhibitors and other agents directly or indirectly affect enzyme activities. Thus each of these can be assessed or monitored or studied according to methods of the invention.

Methods

[0085] It is useful to be able to differentiate non-metastatic primary tumors from metastatic tumors, because metastasis is a major cause of treatment failure in cancer patients. If metastasis can be detected early, it can be treated aggres-

sively in order to slow the progression of the disease. Metastasis is a complex process involving detachment of cells from a primary tumor, movement of the cells through the circulation, and eventual colonization of tumor cells at local or distant tissue sites. Additionally, it is desirable to be able to detect a predisposition for development of a particular cancer such that monitoring and early treatment may be initiated. For instance, an extensive cytogenetic analysis of hematologic malignancies such as lymphomas and leukemias have been described, see e.g., Solomon et al., Science 254, 1153-1160, 1991. Early detection or monitoring using the non-invasive methods of the invention may be useful.

[0086] Solid tumors progress from tumorigenesis through a metastatic stage and into a stage at which several different active proteases can be involved. Some protease are believed to alter the tumor such that it can progress to the next stage, i.e., by conferring proliferative advantages, the ability to develop drug resistance or enhanced angiogenesis, proteolysis, or metastatic capacity.

[0087] Accordingly, in some aspects, the disclosure provides a method for determining metastatic stage of a tumor comprising administering to the lymph node of a subject having a tumor a lymph node biomarker nanoparticle, wherein the lymph node biomarker nanoparticle comprises a modular structure having a carrier domain linked to a lymph node specific enzyme susceptible detectable marker, wherein the lymph node specific enzyme susceptible detectable marker is comprised of an enzyme susceptible domain linked to a detectable marker whereby the detectable marker is capable of being released from the biomarker nanoparticle when exposed to a metastatic tumor-associated enzyme in a lymph node; obtaining a urine sample from the subject for detection of the detectable marker; and, analyzing the urine sample using a capture assay in order to detect the presence of the detectable marker, wherein the presence of the detectable marker in the urine sample is indicative of the subject having a metastatic tumor.

[0088] In addition to harboring nascent metastases, the LN is the site of numerous immune processes that have proven to be critical to anti-tumor therapies. For example, an emerging paradigm in oncology is the use of immunotherapies, whereby a patient's own immune system is directed against the tumor. Checkpoint blockade inhibitors and anti-tumor monoclonal antibodies have proven to be remarkably effective in the clinic for a diverse array of indications, and will likely become incorporated in standard of care for oncology. Anti-tumor immune responses are orchestrated in the tumor-draining LN, the same nodes that harbor metastases, which contain a trove of immunological activity. Thus, in some embodiments, an enzyme susceptible domain linked to a detectable marker releases the detectable marker when exposed to an enzyme associated with an anti-tumor response (e.g., an anti-tumor response resulting from treatment with a checkpoint blockade inhibitor or an anti-tumor monoclonal antibody). In some embodiments, detecting a detectable marker is useful for assessing the endogenous immune response prior to immunotherapy, or assessing efficacy of immunotherapy during administration, for example by having an enzyme-susceptible substrate with readout that is in the urine.

[0089] In some embodiments, a protease detected by methods and compositions described herein is associated with a pathogenic agent and is thus indicative of infection in a subject. Accordingly, in some aspects, the disclosure

provide a method for identifying a pathogenic agent comprising administering to the lymph node of a subject infected or suspected of being infected with a pathogenic agent a lymph node biomarker nanoparticle, wherein the lymph node biomarker nanoparticle comprises a modular structure having a carrier domain linked to a lymph node specific enzyme susceptible detectable marker, wherein the lymph node specific enzyme susceptible detectable marker is comprised of an enzyme susceptible domain linked to a detectable marker whereby the detectable marker is capable of being released from the biomarker nanoparticle when exposed to an enzyme associated with a pathogenic agent; obtaining a urine sample from the subject for detection of the marker; and, analyzing the urine sample using a capture assay in order to detect the presence of the detectable marker, wherein the presence of the detectable marker in the urine sample is indicative of the subject being infected with the pathogenic agent.

[0090] Examples of infectious diseases that can be detected by methods and compositions of the disclosure include but are not limited to bacterial infections, viral infections, fungal infections, and parasitic infections.

Administration

[0091] Compositions described herein can be administered to any suitable subject. As used herein, a subject is a human, non-human primate, cow, horse, pig, sheep, goat, dog, cat, or rodent. In all embodiments human subjects are preferred. In aspects of the invention pertaining to cancer diagnosis in general the subject preferably is a human suspected of having cancer, or a human having been previously diagnosed as having cancer. Methods for identifying subjects suspected of having cancer may include physical examination, subject's family medical history, subject's medical history, biopsy, or a number of imaging technologies such as ultrasonography, computed tomography, magnetic resonance imaging, magnetic resonance spectroscopy, or positron emission tomography.

[0092] As used herein, a biological sample is a tissue sample. The biological sample may be examined in the body, for instance, by detecting a label at the site of the tissue, i.e. urine. Alternatively the biological sample may be collected from the subject and examined in vitro. Biological samples include but are not limited to urine, blood, saliva, or mucous secretion. In preferred embodiments the tissue sample is obtained non-invasively, such as the urine.

[0093] A "plurality" of elements, as used throughout the application refers to 2 or more of the elements.

[0094] The biomarker nanoparticles of the invention are administered to the subject in an effective amount for detecting enzyme activity. An "effective amount", for instance, is an amount necessary or sufficient to cause release of a detectable level of detectable marker in the presence of an enzyme. The effective amount of a compound of the invention described herein may vary depending upon the specific compound used, the mode of delivery of the compound, and whether it is used alone or in combination. The effective amount for any particular application can also vary depending on such factors as the disease being assessed or treated, the particular compound being administered, the size of the subject, or the severity of the disease or condition as well as the detection method. One of ordinary skill in the art can empirically determine the effective amount of a particular molecule of the invention without necessitating

undue experimentation. Combined with the teachings provided herein, by choosing among the various active compounds and weighing factors such as potency, relative bioavailability, patient body weight, severity of adverse side-effects and preferred mode of administration, an effective regimen can be planned.

[0095] Pharmaceutical compositions of the present invention comprise an effective amount of one or more agents, dissolved or dispersed in a pharmaceutically acceptable carrier. The phrases "pharmaceutical or pharmacologically acceptable" refers to molecular entities and compositions that do not produce an adverse, allergic or other untoward reaction when administered to an animal, such as, for example, a human, as appropriate. Moreover, for animal (e.g., human) administration, it will be understood that preparations should meet sterility, pyrogenicity, general safety and purity standards as required by FDA Office of Biological Standards.

[0096] As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, surfactants, antioxidants, preservatives (e.g., antibacterial agents, antifungal agents), isotonic agents, absorption delaying agents, salts, preservatives, drugs, drug stabilizers, gels, binders, excipients, disintegration agents, lubricants, sweetening agents, flavoring agents, dyes, such like materials and combinations thereof, as would be known to one of ordinary skill in the art (see, for example, Remington's Pharmaceutical Sciences (1990), incorporated herein by reference). Except insofar as any conventional carrier is incompatible with the active ingredient, its use in the therapeutic or pharmaceutical compositions is contemplated. The agent may comprise different types of carriers depending on whether it is to be administered in solid, liquid or aerosol form, and whether it need to be sterile for such routes of administration as injection.

[0097] Aspects of the disclosure relate to the discovery that, in some embodiments, lymph node biomarker nanoparticles circulate and sense the lymph node microenvironment after systemic administration to a subject. In some embodiments, the systemic administration is injection, optionally subcutaneous injection. Preferably the material is injected into the body but could also be administered by other routes. For instance, the compounds of the present invention can be administered intravenously, intradermally, intraarterially, intralesionally, intratumorally, intracranially, intraarticularly, intraprostatically, intrapleurally, intratracheally, intranasally, intravitreally, intravaginally, intrarectally, topically, intratumorally, intramuscularly, intraperitoneally, subcutaneously, subconjunctival, intravesicularly, mucosally, intrapericardially, intraumbilically, intraocularly, orally, topically, locally, inhalation (e.g., aerosol inhalation), injection, infusion, continuous infusion, localized perfusion bathing target cells directly, via a catheter, via a lavage, in creams, in lipid compositions (e.g., liposomes), or by other method or any combination of the forgoing as would be known to one of ordinary skill in the art (see, for example, Remington's Pharmaceutical Sciences (1990), incorporated herein by reference).

Example

[0098] Lymph nodes adjacent to tumors integrate several useful diagnostic signals and may serve as the first stop for metastatic tumor cells, and thus are valuable in staging the invasiveness of a patient's cancer. Nodes also house the

coordinated immune response against the tumor and, if molecularly probed, could provide a snapshot view of the current state of tumor immunity in a patient. In spite of this potentially rich source of information, the only current way to functionally probe lymph nodes is via invasive surgical removal, associated with significant morbidity to patients, and subsequent traditional histopathological analysis. Less invasive imaging modalities can help determine whether tumor cells are present in the lymph node, but they fail to provide information regarding invasiveness or immune activity. If clinicians had access to these data, they could make more informed decisions on: whether surgical lymph node excision is required, which nodes to remove, how invasive the tumor is, how well the patient may respond to immunotherapy, and whether additional interventions should be prescribed, etc.

[0099] The following Examples describe some embodiments of approaches for highly multiplexed protease-sensitive nanosensors developed to probe the multitude of signals at the lymph node. Protease cleavage of substrates is assessed via urine measurement of reporter fragments to provide a minimally invasive snapshot of the current state of the node. Peptide substrates are tethered (e.g., conjugated) to serum albumin, which serves the dual purpose of targeting the lymph node via high molecular weight-mediated uptake and excluding injected material from renal filtration prior to proteolytic activation. Only after substrates encounter their cognate proteases are they liberated from their protein carrier, enter the bloodstream and get concentrated in the urine. The development of these urinary monitoring tools for lymph node activity enables physicians to noninvasively monitor cancer progression, stage invasiveness, and understand the immune response.

Lymph Node Specific Synthetic Biomarkers

[0100] Aberrantly expressed proteases are candidate enzymes for cancer detection and analysis because they play critical roles in many cancers. Additionally, proteases are involved in many immune processes, including immune cell trafficking to and from the lymph node and target cell killing (FIG. 1). A set of protease-sensitive substrates is delivered to the lymph node using recently acquired knowledge on trafficking carriers to lymph nodes. Upon encountering their cognate proteases, the protease-sensitive substrates are cleaved and reporter fragments are excreted into urine,

providing a non-invasive diagnostic readout. A subset of the delivered substrates will be responsive to proteases enriched in different stages of tumor invasiveness (e.g., metastasis), and provide the clinician with a high resolution, functionality driven snapshot of lymph node (LN) metastases. The remaining substrates are reactive against immunological proteolytic activity, providing oncologists with an understanding of the ongoing anti-tumor immune response. Together, the two substrate sets provide next-generation functional diagnostics for LN monitoring.

[0101] This Example describes multiplexed, protease nanosensors with urinary readouts that accumulate in primary tumors called ‘synthetic biomarkers’. This example also describes protein carriers that have optimized pharmacokinetic properties such that there is minimal accumulation in the blood stream and other high background organs such as the liver, following subcutaneous injection. The protease nanosensors can be designed to be cleaved by various metastasis-associated proteases. Proteolytic cleavage liberates urinary fragments, which can be detected by mass spectrometry (FIGS. 2A-2B). In some embodiments, delivery of multiplexed, proteolytically-activated sensors described by the disclosure to tumor-draining lymph nodes is useful for diagnosis and prognosis of LN tumor metastasis, or LN immune response, by 1) detecting and characterizing LN metastases via the presence of aberrantly expressed proteases in migratory tumor cells, and 2) defining the localized response via the characterization of immune-associated proteolytic activity. Substrate libraries that profile the proteases involved in tumor metastasis in the lymph node and immune-associated proteases are also produced.

Identification of Protease Signatures for LN Metastases and Immunological Activity

[0102] Candidate proteases are identified by analyzing available RNA transcript data from melanoma samples (e.g., FIG. 3A) to identify lymph node metastasis specific protease profiles. Analysis of these data sets identified candidate proteases including but not limited to ADAM28, MMP9, and MMP12 (FIG. 3B). Immune-related proteases are also identified, such as proteases involved in immune cell trafficking and target cell killing, e.g., granzymes A, B, K and Cathepsin D (FIG. 1). Additional candidate proteases upregulated in lymph nodes of melanoma samples versus primary samples are shown in Table 3.

TABLE 3

Proteases upregulated in RLN samples vs Primary samples from TCGA (the Cancer Genome Atlas) melanoma.					
Gene Name	Score(d)	Numerator(r)	Denominator(s + s0)	Fold Change	q-value(%)
ADAM28	5.6187932246625	291.571949602122	51.8922725830751	5.27392286943209	0
MMP9	5.02194664053601	5776.7374005305	1150.29844281936	3.71777599185352	0
ACE	4.98939405175635	492.792108753316	98.7679272555842	2.04458307299482	0
ADAMDEC1	4.48371075384786	735.351127320955	164.005032369647	4.89371810199986	0
GZMK	4.31642234597524	736.148209549072	170.545917554958	4.44288410276132	0
MMP12	4.07535661102745	292.520225464191	71.7778229941068	4.91482479066734	0
GZMA	3.78388726532043	443.168103448276	117.119795695273	2.60786613495973	0
ADAMTS5	3.37780765594101	188.777519893899	55.8875871933888	2.15412745100027	0
HTRA4	3.20241223082401	36.8902519893899	11.5195200774941	2.59392862770941	0
C2	2.96774560381754	4676.8775596817	1575.90244718605	2.05768709894241	0
REN	2.94443698992391	11.9429708222812	4.05611356709311	7.33708655876144	0
CPA5	2.67466496680941	7.01442307692308	2.62254269748429	3.85652752760592	4.76798637718178
CELA1	2.55069771166091	0.875	0.343043393970129	8	4.76798637718178
MMP16	2.46556009729632	901.373342175066	365.585630284776	2.05725788449019	4.76798637718178
CFI	2.32517417765658	1254.27884615385	539.434360748823	2.12317998260705	4.76798637718178

TABLE 3-continued

Proteases upregulated in RLN samples vs Primary samples from TCGA (the Cancer Genome Atlas) melanoma.					
Gene Name	Score(d)	Numerator(r)	Denominator(s + s0)	Fold Change	q-value(%)
KLK3	1.90207476848199	51.1147214854111	26.8731399692583	25.8407992265549	9.34267600934268
CPA1	1.84692635626155	1.40285145888594	0.759560040999966	4.94315004659832	10.636277302944
ADAMTS6	1.80305667900417	59.3975464190981	32.9426950970302	2.10526835347758	10.636277302944
CPXM1	1.57925185321327	1431.01956233422	906.13764956017	2.18816540778367	15.1761517615176
PRSS33	1.22734278806856	680.528183023873	554.472792474549	2.50013631137758	22.2222222222222
CNDP1	1.13296586861481	416.114088196286	367.278573629969	2.02808193732172	22.2222222222222
CPB1	1.02787802609301	8.97049071618037	8.72719378025565	2.09370578485669	27.7676583687513
KLK15	1.01409062889863	2.18866047745358	2.15824938628079	2.7375625164517	27.7676583687513
CELA2B	0.867216607521151	0.222148541114058	0.25616269244318	12.551724137931	33.2033788174139
RELN	0.806346488754898	345.229442970822	428.140319062963	2.22371718026467	33.2033788174139
PRSS58	0.293044921192387	0.0593501326259947	0.20252912892843	7.17241379310345	34.1189674523008

Optimization and Characterization of In Vivo Pharmacokinetic Properties of Protein-Delivered Synthetic Biomarkers

[0103] It has been observed that subcutaneous injection of protein carriers enables robust trafficking to the lymph nodes in the vicinity of that injection. In particular, data indicate that serum albumin is an exceptionally effective chaperone to deliver peptides to lymph nodes. Synthetic peptides conjugated to albumin are recombinantly produced by reacting serum albumin functionalized with the C-terminal Sortase A recognition motif LPSTG with (G)5-modified protease-sensitive peptide probes to albumin (FIG. 2A). Sortase A is a transpeptidase that enables robust bioconjugation between expressed proteins and synthetic peptides. Here, albumin serves a dual purpose, as it both improves LN uptake and anchors the synthetic biomarkers (e.g., urinary synthetic biomarkers) to a protein that is renally excluded (e.g., serum albumin) prior to proteolytic processing.

[0104] The pharmacokinetic properties of albumin-chaperoned synthetic biomarkers are tested by injecting them into a subject subcutaneously and measuring blood accumulation and end-point biodistribution. Pharmacokinetic data indicate over 30-fold higher average accumulation in inguinal lymph nodes than the liver (FIGS. 4A-4B).

[0105] Other carrier proteins can also be used, for example, antibodies that efficiently drain to the lymph node. Antibody-delivered synthetic biomarkers, in some embodiments, exhibit improved sensitivity due to targeting characteristics and may be multifunctional in their ability to both detect and deplete LN metastases.

[0106] Synthetic biomarker accumulation was also measured in the urine. Healthy mice were administered Albumin-B7 peptide (Albumin-GPLGVRGKGK(Biotin)eGvndneeGffsarK(FAM)) (SEQ ID NO: 75) where the protease cleavable substrate is PLGVRGK (SEQ ID NO: 76) and urinary reporter is ligand coded K(Biotin)eGvndneeGffsarK(FAM) (SEQ ID NO: 77) for detection with ELISA. Lowercase residues indicate *D*-forms of each amino acid. FIG. 5 shows urine concentration of reporters after subcutaneous injection of Albumin-B7 in healthy mice shows peak urine signal at 3 hours post-injection with detectable signal 24 hours post-injection.

Urinary Monitoring of Vaccine Efficacy

[0107] Mice were subcutaneously injected with a cancer-specific peptide vaccine amph-EGP (DSPE-PEG2000-maleimide conjugated to CAVGALEGPRNQDWLGVPRL

(SEQ ID NO: 78)), or PBS, and lymph node-targeting adjuvant (lipo-CpG (DSPE conjugated to class B CpG 1826: 5'-tccatgacgttctctgacgtt-3'; SEQ ID NO: 79)) to stimulate immune response in the lymph nodes. Mice were later boosted to engage both innate and adaptive immunity. Subsequently, mice were administered a LN-targeting pro-diagnostic reagent comprising a LN-specific enzyme susceptible domain (e.g., protease substrate). Cleavage of the pro-diagnostic reagent by metalloproteases in the LN results in production of signature molecules (ligand encoded tags) that are released into the urine of the subject (e.g., mouse). Urine was collected from the mice 3 hours after injection. Reporter signal was quantified by ELISA. Data indicate that reporter signal in vaccinated mice was significantly increased compared to PBS-injected mice, as shown in FIG. 6.

Ex Vivo Peptide Screen of LN from Vaccinated Mice and Control Mice

[0108] Mice were vaccinated in the same manner as described above. Lymph nodes from vaccinated or non-vaccinated mice were harvested. The harvested lymph nodes were homogenized and added to the 58 fluorogenic protease substrates (SEQ ID NOs: 2-59) in 384 well plates. Fluorescent signal was monitored over the period of several hours for each substrate in the well plates. Fluorescence of reporter molecules in lymph nodes of vaccinated mice was compared to non-vaccinated mice (injected with PBS) and reported as the fold difference in cleavage of each substrate between vaccinated and control mice. Data indicate that the two highest cleaved substrates in the LN of vaccinated mice are PQ12 (GGVPRG; SEQ ID NO: 74) and Q10 (f(Pip)KSGGG, where f is a D stereoisomer of Phe and Pip is pipecolic acid; SEQ ID NO: 80) (FIG. 7). The substrate used urinary monitoring experiment described above is referred to as Q7 (PLGVRGK; SEQ ID NO: 76).

Multiplexed Synthetic Biomarker Library for Lymph Node Monitoring

[0109] One embodiment of an approach for mass-encoding protease substrate-urinary reporter tandems is described. A 10-plex albumin-chaperoned library (e.g., an albumin-chaperoned library having mass-encoded reporters) that responds to both metastasis-associated and immune-associated proteases is produced. These albumin-synthetic biomarkers are tested in murine models of melanoma. Melanoma cells are injected into the flank of mice and allowed to metastasize to the lymph node. Sensors are infused into mice and urine is collected at various timepoints. Cleavage pat-

terns are monitored from the mass-encoded reporters using LC-MS/MS and analyzed for evolving signatures that classify lymph node metastasis.

[0110] To demonstrate classification between different indications, the immune system of non-tumor bearing mice is examined. Similarly, the proteolytic signatures identified by the platform that identify immune response are exam-

ined. In some cases, the signatures identified from metastasis are non-overlapping from the signatures identified from immune stimulation.

[0111] The specificity of lymph node sampling is tested using a mouse model of lung metastatic cancer as a negative control. There is minimal lymph node involvement in this model because the sensors should not respond to increased proteolysis occurring in the lungs.

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REGION	1..12	
	note = Synthetic Polypeptide	
SITE	1	
	note = misc_feature - Modified with 5FAM	
REGION	11..12	
	note = misc_feature - Modified with CPQ2-PEG2	
source	1..12	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 19		
GGSEDELQTI KC		12
SEQ ID NO: 20	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
REGION	1..12	
	note = Synthetic Polypeptide	
SITE	1	
	note = misc_feature - Modified with 5FAM	
REGION	11..12	
	note = misc_feature - Modified with CPQ2-PEG2	
source	1..12	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 20		
GGFPHLHSKI KC		12
SEQ ID NO: 21	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
REGION	1..12	
	note = Synthetic Polypeptide	
SITE	1	

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REGION	note = misc_feature - Modified with 5FAM 11..12	
source	note = misc_feature - Modified with CPQ2-PEG2 1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 21 GGGHARLVHV KC		12
SEQ ID NO: 22 FEATURE REGION	moltype = AA length = 12 Location/Qualifiers 1..12 note = Synthetic Polypeptide	
SITE	1 note = misc_feature - Modified with 5FAM	
REGION	11..12 note = misc_feature - Modified with CPQ2-PEG2	
source	1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 22 GGHIANVERV KC		12
SEQ ID NO: 23 FEATURE REGION	moltype = AA length = 12 Location/Qualifiers 1..12 note = Synthetic Polypeptide	
SITE	1 note = misc_feature - Modified with 5FAM	
REGION	11..12 note = misc_feature - Modified with CPQ2-PEG2	
source	1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 23 GGKAAATQKK KC		12
SEQ ID NO: 24 FEATURE REGION	moltype = AA length = 12 Location/Qualifiers 1..12 note = Synthetic Polypeptide	
SITE	1 note = misc_feature - Modified with 5FAM	
REGION	11..12 note = misc_feature - Modified with CPQ2-PEG2	
source	1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 24 GGLATASTMD KC		12
SEQ ID NO: 25 FEATURE REGION	moltype = AA length = 12 Location/Qualifiers 1..12 note = Synthetic Polypeptide	
SITE	1 note = misc_feature - Modified with 5FAM	
REGION	11..12 note = misc_feature - Modified with CPQ2-PEG2	
source	1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 25 GGLGPKGQTG KC		12
SEQ ID NO: 26 FEATURE REGION	moltype = AA length = 12 Location/Qualifiers 1..12 note = Synthetic Polypeptide	
SITE	1 note = misc_feature - Modified with 5FAM	
REGION	11..12 note = misc_feature - Modified with CPQ2-PEG2	
source	1..12 mol_type = protein organism = synthetic construct	

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SEQUENCE: 26
GGLSLPETGE KC 12

SEQ ID NO: 27 moltype = AA length = 12
FEATURE Location/Qualifiers
REGION 1..12
note = Synthetic Polypeptide
SITE 1
note = misc_feature - Modified with 5FAM
REGION 11..12
note = misc_feature - Modified with CPQ2-PEG2
source 1..12
mol_type = protein
organism = synthetic construct

SEQUENCE: 27
GGNLAGILKE KC 12

SEQ ID NO: 28 moltype = AA length = 12
FEATURE Location/Qualifiers
REGION 1..12
note = Synthetic Polypeptide
SITE 1
note = misc_feature - Modified with 5FAM
REGION 11..12
note = misc_feature - Modified with CPQ2-PEG2
source 1..12
mol_type = protein
organism = synthetic construct

SEQUENCE: 28
GGNPGMSEPV KC 12

SEQ ID NO: 29 moltype = AA length = 11
FEATURE Location/Qualifiers
REGION 1..11
note = Synthetic Polypeptide
SITE 1
note = misc_feature - Modified with 5FAM
REGION 11
note = misc_feature - Modified with CPQ2-PEG2
source 1..11
mol_type = protein
organism = synthetic construct

SEQUENCE: 29
GGPFGCHAKK C 11

SEQ ID NO: 30 moltype = AA length = 11
FEATURE Location/Qualifiers
REGION 1..11
note = Synthetic Polypeptide
SITE 1
note = misc_feature - Modified with 5FAM
REGION 10..11
note = misc_feature - Modified with CPQ2-PEG2
source 1..11
mol_type = protein
organism = synthetic construct

SEQUENCE: 30
GGPLGLRWWK C 11

SEQ ID NO: 31 moltype = AA length = 12
FEATURE Location/Qualifiers
REGION 1..12
note = Synthetic Polypeptide
SITE 1
note = misc_feature - Modified with 5FAM
REGION 11..12
note = misc_feature - Modified with CPQ2-PEG2
source 1..12
mol_type = protein
organism = synthetic construct

SEQUENCE: 31
GGQMGVMQGV KC 12

SEQ ID NO: 32 moltype = AA length = 12
FEATURE Location/Qualifiers
REGION 1..12

-continued

SITE	note = Synthetic Polypeptide 1	
REGION	note = misc_feature - Modified with 5FAM 11..12	
source	note = misc_feature - Modified with CPQ2-PEG2 1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 32 GGQTCKCSCK KC		12
SEQ ID NO: 33 FEATURE REGION	moltype = AA length = 12 Location/Qualifiers 1..12 note = Synthetic Polypeptide	
SITE	1 note = misc_feature - Modified with 5FAM	
REGION	11..12 note = misc_feature - Modified with CPQ2-PEG2	
source	1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 33 GGQWAGLVEK KC		12
SEQ ID NO: 34 FEATURE REGION	moltype = AA length = 12 Location/Qualifiers 1..12 note = Synthetic Polypeptide	
SITE	1 note = misc_feature - Modified with 5FAM	
REGION	11..12 note = misc_feature - Modified with CPQ2-PEG2	
source	1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 34 GGRPAVMTSP KC		12
SEQ ID NO: 35 FEATURE REGION	moltype = AA length = 12 Location/Qualifiers 1..12 note = Synthetic Polypeptide	
SITE	1 note = misc_feature - Modified with 5FAM	
REGION	11..12 note = misc_feature - Modified with CPQ2-PEG2	
source	1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 35 GGTLRELHLD KC		12
SEQ ID NO: 36 FEATURE REGION	moltype = AA length = 12 Location/Qualifiers 1..12 note = Synthetic Polypeptide	
SITE	1 note = misc_feature - Modified with 5FAM	
REGION	11..12 note = misc_feature - Modified with CPQ2-PEG2	
source	1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 36 GGTPPPSQGK KC		12
SEQ ID NO: 37 FEATURE REGION	moltype = AA length = 12 Location/Qualifiers 1..12 note = Synthetic Polypeptide	
SITE	1 note = misc_feature - Modified with 5FAM	
REGION	11..12 note = misc_feature - Modified with CPQ2-PEG2	
source	1..12	

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	mol_type = protein organism = synthetic construct	
SEQUENCE: 37 GGTSEDLVVQ KC		12
SEQ ID NO: 38 FEATURE REGION SITE REGION source	moltype = AA length = 12 Location/Qualifiers 1..12 note = Synthetic Polypeptide 1 note = misc_feature - Modified with 5FAM 11..12 note = misc_feature - Modified with CPQ2-PEG2 1..12 mol_type = protein organism = synthetic construct	
SEQUENCE: 38 GGVWAAEAIS KC		12
SEQ ID NO: 39 FEATURE REGION SITE REGION source	moltype = AA length = 13 Location/Qualifiers 1..13 note = Synthetic Polypeptide 1 note = misc_feature - Modified with 5FAM 11..12 note = misc_feature - Modified with CPQ2-PEG2 1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 39 GRQRRALEKG KGC		13
SEQ ID NO: 40 FEATURE REGION SITE REGION source	moltype = AA length = 15 Location/Qualifiers 1..15 note = Synthetic Polypeptide 1 note = misc_feature - Modified with 5FAM 13..14 note = misc_feature - Modified with CPQ2-PEG2 1..15 mol_type = protein organism = synthetic construct	
SEQUENCE: 40 GGGSGRSANA KGKGC		15
SEQ ID NO: 41 FEATURE REGION SITE REGION source	moltype = AA length = 13 Location/Qualifiers 1..13 note = Synthetic Polypeptide 1 note = misc_feature - Modified with 5FAM 11..12 note = misc_feature - Modified with CPQ2-PEG2 1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 41 GKPISLISSG KGC		13
SEQ ID NO: 42 FEATURE REGION SITE REGION source	moltype = AA length = 13 Location/Qualifiers 1..13 note = Synthetic Polypeptide 1 note = misc_feature - Modified with 5FAM 11..12 note = misc_feature - Modified with CPQ2-PEG2 1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 42 GILSRIVGGG KGC		13
SEQ ID NO: 43	moltype = AA length = 8	

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FEATURE	Location/Qualifiers	
REGION	1..8	
	note = Synthetic Polypeptide	
SITE	1	
	note = misc_feature - Modified with 5FAM	
REGION	6..7	
	note = misc_feature - Modified with CPQ2-PEG2	
source	1..8	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 43		
GGGPGKGC		8
SEQ ID NO: 44	moltype = AA length = 14	
FEATURE	Location/Qualifiers	
REGION	1..14	
	note = Synthetic Polypeptide	
SITE	1	
	note = misc_feature - Modified with 5FAM	
REGION	7..8	
	note = misc_feature - Modified with Nval	
REGION	12..13	
	note = misc_feature - Modified with CPQ2-PEG2	
source	1..14	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 44		
GRPKPVEWRK GKGC		14
SEQ ID NO: 45	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
REGION	1..11	
	note = Synthetic Polypeptide	
SITE	1	
	note = misc_feature - Modified with 5FAM	
REGION	9..10	
	note = misc_feature - Modified with CPQ2-PEG2	
source	1..11	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 45		
GHSSKLQGKG C		11
SEQ ID NO: 46	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
	note = Synthetic Polypeptide	
SITE	1	
	note = misc_feature - Modified with 5FAM	
REGION	11..12	
	note = misc_feature - Modified with CPQ2-PEG2	
source	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 46		
GSSQYSSNGG KGC		13
SEQ ID NO: 47	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
	note = Synthetic Polypeptide	
SITE	1	
	note = misc_feature - Modified with 5FAM	
REGION	11..12	
	note = misc_feature - Modified with CPQ2-PEG2	
source	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 47		
GQKGRYKQEG KGC		13
SEQ ID NO: 48	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
	note = Synthetic Polypeptide	
SITE	1	

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REGION	note = misc_feature - Modified with 5FAM 11..12	
source	note = misc_feature - Modified with CPQ2-PEG2 1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 48 GGKAFRRSGG KGC		13
SEQ ID NO: 49 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = Synthetic Polypeptide	
SITE	1	
REGION	note = misc_feature - Modified with 5FAM 11..12	
source	note = misc_feature - Modified with CPQ2-PEG2 1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 49 GIQQRSLGGG KGC		13
SEQ ID NO: 50 FEATURE REGION	moltype = AA length = 10 Location/Qualifiers 1..10 note = Synthetic Polypeptide	
SITE	1	
REGION	note = misc_feature - Modified with 5FAM 8..9	
source	note = misc_feature - Modified with CPQ2-PEG2 1..10 mol_type = protein organism = synthetic construct	
SEQUENCE: 50 GGVPRGGKGC		10
SEQ ID NO: 51 FEATURE REGION	moltype = AA length = 13 Location/Qualifiers 1..13 note = Synthetic Polypeptide	
SITE	1	
REGION	note = misc_feature - Modified with 5FAM 11..12	
source	note = misc_feature - Modified with CPQ2-PEG2 1..13 mol_type = protein organism = synthetic construct	
SEQUENCE: 51 GSGSKIIGGG KGC		13
SEQ ID NO: 52 FEATURE REGION	moltype = AA length = 11 Location/Qualifiers 1..11 note = Synthetic Polypeptide	
SITE	1	
REGION	note = misc_feature - Modified with 5FAM 9..10	
source	note = misc_feature - Modified with CPQ2-PEG2 1..11 mol_type = protein organism = synthetic construct	
SEQUENCE: 52 GAANLTRGKG C		11
SEQ ID NO: 53 FEATURE REGION	moltype = AA length = 10 Location/Qualifiers 1..10 note = Synthetic Polypeptide	
SITE	1	
REGION	note = misc_feature - Modified with 5FAM 8..9	
source	note = misc_feature - Modified with CPQ2-PEG2 1..10 mol_type = protein organism = synthetic construct	

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SEQUENCE: 53		
GGGELRGKGC		10
SEQ ID NO: 54	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
REGION	1..11	
	note = Synthetic Polypeptide	
SITE	1	
	note = misc_feature - Modified with 5FAM	
REGION	5..6	
	note = misc_feature - Modified with Phe(homo)	
REGION	9..10	
	note = misc_feature - Modified with CPQ2-PEG2	
source	1..11	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 54		
GLAQARSGKG C		11
SEQ ID NO: 55	moltype = AA length = 15	
FEATURE	Location/Qualifiers	
REGION	1..15	
	note = Synthetic Polypeptide	
SITE	1	
	note = misc_feature - Modified with 5FAM	
REGION	13..14	
	note = misc_feature - Modified with CPQ2-PEG2	
source	1..15	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 55		
GSPLAQAVRS SGKGC		15
SEQ ID NO: 56	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
REGION	1..10	
	note = Synthetic Polypeptide	
SITE	1	
	note = misc_feature - Modified with 5FAM	
REGION	8..9	
	note = misc_feature - Modified with CPQ2-PEG2	
source	1..10	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 56		
GMERMGGKGC		10
SEQ ID NO: 57	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
	note = Synthetic Polypeptide	
SITE	1	
	note = misc_feature - Modified with 5FAM	
REGION	11..12	
	note = misc_feature - Modified with CPQ2-PEG2	
source	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 57		
GPVPLSLVMG KGC		13
SEQ ID NO: 58	moltype = AA length = 13	
FEATURE	Location/Qualifiers	
REGION	1..13	
	note = Synthetic Polypeptide	
SITE	1	
	note = misc_feature - Modified with 5FAM	
REGION	11..12	
	note = misc_feature - Modified with CPQ2-PEG2	
source	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 58		
GRQSRIVGGG KGC		13
SEQ ID NO: 59	moltype = AA length = 13	

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FEATURE	Location/Qualifiers	
REGION	1..13	
	note = Synthetic Polypeptide	
SITE	1	
	note = misc_feature - Modified with 5FAM	
REGION	11..12	
	note = misc_feature - Modified with CPQ2-PEG2	
source	1..13	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 59		
GSQPRIVGGG KGC		13
SEQ ID NO: 60	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
REGION	1..11	
	note = Synthetic Polypeptide	
source	1..11	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 60		
DICLPRWGCL W		11
SEQ ID NO: 61	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
REGION	1..8	
	note = Synthetic Polypeptide	
source	1..8	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 61		
SLKRYGGG		8
SEQ ID NO: 62	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
REGION	1..8	
	note = Synthetic Polypeptide	
source	1..8	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 62		
AAFRSRGA		8
SEQ ID NO: 63	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
REGION	1..8	
	note = Synthetic Polypeptide	
REGION	1..2	
	note = misc_feature - Xaa can be any naturally occurring amino acid	
REGION	7..8	
	note = misc_feature - Xaa can be any naturally occurring amino acid	
source	1..8	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 63		
XXFRFFXX		8
SEQ ID NO: 64	moltype = AA length = 6	
FEATURE	Location/Qualifiers	
REGION	1..6	
	note = Synthetic Polypeptide	
source	1..6	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 64		
QSVGFA		6
SEQ ID NO: 65	moltype = AA length = 7	
FEATURE	Location/Qualifiers	
REGION	1..7	
	note = Synthetic Polypeptide	
source	1..7	
	mol_type = protein	
	organism = synthetic construct	

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SEQUENCE: 65 LGLEGAD		7
SEQ ID NO: 66 FEATURE REGION source	moltype = AA length = 4 Location/Qualifiers 1..4 note = Synthetic Polypeptide 1..4 mol_type = protein organism = synthetic construct	
SEQUENCE: 66 GPLD		4
SEQ ID NO: 67 FEATURE REGION source	moltype = AA length = 6 Location/Qualifiers 1..6 note = Synthetic Polypeptide 1..6 mol_type = protein organism = synthetic construct	
SEQUENCE: 67 LGV LIV		6
SEQ ID NO: 68 FEATURE REGION source	moltype = AA length = 6 Location/Qualifiers 1..6 note = Synthetic Polypeptide 1..6 mol_type = protein organism = synthetic construct	
SEQUENCE: 68 GLVLVA		6
SEQ ID NO: 69 FEATURE REGION source	moltype = AA length = 6 Location/Qualifiers 1..6 note = Synthetic Polypeptide 1..6 mol_type = protein organism = synthetic construct	
SEQUENCE: 69 PAALVG		6
SEQ ID NO: 70 FEATURE REGION source	moltype = AA length = 7 Location/Qualifiers 1..7 note = Synthetic Polypeptide 1..7 mol_type = protein organism = synthetic construct	
SEQUENCE: 70 GPAGLAG		7
SEQ ID NO: 71 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = Synthetic Polypeptide 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 71 ASPRAGGK		8
SEQ ID NO: 72 FEATURE REGION source	moltype = AA length = 8 Location/Qualifiers 1..8 note = Synthetic Polypeptide 1..8 mol_type = protein organism = synthetic construct	
SEQUENCE: 72 YEADSL EE		8
SEQ ID NO: 73 FEATURE REGION	moltype = AA length = 6 Location/Qualifiers 1..6	

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source	note = Synthetic Polypeptide 1..6 mol_type = protein organism = synthetic construct	
SEQUENCE: 73 YQYRAL		6
SEQ ID NO: 74 FEATURE REGION	moltype = AA length = 6 Location/Qualifiers 1..6 note = Synthetic Polypeptide	
source	1..6 mol_type = protein organism = synthetic construct	
SEQUENCE: 74 GGVPRG		6
SEQ ID NO: 75 FEATURE REGION	moltype = AA length = 25 Location/Qualifiers 1..25 note = Synthetic Polypeptide	
SITE	1 note = misc_feature - Modified with Albumin	
REGION	10..11 note = misc_feature - Modified with Biotin	
SITE	11 note = mod_res - D stereoisomer of Glu	
SITE	13 note = mod_res - D stereoisomer of Val	
SITE	14 note = mod_res - D stereoisomer of Asn	
SITE	15 note = mod_res - D stereoisomer of Asp	
SITE	16 note = mod_res - D stereoisomer of Asn	
SITE	17 note = mod_res - D stereoisomer of Glu	
SITE	18 note = mod_res - D stereoisomer of Glu	
SITE	20 note = mod_res - D stereoisomer of Phe	
SITE	21 note = mod_res - D stereoisomer of Phe	
SITE	22 note = mod_res - D stereoisomer of Ser	
SITE	23 note = mod_res - D stereoisomer of Ala	
SITE	24 note = mod_res - D stereoisomer of Arg	
SITE	25 note = misc_feature - Modified with FAM	
source	1..25 mol_type = protein organism = synthetic construct	
SEQUENCE: 75 GPLGVRGKGK EGVNDNEEGF FSARK		25
SEQ ID NO: 76 FEATURE REGION	moltype = AA length = 7 Location/Qualifiers 1..7 note = Synthetic Polypeptide	
source	1..7 mol_type = protein organism = synthetic construct	
SEQUENCE: 76 PLGVRGK		7
SEQ ID NO: 77 FEATURE REGION	moltype = AA length = 16 Location/Qualifiers 1..16 note = Synthetic Polypeptide	
REGION	1..2 note = misc_feature - Modified with Biotin	
SITE	2 note = mod_res - D stereoisomer of Glu	
SITE	4	

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SITE	note = mod_res - D stereoisomer of Val	
	5	
SITE	note = mod_res - D stereoisomer of Asn	
	6	
SITE	note = mod_res - D stereoisomer of Asp	
	7	
SITE	note = mod_res - D stereoisomer of Asn	
	8	
SITE	note = mod_res - D stereoisomer of Glu	
	9	
SITE	note = mod_res - D stereoisomer of Glu	
	11	
SITE	note = mod_res - D stereoisomer of Phe	
	12	
SITE	note = mod_res - D stereoisomer of Phe	
	13	
SITE	note = mod_res - D stereoisomer of Ser	
	14	
SITE	note = mod_res - D stereoisomer of Ala	
	15	
SITE	note = mod_res - D stereoisomer of Arg	
	16	
source	note = misc_feature - Modified with FAM	
	1..16	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 77		
KEGVNDNEEG FFSARK		16
SEQ ID NO: 78	moltype = AA length = 21	
FEATURE	Location/Qualifiers	
REGION	1..21	
source	note = Synthetic Polypeptide	
	1..21	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 78		
CAVGALEGPR NQDWLGVP RQ L		21
SEQ ID NO: 79	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic Polynucleotide	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 79		
tccatgacgt tcctgacgtt		20
SEQ ID NO: 80	moltype = AA length = 6	
FEATURE	Location/Qualifiers	
REGION	1..6	
SITE	note = Synthetic Polypeptide	
	1	
REGION	note = mod_res - D stereoisomer of Phe	
	1..2	
source	note = misc_feature - Modified with pipecolic acid	
	1..6	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 80		
FKSGGG		6
SEQ ID NO: 81	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
REGION	1..11	
source	note = Synthetic Polypeptide	
	1..11	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 81		
LPSTGHHHHH H		11

1-53. (canceled)

54. A method for detecting cancer comprising:

- a) administering to a subject a biomarker particle, wherein the biomarker particle comprises a modular structure having a carrier domain comprising a trafficking carrier linked via an enzyme substrate to a detectable marker, and wherein the biomarker particle, when exposed to an enzyme, releases the detectable marker from the carrier domain;
- b) analyzing a biological sample from the subject; and
- c) determining whether the detectable marker is in the biological sample, wherein the presence of the detectable marker in the biological sample is indicative of a cancer.

55. The method of claim **54**, wherein the trafficking carrier comprises an antibody, a protein, a polymeric scaffold, or a nanoparticle.

56. The method of claim **54**, wherein the trafficking carrier is a lymph node trafficking carrier.

57. The method of claim **54**, wherein the trafficking carrier is non-immunogenic.

58. The method of claim **54**, wherein the enzyme substrate is a cancer enzyme substrate.

59. The method of claim **58**, wherein the cancer enzyme substrate is ADAM28, MMP9 or MMP12.

60. The method of claim **54**, wherein the enzyme substrate is an immune-associated substrate.

61. The method of claim **54**, wherein the enzyme substrate is a granzyme substrate.

62. The method of claim **54**, wherein the biological sample is urine.

63. The method of claim **54**, wherein the lymph node biomarker nanoparticle is a multiplexed library of lymph node specific enzyme susceptible detectable markers.

64. (canceled)

65. The method of claim **54**, wherein the detectable marker is a mass encoded protease substrate or a ligand encoded protease substrate.

66. The method of claim **54**, wherein the presence of the detectable marker in the biological sample is indicative of an immune status.

67. The method of claim **66**, wherein the immune status indicates sensitivity to immune therapy.

68. (canceled)

69. The method of claim **54**, wherein the analysis of step (b) comprises using mass spectrometry.

70. The method of claim **54**, wherein the analysis of step (b) comprises measuring fluorescence of the detectable marker.

71. The method of claim **54**, wherein the analysis of step (b) occurs in vitro.

72. The method of claim **54**, wherein the analysis of step (b) occurs ex vivo.

73. The method of claim **54**, wherein the analysis of step (b) occurs in vivo.

74. The method of claim **54**, wherein the cancer is a pancreatic cancer, a prostate cancer, a breast cancer, a colon cancer, an ovarian cancer, an oral cancer, an endometrial cancer, a skin cancer, a gastric cancer, an esophageal cancer, or a lung cancer.

75. A method for determining a metastatic stage of a cancer comprising:

- a) administering to a subject a biomarker particle, wherein the biomarker particle comprises a modular structure having a carrier domain comprising a trafficking carrier linked via an enzyme substrate to a detectable marker, and wherein the biomarker particle, when exposed to an enzyme, releases the detectable marker from the carrier domain;
- b) analyzing a biological sample from the subject; and
- c) determining whether the detectable marker is in the biological sample, wherein the presence of the detectable marker in the biological sample is indicative of the metastatic stage of the cancer.

76-95. (canceled)

96. The method of claim **54**, wherein the presence of the detectable marker in the biological sample is further indicative of a metastatic stage of the cancer.

* * * * *