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(54) Title: IMMUNOHISTOCHEMISTRY VIA HYBRIDIZATION CHAIN REACTION

(57) Abstract: The present disclosure relates to methods involving HCR reactions that involve using trigger oligos to activate probes that initiate HCR

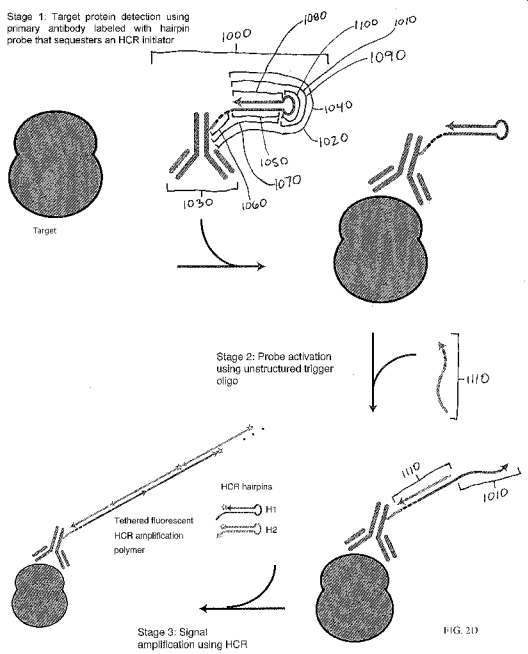

FIG. 1D

[Continued on next page]

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IMMUNOHISTOCHEMISTRY VIA HYBRIDIZATION CHAIN REACTION

INCORPORATION BY REFERENCE TO ANY PRIORITY APPLICATIONS

[0001] This Application claims priority to U.S. Provisional Patent Application No. 62/381474 filed August 30, 2016, the disclosure of which is hereby incorporated by reference in its entirety herein.

STATEMENT REGARDING FEDERALLY SPONSORED R&D

[0002] This invention was made with government support under Grant No. EB006192 awarded by the National Institutes of Health, under Grant No. CCF1317694 awarded by the National Science Foundation, and under Grant No. HR0011-17-2-0008 awarded by the Defense Advanced Research Projects Agency. The government has certain rights in the invention.

BACKGROUND

Field

[0003] The present invention relates generally to methods of hybridization chain reaction (HCR).

Description of the Related Art

[0004] Hybridization chain reaction is a method for the triggered self-assembly of nucleic acid molecules starting from metastable hairpin monomers. Metastable hairpin monomers undergo a chain reaction of hybridization events to form a nicked double stranded amplification polymer when triggered by a nucleic acid initiator strand. The hairpin monomers store the energy to drive the polymerization process in their single stranded loops and toeholds.

SUMMARY

[0005] In some embodiments, a method is provided. The method comprises providing a probe comprising a target-binding region linked to a structured nucleic acid region, wherein the structured nucleic acid region sequesters an HCR initiator. The method further includes adding a trigger oligo, wherein the trigger oligo binds to the structured nucleic acid region, which changes conformation to expose the initiator; and amplifying from the initiator using HCR.

[0006] In some embodiments, a method is provided. The method comprises providing: at least one target-binding moiety labeled with a modified HCR hairpin; a target molecule; a trigger oligo; and a pair of polymerizing HCR hairpins. The trigger oligo binds to the modified HCR hairpin and the pair of polymerizing HCR hairpins do not bind to each other or directly to the modified HCR hairpin unless the trigger oligo has first bound to the modified HCR hairpin. The method further includes performing HCR to produce a polymer; and detecting a signal from the polymer.

[0007] In some embodiments, a method is provided. The method comprises providing: at least one target-binding moiety labeled with a structured probe sequestering an HCR initiator; a target molecule; a trigger oligo; and at least a pair of polymerizing HCR hairpins, wherein the trigger oligo binds to the structured probe and the pair of polymerizing HCR hairpins do not bind to each other or to the sequestered HCR initiator, unless the trigger oligo has first bound to the structured probe. The method further includes performing HCR; and detecting a signal.

BRIEF DESCRIPTION OF THE DRAWINGS

[0008] **FIGs. 1A-1C** depict in situ amplification via hybridization chain reaction (HCR). FIG. 1A depicts an HCR mechanism. FIG. 1B depicts an antibody driven binding embodiment, which includes an HCR amplification stage. FIG. 1C denotes a multiplexed experimental timeline of some embodiments of the process, simultaneously adding initiator-labeled antibodies for each of three targets, washing out unbound antibodies, simultaneously adding hairpin monomers for each of three HCR amplifiers, washing out unpolymerized hairpin monomers.

[0009] **FIGs. 2A-2D** depicts some embodiments of HCR immunohistochemistry (HCR-IHC) using oligo-labeled primary antibodies. FIG. 2A depicts scheme A. FIG. 2B

depicts scheme B. FIG. 2C depicts scheme C. FIG. 2D depicts scheme D. These embodiments can be combined or modified as provided herein. The figures depict both generic and specific embodiments.

[0010] **FIGs. 3A-3D** depicts HCR-IHC using oligo-labeled secondary antibodies. FIG. 3A depicts scheme E. FIG. 3B depicts scheme F. FIG. 3C depicts scheme G. FIG. 3D depicts scheme H. These embodiments can be combined or modified as provided herein. The figures depict both generic and specific embodiments.

[0011] **FIGs. 4A-4C.** Antibody-oligo conjugation scheme.

[0012] **FIG. 5.** Performance results of Scheme E (secondary antibody carrying HCR initiator) vs Scheme F (secondary antibody carrying HCR hairpin) in whole-mount zebrafish embryos.

[0013] **FIGs. 6A-6B.** Relative quantitation of target protein expression via HCR-IHC.

[0014] **FIG. 7.** Scheme for simultaneously mapping protein and mRNA expression via HCR-IHC and HCR in situ hybridization (HCR-ISH).

[0015] **FIGs. 8A-8B.** Multiplexed HCR-IHC/HCR-ISH in whole mount zebrafish embryos.

[0016] **FIG 9.** HCR-IHC using label probes.

DETAILED DESCRIPTION

[0017] Provided herein are embodiments employing immunohistochemistry and hybridization chain reactions. By combining these techniques, superior processes and kits can be obtained for the detection of various targets. In some embodiments, in order to reduce any inadvertent signaling that can occur in a sample, the IHC component of the process is distinguished or separated from the HCR side of the process. This can be achieved in a number of ways, for example, by sequestering an initiator component within (or modifying it or removing it) from the antibody linked component. Thus reducing any inadvertent HCR amplification (or background HCR reactions). In some embodiments, this is done via a trigger oligo, which binds to the modified HCR hairpin on the antibody, so as to then expose the initiator, which can then trigger HCR signal amplification (e.g., FIG. 3C). Other

embodiments are provided herein as well. In some embodiments, the IHC aspect can involve a primary antibody assay or a secondary antibody assay (where the modified HCR hairpin is linked to the secondary antibody, in some embodiments). In some embodiments, any of the methods provided in one or more of the figures can be employed to reduce background or inadvertent triggering events.

[0018] By way of context, Hybridization Chain Reaction (HCR) is a method for the triggered hybridization of nucleic acid molecules starting from metastable hairpin monomers or other metastable nucleic acid structures. See, for example, Dirks, R. and Pierce, N. Proc. Natl. Acad. Sci. USA 101(43): 15275-15278 (2004), and U.S. Patent Application No. 11/087,937, filed March 22, 2005, U.S. Pat. Nos. US 8,105,778, January 31, 2012, and 8,507,204, August 13, 2013, each of which is incorporated herein by reference in its entirety. HCR does not require any enzymes and can operate isothermally. Traditionally, HCR ISH involves an unstructured nucleic acid probe that carries an exposed HCR initiator or a structured nucleic acid probe that initially sequesters an HCR initiator but changes conformation to expose an HCR initiator upon binding to a nucleic acid target. In either scenario, an exposed HCR initiator will trigger polymerization of metastable HCR monomers to form an HCR amplification polymer. By contrast, some of the present embodiments require an additional process or component before polymerization will occur.

[0019] For example, some embodiments provided herein add an additional step or component, such as a trigger oligo, which is used to activate a structured nucleic acid probe carried by an antibody probe. In some embodiments, the structured nucleic acid probe is a hairpin probe that initially sequesters an HCR initiator that is exposed upon binding of the trigger oligo to the input domain of the hairpin probe, enabling the initiator to trigger HCR signal amplification. Prior techniques did not involve a trigger oligo as a part of the target detection and signal amplification cascade. With prior HCR-ISH techniques, in a first scenario, an unstructured nucleic acid probe carries an exposed HCR initiator that is accessible to trigger HCR signal amplification. Hence, if the probe binds non-specifically in the sample, it will nonetheless trigger HCR signal amplification and lead to generation of amplified background. In a second scenario, a structured nucleic acid probe initially sequesters an HCR initiator that is then exposed when the probe selectively hybridizes to the nucleic acid target molecule, thus activating the probe so that it can trigger HCR signal

amplification. Hence, if the probe binds non-specifically in the sample, it will remain inactive and not lead to generation of amplified background. With prior HCR-IHC techniques, an antibody probe carries an exposed HCR initiator that is accessible to trigger HCR signal amplification. Hence, if the antibody binds non-specifically in the sample, it will nonetheless trigger HCR signal amplification and lead to generation of amplified background. Moreover, the unstructured initiator oligos labeling the antibody increase the stickiness of the antibody probe, inhibiting penetration into the sample and increasing non-specific binding. Labeling the antibody probe with multiple exposed HCR initiators in order to increase the signal generated per target molecule further increases the stickiness of the antibody probe due to multivalent non-specific base-pairing between the sample and the multiple exposed HCR initiators, thus further increasing non-specific binding and reducing sample penetration.

[0020] In some embodiments, the use of an antibody probe carrying a hairpin probe sequestering an HCR initiator reduces non-specific binding of the antibody probe and increases the ability of the antibody probe to penetrate the sample. Compared to an exposed HCR initiator, the duplex stem of the hairpin probe reduces the availability of bases to base-pair non-specifically in the sample, thus reducing non-specific binding and increasing sample penetration. In some embodiments, after an antibody probe penetrates the sample and binds selectively to a target within the sample, the hairpin probe labeling the antibody is activated using a trigger oligo that binds to the hairpin probe to expose an HCR initiator, enabling subsequent HCR signal amplification. In some embodiments, an antibody probe is labeled with multiple structured nucleic acid probes such that it penetrates the sample and binds selectively to the target; subsequently each structured nucleic acid probe is activated by a trigger oligo, in each case exposing an HCR initiator; subsequently each exposed HCR initiator triggers self-assembly of an HCR amplification polymer, leading to multiple HCR amplification polymers tethered to the same antibody probe, thus increasing the signal generated per target molecule.

[0021] In some embodiments, the nucleic acid probe attached to the antibody can be any nucleic acid that exposes an HCR initiator upon selective hybridization to the trigger oligo. The trigger oligo can, in turn, include a first HCR initiator, which would otherwise be washed out of the sample, but upon selective binding to the nucleic acid probe, exposes a

second HCR initiator that triggers HCR signal amplification, leading to self-assembly of an HCR amplification polymer tethered to the antibody.

[0022] By way of further context, an HCR amplifier comprises of two kinetically trapped nucleic acid hairpin monomers (H1 and H2) that co-exist metastably in the absence of a cognate initiator strand (I1 with sequence domains 'b*-a*'; FIG. 1A). Arrival of the initiator triggers a chain reaction in which H1 and H2 hairpin monomers sequentially nucleate and open to assemble into a long nicked double-stranded amplification polymer (Dirks and Pierce 2004). Each HCR hairpin monomer includes an input domain with an exposed single-stranded toehold and an output domain with a single-stranded toehold sequestered in the hairpin loop. Hybridization of the initiator to the input domain of H1 (FIG. 1A, 'a-b') opens the hairpin monomer to expose its output domain (FIG. 1A, 'c*-b*'). Hybridization of this output domain to the input domain of H2 (FIG. 1A, 'c-b') opens the hairpin monomer to expose an output domain (FIG. 1A, 'b*-a*') identical in sequence to the initiator. Regeneration of the initiator sequence provides the basis for a chain reaction of alternating H1 and H2 polymerization steps leading to formation of a nicked double-stranded polymer.

[0023] Using HCR-IHC, antibody probes that selectively bind protein targets carry DNA HCR initiators that trigger chain reactions in which metastable fluorophore-labeled DNA hairpins self-assemble into tethered fluorescent amplification polymers (FIG. 1B). The same IHC protocol can be used independent of the number of targets (FIG. 1C): in the detection stage, antibody probes for all targets bind in parallel; in the amplification stage, orthogonal HCR amplifiers carrying spectrally distinct fluorophores operate in parallel for all targets.

[0024] HCR draws on principles from the emerging disciplines of molecular programming and dynamic nucleic acid nanotechnology to provide isothermal enzyme-free signal amplification in diverse technological settings (Zhang et al. 2013; Jung and Ellington 2014; Wang et al. 2014; Ikbal et al. 2015) and it is particularly well-suited to the demands of in situ amplification (Choi et al. 2010; Choi et al. 2014). First, HCR is programmable, providing the basis for straightforward multiplexing using orthogonal amplifiers that operate independently and carry spectrally distinct fluorophores. Use of a protocol independent of the number of target species is convenient for any sample, but essential for delicate samples

such as sea urchin embryos that are easily damaged during serial multiplexing protocols. Second, HCR hairpins do not self-assemble until they encounter a probe carrying the cognate initiator, enabling deep sample penetration prior to growth of bright amplification polymers at the site of target molecules. The fact that the amplification reagents are structured hairpin monomers with a duplex stem reduces the potential for non-specific hybridization within the sample and also increases the ease of engineering multiple orthogonal amplifiers. The fact that amplification polymers carry up to hundreds of fluorophores (Choi et al. 2014) makes it possible to achieve high signal-to-background even when autofluorescence is high (e.g., in whole-mount vertebrate embryos (Choi et al. 2014; Huss et al. 2015; McLennan et al. 2015) or in bacteria contained within environmental samples or other organisms (Rosenthal et al. 2013; Nikolakakis et al. 2015; Yamaguchi et al. 2015)). Third, HCR amplification polymers remain tethered to their initiating probes, preventing signal from diffusing away from targets. Fourth, previously validated HCR amplifiers (Choi et al. 2014) can be used for new studies without modification. In some embodiments, all that is needed to map a new target molecule is an antibody probe labeled with a structured nucleic acid probe sequestering an initiator for a previously validated HCR amplifier. In this scenario, it is not necessary to engineer a new HCR amplifier for each new target molecule.

Definitions and Embodiments

[0025] The term "target binding region" refers to a region in an antibody or fragment thereof that binds to a target molecule.

[0026] The term "structured nucleic acid molecule" refers to a nucleic acid molecule that forms intramolecular base pairs, such as a hairpin probe, which contains a duplex stem comprising intramolecular base pairs. The term "unstructured nucleic acid molecule" refers to a nucleic acid molecule that predominantly does not form intramolecular base pairs, such that all of the bases in the molecule are predominantly available to base-pair.

[0027] The term "HCR initiator" refers to a nucleic acid region that can trigger the polymerization of two metastable HCR hairpin monomer species to form an HCR amplification polymer. An exposed HCR initiator is functional and triggers polymerization of the metastable HCR hairpin monomers under polymerizing conditions. A sequestered HCR initiator is non-functional and does not trigger polymerization of the metastable HCR

hairpins monomers under polymerizing conditions. A sequestered HCR initiator (hence, initially non-functional) can be exposed (hence, becoming functional) upon binding of another molecule to the sequestering molecule.

[0028] The term "trigger oligo" refers to a nucleic acid molecule that binds to a structured nucleic acid probe carried by a target-binding probe (for example, an antibody) such that binding of the trigger oligo to the structured nucleic acid probe exposes a functional HCR initiator. In some embodiments, the initiator is previously sequestered by the structured nucleic acid probe. In some embodiments, the trigger oligo comprises a functional HCR initiator. In some embodiments, the trigger oligo binds to the nucleic acid probe associated with the target-binding probe and thereby exposes a functional HCR initiator.

[0029] The term "hairpin probe" refers to a nucleic acid strand that forms intramolecular base pairs to yield a duplex stem with a single-stranded toehold at one end and a single-stranded hairpin loop at the other.

[0030] The term "toehold" refers to nucleation site of a domain comprising a nucleic acid sequence designed to initiate hybridization of the domain with a complementary nucleic acid sequence. The secondary structure of a monomer may be such that the toehold is exposed or sequestered. For example, in some embodiments, the secondary structure of the toehold is such that the toehold is available to hybridize to a complementary nucleic acid (the toehold is "exposed," or "accessible"), and in other embodiments, the secondary structure of the toehold is such that the toehold is not available to hybridize to a complementary nucleic acid (the toehold is "sequestered," or "inaccessible"). If the toehold is sequestered or otherwise unavailable, the toehold can be made available by some event such as, for example, the opening of the hairpin of which it is a part. When exposed, a toehold is configured such that a complementary nucleic acid sequence can nucleate at the toehold. In some embodiments, nucleation of a complementary nucleic acid sequence at an exposed toehold initiates branch migration that opens up the hairpin of a hairpin monomer.

[0031] The term "stem section" refers to a region on a hairpin probe that hybridizes to a complementary portion of the probe ("complement to the stem section") to form a duplex stem.

[0032] The term "input domain" refers to a region of a hairpin probe that comprises the "toehold" and "stem section".

[0033] The term "output domain" refers to a region of a hairpin probe that comprises the "hairpin loop" and "complement to the stem section".

[0034] The term "hairpin loop" refers to a single-stranded region that loops back on itself and is closed by a base pair.

[0035] The term "complement to the stem section" refers to a region of a hairpin probe that hybridizes to a complementary portion of the same probe ("stem section") to form a duplex stem.

[0036] The term "label binding site" refers to a region on a HCR hairpin monomer that is complementary to the "complement to the label binding site."

[0037] The term "complement to the label binding site" refers to a region on a HCR hairpin monomer that is complementary to the "label binding site."

[0038] The term "reporter molecule" refers to a molecule that can be detected.

[0039] The term "HCR hairpin monomer" when used without further modification, refers to a monomer that is capable of performing HCR signal amplification.

[0040] The term "modified HCR hairpin monomer" as used herein refers to an HCR hairpin monomer with a modified input domain comprising a modified toehold sequence and a sequestered HCR initiator within its output domain, such that it is not capable of trigger HCR on its own, but exposes a functional HCR initiator upon binding of a trigger oligo to the input domain, thus enabling triggering of HCR signal amplification.

[0041] The term "modified input domain" refers to an input domain that has a modified toehold sequence.

[0042] The term "modified toehold sequence" refers a toehold sequence that is not a nucleation site for the complement to a standard toehold sequence.

[0043] The term "nucleic acid" refers to DNA, RNA, 2'OMe-RNA, LNA, or any DNA analog, RNA analog, or synthetic polymer capable of base-pairing.

Methods

[0044] In some embodiments, a method is provided as depicted FIG. 2D. In some embodiments, a probe 1000 is provided, comprising a target binding region 1030 (that can be, e.g., a primary antibody, but is not so limited in all embodiments) that is linked to a structured nucleic acid probe 1040 (that can be, e.g., a hairpin probe, but is not so limited in

all embodiments) that sequesters an HCR initiator 1010. In some embodiments, when the HCR initiator is sequestered, it cannot effectively trigger HCR signal amplification. In some embodiments, the structured nucleic acid probe 1040 is a hairpin probe 1020 that comprises an input domain 1070 and an output domain 1090. In some embodiments, the input domain 1070 comprises a toehold 1060 and a stem section 1050. In some embodiments, the output domain 1090 comprises a complement to the stem section 1080 and a hairpin loop 1100. In some embodiments, the output domain 1090 comprises the HCR initiator 1010. In some embodiments, the HCR initiator is the whole output domain. In some embodiments, the HCR initiator is only a portion of the output domain. Addition of a trigger oligo 1110 results in binding of the trigger oligo 1110 to the hairpin probe 1020 at the toehold 1060 and stem section 1050. This results in a conformation change of the hairpin probe 1020, which exposes the HCR initiator 1010. Exposure of the HCR initiator 1010 enables triggering of HCR signal amplification in which metastable HCR hairpin monomers self-assemble to form an HCR amplification polymer. Additional embodiments of FIG. 2D are described below.

[0045] In some embodiments, a method is provided that comprises providing a probe comprising a target-binding region linked to a structured nucleic acid region. The structured nucleic acid region sequesters an HCR initiator. One then adds a trigger oligo. The trigger oligo binds to the structured nucleic acid region, which changes conformation to expose the initiator. One then amplifies from the initiator using HCR. Washes can occur such that unbound probe and unbound trigger oligo are each removed prior to the next step.

[0046] In some embodiments, a method is provided comprising providing: at least one target-binding moiety labeled with a modified HCR hairpin probe; a target molecule; a trigger oligo; and a pair of metastable HCR hairpins monomer species. The trigger oligo binds to the modified HCR hairpin and the pair of metastable HCR hairpin monomers do not bind directly to the modified HCR hairpin unless the trigger oligo has first bound to the modified HCR hairpin probe; performing HCR signal amplification to produce an HCR amplification polymer; and detecting a signal from the polymer. Washes can occur such that unbound probe, unbound trigger oligo, and unbound HCR hairpin monomers are each removed prior to the next step.

[0047] In some embodiments, a method is provided comprising providing: at least one target-binding moiety labeled with a structured probe sequestering an HCR initiator; a target molecule; a trigger oligo; and at least a pair of metastable HCR hairpin monomer species. The trigger oligo binds to the structured probe and the pair of metastable HCR hairpin monomer species do not bind to the structured probe, unless the trigger oligo has first bound to the structured probe to expose the HCR initiator. The exposed HCR initiator then triggers HCR signal amplification, generating a detectable signal when the target molecule is present. The amplified signal is then detected. Washes can occur such that unbound probe, unbound trigger oligo, and unbound metastable hairpin monomers are each removed prior to the next step.

[0048] In some embodiments, the target-binding region comprises DNA, RNA, LNA, PNA, 2'OMe-RNA, a synthetic nucleic acid analog, amino acid, or synthetic amino acid analog.

[0049] In some embodiments, the target-binding region is an antibody. In some embodiments, the antibody comprises a primary antibody. In some embodiments, the antibody further comprises a secondary antibody. In some embodiments, the antibody comprises a first antibody that binds to the target molecule, and a second antibody that binds to the first antibody, wherein the structured nucleic acid region is linked to the second antibody but is not linked to the first antibody. In some embodiments, an antibody fragment is used. In some embodiments, any molecule or structure that binds to a desired target, suitable for in vitro, in situ, ex vivo, in vivo detection, can be employed.

[0050] In some embodiments, the structured nucleic acid region comprises DNA, RNA, LNA, PNA, 2'OMe-RNA, or a synthetic nucleic acid analog. In some embodiments, the structured nucleic acid region comprises or consists of a hairpin probe. In some embodiments, the hairpin probe comprises: an input domain comprising a toehold and a stem section, and an output domain comprising a hairpin loop and a complement to the stem section, such that the exposed output domain comprises an HCR initiator. In some embodiments, the hairpin probe is an HCR hairpin monomer. In some embodiments, the hairpin probe is not an HCR hairpin monomer.

[0051] In some embodiments, the hairpin probe comprises a modified HCR hairpin monomer with a modified input domain that has a modified toehold sequence,

wherein the modified HCR hairpin monomer is configured such that its output domain is a sequestered HCR initiator that does not trigger HCR, but wherein the trigger oligo hybridizes to the modified input domain to expose the HCR initiator, triggering HCR signal amplification via self-assembly of first and second HCR hairpin monomer species. In some embodiments, the hairpin probe cannot or is not configured to trigger HCR or participate within HCR signal amplification directly. Of course, with the assistance of a trigger oligo, HCR polymerization then becomes possible.

[0052] In some embodiments, the trigger oligo binds to the hairpin probe at a toehold and/or stem section, thereby changing the conformation of the hairpin probe to expose a functional HCR initiator. In some embodiments, the trigger oligo is or comprises a first HCR initiator, such that upon binding to the input domain of the hairpin probe further comprising an output domain that is or comprises a sequestered second HCR initiator, the second HCR initiator is exposed and is thus able to trigger HCR signal amplification.

[0053] In some embodiments, the trigger oligo binds to the input domain, thereby exposing the output domain which is capable of triggering HCR. In some embodiments, the trigger oligo comprises a nucleotide sequence. In some embodiments, the trigger oligo hybridizes to the probe and thereby exposes the initiator (previously sequestered within the structured probe).

[0054] In some embodiments, in any of the binding reactions described herein, binding comprises hybridization. In some embodiments, binding comprises selective protein-protein interaction. In some embodiments, binding comprises selective nucleic acid-protein interaction. In some embodiments, binding comprises ionic binding. In some embodiments, binding comprises covalent bonding.

[0055] In some embodiments, the target molecule is a protein. In some embodiments, the target molecule is a small molecule or nucleic acid. In some embodiments, the target molecule is a complex of two or more proteins, nucleic acids, and/or small molecules. In some embodiments, the target molecule comprises a nucleotide sequence. In some embodiments, the target molecule comprises an amino acid sequence. In some embodiments the target comprises a molecule or a complex of two or more molecules.

[0056] In some embodiments, HCR signal amplification is performed using at least a first and second set of HCR hairpin monomer. In some embodiments, HCR is

performed using a first, second, third, and fourth set of HCR hairpin monomers. In some embodiments, HCR is performed using more than two sets of HCR hairpin monomers, for example, more than 10 sets of HCR hairpin monomers, more than 100 sets of HCR hairpin monomers, more than 1,000 sets of HCR hairpin monomers, more than 10,000 sets of HCR hairpin monomers, or 100,000 sets of HCR hairpin monomers. In some embodiments, the first and second set of HCR hairpin monomers each further comprise a reporter molecule. In some embodiments, the first and second set of HCR hairpin monomers each further comprise a label-binding site that is configured to hybridize to a complement to the label binding site, wherein the complement to the label binding site further comprises a reporter molecule. In some embodiments, the HCR monomers comprise a label-binding site.

[0057] In some embodiments, the reporter molecules are fluorescent molecules, non-fluorescent molecules, FRET molecules, or rare earth elements. In some embodiments, the reporter molecule comprises a quenched or FRET arrangement. In some embodiments, the reporter molecules are rare metal lanthanide complexes. In some embodiments, the reporter molecules are gold nanoparticles. In some embodiments the reporter molecules are dyes such as rhodamine, fluorescein, phycobiliproteins, acridines or cyanine compounds. In some embodiments, any reporter molecule whose presence or absence can be monitored can be employed. In some embodiments, the reporter molecule comprises a fluorescent molecule such as a fluorophore, or a colorimetric compound, that allows the resulting polymers to be visualized. In some embodiments, the reporter molecule is directly observable. In some embodiments, the reporter molecule is indirectly observable. In some embodiments, the reporter molecule comprises an enzyme or is enzymatic, and/or can mediate enzymatic signaling after HCR polymerization. In some embodiments, reporting is achieved by catalyzed reporter deposition ("CARD"). In some embodiments, a label binding site on one or more of the HCR hairpin monomer species can enable binding of a complement to the label binding site, wherein the complement to the label binding site carries a reporter molecule. In some embodiments, one type of reporter molecule carried by the hairpin monomers or the complement to the label binding site can mediate enzymatic signal amplification (CARD) after HCR polymerization such that a second type of reporter molecules deposited in the vicinity of HCR polymers will then be detected. In some embodiments, the reporter molecule is at least one of a luminescent molecule, FRET

molecules, fluorophore/quencher molecular pairs, or other detectable markers. In some embodiments, the reporter molecule can allow for a secondary molecule (such as a secondary antibody) to be employed for detection of the polymerization event. In some embodiments, the hairpin monomers can be labeled with reporter molecules (e.g., a fluorophore and a quencher) such that hairpin monomers are quenched but that the conformation change that occurs during HCR polymerization leads to fluorescent HCR amplification polymers.

[0058] In some embodiments, each HCR amplifier comprises at least two types of kinetically trapped nucleic acid hairpin monomers that co-exist metastably in the absence of the initiator. In some embodiments, each HCR amplifier comprises more than two types of kinetically trapped nucleic acid hairpin monomers, for example, at least 10 kinetically trapped nucleic acid hairpin monomers, at least 100 kinetically trapped nucleic acid hairpin monomers, at least 1,000 kinetically trapped nucleic acid hairpin monomers, at least 10,000 kinetically trapped nucleic acid hairpin monomers, or at least 100,000 kinetically trapped nucleic acid hairpin monomers.

[0059] In some embodiments, any of the methods described herein further comprise washing away any unbound probe from a sample. In some embodiments, washing away any unbound probe requires more than one wash, for example, two washes, three washes, four washes, or five washes.

[0060] In some embodiments, any of the washes provided herein can result in the removal of greater than 50% of any unbound probe from the sample, greater than 55%, greater than 60%, greater than 65%, greater than 70%, greater than 75%, greater than 80%, greater than 85%, greater than 90%, greater than 95%, greater than 99%, greater than 99.9%, greater than 99.99%, greater than 99.999%, or greater than 99.9999999%.

[0061] In some embodiments, a trigger oligo is added to the sample, after unbound probe has been washed from the sample. In some embodiments, any of the methods described herein further comprise: washing the sample to remove unpolymerized HCR hairpin monomers; adding a label probe that comprises a complement to the label binding site and a reporter molecule; washing unbound label probe; and detecting a presence or absence of the reporter molecule. In some embodiments, any of the embodiments provided herein further include washing away the unbound trigger oligo.

[0062] In some embodiments, any of the washes provided herein can result in the removal of greater than 50% of any unpolymerized HCR hairpin monomers from the sample, greater than 55%, greater than 60%, greater than 65%, greater than 70%, greater than 75%, greater than 80%, greater than 85%, greater than 90%, greater than 95%, greater than 99%, greater than 99.9%, greater than 99.99%, greater than 99.999%, or greater than 99.9999999%.

[0063] In some embodiments, amplifying using HCR comprises adding at least two different species of HCR hairpin monomers to the sample. In some embodiments, the two different species comprise a first species comprising a first reporter molecule and a second species comprising a second reporter molecule.

[0064] In some embodiments, amplifying using HCR comprises adding three species, or four species, or five species, or six species, or seven species, or eight species, or nine species, or 10 species of HCR hairpin monomers to the sample. In some embodiments, amplifying using HCR comprises adding more than 10 species of HCR hairpin monomers to the sample, for example, 50 species, 100 species, 150 species, 200 species, 250 species, 300 species, 350 species, 400 species, 450 species, 500 species, 550 species, 600 species, 650 species, 700 species, 750 species, 800 species, 850 species, 900 species 950 species, or 1,000 species. In some embodiments, amplifying using HCR comprises adding more than 1,000 species of HCR hairpin monomers to the sample, for example, 2,000 species, 3,000 species, 4,000 species, 5,000 species, 6,000 species, 7,000 species, 8,000 species, 9,000 species, or 10,000 species. In some embodiments, amplifying using HCR comprises adding more than 10,000 species of HCR hairpin monomers to the sample, for example, 20,000 species, 30,000 species, 40,000 species, 50,000 species, 60,000 species, 70,000 species, 80,000 species, 90,000 species, or 100,000 species. In some embodiments, amplifying provides a fluorescent amplification polymer. In some embodiments, amplifying generates a detectable polymer that indicates a presence of a target molecule, wherein the target molecule is bound by the target-binding region. In some embodiments, amplifying using HCR comprises added three species, four species, five species, six species, seven species, eight species, nine species, or 10 species of HCR hairpin monomers to the sample. In some embodiments, amplifying using HCR comprises adding more than 10 species of HCR hairpin monomers, for example, 100 species

of HCR hairpin monomers, 1,000 species of HCR hairpin monomers, 10,000 species of HCR hairpin monomers, or 100,000 species of HCR hairpin monomers.

[0065] In some embodiments, more than one target is assayed for at a time, wherein each probe comprises a target-binding region selective for each target to be assayed for. In some embodiments, two, three, four, five, six, seven, eight, nine, or 10 targets at a time, wherein each probe comprises a target-binding region selective for each target to be assayed for. In some embodiments, more than 10 targets are assayed for. In some embodiments, more than 100 targets are assayed for at a time, wherein each probe comprises a target-binding region specific for each target to be assayed for. In some embodiments more than 1,000 targets are assayed for, for example, more than 10,000 targets are assayed for, or 100,000 targets are assayed for, wherein each probe comprises a target-binding region selective for each target to be assayed for.

[0066] In some embodiments, multiple targets are assayed for at the same time, wherein each of probe comprises a target-binding region selective for a different target molecule and further comprises a structured nucleic acid probe sequestering an HCR initiator for a different HCR amplifier, such that each structured nucleic acid probe can be activated to expose its HCR initiator by a different trigger oligo. In some embodiments, two, three, four, five, six, seven, eight, nine, or 10 HCR amplifiers are used to perform signal amplification for different targets simultaneously. In some embodiments, more than 10 HCR amplifiers are used to perform signal amplification for different targets simultaneously. In some embodiments, more than 100 HCR amplifiers are used to perform signal amplification for different targets simultaneously. In some embodiments, more than 1000 HCR amplifiers are used to perform signal amplification for different targets simultaneously. In some embodiments, more than 10,000 HCR amplifiers are used to perform signal amplification for different targets simultaneously. In some embodiments, more than 100,000 HCR amplifiers are used to perform signal amplification for different targets simultaneously.

[0067] In some embodiments, any of the methods described herein is an immunohistochemistry assay. In some embodiments, any of the methods described herein is an immunocytochemistry assay. In some embodiments, any of the methods described herein further comprise parallel multiplexing performed for two or more targets simultaneously, wherein the two or more target molecules are each separately bound by selective probes. In

some embodiments, parallel multiplexing is performed for 10 or more targets simultaneously wherein the 10 or more target molecules are each separately bound by selective probes. In some embodiments, parallel multiplexing is performed for 100 or more targets simultaneously wherein the 100 or more target molecules are each separately bound by selective probes. In some embodiments, parallel multiplexing is performed for 1,000 or more targets simultaneously wherein the 1,000 or more target molecules are each separately bound by selective probes. In some embodiments, parallel multiplexing is performed for 10,000 or more targets simultaneously wherein the 10,000 or more target molecules are each separately bound by selective probes. In some embodiments, parallel multiplexing is performed for 100,000 or more targets simultaneously wherein the 100,000 or more target molecules are each separately bound by selective probes.

[0068] In some embodiments, the target-binding moiety comprises a primary antibody. In some embodiments, the target-binding moiety comprises a secondary antibody. In some embodiments, in any of the methods described herein, the method comprises use of more than one target-binding moiety, for example, two target-binding moieties, three target-binding moieties, four target-binding moieties, five target-binding moieties, six target-binding moieties, seven target-binding moieties, eight target-binding moieties, nine target-binding moieties, or 10 target-binding moieties. In some embodiments more than 10 target-binding moieties are used in any of the methods described herein, for example, more than 100 target-binding moieties, more than 1,000 target binding moieties, more than 10,000 target binding moieties, or 100,000 target binding moieties.

[0069] In some embodiments, the modified HCR hairpin comprises a domain that is complementary (will hybridize) to a domain on the trigger oligo. In some embodiments, the modified HCR hairpin comprises a domain that is only partially complementary (will hybridize) to a domain on the trigger oligo. In some embodiments, the modified HCR hairpin does not comprise a domain that is complementary to a domain on the trigger oligo.

[0070] In some embodiments, the structured nucleic acid probe comprises a domain that is complementary (will hybridize) to a domain on the trigger oligo. In some embodiments, the structured nucleic acid probe comprises a domain that is partially complementary (will hybridize) to a domain on the trigger oligo. In some embodiments, the

structured nucleic acid probe does not comprise a domain that is complementary to a domain on the trigger oligo.

[0071] In some embodiments, any of the methods described herein further comprise binding the trigger oligo to the modified HCR hairpin, wherein binding of the trigger oligo to the modified HCR hairpin results in opening of the modified HCR hairpin.

[0072] In some embodiments, the method further comprises binding the trigger oligo to the structured probe, wherein binding of the trigger oligo to the structured probe exposes the previously sequestered HCR initiator.

[0073] In any of the methods described herein, any one or more of the following can be detected and/or assayed for: molecules, DNA molecules, RNA molecules, protein molecules, small molecules, synthetic molecules, or complexes of molecules. In some embodiments, the target is more than one target, such as a complex of proteins, or a complex of a protein and a nucleic acid, etc. In some embodiments, inorganic or non-organic materials can also be assayed for. In some embodiments, the target is a nucleic acid molecule. In some embodiments, the target is a protein. In some embodiments, the target consists of at least one of: mRNA, miRNA, lncRNA, rRNA, non-coding RNA, or genomic DNA. In some embodiments, the target is comprised of an amino acid sequence. In some embodiments, the target is comprised of a complex of molecules. In some embodiments, the target is at least one of: DNA, RNA, protein, or small molecule target molecules or complexes in vitro, in situ, ex vivo, or in vivo. In some embodiments, the target is a complex of molecules that is made up of at least one of: DNA, RNA, protein, or small molecule target molecules. In some embodiments the target comprises a molecule or complex in vitro, in situ, or in vivo.

[0074] FIG. 1A depicts further embodiments involving HCR. In particular, FIG. 1A shows metastable fluorescent hairpins that self-assemble into fluorescent amplification polymers upon detection of a cognate initiator. Initiator I1 nucleates with hairpin monomer H1 via base-pairing to single-stranded toehold 'a', mediating a branch migration that opens the hairpin monomer to form complex I1•H1 containing single-stranded segment 'c*-b*'. This complex nucleates with hairpin monomer H2 by means of base-pairing to toehold 'c', mediating a branch migration that opens the hairpin monomer to form complex I1•H1•H2 containing single-stranded segment 'b*-a*'. Thus, the initiator sequence is regenerated,

providing the basis for a chain reaction of alternating H1 and H2 polymerization steps. Stars denote fluorophores. Arrowhead denotes 3' end of each strand. FIG. 1B shows an immunohistochemistry protocol. Detection stage: antibody probes carrying HCR initiators are hybridized to protein targets and unused probes are washed from the sample. Amplification stage: initiators trigger self-assembly of tethered fluorescent amplification polymers and unused hairpins are washed from the sample. FIG. 1C shows an experimental timeline. The same two-stage protocol is used independent of the number of target molecule species. For multiplexed experiments, antibody probes for different target species carry orthogonal initiators that trigger orthogonal HCR amplification cascades labeled by spectrally distinct fluorophores.

[0075] FIGs. 2A-2B depict further embodiments involving HCR-IHC schemes that use oligo-labeled primary antibodies.

[0076] Scheme A of FIG. 2A depicts an embodiment using a primary antibody labeled with unstructured HCR initiator.

[0077] Stage 1 of Scheme A: Target protein detection using primary antibody labeled with unstructured HCR initiator. Antibody probes are hybridized within the fixed sample and unused probes are washed away.

[0078] Stage 2 of Scheme A: Signal amplification using HCR. HCR hairpins are hybridized within the fixed sample and unused hairpins are washed away. This is a simple 2-stage scheme.

[0079] Performance implications of Scheme A: With Scheme A, unstructured HCR initiators carried by the primary antibody can inhibit sample penetration and/or increase non-specific binding of the antibody probe within the sample, generating amplified background during Stage 2.

[0080] Scheme B of FIG. 2B depicts an embodiment using primary antibody labeled with HCR hairpin. To reduce the potential for non-specific binding of the antibody probe, Scheme B instead labels the primary antibody with one or more HCR hairpins. Because each HCR hairpin contains a duplex stem, the potential for off-target base pairing of the oligo-labeled antibody probe is reduced compared to Scheme A.

[0081] Stage 1 of Scheme B: Target protein detection using primary antibody labeled with HCR hairpin. Antibody probes are hybridized within the fixed sample and unused probes are washed away.

[0082] Stage 2 of Scheme B: Probe activation using unstructured HCR initiator. Initiators are hybridized within the fixed sample and unused initiators are washed away. The HCR initiators open the HCR hairpins carried by the antibody probe, activating the hairpins by exposing an HCR initiator for subsequent triggering of HCR signal amplification in Stage 3.

[0083] Stage 3 of Scheme B: Signal amplification using HCR. HCR hairpins are hybridized within the fixed sample and unused hairpins are washed away.

[0084] Performance implications of Scheme B: Compared to Scheme A, where one or more HCR initiators label the antibody probe, the individual HCR initiators used in Scheme B are less susceptible to non-specific binding within the sample, and there is no potential for polyvalent off-target binding (which does exist with Scheme A if antibody probes carry more than one HCR initiator). With Scheme B, if the HCR initiator binds non-specifically in the sample during Stage 2, it will lead to amplified background during Stage 3.

[0085] Scheme C of FIG. 2C depicts an embodiment using a primary antibody labeled with a modified HCR hairpin. This embodiment reduces background by changing the toehold sequence for the input domain of the modified hairpins labeling the antibody probe, as well as the corresponding sequence in an unstructured trigger oligo that will be used to activate the modified hairpins carried by the antibody probe. For example, the antibody probe can be labeled with modified versions of the H1 hairpin monomer containing input domain ('e-b') instead of the input domain ('a-b') carried by a standard H1 hairpin monomer. This modified version of H1 can be activated by a trigger oligo ('b*-e*') in Stage 2 that is not itself an HCR initiator. As a result, if the trigger oligo binds non-specifically in the sample, it will not generate amplified background in Stage 3.

[0086] Stage 1 of Scheme C: Target protein detection using primary antibody labeled with modified HCR hairpin. Antibody probes are hybridized within the fixed sample and unused probes are washed away.

[0087] Stage 2 of Scheme C: Probe activation using unstructured trigger oligo. The trigger oligos open the modified hairpins carried by the antibody probe, activating the modified hairpins by exposing an HCR initiator for subsequent triggering of HCR signal amplification in Stage 3.

[0088] Stage 3 of Scheme C: Signal amplification using HCR. HCR hairpins are hybridized within the fixed sample and unused hairpins are washed away.

[0089] Performance Implications of Scheme C: Compared to Scheme B, Scheme C has the additional benefit that non-specific binding of the unstructured trigger oligo in Stage 2 does not lead to amplified background in Stage 3. Because the unstructured trigger oligo is not an HCR initiator, only the activated hairpins carried by the antibody probes are capable of triggering growth of HCR amplification polymers in Stage 3.

[0090] Scheme D of FIG. 2D depicts an embodiment using a primary antibody labeled with a hairpin probe that sequesters an HCR initiator. In this embodiment, instead of using a modified HCR hairpin where only the toehold of the input domain is changed relative to a normal HCR hairpin, the hairpin probe that labels the antibody can have domain dimensions and/or domain sequences that differ from a normal HCR hairpin. For example, the toehold length of the input domain could be extended relative to that of a normal HCR hairpin to promote high-yield activation of the hairpin probes carried by the antibody probes. Functionally, the hairpin probe labeling the antibody probe has the property that it predominantly initiates HCR if and only if it has been activated by the trigger oligo in Stage 2. Stage 1 of Scheme D: Target protein detection using primary antibody labeled with hairpin probe that sequesters an HCR initiator. Antibody probes are hybridized within the fixed sample and unused probes are washed away.

[0091] Stage 2 of Scheme D: Hairpin probe activation using unstructured trigger oligo. The trigger oligos open the hairpin probes carried by the antibody probe, activating the hairpin probes by exposing an HCR initiator for subsequent triggering of HCR signal amplification in Stage 3.

[0092] Stage 3 of Scheme D: Signal amplification using HCR. HCR hairpins are hybridized within the fixed sample and unused hairpins are washed away.

[0093] Performance Implications of Scheme D: This scheme has the potential to increase the yield of hairpin activation on antibody probes.

[0094] In some embodiments, instead of labeling the primary antibody with an oligo, another option is to use unlabeled primary antibodies, and instead to use oligo-labeled secondary antibodies to initiate the growth of tethered fluorescent HCR amplification polymers. The following four Schemes (E, F, G, H) of FIGs. 3A-3D parallel the four previous schemes (A, B, C, D) of FIGs. 2A-2D; in each case, there is one extra stage corresponding to the use of a secondary antibody to detect the primary antibody, and the oligo label has been shifted from the primary antibody to the secondary antibody.

[0095] Scheme E of FIG. 3A depicts an embodiment using a secondary antibody labeled with unstructured HCR initiator. Stage 1 of Scheme E: Target protein detection using unlabeled primary antibody. Stage 2 of Scheme E: Primary antibody detection using secondary antibodies labeled with unstructured HCR initiators. Stage 3 of Scheme E: Signal amplification using HCR.

[0096] Scheme F of FIG. 3B depicts an embodiment of a secondary antibody labeled with HCR hairpin. Stage 1 of Scheme F: Target protein detection using unlabeled primary antibody. Stage 2 of Scheme F: Primary antibody detection using secondary antibodies labeled with HCR hairpins. Stage 3 of Scheme F: Probe activation using an unstructured HCR initiator. Stage 4 of Scheme F: Signal amplification using HCR.

[0097] Scheme G of FIG. 3C depicts an embodiment using a secondary antibody labeled with modified HCR hairpin. Stage 1 of Scheme G: Target protein detection using unlabeled primary antibody. Stage 2 of Scheme G: Primary antibody detection using secondary antibodies labeled with modified HCR hairpins. Stage 3 of Scheme G: Probe activation using an unstructured trigger oligo. Stage 4 of Scheme G: Signal amplification using HCR.

[0098] Scheme H of FIG. 3D depicts an embodiment using a secondary antibody labeled with a hairpin probe that sequesters an HCR initiator. Stage 1 of Scheme H: Target protein detection using unlabeled primary antibody. Stage 2 of Scheme H: Primary antibody detection using secondary antibodies labeled with hairpin probes that sequester an HCR initiator. Stage 3 of Scheme H: Hairpin probe activation using an unstructured trigger oligo. Stage 4 of Scheme H: Signal amplification using HCR.

[0099] In some embodiments, a disadvantage of using a secondary antibody (Schemes E, F, G, H of FIGs. 3A-3D) is the need for an extra stage in the protocol (relative to Schemes A, B, C, D of FIGs. 2A-2D).

[0100] Performance Implications: In some embodiments, the advantage of using oligo-labeled secondary antibodies is that a library of orthogonal secondary antibodies can be validated and reused for different primary antibodies. For example, consider a library of five orthogonal secondary antibodies. These could each be reused for 1000 primary antibodies that detect different target proteins.

[0101] In some embodiments, an advantage of using oligo-labeled primary antibodies is the ability to perform highly multiplexed experiments in which multiple target types are detected simultaneously using different primary antibodies that each bind selectively to a single target type; for example simultaneous detection of 10 target types, or 100 target types, or 1000 target types, or 10,000 target types, or 100,000 target types.

[0102] In some embodiments, a method is provided that is depicted in FIG. 9. The method comprises a four-stage scheme: a) Stage 1: target detected using primary antibody probe carrying nucleic acid hairpin probe sequestering HCR initiator; unbound probe washed from sample. Stage 2: Unstructured trigger oligo activates hairpin probe, exposing HCR initiator; unbound trigger oligos washed from sample. Stage 3: signal amplification via polymerization of H1 and H2 hairpins, each carrying label binding site; unbound H1 and H2 hairpins washed from sample. Stage 4: label probes comprising a complement to the label binding site and additionally comprising a detectable reporter are hybridized to the amplification polymers; unbound label probes are washed from the sample.

Examples

Examples of HCR-IHC

Example 1

[0103] An example of an antibody-oligo conjugation scheme is shown in FIGs. 4A-4C. As shown in FIG. 4A, the heterobifunctional linker S-HyNiC is reacted with the amine group of lysine residues within the antibody, functionalizing the antibody with a hydrazide group. In FIG. 4B the oligo is synthesized with an amine group and reacted with a

heterobifunctional linker S-4FB, functionalizing the oligo with an aldehyde group. In FIG. 4C the two functionalized components are incubated together in the presence of an aniline catalyst that promotes the formation of a hydrazone bond, covalently linking the antibody and the oligo.

Example 2

[0104] A HCR-IHC result is illustrated in FIG. 5. Reduced background was observed using Scheme F (secondary antibodies carrying HCR hairpins) relative to Scheme E (secondary antibodies carrying unstructured HCR initiators), indicating that antibodies labeled with HCR hairpins are less prone to non-specific binding than antibodies labeled with unstructured HCR initiators. As shown in FIG. 5, sample penetration was improved and background was reduced using the hairpin-labeled antibodies (Scheme F). Embryos fixed 27 hours post-fertilization (hpf). Scale bar: 50 μm.

Example 3

[0105] The quantitative nature of HCR is illustrated in FIGs. 6A-6B. Using Scheme F of FIG 3B, target proteins were detected using primary antibodies (Stage 1). Then, two batches of secondary antibodies carrying orthogonal HCR hairpins were used to detect the primary antibodies (Stage 2). These probes were then each activated using their orthogonal HCR initiators (Stage 3). HCR amplification was then performed using the two orthogonal HCR systems carrying spectrally distinct fluorophores (Stage 4), leading to redundant imaging of protein expression. If HCR signal scales linearly with primary antibody abundance, a 2-channel scatter plot of voxel intensities will reveal a linear distribution. If primary antibody binding scales linearly with target protein abundance, HCR-ISH will enable relative quantitation of protein abundance within the fixed sample.

[0106] FIG. 6A shows redundant 2-channel mapping of protein expression using two batches of secondary antibody and two orthogonal HCR amplifiers carrying spectrally distinct fluorophores. Row 1: Zebrafish line: wild type. Target protein: Desmin. Primary antibody: rabbit anti-Desmin. Secondary antibody: donkey anti-rabbit. Row 2: Zebrafish line: ct-122a. Target protein: Citrine. Primary antibody: chicken anti-GFP (which binds selectively to Citrine protein). Secondary antibody: goat anti-chicken. FIG. 6B Highly

correlated subcellular voxel intensities within the solid boundary (Pearson correlation coefficient: $r = 0.96$ for Desmin, $r = 0.98$ for Citrine). To avoid inflating the correlation coefficient, voxels were excluded that fell below background thresholds in both channels (excluded voxels lie in the black rectangles at the lower left corner of the correlation plots). For each channel, the background threshold was defined as the mean plus two standard deviations for the voxels in the small white dashed square. Embryos fixed 27 hours post-fertilization. Scale bar: 50 μm.

Example of simultaneously mapping protein and mRNA expression via HCR-IHC/HCR-ISH

Example 4

[0107] In situ hybridization (ISH) using HCR employs nucleic acid probes carrying HCR initiators to map mRNA targets within fixed samples (Choi et al. 2010; Choi et al. 2014). FIG. 7 provides an example of a scheme for simultaneous HCR-IHC and HCR-ISH in a single fixed specimen. HCR signal amplification is performed for all protein and mRNA targets simultaneously.

[0108] As shown in FIG. 7, Stage 1: Target protein detection uses unlabeled primary antibody; unbound primary antibodies washed form the sample. In stage 2: primary antibody detection using secondary antibody labeled with an HCR hairpin; unbound secondary antibodies washed from the sample. In stage 3: target mRNA detection using DNA probes carrying HCR initiators; unbound DNA probes washed from the sample. In stage 4: activation of the hairpin carried by the antibody probe using unstructured HCR initiator as a trigger oligo; unused trigger oligos washed from the sample. In stage 5: HCR signal amplification triggered by exposed HCR initiators carried by DNA probes selectively bound to mRNA targets (from Stage 3) or triggered by exposed HCR initiators carried by antibody probes (activated by trigger oligos in Stage 4); unbound metastable HCR hairpin monomers are washed from the sample. This example uses HCR-IHC Scheme F as the starting point, but any of Schemes A-H can be combined with HCR-ISH similarly.

Example of HCR-IHC/HCR-ISH

Example 5

[0109] Simultaneous mapping of 2 proteins and 2 mRNAs is illustrated in the 4-channel image of FIG. 8A. High signal-to-background was achieved for all four targets. FIG. 8A depicts 4-channel confocal microscopy images showing mapping of 2 proteins and the corresponding 2 mRNAs. One representative optical section is shown for each of 3 replicate embryos. FIG. 8B provides pixel intensity histograms. Signal + Background estimated from voxels within solid boundary; Background estimated from voxels within dashed boundary. Embryos were fixed 27 hours post-fertilization. Scale bar: 50 μm. Signal-to-background (mean ± standard deviation for N=3 embryos): 15 ± 8 for *desmin* mRNA, 14 ± 5 for Desmin protein, 19 ± 9 for *Tg(kdrl:egfp)* mRNA, 17 ± 6 for Tg(kdrl:eGFP) protein.

Methods of HCR Using Trigger Oligos

Example 6

[0110] HCR amplification is performed using a probe that comprises a target-binding region, which is linked to a structured nucleic acid region. The structured nucleic acid region sequesters an HCR initiator. The target-binding region binds selectively to the target, and then unbound probes are washed from the sample. Addition of a trigger oligo to the sample results in binding to the structured nucleic acid region, which results in a conformation change that exposes the HCR initiator. Exposure of the HCR initiator allows for amplification from the initiator using HCR. The resulting HCR amplification polymer contains a combination of fluorescent markers which can be detected and identified as corresponding to the presence of a particular target.

Example 7

[0111] HCR amplification is performed using a trigger oligo by providing at least one target-binding moiety that is labeled with a modified HCR hairpin; a target molecule; a trigger oligo; and a pair of metastable HCR hairpin monomers. The trigger oligo binds to the modified HCR hairpin and the pair of metastable HCR hairpin monomers do not bind directly to the modified HCR hairpin unless the trigger oligo has first bound to the modified HCR hairpin. After binding of the trigger oligo, HCR signal amplification is performed to produce an amplification polymer and a signal is detected from the polymer (where each of

the HCR hairpin monomers that self-assemble to make the polymer include a reporter marker) to identify the target molecule.

Example 8

[0112] HCR amplification can be performed using a trigger oligo by providing (i) at least one target-binding moiety labeled with a structured probe sequestering an HCR initiator (ii) a target molecule, (iii) a trigger oligo, and (iv) at least a pair of polymerizing HCR hairpins. The trigger oligo binds to the structured probe. The pair of metastable HCR hairpin monomers do not bind to the sequestered HCR initiator. The trigger oligo binds to the structured probe to expose the HCR initiator, which triggers self-assembly of the fluorophore-labeled metastable HCR monomers to generate a detectable HCR amplification polymer. If each of the two metastable hairpin species carries a different fluorophore reporter, each amplification polymer will be detectable in 2 channels where the ratio of intensities in the two channels will be approximately constant independent of the length of each amplification polymer (because the number of H1 hairpin monomers in each amplification polymer is either one less, equal to, or one more than the number of H2 hairpin monomers in each amplification polymer).

WHAT IS CLAIMED IS:

1. A method comprising:

providing a probe comprising a target-binding region linked to a structured nucleic acid region, wherein the structured nucleic acid region sequesters an HCR initiator;

adding a trigger oligo, wherein the trigger oligo binds to the structured nucleic acid region, which changes conformation to expose the initiator; and

amplifying from the initiator using HCR.

2. The method of claim 1, wherein the structured nucleic acid region comprises a hairpin probe.

3. The method of claim 2, wherein the trigger oligo binds to the hairpin probe at a toehold and a stem section, thereby changing the conformation of the hairpin probe to expose the HCR initiator.

4. The method of claim 2, wherein the hairpin probe comprises:
an input domain comprising a toehold and stem section,
an output domain comprising a hairpin loop and a complement to the stem section, such that the output domain comprises a sequestered HCR initiator.

5. The method of claim 4, wherein the trigger oligo binds to the input domain, thereby exposing the output domain which is capable of triggering HCR.

6. The method of claim 2, wherein the hairpin probe is an HCR hairpin monomer.

7. The method of claim 6, wherein the trigger oligo is an HCR initiator.

8. The method of claim 4, wherein the hairpin probe comprises a modified HCR hairpin monomer with a modified input domain that has a modified toehold sequence, wherein the modified HCR hairpin monomer is configured such that the hairpin probe does not trigger HCR, but wherein the trigger oligo hybridizes to the modified input domain to expose the output domain that triggers HCR amplification using a set of first and second metastable HCR hairpin monomers.

9. The method of claim 2, wherein the hairpin probe is not an HCR hairpin.

10. The method of claim 9, wherein the hairpin probe is not configured to trigger HCR.

11. The method of any one of the preceding claims, wherein HCR is performed using at least a first and second set of metastable HCR hairpin monomers.

12. The method of claim 11, wherein the first and second set of metastable HCR hairpin monomers each further comprise a reporter molecule.

13. The method of claim 11, wherein the first and second set of metastable HCR hairpin monomers each further comprise a label-binding site that is configured to hybridize to a complement to the label binding site, wherein the complement to the label binding site further comprises a reporter molecule.

14. The method of any one of the preceding claims where the target molecule is a protein.

15. The method of any of claims 1-13 where the target molecule is a small molecule or nucleic acid.

16. The method of any of claims 1-13 where the target molecule is a complex of two or more proteins, nucleic acids, and/or small molecules.

17. The method of any one of the preceding claims where the structured nucleic acid region comprises DNA, RNA, LNA, PNA, 2'OMe-RNA, or a synthetic nucleic acid analog.

18. The method of any of the preceding claims where the target-binding region comprises DNA, RNA, LNA, PNA, 2'OMe-RNA, a synthetic nucleic acid analog, amino acid, or synthetic amino acid analog.

19. The method of any one of the preceding claims, wherein the target-binding region is an antibody.

20. The method of claim 19, wherein the antibody comprises a primary antibody.

21. The method of claim 19, wherein the antibody comprises a first antibody that binds to the target molecule, and a second antibody that binds to the first antibody, wherein the structured nucleic acid region is linked to the second antibody but is not linked to the first antibody.

22. The method of any one of the preceding claims, further comprising washing away any unbound probe from a sample.

23. The method of claim 22, wherein a trigger oligo is added to the sample, after unbound probe has been washed from the sample.

24. The method of any one of the preceding claims, wherein amplifying using HCR comprises adding at least two different species of metastable HCR hairpin monomers to the sample.

25. The method of claim 24, wherein the two different species comprises a first species comprising a first reporter molecule and a second species comprising a second reporter molecule.

26. The method of any of the preceding claims where the reporter molecules are fluorescent molecules, non-fluorescent molecules, FRET molecules, or rare earth elements.

27. The method of any one of the preceding claims, wherein amplifying provides a fluorescent amplification polymer.

28. The method of any one of the preceding claims, wherein the metastable HCR monomers comprise a label-binding site.

29. The method of claim 28, further comprising:

washing the sample to remove unpolymerized HCR hairpin monomers;

adding a label probe that comprises a complement to the label binding site and a reporter molecule;

washing unbound label probe; and

detecting a presence or absence of the reporter molecule.

30. The method of any one of the preceding claims, wherein more than one target is assayed for at a time, wherein each probe comprises a target-binding region selective for each target to be assayed for.

31. The method of any one of the preceding claims, wherein more than 100 targets are assayed for at a time, wherein each probe comprises a target-binding region specific for each target to be assayed for.

32. The method of claim 31, wherein the method is an immunohistochemistry assay.

33. The method of any one of the preceding claims, further comprising parallel multiplexing performed for 2 or more targets simultaneously, wherein the two or more target molecules are each separately bound by selective probes.

34. The method of any one of the preceding claims, wherein each HCR amplifier comprises at least two types of kinetically trapped nucleic acid hairpin monomers that co-exist metastably in the absence of the initiator.

35. The method of any one of the preceding claims, wherein amplifying generates a detectable polymer that indicates a presence of a target molecule, wherein the target molecule is bound by the target-binding region.

36. A method, comprising

(i) providing:

at least one target-binding moiety labeled with a modified HCR hairpin;

a target molecule;

a trigger oligo; and

a pair of metastable HCR hairpin monomers, wherein the trigger oligo binds to the modified HCR hairpin and the pair of metastable HCR hairpin monomers do not bind directly to the modified HCR hairpin unless the trigger oligo has first bound to the modified HCR hairpin;

(ii) performing HCR to produce a polymer; and

(iii) detecting a signal from the polymer.

37. A method, comprising

(i) providing:

at least one target-binding moiety labeled with a structured probe sequestering an HCR initiator;

a target molecule;

a trigger oligo; and

at least a pair of metastable HCR hairpin monomers, wherein the trigger oligo binds to the structured probe and the pair of metastable HCR hairpin monomers do not bind to the sequestered HCR initiator, unless the trigger oligo has first bound to the structured probe;

(ii) performing HCR; and

(iii) detecting a signal.

38. The method of any of claims 36 and 37, wherein the target-binding moiety comprises a primary antibody.

39. The method of any of one of claims 36-38, wherein the target molecule comprises a nucleotide sequence.

40. The method of any of one of claims 36-38, wherein the target molecule comprises an amino acid sequence.

41. The method of any of one of claims 36-38, wherein the trigger oligo comprises a nucleotide sequence.

42. The method of any of one of claims 36-38, wherein the trigger oligo comprises an amino acid sequence.

43. The method of claim 36, wherein the modified HCR hairpin comprises a domain that is complementary to a domain on the trigger oligo.

44. The method of claim 37, wherein the structured probe comprises a domain that is complementary to a domain on the trigger oligo.

45. The method of claim 37, wherein the trigger oligo hybridizes and thereby exposes the initiator.

46. The method of either of claims 36 or 37, further comprising incubating the at least one target-binding moiety with the target molecule to allow for binding of the at least one target-binding moiety to the target molecule.

47. The method of claim 46, further comprising washing away the at least one target-binding moiety that is not bound to the target molecule.

48. The method of claim 36, further comprising binding the trigger oligo to the modified HCR hairpin, wherein binding of the trigger oligo to the modified HCR hairpin results in opening of the modified HCR hairpin.

49. The method of claim 37, further comprising binding the trigger oligo to the structured probe, wherein binding of the trigger oligo to the structured probe exposes the previously sequestered HCR initiator.

50. The method of either of claims 36 or 37, wherein the method is part of an in situ process to image DNA, RNA, protein, or small molecule targets, including DNA in situ hybridization (ISH), RNA in situ hybridization (ISH), and/or protein immunohistochemistry (IHC).

51. The method of either of claims 36 or 37, wherein the method is in vitro or in vivo and wherein the target is not immobilized.

52. The method of either of claims 36 or 37, wherein the target is immobilized on a bead or microarray.

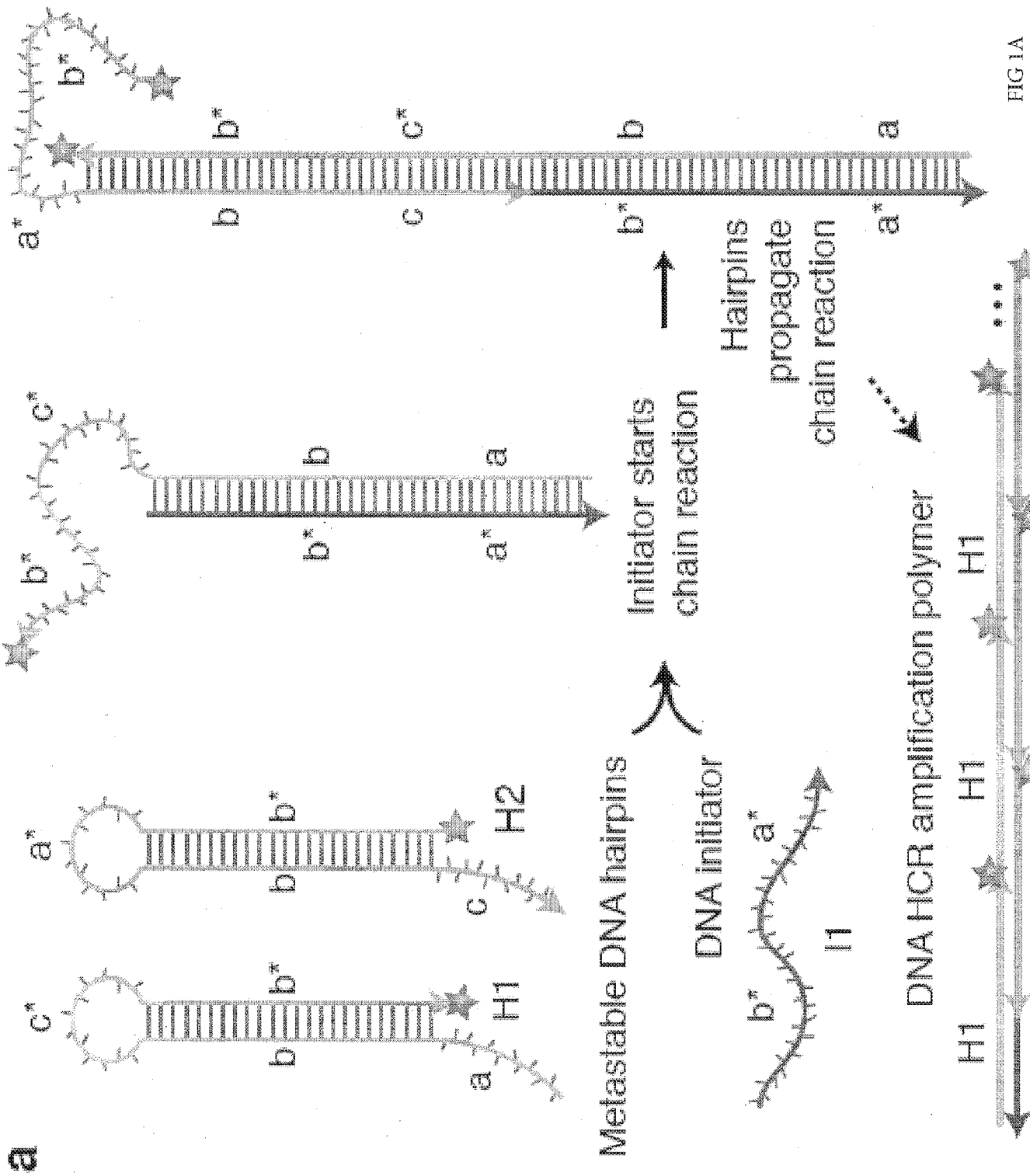

a
Metastable DNA hairpins
DNA initiator
I1
Initiator starts chain reaction
Hairpins propagate chain reaction
DNA HCR amplification polymer
H1
H2

FIG 1A

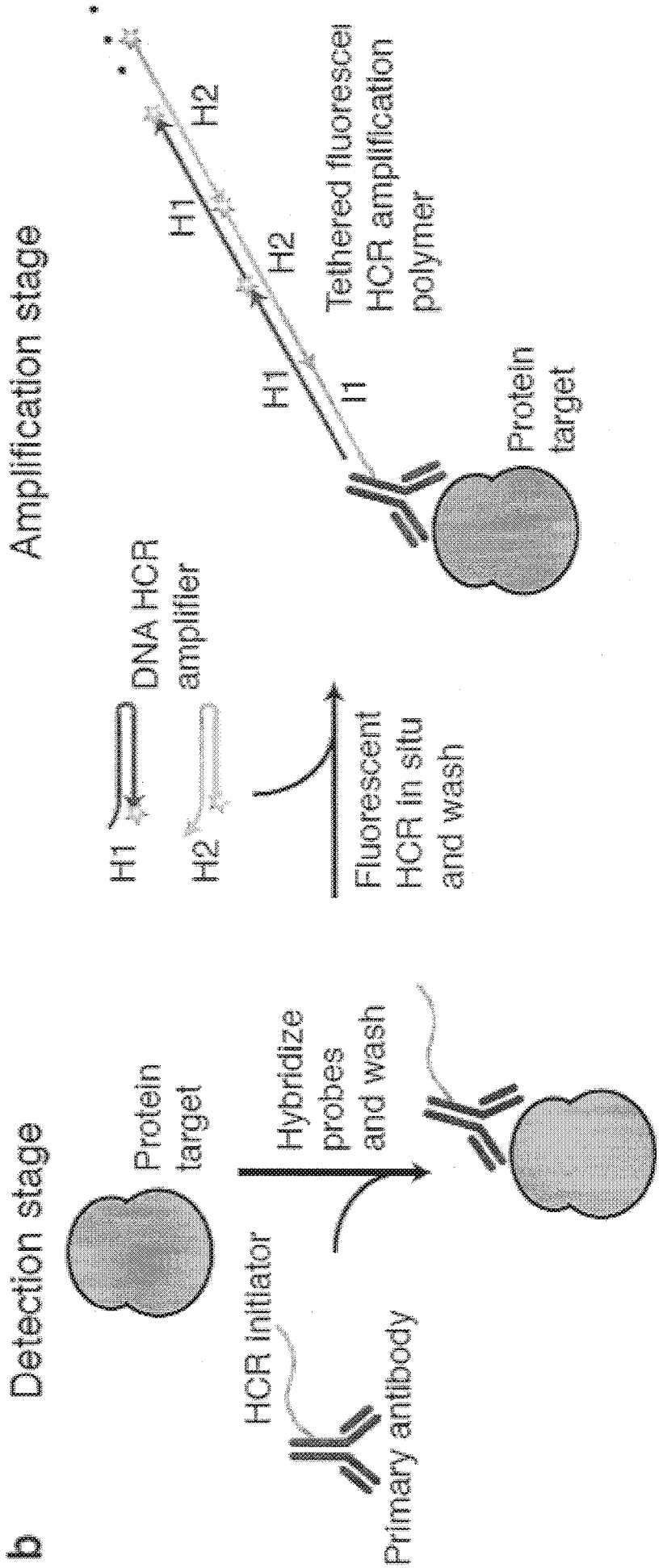

b
Detection stage
Protein target
HCR initiator
Primary antibody
Hybridize probes and wash
Amplification stage
DNA HCR amplifier
H1
H2
Fluorescent HCR in situ and wash
Protein target
I1
H1
H2
H1
H2
Tethered fluorescent HCR amplification polymer

FIG. 1B

C
Antibody 1
Antobody 2
Antibody 3
Add all primary antibodies
Incubation
Wash
Amplifier 1
Amplifier 2
Amplifier 3
Add all DNA HCR amplifiers
Incubation
Wash
0
16
18
34
36
Experimental time (h)

FIG. 1C

(a) Scheme A: Primary antibody labeled with unstructured HCR initiator
Stage 1: Target protein detection using primary antibody labeled with unstructured HCR initiator
Stage 2: Signal amplification using HCR
HCR initiator I1
Primary antibody
Protein target
HCR hairpins
H1
H2
Tethered fluorescent HCR amplification polymer

FIG. 2A

(b) Scheme B: Primary antibody labeled with HCR hairpin
Stage 1: Target protein detection using primary antibody labeled with HCR hairpin
Stage 2: Probe activation using unstructured HCR initiator
HCR hairpin H1
Primary antibody
Protein target
HCR initiator I1

FIG. 2B

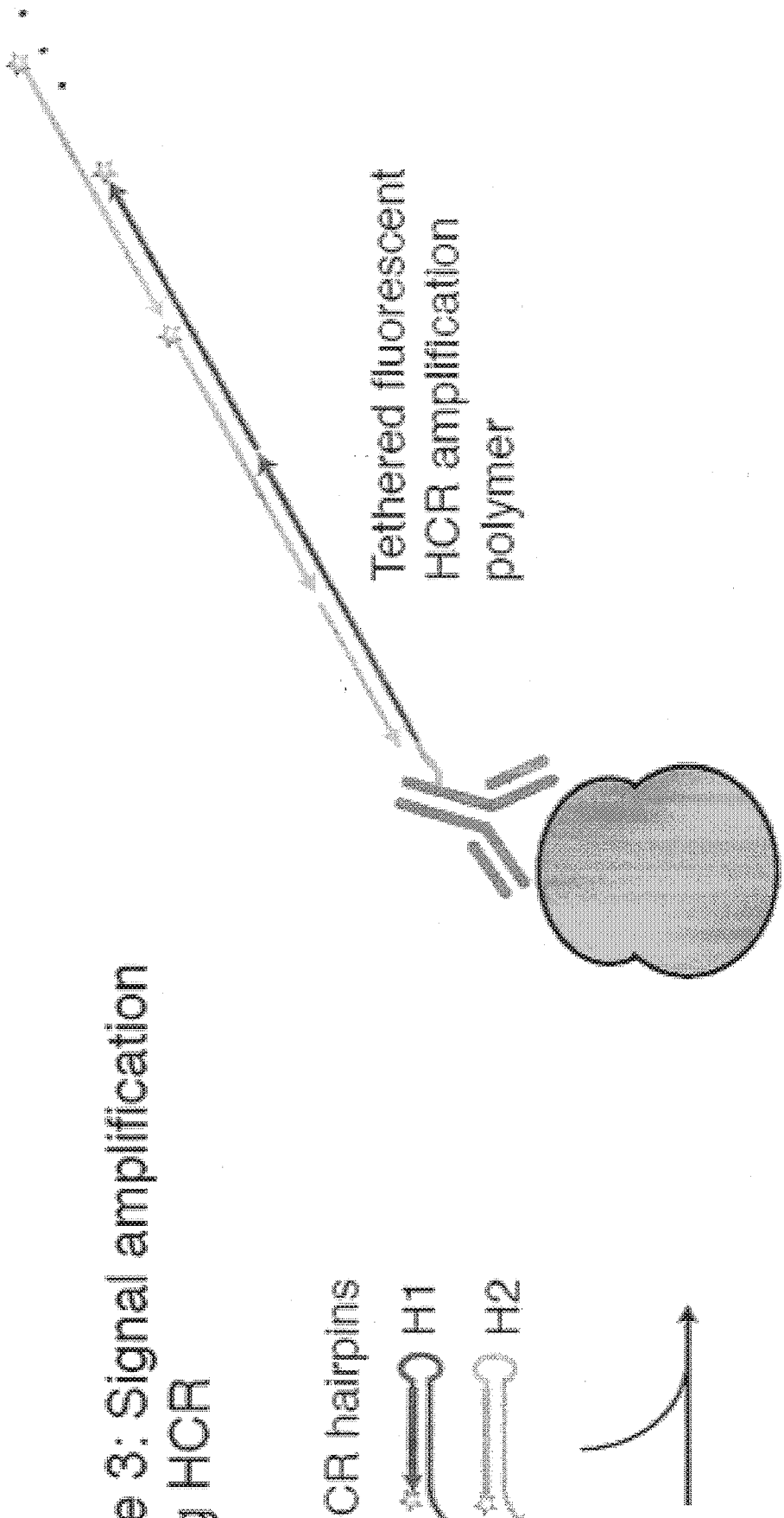

Stage 3: Signal amplification using HCR
HCR hairpins
H1
H2
Tethered fluorescent HCR amplification polymer

FIG. 2B CONTD

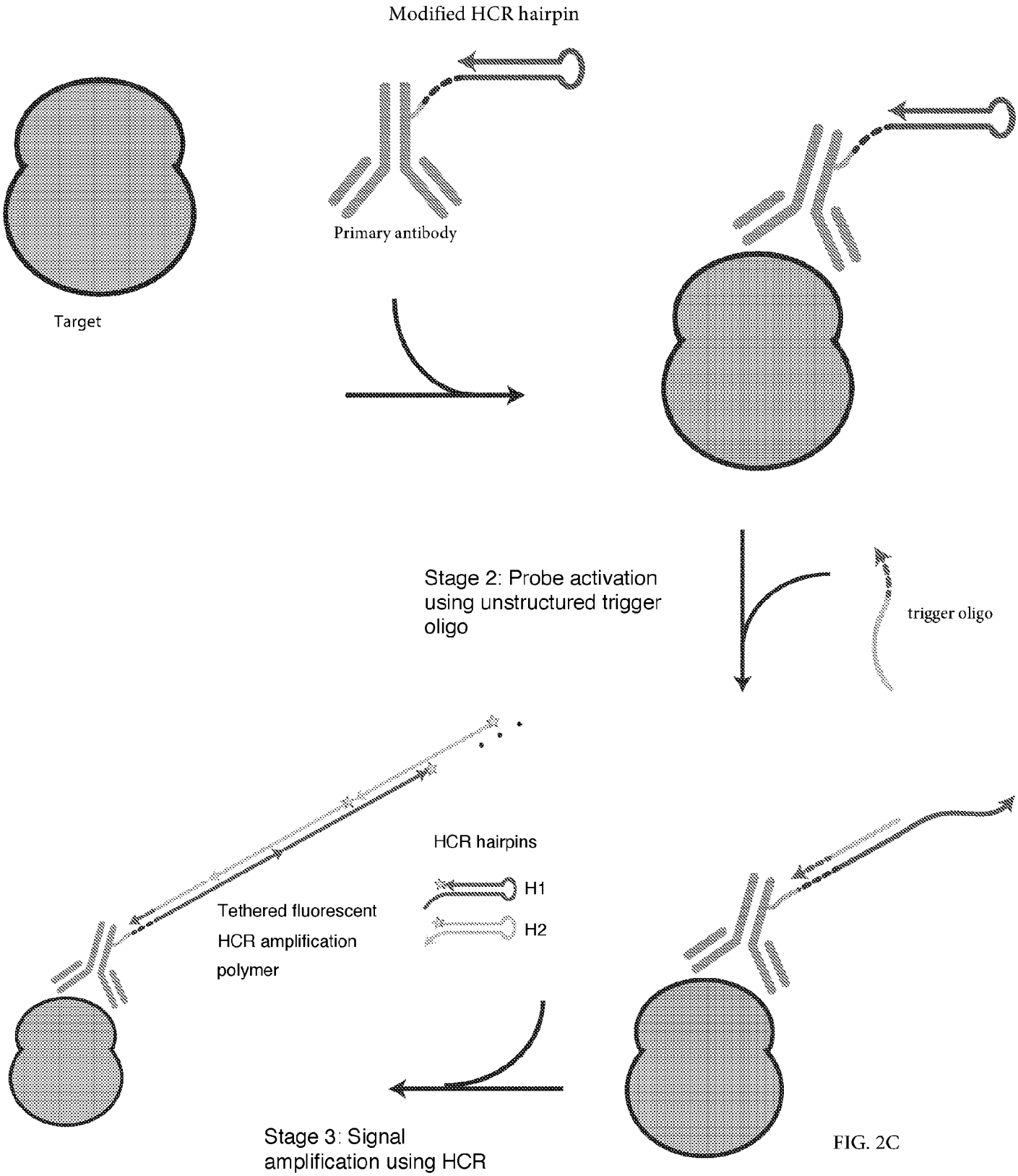

Stage 1: Target protein detection using primary antibody labeled with modified HCR hairpin
Modified HCR hairpin
Primary antibody
Target
Stage 2: Probe activation using unstructured trigger oligo
trigger oligo
HCR hairpins
H1
H2
Tethered fluorescent HCR amplification polymer
Stage 3: Signal amplification using HCR

FIG. 2C

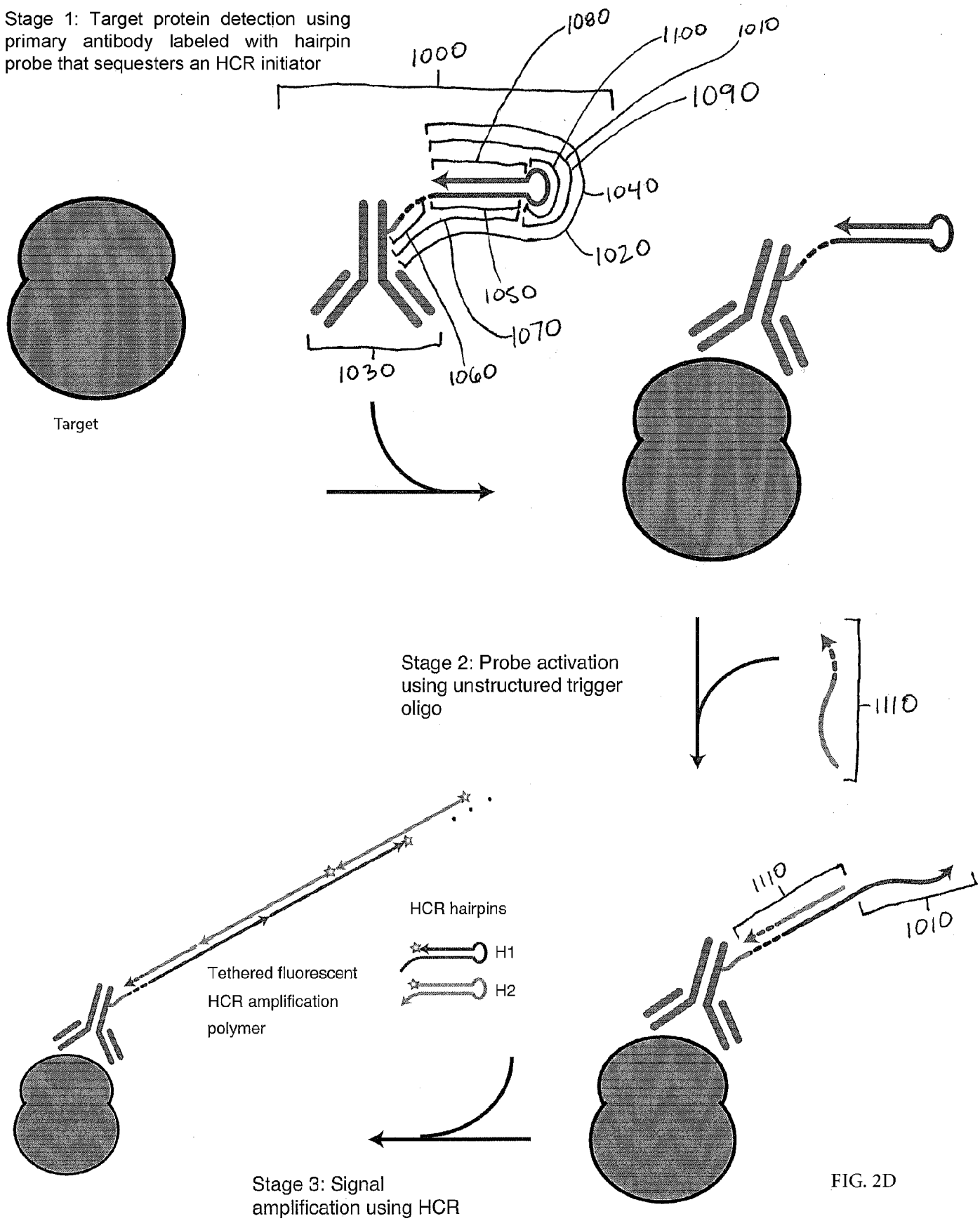

Stage 1: Target protein detection using primary antibody labeled with hairpin probe that sequesters an HCR initiator
1000
1080
1100
1010
1090
1040
1020
1050
1070
1030
1060
Target
Stage 2: Probe activation using unstructured trigger oligo
1110
HCR hairpins
H1
H2
Tethered fluorescent HCR amplification polymer
1110
1010
Stage 3: Signal amplification using HCR

FIG. 2D

(a) Scheme E: Secondary antibody labeled with unstructured HCR initiator

Target protein detection using unlabeled primary antibody

Stage 1:

Stage 2: Primary antibody detection using secondary antibody labeled with unstructured HCR initiator

FIG. 3A

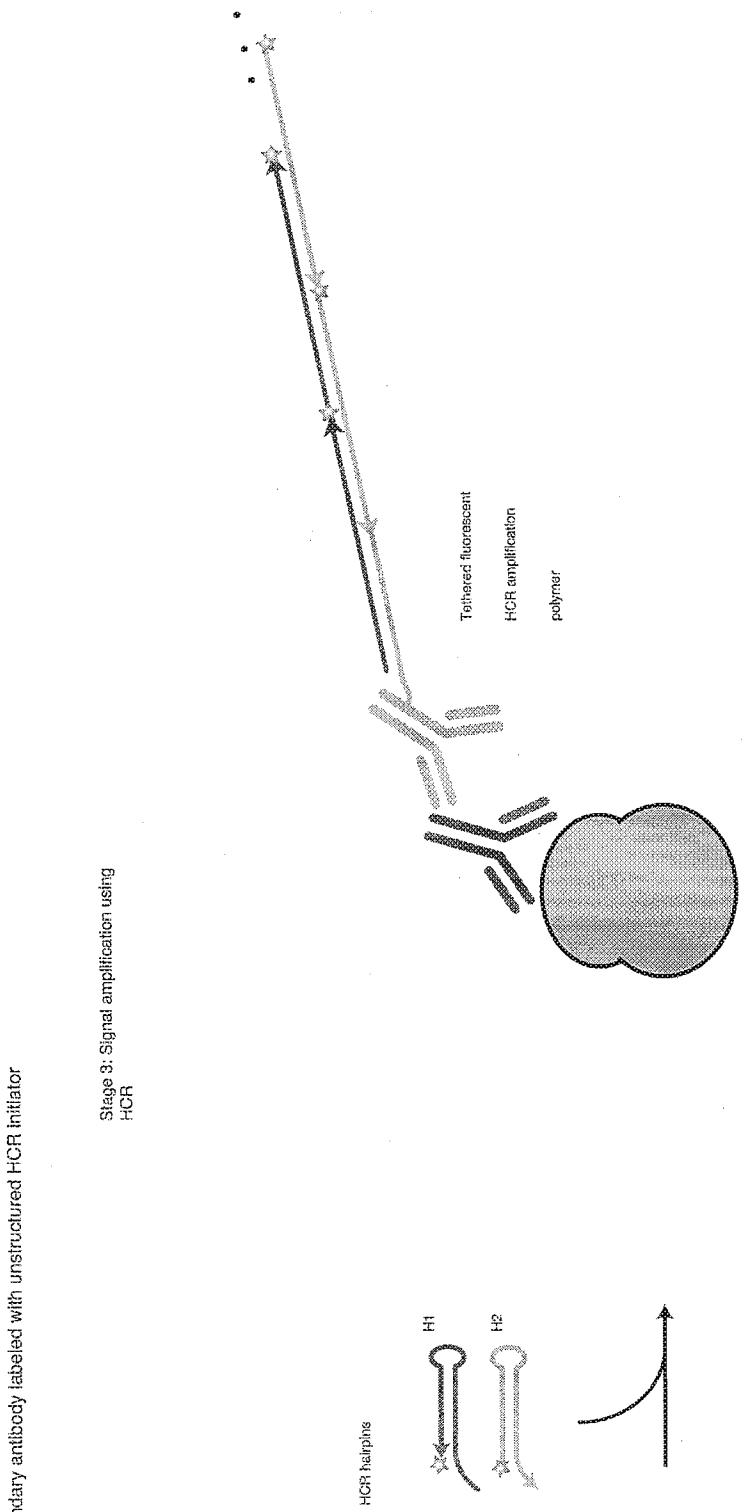

(a) Scheme E: Secondary antibody labeled with unstructured HCR initiator
Stage 3: Signal amplification using HCR
HCR hairpins
H1
H2
Tethered fluorescent HCR amplification polymer

FIG. 3A CONT.

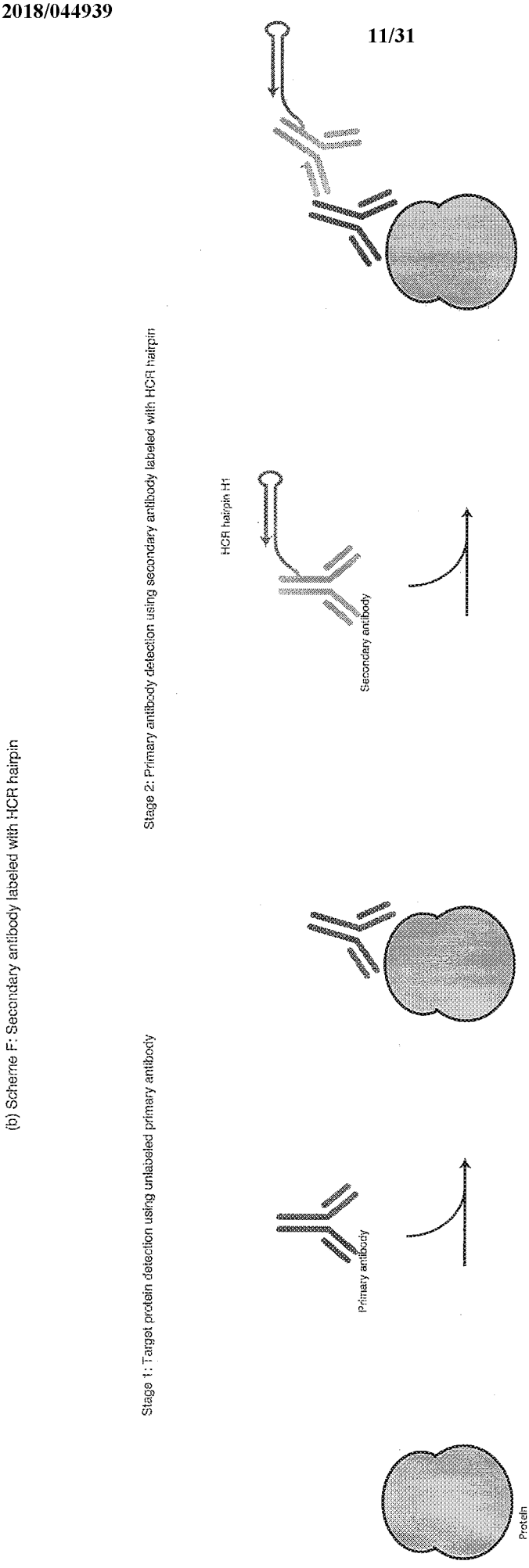

(b) Scheme F: Secondary antibody labeled with HCR hairpin
Stage 1: Target protein detection using unlabeled primary antibody
Stage 2: Primary antibody detection using secondary antibody labeled with HCR hairpin
Protein target
Primary antibody
Secondary antibody
HCR hairpin H1

FIG. 3B

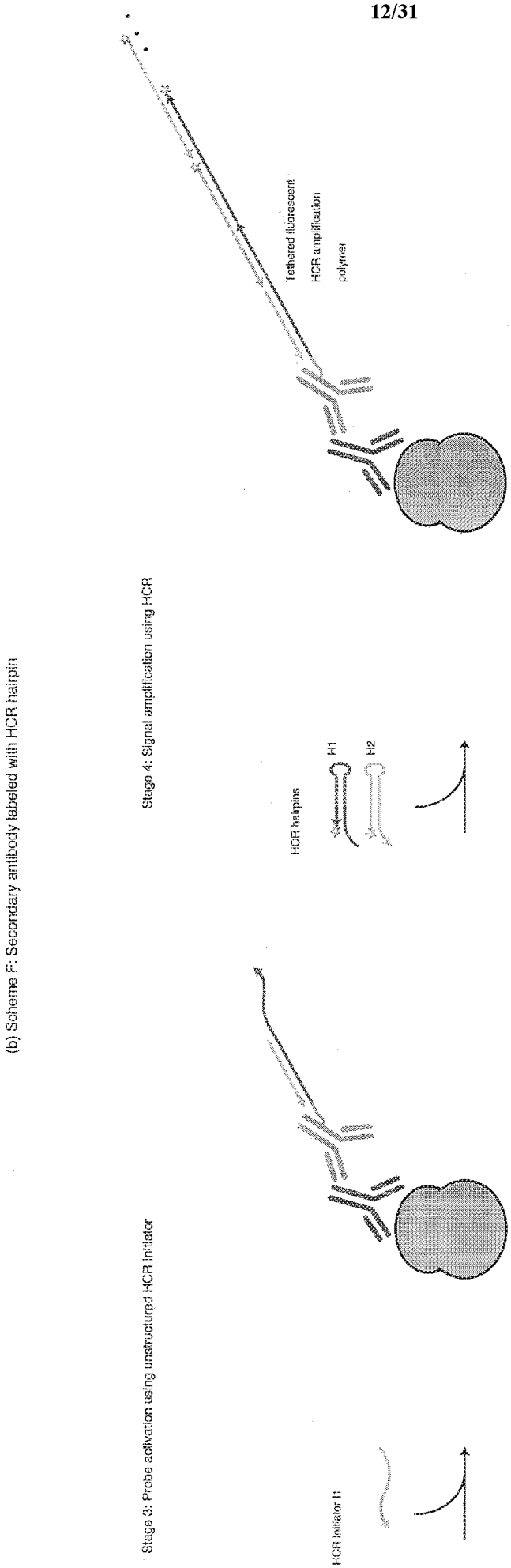

(b) Scheme F: Secondary antibody labeled with HCR hairpin
Stage 3: Probe activation using unstructured HCR initiator
HCR initiator I1
Stage 4: Signal amplification using HCR
HCR hairpins
H1
H2
Tethered fluorescent
HCR amplification
polymer

FIG. 3B CONT.

(c) Scheme G: Secondary antibody labeled with modified HCR hairpin
Stage 1: Target protein detection using unlabeled primary antibody
Protein target
Primary antibody
Stage 2: Primary antibody detection using secondary antibody labeled with modified HCR hairpin
Secondary antibody
Modified HCR hairpin

FIG. 3C

(c) Scheme G: Secondary antibody labeled with modified HCR hairpin
Stage 3: Probe activation using unstructured trigger oligo
Trigger oligo
Stage 4: Signal amplification using HCR
HCR hairpins
H1
H2
Tethered fluorescent HCR amplification polymer

FIG. 3C
CONT.

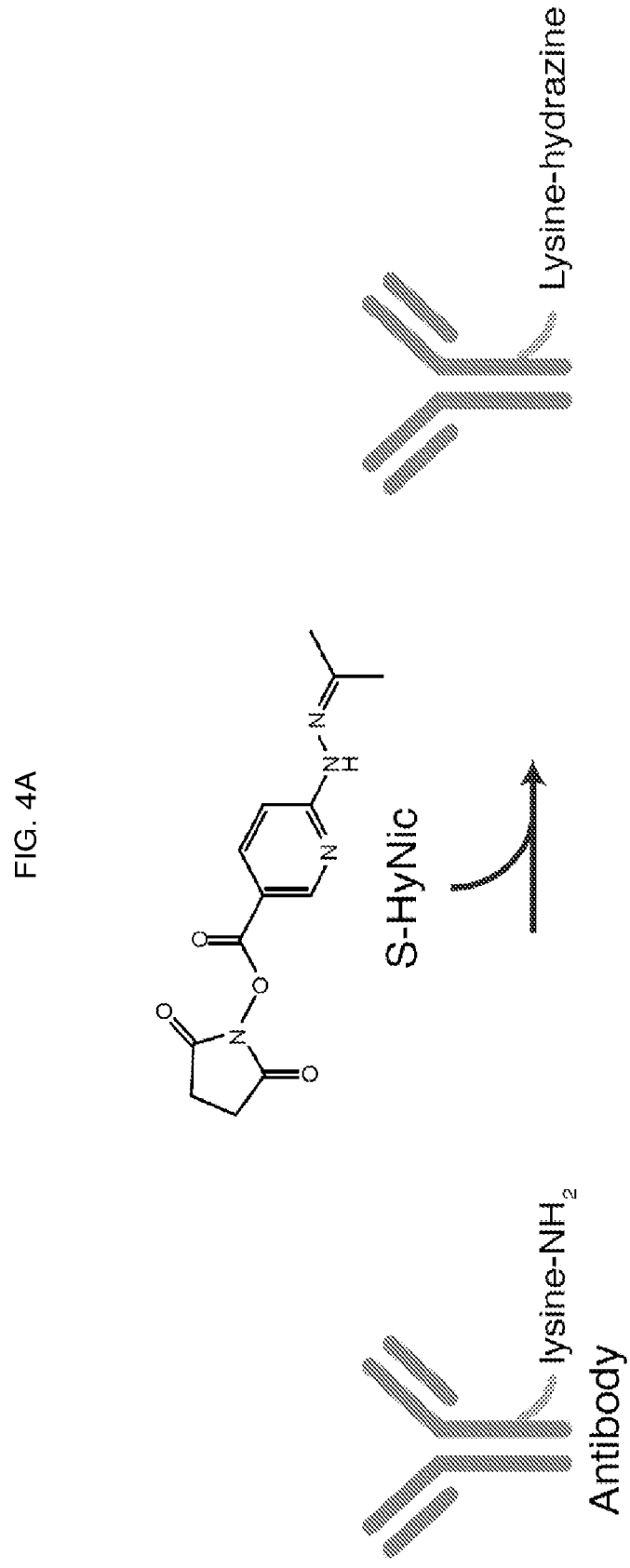
(d) Scheme H: Secondary antibody labeled with hairpin that sequesters an HCR initiator

FIG 3D.

(d) Scheme H: Secondary antibody labeled with hairpin that sequesters an HCR initiator
Stage 3: Probe activation using unstructured trigger oligo
Stage 4: Signal amplification using HCR
Trigger oligo
accessible
HCR initiator i2
HCR hairpins
H1
H2
Tethered fluorescent
HCR amplification
polymer

FIG 3D.
CONT.

FIG. 4A



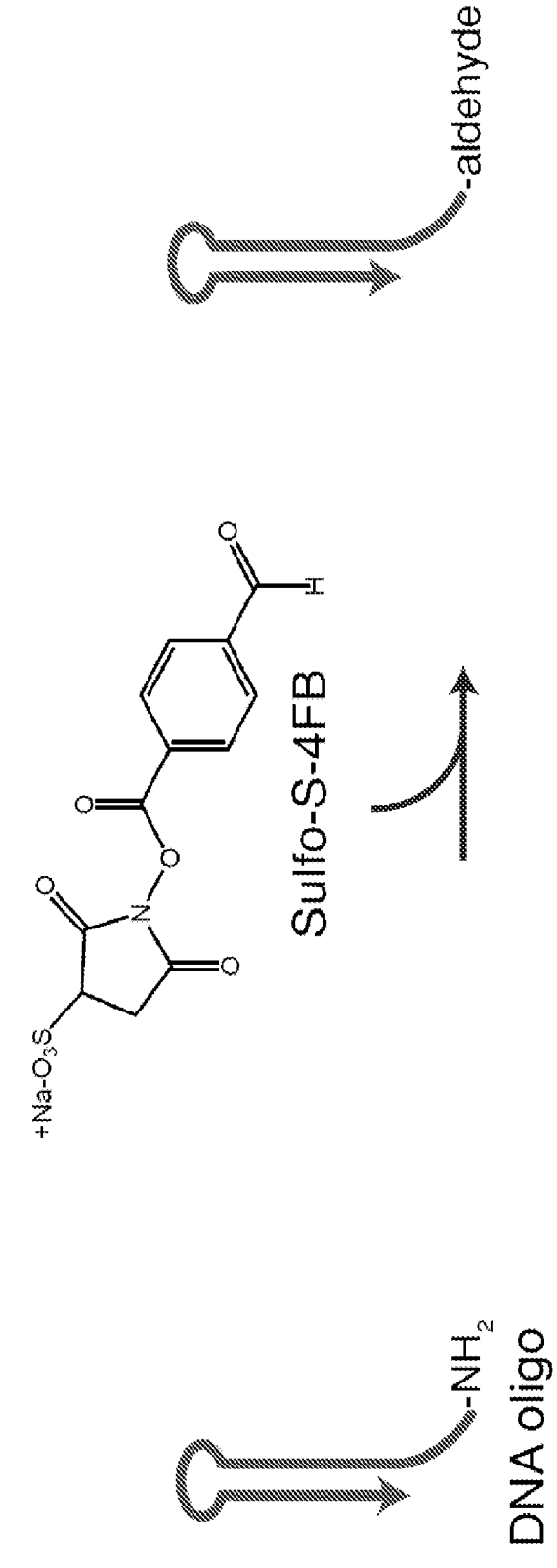


FIG. 4B

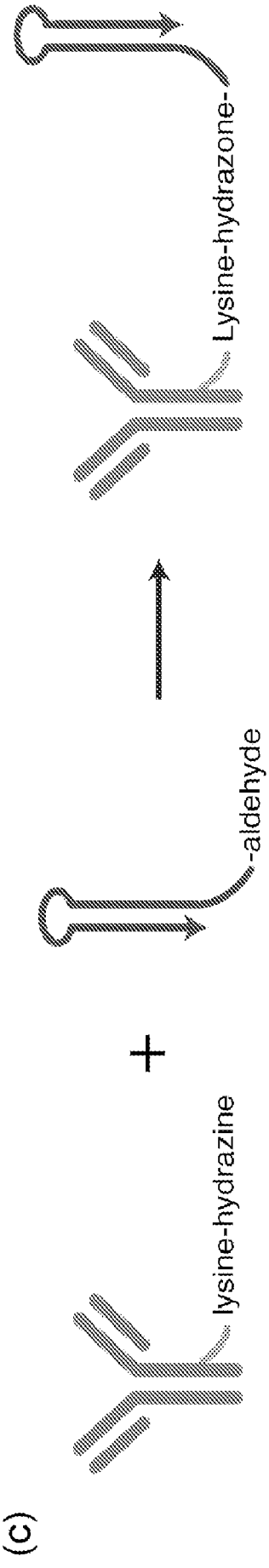


FIG. 4C

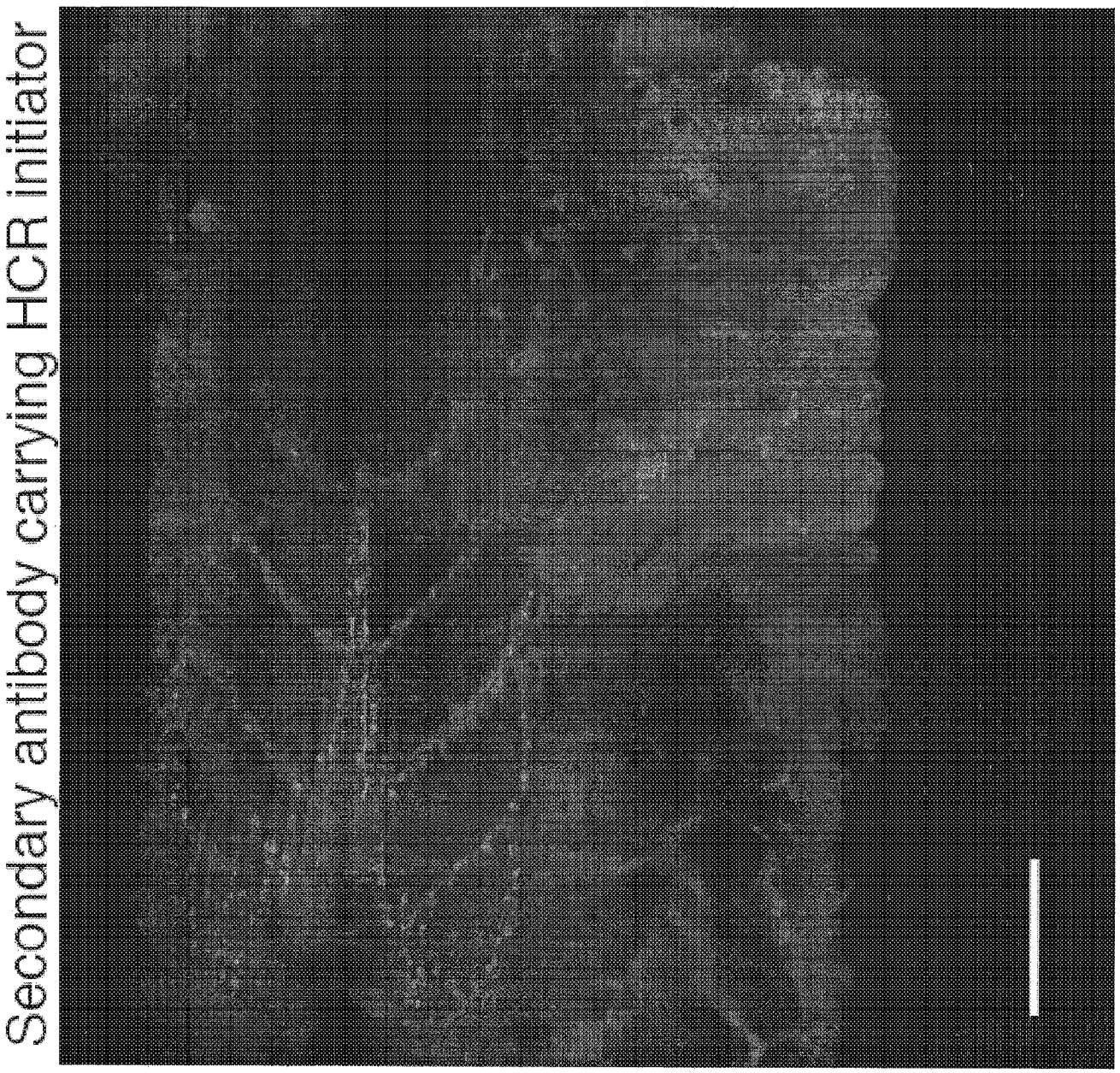


FIG. 5

Scheme F

Secondary antibody carrying HCR hairpin

FIG. 5 CONT

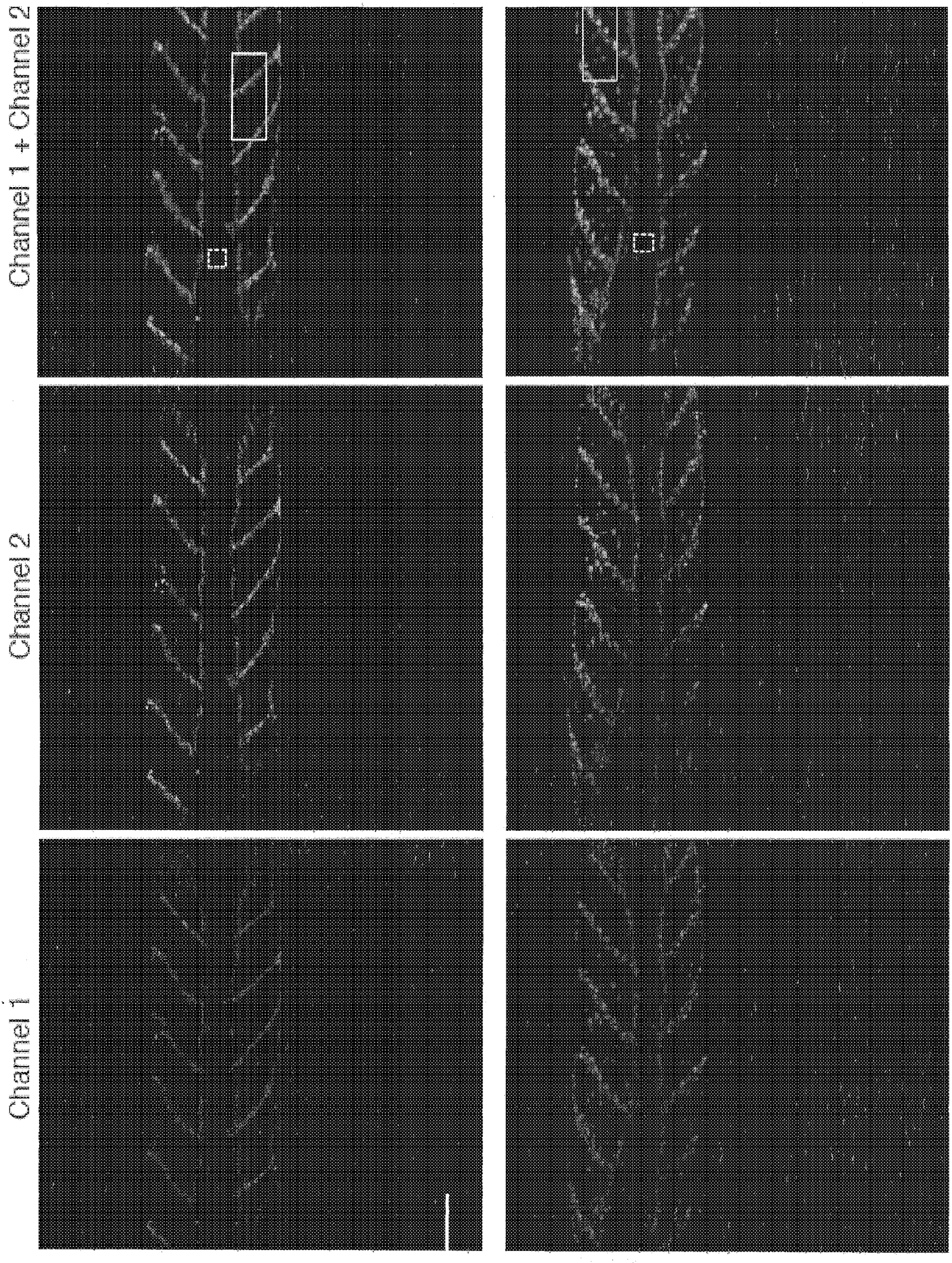
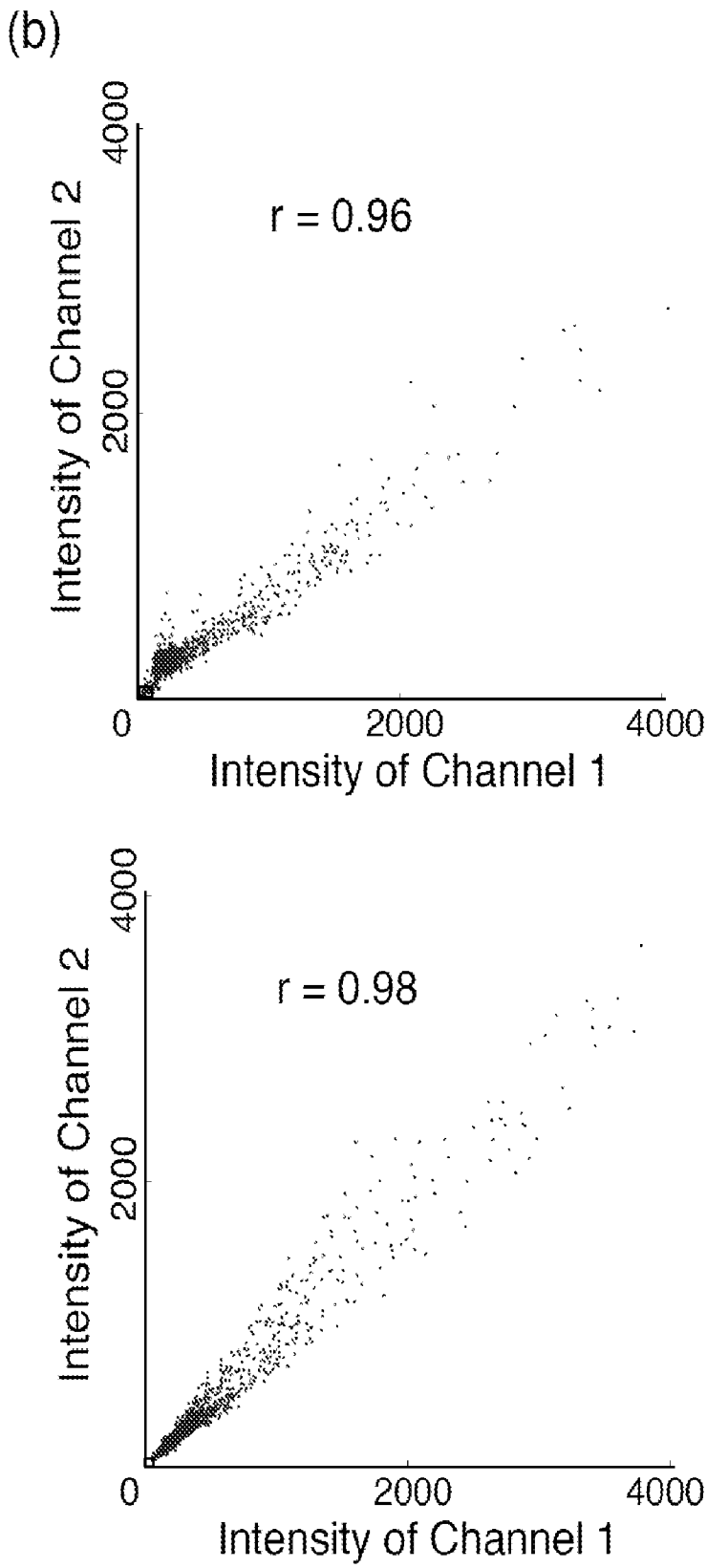


FIG. 6A

FIG. 6B


(b)
r = 0.96
Intensity of Channel 2
Intensity of Channel 1
0
2000
4000
r = 0.98
Intensity of Channel 2
Intensity of Channel 1
0
2000
4000

Stage 1: Target protein detection
using unlabeled primary antibody
Protein target
Primary antibody
Wash out unused
primary antibody
mRNA target

FIG. 7

Stage 2: Primary antibody detection
using secondary antibody
labeled with HCR hairpin
Hairpin H1 of
HCR amplifier 1
Wash out unused
secondary antibody
and fix
Secondary antibody

FIG. 7. CONT.

Stage 3: Target mRNA detection using
DNA probes carrying HCR initiators
DNA probe set with initiators
of HCR amplifier 2
Initiators of HCR amplifier 2
Wash out unused
DNA probes

FIG. 7 CONT.

Stage 4: Antibody probe activation
using unstructured HCR initiator
Wash out unused
unstructured HCR
initiator
Initiator I1 of HCR amplifier 1

FIG. 7 CONT.

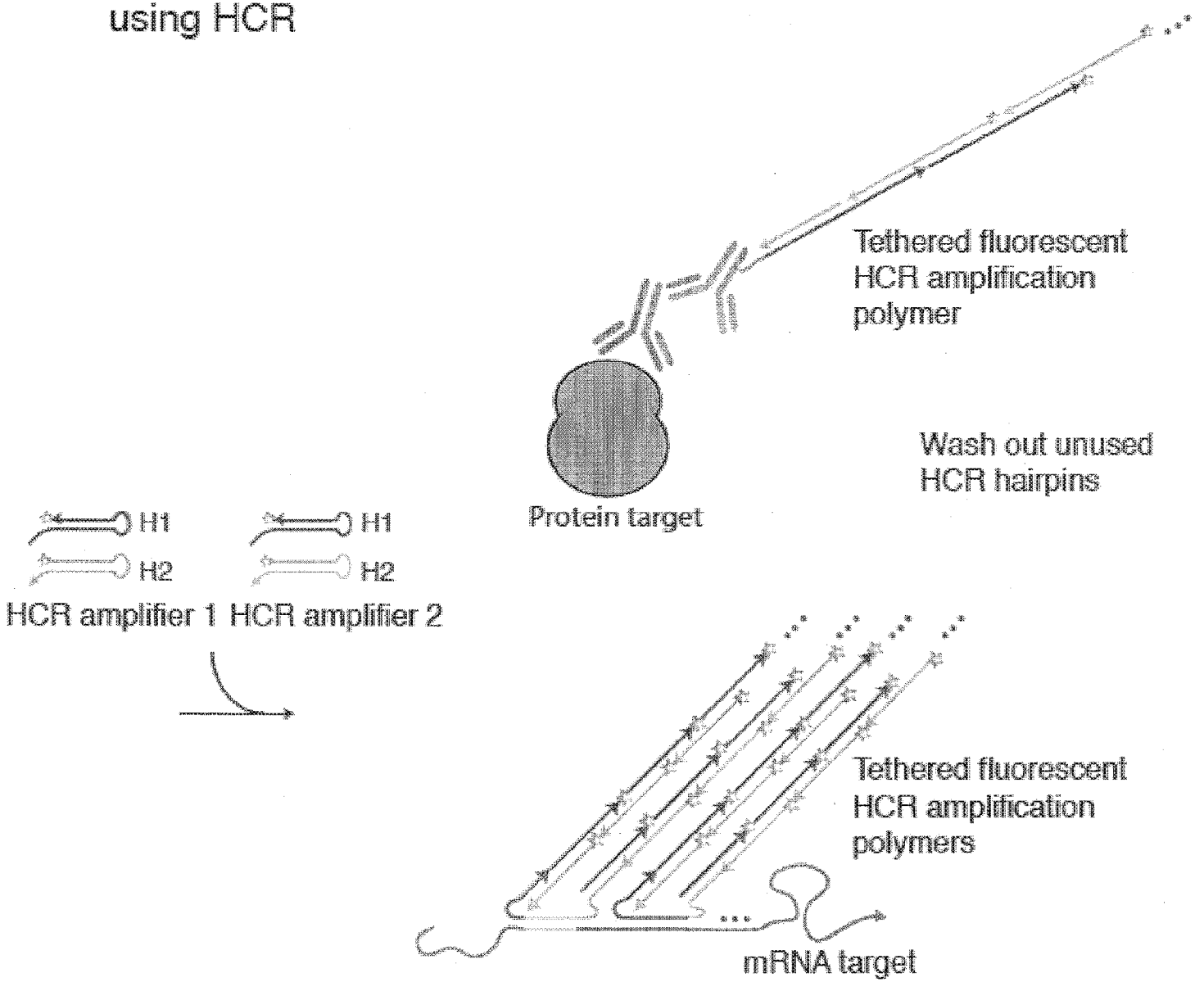
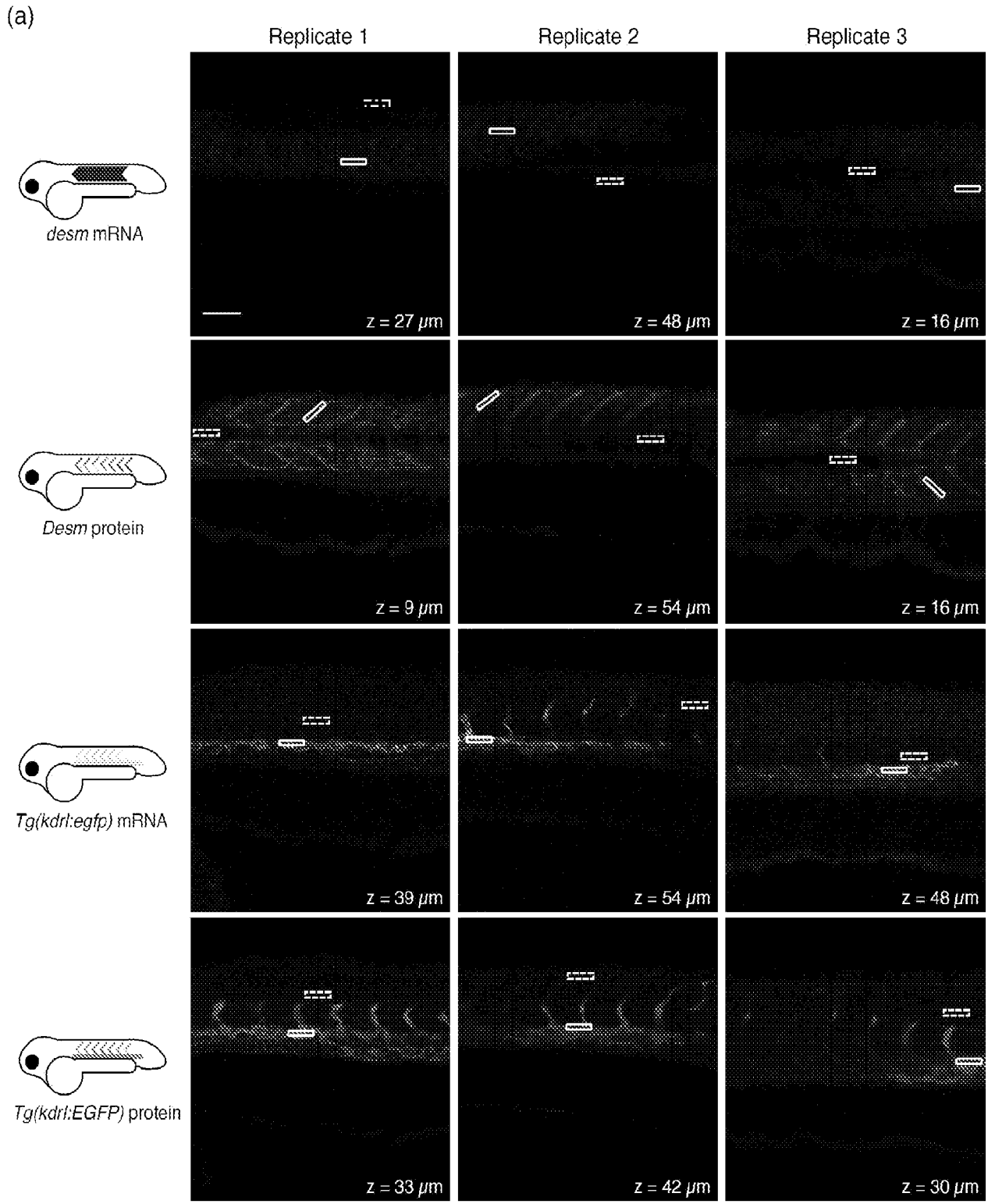

Stage 5: Signal amplification using HCR
Tethered fluorescent HCR amplification polymer
Wash out unused HCR hairpins
Protein target
H1
H2
H1
H2
HCR amplifier 1
HCR amplifier 2
Tethered fluorescent HCR amplification polymers
mRNA target

FIG. 7 CONT.

FIG. 8A


(a)
Replicate 1
Replicate 2
Replicate 3
desm mRNA
Desm protein
Tg(kdrl:egfp) mRNA
Tg(kdrl:EGFP) protein
z = 27 μm
z = 48 μm
z = 16 μm
z = 9 μm
z = 54 μm
z = 16 μm
z = 39 μm
z = 54 μm
z = 48 μm
z = 33 μm
z = 42 μm
z = 30 μm

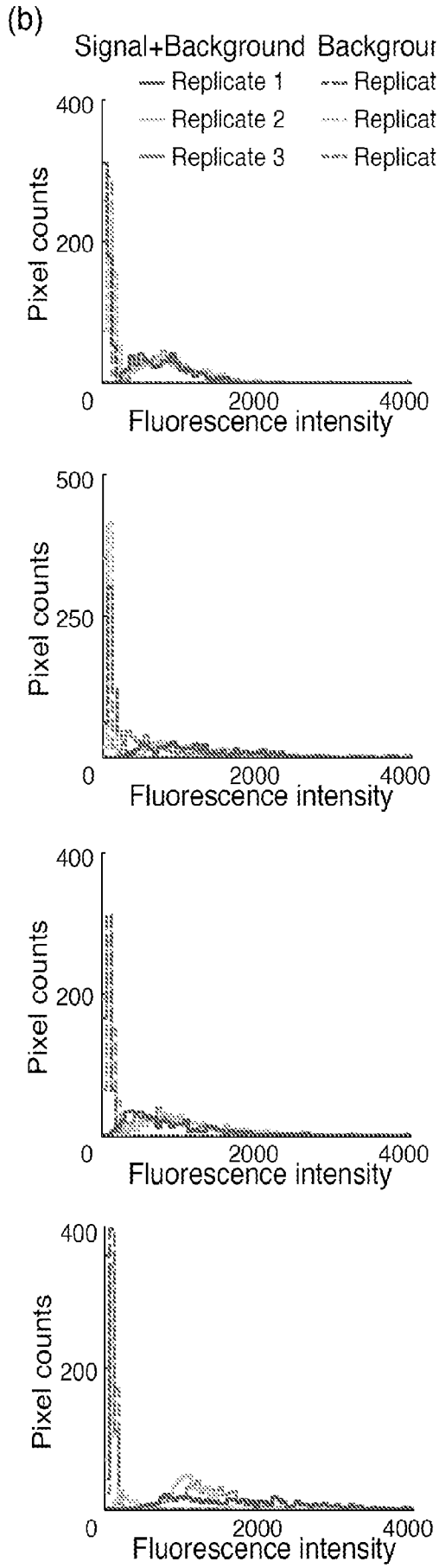

(b)
Signal+Background
Backgrour
Replicate 1
Replicat
Replicate 2
Replicat
Replicate 3
Replicat
Pixel counts
400
200
0
2000
4000
Fluorescence intensity
500
250
0
2000
4000
Fluorescence intensity
400
200
0
2000
4000
Fluorescence intensity
400
200
0
2000
4000
Fluorescence intensity

FIG. 8B

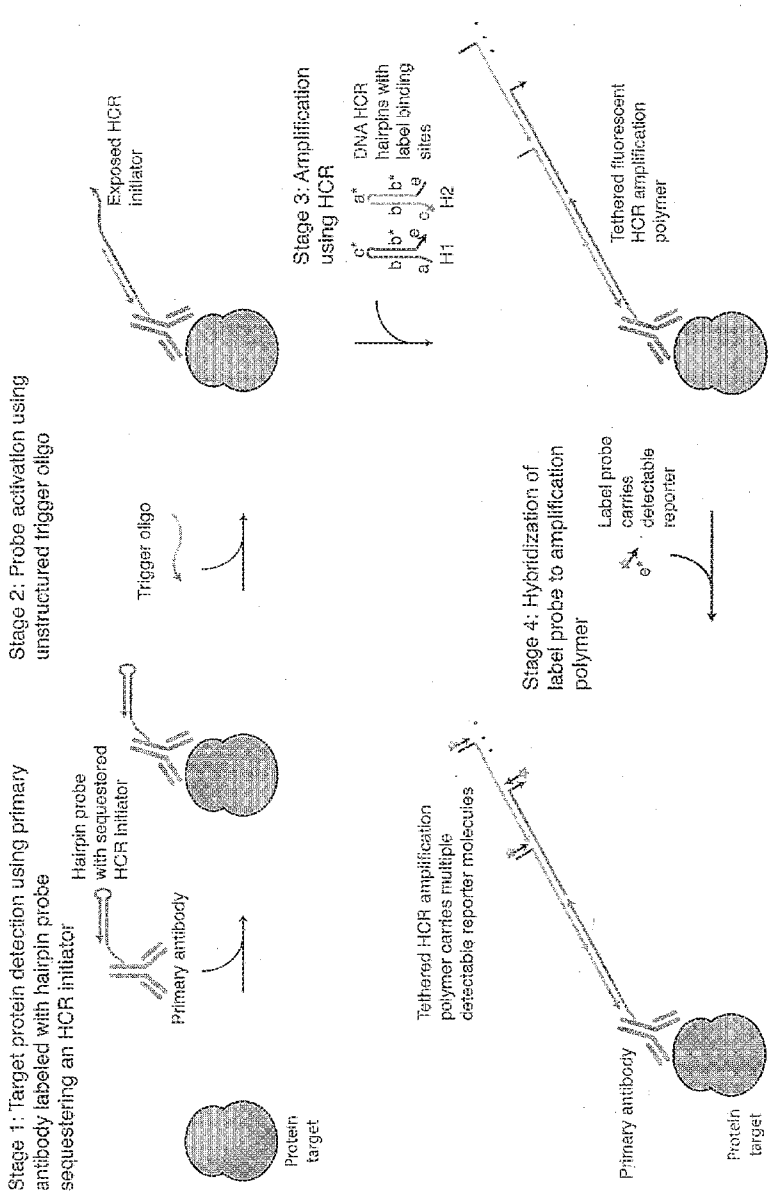

Stage 1: Target protein detection using primary antibody labeled with hairpin probe sequestering an HCR initiator
Hairpin probe with sequestered HCR initiator
Primary antibody
Protein target
Stage 2: Probe activation using unstructured trigger oligo
Trigger oligo
Exposed HCR initiator
Stage 3: Amplification using HCR
DNA HCR hairpins with label binding sites
H1
H2
Tethered fluoresent HCR amplification polymer
Stage 4: Hybridization of label probe to amplification polymer
Label probe carries detectable reporter
Tethered HCR amplification polymer carries multiple detectable reporter molecules
Primary antibody
Protein target

FIG. 9

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US17/49198

A. CLASSIFICATION OF SUBJECT MATTER

IPC - C07H 21/02, 21/04; C12Q 1/68; G01N 33/58 (2017.01)

CPC - C07H 21/02, 21/04; C12Q 1/6825, 1/6841, 1/6876; G01N 33/58

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

See Search History document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ---- Y	US 2012/0190835 A1 (PIERCE, NA et al.) 26 July 2012; paragraphs [0010], [0011], [0012], [0013], [0038], [0039], [0042], [0045], [0069]), [0076], [0083], [0085]), [0091], [0092], [0093], [0096], [0097], [0099]. [0100], [0102], [0114], [0115]; Figures 1A, 1B, 1C, 8B, and 9	1-2, 6-7, 9-10, 11/1-2, 11/6-7, 11/9-10, 12-13/11/1-2, 12-13/11/6-7, 12-13/11/9-10, 36-37, 38/36-37, 43-45, 46/36-37, 47/46/36-37, 48-49, 50-51/36-37 ---------- 3-5, 8, 11/3-5, 11/8, 12-13/11/3-5, 12-13/11/8, 52/36-37
Y	(CHOI, HMT et al.) Programmable in situ amplification for multiplexed imaging of mRNA expression, Nature Biotechnology, November 2010, Epub 31 October 2010, Vol. 28, No. 11; pages:1208-1212; page 1208, 2nd column, 2nd paragraph; page 1209, 1st column, 3rd paragraph; Figure 1a; DOI: 10.1038/nbt.1692	3-5, 8, 11/3-5, 11/8, 12-13/11/3-5, 12-13/11/8
Y	(CHEN, Y et al.) Arrayed Profiling of Multiple Glycans on Whole Living Cell Surfaces. Analytical Chemistry. 19 November 2013, Epub 30 October 2013, Vol. 85, No. 22; pages 11153-11158; abstract; DOI: 10.1021/ac403150n	52/36-37

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
18 October 2017 (18.10.2017)	06 NOV 2017

Name and mailing address of the ISA/	Authorized officer
Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-8300	Shane Thomas PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

Form PCT/ISA/210 (second sheet) (January 2015)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US17/49198

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 14-35, 39-42
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.