(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
9 October 2014 (09.10.2014)

WIPO | PCT

(10) International Publication Number
WO 2014/164479 Al

(51) International Patent Classification:
C12Q 1/68 (2006.01)

(21) International Application Number:
PCT/US2014/022534

(22) International Filing Date:
10 March 2014 (10.03.2014)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/776,256 11 March 2013 (11.03.2013) US

(71) Applicant: **ELITECH HOLDING B.V.** [NL/NL]; Van Rensselaerweg 4, NL-6956 AV Spankeren (NL).

(72) Inventors; and
(71) Applicants *(for US only):* **BELOUSOV, Yevgeniy, S.** [US/US]; 2717 144th Court SE, Mill Creek, WA 98012 (US). **ALABEYEV, Boris** [US/US]; 3732 156th Street SW, Apt. 1, Lynnwood, WA 98087 (US). **SCARR, Noah** [US/US]; 12522 North Park Avenue N, Seattle, WA 98133 (US).

(74) Agents: **BORRELLI, Sara K.** et al; Jackson Walker L.L.P., 901 Main Street, Suite 6000, Dallas, TX 75202 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available):* AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

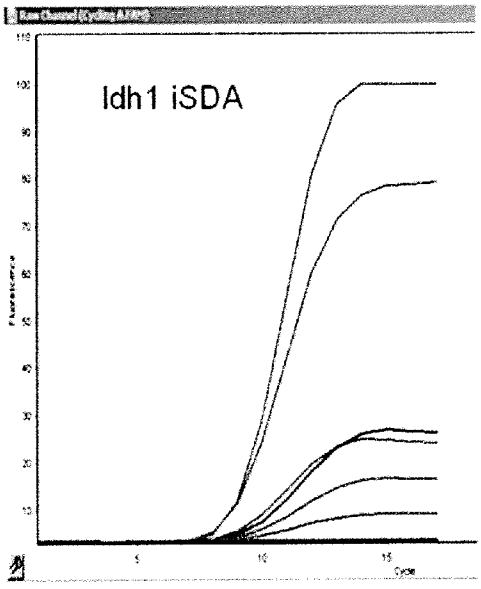
(84) Designated States *(unless otherwise indicated, for every kind of regional protection available):* ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM,

[Continued on next page]

(54) Title: METHODS FOR TRUE ISOTHERMAL STRAND DISPLACEMENT AMPLIFICATION

(57) Abstract: Methods, primers and probes are provided for the isothermal amplification and detection, without denaturation, of double stranded nucleic acid targets for polymerase strand displacement amplification ("iSDA"), The methods and compositions disclosed are highly specific for nucleic acid targets with high sensitivity, specificity and speed that allow detection of clinical relevant target levels. The methods and compositions can easily be used to amplify or detect nucleic acid targets in biological samples.

Figure 2



WO 2014/164479 A1

TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

— *with international search report (Art. 21(3))*

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

METHODS FOR TRUE ISOTHERMAL STRAND DISPLACEMENT AMPLIFICATION

BACKGROUND

[0001] This application claims priority to U.S. Provisional Patent Application Serial No. 61/776,256, filed March 11, 2013, entitled "Methods for True Isothermal Strand Displacement Amplification," the entire contents of which are hereby incorporated by reference.

[0002] This disclosure pertains to methods for isothermal strand displacement amplification that accomplishes efficient primer extension amplification with target specific primers and does not require pre-denaturation.

[0003] Isothermal amplification requires single stranded targets for efficient primer extension. Helicase dependent amplification of nucleic acids also requires helicase enzyme for unwinding double strands to allow amplification with a DNA polymerase (US Patent No. 7282328). Exponential strand displacement amplification ("SDA") as described in US Patent No. 5,455,166 requires an initial denaturation of the target into single-stranded DNA (ssDNA), generation of hemiphosphorothioate sites which allow single strand nicking by restriction enzymes, and extension by a polymerase lacking **5'-3'** exonuclease activity. Raising the temperature of the reaction to approximately 95°C to render double strands into single strands is required to permit binding of the primers to the target strands. State of the art SDA amplification requires the denaturation of the target at elevated temperature to yield ssDNA for strand displacement isothermal amplification.

[0004] The use of a nicking enzyme to cleave one of the strands of a target instead of the generation of hemiphosphorothioate sites in SDA amplification was described in (Ehses et al, J. Biochem. Biophys. Methods. 63:170-86 (2005)). The design of primers to reduce non-predictable byproducts was also described. Denaturation at 95°C was required by Ehses et al. after the addition of target and before the addition of any enzymes. Nicking enzyme SDA amplification without denaturation of target at 95°C was reported in U.S. Patent Application Publication No. 2009/0092967. However, a limitation of the latter method is that a limited number of nicking enzymes are available and quite often no natural nicking site is present in a target region of interest. An abasic site

endonuclease amplification assay was disclosed in U.S. Patent Application Publication No. 2004/0101893. The use of this assay as a post amplification detection system in combination with other amplification systems was also disclosed. These assays require a denaturation step of dsDNA.

[0005] It is known in the art that double stranded (ds) nucleic acid can be denatured in different ways. Heat denaturation is state of the art to separate ds DNA into single strands. Native DNA denatures at about 85°C. (White, Handler and Smith, Principles of Biochemistry 5th Edition, McGraw-Hill Kogakush, Ltd, pages 192-197, 1993). Early on, it was established that primer extension in amplification required the binding of a primer to a single strand DNA strand. This was preferably achieved by heating the sample at about 95°C (M Panaccio and A Lew. PCR based diagnosis in the presence of 8% (v/v) blood. Nucleic Acids Res., 19: l 151 (1991)). It was recently reported that Watson-Crick pairs in naked DNA spontaneously flip into Hoogstein pairs under ordinary conditions, suggesting that DNA breathes (Fran-Kamentskii. Artificial DNA; PNA & XNA, 2:1, 1-3 (201 1)).

[0006] A few nucleases cut just one strand of DNA thereby introducing a nick into DNA (Besnier and Kong, EMBO Reports, 21: 782-786 (2001)). Most such proteins are involved in DNA repair and other DNA-related metabolism and cannot easily be used to manipulate DNA. They usually recognize long sequences and associate with other proteins to form active complexes that are difficult to manufacture (Higashitani et al., J. Mol. Biol., 237: 388-4000 (1994)). Single strand nicking endonucleases which nick only one strand of the DNA double strands and traditional restriction endonucleases are listed and updated in the REBASE Database (rebase.neb.com ; Roberts et al., Nucl. Acids Res., 31: 418-420 (2003)). Engineering of a nicking endonuclease has been described (Xu et al, PNAS 98: 12990-12995 (2001)).

[0007] Other methods using isothermal amplification have been disclosed recently (Niemz et al., Trends in Biotechnol., 29:240-250 (201 1)). However, these amplification methods also utilize thermal or other denaturation.

SUMMARY

[0008] The present invention relates generally to an isothermal assay which utilizes the advantages of target nucleic acid amplification without the requirement for dsDNA denaturation. The present methods enable efficient detection of target nucleic acids with exquisite specific amplification. The present disclosure unexpectedly determined that primers designed according to a particular method allow efficient primer extension amplification of target specific primers without pre-denaturation. Generally, the present disclosure provides methods, primers and probes for the isothermal amplification without denaturation of nucleic acid targets for polymerase primer extension (isothermal strand displacement amplification ("iSDA")) in samples including biological samples (e.g., blood, nasopharyngeal or throat, swab, wound swab, or other tissues). The nucleic acid targets may be double stranded or they may be single stranded, such as RSV virus. RNA targets may be single stranded or double stranded.

[0009] The method described herein utilizes primer oligonucleotides that allow primer extension without denaturation of nucleic acid targets. In some examples the primers have modified bases to improve stability or to eliminate primer self-association. In one embodiment modified bases are used to limit primer self-association.

[0010] In certain examples the primer comprises a 5'-non-complementary tail wherein said tail further comprises a nicking enzyme specific sequence.

[0011] In the methods described herein, the nucleic acids present in a clinical or test sample obtained from a biological sample or tissue suspected of containing a clinical target (microorganisms or tissue, for example) are extracted with methods known in the art. The target nucleic acids are amplified without denaturation and detected. More specifically the target specific primers contain a sequence specific for target and a non-target complementary 5'-tail, wherein the tail contains a sequence specific for a nicking enzyme when hybridized to its complementary sequence. At least one amplification cycle provides a double stranded amplicon containing a nicking site which allows strand displacement in a second amplification cycle. The amplified nucleic acid can be detected by a variety of state of the art methods including fluorescence resonance energy ("FRET"), radiolabels, lateral flow, enzyme labels, and the like.

[0012] The methods described herein also include methods for the design of primers allowing amplification of at least one cycle of amplification without dcnaturation of duplex DMA target.

[0013] In certain methods provided herein the methods comprise the detection of iSDA or RT-iSDA amplified targets by lateral flow.

[0014] Those skilled in the art will appreciate that the present disclosed amplification method can be performed in combination with other methods. In one embodiment the amplification method described in U.S. Patent Application Publication No. 2009/0092967 can be combined with the method of the present disclosure.

[0015] This disclosure provides an isothermal method for specifically detecting a nucleic acid sequence in a biological sample from an individual. The disclosure also provides oligonucleotide primers and probes comprising nucleotide sequences characteristic of specific genomic nucleic acid sequences. The method includes performing isothermal amplification without a denaturation step prior to amplification. The amplification step includes contacting the sample nucleic acid with pairs of primers to produce amplification product(s) if the specific genomic nucleic acid target is present. The preferred primers target a specific region of a specific target gene. Each of the preferred primers has a 5'-oligonucleotide tail non-complementary to the target where said non-complementary tail contains a sequence when hybridized to a complementary sequence contains a nicking enzyme cleavage site. The oligonucleotide probes detect the amplified target directly or indirectly. The preferred oligonucleotide probe is a 5'-minor groove binder-ftuorophore-oligonucleotide-quencher-3' conjugate that fluoresces on hybridization to its complementary amplified target. In some embodiments one or more primer is labeled. In some embodiments a double strand binding fluorescent dye is used. In some embodiments one or more bumper oligonucleotides are provided. In some embodiments the probe(s) is omitted. In some embodiments the amplified target is captured on a solid support or membrane and detected by a labeled probe. In some embodiments the primer concentrations are present in different concentrations. In some embodiments an internal control is provided.

BRIEF DESCRIPTION OF THE DRAWINGS

[0016] Figure 1 shows a schematic of an example of dual capture and detection of iSDA amplified amplicon by pDNA immobilized on a solid surface;

[0017] Figure 2 shows an example of real-time iSDA amplification of different concentrations of the *Idhl* gene with fluorescence detection utilizing a Pleiades probe;

[0018] Figure 3 shows an example of lateral flow colorimetric detection of an *Idhl* iSDA amplified amplicon with the approach provided in Figure 1;

[0019] Figure 4 shows an example of real-time iSDA amplification of two different *mecA* designed assays with fluorescence detection utilizing a Pleiades probe;

[0020] Figure 5 shows an example of real-time iSDA amplification with different polymerases;

[0021] Figure 6 shows an example of gel analysis of the valuation of Nt.AIw I on PCR Amplified target containing Nt.AIw I cleavage site;

[0022] Figure 7 shows an example of lateral flow detection of iSDA biplex-amplified *Idhl* and IC amplicons;

[0023] Figure 8 shows a schematic representation of a primer containing a complementary- and non-complementary-sequence;

[0024] Figure 9 shows the probe specific iSDA detection and differentiation of *Idhl* gene in *S. aureus* and of *S. epidermis;*

[0025] Figure 10 shows the specific real-time iSDA amplification of *S. aureus* nucleic acid extracted with five different extraction methods;

[0026] Figure 11 shows the results of amplification reactions comparing amplification with primers and probes optimized for use in the present isothermal strand displacement amplification method and traditional primers and probes;

[0027] Figure 12 shows the specific reverse transcriptase-iSDA (RT-iSDA) amplification of Respiratory syncytial virus (RSV) extracted RNA nucleic acid using both real-time fluorescence detection and post-amplification lateral flow detection; and

[0028] Figure 13 shows the real-time iSDA amplification of native and denatured *Plasmodium falciparum* DNA.

DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

I. General

[0029] Generally, the present disclosure provides methods, primers and probes for the isothermal amplification and detection, without denaturation, of double stranded nucleic acid targets for polymerase strand displacement amplification ("iSDA"). The methods and compositions disclosed are highly specific for nucleic acid targets with high sensitivity, specificity and speed that allow detection of clinical relevant target levels. The methods and compositions can easily be used to amplify or detect nucleic acid targets in biological samples.

[0030] According to Ehses et al. (J. Biochem. Biophys. Methods. 63:170-86 (2005), incorporated herein by reference), primers can be designed using the Vienna Folding Package (tbi.univie.ac.at/ivo/RNA/) that identifies analyzes sequences that allowing one to minimize the accumulation of non-predictable byproducts especially for longer incubation times and low concentrations of initial template DNA. More specifically, the Vienna Folding Package is a software product that predicts a secondary structure of the primers based on the calculations of the minimum free energy of the hybridization reaction and calculates the probabilities of alternative DNA/DNA duplex structures. Primers designed using software such as the Vienna Folding Package are considered to have an improved hybridization stringency, and thus permit efficient elongation of a target sequence. The T_m of the selected primers can then be adjusted by calculation with a preferred software package, such as the Eclipse Design Software 2.3 (Afonina et al., Single Nucleotide Polymorphism Detection with fluorescent MGB Eclipse Systems in A-Z of Quantitative PGR, Ed. S. A. Bustin, International University Line, La Jolla, CA, pages 718-731 and XII-XIII, 2004; see also U.S. Patent Nos. 6683173 and 7751982). The software adjusts the Tm of the primers for optimum extension as well, by calculating duplex stabilities using an algorithm applying a nearest-neighbor model for duplex formation thermodynamics for each of the neighboring base pairs. Each nearest neighbor thermodynamic parameter defines a thermodynamic contribution of two corresponding neighboring bases. A preferred oligonucleotide primer sequence is then selected having the desired duplex stability. The primers can also be designed, if necessary or desired, to include modified bases (see US 7,045,610; US 6,127,121 ; US

6,660,845; US 5,912,340 and US Application Publication No. 2010/057862, all incorporated by reference). In the case of probes or MGB probes, the same software package (such as Eclipse Design Software 2.3) can be used.

II. Definitions

[0031] A "sample" as used herein refers to a sample of any source which is suspected of containing a target sequence. These samples can be tested by the methods described herein. A sample can be from a laboratory source or from a non-laboratory source. A sample may be suspended or dissolved in liquid materials such as buffers, extractants, solvents, and the like. Samples also include biological samples such as plant, animal and human tissue or fluids such as whole blood, blood fractions, serum, plasma, cerebrospinal fluid, lymph fluids, milk, urine, various external secretions of the respiratory, intestinal, and genitourinary tracts, tears, and saliva; and biological fluids such as cell extracts, cell culture supernatants, fixed tissue specimens, and fixed cell specimens. Samples include nasopharyngeal or throat swabs, stools, wound or rectal swabs. Biological samples may also include sections of tissues such as biopsy and autopsy-samples or frozen sections taken for histological purposes. A biological sample is obtained from any animal including, *e.g.,* a human. A biological sample may include human and animal pathogens that includes microbes or microorganisms such as a viruses, bacteria, or fungi that causes disease in humans. Biological samples may further also include products of gene mutated-metabolic disorders.

[0032] The terms "flap primer" or "overhang primer" refer to a primer comprising a 5' sequence segment non-complementary to a target nucleic acid sequence, wherein said tail further comprises a nicking enzyme specific sequence and a 3' sequence segment complementary to the target nucleic acid sequence The flap primers are suitable for primer extension or amplification of the target nucleic acid sequence The primers may comprise one or more non-complementary or modified nucleotides (e.g., pyrazolopyrimidines as described in US 7,045,610 which is incorporated herein by reference) at any position including, e.g., the 5' end.

[0033] The term "isothermal strand displacement amplification" ("iSDA") refers to primer extension using a primer that comprises a 5' sequence segment non-

complementary to a target nucleic acid sequence, wherein said tail may further comprise a nicking enzyme specific sequence and a 3' sequence segment complementary to the target nucleic acid sequence.

[0034] The term "fluorescent generation probe" refers either to a) an oligonucleotide having an attached minor groove binder, fluorophore, and quencher, b) an oligonucleotide having an attached fluorophore, and quencher, c) an oligonucleotide having an attached minor groove binder, and fluorophore, d) an oligonucleotide having an attached fluorophore and quencher, e) an oligonucleotide having an attached fluorophore, or f) a DNA binding reagent. The probes may comprise one or more non-complementary or modified nucleotides (e.g., pyrazolopyrimidines as described in US 7,045,610) at any position including, e.g., the 5' end. In some embodiments, the fluorophore is attached to the modified nucleotide. In some embodiments the probe is cleaved to yield a fluorescent signal.

[0035] Preferably, modified bases increase thermal stability of the probe-target duplex in comparison with probes comprised of only natural bases (i.e., increase the hybridization melting temperature of the probe duplexed with a target sequence). Modified bases can decrease probe and primer self-association compared to only normal bases. Modified bases include naturally-occurring and synthetic modifications and analogues of the major bases such as, for example, hypoxanthine, 2-aminoadenine, 2-thiouracil, 2-thiothymine, inosine, 5-N^4-ethenocytosine, 4-aminopyrrazolo[3,4-djpyrimidine and 6-amino-4-hydroxy-[3.4-d]pyrimidine. Any modified nucleotide or nucleotide analogue compatible with hybridization of probe with a nucleic acid conjugate to a target sequence is useful, even if the modified nucleotide or nucleotide analogue itself does not participate in base-pairing, or has altered base-pairing properties compared to naturally-occurring nucleotides. Examples of modified bases are disclosed in U.S. Pat. Nos. 7,045,610; 5,824,796; 6,127,121; 5,912,340; and PCT Publications WO 01/38584; WO 01/64958, each of which is hereby incorporated herein by reference in its entirety. Preferred modified bases include 5-hydroxybutynyl uridine for uridine; 4-(4,6-Diamino-1H-pyrazolo[3,4-d]pyrimidin-3-yl)-but-3-yn-1-ol, 4-amino-1H-pyrazolo[3,4-d]pyrimidine, and 4-amino-1H-pyrazolo[3,4-d]pyrimidine for adenine; 5-(4-Hydroxy-but-1-ynyl)-1H-pyrimidine-2,4-dione for thymine; and 6-amino-1H-pyrazolo[3,4-d]pyrimidin-4(5H)-one

for guanine. Particularly preferred modified bases are "Super A®: 4-(4.6-Diamino-I H-pyrazolo[3,4-d]pyrimidin-3-yl)-but-3-yn-l-ol," "Super G®: 4-hydroxy-6-am ino pyrazolopyrimidine" (www.elitechgroup.com) and "Super T®: 5-(4-hydroxy-but- 1-ynyl)-1H-pyrimidine-2.4-dione". "Super-D™: 3-Alkynyl pyrazolopyrimidine" analogues as universal bases are disclosed in U.S. Patent Application Publication No. 2012/0244535, incorporated by reference.

[0036] The terms "fluorescent label" or "fluorophore" refer to compounds with a fluorescent emission maximum between about 400 and about 900 nm. These compounds include, with their emission maxima in nm in brackets, Cy2™ (506), GFP (Red Shifted) (507), YO-PRO™-l (509), YOYO™-l (509), Calcein (517), FITC (518), FluorX™ (519), Alexa™ (520), Rhodamine 110 (520), 5-FAM (522), Oregon Green™ 500 (522), Oregon Green™ 488 (524), RiboGreen™ (525), Rhodamine Green™ (527), Rhodamine 123 (529), Magnesium Green™ (531), Calcium Green™ (533), TO-PRO™-l (533), TOTO®-1 (533), JOE (548), BODIPY® 530/550 (550), Dil (565), BODIPY® 558/568 (568), BODIPY® 564/570 (570), Cy3™ (570), Alexa™ 546 (570), TRITC (572), Magnesium Orange™ (575), Phycoerythrin R&B (575), Rhodamine Phalloidin (575), Calcium Orange™ (576), Pyronin Y (580), Rhodamine B (580), TAMRA (582), Rhodamine Red™ (590), Cy3.5™ (596), ROX (608), Calcium Crimson™ (615), Alexa™ 594 (615), Texas Red® (615), Nile Red (628), YO-PRO™-3 (631), YOYO™-3 (631), R-phycocyanin (642), C-Phycocyanin (648), TO-PRO™-3 (660), TOTO®-3 (660), DiD DilC(5) (665), Cy5™ (670), Thiadicarbocyanine (671), and Cy5.5 (694). Additional fluorophores are disclosed in PCT Patent Publication No. WO 03/023357 and U.S. Patent No. 7,671,218. Examples of these and other suitable dye classes can be found in Haugland et al., Handbook of Fluorescent Probes and Research Chemicals, Sixth Ed., Molecular Probes, Eugene, Ore. (1996); U.S. Patent Nos, 3,194,805; 3,128,179; 5,187,288; 5,188,934; 5,227,487, 5,248,782; 5,304,645; 5,433,896; 5,442,045; 5,556,959; 5,583,236; 5,808,044; 5,852,191; 5,986,086; 6,020,481 ; 6,162,931 ; 6,180,295; and 6,221,604; EP Patent No. 1408366; Smith et al, J. Chem. Soc. Perkin Trans. 2:1 195-1204 (1993); Whitaker, et al, Anal. Bioehem. 207:267-279 (1992); Krasoviskii and Bolotin, Organic Luminescent Materials, VCH Publishers, NY. (1988); Zolliger, Color Chemistry, 2nd Edition, VCH Publishers, NY. (1991); Hirschberg et al., Biochemistry 37:10381-10385 (1998); Fieser and Fieser, REAGENTS FOR ORGANIC

SYNTHESIS, Volumes 1 to 17, Wiley, US (1995); and Geiger et al., Nature 359:859-861 (1992). Still other dyes are provided via online sites such as www.zeiss.com. Phosphonate dyes are disclosed in co-owned US 7,671,218 and US 7,767,834.

[0037] There is extensive guidance in the art for selecting quencher and fluorophore pairs and their attachment to oligonucleotides (Haugland, 1996; U.S. Patent Nos. 3,996,345 and 4,351,760 and the like). Preferred quenchers are described in U.S. Patent No. 6,727,356, incorporated herein by reference. Other quenchers include bis azo quenchers (U.S. Patent No. 6,790,945) and dyes from Biosearch Technologies, Inc. (provided as Black Hole™ Quenchers: BH-1, BH-2 and BH-3 quenchers), Dabcyl, TAMRA and carboxytetramethyl rhodamine.

[0038] The term "linker" refers to a moiety that is used to assemble various portions of the molecule or to covalently attach the molecule (or portions thereof) to a solid support, surface or membrane. Typically, a linker or linking group has functional groups that are used to interact with and form covalent bonds with functional groups in the ligands or components (e.g., fluorophores, oligonucleotides, minor groove binders, or quenchers) of the conjugates described and used herein. Examples of functional groups on the linking groups (prior to interaction with other components) include -NH2, -NHNH2, -ONH$_2$, -NHC=(0)NHNH$_2$, -OH, and -SH. The linking groups are also those portions of the molecule that connect other groups (e.g., phosphoramidite moieties and the like) to the conjugate. Additionally, a linker can include linear or acyclic portions, cyclic portions, aromatic rings, and combinations thereof.

[0039] The term "solid support" refers to any support that is compatible with oligonucleotide attachment, including, for example, glass, controlled pore glass, polymeric materials, polystyrene, beads, coated glass, and the like.

[0040] Lateral flow assay technology is well known in the art and is performed on strips of porous paper or sintered polymer see for example US 6,485,982, US 7,799,554, and US 7,901,623.

[0041] In the description herein, the abbreviations MGB, FL, Q, CPG, and ODN refer to "minor groove binder," "fluorescent label" or "fluorophore," "quencher," "controlled pore glass" (as an example of a solid support), and "oligonucleotide" moieties

or molecules, respectively, and in a manner which is apparent from context. The terms "probe" and "conjugate" are used interchangeably and refer to an oligonucleotide having an attached minor groove binder, fluorophore, and quencher.

[0042] The terms "oligonucleotide," "nucleic acid," and "polynucleotide" are used interchangeably herein. These terms refer to a compound comprising nucleic acid, nucleotide, or its polymer in either single- or double-stranded form, e.g., DNA, RNA, analogs of natural nucleotides, and hybrids thereof. The terms encompass polymers containing modified or non-naturally-occurring nucleotides, or to any other type of polymer capable of stable base-pairing to DNA or RNA including, but not limited to, peptide nucleic acids as described in Nielsen et al., Science, 254:1497-1500 (1991), bicyclo DNA oligomers as described in Bolli et al., Nucleic Acids Res., 24:4660-4667 (1996), and related structures. Unless otherwise limited, the terms encompass known analogs of natural nucleotides that hybridize to nucleic acids in a manner similar to naturally-occurring nucleotides. Examples of such analogs include, without limitation, phosphorothioates, phosphoramidates, methyl phosphonates, chiral-methyl phosphonates, 2-O-methyl ribonucleotides, and peptide-nucleic acids (PNAs). A "subsequence" or "segment" refers to a sequence of nucleotides that comprise a part of a longer sequence of nucleotides. In some embodiments, nucleotides may include analogs of natural nucleotides which exhibit preferential binding to nucleotides other than naturally occuring DNA or RNA; an example of such nucleotides is pDNA (Eschenmoser et al, Helvetica Chimica Acta, "Why Pentose- and Hexose-Nucleic Acids?", pp. 76: 2161-2183 (1993)).

[0043] The term "Nicking Enzyme (or nicking endonuclease)" describes an enzyme that cuts one strand of a double-stranded DNA at a specifically recognition recognized nucleotide sequences known as a nicking site. Such enzymes hydrolyse (cut) only one strand of the DNA duplex, to produce DNA molecules that are "nicked", rather than cleaved. These nicking enzymes include N.Alw I, Nb.BbvCl, Nt.BbvCl, Nb.BsmI, Nt.BsmAI, Nt.BspQl, Nb.BsrDI, **Nt.BstNBI, Nb.BstsCI,** Nt.CviPII, Nb.BpulOI, Nt.BpulOI and Nt.Bst9I which are commercially available from www.neb.com, www.fermentas.com and www.sibenzyme.com, respectively. The New England Biolabs REBASE website (rebase.neb.com/cgi-bin/azlist?nick) lists 917 nicking enzymes. Designing of artificial nicking endonucleases on the basis of restriction endonucleases was

reviewed by Zheleznaya et al., Biochemistry (Mosc). 74:1457-66 (2009), incorporated by reference. "Nicking Enzyme" also includes engineered enzymes that cut one strand of a double stranded DNA, for example, zinc finger nucleases.

[0044] The term "Lateral Flow" describes a porous membrane capable of nonabsorbent lateral flow used as assay substrate; a member of the binding pair is affixed in an indicator zone defined in the substrate. The sample is applied at a position distant from the indicator zone and permitted to flow laterally through the zone; any analyte in the sample is complexed by the immobilized specific binding member, and detected. Lateral flow utilizing immuno-binding pairs is well known in the art (US 4,943,522). Lateral flow using DNA binding pairs was disclosed in US US7488578. pDNA binding pairs are disclosed in co-owned US application 2012-0015358 Al. Biotin-streptavidin affinity pairs are well known in the art and commercially available. Streptavidin-coated label may be a covalent or adsorptively bound streptavidin or other biotin-binding species, and the label may be a polystyrene nanoparticle doped with fluorescent or visible dye, a carbon black nanoparticle, a metal colloid, or other species detectable by fluorescence, radioactivity, magnetism, or visual acumen. The lateral flow buffer may be an aqueous suspension containing detergents, proteins, surfactants, and salts. The lateral flow strip may be a porous matrix composed of nitrocellulose, modified nitrocellulose, polyethersulfone, cellulose, glass fiber, polyvinylidene fluoride, or nylon. The lateral flow strip has at least one detection region composed of affinity pairs specific to the iSDA reaction products.

[0045] The practice of the methods described herein will employ, unless otherwise indicated, conventional techniques in organic chemistry, biochemistry, oligonucleotide synthesis and modification, bioconjugate chemistry, nucleic acid hybridization, molecular biology, microbiology, genetics, recombinant DNA, and related fields as are within the skill of the art. These techniques are fully explained in the literature. See, for example, Sambrook, Fritsch & Maniatis, MOLECULAR CLONING: A LABORATORY MANUAL, Second Edition, Cold Spring Harbor Laboratory- Press (1989); Ausubel, et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons (1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996); Gait (ed.), OLIGONUCLEOTIDE SYNTHESIS: A PRACTICAL APPROACH, IRL Press (1984);

and Eckstein (ed.), OLIGONUCLEOTIDES AND ANALOGUES: A PRACTICAL APPROACH, IRL Press (1991).

III. Descriptions

[0046] In one aspect, this disclosure provides an isothermal method for specifically detecting a nucleic acid sequence in a biological sample from an individual. The isothermal method can be carried out entirely at room temperature, or between about 40°C and about 65°C, or more preferably between about 45°C and about 55°C. The disclosure also provides oligonucleotide primers and probes comprising nucleotide sequences characteristic of a specific genomic nucleic acid sequences. The method includes performing of isothermal amplification without a denaturation step prior to amplification. The amplification step includes contacting the sample nucleic acid with pairs of primers to produce amplification product(s) if the specific genomic nucleic acid target is present. The primer "a-b" comprises a complementary sequence "b" and comprises a non-complementary nicking enzyme recognition sequence site "a" when hybridized to a complementary sequence (Figure 8). Primer a-b further comprises sequences selected by free energy minimization for specific hybridization and efficient elongation. The primers target a specific region of a specific target gene that allows amplification without thermal denaturation. Bumper primers hybridize upstream of the 5'-end of the flap primers to generate a target specific single stranded DNA newly synthesized amplicon by strand displacement (Nuovo GJ, .Diagn Mol Pathol. 2000 Dec;9(4): 195-202.). The oligonucleotide probes detect the amplified target directly or indirectly. The preferred oligonucleotide probe is a 5'-minor groove binder-fluorophore-oligonucleotide-quencher-3' conjugate that fluoresces on hybridization to its complementary amplified target.

[0047] In some embodiments the probe(s) is omitted. In some embodiments the amplified target is captured on a solid support, surface or membrane and detected by a labeled probe. In some embodiments the primer concentrations are present in different concentrations. In some embodiments an internal control is provided.

[0048] In a particular embodiment human, animal, and/or plant pathogen nucleic acids are amplified and detected.

[0049] In another embodiment the amplified target nucleic acid is RNA and the method further comprises a reverse transcriptase step.

[0050] In another aspect, the 5' non-complementary sequence comprises a sequence for a nicking site. Although any enzyme with a suitable nicking site can be used, preferred nicking enzyme recognition sequences are selected from N.Alw I, Nb.BbvCl, Nt.BbvCl, Nb.BsmI, **Nt.BsmAI,** Nt.BspQI, Nb.BsrDI, Nt.BstNBI, Nb.BstsCI, Nt.CviPII, Nb.Bpu10I, NiBpulOI and Nt.Bst9I, Nb.Mval269I and endo nuclease V.

[0051] In another embodiment, a complementary primer sequence comprises a sequence with an Endonuclease V ("Endo V") cleavage site requiring no heat or chemical denaturation, as more fully described in U.S. Patent No. 8,202,972 or U.S. Patent Application Publication No. 201 1/01 71649 incorporated by reference, which describes Endo V-based amplification primers. More specifically Endonuclease V is a repair enzyme recognizing DNA oligonucleotides containing deaminated modified bases such as inosine. Endo V cleaves the second or third phosphodiester bond 3' to the modified base, such as inosine. U.S. Patent No. 8,202,972 describes an Endonuclease V-based amplification method that extends a forward- and reverse-primer containing inosine adjacent to 3'-end terminal base. In the second round of amplification the Endo V cleaves the second or third phosphodiester bond 3' to the inosine in the same strand. The 3'-hydroxyl of the nick is extended by DNA polymerase in a template-directed manner. Employing a series of nested primer pairs complementary upstream of the 5'-end of the inosine containing primer pair, a series of extension products are generated. U.S. Patent No. 8,202,972 requires that "target dsDNA may be thermally denatured, chemically denatured, or both thermally and chemically denatured' *.

EXAMPLES

[0052] The following examples are provided to illustrate, but not to limit, the subject matter described herein.

[0053] In these examples, iSDA was performed using final concentrations of 3.75 mM $MgSO_4$, 50 mM KH_2PO_4 pH 7.6, 250 nM forward primer, 1 μM reverse primer, 50 nM bumper oligonucleotides, 200 nM probe, 0.2 mM dNTPs, 40 μg/mL BSA, 10 ng genomic DNA. 4U N.BbvClB and 3.6U Bst DNA polymerase in a total volume of 20 μL

(mono-reagent). Twenty microliters of the mono-reagent was introduced in a 96 well PCR plate with 10 μL of sample nucleic acid. Sample nucleic acid was obtained by extraction with easyMag using NucliSENSE easyMAG extraction reagents (Biomerieux, l'Etoile, France). The plate was sealed with MicroAmp® Optical Adhesive Film (Applied Biosystems, Foster City, CA) and then centrifuged to collect the assay solution in the bottom of the plate well. The assay was then performed in an AB1 7500 DX Fast Block Real-time PCR machine at 48°C for 30 minutes.

EXAMPLE 1.

[0054] This example demonstrates the efficient iSDA amplification without denaturation of the *Idhl* gene from easyMag extracted nucleic acid from cultured *S. aureus subsp. aureus COL* (gi|57650036 :262250-263203). The primer, bumper and probe sequences are shown in Table 1.

[0055] Table 1 below illustrates *Idhl* oligonucleotide sequences for iSDA amplification. Underlined sequences represents the nicking site for N.BbvClB. The upper case sequence is *Idhl* specific, the 5'-end lower case sequence is non-complementary to the *Idhl* target, and the pDNA sequence is shown in brackets. Q14 is a hexaethylene glycol linker, MGB is a DPI_3 minor groove binder, FAM is fluorescein, and EDQ is the Eclipse® dark quencher (quenching range 390-625 nm, maximum absorption 522 nm, Epoch Biosciences, Inc., Bothell, WA).

Table 1

Seq ID #	Description	Oligonucleotide sequence
1	Forward Primer	gcataatactaecagtctcctcagcAAGCTACGCATTTTCATTAG
2	Reverse Primer	tagaatagtcgcatacttcctcagcCATAACATCTCCTCGAACT
3	Probe	MGB-FAM-CTAATTCATCAACAATGC-EDQ
4	Forward Bumper	AGGTAATGGTGCAGTAGGT
5	Reverse Bumper	CCAGCTTTCACACGAAC
6	pDNA Capture Probe	[TTTTTTTTCKQ14)-CAGTGTCTAAATCAATGATG
7	Biotinilated Detection Probe	CTAATTCATCAACAATGC-biotin

[0056] Real-time iSDA amplification with oligonucleotide 1 to 5 was performed as described above with target concentrations ranging from 10 to 500 copies per reaction. The results are shown in Figure 2.

Lateral Flow:

[0057] A similar iSDA amplification was performed except that probe 3 was replaced with probes 6 and 7 that allow capture and detection in a lateral flow format, as schematically depicted in Figure 1, with the results shown in Figure 3. Once the iSDA reaction was complete, 2 μL of the product was aliquoted into a well containing a streptavidin-coated label and a volume of buffer for running the lateral flow assay on HF135 nitrocellulose (Millipore), then the lateral flow strip was added to the well. In one example, 2 μL of the iSDA *Idhl* reaction mixture was diluted in 100 μL of lateral flow buffer with the formulation 15 mM HEPES (pH 8), 1% Triton X-100, 0.5% BSA, 400 mM NaCl, 0.05% NaN_3, and 100 ng/μL streptavidin-coated 300 nm diameter blue-dyed polystyrene nanoparticles (Seradyn). To the diluted product was then added a nitrocellulose strip, 4 x 25 mm, containing an immobilized pDNA oligo complementary to the pDNA capture probe 6. The pDNA was immobilized via a cross-linked polythymidine tail at a concentration of 120 pmol/cm and a line width of approximately 1 mm. Positive results were visualized easily by the naked eye (as seen in Figure 3).

EXAMPLE 2.

[0058] This example illustrates the versatility of the design of primers from *mecA* gene sequences to allow iSDA amplification without denaturation. Nucleic acid was easyMag extracted from cultured *S. aureus subsp. aureus COL*. The primer, bumper and probe sequences of Design 1 and 2 are shown below in Table 2. The pDNA sequence is shown in brackets.

[0059] Table 2 below shows Designs 1 and 2 oligonucleotide sequences for *mecA* amplifications. Underlined sequences represent the nicking site for Nt.BbvClB, the upper case sequence is *mecA* specific, the 5'-end lower case sequence is non-complementary to the *mecA* target, the pDNA sequence is shown in brackets, A* is Super A (US 7,045,610), and Q14 is a hexaethylene glycol linker.

Table 2

Seq ID #	Description	Oligonucleotide sequence
Design 1		
8	Forward Primer	gaaacaatgtacctgtcacctcagcGACCGAAACAATGTGGAAT
9	Reverse Primer	ttcaatagtcagttacttcctcagcGGAACGATGCCTAATCTCA
10	Probe	MGB-FAM- CCAATACAGGAACACAT -EDQ
11	Forward Bumper	GAAAATTTAAAATCAGAACGTGG
12	Reverse Bumper	GCTTTA*TAATCTTTTTTAGATAC
13	pDNA Capture Probe	[TTTTTTTTC]-(Q14-CAATGTGGA*ATTGG
14	Biotinilated Detection Probe	CCAATACAGGAACACAT-biotin
Design 2		
15	Forward Primer	ccattatactacctgtctcctcagcGGCAAAGATATTCAACTAAC
16	Reverse Primer	tagaatagtcagttacttcctcagcGCCATAATCATTTTTCATGTTG
17	Probe	MGB-FAM- CTTTTGAACTTTAGCATC-EDQ
18	Forward Bumper	GATAATAGCAATACAATCGCACA
19	Reverse Bumper	GTGCTAATAATTCACCTGTTTGA
20	pDNA Capture Probe	[CAAGAATC]-(Q14)-CTTTAGCATCAATAGTTAG
21	Biotinilated Detection Probe	GTTA*TAAATA*CTCTTTTGA-biotin

[0060] Using primers, probe and bumper oligonucleotides (Design 1, Seq. ID# 8-12 and Design 2, Seq. ID # 15-18) in the same way described in Example 2, efficient real-time iSDA was achieved as shown in Figure 4.

EXAMPLE 3.

[0061] This example demonstrates the use of different polymerases in the real-time iSDA amplification. iSDA amplification was performed as described above using either *Bst* DNA Polymerase (portion of *Bacillus stearothermophilus* DNA Polymerase, New England BioLabs Inc., Ipswich, MA) or *Bst2.0* Warm Start (an *in silico* designed homologue of *Bacillus stearothermophilus* DNA Polymerase I, New England BioLabs

Inc.). The latter enzyme amplified *mecA* target and is active above 45°C. The results are shown in Figure 5, indicating better performance with the *Bst2. 0* **WarmStart** enzyme.

EXAMPLE 4.

[0062] This example demonstrates that although the Nt.Alwl nicking enzyme successfully cut a PCR amplicon into which the NtAlwl nicking site was designed, it did not cut extracted genomic DNA even though the *Idhl* gene contains a natural nicking site for NtAlwl.

[0063] The sequences below in Table 3 were used to incorporate a nicking site into a PCR amplicon. The Idhl specific sequences were designed with traditional PCR design software.

[0064] In Table 3 below, Design 3 and **4** oligonucleotide sequences for *Idhl* amplifications were generated with the Eclipse Design Software 2.3. Underlined sequences represent the nicking site for NtAlwl, the upper case sequence is *Idhl* specific, and the 5'-end lower case sequence is non-complementary to the *Idhl* target.

Table 3

Seq ID #	Description	Oligonucleotide sequence
Design 3		
22	Limiting primer-L1	aataaatcataaggatcAACGTGTTATAGGTTCTGGTACA
23	Excess primer -E1	aataaatcataaggatcTGAGCATCGACGCTACGTG
24	Forward Bumper1	ATGGAAATTCTCTGGT
25	Reverse Bumper1	TGTCACCATGTTCAC
Design 4		
26	Limiting primer-L2	aataaatcataaggatcTGGTGAACATGGTGACACTGAAT
27	Excess Primer E2	aataaatcataaggatcGCCCTCAGGACGTTGTTCAAG
28	Forward Bumper2	AGCGTCGATGCTCA
29	Reverse Bumper2	AATTTGTTCAATTTGCG

[0065] Primers of Design 3 and Design 4 were used to generate PGR amplicons which contain a nicking site for NtAlwl, yielding a convenient target containing a nicking site for NtAlwl. iSDA with the PCR-generated amplicon was analyzed on an agarose gel and the results are shown in Figure 6.

EXAMPLE 5.

[0066] This example illustrates the iSDA bi-plexing of *Idhl* and an internal control ("IC"). The IC template contains nonsense, non-specific target DNA fragment in a plasmid vector. Preferably, the control nucleic acid comprises the sequence shown in Table 4 below.

[0067] In Table 4 below, oligonucleotide sequences for the amplification of the IC were generated as described above for iSDA amplification. Underlined sequences represent the nicking site for Nt.BbvClB, the upper case sequence is IC- specific, and the 5'-end lower case sequence is non-complementary to the IC target. The same *Idhl* primers, bumper, capture and detection oligonucleotides (Seq. ID# 1, 2 4-7, Table 1) were used for the bi-plexing of the *Idhl* with the IC . The IC primers, bumpers, capture and detection probes sequences are shown in Table 4.

Table 4

Seq ID #	Description	Oligonucleotide sequence
30	Limiting primer-L1	ccaatatagtaacagtctcctcagcATTCGCCCTTCTGCACG
31	Excess primer -E1	ttcaaaagacccatacttcctcagCCTTCTCATTTTTTCTACCG
32	Forward Bumper1	TCGGATCCACTAGTAAC
33	Reverse Bumper1	GTGATGGATATCTGCAGAAT
34	Chimeric pDNA/DNA	[ACATCACA]-Q14-GATCTTGTACCAATGC
35	Biotinilated probe	CGTGGTCCGTAAAG -biotin TEG
36	IC2	TTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTATTTAG GTGACACTATAGAATACTCAAGCTATGCATCAAGCTTGGTACCGAGC TCGGATCCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTCT GCACGGACCAG*TTACTTTACGGACCAC*GTACCGCATTGGTACAAGATC TCCGGTAGAAAAAATGAGAAGGGCGAATTCTGCA*GATATC*CATCACA

		CTGG

[0068] iSDA amplification was performed as described above, except that the concentration for both ***Idhl*** and the IC primers were 250nM for the limiting primer and 500nM for excess primer, forward and reverse bumper primers were at 50nM, the chimeric pDNA-DNA probe and biotinylated probe at 200nM each. Each target dilution contained 5000 IC2 copies. The amplification reaction was incubated at 48°C for 30 minutes then it was analyzed by lateral flow analysis as described above. The lateral flow analysis is shown in Figure **7** indicating for this particular assay a lower detection limit of 60 copies.

EXAMPLE 6

[0069] This example illustrates the probe specific iSDA detection and differentiation of *S.aureus* (BAA-1556, ATCC) and *S.epidermidis* (12228, ATCC).

[0070] Cultures of *S.aureus and S. epidermidis* (5xl0 ^{8} cfu/mL) were sonicated for 10 min in the waterbath sonicator (Branson 55 10, Bransonic) The crude lysates were assayed for the *Idhl* gene according to the method described in Example 1 at a concentration of 5x1 0^{4} cfu/reaction. Efficient specific detection of the *Idhl* gene in *S. aureus* only is shown in Figure 9.

EXAMPLE 7

[0071] This example illustrates the iSDA amplification of nucleic acid from the same sample extracted with different methods.

[0072] A *S. aureus* sample was extracted using the following extraction methods:

a) Extraction with chaotropic salts (8M guanidinium HC1 or 4M guanidinium thiocyanate) , with and without the silica spin column.

Bacterial cells (5xl0 ^{8} cfu) were extracted according to the procedure described in Molecular Cloning: a laboratory manual. (pages **7**-19, **7**-24). DNA from each extraction was resuspended in *200*µL of the TE buffer and divided into two IOOµE aliquots. One aliquot was set aside for PCR and iSDA analysis, and another one was further purified on

QIAmp DNA Mini Kit (Qiagen) spin columns according to the product manual. DNA was cluted in 100 µL of the elution buffer.

b) Phenol/chloroform extraction followed by ethanol precipitation. (Molecular Cloning: a laboratory manual, App.E3-E4).

c) Sonication for 10 min in the waterbath sonicator(Branson 5510, Bransonic).

d) 10% final concentration of Triton X100 incubation at room temperature followed by ethanol precipitation.

[0073] The concentrations of different non-denatured DNA nucleic acid fractions were normalized at 500 copies/reaction by real-time *Idhl* PCR assay (described in U.S. Patent Application Serial No. 13/479,557). As shown in Figure 10, all five extractions gave essentially the same signal result at around cycle 9 (9 min). The NTC showed no amplification and is not shown.

EXAMPLE 8

[0074] This example illustrates the iSDA amplification of the *Idhl* gene with primers and probes designed with the current disclosure in comparison with traditional designed primers and probes shown in Table 5

[0075] Using the method described in Example 1, the primers and bumper primers for the *Idhl* gene described in Tables 1 and 5 were tested in which both sets of primers had target concentrations ranging from 5 xlO^3 to 5 xlO^5 target copies/reaction. The amplification reactions were analyzed by agarose gel electrophoresis as shown in Figure 11A and B. The arrows in Figure 11A and B refer to the amplicon products of amplification. As shown the amplification with the primers of the current disclosure showed substantial amplification at all three concentrations, while the conventional designed primers showed poor amplification Figure 11A.

Table 5

Seq ID #	Description	Oligonucleotide sequence
37	Limiting primer-Ll	gcattatagtacctgtctcctcagcTGGTGAACATGGTGACACTGAAT
38	Excess	ttgaatagtcggttacttcctcag_cGCCCTCAGGACGTTGTTCAAG

	primer -E 1	
39	Forward Bumperl	AGCGTCGATGCTCA
40	Reverse Bumperl	AATTTGTTCAATTTGCG

EXAMPLE 9

[0076] This example illustrates the one step RT-iSDA amplification of RSV nucleic acid. RT-iSDA uses the same final concentrations as disclosed for iSDA in [0049], except that 8U WarmStart Bst Polymerase was substituted for Bst Polymerase, 8U Nt.BbvCl nicking enzyme was used per 10 μL reaction. In addition the reaction mixture contains 10U RNA inhibitor (Life Technologies), 0.5 μL Omniscript Reverse Transcriptase (Qiagne), template RNA and 1 μg BSA per 10 μL/reaction. Reaction mixture was followed in real-time for 25 minutes at 49°C as illustrated in Figure 12a) and lateral flow detection in Figure 12b). Primers, bumper primers and probes are shown in Table 6 below. T*= Super T and other abbreviations have been described above. The lateral flow membrane has a test line of pDNA (immobilized by cross-linked polythymidine tail) and a BSA-biotin line as flow control.

Table 6

Seq ID #	Description	Oligonucleotide sequence
41	Limiting primer-L1	gcattatagtacctgtctcctcagcGAATTCCCTGCATCAATAC
42	Excess primer -E1	gcattatggtacctctctcctcagcTA*TGTCA*ATATCT*T*CATC
43	Forward Bumper1	AACTAAGGCCAAAGCTTATAC
44	Reverse Bumper1	CAGTCAGTAGTAGACCATG
45	Chimeric pDNA/DNA	[TTTTTTTTC]-(Q14)-CTACAAATTATCACTTTGA
46	Biotinilated probe	TA*ATCGCATATTAACAG-biotin TEG
47	FAM probe	MGB-FAM-TAATCGCATAT*T*AACAG-EDQ

EXAMPLE 10

[0077] This example illustrates the iSDA amplification of native and denatured *P.falciparum genomic* DNA. Primers and probes were designed using mitochondrial DNA (Polley et.al,. J. Clin. Microbiol, 48:2866-2871 (2010)) as a target and is shown in Table 7 below. Extraction from *Plasmodium falciparum,* strain NF54 and iSDA amplification were performed as described above. Figure 13A shows identical real-time iSDA amplification for native and denature DNA at 95°C for 5 minutes. Figure 13B shows the amplification of native DNA at 100 and 1000 copies.

Table 7

Seq ID #	Description	Oligonucleotide sequence
48	Limiting primer-Ll	gaatagacccatacatcctcagcGACTTGAGTAATGATAAATTGATAG
49	Excess primer -E 1	gaatagaeccatacatccteagcGACTTGAGTAATGATAAATTGATAG
50	Forward Bumper1	CCA *CTTGCTT ATAACTGT ATG
51	Reverse Bumper 1	GTTTCCA*TAGAAACCTTCAT
52	FAM probe	MGB-FAM-ATTGATTCCGTTTTGAC-EDQ

REFERENCES CITED

The following documents and publications are hereby incorporated by reference.

U.S. and Foreign Patent Documents

US 5,824,796

US 5,912,340

US 5,455,166

US 7,282,328

US 4,943,522

US 7488578

US Application Publication No. 2012-0015358 A

US 5,624,825

US RE39885

US 5,455,166

US 5,422,252

US 5,624,825

US 5,712,124

US 5,270,184

US 5,470,723

US 5,56 1,944

US 5,736.365

US 6,127,12 1

US 6,660,845

US 6683173

US 7045610

US 7751982

US 7,799,554

US 8,202,972

U.S. Patent Application Publication No. 2010/057862

U.S. Patent Application Publication No. 201 1/0171649

U.S. Patent Application Publication No. 2012/0244535

PCT Publication WO 0 1/38584

PCT Publication WO 01/64958

Non-Patent References

Afonina et al., Single Nucleotide Polymorphism Detection with fluorescent MGB Eclipse Systems in A-Z of Quantitative PCR, Ed. S. A. Bustin, International University Line, La Jolla, CA, pages 718-73 1 and XII-XIII, 2004)

Besnier and Kong, EMBO Reports, 2 1: 782-786 (2001)

Ehses et al., J. Biochem. Biophys. Methods. 63:170-86 (2005).

Eschenmoser et al, Helvetica Chimica Acta, 76: 2161-2183 (1993)

Fran-Kamentskii. Artificial DNA; PNA & XNA, 2:1, 1-3 (201 1)

Molecular Cloning: a laboratory manual

Niemz et al., Trends in Biotechnol., 29:240-250 (201 l))

Nuovo, Diagn Mol Pathol. 9(4): 195-202 (2000)

M Panaccio and A Lew. PCR based diagnosis in the presence of 8% (v/v) blood. Nucleic Acids Res., 19: 1l 5 1 (1991)

Policy et al. J. Clin. Microbiol. 48:2866-2871 (2010)

Ramirez et al. Nucl. Acids Res., 40:5560-8 (2012)

Roberts et al., Nucl. Acids Res., 3 1: 418-420 (2003)

Walker et al.. NAR 20: 1691- 1695 (1992)

Walker, PGR Methods and Applications, 3: 1-6 (1993)

Walker et al., NAR 22: 2670 (1994)

Walker et al., Clin. Chem.. 42: 9-13 (1996)

Walker et al., Clin. Chem., 42: 1604-8 (1996)

Walker et al, NAR 24:349 (1996)

Wang et al., Clin. Chem., 49: 1599 (2003)

White. Handler and Smith. Principles of Biochemistry 5th Edition. McGraw-Hill Kogakush, Ltd, pages 192-197, 1993

Xu et al, PNAS 98: 12990-12995 (2001)

Zheleznaya et al., Biochemistry (Mosc). 74:1457-66 (2009)

WHAT IS CLAIMED IS:

1. An isothermal strand displacement amplification method, the method comprising:

(a) contacting a genomic nucleic acid having a target nucleic acid sequence with an amplification reaction mixture comprising:

a forward primer and a reverse primer,

wherein the forward primer has the formula:

A-B,

wherein B comprises a portion of the forward primer that is complementary to the target nucleic acid sequence, and wherein A comprises a portion of the forward primer that is non-complementary to the target nucleic acid sequence and comprises a forward nicking enzyme recognition sequence,

wherein the reverse primer has the formula:

A'-B',

wherein B' comprises a portion of the reverse primer that is complementary to the target nucleic acid sequence, and wherein A' comprises a portion of the reverse primer that is non-complementary to the target nucleic acid sequence and comprises a reverse nicking enzyme recognition sequence, and

wherein the forward primer and the reverse primer comprise sequences optimized by software for specific hybridization and efficient elongation,

a polymerase enzyme having strand displacement activity, and

a nicking enzyme specific for the nicking enzyme recognition sequence;

(b) incubating the amplification reaction mixture and the genomic nucleic acid under amplification conditions suitable for amplification of the target nucleic acid to produce an amplified target nucleic acid,

wherein the contacting step and the incubating step are carried out at a temperature between about 40°C and about 65°C and amplification of the target nucleic acid occurs without thermal denaturation; and

(c) detecting the amplified target nucleic acid.

2. The method of claim 1 wherein the amplification reaction mixture further comprises one or more bumper oligonucleotides.

3. The method of claim 1 wherein the genomic nucleic acid is RNA and wherein the amplification reaction mixture further comprises a reverse transcriptase enzyme.

4. The method of claim 1 wherein the genomic nucleic acid is double stranded.

5. The method of claim 1 wherein the target nucleic acid sequence is single stranded.

6. The method of claim 1 wherein the step of detecting the amplified target nucleic acid comprises using fluorescence resonance energy (FRET), radiolabels, lateral flow, or enzyme labels.

7. The method of claim 1 wherein the step of detecting the amplified target nucleic acid comprises hybridizing an oligonucleotide probe to at least a portion of the amplified target nucleic acid.

8. The method of claim 6 wherein the oligonucleotide probe is a fluorescent generation probe.

9. The method of claim 7 wherein the oligonucleotide probe comprises a minor groove binder (MGB), a fluorophore, and a quencher.

10. The method of claim 7 wherein the oligonucleotide probe is a FRET probe.

11. The method of claim 7 wherein the oligonucleotide probe fluoresces when hybridization to the amplified target nucleic acid occurs.

12. The method of claim 7 wherein the oligonucleotide probe is cleaved to produce a fluorescent signal.

13. The method of claim 1 wherein the step of detecting the amplified target nucleic acid comprises using lateral flow.

14. The method of claim 1 wherein at least one of the forward primer and reverse primer comprises a fluorescent label.

15. The method of claim 1 wherein the step of detecting the amplified target nucleic acid comprises attaching the amplified target nucleic acid to a solid support and detecting the amplified target nucleic acid with an oligonucleotide probe having a fluorescent label.

16. The method of claim 1 wherein the amplification reaction mixture further comprises an internal control.

17. The method of claim 1 wherein the software comprises the Vienna Folding Package.

18. The method of claim 1 wherein the software comprises software for adjusting the T_m of the forward primer and the reverse primer by calculating duplex stabilities using an algorithm applying a nearest-neighbor model for duplex formation thermodynamics for each neighboring base pair.

19. The method of claim 1 wherein the forward primer and the reverse primer are present in different concentrations in the amplification reaction mixture.

20. The method of claim 1 wherein at least one of the forward primer and reverse primer is substituted with at least one modified base.

21. The method of claim 1 wherein at least one of the forward nicking enzyme recognition sequence and the reverse nicking enzyme recognition sequence comprises a cleavage site for Endonuclease V.

22. The method of claim 1 wherein the contacting step and the incubating step are carried out at a temperature between about 45°C and about 55°C.

23. A method of claim 1 wherein A' comprises a sequence for a cleavage site.

Figure 1

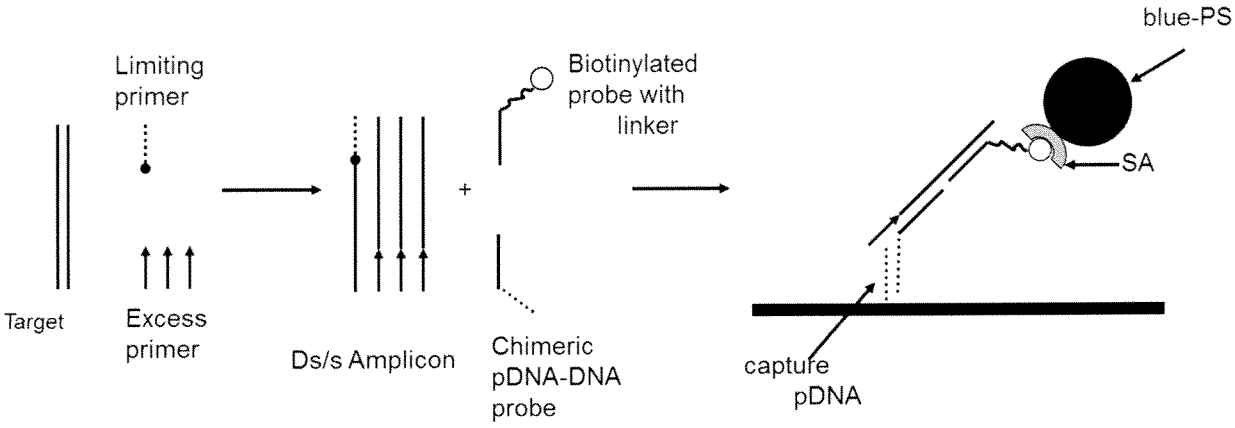

Limiting primer
Biotinylated probe with linker
blue-PS
SA
Target
Excess primer
Ds/s Amplicon
Chimeric pDNA-DNA probe
capture pDNA

Figure 2

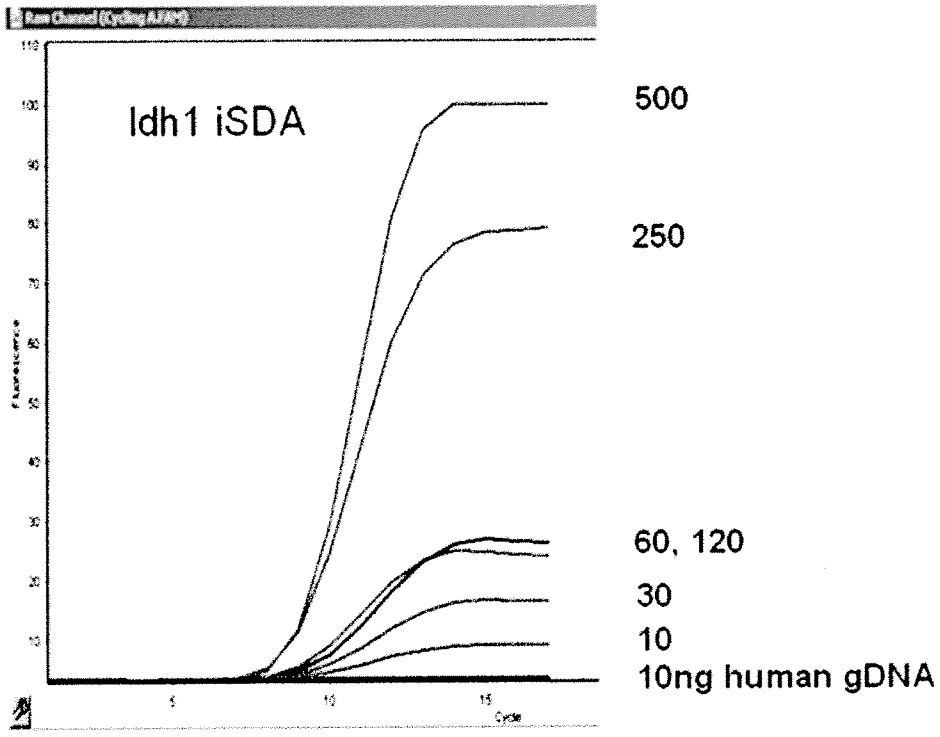


Figure 3

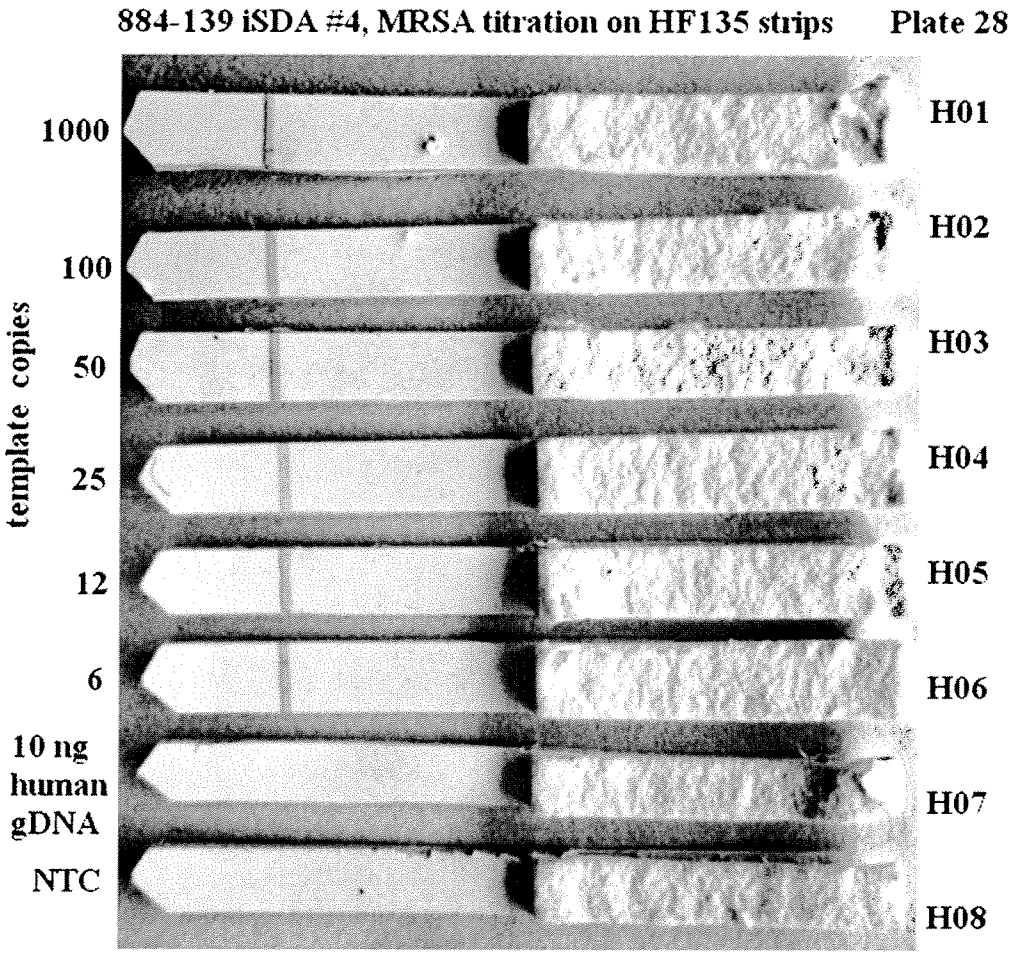

884-139 iSDA #4, MRSA titration on HF135 strips
Plate 28
template copies
1000
100
50
25
12
6
10 ng human gDNA
NTC
H01
H02
H03
H04
H05
H06
H07
H08

Figure 4

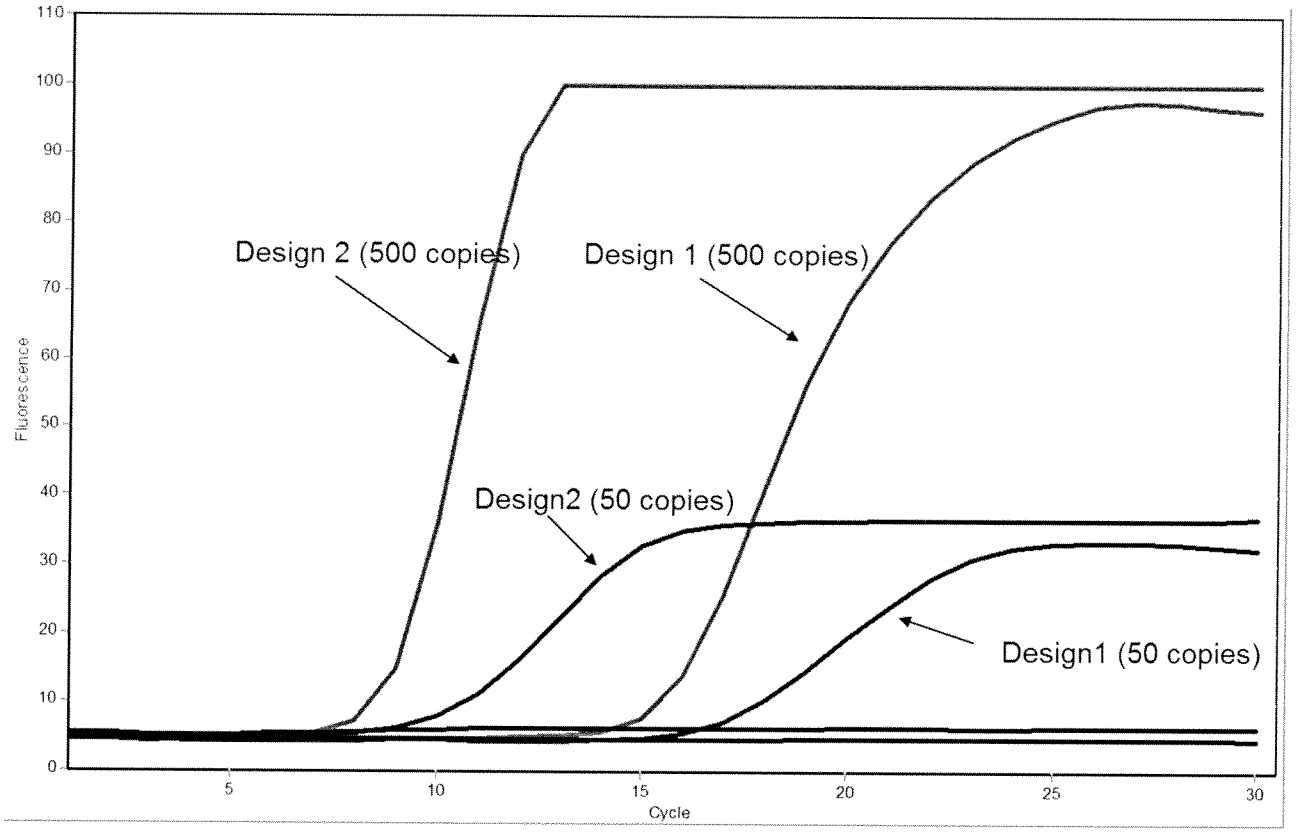

110
100
90
80
70
60
50
40
30
20
10
0
Fluorescence
5
10
15
20
25
30
Cycle
Design 2 (500 copies)
Design 1 (500 copies)
Design2 (50 copies)
Design1 (50 copies)

Figure 5

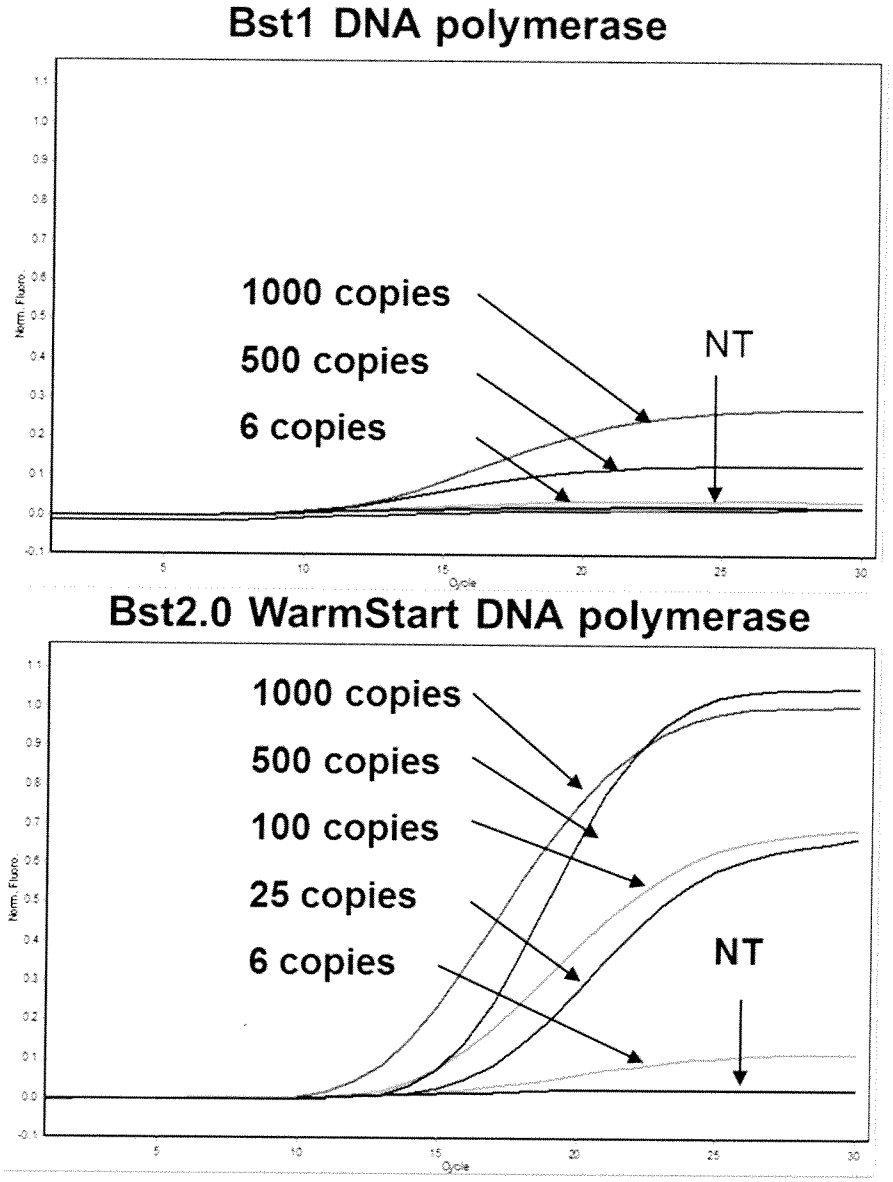
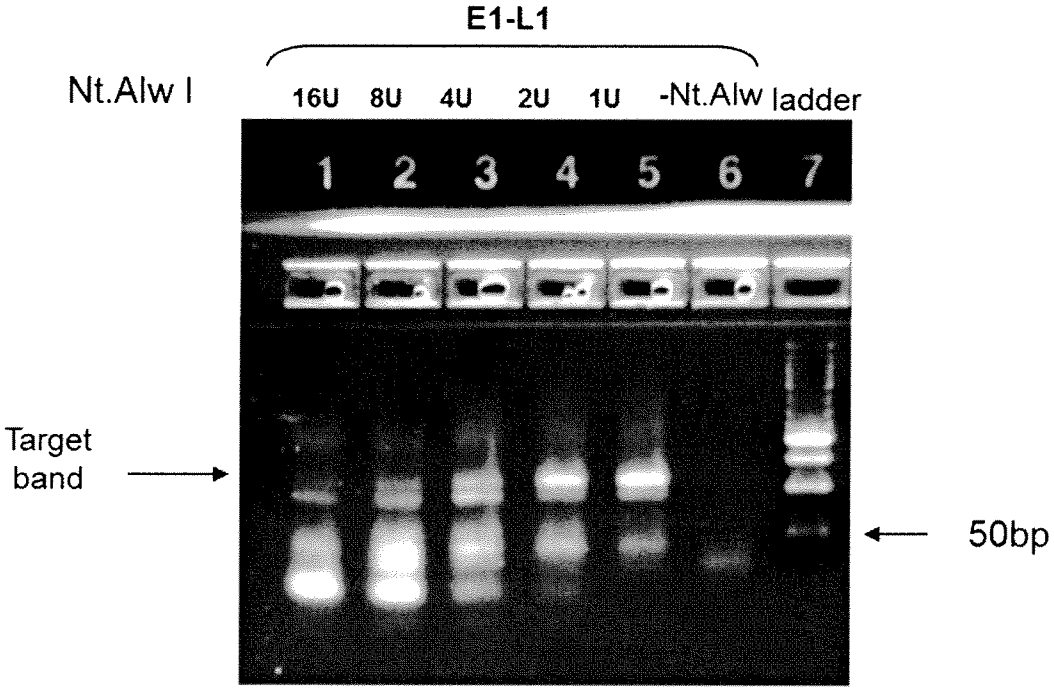

Bst1 DNA polymerase
1000 copies
500 copies
6 copies
NT
Norm. Fluoro.
Cycle
Bst2.0 WarmStart DNA polymerase
1000 copies
500 copies
100 copies
25 copies
6 copies
NT
Norm. Fluoro.
Cycle

Figure 6



Template – 1ul of 1:100 dilution of PCR product

Figure 7

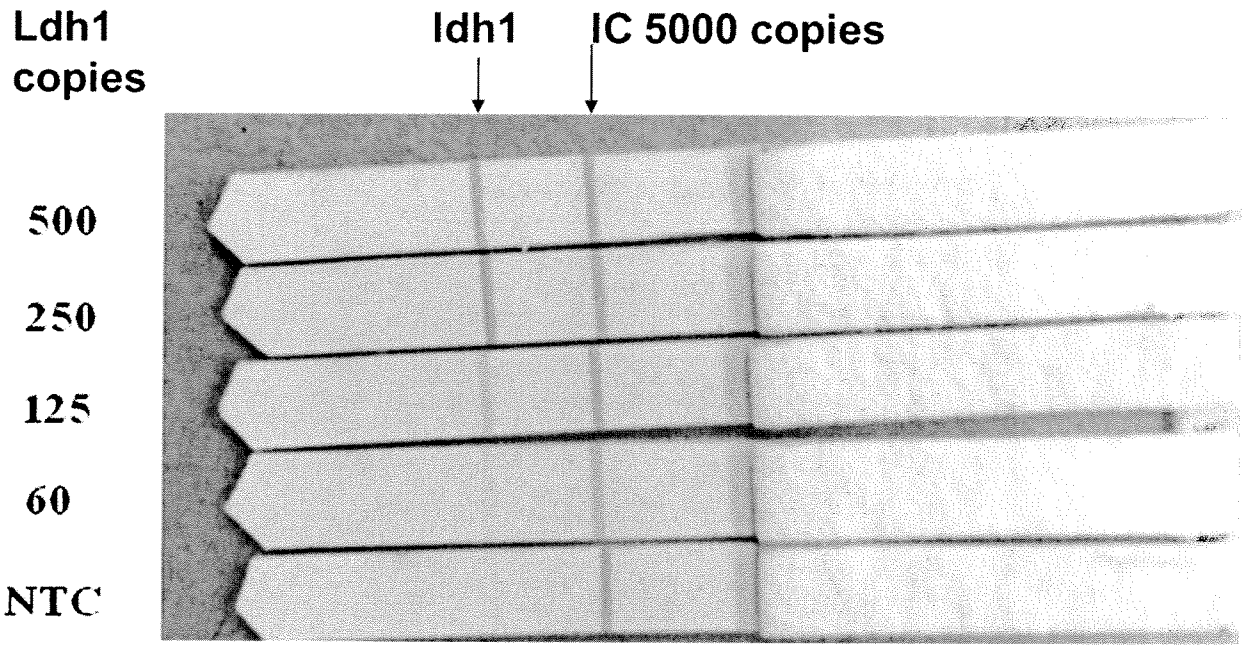


Figure 8

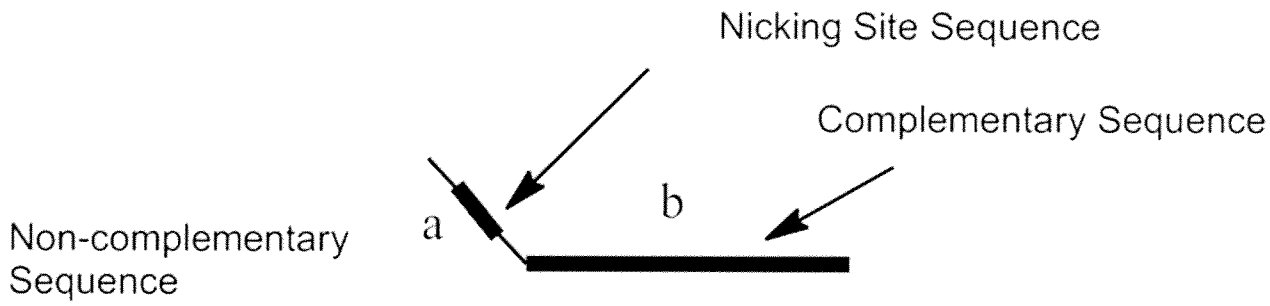

Nicking Site Sequence
Complementary Sequence
Non-complementary Sequence
a
b

Figure 9

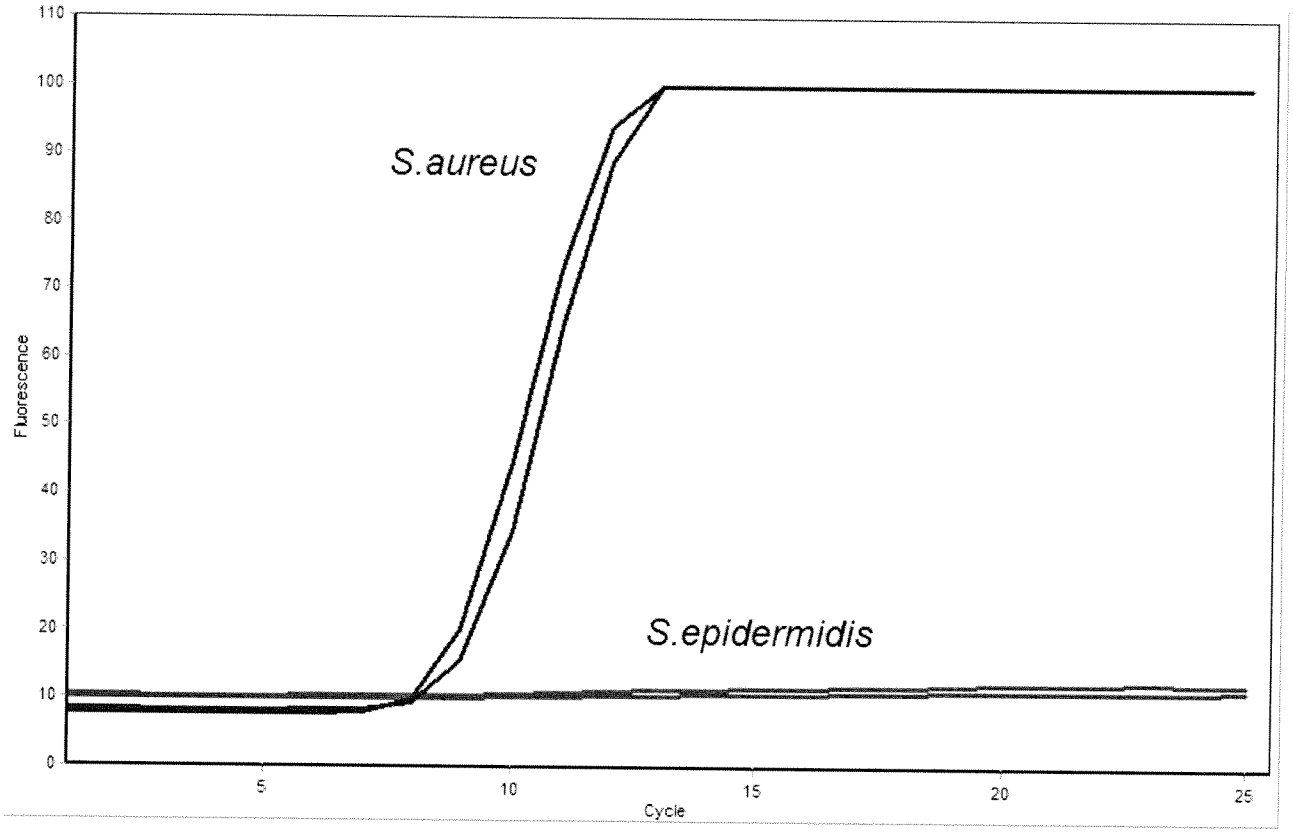

110
100
90
80
70
60
50
40
30
20
10
0
Fluorescence
S.aureus
S.epidermidis
5
10
15
20
25
Cycle

Figure 10

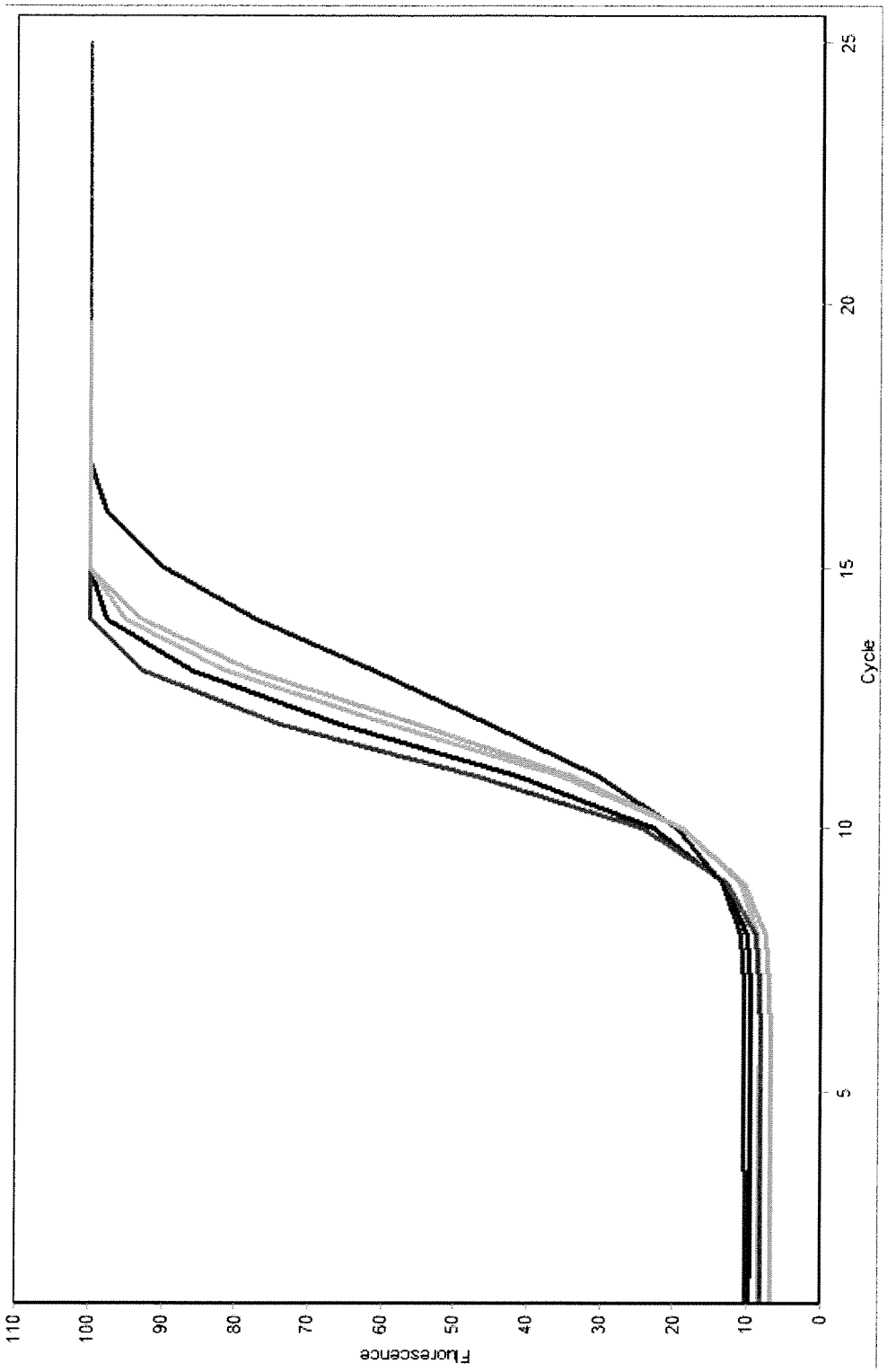


Figure 10
Fluorescence
110
100
90
80
70
60
50
40
30
20
10
0
Cycle
5
10
15
20
25

Figure 11

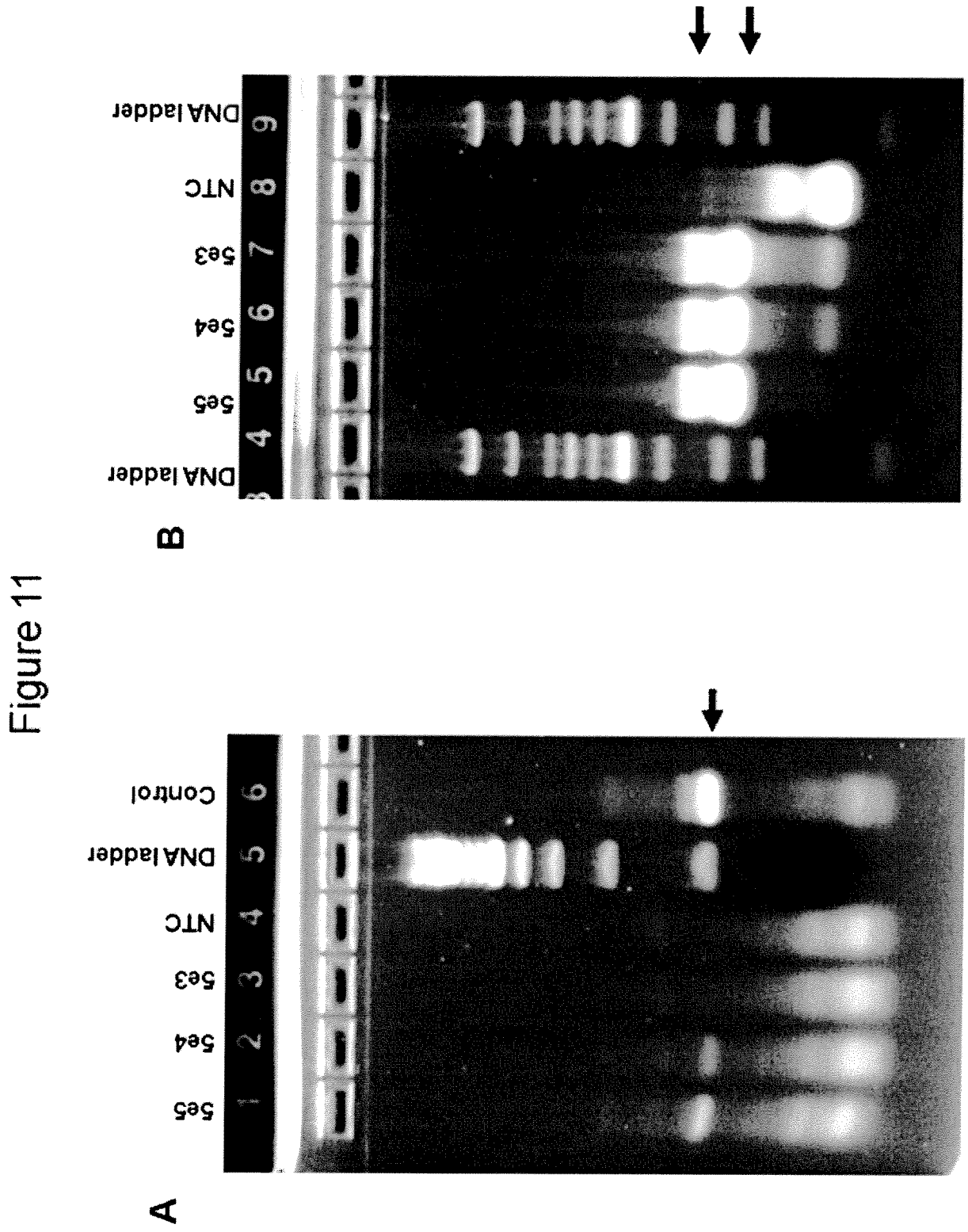
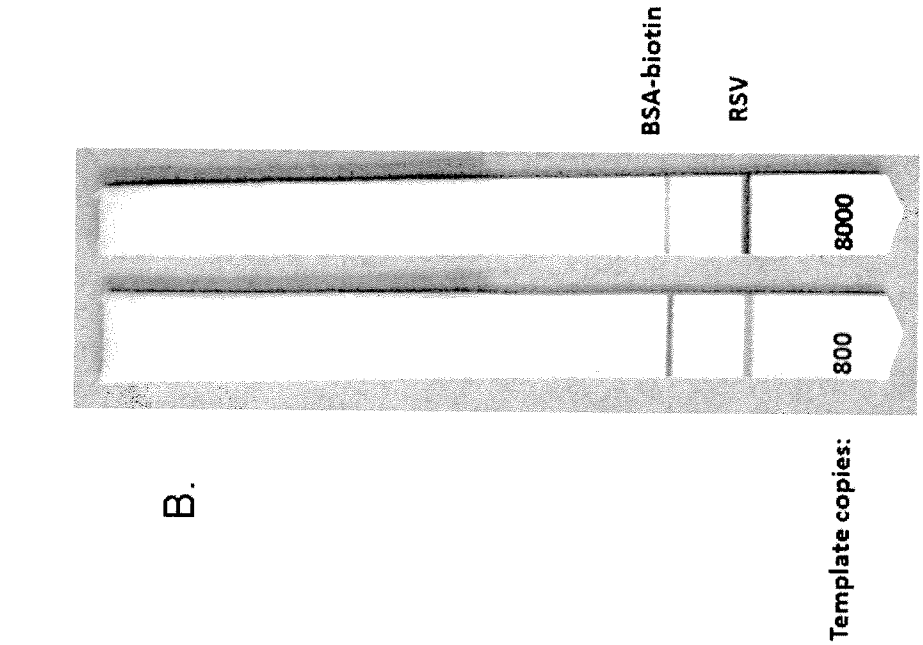


Figure 11
B
DNA ladder
NTC
Se3
Se4
Se5
DNA ladder
9
8
7
6
5
4
A
Control
DNA ladder
NTC
Se3
Se4
Se5
6
5
4
3
2
1

Figure 12



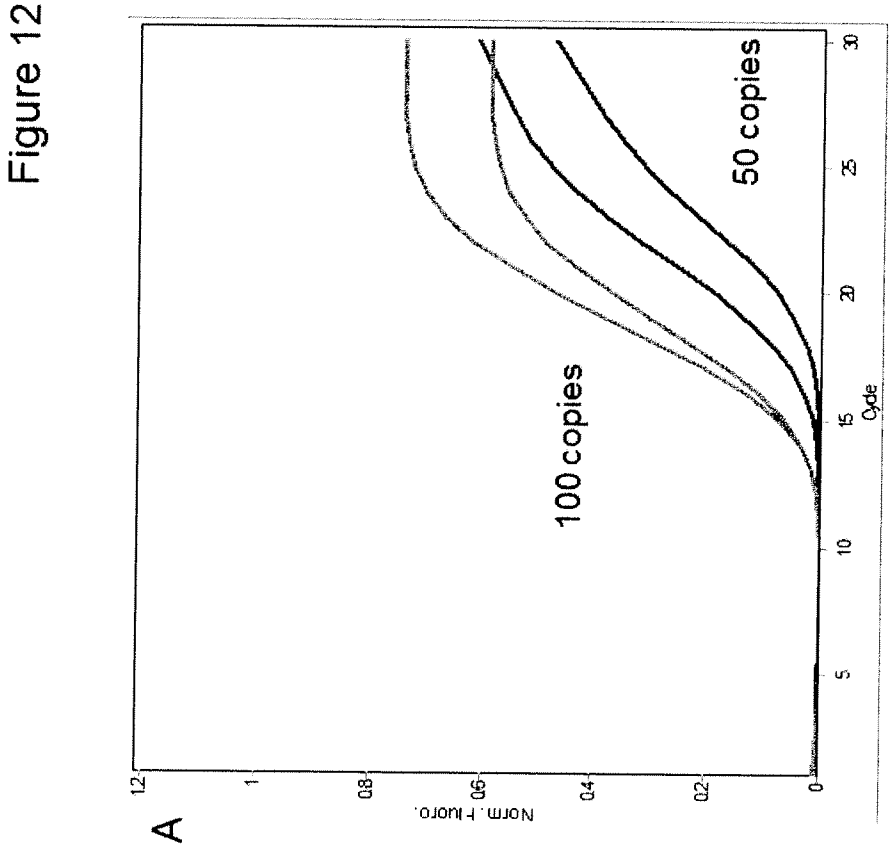


Figure 12

Figure 13

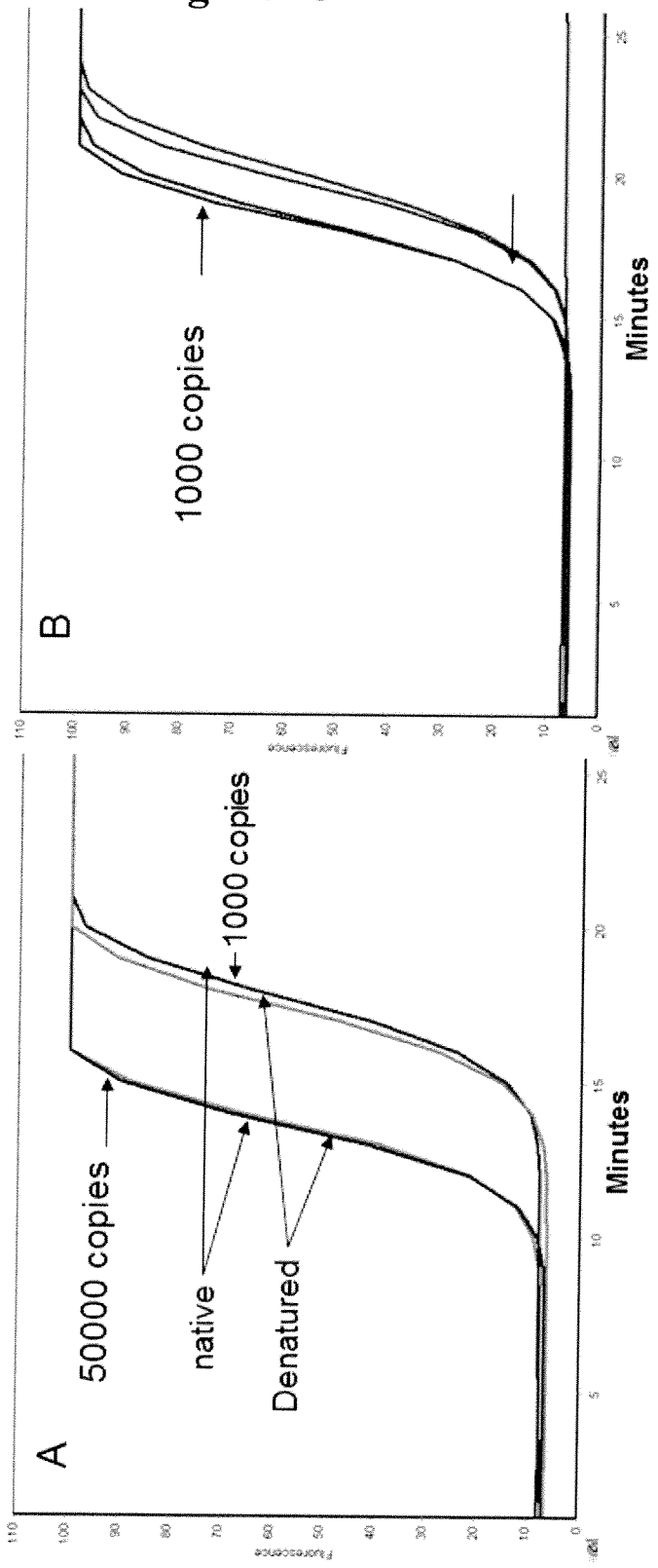


Figure 13

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2014/022534

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68
ADD.

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)
C12Q

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

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal , BIOSIS, Sequence Search , EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2010/255546 Al (UEMATSU CHIHIRO [JP] ET AL) 7 October 2010 (2010-10-07) see whole doc. esp. claims aND fIGURES. -----	1-23
X	US 6 063 604 A (WICK JAMES F [US] ET AL) 16 May 2000 (2000-05-16) see whole doc. esp. claims and Figures -----	1-23
X	EP 0 678 582 Al (BECT0N DICKINSON CO [US]) 25 October 1995 (1995-10-25) the whole document -----	1-23
X	W0 2008/002920 A2 (EPOCH BIOSCIENCES INC [US] ; YA0 ZUXU [US] ; LIDGARD GRAHAM [US] ; BEL0US) 3 January 2008 (2008-01-03) cited in the application see whole doc., esp. Figures 1B/C, -----	1-23
	-/--	

[X] Further documents are listed in the continuation of Box C.

[X] 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" documentwhich may throw doubts on priority claim(s) orwhich 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
3 September 2014	15/09/2014

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Muel l er, Frank

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2014/022534

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ANGELIKA NIEMZ ET AL: "Point-of-care nucleic acid testing for infectious diseases", TRENDS IN BIOTECHNOLOGY, vol. 29, no. 5, 4 March 2011 (2011-03-04), pages 240-250, XP028194817, ISSN: 0167-7799, DOI: 10.1016/J.TIBTECH.2011.01.007 [retrieved on 2011-01-25] cited in the application see esp. Figure 3	1-23
A	EHSES S ET AL: "Optimization and design of oligonucleotide setup for strand displacement amplification", JOURNAL OF BIOCHEMICAL AND BIOPHYSICAL METHODS, AMSTERDAM, NL, vol. 63, no. 3, 30 June 2005 (2005-06-30), pages 170-186, XP027670200, ISSN: 0165-022X [retrieved on 2005-06-30] cited in the application the whole document	1-23

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/US2014/022534

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
US 2010255546 Al	07-10-2010	JP 2008136451 A	19-06-2008
		us 2010255546 Al	07-10-2010
US 6063604 A	16-05-2000	AU 723678 B2	31-08-2000
		AU 2329497 A	10-10-1997
		CA 2249717 Al	25-09-1997
		EP 0914462 Al	12-05-1999
		JP 2000505312 A	09-05-2000
		US 6063604 A	16-05-2000
		WO 9735026 Al	25-09-1997
EP 0678582 Al	25-10-1995	AT 220724 T	15-08-2002
		AU 685903 B2	29-01-1998
		AU 1502395 A	26-10-1995
		BR 9501582 A	16-09-1997
		CA 2145576 Al	19-10-1995
		DE 69527392 Dl	22-08-2002
		DE 69527392 T2	06-03-2003
		EP 0678582 Al	25-10-1995
		ES 2177590 T3	16-12-2002
		JP 2674737 B2	12-11-1997
		JP H07289299 A	07-11-1995
		SG 34216 Al	06-12-1996
		US RE39885 El	16-10-2007
		US 5547861 A	20-08-1996
		US 5593867 A	14-01-1997
W0 2008002920 A2	03-01-2008	US 2009092967 Al	09-04-2009
		WO 2008002920 A2	03-01-2008